A COMBINED EXPERIMENTAL AND SIMULATIONAL APPROACH TO THE STUDY OF OPTICAL EMISSIONS RESULTING FROM THE DISSOCIATIVE ELECTRON–ION RECOMBINATION OF SMALL POLYATOMIC IONS

by

BETHANY LACHELE FOLEY

(Under the Direction of NIGEL GRAHAM ADAMS)

ABSTRACT

Current experimental approaches to and theoretical descriptions of the study of electron-ion recombination are presented with focus on dissociative recombination. The experimental apparatus, chemical methodology and means of data analysis used in these studies are described. Photoemissions due, or likely to be due, to electron-ion recombination are reported and quantified for the following recombining parent ions: CH_5^+ , HCO^+ , CO_2^+ , HCO_2^+ , CS_2^+ , NH_4^+ , HNO^+ , N_2OH^+ , SH_3^+ and XeH^+ . Practical issues regarding the composition of the plasma in which the recombinations occur and the characteristics of injection and mixing of the reagent parent gases are discussed; solutions to difficulties are suggested. A program that simulates rovibronic spectra is described. Also, a program that simulates the idealized injection into the reactive flow of a neutral reagent gas is described.

INDEX WORDS: Electron-ion recombination, Dissociative recombination, Spectroscopic products, Plasma chemistry, Gas-phase ion chemistry, Rotational spectroscopy, Rovibronic transitions, Simulation, Flowing afterglow, Rotational temperatures, Vibrational distributions, Mixing of gases

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2002

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[] reference amu atomic mass units cm^{-1} wavenumbers DP diffusion pump e^- an electron e-i electron-ion FA flowing afterglow GPC gated photon counter h Planck's constant i-n ion-neutral IP ionization potential k reaction rate constant LIF . . . laser-induced fluorescence MeV $\ldots \ldots \ldots 10^6$ electron–volts MS mass spectrometer nm nanometers $\mathcal{O}()$. . order of magnitude of () PE potential energy RIP resonant ion pair s seconds slm . . . standard liters per minute τ general spatial coordinate Tls^{-1} torr-liters per second VUV vacuum ultraviolet XYZ polyatomic molecule

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eV					•			e	eleo	ctr	on	vo	olts	
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$h\nu$					•					a	p	hot	ton	
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J.					•	•		•	•			Jou	ıles	
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$ au_{rad}$					•		ra	dia	ati	ve	lif	eti	me	
UV-	VI	\mathbf{S}				I	ult	ra	vic	let	5— v	visi	ble	
XY					•	C	lia	to	mi	сr	no	lec	ule	

LIST OF ABBREVIATIONS

CHAPTER 1 ELECTRON–ION RECOMBINATION: DEFINITIONS AND INTRODUCTION

1-1 Definitions

Electron-ion recombination is the process by which a positive ion, I^+ , and an electron, e^- , react with each other:

$$I^+ + e^- \to products$$
 1

The process can occur, with varying efficiencies, between any positive ion and an electron. Depending on the nature of the process, more specific terms are often used. When the products are a single neutral particle and a photon, the process is called *radiative recombination*. When a second electron is involved in the process, it is termed *dielectronic recombination*. When a neutralized polyatomic ion breaks into smaller fragments, the process is called *dissociative recombination* (DR).

Recently it has been found that those smaller fragments are sometimes a positive and a negative ion, e. g.

$$XY^+ + e^- \to X^+ + Y^- \tag{2}$$

In this case, the process is said to have produced a *resonant ion pair* (RIP) [See Appendix A]. The study of the process is very new, and there is an apparent disagreement on whether RIP formation should be considered a separate process from DR, even though both processes result in "dissociation." For example, one paper [Lange 1999] has the title "Threshold Effects and Ion–Pair Production in the Dissociative Recombination of HD⁺," which suggests that they consider ion–pair production a subset of

the possible outcomes of DR. Another paper [Zong 1999] makes an obvious distinction between the processes, avoiding the term *recombination* altogether except when speaking of the formation of neutral products. Instead, they use "electron collisions with molecular ions." In this manuscript, RIP will be considered a subset of DR, but only neutral products of DR will be discussed in detail.

Many other electron-ion recombination processes are well known and more solidly defined. For example, when the products are stabilized by the release of a photon, the term *radiative stabilization* is used. If collisions with other particles become involved in radiative stabilization of the electron-ion system, the process is called *collisional radiative recombination*. The ejection of an electron from the intermediate complex (either the incident electron or some other electron) is called *autoionization*. For a brief, but more technical description of the various processes than is presented here, the reader is referred to the *Atomic, Molecular and Optical Physics Handbook* published by The American Institute of Physics [Drake 1996, Section 52.1].

Recombination between atomic ions and electrons is very slow, with a rate coefficient of $\sim 4 \times 10^{-12} \ cm^3 molecule^{-1} s^{-1}$ [Murad 1986], so is of little interest to the type of study described in this document. Even so, it is important to know something of the process, as it provides a foundation from which to better understand the more complicated process of polyatomic ion recombination. When recombination between a solitary atomic ion and an electron does occur, energy must be lost from the system in order for the neutral to stabilize (and not autoionize). In the case of a single atom, the paths available are interactions with the atomic core (e.g., electron capture), translational excitation and photo–emission. Mechanisms for rotational or vibrational excitation, of course, do not exist, in contrast to the case with diatomic and polyatomic ions. Of the three available mechanisms, translational excitation plays very little part in the process. Rarely are there efficient mechanisms by which an incident electron can transfer translational energy to an ion. Even at high kinetic energies, the electron is more likely to cause other electron(s) to be released from the ion than to cause the ion as a whole to move [the process is well known and is called *electron impact ionization*]. So, it is unlikely that energy possessed by the electron will be turned into sufficient kinetic energy in the electron–ion pair to stabilize the system. Nor do nuclear interactions play an important role. It is certainly possible, in some cases, to study the recombination of an ambient electron with an unstable nucleus, but, if the literature contains any references to that sort of experiment, this author has been unable to find them.

Whatever the case, the dominant stabilization processes for atomic-ion/electron recombination are collisional stabilization or photoemission. The only other significant non-radiative option available is, as was mentioned earlier, the re-ejection of an electron, where the net result is that recombination does not occur. In fact, in most of these interactions, autoionization is by far the dominant process. If one compares, in general, the efficiency for changes in internal motion, e. g., the re-ejection of an electron (timescales $\leq 10^{-14}$ s [Adams 1992]), and the emission of a photon ($\tau \geq 10^{-9}$ s), one finds that the re-ejection is significantly more efficient. It is this relative efficiency for re-ejection compared to radiation that makes atomic-ion/electron recombination such an inefficient process.

But even though inefficient, the process is worthy of study for certain applications. Radio astronomers, for example, use emissions from very high–orbital transitions of atomic hydrogen to study the structures and properties of objects in the interstellar medium [Dupree 1970]. These transitions are called *radio recombination lines* [De-Pree 2000]. One might argue that these "recombination" lines are merely transitions between high–level atomic orbitals. This is true; but, the lines are generally thought to be the cascade of an electron down the orbitals of a hydrogen atom as the electron and proton become successively more stabilized to form a neutral atom. So, it is not unreasonable to consider this to be sub–processes of recombination. At higher pressures and/or higher ionization (charged particle) densities, the process of collisional radiative recombination [Drake 1996] can increase the probability of any recombination, including recombinations between single atoms and electrons. It occurs when one or more "third" bodies are involved in the recombination process. The third body might be any other ion or neutral and can also be an electron. At high pressures, collisions with "third" bodies may be important. In this process, the effect of collisions on the cascade of the electron to lower energy states may be coupled to the emission of radiation. Generally speaking, collisional effects are more important for high n levels where the radiative lifetimes are long. Radiation becomes more important as the electron transits to lower n levels. If one also considers re-absorption of light and effects of electron temperature and plasma pressure, the process becomes complex. However, at the pressures used in this study, such threebody interactions happen infrequently — far less frequently than binary DR — and can be safely ignored.

Dissociative recombination (DR) can only occur when the ion is capable of fragmentation upon recombination, so, DR applies only to molecular ions. DR occurs when the addition of an electron to a molecular ion results in the formation of two or more particles as products. The process is often followed by photoemission from at least one of the product fragments. Rate coefficients for DR are generally on the order of $10^{-6} - 10^{-7} cm^3 s^{-1}$ [Johnsen 1987]. Although it is possible for the recombination of a polyatomic ion to occur without product fragmentation, the process is not significant compared to dissociative recombination.

The most commonly observed products of DR are neutral atoms and molecules, but, as mentioned above, ion-pair production is also possible. Little, if any, information on resonant ion pair (RIP) production,

$$XY^+ + e \to X^+ + Y^- \tag{3}$$

is available for the case of triatomic and larger molecules. However, based solely on results for diatomic species, the possibility of the process being significant for larger polyatomics cannot be ignored. Many of these diatomic systems were studied at high interaction energies $(k_B T \text{ corresponding to effective temperatures much greater than})$ 300 K). For example, in the recombination of HeH⁺, Larson and Orel [Larson 1999] calculated that the branching fraction for ion-pair formation might be as high as 10%of the total at energies on the order of 20 eV. For some species, such large energies are necessary for the system to be able to produce an ion pair. However, RIP has been observed to occur at lower energies for some systems. Zong, et al., [1999] observed ion-pair formation in the recombinations of HD⁺ and HF⁺. Although they found that a threshold energy of about 1.91 eV is necessary for RIP production in the collision of an electron with HD⁺, they report finite rate coefficients for RIP in HF⁺ at energies as low as 10^{-4} eV. RIP occurs more readily in HF⁺ because the net energy change during the process is small. In the case of HD⁺, the difference between the energy for dissociation to H⁺ and D ($D_{ion} = 2.6677$ eV [Zong 1999]) and the electron affinity of D $(EA_D, 0.7546 \text{ eV} [\text{Zong 1999}])$ requires an energy of 1.913 eV be added to the system for RIP formation. However, in the case of HF^+ , the electron affinity ($EA_F =$ 3.412 eV, [Zong 1999]) and the dissociation energy of the ion ($D_{ion} = 3.417 \text{ eV}$, [Zong 1999) are within thermal energies of each other. Zong, et al., [1999] also found for this system that, at 0 eV, the ratio of RIP to the production of neutral products (DR, in their paper) is about 0.3. It is possible that, for larger polyatomic species, further studies will find that the additional vibration and rotation in the channels available for the dispersal of energy will make the RIP channel less important. However, without further experimental and theoretical investigation, significant RIP formation in the DR of polyatomic ions remains only a possibility at the present time.

Whatever the products, electron–ion recombination is, generally speaking, highly energetic. The energy gained by electron and ion is equal to the recombination energy of the ion plus the relative kinetic (thermal) energies of the ion and the electron. That energy must be dissipated in some manner; for triatomic or larger ions, there are numerous possibilities, most involving the cleavage of one or more bonds. Stabilization can also be provided by translational, rotational, vibrational or electronic excitation in the fragments. Indeed, the breaking of one or more bonds is often accompanied by the emission of light from a number of ro–vibronic states in the fragments. A common symbolism for the process is:

$$XYZ^+ + e^- \to XY^* + Z^*$$
$$\hookrightarrow XY + h\nu \qquad 4$$

where the asterisk (*) denotes excitation (electronic, vibrational, etc.) in that product. Note that this symbolism does not reflect all possibilities for all types of polyatomic ion; it is merely a representation of the primary classes of products from the process. Note also that the equations do not include the neutral molecule corresponding to the unfragmented polyatomic ion. It is unlikely that a particle analogous to the neutralized ion ever exists as anything more stable than a transition state (except, perhaps, for larger molecular structures; the detailed mechanisms of dissociative recombination will be discussed more thoroughly in Section 1-2.).

The possible emission of light makes the process interesting because it can be studied passively — that is, information can be obtained about the process without interfering with the process. This aspect is valuable for monitoring remote environments such as ionized clouds of gas in the interstellar medium. Even the absence of photoemission, where there is sufficient energy for the production for certain photons, can tell us much about the dynamics of the process.

1-2 Theoretical Descriptions of Dissociative Recombination

Details and summaries of various theoretical treatments of dissociative recombination have been presented elsewhere; so, only a brief synopsis of the theory, as it applies to the current study, will be provided here. For example, although any description of the mechanism by which an electron and an ion recombine will, to some extent, apply to ion-pair formation as well as to neutral products, only the formation of neutral products will be considered in any detail. Computational models will not be presented; instead, the focus will be on theory. However, the Reference section contains references to works that address all of these issues and many others. In Appendix A there is a listing of references arranged by category.

Since an electron has very little mass compared to a nucleus, it is not appropriate to consider the collisional momentum of the electron as being the direct reason that the nuclei move apart. As was stated in the last section, even at high kinetic energies, the electron is more likely to cause the ejection of other electron(s) than to move the ion as a whole. Certainly, though, it is possible for a recombining polyatomic ion to dissociate, and this generally occurs. In such a case, the fragments typically gain translational linear momentum with respect to each other. But, the translational momentum does not result directly from the addition of momentum from the electron.

A better way to think of the process is that the addition of the incident electron changes the shape of the potential field in which the nuclei find themselves. Due to this change in the potential field, a bond might be broken between two atomic cores in the molecule (i. e., the system moves onto a repulsive potential). In this case, the two parts of the molecule might experience a repulsive force and begin to move apart. The observation of vibrational, rotational and translational momentum in DR products has prompted theorists to investigate the source of such excitation. For example, Bates [1993b] presented a theory describing mechanisms for vibrational excitation in polyatomic DR products. The theory involves contributions from two



Figure 1-2.1: Schematic diagram of a curve crossing. If recombination occurs by curve crossing, the potential energy curve for the unbound, neutral state (X + Y) crosses that for the bound ion, XY^+ . This process becomes likely when the curve crossing occurs at an internuclear separation probable for the ion. In this schematic, the crossing is not near the potential minimum for the bound ion, and one would expect vibrational excitation in the ion to be necessary for recombination to occur via the curve crossing mechanism.

mechanisms that he called *impulse* and *relic*. A summary description of this theory can be found a few paragraphs below, just after a summary of current ideas involving the change in potential caused by the incident electron.

Two important DR mechanisms are called *crossing* and *tunneling*, respectively. Their names are based on the relative positions of potential energy curves that describe the process. In the crossing mechanism (see Figure 1-2.1) there is direct interaction between the potential energy curves for a bound ionic state and an unbound neutral state (a *curve crossing*). No such direct interaction is present in the case of the tunneling mechanism (see Figure 1-2.2). In 1994, Bates [Bates 1994] published an article detailing the history, development, and current state of understanding of the two mechanisms. Briefly, this is as follows.

When describing DR, the potential energy curves that are presented usually include, but are not limited to, one curve describing the bound ion and a curve describing at least one unbound, neutral state. Schematic diagrams of possible arrangements of these curves are shown in Figures 1-2.1 and 1-2.2. Figure 1-2.3 is another schematic describing one type of behavior that a dissociating system might undergo. Curves for specific systems can be found in many of the papers in the reference section, especially those categorized under "Computational and Theoretical — DR" in Appendix A.

In the crossing mechanism, the potential energy curves for the recombining ion and the dissociating products cross each other at a molecular geometry probable for the ion (see Figure 1-2.1). Upon neutralization by the electron, the system is considered to leave the bound curve (XY^+ in Figure 1-2.1) and begin to separate along the unbound potential curve (X + Y). Quantum-mechanical descriptions of systems allow all internuclear separations: some are simply far more probable than others. So, the physical interpretation of the curve-crossing mechanism is that there exists a probable internuclear separation for the recombining ion that has the same energy as the (neutral) dissociated particles would have at that same separation. Thus, the dissociation portion of the recombination is the reverse of a half-collision between the two unbound particles. Geometries for these systems are typically described in terms of the separation between the two atoms involved in the bond that is breaking. With more complex polyatomics, there is, of course, the possibility that such a simple description will not be sufficient. Even so, the one-dimensional picture serves to illustrate the mechanism well

Sometimes, the potential curves never cross or only cross at high energies. If there is no common energy/separation accessible to the bound ion and to the neutral products, the recombination may proceed via quantum mechanical tunneling (see



Figure 1-2.2: Schematic diagram of the relative positions of two potential curves for a system in which recombination via tunneling is likely. In this diagram, the potential curve for the unbound, neutral state (X + Y) does not cross the potential curve for the bound ion, XY^+ , at an internuclear separation probable for the ion. No intermediate states are involved in the interaction.

Figure 1-2.2), from a point on the bound curve across to the isoenergetic point on the unbound curve.

When two (or more) potential curves cross each other, there is also, in some circumstances, the possibility for the curves to "mix" and produce what is termed an *avoided crossing*. This can occur whenever the two curves describe what Herzberg [Herzberg 1989] called "states of the same species." His use of the term "species" does not refer to the atomic or molecular identity of the particle. Instead, it refers to the characteristics of two electronic states within the same molecule. The concept is similar to the splitting of rotational states that would otherwise be degenerate, except that, here, it is being applied to a standard potential energy curve constructed for a rotationless, vibrationless system. For the avoided crossing to occur, all symmetry



Figure 1-2.3: Schematic for an avoided crossing. The intent of this figure is to depict the possible "routes" that can be taken by the newly-recombined activated complex, XY** in the event that it encounters an avoided crossing. Consider the complex to be dissociating along path (A). The dashed lines represent the crossing that is being avoided. Note: the middle curve (A–B) describes an excited bound state of XY correlating to excited states of the separated atoms X and Y; the ground state neutral, XY, is weakly bound and will apparently predissociate along (D) at some excited rotational or vibrational level. See text for further discussion of the figure.

properties must be the same; these include: Λ , the total orbital angular momentum; S, the electron spin vector; Ω , the vector describing the interaction of Λ and S; for Σ states, the symmetry of the wavefunction reflected across the internuclear axis (+ or -); and, for homonuclear systems, the parity (gerade or ungerade);

If the crossing is avoided, the potential curves that would cross in a first approximation serve as something similar to asymptotes to the proper curves. The term "avoided" is only partially descriptive, however. A crossing is only fully avoided in the limit of infinitely slow change of internuclear separation. So, for high vibrational levels or rapid dissociations, the crossing will not be completely avoided, and in the limit of high velocity the crossing will never be avoided. Herzberg [1989, ca p 295] describes this effect in detail. The practical effect is that the "avoided crossing" and the "crossing" exist simultaneously. Figure 1-2.3, a schematic of an avoided crossing, depicts two possible states that could result from the recombination of the ion XY^+ . Consider the activated complex, XY^{**} , resulting from the ion, XY^+ , having just been neutralized by an electron. The neutralized ion initially separates along the repulsive potential labeled (A). The presence of the avoided crossing implies that the activated complex is most likely to dissociate via path (B). However, the system can also dissociate along (D). Given that the momentum of the system is in the direction of separation, the complex is unlikely to take route (C) and become the bound neutral molecule, XY. But, even if it does "go" that route, either directly or via path (B), the complex contains sufficient energy to dissociate and will do so unless it is stabilized via collision or radiation. A system $(N_2^+ + e)$ whose product potentials include an avoided crossing has been discussed by Bates [Bates 1994, ca. page 446] as having been studied both computationally [Guberman 1991] and experimentally [Helm 1989]. The "avoided" route $(N(^2D) + N(^4S))$, equivalent to (D) in Figure 1-2.3, was found by both studies to be the primary channel for dissociation (88%). However, another study [Queffelec 1985] found the branching ratio for the avoided channel to be, at most, 0.15.

Theoretical descriptions of DR can include transitions involving any number of electrons, up to the total number of electrons present in the system. However, the descriptions are sometimes limited to single– or two–electron transitions due to mathematical complexity or computational expense.

In the case of tunneling, the transitions are often considered to be single-electron transitions. Bates discusses only two classes of single-electron transition in detail. In one, the valence decrease class, the incident electron enters an orbital around one atom in the ion. The occupation of this orbital precipitates the dissolution of one (or more) of the existing bonds between the atom to which the electron was added and other atoms in the ion. The other class, consisting of cluster ions containing a proton-bridge bond, i. e. $A \cdots H^+ \cdots B$, is intuitively similar. It is only in the mathematical treatment that distinctions arise [Bates 1994]. In this case, the incident electron moves into the 1s orbital around the bridging proton. Again, this precipitates dissolution of a bond. As in the former class, the bond broken is between the bridging hydrogen and one or more of the sub-particles for which it served as a bridge.

In the case of a curve–crossing (Figure 1-2.1), a single–electron transition is not possible [Bates 1994]. Two dominant descriptions of the curve–crossing process are called *direct* and *indirect* (see Figure 1-2.4). In *direct* recombination, the incident electron initiates a two–electron transition directly to the repulsive state of the unbound neutral. An expression for the recombination coefficient for the direct mechanism is presented in Equation 6 with discussion following. *Indirect* recombination, a theory initiated by Bardsley [1968a,b], and described by Bates [1994, ca. p. 437], involves two radiationless transitions. Here, the first transition is into a Rydberg state of the neutralized ion. Then, the second transition is into the same unbound, repulsive state as accessed in the direct mechanism. Bates [1994] gives the rate coefficient for the *indirect* mechanism as:

$$\alpha_I' = \int \left\{ \frac{8}{\pi m (k_B T)^3} \right\}^{1/2} \epsilon \, \sigma'(E) \exp\left(\frac{-\epsilon}{k_B T}\right) \, \mathrm{d}\epsilon \tag{5}$$



Figure 1-2.4: Schematic diagram depicting the difference between the direct and indirect mechanisms. (a) In the direct mechanism, the system moves directly from the bound state of the ion, XY^+ (1), to the repulsive neutral curve, X + Y (2). (b) In the indirect mechanism, the system (1) first transits to a high vibrational level of a Rydberg state of the neutral, XY^* (2), and then transits to the repulsive neutral curve, X + Y (3). In either case, the transitions do not involve radiation, so the system retains its initial total energy, E.

Here, π , k_B and T have their usual meanings [see the List of Abbreviations]; ϵ is the energy of the incident electron and $\sigma'(E)$ is the cross section for an electron with energy ϵ .

The following expression, given by Bates [1994] describes the recombination coefficient, $\alpha_D(v)$ for a *direct, two-electron* transition from vibrational level v in the ion where there exists a favorable curve-crossing to a repulsive neutral potential curve and where all products dissociate:

$$\alpha_D(v) = \frac{Srh^3}{2(2\pi mk_B T)^{3/2}} \cdot \frac{2\pi\hbar}{me^4} \int \left|\psi_v(R)V(R)\phi_\epsilon(R)\right|^2 \mathrm{d}R \quad \exp\left(\frac{-\epsilon}{k_B T}\right) \mathrm{d}\epsilon \qquad 6$$

where S is defined below; r is the statistical weight of the neutral compared to the corresponding ground-state ion; m is the reduced mass of the electron-ion system; T is the temperature of the system; π , k_B , h and \hbar have their standard meanings [see the List of Abbreviations]; e is the elementary charge; $\psi_v^*(R)$ is the vibrational wave-function for the ion; V(R) represents the "interaction causing the autoionization;" ϕ_{ϵ} is the wavefunction describing the separating particles; R is the internuclear distance; and ϵ is the energy of the system.

Bates's [1994] derivation of Equation 6 begins with a modification of an expression for the dielectronic recombination rate coefficient:

$$\alpha(p) = \frac{A(st)A(au)}{A(st) + A(au)} \frac{rh^3 \exp\left(-\epsilon/kT\right)}{2(2\pi mkT)^{3/2}}$$
7

In this expression, A(au) is the autoionization rate for a system consisting of a coupled ion-electron pair with an excited state, p, at energy ϵ above the ionization potential of the neutral particle. A(st), in terms of plasma dynamics, is the rate at which neutrality of the plasma is maintained by loss of energy in excess of ϵ ; in terms of dissociative recombination, it is the rate at which the electron-ion complex is stabilized by dissociation. Equation 7 is based on the assumption that the system is in steady-state and is valid for recombinations via level p. The expression in Equation 6 is then generated by first making the following substitution:

$$\frac{A(st)}{A(st) + A(au)} \equiv S$$
8

This definition allows S to be treated separately from the integral in Equation 6. The separate treatment of S is based on the assumption that the stabilization rate will be much greater than the autoionization rate (due to the rapid dissociation of the recombined ion), and the value of S is generally considered to be approximately one. Next, it is necessary to find an expression for the autoionization rate, A(au), that remains after the substitution of S. Bates uses methods familiar to quantum mechanics in his treatment of A(au):

$$A(au) = \frac{2\pi\hbar}{me^4} \left| \int \psi^*(R) V(R) \phi_\epsilon(R) \, \mathrm{d}R \right|^2$$
9

The symbols in Equation 9 are defined after Equation 6, above.

Although the theoretical descriptions can become complex, a visceral understanding of the processes and of the effects of environmental factors, such as temperature, can be gained by inspection of the relevant potential energy curves. For example, one very important concept is the effect of collision, or interaction, energy on the potential curves. The reason the concept is important is that the collision energy effectively changes the position of the potential curve for the recombining ion, but not for the products [Bates 1994, e. g., p. 436 & 466]. That this is the case can be deduced by considering other possibilities. For example, consider that the ion is in vibrational state v of the electronic state described by potential (a) in Figure 1-2.5. If the system is placed at a higher energy by the proximity of an electron with kinetic energy, E, that extra energy is not likely to correspond to vibrational excitation in the ion. The potential field generated by the motion of the electron might distort the electronic structure surrounding the ion, but it is not expected, necessarily, to provide vibrational excitation. Instead, it is the vertical position of the potential that will change. The potential for the neutral products of recombination, however, will not be influenced by the presence of the high-energy electron (especially since the electron is no longer free). Figures 1-2.6 — 1.2.8 illustrate the effect for a few hypothetical systems, with Figures 1-2.6 and 1-2.7 focusing on the effect where a curve–crossing appears.

The effect of interaction energy in the case of a curve–crossing is easily seen by plotting the potential curve for the ion with and without an increase of interaction energy (collision energy). Figure 1-2.6 is a schematic of a system where an increase in electron energy favors the curve–crossing mechanism for low vibrational levels of



Figure 1-2.5: Illustration of the effect of the kinetic energy of an electron on the potential of the ion. Rather than causing vibrational excitation (a), the presence of the energetic electron raises the ion's potential (b) relative to the neutral products (not pictured).

the ion. To account for the energy of the electron, the position of the PE curve for the ion, initially at (a), must be raised to (b). Note that the unbound curve, (c), does not move. The opposite situation is depicted in Figure 1-2.7. For that system at low electron energy, the unbound potential crosses the ion potential near the potential minimum. But, the addition of electron energy effectively moves the crossing point to higher vibrational levels of XY^+ .

In the case of tunneling (Figure 1-2.8), the situation is not as simple. One must consider the probability that the electrons already bound to the ion and the neutralizing electron will arrange themselves in a manner consistent with formation of two unbound particles. A discussion of the electron–orbital implications appears below, and certainly the incident electron affects the shape of the orbitals. But, for the sake of this argument, consider that the electron's effect on the orbitals is not altered by a change in the electron temperature. Assume that the only change is in the relative energies of the two states, ionic and unbound. Consider Figure 1-2.8 as depicting the



Figure 1-2.6: Hypothetical system where an increase in interaction energy, moving the curve from (a) to (b), favors curve–crossing DR from low vibrational levels of the recombining ion (see text).

potential recombination of an ion, XY^+ , in its zeroth vibrational level. A horizontal, isoenergetic line is included for convenience, as are schematic representations of bound and unbound vibrational wavefunctions at that energy. If the orbital shapes do not change, then changing the electron temperature only changes the particular unbound wavefunction that is to be considered when calculating an overlap. Since there is not an exchange of photons (an implicit assumption thus far), the change in state must be isoenergetic, and only the wavefunctions at that energy (ignoring uncertainties) are important. If the position of the bound curve were moved higher or lower, the nature of the overlap would necessarily change. Intuitive prediction of the manner in which the overlap will change is not a trivial task, but, a few generalizations can



Figure 1-2.7: Hypothetical system where an increase in interaction energy, moving the curve from (a) to (b), does not favor curve–crossing DR from low vibrational levels of the recombining ion (see text).

be made. For example, in the situation depicted in the Figure 1-2.8, a decrease in interaction energy would cause an increase in DR probability, since a low–energy unbound wavefunction would have a broad peak coincident with the zeroth vibrational level of the ion.

It is not completely correct, as was assumed for the arguments in the tunneling example, to assume that the incident electron does not have an effect on the orbitals, and that a difference in initial electron velocity will not change the magnitude of that effect. A brief look at elementary electrodynamics [Bueche 1986, or most undergraduate physics texts] informs us that the magnetic field induced by the motion



Figure 1-2.8: Schematic depicting some of the factors important to tunneling DR (see text). The factors illustrated are: the bound potential curve of the ion (XY^+) and the wavefunction for vibration of the ion in the zeroth vibrational level (a); the unbound potential curve for the product neutral (X + Y) and the wavefunction for the unbound system at an energy coincident with the energy of the zeroth vibrational level of the ion (b). The wave functions are not normalized.

of charged particles is directly proportional to the current, or speed, of the charged particles. So, in this way, the initial velocity of the electron is certainly expected to have an effect on the recombination. The initial trajectory of the electron with respect to the ionic structure should have an effect as well. Although the ion is positively charged, overall, the existence of electronic structure implies the possibility that different effective charges will be experienced at different collision geometries. Harland and Vallance [Harland 1998] present detailed accounts of orientation effects in electron–impact ionization. Both processes, electron–impact ionization and electron–ion recombination, involve the collision of an electron with a particle. If orientation is important for electron–impact ionization then there should be orientation effects present for electron–ion recombination as well.

To illustrate this, consider the dissociative recombination of a heteronuclear diatomic ion, HF⁺. It is generally well known that most of the electron cloud surrounding HF⁺ is "owned" by the fluorine atom, and that the bulk of the positive charge in the vicinity of the hydrogen. If an electron collides with this ion, it seems natural to assume that an electron approaching from the hydrogen side encounters a different environment than one approaching from the fluorine side. Of course, the ion will generally be vibrating and likely rotating, which complicates the picture presented here. Uncertainties about the wave/particle characteristics of the electron complicate things further. However, the electron is not approaching the ion from all directions at the same time. In other words, the electron, be it particle or wave, must approach the ion from a particular direction. It is possible that an electron approaching the ion could take a trajectory such that it collides with the ion in an area that is more fluorine atom than hydrogen ion. Since fluorine is the most electronegative element known, with a large electron affinity, one might expect the electron to enter an orbital around the fluorine. In the case of a subsequent dissociation, an ion-pair would be formed. Indeed, recent storage-ring experiments have found [Zong 1999] that the interaction between an electron and an HF⁺ ion at 0 eV produces an ion-pair about 1/3 as often as it produces two neutral atoms.

It is clear from the above that the trajectory of the incoming electron needs to be considered. The influence of the electron on the ion's electronic orbitals has been shown to be important, as has the effect of collision energy on the position of the potential curve for the ion. The effect of vibrational overlap between the initial and final states has been discussed. Many other possible interactions have not been discussed here, but should be considered. These include, at least, the s-character or p-character of the incident electron, the influence of Rydberg states (the *indirect* mechanism), rotational excitation and, most importantly, the changes within the atomic and molecular orbitals.

As mentioned earlier, another part of the process that aroused the interest of Bates [1993b] was the suggestion that some diatomic products of polyatomic recombination are vibrationally excited [Duley 1992]. He presented two theoretical approaches to account for this, which he called the *relic* and *impulse* mechanisms. The relic mechanism is based on the notion that, for example, in the recombination of triatomic ion XYZ^+ , to form X + YZ, a portion of the wavefunction describing the molecular orbital around the ion is associated with the neutral, YZ. The nature of the overlap between this part of the molecular orbital of XYZ⁺ and the free YZ molecule will be different for different vibrational levels. According to Bates, it is this "relic" of the wavefunction that serves as one mechanism for vibrational excitation in the neutral diatomic product. His other mechanism is based on the fact that, as the two products, X and YZ, repel each other, the initial repulsion will affect atom Y before atom Z, therefore providing an impulse to Y, initiating vibration in the product. His treatments involve the simple harmonic oscillator assumption for vibrations and he treated directly only diatomic products in the ground electronic state. Neither of these mechanisms has held up well to comparison with experiment for vibrational excitation in electronically excited states [Adams 1994a].

Since electron-ion recombination involves a radiationless transition between a bound state and an unbound state, the process has similarity to predissociation. Herzberg [1989, ca pp 420-421] suggests that the dominant feature controlling vibrational excitation in the case of predissociation is simply the overlap between the vibrational wavefunctions of the bound and unbound states at the interaction energy. So, it is possible that a similar relationship holds in the case of DR.

If an electron is in some electronic orbital of very large n^{\dagger} (Rydberg state or beyond) of a polyatomic molecule, XYZ, then the ion core, XYZ⁺ could be considered to be, largely, ignorant of the high-orbital electron. Indeed, there will be little difference to the ion core if the electron is removed altogether. In such a case, the potential energy curve of the ion core would have nearly the same sort of shape as if it were considered to be a solitary ion. This line of reasoning doesn't take one directly to an overall recombination coefficient, but it does lead to a means for calculating the relative populations of vibrational excitation in the products. Viewed from this perspective, DR is very similar to predissociation. In fact, it is, essentially, equivalent to predissociation. The primary difference is that instead of dissociating from a low-lying bound electronic state, the dissociation occurs from a high-level Rydberg state. So, the relative vibrational population resulting from DR can be calculated in a manner similar to that for any other electronic transition — essentially, by taking a Franck–Condon overlap between the two states and squaring the result. It is probable that this description will lead only to approximate results, but it is simple and can serve as a starting point for the development of more rigorous calculations. Consider the relative vibrational excitation in the diatomic product XY from the DR of ion RXY⁺, where R is one or more atoms, and X is bonded directly to Y. Y is, of course, not bound to atoms other than X, but that situation could be handled in a manner analogous to this treatment. In the following expression, $\psi_{v'_{RXY}}(\tau)$ is the

[†] The principal quantum number.

wavefunction describing vibration in the ion, $\psi_{v'_{XY}}(\tau)$ is the wavefunction describing vibration in XY and $f_{v'_{XY}}$ is the *fractional* excitation in vibrational level v''_{XY} of XY. τ is a generalized spatial coordinate, the applicable volume element. In the simplest case, τ could be replaced by r, the internuclear distance between R and X. Note that the quantum number v''_{XY} is not necessarily the same as the quantum number v'_{RXY} .

$$f_{v_{XY}^{\prime\prime}} \propto \left| \int \psi_{v_{RXY}^{\prime}}(\tau) \psi_{v_{XY}^{\prime\prime}}(\tau) \ d\tau \right|^2 \tag{10}$$

In essence, this is the Franck–Condon overlap between the two vibrational wavefunctions. Note also that the calculation can be simplified somewhat. Since the vibrational wavefunction for the diatomic molecule decays rapidly to zero beyond the classical turning points, it is only necessary to consider that part of the ion's wavefunction in the vicinity of the diatomic product.

A few reasonable simplifications and approximations make such a calculation trivial, but not very predictive at this time. The technique holds promise, but it will be necessary to have better descriptions of the ionic states than are currently available [Jacox 2002] before it can be thoroughly tested. If accurate descriptions of recombining ions make the method more predictive, it would be useful in its simplicity, both conceptually and computationally.

One recent paper uses methods that have similarity to the preceding discussion, but with a far more rigorous approach and considerable success [Tomashevsky 1998]. They base their calculations on the *relic* and *impulse* mechanisms proposed by Bates [1993b]. But, their method also includes the effects of Franck–Condon overlap. They do not treat Bates's two mechanisms separately, but include them both in their calculations. They use both classical and quantum mechanical solutions to the equations of motion. Their results compare far more favorably to experiment [Adams 1994a and Butler 1997] than did either of Bates's mechanisms alone.

1-3 Experimental Studies

Experimental studies of electron-ion recombination have been carried out on a number of systems. Appendix A lists references arranged by category, and there is a large section devoted to studies of electron-ion recombination. Although the focus of this document is on photoemissions from dissociative recombination, it is useful to consider other studies of the process as well.

Studies of dissociative recombination can be classified by the type of information they determine about the process, the main information types being kinetic and product-related. Studies of recombination kinetics generally base results on the decay of an ion signal as detected by a mass spectrometer, Langmuir probe, or other ionization detection device. These studies can be successfully carried out without the researcher being concerned about the nature of the products. Product-related studies are the opposite — they are less concerned with the rate at which the reaction proceeds than with the final outcome of the recombination. Section 1-2 contains a somewhat detailed discussion of different mechanisms of recombination, including the different product classes that are possible. Some experiments, of course, study kinetics and products at once. See Appendix A under heading "Experimental Results — DR" for references. Experiments with more than one goal (e. g. those that study both kinetics and products) appear under multiple sub-headings.

The two most important techniques currently being used are the flowing afterglow [Adams 1988a] and the ion storage ring [next paragraph]. Either of these techniques can be used to study kinetics or products, if the experiment and the experimental apparatus are designed appropriately. An older technique, the predecessor of the flowing afterglow, is the stationary afterglow [Schmeltekopf 1963, Weller 1967]. Also, Mitchell and Rowe [Mitchell 2000] have made suggestions for new experiments, all involving storage rings or flowing afterglows.
Use of storage rings is fairly new, with details of the experiment and apparatus being described elsewhere [Strömholm 1996 and other references in this paragraph], so the method will only be described briefly here, mostly with respect to typical results obtained. The storage rings used for the studies are ASTRID (Aarhus, Denmark) [Jensen 1999], CRYRING (Stockholm, Sweden) [Zong 1999], TARN (Tokyo, Japan) [Tanabe 2000], and the TSR (Heidelberg, Germany) [Habs 1989]. Although the devices are called rings, they are shaped more like squares or rectangles with rounded corners. The basic feature of the device is the ability to contain ions electromagnetically for relatively long periods of time (of the order of a few seconds). This feature allows for vibrational, rotational and off-axis[†] translational cooling of ions prior to reaction; but, the cooling is radiative and is limited by the temperature of the walls. The ions travel around the ring at high energies, encountering different environments as dictated by experimental needs. The square-ish shape allows for sections of long, straight trajectories, and curved sections allow neutrals or selected ions to be extracted while the rest of the beam is bent around the orbital path. The apparatus gives the researchers great flexibility in terms of manipulating reactants and in observing products. Until very recently, storage rings were mainly used to study small $\mathrm{HX^{+},\ H_{2}X^{+}}$ ions and their deuterated analogs [Amitay 1999, Jensen 1999, Lange 1999, Schneider 2000a, b, Strömholm 1996, Zong 1999]. Even the most recent [Larson 1998, Semaniak 1998, several articles in Larsson 2000] studies have not been for very massive ions, and most concentrate on H_nX^+ variants $(n \leq 5)$. A recent conference proceedings [Larsson 2000] contains articles discussing these experiments. Often, the interaction energies are very large (several eV to several MeV). But, lower energy interactions, as are comparable to the work presented in this document, are usually included [see previous list]. Since the numbers of ions recombining is low, these experiments do not observe photoemissions. But, they are able to deduce the energy

 $[\]dagger$ e. g., perpendicular to the forward motion of the ions around the ring.

content of the products in some cases and, therefore, deduce their electronic state [Strömholm 1996, Zong 1999]. The studies nearly always concern themselves with calculation of recombination cross sections [all references in this paragraph]. They sometimes also report recombination rate coefficients [Amitay 1999, Zong 1999] and branching ratios for the various product pathways [Jensen 1999, Larson 1998, Semaniak 1998]. These studies keep the ions trapped in the ring prior to recombination long enough for vibrational relaxation by photoemission, but most do not determine the vibrational state of the ion directly. One study [Amitay 1999], however, selects for the initial vibrational state of the ion. The vibrational state is determined using a technique called coulomb explosion imaging (CEI). This technique strips the electrons off an ion very rapidly. The nuclei then move rapidly apart by coulombic repulsion (hence "explosion"). The researchers use the fragment pattern to determine the vibrational state of the nuclei at the point at which the electrons were stripped.

The new research reported in this dissertation employed a flowing afterglow, and details of design and use can be found in Chapter 2. The primary advantage of using a flowing afterglow, rather than other devices such as a stationary afterglow, is that the behavior of a reaction in time is stretched out along a flow-tube. This feature is particularly useful to kinetic studies. The familiar rate law describing a bimolecular recombination (here, e–i recombination):

$$Rate = \frac{\mathrm{d}[R]}{\mathrm{d}t} = -\alpha[e^{-}][XY^{+}]$$
 11

is no longer written in terms of time, but of distance:

$$\frac{\mathrm{d}[R]}{\mathrm{d}t}\frac{\mathrm{d}t}{\mathrm{d}z} = \frac{\mathrm{d}[R]}{\mathrm{d}z} = -\frac{\alpha}{v}[e^{-}][XY^{+}]$$
12

where, R stands for either reactant, the electron, e^- , or the ion, XY^+ , and [] indicates the concentration of the reactant. α is the rate coefficient, v is the velocity of the plasma, t is the reaction time, and z is distance, axially, along the tube. The disadvantage is that studies are complicated by flow effects such as diffusion. Since the particles are charged, the species are lost to recombination at the walls as well as to processes occurring within the volume of the flow. The process governing the loss at the walls is called *ambipolar diffusion* and is discussed in texts dealing with plasmas [for example, Adams 1975, Drake 1996, Hazeltine 1998]. With a sufficiently high pressure (~ 1 torr) of a neutral carrier gas, such as helium, and a reasonably high number density of electrons (~ $10^{10}cm^{-3}$) loss to the walls is slow compared to loss due to recombination [Adams 1984]. In this case, the standard second–order kinetics, as written in equation 13 provides a sufficient description, with a well–known solution [for example, Atkins 1998]. If we use position references of z_1 for the initial position along the tube and z_2 for the final position along the tube, then an expression relating electron concentration and position to the recombination coefficient is:

$$\ln\left(\frac{[XY^+]_{z_1}[e^-]_{z_2}}{[e^-]_{z_1}([XY^+]_{z_1} - [e^-]_{z_1} + [e^-]_{z_2})}\right) = \alpha \frac{[e^-]_{z_1} - [XY^+]_{z_1}}{v} (z_2 - z_1)$$
 13

Variations on this expression can be formulated for dependence on ion density as a function of position or for both densities as a function of position. Such variations are useful for different experimental setups. The formulation given in Equation 14 is useful in cases where it is convenient to measure electron density as a function of position (such as with a movable Langmuir probe), but where the ion density could only be known at the start position, perhaps due to the presence of multiple ion types. In cases where there is only one positive ion type and there are no negative ions, it is acceptable to assume that the ion density equals the electron density, since the plasma is quasi-neutral. It is, then, only necessary to ensure that sufficient XYprecursor is added to make certain that all the positive ions are converted to XY^+ . If this is the case, the reaction reduces to one of general type:

$$\frac{\mathrm{d}[R]}{\mathrm{d}x} = -\frac{\alpha}{v}[e^{-}]^2 \tag{14}$$

to which the solution is well known as:

$$\frac{1}{[e^-]_{z_2}} - \frac{1}{[e^-]_{z_1}} = \alpha \frac{(z_2 - z_1)}{v}$$
 15

For a thorough discussion of the usefulness of this sort of technique, see the temperature dependence work by Adams and Smith [Adams 1984]. In 1987, Johnsen [Johnsen 1987] published a comparative review of recombination rate coefficients available at that time. Although many of the recent rate coefficient determinations have come from storage ring experiments, the flowing afterglow has still been used in a number of studies. For example, rate coefficients have been determined recently in a flowing afterglow for recombinations of H_3^+ , D_3^+ and HCO^+ [Laubé 1998a]. Another group has been studying the recombinations of larger hydrocarbons noting isomeric differences where possible [Rebrion–Rowe 2000a,b].

A few experiments in afterglows (either flowing or stationary) have been concerned with atomic or molecular products of DR but not with direct photoemission from those products. These experiments often involve laser-induced fluorescence (LIF) of the products [Herd 1990, Adams 1991, Gougousi 1997a,b] and/or vuv absorption [Kley 1977, Herd 1990, Adams 1991, Williams 1999]. In the LIF studies, the OH radical is monitored as a product of recombination. The OH density is determined by excitation of molecules from the ground $(X^2\Pi)$ state up to an excited state $(A^2\Sigma^+)$ and then observing the light emitted (fluorescence) when the OH returns to its ground state. This method was initially used to quantify OH in the $X^2\Pi$ v=0 and v>0 states [Herd 1990, Adams 1991]. More recently, yield has been determined for relative populations of the v=0 and v=1 vibrational levels in OH [Gougousi 1997a,b]. These latter studies did not determine the contribution for levels greater than v=1. The absorption studies were used to examine H atom production [Herd 1990, Adams 1991] and N (^{2}D) production [Kley 1977]. If one considers the storage-ring experiments, a larger number of products have been determined, but even then, the body of information is hardly extensive.

The number of studies that have examined photo–emissions as products of recombination is also small relative to the number of possibilities. This number, however, appears to be growing, so there might soon be a considerable body of information on the subject. One of the earliest mentions of the phenomenon comes from a study of emissions in a flowing afterglow [Taieb 1977]. In this study, the experimenters injected neutral molecules into a plasma flow and observed the resulting emissions. They found that some of the emissions came from neutral species that were smaller than the injected molecules. The researchers suggested that those emissions might have been the result of recombinations of larger ions with electrons. Based on experiments done since then, it now seems very likely that they were correct in that assertion. Thus far, there have been no observations of emissions from triatomic or larger products. Only two papers, both by Zipf [1979, 1980b] report observation of atomic emission as a result of recombination. Table 1-3.1 lists ions and products for studies since the observation in 1977 by Taieb and Broida. Several of the studies listed in the Table will be discussed in greater detail in Chapter 4 of this document. _____ Table 1-3.1 _____

Molecule	$\mathbf{State}(\mathbf{s})$	Parent Ion †	Reference	Note
Ο	^{1}S	O_2^+	Zipf 1979, 1980	
CH	$A^2\Delta, B^2\Sigma^-, C^2\Sigma^+$	$\overline{CH_4}$	Tsuji, 1991	
	$A^2\Delta, B^2\Sigma^-$	$CH_4 + H_2$	This work	a, b
CO	$A^{1}\Pi$	CO_2^+	Valée, 1986	a
			Tsuji, 1995	
			This work	a
		$\rm HCO^+/\rm COH^+$	This work	a, b
		HCO_2^+	This work	a, b
	$a^3\Pi_r$	HCO^{+}	Adams, 1994a, b $% =1000000000000000000000000000000000000$	
			Butler, XXXX	
			This work	
		DCO^+	Butler, XXXX	
		$\rm HCO^+/\rm COH^+$	Johnsen, 2000	
			This work	b
		CO_2^+	Tsuji, 1995	
			Skrzypkowski, 1998	
			Johnsen, 2000	
			This work	a
		HCO_2^+	This work	b
	$a'^3\Pi_r, d^3\Delta_i, e^3\Sigma^-$	$\rm HCO^+/\rm COH^+$	Johnsen, 2000	
		CO_2^+	Tsuji, 1995	
	$a'^3\Pi_r, d^3\Delta_i$	CO_2^+	This work	
		HCO_2^+	This work	a, b
CS	$A^{1}\Pi$	CS_2^+	This work	b
	$a^3\Pi_r$	CS_2^+	This work	b

Emitting States for Observed Photoproducts of Recombination

Table continues

[†] If neutral parents are listed, the exact identity of the parent is complex or uncertain. The neutrals listed are the species injected into the plasma.

NH	$A^3\Pi_i$	$NH_3 + H_2$	This work	b
		HNO ⁺	This work	b
		N_2OH^+	Foley, 1993	
			Johnsen, 2000	
	$c^{1}\Pi$	$NH_3 + H_2$	This work	a, b
		N_2OH^+	This work	b
N_2	$B^3 \Pi_q$	N_2H^+	Adams, 1994a, b	
	5		Butler, XXXX	
		N_2D^+	Butler, XXXX	
		N_2O^+	Tsuji, 2000	
		N_2OH^+	This work	a, b
NO	$A^2\Sigma^+$	HNO^+	Johnsen, 2000	
	$A^2\Sigma^+, B^2\Pi_r$	N_2O^+	Johnsen, 2000	
		HNO^+	This work	b
OH	$A^2\Sigma^+$	H_2O^+	Sonnenfroh, 1993	c
			Johnsen, 2000	
		O_2H^+	Foley, 1993	
		N_2OH^+	Foley, 1993	
			Johnsen, 2000	
		HNO^+	This work	b
		HCO_2^+	Johnsen, 2000	
		-	This work	b
\mathbf{SH}	A?	H_3S^+	This work	d

Notes:

a: Apparent vibrational excitation in recombining ion.

b: Tentative: likely due to recombination, but other sources are possible.

c: T_e ~ 1000k.

d: Electronic state uncertain.

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CHAPTER 2

EXPERIMENTAL APPARATUS AND DESIGN

The first part of this chapter, Section 2-1, describes the physical design of the experimental apparatus. First, the overall layout of the system is presented. Following that, the major components are discussed separately and in moderate detail.

The chemical aspects of the experiments are described in Section 2-2. As in Section 2-1, a general overview of the design is followed by a more detailed discussion of important reactions.

2-1 Experimental Apparatus

The experiments described in Chapters 3–5 were carried out in a flowing afterglow (FA), a schematic of which is given in Figure 2-1.1. A flowing afterglow consists of a tube, often stainless steel, through which one or more gases flow. Reactions begin, generally, at or near the upstream end, where ionization is produced in a neutral gas, called a *carrier* gas. In these studies, He was used exclusively as the carrier gas, but other gases, N_2 for example, can be used. The carrier gas makes up the bulk of the gaseous pressure in the apparatus and acts as the medium in which the chemical reactions take place. Since the gas also inhibits, or "buffers," diffusion of the reacting species, it is sometimes referred to as a *buffer* gas, but will be referred to here exclusively as a carrier gas. The partially ionized carrier gas then flows down the length of the tube and carrier is pumped away at the downstream end. To control the chemistry occurring in the flow, additional gases are added at various points along the tube.

Gas manifolds (not shown here): 1

Inlet ports RP1-RP6: 3





Figure 2-1.1: Schematic of the flowing afterglow apparatus. Numbers following labels indicate the subsection(s) of Section 2-1 in which that component is discussed. The figure is not drawn to scale, but is somewhat representative of the relative sizes of the real components. To reduce clutter, the gas manifolds, gas flow systems and pumping systems are illustrated separately in Figures 2-1.2, 2-1.3 and 2-1.7.

This section is devoted to discussions and figures describing the flowing afterglow and ancillary equipment used in the studies presented here. Figure 2-1.1 is a schematic of the central portions of the apparatus, i. e., the "reaction vessel." In the figure, portions of the apparatus are numbered; discussions of numbered portions appear on the following pages in the order indicated by the numbering. Portions of the apparatus that are not pertinent to flowing afterglow reactions, but which are included for completeness' sake, will only be discussed briefly here. Some of the systems needed for experimentation are not included in this schematic because their inclusion would render the figure unnecessarily cluttered. Separate figures (see below) are devoted to those systems.

2-1.1 The Gas Manifolds, Flow Control and Reagent Purification

This subsection describes the systems that control the movement of gases into and out of the flowtube. Also included here is a discussion of gas purification.

Coarse flow of gases into the system is handled by two gas manifolds: one used primarily for helium and the other, primarily for reagent gases. Gas flows are more precisely controlled by a series of valves and flow controllers within a gas manifold. During experimentation, the outflow of gases from the flowtube is controlled by use of a Roots pump. Gases are removed from other parts of the system, and from the flowtube when idle, via a series of diffusion pumps. Gases that are input in high concentrations (He, Ar and H₂) are purified by passage through one or two molecular sieves. These components of gas–flow control — the gas manifolds, inflow and outflow of gases and reagent purification — are discussed separately.

The gas manifolds

The gas manifolds consists of two sections. The first section, the *helium manifold* (Figure 2-1.2), primarily controls the flow of the carrier gas, which, in this study, is exclusively helium. The other section, the *reactant manifold* (Figure 2-1.3), directs



Figure 2-1.2: Schematic of the Helium Manifold.

Legend for Figures 2-1.2 & 2-1.3:



the flow of almost all the other gases. The exceptions are hydrogen and argon. Since they are often input in larger quantities and usually purified in cooled molecular sieves (see Table 2-1.1), they are also controlled from the helium manifold. Helium and hydrogen can also be, and routinely are, directed through the reactant manifold.



Figure 2-1.3: Schematic of the Reactant Manifold gas-inlet systems. Only one inlet system (of four) is illustrated here. Each of the four systems leads from one cylinder to a set of four reactant inlet ports. Volatile liquids are injected into the system by replacing the gas cylinder and regulator with a vial of the liquid: liquid vapor pressures are low enough that a regulator is not necessary. A legend describing the symbols used here is given with Figure 2-1.2 (previous page). The letters i, j, k and l associated with the reactant ports (RP's) refer to any four of the reactant ports RP1-RP6.

Both manifolds are designed (Figures 2-1.2 & 2-1.3) so that each section can be shut off from all the others. This allows for evacuation or modification of each section at any time, but especially during experimentation, with no significant disturbance of flow through other sections. Each system attaches separately to a primary manifold. The primary manifold (labeled "Gas Manifold" in the figures) is roughed by a mechanical pump and then brought to a pressure on the order of 10^{-5} to 10^{-7} Torr by a diffusion pump (see subsection 2-1.9 for more technical information on pumps). Shutoff valves are used wherever gas flow needs only be turned on or off. Mechanical needle valves, alone or in conjunction with more precise instruments (generally a Granville–PhillipsTM valve), are used where reagent gas throughput needs to be more carefully regulated.

Bulk gas flow control

During experimentation, the bulk throughput of helium is regulated by an MKSTM flow controller. He pressure in the tube is controlled by throttling the Roots pump. For typical experimentation, the helium throughput was 222 Tls^{-1} (16.0 slm, standard liters per minute, as measured on the MKSTM) and the Roots pump was throttled such that the pressure inside the tube was 1.8 Torr. Since the argon needed only be injected in excess, rather than in precise quantities, its input was typically controlled by a needle valve. The valve was opened until the reading on the BaratronTM pressure gauge changed by about 1 mT. In a number of cases H₂ was also added using this method.

Reactant gas flow control

The injection of other reagent gases needed to be controlled much more precisely. To this end, a combination of a Granville–PhillipsTM valve and a mechanical needle valve was used, together with measurements of pressure in a calibrated capillary, to determine reagent gas flow. The pressure into the capillary tube (p_1 or p_{in} , below) was primarily regulated by the Granville–PhillipsTM valve. The pressure drop across the capillary ($p_1 - p_2$ or Δp , below) was primarily controlled by adjusting the mechanical needle valve. Using this combination the throughput appropriate to each experiment was achieved. The range of injection throughputs is about 3×10^{-4} to 2 Tls⁻¹.

The throughput, Q, of a viscous gas can be measured by using a variant of Poiseuille's formula:

$$Q = \frac{(p_1^2 - p_2^2)\pi r^4}{16\ell\eta} = \frac{(p_{in} - \frac{\Delta p}{2})\Delta p \,\pi r^4}{8\ell\eta}$$
 16

where r and ℓ are the radius and length of the tube, η is the viscosity of the gas, p_1 or p_{in} is the pressure into the capillary, p_2 is the pressure out, Δp is pressure difference across the capillary, and π has its usual trigonometric meaning.

This method worked well for most reagent gases, since they were injected at pressures well suited to the Granville–PhillipsTM valves and the pressure measuring devices. The attaching gas (see Section 2-2), however, needed to be injected at pressures near the low end of the usefulness of the valves. At these low pressures, without servo devices installed, the pressure measurements for the gases tended to rise or fall slowly, requiring continual manual adjustment during that phase of experimentation. Also, at such low throughputs, the flow becomes non–viscous, and Poiseuille's equation (above) is no longer valid. Mixtures of low–flow gases with helium can be used to overcome this problem.

Gas purification

For cleaning the gases, traps filled with molecular sieve were used. These *sieve* traps, are constructed of subdivided, stainless steel tubes (see Figure 2-1.4) filled with the appropriate sieve material (see Table 2-1.1). The specifications given in the table refer to the manufacturer's description of the material. The traps, except for the one used to purify argon, are cooled by liquid nitrogen. Since the boiling point for argon is higher than that for nitrogen, its trap was immersed in a methanol bath cooled to around -90° C by the cooling finger of a two stage refrigerator. In all cases, impurity gases, such as O_2 , H_2O , etc., condense onto the cold sieve material, purifying the primary gas.



Figure 2-1.4: Cross–sectional diagram of the sieve trap used to purify the helium used in these studies.

Table 2-1.1				
Reactant Purification				
Gas	Helium	Argon	Hydrogen	Reactant Gases
Purification	Molecular Sieve	Molecular Sieve	Molecular Sieve	Generally Not
Type	5A & 13X	5A & 13X	3A	Purified

Since the pressure of helium in the flowtube is so much larger than that for other gases, it is necessary that the helium be very pure. During experimentation, the number density of helium is several orders of magnitude higher than that of the reacting species. Helium that is 99.95% pure contains impurities at far higher concentrations than that of the reactants. In order to sufficiently purify the helium, it is passed, successively, through two identical, specially designed sieve traps (see Figure 2-1.4). Each trap is designed such that the helium makes four full passes through the sieve material before exiting the trap. Since the reactant gases are used in such relatively small amounts, any impurities they have are generally not significant, and, for this study, they were usually not purified. However, it should be noted that an impurity more reactive than the species of interest, even when present in small concentration, can become significant. In these cases, higher purity reagents are used.



Figure 2-1.5: Schematic of the flowing afterglow arm of the flowtube and RP1, the flowing afterglow's helium inlet port. Both the flowing afterglow arm and RP1 are made of pyrex. The microwave discharge cavity (see Figures 2-1.1, 2-1.7 and 2-1.8) is not illustrated here.

2-1.2 The Flowing Afterglow Arm

The primary point of entry for the helium, and its sole point of entry as a carrier gas, is through the flowing afterglow arm of the flowtube. The flowing afterglow arm is a specially made pyrex tube (Figure 2-1.5). Near the upstream end, helium is let in through a port that attaches to the gas manifold via a glass-to-metal seal. At the downstream end, the flowing afterglow arm splits into two concentric tubes. The inner tube fits into the flowtube, and the outer tube, the vacuum jacket.

Helium can also be introduced through a pyrex reactant port, RP1, situated inside the flowing afterglow arm (see figure). RP1 consists of a bent $\frac{1}{4}''$ pyrex tube that fits into an inlet port just inside the flowtube (Figure 2-1.5). Its purpose is to begin the helium flow in the center of the flowing afterglow arm. With this construction, the helium upstream of the port is hardly flowing, whereas the helium downstream of it is flowing rapidly. Thus, by controlling the position of the microwave cavity (Section 2-1.4) along the length of the FA arm, large variations in the downstream ionization density can be produced. Its glass construction ensures that it does not interfere with the oscillation of the microwaves within the discharge cavity. The inlet for RP1 (see Figure 2-1.5) is situated inside the flowtube to facilitate temperature control if required in an experiment.

2-1.3 Inlet Ports

At the time these experiments were conducted, there were six inlet ports along the length of the flowtube. Reactant ports (RP's) RP1, RP2 and RP3 were used in this study. RP4, RP5, and RP6, were not used in this study, but are presented here for completeness. Schematics of RP2 and RP3, and a representative for RP4-RP6 can be found in Figure 2-1.6. Figure 2-1.7 contains photographs of RP1 and RP3. Approximate positions of the ports are illustrated on Figure 2-1.1. A schematic of RP1 was given in Figure 2-1.5, with accompanying discussion in Section 2-1.2.



Figure 2-1.6: Schematics of the inlet ports: (a) RP2, which is simply an opening in the side of the flowtube; (b) RP3 is a tube 0.065", outer diameter; the curvature directs the gas flow into the center of the flowtube in a direction opposite the helium flow. (c) RP's 4-6 are closed-end tubes 0.060" outer diameter, bent into a partial circle and bored with six 1 mm holes. Note that the ring injection speeds the mixing of reactant gases evenly into the flow. In (b) and (c) a small flow of purified He is often mixed with the reactant gas to speed injection into the flowtube.

Reactant port two (RP2) is merely an opening in the wall of the flowtube (Figure 2-1.6 a). It is used to inject gases that alter the plasma composition necessary for



Figure 2-1.7: Color photographs of RP1 (a) and RP3 (b). (a) The dark object surrounding the flowing afterglow arm (in which RP1 is suspended) is the microwave discharge source. The color of the gas within and surrounding RP1 is due to excitation in the helium as it flows through the μ -wave cavity. (b) The greenish glow surrounding RP3 is due to the combination of helium emissions that are propagated down the flowtube and emissions arising from the addition of argon at RP2. No reagents are being added at RP3 (see Chapters 3 and 4 for photographs of RP3 when a reactant gas is being added).

the reactions occurring downstream at ports RP3-RP6. A simple opening is sufficient because the gases do not need to be mixed rapidly into the bulk flow. In these studies, the only gases injected through RP2 are the attaching gas (see Section 2-2) and argon.

Reactant port three (RP3) consists of a single, thin-walled, 0.065" diameter tube (Figure 2-1.7 b). The tube is bent so that the gas in injected into the flowtube in a direction opposite the flow of the carrier gas (Figure 2-1.6 b). This reverse injection causes the portion of the reaction observed by the spectrometers to be maximized. A perspective equivalent to that of the spectrometer is shown in the photograph in

Figure 2-1.7 b. The profile of the injection plume is either roughly paraboloid or spherical depending on the nature of the interaction between the injected species and the oncoming plasma (see Chapter 5).

Reactant ports four through six (RP4-RP6) are *ring ports*. They are made from a piece of 0.065" diameter tubing that has been bent into a circle and into one side of which several holes have been bored (Figure 2-1.6 c). The gas exits the port through these holes. The holes face upstream so the gas exits contra-flow (like RP3). The purpose of this design is to minimize the time required for the injected gas to mix with the other gas(es) in the flow.

2-1.4 Gas Ionization

Gas ionization in the flowtube is generated in either a microwave discharge cavity situated around the FA arm or in an ionization source appropriate for use with a SIFT (defined shortly). It is not practical (or, so far, desirable) to have ionization produced in both simultaneously. Only the microwave cavity is of interest to this study, and it is discussed in some detail below. SIFT stands for "Selected Ion Flow Tube." A SIFT selects single ion types by mass and injects them into a flow of neutral He carrier gas. Ions from a remote ion source are selected using a quadrupole mass spectrometer. A series of electrical lenses then directs the stream of single–mass ions into the flowtube. The apparatus has been described elsewhere in detail [Adams 1988a].

The microwave discharge cavity was made specifically for this flowtube. It is constructed of two hollow cylindrical brass sections. The two sections (Figure 2-1.8) fit top-into-bottom and are cut so that the two sections fit loosely around the glass flowing afterglow arm. A power supply (OpthosTM) provides a source of intense microwave radiation. Adjustment of a tuning rod and screw (see diagram) tune the cavity for resonance with the microwaves, helping to maximize absorption of the radiation by the flowing helium. The discharge source works by causing electrons to be accelerated



Figure 2-1.8: A three dimensional drawing of the microwave discharge source. The top piece fits into the bottom piece, as shown, and around the flowing afterglow arm.

back and forth within the microwave field generated by the resonant oscillation of the microwave radiation. A spark provided by a tesla coil provides an initial supply of electrons to the cavity to initiate the discharge. A few of these electrons are trapped inside the oscillating microwave field. As they move back and forth, they impact the flowing helium atoms, causing electronic excitation and ionization.

The position of the microwave discharge source along the flowing afterglow arm is adjustable. The position of the cavity affects the ionization density in the tube (see Section 2-1.2). When higher ionization densities are desired, the cavity is slid to its most downstream position (next to the flowtube's vacuum jacket). Higher ionization densities are desirable for recombination studies. But, higher ion densities are also likely to cause damage to the ion detection system. So, whenever mass spectra are being taken, the cavity is positioned (approximately) around the crook in RP1. Consequently, mass spectra are not taken while recombination spectra are being recorded. However, the flow control and pumping systems are stable and the number and type of ions present in the tube is not likely to change during a typical run. On several occasions, this assumption was tested (by taking mass spectra between or after recombination experiments) and was found to be valid.

2-1.5 The Spectrophotometers and Supporting Equipment

The two monochromators used in these experiments cover a wavelength range from $\sim 140 - 800$ nm, with about 200 nm of wavelength overlap for comparison between the two: the vacuum ultraviolet (VUV) spectrometer has an upper limit of around 400 nm due to the range of the photomultiplier tube, and the ultraviolet– visible (UV–VIS) spectrometer's efficiency has a lower limit of about 180 nm due to absorption by the air. Both spectrometers disperse light with diffraction gratings, detect photons using cooled photomultiplier tubes and record numbers of photons using gated photon–counting devices interfaced to computers.

The VUV spectrometer is evacuated via a turbomolecular pump to $\sim 5 \times 10^{-5}$ Torr (a turbomolecular pump is used here instead of a diffusion pump to eliminate the condensation of oil onto the diffraction grating, which would reduce its efficiency).

	Typical Operating Conditions	
Spectrometer	\mathbf{UV} - \mathbf{VIS}	VUV
Slit Width	$0.27 \mathrm{~mm}$	$0.81 \mathrm{~mm}$
PMT Power	1.85 kV	1.85 kV
Scan Rate	1.5 nm/min (180-400 nm) 5.0 nm/min (400-800 nm)	$1.5 \mathrm{~mn/min}$
Count Period	4 sec (180-400 nm) 3 sec (400-800 nm)	$4 \sec$

____ Table 2-1.5.b ____

The diffraction gratings for the two spectrometers are interchangeable. The blaze and number of grooves per millimeter are chosen for efficiency in the desired wavelength ranges. The grooves are blazed to enhance diffraction in the wavelength region and diffraction order of interest. Table 2-1.5.a lists specifications for the two systems, and Table 2-1.5.b summarizes typical operating conditions.

2-1.6 The Vacuum Jacket and Temperature Control

The structure of the flowtube, including the vacuum jacket, is illustrated in Figure 2-1.1. The vacuum jacket is used for thermal insulation during experiments. In these studies, it served mainly to minimize the effects of any leaks that might have existed along the length of the flowtube and to provide a light–proof enclosure for the flowtube. The tube itself can be heated with heating tape or cooled by tubes filled with coolant, thus enabling studies of the temperature dependence of reactions.

2-1.7 Viewports

Viewports are positioned along the flowtube at several locations (see Figure 2-1.1). The ports of interest to this study are those that allow for observation of RP3. In addition to the ports indicated on the figure, there are ports in equivalent positions above and below the flowtube (only ports to either side of the tube are shown in the figure). The photograph in Figure 2-1.7(b) was taken from the viewport directly above RP3. Spectra were taken through the side ports, as is shown in Figure 2-1.1. The material for each viewport window was chosen based on spectral transmission. For example, windows associated with the VUV spectrometer are made of magnesium fluoride (MgF₂), which transmits light down to about 140 nm.

Table 2-1.6					
Mass Spectrometer Specifications					
Mass Range (typical, amu)	Type	Detector	Typical Working Pressure (Torr)		
0 - 200	Quadrupole	Channeltron	$< 1 \times 10^{-4}$		

2-1.8 Ion Mass Analysis and Detection

The detection system is composed of a quadrupole mass filter with a ChanneltronTM channel electron multiplier as detector (see Figure 2-1.1). Signals from the Channeltron are interpreted by a pulse counter which is interfaced to a computer that records and displays the data. See figures Appendix D for sample data output from the mass spectrometer. While the flowtube is idle, a diffusion pump maintains vacuum within the flowtube and the detection chamber. But, during experimentation, the primary flow is directed to a Roots pump. An electronic lens 0.3 mm from the orifice draws ions from the flow into the detection region. Here, the diffusion pump previously used to evacuate both flowtube and detection chamber keeps the detection chamber under sufficient vacuum for operation of the mass spectrometer and ion detector.

2-1.9 Pumping Systems

In all but two cases, the various parts of the system are pumped by diffusion pumps backed by standard mechanical pumps. The two exceptions are the turbo-



Figure 2-1.9: Schematic of pumps and their approximate positions along the apparatus. See the legend for pump types represented by the various symbols. The numbers assigned to the pumps correspond to those in Table 2-1.7. Each pump shown here requires a backing pump, specifications for which are in Table 2-1.7.

molecular pump used for the VUV spectrometer (see section 2-1.5) and a large Roots blower used during experiments to maintain a steady pressure for constant throughput of carrier and reactant gases. Pump positions, sizes, approximate loads, pumping speeds and other information are contained in Figure 2-1.9 and Table 2-1.7

2-1.10 Computer Interface and Supporting Software

Except during initial tests of equipment, all data were collected on-line using computer interfaces (RS232 and IEEE) to the gated photon counter for data analysis and to the mass and optical spectrometers for component control. All software used was written by group members in Quick Basic.

Table 2-1.7					
Pump Number	Section	$\begin{array}{c} Pump\\ Type^a \end{array}$	Model Number ^b	Backing Pump Size (in)	
1	Reactant Manifold	DP	63	5	
2	Helium Manifold	DP	63	5	
3	Sift Chamber	DP	100	8	
4	VUV Spectrophotometer	TMP	STP300	12	
5	Tank	DP	63	5	
6	Flowtube	Roots	17215		
7	Flowtube/Detection	DP	160	18	

^{*a*} DP = Diffusion Pump; TMP = Turbomolecular Pump. ^{*b*} Diffusion pumps and backing pumps manufactured by EdwardsTM; turbomolecular pump manufactured by Seiko Seiki; Roots pump manufactured by Stokes Vacuum.

2-2 Experimental Design

This section outlines the sequence of reactions used to control the chemistry occurring in the flowtube. The reaction scheme is well established, and similar descriptions have appeared elsewhere [Adams 1992]. Discussions of apparent deviations from this chemistry are given in Chapter 4.

The goal of these experiments is to observe and quantify photons emitted as a result of the reactions of small, polyatomic ions with electrons. Such reactions are generally highly exothermic. If only the exothermicity is considered, a variety of products is possible, but, not all possible products are, in fact, observed. Reactions 2 and 3 describe two possible outcomes from a hypothetical recombination.

In order to observe emissions from recombination, especially weak emissions from less–populated states or forbidden transitions, it is necessary to have a relatively large number of recombination reactions occur in a relatively small volume. Arranging this is a difficult task, and the primary challenge in these experiments. Polyatomic ions react with electrons very rapidly (with rate constants on the order of 10^{-6} cm³s⁻¹. [Johnsen 1987]). So, it is necessary to keep the polyatomic ions and the electrons separated until they are in a location such that the results of their reaction can be recorded.

This is achieved by creating a stable, flowing plasma that is not recombining and then injecting a neutral reagent into the the flow in a region convenient to observation. Initially, the flowing plasma contains only free electrons and positive atomic ions[†] within a neutral, helium carrier gas. If an unprotonated recombining ion is desired, the appropriate parent polyatomic gas is injected into the plasma at the point where the plasma flows through a region observed by the spectrometers. The atomic ions charge–transfer rapidly to the polyatomic molecules, and the newly–formed polyatomic ions react with the ambient electrons almost immediately. When a protonated recombining ion is desired, the procedure is similar except that H₂ is also added in great excess. Details of these procedures are discussed below.

With the reactions thus confined mainly to one region of the flow, emissions from recombination can more easily be observed. However, there are other species besides the recombining ions present in the flow, many in excited states. In any spectra taken, emissions from processes associated with these species, as well as emissions from the ion source, may be present, along with emissions due to recombination. In order to differentiate recombination emissions and emissions due to these other processes, two spectra are taken. The first is the spectrum resulting from the sequence of reactions

 $^{^\}dagger$ See Chapter 1 for a discussion of the stability of atomic ions in the presence of electrons.

as described in this section. The second spectrum is taken after a small amount of a gas that rapidly attaches electrons, an *attaching gas*, is added upstream of the reaction region (at RP2, 27.62 cm upstream of RP3). Addition of this gas removes free electrons from the flow, making electron-ion recombination no longer possible. The amount of attaching gas required is not sufficient to significantly affect the ion chemistry in the flow. At the high pressures used (1.8 Torr), diffusion is minimal so effects on this due to the switch from electrons to negative ions will not be significant. Comparisons of the spectra taken before and after the addition of the attaching gas help to differentiate the various classes of emissions. A brief description of these spectral comparisons is in Section 2-2.2, but a more detailed analysis of the technique can be found in Chapter 3. Specific examples can be found in Chapter 4.

2-2.1 Sequence of Reactions Resulting in Controlled Recombination

As was stated earlier, the primary challenge with these experiments is to somehow cause a large number of electrons and positive, polyatomic ions to coexist in the same small region so that their reactions can be observed. The next several paragraphs describe the sequence of reactions used for that purpose in the experiments presented here.

At the very upstream end of the flowtube, neutral helium is injected through RP1^{\dagger} into a region within the microwave discharge source. Inside the self–sustaining discharge source, free electrons (Section 2-1.4) ionize the neutral helium:

$$He + e^{-*} \longrightarrow He^+ + 2e^- \tag{19}$$

Since the pressure of the helium is high (~ 1.8 Torr), the He⁺ undergoes a three– body reaction very rapidly [Ikezoe 1987] to produce He₂⁺.

$$He^+ + 2He \quad - \underbrace{k \sim 6 \times 10^{-32} cm^6 s^{-1}}_{mean} \longrightarrow \quad He_2^+ + He^* \qquad 20$$

^{\dagger} See Figures 2-1.1 and 2-1.5 for locations of the reactant ports (RP's) and for diagrams of the flowtube.

(*) represents translational excitation of the third helium atom, providing the necessary stabilization of the helium dimer ion.

Argon injected into the flow at RP2 then reacts with the helium dimer ion to produce Ar^+ [Ikezoe 1987].

$$He_2^+ + Ar \quad --- \xrightarrow{k \sim 2 \times 10^{-10} cm^3 s^{-1}} \longrightarrow \quad Ar^+ + 2He \qquad \qquad 21$$

The argon will also undergo Penning ionization [Bolden 1970, Schmeltekopf 1970, Lindinger 1974] with any helium metastable species that were created in the discharge:

$$He(2s^{1}S, 2s^{3}S) + Ar \longrightarrow Ar^{+} + He + e^{-*}$$
 22

The * indicates translational excitation in the electron. This creates a condition where the primary reactive constituents of the flow are the Ar⁺ and electrons. Gas-phase reaction between a positive atomic ion and an electron is extremely slow (see Chapter 1), so this plasma is quite stable.

While the He₂⁺ is also quite stable and could be used as the charge carrier for the system, Ar has a much lower ionization energy (15.76 rather than 22.23 eV for He₂) [Radzig 1985 for all ionization energies this paragraph]. At 22.23 eV, the dihelium ion would transfer enough energy to not only ionize the polyatomic molecule, but also to fragment it. Most of the polyatomics of interest to these studies have ionization energies around 9-13 eV. Charge transfer from argon is far less destructive. Use of a heavier noble gas, such as krypton (IE = 14.00 eV) or xenon (12.13 eV) would cause even less excitation in the newly ionized polyatomic. This is a possible variation to try in future studies.

In cases where a protonated recombining ion is desired, hydrogen is injected at RP3. The following series of reactions occurs [Ikezoe 1987], resulting in the production of H_3^+ , which will readily proton transfer to most neutral atoms and molecules:

$$Ar^{+} + H_2 \xrightarrow{k \sim 7 \times 10^{-10} cm^3 s^{-1}} ArH^{+} + H \qquad 23$$

Helium Throughput 16.0 slm	Argon Pressure	$\sim 1 mTorr$
Hydrogen Throughput . $\sim 14~\mathrm{mTorr}$	Flowtube Pressure	1.8 Torr
XYZ Throughput $\sim 15 \frac{\text{mTorr} \cdot L}{s}$	Ionic Species Velocity	$4500~{\rm cm/s}$
Attaching Gas Throughput $\sim 0.4 \frac{\text{mTorr} \cdot L}{s}$	Neutral Species Velocity	$3000~{\rm cm/s}$

$$ArH^+ + H_2 \longrightarrow k \sim 2 \times 10^{-9} cm^3 s^{-1} \longrightarrow H_3^+ + Ar$$
 24

A small amount of H_2^+ is also produced by Reaction 8, but that also reacts with H_2 to produce H_3^+ [Ikezoe 1987].

Either alone or while the hydrogen is being added, a neutral molecule, XYZ, is injected (also at RP3). In cases where hydrogen has been added, both of the following reactions occur, with the second reaction dominating. In cases where hydrogen is not added, only the first reaction occurs [both reactions and coefficients: Ikezoe 1987].

$$Ar^{+} + XYZ \longrightarrow k \sim (5 \times 10^{-10}) cm^{3} s^{-1} \longrightarrow XYZ^{+} + Ar$$
 25

$$H_3^+ + XYZ \longrightarrow k \sim (1 \times 10^{-9}) cm^3 s^{-1} \to XYZH^+ + H_2$$
 26

The newly created ion then recombines readily with the ambient electrons. A few possible outcomes of a generic recombination are given in Reactions 2 and 3. Although one might initially consider it to be possible, the following reaction is highly inefficient:

$$XYZ^+ + e^- \longrightarrow XYZ + h\nu$$
 27

The reasons for this are discussed in Chapter 1.

2-2.2 Distinguishing Emissions Due to Recombination from Other Emissions

In order to distinguish radiations due to e-i recombination from radiations due to other side processes, as mentioned above, a small amount of a gas that rapidly attaches electrons is added at RP2. Often, as illustrated below, the attaching gas (ABC) will dissociate in some manner upon attaching an electron.

$$ABC + e^- \to AB^- + C \tag{28}$$

$$\rightarrow AB + C^{-}$$
 29

Regardless of the attachment process, the addition of the gas removes electrons from the flow, thus preventing electron–ion recombination.

Attaching gases are chosen for the speed with which they attach electrons and for the small energy changes associated with that attachment. It is also necessary that the attaching gas and the products of its attachment to an electron be unreactive with other species in the flow. Only very small amounts of the attaching gas are required, so the side-reactions are minimized. The three attaching gases used in this study are SF_6 , CH_3I and CCl_4 which yield SF_6^- (with some SF_5^-)m I⁻ and CL^- , respectively.

Spectra are taken before and after the addition of this attaching gas. A spectrum taken without an attaching gas present is referred to an *origin* spectrum (since this spectrum is the one to which others are compared), and the other is called a *back-ground* spectrum. The two spectra are compared by ratio and by difference. As is implied by the names, a difference plot is make by plotting the difference between the origin and background spectra, and the ratio plot, by plotting their ratio. Each type of comparison has advantages and disadvantages. They are discussed in detail in Chapter 3 and examples are presented in Chapter 4.

CHAPTER 3 METHODS OF DATA ANALYSIS

Methods of data analysis are presented. The order of presentation follows the order in which the methods were typically applied to the data.

3-1 Correction of Data for Optical System Transmission Efficiency

In order to properly compare the intensity of emissions in different spectral regions, a mathematical description of the transmission efficiency of the optical path from photoemission through detection was constructed. This efficiency takes account of all devices in the optical train: windows, mirrors, gratings, lenses, photomultiplier tubes and, where appropriate, air. The efficiencies of individual optical components were from factory issued response curves and taken at intervals of 20 nm. The absorption due to air was taken from a geophysical reference and made little difference to the final efficiency. The transmission efficiencies of the individual components, expressed as a fraction of one, were multiplied together at each wavelength to give the overall system efficiency.

The entire collection of data points versus wavelength was not well described by a polynomial; so, the spectral range was broken into smaller segments. Each of these segments was fit to a polynomial of order between 2 and 10 (see Appendix E for the exact form of the polynomials). Photon counts were then corrected for transmission efficiency by dividing the observed numbers of counts by the value of the polynomial at each wavelength. In many cases, the thermal background noise



Figure 3-1.1: Optical transmission efficiencies for the UV-VIS (upper graph) and VUV (lower graph) spectrometry systems.

from the photomultiplier tube (PMT) became significant. Whenever this occurred, it was necessary to subtract out as much of the noise as possible prior to correction.

The transmission efficiency could not properly be corrected between 400-415 nm because of the addition of a cut-off filter for which the efficiency is unreliable in that region. The filter is inserted into the optical train when taking spectra above 400 nm to block second order dispersions from the grating.

In all, this method of correcting the spectra for transmission efficiency has performed well. The simulation of the argon emissions in the base plasma (see Section 4-2) indicates a shift in the true efficiency that is not accounted for by the transmission efficiency polynomials. The shift occurs at about 440 nm. Efficiencies from that point down to about 415 nm appear to underestimate the corrected number of photon counts by about a factor of two. Efficiencies within that region appear to be correct relative to each other, and efficiencies above that region also appear to be correct relative to each other (within 5-10% in both cases). The cause of this discrepancy is yet unknown, but could be related to the cut-off filter. This finding does not impact the data presented here; there are no emissions in this region that are significant to the results. No systems have been found that have allowed such rigorous testing of the UV-VIS efficiency below 400 nm or in the VUV. But, there have been many opportunities for comparisons of the relative intensities of a series of vibrational transitions from a single upper vibrational level, and no significant discrepancies have been found.

3-2 Identification of Photoemissions

The identification of photoemissions in the data is not a straightforward procedure. For diatomic molecules, the task has become fairly automated. For atomic species, because of the great number of possibilities, the process is more tedious, but is possible to make identifications and the results are reliable. For polyatomics, unless a published spectrum is available, identification is difficult. A list of transition wavelengths can also be useful, but precise relative intensities and other information related to band structure are often not included.

Intense or well–resolved atomic species can generally be identified by simple comparison of observed wavelengths to those tabulated in the literature. There are usually a number of intense emissions from the same atom within range of our spectrometers that can be used to confirm identification. If a single upper atomic state decays to a series of lower states, as is the case with the Ar emissions described in Section 4-2, or if a number of intense emissions from a given atom are present at proper relative intensities, identification is certain. Collections of atomic line positions, often with transition probabilities, can be found in a number of locations [for example: Bashkin 1975, NIST 2001b, Radzig 1985].

The identification of diatomic emissions was made reliable by a program for calculating Franck–Condon factors [Ervin 1993]. The program depends on a Morse potential for its calculations. While a Morse potential is not a perfect model for diatomic motion, it is very close and greatly facilitates identification. A program that automates input and output for Ervin's program was also developed. Collectively, the process is called "CASI," an acronym for computer assisted spectral identification. CASI provides a graphical representation of the spectrum to expect from vibrational transitions between two electronic states in a diatomic molecule. The graph consists of a series of vertical lines at expected transition wavelengths. Each line's height is scaled to the intensity expected for that vibronic transition. Across the top of the graph, the vibrational quantum numbers for each transition are indicated. A sample graph from the most recent manifestation of CASI is presented in Figure 3-2.1a. The graph simulates transition wavelengths and intensities for the first five vibrational levels of the CO $a^3 \Pi_r \rightarrow X^1 \Sigma_g^+$ transition. For comparison, an observed CO $a \rightarrow X$

Figure captions for Figures 3-2.1 a and b

Figure 3-2.1a: Simulation of vibronic transition positions and intensities as output from the graphical portion of the set of computer programs called CASI (see text). The simulation presented here is of the CO $a \rightarrow X$ emission spectrum expected from the lowest five vibrational levels of the a state. All upper-state vibrational levels are assigned equal populations.

The vertical lines in the lower portion of the graph correspond to the band origin positions for each $v \rightarrow v$ transition included in the simulation. The intensities of the lines are "pseudo-Einstein A coefficients," P_T (see *Relative vibrational populations* in Section 3-3).

Symbols in the upper portion of the graph identify the upper and lower vibrational quantum numbers corresponding to the line directly beneath. Since vibrational transitions are often clustered, the symbols in the upper graph are color-coded to the vertical lines in the lower graph. The result is not visually appealing, but is easier to read than a monochromatic system. Closed symbols and crossed \times 's correspond to the vibrational quantum number in the upper electronic state; open symbols and uncrossed \times 's, similarly, to the lower state. The value of the vibrational quantum number is read from the axis at the right of the graph.

Figure 3-2.1b: An experimental spectrum taken of the plasma containing recombining CO_2^+ ions for comparison with the graphical output from CASI (Figure 3-2.1a). Identifications are omitted to illustrate the usefulness of spectral simulation in identification. For this spectrum with identifications, see Chapters 4 and 5.








- Figure 3-2.1b -

spectrum in the same region is given in part b of the same figure. The usefulness of the program is self-evident. Note that the program does not assign relative populations to the vibrational states, so it does not automatically reproduce all of the intensities in the observed spectrum.

While some spectroscopic constants exist for polyatomic molecules, only the fundamental frequencies are generally reported. Anharmonicities must be inferred, and software for generating Franck–Condon factors for polyatomics is not available. So, unless rotational resolution is available (which is not always the case), identification of polyatomic emissions must proceed via less well defined methods. Typically, published spectra at similar resolution are consulted. Because each spectrum has individual characteristics, identification is quite certain. But, if a published spectrum is not available, identifications are made by estimates based on energetic considerations. Even when the published spectrum is available, care must be taken. Emissions from different species can have similar appearance. For a diatomic example of this, see the discussion on the recombination of H_3S^+ (Section 4-1.8).

In all of the cases, energetics and predictions based on species known to be present in the flow can only be considered guiding principles. On many occasions, a species thought too energetic or otherwise unlikely to be present in the flow has been identified. Two obvious examples are the identifications of the excited states of Ar^+ and He₂. Hints for the presence of He₂ came from a tabulated list of species and corresponding wavelengths [Pearse 1976], but the identification of Ar^+ excited states as a possible emission source came only from extensive and thorough analysis.

3-3 Assignment of Vibrational Populations and Rotational Temperatures

Given the tools and the information available, it has been possible to assign relative populations for atomic and diatomic species for which there are reliable, tabulated spectroscopic constants. Little is generally known about the spectra of polyatomics; so, many of them could not be treated in detail. This is of little importance here since the photoproducts of dissociative recombination that are identified, either tentatively or with certainty, all result from transitions in diatomic or atomic species. Assignment of the relative populations of electronic states (whether atomic, diatomic or polyatomic) is discussed at the start of Chapter 5, where such discussion is more convenient.

Relative vibrational populations

Within any electronic state of a diatomic molecule, there exists a number of vibrational and rotational states. The relative populations of vibrational states can be determined by comparing intensities of their transitions to transition probabilities. For $v \rightarrow v$ transitions between two electronic states in a molecule, the probability, P_T , that a transition will occur is proportional to the square of the Franck–Condon factor, $F_{i,j}$ multiplied by the cube of the transition energy, ν :

$$P_T \propto \nu^3 F_{i,j}^2 \tag{30}$$

where *i* and *j* represent the vibrational quantum numbers for the upper and lower electronic states, respectively. ν is typically expressed as a transition frequency in wavenumbers. For calorimetric detection methods, the observed intensity, which is not the same as the transition probability, depends on ν^4 . These experiments employ photon counting rather than calorimetric detection, so the cubed factor is appropriate. The term used for P_T is "pseudo–Einstein A coefficient" because it contains all transition probability information that is not constant for transitions between different vibrational levels in two electronic states.

The relative population for a series of vibrational states, v, within the same electronic state can be determined by dividing the observed emission intensity, I_{obs} by the appropriate P_T :

Relative Vibrational Population =
$$I_{obs,v}/P_{T,v}$$
 31

Populations determined in this manner are only as good as the Franck–Condon factors (FCF's) used to calculate them. In general, as is expected, FCF's based on a Morse potential fit observed data better near the bottom of the potential well, e. g., for low vibrational quantum numbers, but become progressively less accurate for higher vibrational excitation. Despite this restriction, the relative vibrational populations presented in Chapter 4 are reliable. Rotational characteristics are usually similar for different vibrational levels in the same electronic state; so, changing the rotational temperature has little effect on calculated relative vibrational populations. The time the species spends in viewing range of the spectrometer does not introduce uncertainty either (see Chapter 5) since all the vibrational levels are decaying from a single upper electronic state.

Rotational temperatures

Rotational temperatures were determined by fitting results from the program RVESIM (rotational vibrational electronic simulation, see Chapter 6) to the observed rotational emission manifold. RVESIM, at this time, treats only Hund's Cases a and b and does not treat transitions between the two cases. The rules for transition frequencies and intensities are taken from Herzberg [1989]. For the results presented here, all rotational populations were assumed to be thermal. This is a reasonable assumption since the frequent collisions with He $(10^7 s^{-1})$ are efficient at rotational relaxation. For two of the emitting species, NH and OH, the rotational distribution might not be thermal; see Chapters 4 and 6 for further details. Again, the assigned rotational temperatures can only be as good as the spectroscopic constants used to determine them. In nearly all cases, spectroscopic constants were taken from NIST [2001a]. Where necessary, supplemental values were obtained from another source [Radzig 1985].



Figure 3-3.1a: Illustration of the effect of assumed rotational temperatures on electronic state populations determined by fitting RVESIM simulations to the rotational transition manifold. Solid, red lines are results from the simulation. Green, dashed lines are experimental data (CO_2^+ recombination) except for the "atomic" peak, which has been included for illustration. Each diatomic peak is a single vibronic transition of CO $a \rightarrow X$. The width of each diatomic peak is due to the rotational temperature and spectral resolution of the photon detection system. The width of the atomic peak is due only to spectral resolution. (a) A rotational temperature of 200 K is too low to reproduce the molecular features, but the maximum intensities of the features are correct. (b) When the temperature is taken as 400 K, the peak shapes mimic experimental data better, but the maxima of the molecular features change relative to the atomic peak.



Figure 3-3.1b: Illustration of the effect of assumed rotational temperatures on rotational transition intensities. Each vertical line is a rotational transition within the simulation of the peak near 228 nm in the graphs in Figure 3-3.1a. P, Q and R branches are indicated on each graph. (a) When a temperature of 200 K is assumed, fewer upper-state rotational levels are significantly populated, and the simulated peak is narrower and taller. (b) When 400 K is the assumed temperature, a greater number of upper-state rotational levels have significant populations, resulting in a less intense peak maximum.

It is important to note that the assigned rotational temperature will affect the reported relative electronic population. This is illustrated in Figure 3-3.1. When the temperature of a species is increased, the number of rotational sub-states within each vibronic state is increased. The number of total species in the electronic state must be divided among the number of sub-states populated. In order for a feature to retain a constant relative intensity when the temperature is increased, the occupation of the electronic state must be increased. For this reason, it is important to note the temperature at which relative electronic populations were determined. If the relative temperature determined for a state is taken to be too high a value, the relative population of the electronic state will have been overestimated, too. The intensity change between Figure 3-1.1a (a) and (b) might not appear to be significant on the graph, but the CO a state population relative to that of the "atomic" line must be increased by about 25% to make the maxima match again in (b).

3-4 Plots of Spectral Differences and Ratios

The addition of an electron attaching gas is expected to decrease the intensity of emissions from electron-dependent processes more than other processes. In practice, the situation isn't so straightforward. Such practical issues are presented in detail in Chapter 4 and will be mostly discussed there. Spectra taken without (origin) and with (background) an attaching gas added are compared by taking their difference and ratio. A schematic illustration of such comparisons is presented in Figure 3-4.1. Both the ratio and the difference plot have their usefulness and their limitations. Neither is, by itself, an infallible method for determining which emissions are photoproducts of dissociative recombination (DR).

The advantage to a difference plot is that it retains the original appearance of the emission. For this reason, the difference plot is often invaluable for identifying and quantifying emissions, as it can be used to subtract out emissions from other



Figure 3-4.1: Schematic illustration of ratio and difference plots when applied to emissions arising from different sources. e-i: electron-ion recombination; n-n: neutral-neutral reactions; i-n: ion-neutral reactions.

processes. There are two difficulties with the difference plot. The first is that if there are emissions resulting from DR that are of low intensity, they can be easily missed in a difference plot. One of the original reasons for creating a ratio plot was to address this issue (see later). The other problem is that some emissions do not behave as expected and will be quenched even though they cannot be products of recombination. An example of this is illustrated schematically in Figure 3-4.1; see the emissions categorized as arising from a neutral-neutral reaction ("n-n"). The emission in the origin spectrum is so intense that, although much of it was quenched, it remains a prominent feature in the difference plot. Other examples are given in Chapter 4.

Ratio plots are useful for detecting DR photoproducts at low intensity. In the ideal case, the ratio for a set of emissions resulting from the same process is the same regardless of the initial intensity of the peak (see Figure 3-4.1). In reality, the presence of system noise and the limit on the number of counts to integers complicates the use of the ratio plot at low signal levels.

The ratio, r, at each point includes the native origin counts, o, the native background counts, b, and the average level of noise $n \pm \delta n$:

$$r = \frac{o + n \pm \delta n}{b + n \pm \delta n} \tag{32}$$

The desired ratio is a "true ratio," R which does not include noise:

$$R = o/b \tag{33}$$

If o and b are both large compared to $n \pm \delta n$, then $r \approx R$. But the emissions for which the ratio plot is most useful are those that are at low intensities, where o and b are not likely to be large. In the case that they are both small relative to $n \pm \delta n$, then for all points $r \approx 1$. In the case that o and b are both very small, the best solution, of course, is to increase the count period, thereby increasing the signal to noise ratio.

In order to make the ratio plot the most useful in the cases where it is most needed, the effects of noise in the system must be addressed. One way to address noise in the system is to attempt to subtract it out. A number of counts, c is subtracted from both the origin and the background spectra prior to taking the ratio. c must be chosen so that it is the maximum value possible subject to the requirement that $c < n - \delta n$. This is generally effective. If o and b are on the order of δn , then they



Figure 3-4.2: Comparison of three methods for generating ratio plots (top graph) to the origin spectrum (bottom graph) from the data used to generate them. The ratio methods (see text) are: *upper line:* simple ratio; *middle line:* ratio using subtraction of noise; *lower line:* adjusted relative difference. The top two lines are offset and the adjusted relative difference is multiplied by a factor of five for clarity. In the lower graph, the emissions from 200 to about 280 are CO $a \to X$ emissions and the double peak near 290 is the $CO_2^+ \tilde{B} \to \tilde{X}$ emission.

will probably never be detected in the first place. In most cases, they will be more easily detected using this subtraction method.

An alternate method for addressing system noise was suggested by Brian Decker [1993]. He calls this method an "adjusted relative difference," the symbol $d_{a,r}$ will be used here. It is a hybrid of ratio and difference plots:

$$d_{a,r} = \frac{o - -b}{\frac{1}{2}(o+b) + n}$$
 34

It does a far better job at producing rectangular peak shapes than do the plain ratio or the ratio with noise subtracted. But, it is not quite as good as the subtracted method for low initial intensities. A comparison of the three methods can be found in Figure 3-4.2.

3-5 Color Photographs

Color photographs were taken of the reactive flow near RP3 under a variety of conditions in order to examine the mixing of the reactant gas with the oncoming plasma. Measurements were taken from features in the photos. Details are provided in Chapter 5.

3-6 Assessment of Vibrational Relaxation in Recombining Ions

Whenever possible, it is desirable to ensure that the recombining ion is in a vibrationally relaxed state, or, at least, in a known state of vibrational excitation; this is desirable because vibrational excitation complicates analysis, making detailed understanding of the recombination mechanism more difficult. The methods by which the extent of collisional relaxation in the recombining ions was assessed are presented in this section (information regarding collisional relaxation comes from the text by J. D. Lambert [1977]).

Modes of Collisional Relaxation and Their Efficiencies

Collisional vibrational relaxation of molecular species can proceed via three transfer mechanisms: vibration \rightarrow vibration, vibration \rightarrow rotation and vibration \rightarrow translation. In all cases, transfer is most likely to occur if the amount of energy, ΔE_T , that must be put into translation is small. The probability, P of such a transfer is usually proportional to an exponential in ΔE_T :

J

$$P \propto e^{-\Delta E_T}$$
 35

Resonant vibrational relaxation is very fast. For instance, CO_2 will relax itself in fewer than 10 collisions, but N₂O takes about 50 collisions to relax CO_2 (from its lowest asymmetrical stretch mode). Infrared-active modes relax more efficiently than infrared-inactive modes. A vibrational energy difference (between modes on different molecules) of ≤ 50 cm⁻¹ is considered resonant. For differences over 200 cm⁻¹, relaxation is effectively vibrational-translational.

For non-resonant (vibrational-translational) relaxation, an empirical relationship [Lambert 1977] is available. It estimates the number of collisions, Z, required to relax a molecule as:

$$Z = e^{C\nu_{min}}$$
 36

where ν_{min} is the frequency of the lowest energy vibrational mode expressed in cm⁻¹, and *C* is a constant. For atoms containing one or more hydrogen atoms, C = 0.0083. For other molecules, the number is 0.017. The equation is intended for vibrational relaxation from v=1 to v=0 in a pure sample of the gas and was developed for neutral species. But, even with those limitations, its use should provide a rough estimate, which is sufficient for our purposes.

A similar set of rules is not available for vibration–rotation transfer; therefore, only pseudo–quantitative statements can be made. As was stated earlier, the greater the energy that must be transferred to translation, the lower the probability for

transfer. Since vibrational quanta are generally much larger than rotational quanta, this means transfer favors large changes in $J(\Delta J)$ or large values for B (the rotation constant). This effect is countered by the requirement that angular momentum be conserved. So, for small molecules, like N₂ and O₂, the most probable transitions are $\Delta J = \pm 0, 2$ with $\Delta J = \pm 4$ being three orders of magnitude less probable [Lambert 1977, p. 51]. Larger (more massive) molecules are more likely to undergo large changes in J. For I₂ [Lambert 1977], the optimum ΔJ is $\pm 6-8$ with a maximum around $\Delta J = 14$. None of the molecules in this study are as massive as I₂, the closest being CS_2^+ (76 amu), which has about 30% the mass of I₂. So, small changes in J should be favored. The rigid-rotor value for the rotational constant of CS_2 is about 0.1 cm^{-1} , and the lowest vibrational frequency for CS_2^+ is around 300 cm⁻¹. Since the CS_2 will, presumably, be acquiring energy from vibration in CS_2^+ , it makes sense to consider positive values for ΔJ . Assuming the large value given for ΔJ for I₂ $(\Delta J = +14)$, the starting value of J (in the CS₂) would need to be 32. For smaller ΔJ values, the starting J is a larger number; for example, 215 for $\Delta J = +6$. The Boltzmann probability at 300 K for a J value of 215 is about 2×10^{-10} . For the lower value of J the Boltzmann probability is about 0.6, but this value of J will relax far less efficiently. The point is that vibration–rotation transfer will be more efficient than pure vibration-translation transfer, but it is still unlikely to be significantly efficient. Given that, and the lack of a convenient formula for comparison, the empirical formula given in Equation 7 will be used in cases where vibrational resonance is absent.

3-7 Rate Comparisons for Several Relevant Processes

A number of comparisons are made between the rates at which certain processes occur in the plasma. In all cases, the comparison is between two different processes that a single species might undergo. For example, it is useful to estimate the number of collisions that a molecular ion will undergo (with atomic or molecular species) before it recombines. This estimation allows one to judge the likelihood of vibrational relaxation prior to recombination. The methods used to make this, and other, comparisons are described below; the results of these comparisons are in Table 4-1.7.

For all parent ions, a comparison, $f_{\nu,XYZ}$, is made between its recombination rate, $Rate_{XYZ^+,e^-}$, and the collision rate, $Z_{XYZ^+,XYZ}$, of the ion with its neutral parent, XYZ. A similar comparison, $f_{\nu,He}$, is made between the recombination rate and the collision rate, $Z_{XYZ^+,He}$, of the ion and the bulk neutral helium. The subscript ν is used to indicate that the reason for this comparison is vibrational relaxation of the recombining ion.

For these comparisons, the collision density for a mixture of ideal gases will be used. The collision density, $Z_{A,C}$, between two non-reactive, neutral species A and C is given by [physical chemistry texts, for example, Atkins 1998]:

$$Z_{A,C} = [A][C]\sigma \left(\frac{8k_BT}{\pi\mu}\right)^{1/2}$$
37

where σ is the hard–sphere collisional cross section, μ is the reduced mass and all other symbols have their usual meanings. A binary rate law for the reaction of A with some other reagent B is:

$$Rate_{A,B} = k[A][B]$$

$$38$$

where k is the rate constant. The rate at which A collides with C can be compared to the rate at which A reacts with B, even if the concentration of A is unknown, by taking the ratio of $Z_{A,C}$ and $Rate_{A,B}$, i. e.:

$$f_{\nu,XYZ} = \frac{Z_{XYZ^+,XYZ}}{Rate_{XYZ^+,e^-}}$$

$$39$$

$$f_{\nu,He} = \frac{Z_{XYZ^+,He}}{Rate_{XYZ^+,e^-}}$$

$$40$$

For protonated parent ions, two other comparisons, f_{R,Ar^+} and f_{R,XYZ^+} , are also made. f_{R,Ar^+} is the ratio of the rate at which Ar⁺ will react with H₂ compared to the rate at which Ar^+ will react with the unprotonated neutral parent. f_{R,XYZ^+} is the ratio of the rate at which XYZ^+ will react with H₂ compared to the rate at which it will recombine.

$$f_{R,Ar^{+}} = \frac{Rate_{Ar^{+},H_{2}}}{Rate_{Ar^{+},XYZ}} \qquad f_{R,XYZ^{+}} = \frac{Rate_{XYZ^{+},H_{2}}}{Rate_{XYZ^{+},e^{-}}}$$

$$41$$

In all cases, an electron density of 1×10^{10} cm⁻³ is assumed. Where a recombination coefficient is not known, 1×10^{-6} cm³s⁻¹ is assumed if the molecule is triatomic or larger. 2×10^{-7} cm³s⁻¹ is assumed for diatomics. Atomic ions not treated in this manner. The rate constant for all reactions between H₂ and XYZ⁺ is assumed to be 1×10^{-9} cm³s⁻¹. Other ion-neutral rate constants that are not known are also assigned a value of 1×10^{-9} cm³x⁻¹. The temperature is assigned a value of 300 K.

CHAPTER 4 DATA ANALYSIS AND RESULTS

In this chapter, the results from a number of experiments will be presented. In the first two sections, results pertinent to the main goal of these studies — the observation and characterization of photoemissions from dissociative recombination — are given. In the last section, experimental findings that were not the original focus of the experiments are included. Relevant portions of the spectra from which conclusions were made are included with the discussion of each set of experimental results.

4-1 Spectral Responses to the Addition of an Attaching Gas

In the ideal case, the addition of a small quantity of attaching gas will remove electrons from the flow, thereby quenching emissions that result from recombination, but not others. This assumption appears to be mostly accurate, but results from the experiments presented in this section and in Section 4-3 indicate that the situation is a bit more complex.

Spectra were taken at a single flow of CO_2 (through RP3^{\dagger}) and a series of flows of the attaching gas CCl_4 (upstream, through RP2^{\dagger}). The spectra, taken at a resolution of about 0.5 nm (full width at half maximum, FWHM), include examples of features that can and cannot arise from recombination of ground–state CO_2^+ ions. Samples of these spectra are presented in Figures 4-1.1 and 4-1.2. Both figures compare the

 $[\]overline{\dagger}$ "RP" refers to "reactant port." See Section 2-1.

Figures 4-1.1 and 4-1.2

Figures 4-1.1 and 4-1.2: Plots of spectral peak intensities in a plasma containing recombining CO_2^+ ions at a series of CCl_4 flows (CCl_4 added at RP2).

Each graph contains a series of lines, each corresponding to a different throughput of CCl_4 . Since the intensities of the lines change as a function of wavelength, line styles (solid, dash, etc.) differ to help guide the eye (they do not have additional meanings). Line that have, overall, greater intensity correspond to larger throughputs of CCl_4 . CCl_4 throughputs range from 0 to 0.001 Torr*L/s.

Photon counts are not corrected for optical system transmission efficiency. The resolution in these spectra is about 0.5 nm, FWHM.



Figure 4-1.1: (a) Emissions from CO are possible products of recombination. (b) Emissions from CO_2^+ are not likely to be products of recombination. The CO_2^+ emissions in the spectra are believed to be due to reactions of CO_2 with He metastable atoms (see text). See also the caption on the previous page.



Figure 4-1.2: (a) Emissions from CO are possible products of recombination. (b) Emissions from CO^+ are not likely to be products of recombination. The CO^+ emissions in the spectra are believed to be due to reactions of CO_2 with He⁺ atoms or He₂⁺ molecules in vibrationally excited states (see text). The production mechanism for the Ar emissions is uncertain (see Section 4-3). See also the caption preceding Figure 4-1.1.

behavior of a set of emissions thought to result from recombination (top graph) to a set of emissions that are not expected to depend on electron density (bottom graph). Note that all features in all four spectra respond to the addition of the attaching gas. There is a difference between their behaviors, though: the intensities of the emissions in the lower graphs decrease more regularly (as graphed here) than the emissions in the upper graphs.

To examine these different responses, emission intensities at selected wavelengths from the spectra in Figures 4-1.1 and 4-1.2 are plotted as a function of CCl₄ throughput on ln–linear (Figure 4-1.3) and on linear–linear scales (Figure 4-1.4). Figures 4-1.5 and 4-1.6 contain similar information, but the data plotted in graph (a) on both figures are not shown in the spectra in Figures 4-1.1 and 4-1.2. Curves superimposed on the data points in all eight graphs were fit by hand. Note the difference between the behavior of emissions that are likely to be products of recombination (CO, Figures 4-1.3 — 4-1.6) and emissions that cannot result from recombination (CO⁺₂, Figures 4-1.3 and 4-1.4; CO⁺, Figures 4-1.5 and 4-1.6). Note especially that the CO emissions decay linearly as a function of attaching gas flow as is expected from previous analysis of reaction kinetics associated with the addition of the attaching gas to the flow [Foley 1993].

If the CO emissions result primarily from dissociative recombination, as is expected, the x-axis intercept corresponds to an electron density of about 1×10^{11} cm⁻³. This figure correlates well with the electron density expected for the region around RP2.

The initial decays of the CO_2^+ and CO^+ emissions in Figures 4-1.4 and 4-1.6 are also linear. A linear decay is expected for any species that is destroyed, either directly or indirectly, by the addition of the attaching gas rapidly enough that the amount left at RP3 is determined stoichiometrically. In graphs of emissions from both ions the initial, linear portion of the decay corresponds to a species that responds to the Figures 4-1.3 — 4-1.6: Comparison of the change in emission intensity for selected emissions as a function of throughput of the attaching gas CCl_4 when an emission is (a) probably due to recombination and (b) probably not due to recombination.

Photon counts have not been corrected for optical system transmission efficiency. Wavelengths chosen (see legends) are the points at which the maximum number of counts were observed for that feature. Throughputs are approximate. To convert the throughput to the number density of the attaching gas once it has fully expanded into the flowtube, multiply the throughput by 2.4×10^{14} .

Numbers in parentheses in the legend for transitions in diatomic molecules (CO and CO⁺) are the vibrational quantum numbers for the upper and lower levels $(v' \rightarrow v'')$ involved in the transition.

Curves superimposed onto data points are fits by hand.

See also the additional information below.

Figures 4-1.3 and 4-1.5: Semilogarithmic plots of spectral emission intensities versus CCl_4 throughput. Data points were taken up to CCl_4 flows much higher than that typically used during experimentation.

Figures 4-1.4 and 4-1.6: Linear plots of spectral emission intensities versus CCl_4 throughput. These graphs are of the same data as in Figures 4-1.3 and 4-1.5, but on linear scales with an abbreviated range of CCl_4 throughputs. Note especially the linear portions of the curves.



See also additional caption on previous page. from the CO ${\cal A}$ Figure 4-1.3: Selected emissions intensities versus CCl_4 flow. (b) are from the $CO_2^+ \tilde{B} \rightarrow \tilde{X}$ transition and are not likely to result from recombination. $\rightarrow X$ transition and are probably due to recombination. Emissions in (a) are Emissions in



from the CO ${\cal A}$ See also additional caption preceding Figure 4-1.3 Figure 4-1.4: Selected emissions intensities versus CCl_4 flow. (b) are from the $\operatorname{CO}_2^+ \widetilde{B} \to \widetilde{X}$ transition and are not likely to result from recombination. \downarrow \boldsymbol{X} transition and are probably due to recombination. Emissions in (a) are Emissions in



See also additional caption preceding Figure 4-1.3 are from the CO^+ the CO aFigure 4-1.5: Selected emissions intensities versus CCl_4 flow. Emissions in (a) are from \downarrow \boldsymbol{X} transition and are probably due to recombination. $A \to X$ transition and are not likely to result from recombination Emissions in (b)



See also additional caption preceding Figure 4-1.3 are from the CO^+ the CO aFigure 4-1.6: Selected emissions intensities versus CCl_4 flow. Emissions in (a) are from \boldsymbol{X} transition and are probably due to recombination. $A \rightarrow$ X transition and are not likely to result from recombination. Emissions in (b)

Process $\Delta E \ (eV)^{\dagger}$		Uncertainty	Reference
$H^+ + e^- \to H$	-13.5985	А	Radzig, 1985
$H_3^+ \to H_2 + H^+$	4.38	< 10%	Radzig, 1985
$He(^1S_0) \to He$	-20.616	В	NIST, 2001
$He(^{3}S_{1}) \to He$	-19.820	В	NIST, 2001
$He^+ + e^- \to He$	-24.5876	А	Radzig, 1985
$He_2^+ + e^- \rightarrow 2He$	-22.22	< 1%	Radzig, 1985
$He_2^+ \to He + He^+$	2.36	< 1%	Radzig, 1985
$HeH^+ \to H^+ + He$	1.845	< 1%	Radzig, 1985
$Ar(4s[3/2]_2^0 {}^3P_2^0) \to Ar$	-11.548	В	NIST, 2001
$Ar(4s'[1/2]_0^0 {}^3P_0^0) \to Ar$	-11.723	В	NIST, 2001
$Ar^+ + e^- \to Ar$	-15.760	А	Radzig, 1985
$Ar^+({}^4P^0, {}^4D^0, {}^2D^0) \to Ar^+$	-19.223 to -19.762	В	NIST, 2001
$ArH^+ \to Ar + H^+$	3.87	< 1%	Radzig, 1985

Energy Changes of Relevant Processes Occurring in the Flow

Table 4-1.1: Energetics for several processes known to be occurring in the reactive mixture in the flowtube. Many of these occur in conjunction with other processes during reactions; for example, $H_3^+ \rightarrow H_2 + H^+$ does not occur alone, but does occur as a half-reaction in a proton transfer from H_3^+ to a parent gas. Energetics refer to the ground states of all relevant species unless otherwise indicated. A: these numbers are certain to ± 2 in the last significant figure. B: the accuracy of these numbers is limited, to ± 1 in the last digit, by the conversion from wavenumbers (using 1 cm⁻¹=8065.5 eV). [†] Negative values of ΔE indicate an exothermic process.

_ Table 4-1.2 _

Energetics for Processes Relevant to Section 4-1.1

$\begin{array}{l} \mathbf{Process} \\ \mathrm{CO}_2^+ + \mathrm{e}^- \end{array}$	Products CO + O	$\begin{array}{c} \Delta E \ (eV)^{\dagger} \\ \text{-8.3} \end{array}$	Accessible States CO: $a^{3}\Pi_{r}(11)$, $a'^{3}\Sigma^{+}(9)$, $d^{3}\Delta_{i}(5)$, $e^{3}\Sigma^{-}(2)$, $A^{1}\Pi(0)$, $I^{1}\Sigma^{-}(1)$, $D^{1}\Delta(0)$	Notes a
	$C + O_2$	-2.4	O ₂ : $a^{1}\Delta_{g}(7), b^{1}\Sigma_{g}^{+}(4)$	b
	$\mathrm{CO^{+} + O^{-}}$	+4.2	—	c
$\mathrm{CO}_2^+(\tilde{\mathrm{A}}) + \mathrm{e}^-$	CO + O	-11.8	CO: See Notes	d, e
	$\mathrm{CO^{+} + O^{-}}$	+0.7	—	c
$\mathrm{CO}_2^+(\tilde{\mathrm{B}}) + \mathrm{e}^-$	CO + O	-12.6	CO: See Notes	d, e
	$\mathrm{CO}^+ + \mathrm{O}^-$	-0.1		f
$\mathrm{CO}_2^+(\tilde{\mathrm{C}}) + \mathrm{e}^-$	CO + O	-13.9	CO: See Notes	d, e
	$\mathrm{CO}^+ + \mathrm{O}^-$	-1.4	_	f
$CO_2 + Ar^+$	$\mathrm{CO}_2^+ + \mathrm{Ar}$	-2.0	_	
	$\rm CO^+ + O + Ar$	+3.7		
	$\rm CO + O^+ + Ar$	+3.3		
$\rm CO_2 + He_2^+$	$\mathrm{CO}_2^+ + 2\mathrm{He}$	-8.4	$\tilde{A}, \tilde{B}, \tilde{C}$	
	$\rm CO^+ + O + 2He$	-2.8	CO^+ : $\mathrm{A}^2\Pi_i(0)$	
	$\rm CO + O^+ + 2He$	-3.2	_	
$\rm CO_2 + He^+$	$\mathrm{CO}_2^+ + 2\mathrm{He}$	-10.8	$\tilde{A}, \tilde{B}, \tilde{C}$	
	$\overline{\mathrm{CO}^{+}}$ + O + He	-5.1	CO ⁺ : $A^2 \Pi_i(14)$	
	$\rm CO + O^+ + Ar$	-5.5	_	
$CO_2 + He2s^1S_0$	$\mathrm{CO}_2^+ + \mathrm{Hel}s^1S_0$	-6.8	$\tilde{A}, \tilde{B}, \tilde{C}$	
	$\overline{\mathrm{CO}^{+}}$ + O + Hels ¹ S ₀	-1.2		
$CO_2 + He2s^3S_1$	$\mathrm{CO}_2^+ + \mathrm{Hel}s^1 S_0$	-6.0	$\tilde{A}, \tilde{B}, \tilde{C}$	
	$\overline{\mathrm{CO}^{+}}$ + O + Hels ¹ S ₀	-0.4		

Table Notes:

- [†] Negative values of ΔE indicate an exothermic processes.
- a Transitions from the D and I states are not observed.
- b None of the accessible products are observed.
- c Resonant ion pair production (RIP) is not energetically accessible.
- d For comparison, the CO X-state bond energy is 11.09 eV and the ionization potential of CO is 14.01 eV.
- $e\,$ All tabulated electronic states of CO [NIST 2001] are accessible, but some are not accessible at all vibrational levels.
- f RIP is energetically accessible.

presence of the attaching gas in a manner similar to electrons, e. g., stoichiometrically, and that is present in about half the concentration of electrons at RP3 (the x-axis intercept corresponds to a number density of $\sim 5 \times 10^{10}$ cm⁻³). The other, less linear portions of the CO₂⁺ curves most probably correspond to production of the emissions via Penning ionization reactions of metastable helium atoms with CO₂. Metastable He atoms, like the He₂⁺, should have mostly reacted with Ar and no longer be present in significant quantities at RP3. He⁺ reacts slowly with Ar [Ikezoe 1987], but it is not expected to be present in great quantities (see below). But, emissions in the plasma (Section 4-3) indicate the presence of the metastables in the flow. Additionally, there are few species whose presence in the flow is plausible (see Table 4-1.1) and that possess sufficient energy to create CO₂⁺ in excited electronic states (see Table 4-1.2).

If the portion of the CO_2^+ emissions that persist after the addition of the attaching gas is due to Penning ionization, it must necessarily involve He species that are not affected by the presence of electrons. The electronically excited states of He, He₂, Ar and Ar⁺ that are observed in spectra from the base plasma (when no reactant gases have been added — see Section 4-3) are all quenched by the addition of an attaching gas. So, none of those species are likely to be the source of the emissions. Since the injected argon is expected to react away any helium metastable species, a mechanism by which the helium metastables could persist is needed. The most likely possibility is that the metastable concentration in the flow exceeds that of the injected Argon. Such a situation would also facilitate the propagation of the observed emissions from He and Ar species.

That the CO⁺ $A \to X$ emissions are present at all is unexpected. There are few species that could be present in the flowtube that are energetic enough to produce those emissions, see Tables 4-1.1 and 4-1.2. In addition to those listed in the tables, atomic helium states at or above $3s^3S_1$ have sufficient energy, as do all electronically excited states of Ar^+ (assuming deexcitation to the ground state of neutral Ar for lower levels of Ar^+).

Kinetic models do not support the presence of He_2^+ , He^+ . Neither do they support the presence of either of the He metastables unless they are initially present in concentrations in excess of 3×10^{13} cm⁻³. Instead, they show that these states should have almost completely reacted away by the time the plasma reaches RP3. Of these, the species with the greatest concentration should be He⁺, but its concentration is expected to be very low. Between RP1 and RP2, the termolecular reaction to form He₂⁺ is the primary loss mechanism for He⁺:

$$He^+ + 2He \xrightarrow{k \sim 1 \times 10^{-31} cm^3/s} He_2^+ + He^*$$

$$42$$

where the asterisk indicates translational excitation in the He. Assuming initial concentrations of 1×10^{11} cm⁻³ for He⁺ and 6×10^{16} cm⁻³ for neutral He at RP1 with no diffusive losses, the concentration of He⁺ at RP2 should be about 1×10^{10} cm⁻³. If reactions with Ar are ignored, the concentration of He⁺ at RP3 should be about 1×10^9 cm⁻³. If diffusive losses are still ignored, the concentration of electrons should be 1×10^{11} , so it is reasonable to expect the He⁺ concentration to be, at most, a tenth of the electron concentration at RP2 and much lower at RP2. The plots in Figures 4-1.3 - 4-1.6, however, indicate a species that is highly energetic and is present at about half the concentration of the electrons. Since the emissions observed in the plasma (see Section 4-3) definitely indicate the presence of excited states of He and He₂ (with evidence of excitation to near the ionization limit of both species), a mechanism is implied by which He⁺ and He⁺₂ are present as well, despite what the kinetic models predict. If the process described in Section 4-3:

$$He(n \ge 3) + He \rightleftharpoons He_2^+ + e \tag{43}$$

is occurring, then the presence of He_2^+ is explained. But, there is no process available for explaining a similar "hidden" population of He^+ .



Figure 4-1.7a: Comparison of typical origin spectra (not corrected for optical system efficiency) for a plasma containing recombining CO_2^+ ions (red, solid line) and a plasma containing recombining HCO_2^+ ions (green, dashed line). Labels of the form $n_1 \rightarrow n_2$ denote the upper and lower vibrational levels, respectively, of the CO^+ $A \rightarrow X$ transition. The key to the alpha-numeric labels is in Appendix B-b. See text for further discussion.



information on labeling. See text for further discussion. have been added to the flow (green, dashed line). See the caption of Figure 4-1.7a for the spectrum obtained when no reagent gases besides He (at RP1) and Ar (at RP2) system efficiency) for a plasma containing recombining CO_2^+ ions (red, solid line) to Figure 4-1.7b: Comparison of a typical origin spectrum (not corrected for optical

There is another reason to doubt that He⁺ is the species involved in the production of the CO⁺ emissions. Only the lowest three vibrational levels of the CO⁺ A state are observed in the spectra (see Figures 4-1.7 for sample emissions). There is sufficient energy to populate the CO⁺ A state to v=14 in the reaction of He⁺ with CO₂; therefore, observation of vibrational states above v=2 would be likely (though not necessary). It should be noted that, by the energetics calculations provided in Table 4-1.2, only the v=0 vibrational level of CO⁺(A) is accessible from the reaction of CO₂ with He⁺₂. But note that there is likely to be vibrational excitation in the He⁺₂, especially if it is formed by reactions of excited helium atoms ($n \ge 3$) and ground state He, as is suggested in Reaction 2.

The production of the CO^+ emissions by reaction of CO_2 with excited states of He, Ar and Ar⁺, whose emissions are observed in the base plasma, can also be discounted. The origin spectra for CO_2^+ and HCO_2^+ are compared in Figure 4-1.7. The wavelength range 470-530 nm was chosen because it contains intense emissions from CO^+ , He, Ar and Ar⁺. The amount of CO_2 added in the HCO_2^+ spectra is about half that added in the CO_2^+ spectra. As is expected, the intensities of the CO^+ emissions in the HCO_2^+ spectra are lower than those in the other. If the CO_2 were reacting with the Ar⁺, the intensities of the Ar⁺ emissions should be lower in the CO_2^+ spectrum. Instead, they are significantly lower in the HCO_2^+ spectrum. Note, also, that the relative intensities of the He and Ar neutral emissions did not change significantly. The conclusions, therefore, are that the H₂ reacts with the excited Ar⁺, but that the CO_2 does not react, or reacts slowly, with any of the excited species (He, Ar and Ar⁺), or, if the reaction occurs, that it does not produce CO^+ in the A state.

Part (b) of Figure 4-1.7 compares emissions from the plasma when only He and Ar have been added to emissions when CO_2 has been added as well. The atomic emission intensities are definitely lower in the spectra where CO_2 has been added. It is certainly possible that the decrease is due to reactions of the excited species in the flow with the injected CO_2 . But, other explanations should be mentioned. One, the flowtube pressure was 1.9 Torr for the plasma-only emissions, higher than the 1.8 Torr when CO_2 was added as well; the additional pressure might favor the production or maintenance of the excited species. Two, the in-flow of argon in the system, under typical conditions is only controlled to one unit of precision, and the change in emission intensity is not greater than that. Three, the injection of the CO_2 at RP3 disturbs the flow of the oncoming plasma and might be causing many emitting species to be diverted out of the main viewing area of the spectrometers.

Based on analysis of the current set of data, then, two conclusions can be drawn. One, it is likely that reactions of CO_2 with vibrationally excited states of He_2^+ produce most or all of the observed CO^+ emissions and part of the observed CO_2^+ emissions. Two, the remaining CO_2^+ emissions are produced by reaction of CO_2 with metastable states of He. These conclusions should be tested. The electron density as a function of attaching gas could be measured with a Langmuir probe. If the electron density is affected less than is expected by the addition of the attaching gas, then a buffering reaction such as the one given in Reaction 4 might be occurring. Similarly, given a robust ion-mass detection system, the concentration of He_2^+ ions, if there are any at all, could be measured as a function of attaching gas flow. To test for a large population of He metastables, the presence of CO_2^+ emissions could be monitored as a function of Ar flow, preferably while a suitable amount of attaching gas is also being added (to quench the electron-dependent emissions). If the additional Ar quenches the emissions, then there are probably many more metastable species in the flow than are expected.

If such a buffering reaction is, indeed, an important mechanism, then it is necessary to explain why the attaching gas affects the He_2^+ as well. The mechanism is fairly simple. First, the attaching gas, AG, reacts with electrons:

$$AG + e^{-} \xrightarrow{k \sim 3 \times 10^{-7} cm^3/s} A + G^{-}$$

$$44$$

Here, the exact nature of the products should not be taken literally: the attachment might not be dissociative. Rather, the point is that some negative ion, G^- has been formed which will then react rapidly with He_2^+ via mutual neutralization:

$$G^{-} + He_2^{+} \xrightarrow{k \sim 5 \times 10^{-8} cm^3/s} G + 2He$$

$$45$$

While the negative ion can also react with Ar^+ , it is expected to do so more slowly unless G^- is polyatomic ion. If G^- is atomic (as it is in the attachment of CCl_4 and CH_3I), then the reaction with Ar^+ will be slower, due to the increased number of available channels in the diatomic He_2^+ , unless there is an accidental resonance. In the event that G^- is also polyatomic, there will be many accessible channels for reactions with both He_2^+ and Ar^+ , with more expected for He_2^+ . In all of these cases, of course, the presence of favorable energetics, e. g., curve–crossings, will increase the reactivity of G^- with Ar^+ .

Ratio and Difference Plots

Recall from Section 3-4 that a common method for determining the presence of emissions resulting from recombination is to take spectra without and with the presence of an attaching gas. These spectra are called "origin" and "background," respectively. They are compared to each other by taking their ratio and difference. This section discusses practical issues regarding the use of ratio and difference plots.

In recording a set of data, it is desirable to take one origin spectrum and only one background spectrum. The reason for this is entirely practical. The time required to take one origin and one background spectrum across the full 700 nm available spectral range, at a resolution that is only barely high enough for analysis, is around 15 to 20 hours. During this time, the constant attention of the researcher is required and large quantities of reagents are being used. To produce curves like those found in Figures 4-1.3-6 for the entire range would require, then, 60-80 hours. Of course, the time taken can be greatly reduced by taking a lower resolution spectrum first and then studying regions of interest in more detail. But, even so, research costs are greatly increased if the intensity of every interesting feature must be followed as a function of attaching gas flow.

Before the data presented in this section were analyzed, the understanding of the reactions occurring in the flow was as follows. Side reactions were known to occur in fairly significant quantities [Foley 1993]. But, it was deduced, quite reasonably, that the addition of an attaching gas would always affect emissions due to recombination much more strongly than emissions arising from other sources. Exotic excited states of helium, argon and dihelium were not thought to be present in great quantity. However, in the last section, it was shown that those exotic states are, indeed, present in significant quantities. In this section, it will be shown that a difference or ratio plot is not, by itself, enough data to conclusively identify an emission as being a photoproduct of electron–ion recombination.

The data plotted in Figures 4-1.3 — 4-1.6 can be turned into a series of ratios or differences that would be observed at that wavelength upon addition of each quantity of attaching gas. Calculating a difference is just as simple as calculating a ratio. But, if two features have very different initial intensities, the difference between origin and background will be difficult to compare without knowledge of the initial intensity. Ratios are easy to compare without knowing the initial intensity. So, in order to more easily make meaningful comparisons, ratios of counts are presented here. The ratios of counts observed at several single wavelengths as a function of CCl₄ flow are presented in Figure 4-1.8. The ratio at each point was taken by dividing the number of counts at zero–flow of CCl₄ by the number of counts at each flow of CCl₄. Points in that figure are connected only to help guide the eye.

The emission ratios plotted in Figure 4-1.8 arise from a variety of different sources (indicated on the figure), only two of which, the CO emissions, are likely to be products of the recombination of CO_2^+ . Note that at low flows of CCl_4 , the two CO


Observed Ratio of Counts

Figure 4-1.8: Comparison of the heights in a ratio plot[†] that would be observed for several different types of emission as a function of approximate CCl_4 throughput. Emissions b, d and e are unlikely to result from recombination. Emissions a and c that are thought to be due to recombination. See also Figures 4-1.1 and 4-1.2. Transition wavelengths: (a) 156.1 nm, (b) 507.8 nm, (c) 641.8 nm, (d) 522.3 nm, (e) 288.5 nm. [†] See Section 3-4.

features have very similar ratios. This result is encouraging. Not only are the initial intensities of the peaks different (2,000 counts for the $d \rightarrow a$ and 40,000 for the $A \rightarrow X$), but they also occur in different spectral regions. The difference between their ratios at high flows is a function of the signal-to-noise for the particular peak.

The problematic result is that at low CCl_4 flows, where recombination emissions behave most predictably, emissions that are not expected to result from recombination have comparable or, in most cases, larger ratios. The reason for this is, obviously, that the attaching gas, or a derivative of the attaching gas, is reacting with species in the flowtube other than electrons. But, knowing this does not make a ratio plot more useful.

The next figure, 4-1.9, is a bit cluttered, but shows that the data plotted in Figure 4-1.8 are not exceptional. Figure 4-1.9 is similar to 4-1.8 but includes all the major peak-tops in Figures 4-1.1 and 4-1.2, as well as those from other data taken at the same time. Data points are connected only to help guide the eye and are colored according to the general line shape. Although each set of points is not labeled separately, a listing of the features grouped by color can be found in Table 4-1.3.

Single ratio and difference plots do not provide sufficient evidence that a feature is a photoproduct of recombination. But, features due to recombination can still be identified using this technique. What is required, though, for conclusions to be certain, is to follow a given feature as a function of small flows of attaching gas. If the emission decays linearly with attaching gas throughput, with an x-axis intercept corresponding to the electron density in the injection region, the feature can be identified as a photoproduct of recombination.

Another option is to find a better way to control the makeup of the basic plasma composition (see Section 4-3 for a detailed description of the base plasma). As can be seen by inspection of Table 4-1.2, the excited states of CO^+ and CO^+_2 (which



Observed Ratio of Counts

Figure 4-1.9: Height in ratio plots (see Figure 4-1.8) as a function of approximate attaching gas (CCl₄) throughput for many emissions. Note that the quenching of emissions appears, at low throughputs, to arise from three mechanisms. See Table 4-1.3 for further information including a list of feature identifications for each line color. Line styles differ for viewing in black and white copy (see Table 4-1.3).

Table 4-1.3

	•	T ¹	1 1 0
Hooturog	in	Huguro	
reatures	111	rigure	4-1.9

Green Lines (long dash):

148.7009	$CO A(2) \to X(0)$	151.1021	$CO A(1) \rightarrow X(0)$
154.5039	$CO \ A(0) \to X(0)$	156.1047	$CO A(1) \rightarrow X(1)$
199.3007	$CO \ a(1) \to X(0)$	201.1016	$CO a(2) \rightarrow X(1)$
205.3038	$CO \ a(4) \to X(3)$	206.3043	$CO a(0) \rightarrow X(0)$
210.1063	$CO \ a(2) \to X(2)$	598.2526	$CO d(4) \rightarrow a(0)$
601.2545	$CO d(4) \rightarrow a(0)$	603.756	$CO d(4) \rightarrow a(0)$
641.7511	$CO \ d(3) \to a(0)$	643.252	$CO d(3) \rightarrow a(0)$
646.7542	$CO \ d(3) \to a(0)$		
Blue Lines (she	ort dash):		
288.5008	$\operatorname{CO}_2^+ \tilde{\operatorname{B}} \to \tilde{\operatorname{X}}$	289.7014	$\operatorname{CO}_2^+ \tilde{\operatorname{B}} \to \tilde{\operatorname{X}}$
337.3012	$\operatorname{CO}_2^+ \tilde{\operatorname{A}} \rightarrow \tilde{\operatorname{X}}^a$	337.9015	$\operatorname{CO}_2^+ \tilde{A} \rightarrow \tilde{X}^a$
340.1026	$\operatorname{CO}_2^+ \tilde{\operatorname{A}} \rightarrow \tilde{\operatorname{X}}^a$		
Red Lines (soli	d):		
341.7035	Unknown	343.1042	Unknown
501.2508	He 9B	504.7532	$\mathrm{CO}^+ A(1) \to X(1)$
507.7552	$\mathrm{CO}^+ A(1) \to X(1)$	516.2607	Ar 9U
518.7622	Ar 9W	522.2643	Ar 9DD
525.2662	Ar 10A		

Table 4-1.3: Figure 4-1.9 compares the height that would be observed in a ratio plot (see Section 3-4) for many different emissions as a function of CCl_4 flow. Lines are colored according to their behavior at number densities less than $2 \times 10^{12} \text{ cm}^{-3}$. There are too many lines to easily identify each individually on the graph. The point is that all emissions respond to attaching gas flow, with processes related to three different mechanisms. The nature of these mechanisms is discussed in the text. ^{*a*} tentative assignment.

have not been previously detected) can, energetically speaking, only be produced by plasma species whose presence is unwanted. It would be useful if the ions and neutrals in the plasma could be electronically relaxed so that the excited states are no longer present (see Section 4-2). This should begin at the ionization source, with enhanced production of ground state He⁺ ions and a reduction in excited neutral He species. The types of species produced could be better controlled if there were a device capable of precisely controlling the energy with which the free electrons impact the helium (this is not possible with current technology). To select for ground state He⁺ ions, the energy would need to be controlled to within a couple eV. The first excited state of He⁺ is 40 eV above the ground state, leaving a significant energy gap between the energy needed to ionize He (~ 25 eV) and the energy needed to excite the ion. If the electrons resonating in the microwave cavity were provided with an energy intermediate between 25 and 40 eV, they should be more likely to ionize the helium atoms than to merely excite them. If the energy were kept close to 25 eV, then electrons that have already ionized a helium atom would not be left with sufficient energy (~19 eV) to electronically excite other He atoms.

4-2 Photoproducts of Dissociative Recombination

Techniques used for analysis, difference and ratio plot, comparisons to Franck– Condon factors, etc., will be mentioned or implied frequently. These techniques are discussed in moderate detail in Chapter 3.

A survey of emissions likely to be products of recombination is presented here. The systems to be presented and the subsection in which they can be found are:

Parent Molecule(s)	Primary Ion(s)	Section Number	$\begin{array}{l} \text{Parent} \\ \text{Molecule}(s) \end{array}$	$\begin{array}{c} \text{Primary} \\ \text{Ion}(s) \end{array}$	Section Number
CH_4/H_2	CH_5^+	4-1.1	$\rm NH_3/H_2$	NH_4^+	4-1.6
$\rm CO/H_2$	HCO^+	4-1.2	NO/H_2	HNO^+	4-1.7
CO_2	CO_2^+	4-1.3	N_2O/H_2	N_2OH^+	4-1.8
$\rm CO_2/H_2$	$\rm CO_2H^+$	4-1.4	H_2S/H_2	SH_3^+	4-1.9
CS_2	CS_2^+	4-1.5	$\rm Xe/H_2$	XeH^+	4-1.10

It is important, for each system, to determine whether the observed emissions can possibly be produced by processes other than electron–ion recombination. To facilitate this determination, two tables of energetics are included here. The first, Table 4-1.1 (presented in Section 4-1), contains enthalpy changes associated with processes involving species known to be present in the plasma. The second, Table 4-2.11, lists the energies required to generate, from neutral, ground state parent molecules, the excited states whose emissions are observed in the spectra. Ground state exothermicities for relevant recombination paths are included in the tables (Tables 4-2.1 – 4-2.10) accompanying the discussion of each recombining system. In the case of unprotonated recombining ions, the exothermicity of charge transfer from ground state Ar^+ is also included; for protonated recombining ions, the exothermicity for proton transfer from H_3^+ is included. When the tabulated information is not sufficient, the reader will need to refer to other sources for the pertinent data, e. g., the references in Table 4-1.1.

It is also important to determine the relative frequencies with which certain processes occur. For all recombining ions, a primary issue is the likelihood of collisional vibrational relaxation prior to recombination. Collisional vibrational relaxation proceeds most efficiently when there exist normal modes that are resonant between the excited species and the relaxing agent. But, for small molecules, vibrational frequencies are often different in the neutral species than in the ion (see Section 3-6 for further discussion on vibrational relaxation). Also, while a greater number of collisions increases the likelihood of non-resonant relaxation, the injection of the necessary amount of reagent can cause other problems, such as forcing the injected gas several centimeters up the flowtube. In order to facilitate discussion of the extent of vibrational relaxation, Table 4-2.12 contains an estimated number of collisions, $Z_{V,T}$, required to relax an ion via non-resonant (e. g., vibrational-translational) relaxation and an estimated number of collisions the ion will undergo with the neutral parent, $f_{v,XYZ}$, and with He, $f_{v,He}$, before it recombines.

When the recombining ion is protonated, two additional relationships are calculated. The first is a comparison of the frequency with which Ar^+ will react with H_2 to the frequency with which it will react with the unprotonated, neutral parent. This gives an idea whether a significant portion of the observed spectrum is likely to be due to recombination of the unprotonated ion. The second relationship is the frequency with which any unprotonated ions formed will react with H_2 rather than recombining. For this last relationship, the nature of the products is less important than the fact that there will be fewer unprotonated parent ions recombining. These comparisons are discussed in Section 3-7 and in relevant discussions in Sections 4-2.1 - 4-2.10.

In cases where spectra were obtained at high enough resolution to determine precise values for vibrational level populations, normal-mode frequencies for the parent molecules and ions are listed in Table 4-2.13. In a number of cases, experimental values for one or more normal-mode frequencies were not available. Because of this, normal-mode frequencies were calculated for each of the molecules in its ground electronic state. In order to maintain as much consistency as possible, all colliding partners were treated with identical calculation methods. The calculations used the Hartree–Fock approximation with self consistent field. Since approximate values are sufficient for this comparison, the basis sets were chosen for economy. A slightly larger basis set was required for the nitrogen containing species (see the table for specifics). The implications of results presented in Table 4-2.13 are discussed in each of the appropriate sections below.

The program RVESIM (<u>r</u>otational <u>v</u>ibrational <u>e</u>lectronic <u>sim</u>ulation) was used to determine relative vibrational and electronic populations and to estimate the temperature of each of the emitting species. See Chapters 6 and 3, respectively, for further discussion of the program and of the techniques employed in data analysis. For each recombination, one or more graphs comparing the experimental spectrum to the simulated spectrum are presented in the section discussing that recombination. Specific information regarding observed spectra can be found in the tables, figures and discussions in Sections 4-2.1 — 4-2.10. Pre-run mass spectra for as many runs as are available are included in Appendix D. Recombination spectra with simulation fits are included in the text. Brief information specific to reaction conditions for each experiment is given in the table associated with that experiment. Unless otherwise indicated, all experiments share the following characteristics: He throughput is 220 Tls^{-1} and the overall flowtube pressure is 1.8 Torr; Ar is added at about 1 mT pressure through RP2; H₂ is also added at about 1 mT pressure through RP3; the throughput of the attaching gas is approximately $9 \times 10^{10} \text{cm}^{-3}$.

All recombining systems surveyed here, except CO_2^+ , were studied before the diagnostic experiments described in Section 4-1.1. Although emissions observed in spectra from those other systems are likely to be photoproducts of recombination, recombination cannot unequivocally be identified as their source. Despite the fact that these survey experiments were not conducted under the circumstances dictated by the results from the CO_2^+ studies, they contain useful information that can facilitate future studies.

4-2.1 Emissions from a plasma dominated by recombination of CH_5^+ ions

The Ar⁺ in the system is expected to react with CH₄ rather than with H₂ about 20% of the time (see Table 4-2.12). Of that 20%, only about 20% will recombine before reacting with H₂. Therefore, $\leq 4\%$ of the recombinations whose emissions appear in these spectra will be due to CH₂⁺, CH₃⁺ or CH₄⁺ recombining rather than CH₅⁺.

The emissions in this spectrum are very weak. They are dwarfed by the helium and argon emissions in the base plasma. But, the spectrum fit by RVESIM clearly indicates the presence of emissions from the $A \to X$ and $B \to X$ transitions of CH (see Figure 4-2.1 and Table 4-2.1). The recombination of ground state CH_5^+ does not release sufficient energy to produce the B state of CH. The presence of the B state _Table 4-2.1 _

Emissions from a plasma containing recombining CH_5^+ ions

Recombination products [exothermicity,^{*a*} eV]: CH₄ + H [7.97]; CH₃ + H₂ [7.94]; CH + 2H₂ [3.29] Non-destructive protonation exothermicity^{*a*,*b*} [1.26]

Product	СН				
State $ au, \ \mu s^{\ a}$ $v_{max}, \ v_{max}^{*}^{\ b}$	$ \begin{array}{c} A^2 \Delta^n \\ 0.5 \\ 0, 5 \end{array} $	$B^{2}\Sigma^{-m,n}$ 0.36 $j, 5$			
Rel. Pop. ^c Rot. Temp., K ^d v ^e	1 2500 K	0.4 2000 K			
0	1	1			

Reagent(s)^r (cm⁻³): CH₄, 3.6×10^{12} ; H₂, 2.3×10^{13} Attaching gas^r (cm⁻³): SF₆, 1×10^{11}

Relative electronic populations, relative vibrational populations and rotational temperatures are new data. All other values were taken or derived from other sources [Radzig 1985, NIST 2001]. $^{a-r}$ Notes for Tables 4-2.1 — 4-2.9 are in Table 4-2.10

is probably due to excitation in the recombining ion. The extra energy needed by the recombining system is .05 eV (406 cm⁻¹). At room temperature, the Boltzmann distribution predicts that about 12% of the molecules possess this much energy. So, 12% of the CH_5^+ ions will have this much energy even if they have been collisionally relaxed.

The results presented here are in agreement with earlier results on a similar system [Tsuji 1991]. The previous work concerns recombinations of CH_n^+ where n = 2 - 4. In that work, the $C^2\Sigma^+$ state of CH was also observed. The C state of CH is



Figure 4-2.1: Comparison of the simulated spectrum (red, solid) to the experimental spectrum (green, dashed) observed in a plasma containing recombining CH_5^+ ions. See Table 4-2.1 for additional information. Emissions not identified here are emissions in the base plasma; see Appendix B for specific identifications. Observed photon counts are corrected for the optical system transmission efficiency.

not accessible in the recombinations of either CH_4^+ or CH_5^+ . So, it is not expected here and was not observed. Rotational temperatures were assigned to individual vibrational levels in the previous work. Such precision is not possible in these studies, but rotational temperatures reported here (see Table 4-2.1) are within the range of temperatures reported in the other study. The temperatures reported by the previous work range from 500 to 3200 K for the A state and 600 to 3200 for the B state; rotational temperatures for the C state were not reported. Vibrational distributions in the two studies are also similar, but not exactly the same. While both studies $_Table 4-2.2 _$

Emissions from a plasma containing recombining HCO^+ ions

Recombination products [exothermicity,^{*a*} eV]: H + CO [7.45,[†] 9.18[‡]]; C + OH [0.73,[†] 2.46[‡]]; O + CH [-0.17,[†] 1.55[‡]] Non-destructive protonation exothermicity^{*a,b*} [1.78,[†] 0.04[‡]]

Product

CO

State	$A^1\Pi \ ^{n,o}$	$a^3 \Pi_r n$	$a'^3\Sigma^{+\ m,o}$	$d^3\Delta_i {}^{m,o}$	$e^{3}\Sigma^{-m,n,o}$
$ au,\mu\mathrm{s}^{\;a}$	0.011	8000	10^l	7.3^l	2^l
$v_{max}, v_{max}^* \stackrel{b \dagger}{=}$	j,6	6, 16	3, 17	j, 12	j,9
$\mathbf{v}_{max}, \mathbf{v}_{max}^* ^b \ddagger$	5, 6	16, 16	16, 17	11, 12	9, 9
Rel. Pop. ^c	0.15	0^s	1	1	≤0.04
Rot. Temp., K d	$600 \mathrm{K}$		$400 \mathrm{K}$	$600 \mathrm{K}$	g
v^{e}					
0	1	—	i	i	1
1	0.1		i	1^f	
2	0.1		i	0.5	
3	0.05		i	0.5	
4			i	0.2	
5			1^f	0.1	
6			0.4		
7			0.1		

$\dagger \mathrm{HCO^{+};\ \ddagger COH^{+}}$

Reagent(s)^r (cm⁻³): CO, 5.2×10^{12} ; For protonated parent gas: H₂, 2.2×10^{13} Attaching gas^r (cm⁻³): SF₆, 1×10^{11}

Relative electronic populations, relative vibrational populations and rotational temperatures are new data. All other values were taken or derived from other sources [Radzig 1985, NIST 2001]. $^{a-r}$ Notes for Tables 4-2.1 — 4-2.9 are in Table 4-2.10

report population only in the v=0 level of the B state, the A state populations differ. Scaled relative to 1, the results from Tsuji, et al, are 1, 0.4 and 0.1 for vibrational



Figure 4-2.2a: Comparison of the simulated spectrum (red, solid) of triplet-triplet transitions to the spectrum (green, dashed) observed in a plasma containing recombining HCO⁺ and COH⁺ ions. See Table 4-2.2 for additional information. Emissions from the base plasma are not simulated here; see Appendix B for specific identifications. Observed photon counts are corrected for the optical system transmission efficiency.

levels 0, 1 and 2, respectively, of the CH A state. Here, only population in the v=0 state is reported.

There is slim evidence of cluster formation in the mass spectrum (see Appendix D). The peak at mass 29 could be $C_2H_5^+$, but the presence of a peak around 19 amu (H_3O^+) suggests a significant level of impurities in the flow. Because of this, the peak at 29 amu is probably N_2H^+ instead. Additionally, the ion detection system nearly a meter downstream of RP3, giving ample time for ion-molecule reactions to occur.



Figure 4-2.2b: Comparison of the simulated (red, solid) CO $a \to X$ cascade (from higher triplet levels) spectrum to the spectrum (green, dashed) observed in a plasma containing recombining HCO⁺ and COH⁺ ions. See Table 4-2.2 for additional information. The very intense emissions that are not simulated here are emissions from CO⁺ $B \to X$. Weaker emissions from 180-200 nm are CO $A \to X$ transitions. Observed photon counts are corrected for the optical system transmission efficiency.

Since clusters do not appear to be forming in the injection region, an increased flow of CH_4 would probably improve the signal to noise in the spectrum. Since the emissions are so weak despite the relatively short radiative lifetimes of the CH A and B states (0.5 and 0.36 μ s, respectively), it is possible that they are produced by the reaction with CH_4 of one of the excited species known to exist in the flow. The ionic species in the flow do not possess enough energy to produce the A and B states, but several neutral species could (see Tables 4-1.1 and 4-2.11).



Figure 4-2.2c: Comparison of the 180-300 nm region of the simulated spectrum (red, solid) to the spectrum (green, dashed) observed in a plasma containing recombining HCO^+ and COH^+ ions. See Table 4-2.2 for additional information. Included in this simulation are cascade from the a', d and e states of CO, the very intense emissions from $CO^+ B \to X$ and the weaker emissions (180-200 nm) of $CO A \to X$ transitions. No native population of CO was included. Observed photon counts are corrected for the optical system transmission efficiency.

4-2.2 Emissions from a plasma dominated by recombination of HCO^+ and COH^+ ions

The triplet-triplet transitions $(d, e \text{ and } a' \rightarrow a, \text{ see Figure 4-2.2a})$ are the most obvious features likely to result from recombination. The lower wavelengths (180-280 nm) are dominated by CO⁺ $B \rightarrow X$ emissions (see Figures 4-2.2b and 4-2.2c). Some _Table 4-2.3 _

Relative Populations of Emissions Resulting from the Recombination of CO_2^+

Recombination products [exothermicity,^{*a*} eV]: CO + O [8.26]; C + O₂ [2.27]

Non-destructive charge transfer exothermicity^{a,b} [1.98]

CO

State	$A^1\Pi$	$a^3\Pi_r$	$a'^3\Sigma^+$	$d^3\Delta_i$	$e^3\Sigma^-$
$ au, \ \mu { m s}^{\ a}$:	0.011	8000	10^l	7.3^l	2^l
$v_{max}, v_{max}^* b$	0, 13	11, k	9, k	5, k	2, 19
Rel. Pop. c	0.06	1^s	0.09	0.06	≤0.003
Rot. Temp., K d	$600 \mathrm{K}$	$300 \mathrm{K}$	$400 \mathrm{K}$	$400 \mathrm{K}$	g
$_{ m V}~^{e}$					
0	1	1	i	i	1
1	0.7	0.6	i	1	
2	0.2	0.4	i	0.9	
3	0.1	0.2	i	0.9	
4	0.05	0.1	i	0.5	
5			1	0.2	
6			0.1	0.05	
7			0.1		

 $Reagent(s)^r (cm^{-3}): CO_2, 1 \times 10^{14}$

Attaching gas^r (cm^{-3}) : CH₃I, 1 × 10¹¹

Relative electronic populations, relative vibrational populations and rotational temperatures are new data. All other values were taken or derived from other sources [Radzig 1985, NIST 2001]. $^{a-r}$ Notes for Tables 4-2.1 — 4-2.9 are in Table 4-2.10

transitions from CO $A \to X$ are evident as well. See table 4-2.2 for a summary of the results.

The results from the simulation (Figure 4-2.2b) of the spectrum due only to cascade (see Chapter 6) from the a', d and e states, implies that no CO $a^3 \Pi_r$ is



Figure 4-2.3a: Comparison of the simulated spectrum (red, solid) of triplet-triplet transitions to the spectrum (green, dashed) observed in a the recombination of CO_2^+ . See Table 4-2.3 for additional information. Molecular emissions not simulated here are $CO^+ A \rightarrow X$. Atomic emissions not simulated are emissions in the base plasma; see Appendix B for specific identifications. Observed photon counts are corrected for the optical system transmission efficiency.

produced directly from any process. Note that the simulation is based on the estimates of the simulator rather than on a more rigorous mathematical deduction. The most uncertain estimate is that the CO molecules spend 0.3 ms in the viewing region (see Table 4-2.10, note s). If the time in the viewing region is less than this, then some CO a might be produced directly. A longer residence time would indicate that the system efficiencies at low and high wavelengths are incorrect with respect to each other. Even with the uncertainties, it appears that only small quantities, if any, of the



Figure 4-2.3b: Comparison of the simulated (red, solid) CO $a \to X$ cascade (from higher triplet levels) spectrum to the spectrum (green, dashed) observed in the recombination of CO₂⁺. See Table 4-2.3 for additional information. The very intense emissions that are not simulated here are: 280-300nm, CO₂⁺ $\tilde{B} \to \tilde{X}$; 140-200 nm, CO $A \to X$; and, 180-300 nm, CO $a \to X$ produced directly from the recombination of CO₂⁺ (see next figure for a simulation including CO $a \to X$ produced directly). Observed photon counts are corrected for the optical system transmission efficiency.

a state of CO are being produced directly by any process (including recombination). The presence of CO d and A emissions (and possibly e) indicates that either some COH^+ is reacting or that the HCO^+ is vibrationally excited.

The results for the *a* state do not agree with previous findings [Adams 1994a,b]. In that study, emissions from higher triplet states were not observed and therefore, cascade was not considered. Emissions from the A state were also not observed. The



Figure 4-2.3c: Comparison of the 140-300 nm region of the simulated spectrum (red, solid) to the spectrum (green, dashed) observed in the recombination of CO_2^+ . See Table 4-2.3 for additional information. Included in the simulation are cascade from the a', d and e states of CO, and CO $a \to X$ and $A \to X$ emissions from native (nascent) populations. The intense CO_2^+ $\tilde{B} \to \tilde{X}$ emission (280-300 nm) is not included in the simulation. Observed photon counts are corrected for the optical system transmission efficiency.

reason for the difference is not yet known. The inability to quantitatively consider cascade from higher states has been a hindrance elsewhere [Tsuji 1998, Johnsen 2000b], and is one of the reasons that RVESIM (see Chapter 6) was created. Emissions from the a, a', d, e and A states of CO were observed in another study [Johnsen 2000b], but they were not quantified.

4-2.3 Emissions from a plasma dominated by recombination of CO_2^+ ions

Emissions from the recombination of CO_2^+ have been studied here, extensively, and elsewhere to varying degrees [Johnsen 2000b, Skrzypkowski 1998, Tsuji 1995, Valée 1986, Weller 1967]. This system required extensive study here because it produced an unexpected result that has not been indicated in other studies: emissions from a species, CO^+ , that should not be a product of recombination, were quenched by the addition of an attaching gas (this occurs with the HCO_2^+ system as well). Also, vibrational levels that are not energetically accessible products of recombination of the ground state ion were observed (see Tables 4-2.3). These were not observed in great quantity, and the exothermicity of charge transfer from Ar^+ is sufficient to account for the residual excitation. The unexpected behavior of the CO^+ was addressed in detail in Section 4-1.

Since a series of emissions from a plasma dominated by CO_2^+ recombinations were recorded as a function of attaching gas flow, it is possible to identify some of them as being photoproducts of recombination. The emissions from neutral CO all decayed linearly as a function of attaching gas flow, with intercepts corresponding to electron densities typical of the region around RP2. The electronic states observed, their temperatures and relative electronic and vibrational populations, are included in Table 4-2.3. Relative vibrational populations were determined using RVESIM (see Chapter 6).

Previous studies [Tsuji 1998, Skrzypkowski 1998, Johnsen, 2000b] were unable to estimate the amount of CO a state that is produced nascently (directly) in the recombination of CO₂⁺ rather than by cascade from the higher triplet states (a', d and e). Tsuji, et al., suggested that the recombination of CO₂⁺ produces exclusively the upper states (A, a', d and e) of CO. However, in the current study, cascade from the upper states is not sufficiently intense to account for the observed $a \rightarrow X$ emissions. Tsuji, et al., also report significant population in the e state at v=2 and 3, which is not observed here. In other respects, there is fair agreement between this work and that of Tsuji, et al. [1998], but in the case of the d state populations, the current results are in better agreement with their predictions based on statistical theory:

СО	d	v:	1	2	3	4	5	6
	This work:		1	.9	.9	.5	.2	.05
	Tsuji et al. (obs	.)	1	1.4	1.6	0.5	0.1	0.09
	Tsuji et al. (pre	d.)	1	0.7	0.5	0.3	0.1	0.02
СО	a'	v:	5	6	7			
	This work:		1	.1	.1			
	Tsuji et al. (obs	.)	1.00	0.40	0.11			
	Tsuji et al. (pre	d.)	1	0.7	0.52			
СО	A	v:	0	1	2	3	4	
	This work:		1	.7	.2	.1	.05	
	Tsuji et al. (obs	.)	1.00	0.58	0.09			

Here, "pred." refers to Tsuji, et al.'s predicted populations based on statistical theory and "obs." indicates their experimental values. Values for relative vibrational distributions are scaled for comparison with this study so that values of one occur at the same vibrational level in both data sets. Skrzypkowski, et al., [1998] reported vibrational distributions for the CO a state based on the $a \rightarrow X$ emissions. They were also unable to account for cascade. But, according to the simulation in the present study, the contribution from cascade is small, so their vibrational populations should be fairly accurate. The agreement with the current study is quite good:

CO	a	v:	0	1	2	3	4
	This work:		1	.6	.4	.2	.1
	Skrzypkowski, et	al.	1	0.51	0.35	0.20	

They [Skrzypkowski 1998] describe the distribution as approximately Boltzmann with a vibrational temperature of 4200 ± 300 K. They do not report a rotational temperature.

Tsuji, et al., generally report separate rotational temperatures for each vibrational level. Currently, RVESIM (see Chapter 6) is not capable of making that sort of distinction. To the extent possible, however, the temperatures reported here and by Tsuji, et al., will be compared. For the A state, they report temperatures for the v=0, 1 and 2 levels of 1000, 700 and 400 K, respectively. Here, our reported value is 600 K, well within their range. The temperatures they report for the a' state range from 400-550 K, which is also in agreement with the value presented here (400 K). However, they report temperatures in the range 500-750 K for the d state, which is somewhat higher than the 400 K observed here.

4-2.4 Emissions from a plasma dominated by recombination of HCO_2^+ ions

Here, as is also the case in the CO_2^+ system, $\operatorname{CO}^+ A \to X$ emissions are present and quenched by the addition of an attaching gas (see also Sections 4-1 and 4-2.3). Also, other species in the flow (He^{*}, He⁺, He^{*}₂, Ar^{*}, Ar^{+*}) possess sufficient energy to create all observed neutral emissions. However, with the exception of excited states of Ar neutrals, those species contain so much energy that to observe only such low–energy products seems unlikely. For example, the more energetic of the two metastable Argon atoms (11.72 eV), could react with CO_2 to produce the v=0 level of the $a^3\Pi_r$ state of CO but not any other excited states. On the other hand, the lowest energy metastable He state contains sufficient energy (19.82 eV) to either completely dissociate CO_2 into atoms or to produce CO^+ (ground state) and an O atom. Thus, the ionized species either do not have enough energy to produce excited states of neutral CO (ground state Ar⁺) or the have energies greatly in excess of that needed (He⁺, He⁺₂, Ar^{+*}). The emissions are also intense, and reactions between $_Table 4-2.4$

Emissions from a plasma containing recombining HCO_2^+ ions

Recombination products [exothermicity, a eV]:

 $CO_2 + H [8.00]; CO + OH [6.92]; O_2 + CH [0.02]$

Non-destructive protonation exothermicity a,b [1.23]

Product			CO			OH^n
State $ au, \ \mu s \ ^{a}$ $v_{max}, \ v_{max}^{*} \ ^{b}$	$ \begin{array}{c} A^{1}\Pi \\ 0.011 \\ j, 0 \end{array} $	$a^{3}\Pi_{r}$ 8000 3, 10	$\begin{array}{c} a^{\prime 3}\Sigma^{+m,o} \\ 10^l \\ j, 8 \end{array}$	$\frac{d^3 \Delta_i{}^{m,o}}{7.3^l}$ $j, 3$	$e^{3\sum^{-m,n,o}} \frac{2^l}{j, 0}$	$ \begin{array}{c} \overline{A^2 \Pi_i{}^m} \\ 0.69 \\ 9, k \end{array} $
Rel. Pop. c	0.07	0.7^{s}	1	0.8	≤ 0.05	0.12
Rot. Temp., K d	$800 \mathrm{K}$	$300 \mathrm{K}$	$400 \mathrm{K}$	$400 \mathrm{K}$	g	$1000 \mathrm{K}$
v^{e}						
0	0.8	1	i	i	1	0.7
1	1	0.5	i	1^f		1
2	0.4	0.3	i	0.4		.2
3	0.1	0.3	i	0.3		
4		0.1	i	0.2		
5			1^f	0.2		
6			0.2	0.1		
7			0.2			
8			0.1			
9			0.1			

Reagent(s)^r (cm⁻³): CO₂, 6×10^{13} ; H₂, 1×10^{14}

Attaching gas^r (cm^{-3}) : CH₃I, 1 × 10¹¹

Relative electronic populations, relative vibrational populations and rotational temperatures are new data. All other values were taken or derived from other sources [Radzig 1985, NIST 2001]. $^{a-r}$ Notes for Tables 4-2.1 — 4-2.9 are in Table 4-2.10

neutrals are slow, so it is unlikely that they are the result of a reaction between two neutral species.



Figure 4-2.4a: Comparison of the simulated spectrum (red, solid) of triplet-triplet transitions (indicated on plot) to the spectrum (green, dashed) observed in a plasma containing recombining HCO_2^+ ions. See Table 4-2.4 for additional information. Molecular emissions not simulated here are $\text{CO}^+ A \to X$. Atomic emissions not simulated are emissions in the base plasma; see Appendix B for specific identifications. Observed photon counts are corrected for the optical system transmission efficiency.

It is also very likely that the primary recombining ion is HCO_2^+ . Inspection of Table 4-2.12 shows that Ar^+ is expected to react with CO_2 with half the frequency of reactions with H₂. But, once formed, the CO_2^+ will only recombine once for every 20 reactions with H₂. So, only 1-2% of the recombining ions are expected to be CO_2^+ . The differences between the HCO_2^+ spectrum (see Figures 4-2.4) and the CO_2^+ spectrum support this assertion as well. In the CO_2^+ recombination, the $CO \ a \to X$ emissions are considerably more intense than the a', d and $e \to a$. Additionally,



Figure 4-2.4b: Comparison of the simulated (red, solid) CO $a \to X$ cascade (from higher triplet levels) spectrum to the spectrum (green, dashed) observed in a plasma containing recombining HCO_2^+ ions. See Table 4-2.4 for additional information. The CO $a \to X$ emissions simulated here are due only to cascade from the higher electronic states a', d and e. Observed photon counts are corrected for the optical system transmission efficiency.

there is an intense OH emission in the HCO_2^+ spectrum that cannot be due to the recombination of CO_2^+ .

As can be seen in Table 4-2.4, although emissions from several other states are observed, only the $a^3\Pi_r$ (v=3) state of CO and the $A^2\Pi_i$ (v=9) state of OH are energetically accessible in the recombination of ground state HCO_2^+ . That high vibrational levels are observed indicates that the HCO_2^+ is in a vibrationally excited state. It is unlikely that a significant quantity of CO_2^+ is recombining, and this is



Figure 4-2.4c

Figure 4-2.4c: Comparison of the 140-300 nm region of the simulated spectrum (red, solid) to the spectrum (UV-VIS: green, dashed and VUV: blue, dashed) observed in a plasma containing recombining HCO_2^+ ions. See Table 4-2.4 for additional information. Included in the simulation are cascade from the a', d and e states of CO and CO $a \to X$, CO $A \to X$ and OH $A \to X$ emissions from native (nascent) populations. The intense CO_2^+ $\tilde{B} \to \tilde{X}$ (280-300 nm) and CO_2^+ $\tilde{A} \to \tilde{X}$ (300-340 nm) emissions are not included in the simulation. Due to the strong deviation of the OH A state from Hund's case b, the observed $A \to X$ transition is not simulated well here. An anomalously high noise level in the VUV spectrum (blue, dashed) does not prevent assessment of the relative vibrational levels within the A state, but does create uncertainty about the population of the A state relative to the others. Observed photon counts are corrected for the optical system transmission efficiency.

_Table 4-2.5 _

	1	0	0	4
Recombination products [e	xothermicity,	^{a} eV]:		
$S + CS [5.51]; C + S_2$	[2.53]			
Non-destructive charge	transfer exot	hermicity a,b	[5.51]	
Product	(CS		
State	$A^{1}\Pi$	$a^3 \Pi_r n$		
$ au,\mu\mathrm{s}^{-a}$	0.22	16000		
$v_{max}, v_{max}^* b$	4, k	15, k		
Rel. Pop. c	0.7	1^t		
Rot. Temp., K d	$800 \mathrm{K}$	$700 \mathrm{K}$		
$\mathrm{v}^{\;e}$				
0	1	1		
1	0.7	1		
2	0.7	1		
3	0.5	0.6		
4	0.4	0.2		
5	0.2	0.1		

Emissions from a plasma containing recombining CS_2^+ ions

Reagent(s)^r (cm⁻³): CS₂, 1.4×10^{12} ; CO₂, 1.7×10^{14}

Attaching gas^r (cm^{-3}): CH₃I, 8×10^{10}

Relative electronic populations, relative vibrational populations and rotational temperatures are new data. All other values were taken or derived from other sources [Radzig 1985, NIST 2001]. $^{a-r}$ Notes for Tables 4-2.1 — 4-2.9 are in Table 4-2.10

supported by the low intensity of the CO $a \to X$ emissions that would otherwise be more intense. In fact, it appears to be excited beyond what is available from the protonation of the CO₂. The greatest amount of excitation required above the total recombination energy available, including protonation, is that of the highest observed vibrational level in the A state (7100 cm⁻¹). The cause for this discrepancy is un-



Figure 4-2.5a: Comparison of the simulated (red, solid) $CS \ A \to X$ spectrum to the spectrum (green, dashed) observed in a plasma containing recombining CS_2^+ ions. See Table 4-2.5 for additional information. Observed photon counts are corrected for the optical system transmission efficiency.

certain and indicates that intensities of individual features need to be observed as a function of attaching gas flow to determine their source.

In the only other known study of the recombination of HCO_2^+ [Johnsen 2000b], there is only a mention of the observation of the OH $A \to X$ transition, and relative vibrational populations are not reported.

4-2.5 Emissions from a plasma dominated by recombination of CS_2 ions

The $A \to X$ and $a \to X$ transitions of CS were observed in this system (Table 4-2.5 and Figure 4-2.5). All observed states in the CS₂⁺ recombination are energetically



Figure 4-2.5b: Comparison of the simulated (red, solid) CS $a \to X$ spectrum to the spectrum (green, dashed) observed in a plasma containing recombining CS₂⁺ ions. See Table 4-2.5 for additional information. The molecular peaks not included in the simulation are tentatively identified as CO⁺ $A \to X$ emissions. The atomic line is a He emission from the base plasma; see Appendix B for further identification. Observed photon counts are corrected for the optical system transmission efficiency.

accessible. The v=5 level of the A state is not accessible by recombination energy, but has a Boltzmann probability of about 0.74 at 289 K.

 CO_2 was added to facilitate vibrational relaxation of CS_2^+ ions prior to recombination. CO_2 has vibrational modes that are slightly more resonant with CS_2^+ than are modes of CS_2 , and, in particular, the differences in energy between a few states are favorable (see also Tables 4-2.5 and 4-2.13a):

$$CS_2^+$$
 Mode $[\nu, eV]$ CO_2 Mode $[\nu, eV]$ $\Delta\nu, cm^{-1}$

Emissions from a plasma containing recombining NH_4^+ ions

Recombination products [exothermicity, a eV]:

 $NH + H_2 + H [0.37]$

Non-destructive protonation exothermicity a,b [4.47]

 NH^h Product $A^3 \Pi_i m$ $c^1\Pi \ ^m$ State $\tau,\,\mu {\rm s}^{~a}$ 0.430.44 $v_{max}, v_{max}^* {}^b$ j, 2j, jRel. Pop. c 1 0.2Rot. Temp., K d 3000 K3000 K v^{e} 0 1 1 1 0.3

Reagent(s)^r (cm⁻³): NH₃, 3.6×10^{12} ; H₂, 2.3×10^{13} Attaching gas^r (cm⁻³): SF₆, 1×10^{11}

Relative electronic populations, relative vibrational populations and rotational temperatures are new data. All other values were taken or derived from other sources [Radzig 1985, NIST 2001]. $^{a-r}$ Notes for Tables 4-2.1 — 4-2.9 are in Table 4-2.10

Symmetric Stretch [617]	Bend [667]	-50
Asymmetric Stretch [1200]	Symmetric Stretch [1333]	-133

Since the CS_2^+ frequencies are lower than the CO_2 frequencies, vibrational relaxation would have to be accompanied by translational and/or rotational relaxation.

The spectrum is at fairly high resolution and uncluttered by impurity emissions. The presence of the CO₂ results in the production of emissions from the recombination of CO₂⁺ (see Figure 4-2.2), but these only overlap a few of the less intense CS $A \to X$ emissions, and are easily accounted for in the simulated spectrum. The only significant



Figure 4-2.6: Comparison of the simulated (red, solid) spectrum to the spectrum (green, dashed) observed in a plasma containing recombining NH_4^+ ions. See Table 4-2.6 for additional information. The molecular species included in the simulation are the $c \rightarrow a$ (as visible here, roughly 320–335 nm) and $A \rightarrow X$ (roughly 330–350 nm) transitions of NH. Observed photon counts are corrected for the optical system transmission efficiency.

sources of uncertainty in the results arise from the models used during analysis. The calculated Franck Condon factors, since they are calculated from a Morse potential, are best near v=0.

4-2.6 Emissions from a plasma dominated by recombination of NH_4^+ ions

It is not energetically possible, in the recombination of ground state NH_4^+ to produce the observed excited states of NH (Figure 4-2.6 and Table 4-2.6), so either the emissions are being produced by some process other than recombination, significant amounts of NH_3^+ are recombining or the NH_4^+ is vibrationally excited. If all emissions are due to NH_4^+ recombining, then it must have obtained energy at least 5900 cm⁻¹ in excess of the protonation exothermicity in order to populate the v=0 level of the NH c state (this is the only vibrational level of the c state that is observed). Ar⁺ reacted with NH_3 about once for every 3.6 reactions with H_2 , and any ions formed from that reaction will react with H_2 about 4.6 times for every recombination. So, the NH_3^+ ion might account for as many as 4% of the recombinations. Data oon emissions from the recombination of NH_3^+ is not available in this study or from the literature for comparison. This system will require a more detailed investigation before emissions can be definitely identified as being products of the recombination of vibrationally excited NH_2^+ .

Accurate simulation of the NH $A \rightarrow X$ transition was difficult (see Figure 4-2.6). It is likely that the algorithm used in RVESIM (see Chapter 6) does not treat NH well. It is also possible that the rotational distribution in the NH is nonthermal. Without a higher resolution spectrum, it is difficult to tell which of these is the case.

4-2.7 Emissions from a plasma dominated by recombination of HNO^+ ions

The combination of low resolution and overlapping features makes quantitation of species populations very difficult in this case (Figure 4-2.7). But, the electronic species listed are present (Table 4-2.7), even though the exact vibrational and electronic distributions are uncertain.

Values for the proton affinity of NO available in the literature do not specify whether the protonation occurs at N or O. An ab-initio calculation (Hartree–Fock with the $6-31+G^*$ basis set in Spartan '02 by Wavefunction, Inc.) indicates an energy difference of about 0.09 eV with the higher energy state being protonation at O. In Emissions from a plasma containing recombining HNO^+ ions

Recombination products [exothermicity, a eV]:

H + NO [8.09]; O + NH [4.80]; N + OH [5.98]

Non-destructive protonation exothermicity^{a,b,q} [1.13]

	4 ² 5+
State $A^2 \Sigma^+$ $B^2 \Pi_r{}^{m,n,p}$ $A^3 \Pi_i$	$A^{2}\Sigma^{+}$
$ au, \ \mu s^{\ a} \qquad \qquad 0.2 \qquad \qquad 3.1 \qquad \qquad 0.43$	0.69
$v_{max}, v_{max}^* {}^b \qquad 9, 13 \qquad k, k \qquad 6, 6$	5, 11
Rel. Pop. c 1 ≤ 0.2 0.7	0.3
Rot. Temp., K d 3000 K — 4000 K	2000 K
v^{e}	
0 1 (1) 1	1
1 0.7 (1)	0.3
2 0.5	0.1

Reagent(s)^r (cm⁻³): NO, 1.7×10^{13} ; H₂, 3×10^{13}

Attaching gas^{*r*} (*cm*⁻³): SF₆, 5.2×10^{11}

Relative electronic populations, relative vibrational populations and rotational temperatures are new data. All other values were taken or derived from other sources [Radzig 1985, NIST 2001]. $^{a-r}$ Notes for Tables 4-2.1 — 4-2.9 are in Table 4-2.10

terms of vibrational and electronic states, that is a small amount of energy, and much less than the protonation exothermicity, regardless where the proton attaches.

Previous results [Johnsen 2000b] report the NO $A \rightarrow X$ bands as the only significant photoproduct of the recombination of HNO⁺; however, they do not specify a vibrational distribution.



Figure 4-2.7: Comparison of the simulated (red, solid) spectrum to the spectrum (green, dashed) observed in a plasma containing recombining HNO⁺ ions. See Table 4-2.7 for additional information. The molecular species included in the simulation are the NO $B \rightarrow X$ and $A \rightarrow X$ (overlapping and intense from 200–300 nm), the OH $A \rightarrow X$ transition (roughly 300–325 nm) and the NH $A \rightarrow X$ transition (roughly 325-350 nm). Observed photon counts are corrected for the optical system transmission efficiency.

4-2.8 Emissions from a plasma dominated by recombination of N_2OH^+ ions

The published data [Foley 1993] for this system were taken at the lower resolution of the data sets in this series, and therefore, quantitative information about the NH state could not be presented. Results from analysis of the higher resolution data in this study are given in Table 4-2.8.

Emissions from a plasma containing recombining N_2OH^+ ions

Recombination products [exothermicity, a eV]:

NNO + H [7.64,[†] 7.90[‡]]; N₂ + OH [10.34,[†] 10.61[‡]]; NH + NO [5.91,[†] 6.17[‡]] Non-destructive protonation exothermicity^{*a,b*} [1.58,[†] 1.32[‡]]

Product	NH^h		N_2	OH^h	
State	$A^3 \Pi_i m$	$c^1\Pi^{m,n}$	$\overline{B^3 \Pi_q}^{m,o}$	$\overline{A^2\Sigma^{+\ m}}$	
$ au, \mu { m s}^{\ a}$	0.43	0.44	8	0.69	
$v_{max}, v_{max}^* \overset{b}{\dagger}$	6, k	1, k	15, k	k, k	
$\mathbf{v}_{max}, \mathbf{v}_{max}^* \stackrel{b}{=} \frac{1}{2}$	7, k	2, k	13, k	k, k	
Rel. Pop. ^c	0.07	0.07	1	0.4	
Rot. Temp., K d	$4000~{\rm K}$	3000 K	300 K	2000 K	
v ^e					
0	1	1	i	1	
1	0.5	0.5	i	0.4	
2	0.1		1^f	0.1	
3			0.4		
4			0.5		
5			0.4		
6			0.3		
7			0.2		
8			0.1		
9			0.1		

†NNOH⁺; ‡HNNO⁺

Reagent(s)^r (cm⁻³): N₂O 2.6 × 10¹³; H₂, 3 × 10¹³

Attaching gas^r (cm^{-3}) : CH₃I, 1 × 10¹¹

Relative electronic populations, relative vibrational populations and rotational temperatures are new data. All other values were taken or derived from other sources [Radzig 1985, NIST 2001]. $^{a-r}$ Notes for Tables 4-2.1 — 4-2.9 are in Table 4-2.10



Figure 4-2.8: Comparison of the simulated (red, solid) spectrum to the spectrum (green, dashed) observed in a plasma containing recombining N₂OH⁺ and HN₂O⁺ ions. See Table 4-2.8 for additional information. The molecular species included in the simulation are the OH $A \rightarrow X$ (roughly 280–310), the NH $A \rightarrow X$ and less intense $c \rightarrow a$ (overlapping from about 325–350 nm) and the N₂ $B \rightarrow A$ transition (roughly 600–800 nm). Emissions from N₂O⁺ (roughly 325–400 nm) are not included in the simulation. Other emissions are from the base plasma; see Appendix B for further identification. Observed photon counts are corrected for the optical system transmission efficiency.

All observed states are energetically accessible in the recombination of either protonated isomer. This system is one of the systems more likely to be vibrationally relaxed according to the approximate empirical formula by Lambert (see Table 4-2.12 and Section 3-6). A comparison of the output from the simulation to the observed spectrum is given in Figure 4-2.8.

The current data include previously unobserved emissions from the $c \to a$ transition of NH and the $B \to A$ transition of N₂. The N₂ $B \to A$ emissions have previously been observed for recombinations of N₂O⁺ [Tsuji 2000], but those emissions have not previously been reported in the recombination of N₂OH⁺. Since there is N₂O⁺ present in the experimental spectrum, it is possible that some N₂O⁺ ions are recombining. However, the N₂O⁺ ion will react with H₂ six times for every recombination (see Table 4-2.12), Also, the NO $A \to X$, NO $B \to X$ and N₂ $C \to B$ emissions observed previously [Johnsen 2000b] in the recombination of N₂O⁺ are either too weak for positive identification or not present at all in this study, indicating that only small amounts, if any, of N₂O⁺ ions are recombining. The observed NH and N₂ emissions are thus very likely to origination from the recombination of protonated N₂O⁺.

4-2.9 Emissions from a plasma dominated by recombination of H_3S^+ ions

The emissions in this spectrum are only identified tentatively (see Table 4-2.9). They appear to be from SH, but do not match known spectroscopic constants. One of the peaks has an appearance very similar to the $A \rightarrow X$ emission of NH, but, this is not possible because the pre-run mass spectrum (see Appendix D) does not indicate the presence of nitrogen in any form. Figure 4-2.9 presents, among other things, a comparison between the emission observed for this system and the NH emission observed in the NH⁴₄ recombination.

If the emission is, indeed, SH, there are two possibilities. One is that the literature values for T_{00} are all too high. The lack of certainty in the value was mentioned in a recent paper [Resende 2001]. The lowest value mentioned there, also the one reported by NIST [2001a], is around 30662 cm⁻¹. The transition observed in these spectra corresponds, if it is the 0-0 transition, to a T_{00} of around 28600 cm⁻¹. The other
Emissions from a plasma containing recombining H_3S^+ ions

Recombination products [exothermicity,^{*a*} eV]: H + H₂S [6.29]; SH + H₂ [6.89] Non-destructive protonation exothermicity^{*a,b*} [2.93]

Product	SH
State $ au, \ \mu s^{\ a}$ $v_{max}, \ v_{max}^* \overset{b}{}$	$\begin{bmatrix} \sim \mathbf{A}^2 \Sigma^+ & p \end{bmatrix}$
Rel. Pop. ^c Rot. Temp., K ^d	1 [800 K]
v O	[1]

Reagent(s)^r (cm⁻³): H₂S, 3.5×10^{12} ; H₂, 6.2×10^{13} Attaching gas^r (cm⁻³): SF₆, 1×10^{11}

Relative electronic populations, relative vibrational populations and rotational temperatures are new data. All other values were taken or derived from other sources [Radzig 1985, NIST 2001]. $^{a-r}$ Notes for Tables 4-2.1 — 4-2.9 are in Table 4-2.10

possibility is that the observed transition is from v=1, but the Franck Condon factors (including those calculated by Resende, et al.) are very inaccurate, and such an identification is inconclusive (see Figure 4-2.9 for details). Since the Franck Condon factors are independent of T_e , the possibility of a misplaced T_e is possible. It could also be possible that this is some other transition of SH that is similar to the $A \to X$, but none has, so far, been identified. The issue could be resolved if high-resolution study of the system were performed. According to the Resende paper, experimental production of the $A \to X$ transition has been difficult. If the observed transition is



Figure 4-2.9: Illustration of the similarity to the SH $A \to X$ transition of the unknown emission in the spectrum from a plasma containing recombining SH₃⁺ ions. (a) Although one of the major features in the H₂/H₂S system (green, dashed) is similar to the NH $A \to X$ transition (red, solid, taken from the NH₄⁺ data presented earlier), they are not the same emission. (b) Transitions from the SH $A(v = 1) \to X$ state match energies for the two observed features, but the relative intensities are not correct. (c) A simulation of emissions from SH $A(v = 0) \to X$ matches the observed intensities, but the T₀₀ appears to be shifted. (d) Appearance of the spectrum if the simulated SH $A \to X$ transition is calculated with Te changed from 31040 to 30310.

the SH $A \to X$, then it is produced quite easily in the flowing afterglow and could be studied in some detail for its spectroscopic significance.





Figure 4-2.10: Detail of Xe emission from the recombination of XeH⁺. The oscillatory behavior evident to either side of the main emission is probably due to the variation in the proximity of the H and Xe atoms when the Xe emits.

4-2.12 Emissions from a plasma dominated by recombination of XeH^+ ions

Reagents added at RP3, number density: Xe, 6.2×10^{13} ; H_2 , 1.6×10^{13} . Attaching gas added at RP2, number density: CH_3I , 1×10^{11} .

XeH⁺ has been found to recombine fairly rapidly ($\alpha_e = 8.3 \times 18^{-8} \text{ cm}^{-3} \text{s}^{-1}$) [Le Padellec 1997]. The recombination is exothermic by 8.5 eV, an energy nearly resonant with the ${}^{3}P_{1}^{0} 6s[3/2]_{1}^{0}$ state of atomic Xe [Radzig 1985]. Since that state has a radiative lifetime of about 280 ns [Radzig 1985], observation of that atomic emission as a photoproduct of recombination is likely and, has, indeed, been observed (see Figure 4-2.10). Given the short lifetime, the hydrogen atom is likely, in a small percentage of cases, to be close to the xenon atom at the time of de–excitation. This proximity of the two atoms should have an effect on the observed spectrum. Figure 4-2.10 clearly shows the oscillatory behavior typical of a bound \rightarrow continuum transition. This recombination could be very useful as an intensity calibration since a photon has to be emitted for every recombination.

_Table 4-2.10_____

Notes for Tables 4-2.1 - 4-2.9

^{*a*} Where possible, exothermicities were calculated exclusively from thermodynamic data found in the NIST WebBook [NIST 2001], with supplemental information taken, as needed, from the compilation by Radzig and Smirnov [Radzig 1985]. Radiative lifetimes come exclusively from the latter.

^b v_{max} is the quantum number for the maximum vibrational level that can be populated by the recombination of a ground-state parent ion. The determination of v_{max}^* includes the protonation or charge transfer exothermicities, as appropriate, as well as the recombination energy. So, v_{max}^* is the quantum number for the maximum vibrational level that can be populated by the recombination of a parent ion in an excited state assuming that the excess energy is due only to the charge or proton transfer.

^c The relative population of each electronic state is based on the sum of photons observed to originate from that state. Implicit in this assumption is that any given upper state decays exclusively via the observed emissions. This assumption is necessary because state-to-state transition probabilities are generally not available for molecules (diatomic or otherwise). See also notes d, i and j. For emitting states with long radiative lifetimes, see also notes s and t.

^d Rotational temperatures are based on results from RVESIM (see Chapter 6), which uses a fairly simple algorithm. States that do not conform well to Hund's cases a and b, or that exhibit strong splitting, will not be treated well by the program. Electronic states that represent two or more near-degenerate variants (Π states for systems with an odd number of electrons, for example) for which only one set of spectroscopic constants is available will also be treated poorly by RVESIM. In all cases, thermal distributions are good to about 50% of the significant digit. Note that rotational distributions affect relative vibrational and electronic populations.

^e Relative vibrational populations are based on Franck-Condon factors calculated from a Morse potential. The vibrational potentials of many diatomic species are approximated fairly well by a Morse potential, but few are truly Morse potentials. Vibrational populations will be most reliable at lower vibrational quanta (v) where the Morse potential is most reliable. See also notes h and i.

^f Due to a rapidly changing system efficiency in the spectral region from about 750 nm up, the populations of the following states might be overestimated: CO d, v=1 and a', v=5; N₂ B, v=2.

 g Emissions from the *e* state of CO are weak, if present, and obscured by emissions from the *d* and *a'* states in all spectra considered here. So, it is not possible to determine a rotational temperature for the *e* state.

 h Either the A states of OH and NH have non-thermal rotational distributions or they deviate strongly from the standard model used in RVESIM (see Chapter 6). See also note d.

 i Either there are no emissions from this state within the available spectral range or the emissions have very small transition probabilities.

 j This state is not energetically accessible, but it is observed.

^k There is sufficient energy to either vibrationally dissociate this state or to populate it at $v \ge 20$ (calculated using a Morse potential).

^l Radiative lifetimes for the following electronic states of CO are available only for single vibrational states: a', v=4; d, v=1; e, v=4.

 m This emission is partly or totally obscured by another emission.

 n This emission or set of emissions were of sufficiently low intensity as to make positive identification and/or quantification difficult.

 o One or more intense emissions from this state occur outside the available spectral range.

 p There are uncertainties about the spectroscopic characteristics of the SH A state [Resende 2001], and this identification is uncertain. See text.

^q Values for protonation at different positions in this molecule are not available (as they are for CO and NNO, for example).

 r Reagent gases were added through RP3. Attaching gases were added through RP2.

^s The emissions from this state are partly or wholly due to cascade from the higher, triplet, electronic states of CO. This observation has been used to set an upper limit for the time CO molecules in the *a* state spend in viewing range of the spectrometers. The upper limit assumes that: (1) the higher triplet states (*d*, *a'* and *e*) will all have radiated within the viewing region; (2) that the $a \to X$ emissions are collected starting from the moment of the formation of the *a* state; (3) the simulation algorithm employed in RVESIM and the corrections for optical system transmission efficiency are sufficiently accurate. Based on these assumptions, the maximum time the *a* state was within the viewing region is about 0.3, 1 and 0.7 ms, respectively, for the HCO⁺, CO⁺₂ and HCO⁺₂ systems.

 t CS *a* state populations are based on the assumption that CS molecules in the *a* state were formed within the viewing region of the spectrometers and that they stayed within that region for about 2 ms.

Table 4-2.11 _____

Table 4-2.11: The energies required to produce observed emissions directly from neutral, unprotonated parent molecules (that is, not via recombination). The first column contains the parent molecule. The second column contains one or more ground state fragmentation paths, with required energy for the production of the indicated vibronic state. In the third column are listed the excited states observed for that system with total energy (including the energy from the second column) required for the indicated excitation. Letters in the third column indicate excited electronic states and numbers in parentheses indicate the vibrational level for which the energy was calculated. Energies were calculated for the zeroth vibrational level and the highest observed vibrational level (out of all spectra) for observed electronic states. All energies are given in eV and enclosed in square brackets.

Energies Required to Produce Observed Emissions

From Neutral Parent (Reagent) Molecules

Parent Children [Required Energy, eV]

	To Ground–State	With Indicated Excitation				
Processes	Involving Ions:					
CH_4	$CH + H^+ + H_2 [22.8]$	CH:	A(0) [25.8];	A(2) [26.5];	B (0) [26.1]	
$\rm CO_2$	$O^+ + CO [19.1]$	CO:	a(0) [25.3];	a(4) [26.1];		
			A(0) [27.3];	A(5) [28.2]		
CS_2	$S^{+} + CS [14.9]$	CS:	a(0) [18.4];	a(4) [19.0];		
			A(0) [19.8];	A(5) [20.4]		
H_2S	$H^{+} + SH [17.5]$	SH:	A(0) [21.5]			
NH_3	$NH + H_2^+$ [19.8]	NH:	A(0) [23.7];	A(1) [24.1];	c(0) [25.4]	
N_2O	$N_2 + O^+ [15.4]$	N_2 :	B(0) [22.8];	B(9) [24.6]		
	$N^{+} + NO [19.5]$	NO:	A(0) [25.1];	A(2) [25.7];	B(0) [25.3]	
Neutral F	Processes:					
CH_4	$CH + H + H_2$ [9.2]	CH:	A(0) [12.3];	A(2) [12.9];	B(0) [12.5]	
$\rm CO_2$	O + CO [5.5]	CO:	a(0) [11.7];	a(4) [12.5];		
			A(0) [13.7];	A(5) [14.5]		
CS_2	S + CS [4.6]	CO:	a(0) [8.1];	a(4) [8.6];		
			A(0) [9.5];	A(5) [10.1]		
H_2S	H + SH [3.9]	SH:	A(0) [7.9]			
NH_3	$NH + H_2$ [4.4]	NH:	A(0) [8.3];	A(1) [8.6];	c(0) [10.0]	
N_2O	$N_2 + O[1.7]$	N_2 :	B(0) [9.2];	B(9) [11.0]		
	N + NO[5.0]	NO:	A(0) [10.6];	A(2) [11.2];	B(0) [10.7]	

See description on previous page

Table 4-2.12: Comparisons of relative frequencies for several important processes occuring in the reactive flow. For definitions of all comparisons, f, see Section 3-7. Also included in the table are results for use of the empirical equation for the number of collisions, $Z_{V,T}$, required to relax a gas by vibrational-translational energy transfer (see Equation 3-7 and all of Section 3-6). The value of the lowest vibrational frequency for the ion, ν_{min} , is also given. The letter following ν_{min} , indicates the source of the number as <u>NIST [NIST 2001]</u>, <u>H</u>erzberg [Herzberg 1991] or <u>C</u>alculation using Hartree– Fock self-consistent field theory [Wavefunction, Inc. 2001]. The particular basis set varied according to the complexity of the ion, but was always part of the 6-31(G) series of basis sets.

Keep in mind the limitations of the empirical form of $Z_{V,T}$ (Equation 3-7, also below). It assumes pure, neutral gas and describes the average number of collisions needed to relax the least energetic mode by a single vibrational quantum. The number is still useful, though. It provides us with a best–case scenario. If the number of collisions prior to recombination is less than or even comparable to $Z_{V,T}$ then there is little chance that a significant number of the recombining ions are vibrationally relaxed.

Information regarding reagent concentrations and, where available, recombination coefficients, can be found at the beginning of the section for that reactive system (Sections 4-1.1-10).

The following definitions are also in Sections 3-7 and 3-8.

$$Z_{V,T} = e^{C\nu_{min}}$$
 3-7

$$f_{\nu,XYZ} = \frac{Z_{XYZ^+,XYZ}}{Rate_{XYZ^+,e^-}}$$

$$3-10$$

$$f_{\nu,He} = \frac{Z_{XYZ^+,He}}{Rate_{XYZ^+,e^-}}$$
 3-11

$$f_{R,Ar^{+}} = \frac{Rate_{Ar^{+},H_{2}}}{Rate_{Ar^{+},XYZ}} \qquad f_{R,XYZ^{+}} = \frac{Rate_{XYZ^{+},H_{2}}}{Rate_{XYZ^{+},e^{-}}}$$
3-12

Reactive System	Recombining Ion	$ \nu_{min} $ (cm ⁻¹)	$Z_{V,T}$ (collisions)	$f_{\nu,XYZ}$	$f_{\nu,He}$	f_{Ar^+}	f_{XYZ^+}
CO_2	CO_2^+	462 (H)	2600	7.0	5400		
$\rm CO_2/H_2$	HCO_2^+	598 (C)	140	5.1	7900	2.1	20
$\mathrm{CH}_4/\mathrm{H}_2$	CH_5^+	605 (C)	150	0.1	2500	4.7	4.6
$(\mathrm{CH}_3)_2\mathrm{OH}^+/\mathrm{H}_2$	HCO_2^+	144 (C)	3	0.2	2500	4.7	4.0
$\rm CO/H_2$	HCO^+ COH^+	983 (C) 54 (C)	$3500 \\ 1.6$	1.8	2.7×10^4	33	2×10^{4}
CS_2 The collision	CS_2^+ partner for CS_2^+	305 (H) $S_2^+ is CO_2$	180	11	5400		
$\mathrm{H}_{2}\mathrm{O}/\mathrm{H}_{2}$	H_3O^+	526 (N)	79	373	2700	15	20
$\mathrm{H}_2\mathrm{S}/\mathrm{H}_2$	H_3S^+	1033 (N)	5300	0.3	7300	13	12
$\mathrm{NH}_3/\mathrm{H}_2$	NH_4^+	1447 (N)	1.6×10^{5}	0.1	1900	3.6	4.6
$\rm NO/H_2$	HNO^+ NOH^+	1055 (C) 1301 (C)	$6400 \\ 4.9 \times 10^4$	2.9	1.4×10^{4}	1.3	3.0×10^{4}
N_2O/H_2	$N_2 OH^+$	475 (C)	51	2.1	6400	4.3	6.0
O_2/H_2	O_2H^+	1307 (C)	5.1×10^{4}	0.09	5400	84	4.6
OCS	OCS^+	419 (N)	1200	0.01	5400		
OCS/H_2	$OCSH^+$ $HOCS^+$	368 (C) 410 (C)	$21\\30$	0.01	5400	80	4.2
Xe/H_2	XeH^+	2180 (C)	7.2×10^{7}	15	3.4×10^{4}		

Relative Frequencies for Selected Processes

Table 4-2.12 _____

See the description on the previous page.

Tables 4-2.13a and 4-2.13b $_$

Tables 4-2.13a and 4-2.13b: ν_{HF} values were calculated in Spartan '02 [Wavefunction, Inc 2001] using Hartree Fock (HF) self-consistent field (SCF) at the 6-31G* (4-2.13a) and 6-31+G* (4-2.13b) levels of theory. Experimental values are from NIST [NIST 2001] except starred (*) values [Herzberg 1991]. Values for infrared inactive modes are italicized and underlined. ^{*a*} The HOCO⁺ molecule is bent in the ground state (according to the HF calculation): the OCO portion of the molecule is linear, but the hydrogen is angled with respect to the other three atoms. In the OCO || bend mode, the OCO portion of the molecule bends in the plane formed by the angled hydrogen. Similarly, in the OCO \perp bend mode, the OCO portion is bending perpendicular to the plane formed by the hydrogen. HNNO⁺ and NNOH⁺ have similar structures, with analogous designations. ^{*b*} The || and \perp designations are with respect to the nodal plane of the highest occupied molecular orbital.

$\rm CO_2$			HCO_{2}^{+}			
Mode Bend Symm. Str Asym. Str	$ $	$ $	Mode OCO \parallel Bend ^{<i>a</i>} OCO \perp Bend ^{<i>a</i>} HOC Bend	$ $	ν _{Exp.}	
Bend	CO_2^+	462 6-719 7	Symm. OCO Stretch Asym. OCO	1369.13	1500	
Symm. Str Asym. Str	<u>1355.5</u> 961.37	<u>1244.3</u> 1422	Stretch OH Stretch	2696.08 3736.23	2300 3375.37	
	CS_2			CS_2^+		
Mode Bend Symm. Str Asym. Str	ν _{HF} 445.49 <u>724.94</u> 1582.9	$ u_{Exp.} $ 396* <u>657.98</u> * 1535.4*	Mode Bend \parallel^b Bend \perp^b Symm. Str Asym. Str	$ $	$ $	

Normal–Mode Frequencies (cm^{-1}) for Selected Molecules and Ions

_____ Table 4-2.13a _____

See the description on the previous page.

_ Table 4-2.13b _

 $HNNO^+$ $NNOH^+$ Mode Mode ν_{HF} $\nu_{Exp.}$ ν_{HF} $\nu_{Exp.}$ ONN \parallel Bend NNO || Bend 713.69 474.52 $\mathrm{ONN}\perp\mathrm{Bend}$ 698.34NNO \perp Bend 532.94 HNN Bend 472.23HON Bend 1534.34Symm. NNO Symm. ONN Stretch 1632.25Stretch 1077.36 Asym. ONN Asym. NNO Stretch 2639.47 Stretch 2813.25 OH Stretch NH Stretch 3621.14 3744.05 3330.91 N_2O Mode ν_{HF} $\nu_{Exp.}$ Bend 669.45 588.78^{*} Symm. Str 1376.83 1284.9^{*} Asym. Str 2623.09 2223.76^{*}

Normal–Mode Frequencies for Selected Molecules and Ions

See the description preceding Table 4-2.13a.

4-3 Other (Non–Recombination) Results

The presence of emissions (see Section 4-1) that behave, to some degree, as though they arise from electron-ion recombination, but that are not energetically accessible products of the process, led to more detailed investigations of the experimental procedure. In particular, the sequence of reactions that were assumed to culminate in dissociative recombination have been considered. These investigations have produced a number of interesting, and often unexpected, results.

The primary focus of these investigations is the flowing plasma, called here the *base plasma*, into which the other reactants were injected. Section 4-3.1 presents a detailed description of the species present in the base plasma, including probable production mechanisms. Some of the more interesting species observed in the spectra were electronically excited states of neutral dihelium and of Ar^+ , also called Ar(II). In Section 4-3.2, the effect of addition of an attaching gas on the base plasma is discussed. It is found that the addition of an attaching gas quenches nearly all the emissions. The exceptions are a few excited states of atomic helium. A possible explanation for this behavior is presented.

4-3.1 Characterization of the He and He-Ar Plasmas

Spectra were taken of the base plasma before and after the addition of argon. That is to say, one set of spectra were taken in a pure He afterglow, where only Reactions 2-3 and 2-4 could occur and another set of spectra were taken after the addition of Ar, where 2-5 could also occur. Most of the emissions in these spectra have been identified, and a few of the identifications are surprising. Details of the contents of the plasmas before and after the addition of argon can be found in a series of graphs in Appendix B. Relative populations for the various species have been determined using the atomic simulation feature in RVESIM (rotational vibrational

_ Table 4-3.1 _____

Table 4-3.1: Atomic helium transitions observed in the base plasma and the relative upper state populations implied by the emission intensities. Upper state populations are corrected for *J*-value statistics (see text); values presented are relative to each other with the most populated state assigned a value of one. Underlined transitions survived addition of the attaching gas (see section 4-2.2). Legend: *ns* and *np* are the orbital occupied by the electron that changes during the transition. nm is the wavelength at which the transition occurs. Pop. is the relative population for that state. Numerical entries of the form X(Y) are abbreviations for $X \times 10^{Y}$. _____ Table 4-3.1 _____

Observed Atomic Helium Transitions and Implied Relative Upper State Populations

Trans	itions to:	$2p \ ^{3}P_{0,1}^{0}$,2	From Se	eries:	$ns \ ^3S_1$		
ns	10s	8s	6s	5s	4s	$\underline{3s}$		
nm	356.3	365.2	386.8	412.1	471.3	706.5		
Pop.	6.6(-4)	9.4(-4)	1.2(-3)	1.1(-2)	4.1(-2)	<u>5.8(-1)</u>		
Trans	itions to:	$2s \ {}^{3}S_{1}$		From Se	eries:	$np {}^{3}P_{0,1,}^{0}$	2	
np	10p	$9\mathrm{p}$	$8\mathrm{p}$	$7\mathrm{p}$	6p	5p	4p	$\underline{3p}$
nm	267.7	269.6	272.3	276.4	282.9	294.5	318.8	<u>388.9</u>
Pop.	4.8(-3)	6.9(-3)	8.4(-3)	1.9(-2)	5.4(-2)	4.6(-2)	4.9(-2)	<u>1.5(-1)</u>
Trans	itions to:	$2p \ ^{3}P_{0.1}^{0}$.2	From Se	eries:	$nd \ ^{3}D_{1,2}$.3	
nd	10d	9d	8d	7d	6d	5d	<u>4d</u>	<u>3d</u>
nm	355.4	358.7	363.4	370.5	382.0	402.6	447.2	<u>587.6</u>
Pop.	1.9(-3)	1.8(-3)	3.2(-3)	5.5(-3)	8.3(-3)	9.2(-2)	<u>1.1(-1)</u>	5.5(-1)
		. ,						
Trans	itions to:	$2p \ ^{1}P_{1}^{0}$		From Se	eries:	$ns \ ^1S_0$		
Trans ns	itions to: 8s	$2p \ ^{1}P_{1}^{0}$ 7s	6s	From Se 5s	eries: 4s	$ns {}^1S_0$ <u>3s</u>		
Trans ns nm	itions to: 8s 393.6	$2p {}^{1}P_{1}^{0}$ 7s 402.4	6s 416.9	From Se 5s 443.8	eries: 4s 504.8	$ns {}^{1}S_{0}$ $\underline{3s}$ $\underline{728.1}$		
Trans <i>ns</i> nm Pop.	itions to: 8s 393.6 7.9(-3)	$2p {}^{1}P_{1}^{0}$ 7s 402.4 1.7(-2)	6s 416.9 1.4(-2)	From Se 5s 443.8 2.5(-2)	eries: 4s 504.8 1.5(-1)	$ns {}^{1}S_{0}$ $\underline{3s}$ $\underline{728.1}$ $\underline{2.8(-1)}$		
Trans <i>ns</i> nm Pop.	itions to: 8s 393.6 7.9(-3)	$2p {}^{1}P_{1}^{0}$ 7s 402.4 1.7(-2)	6s 416.9 1.4(-2)	From Se 5s 443.8 2.5(-2)	eries: 4s 504.8 1.5(-1)	$ns {}^{1}S_{0}$ $\underline{3s}$ $\underline{728.1}$ $\underline{2.8(-1)}$		
Trans ns nm Pop. Trans	itions to: 8s 393.6 7.9(-3) itions to:	$2p {}^{1}P_{1}^{0}$ 7s 402.4 1.7(-2) $2s {}^{1}S_{0}$	6s 416.9 1.4(-2)	From Se 5s 443.8 2.5(-2) From Se	eries: 4s 504.8 1.5(-1) eries:	$ns {}^{1}S_{0}$ $\underline{3s}$ $\underline{728.1}$ $\underline{2.8(-1)}$ $np {}^{1}P_{1}^{0}$		
Trans ns nm Pop. Trans <i>np</i>	itions to: 8s 393.6 7.9(-3) itions to: 10p	$2p {}^{1}P_{1}^{0}$ 7s 402.4 1.7(-2) $2s {}^{1}S_{0}$ 9p	6s 416.9 1.4(-2) 8p	From Se 5s 443.8 2.5(-2) From Se 7p	eries: 4s 504.8 1.5(-1) eries: 6p	$ns {}^{1}S_{0}$ $\underline{3s}$ $\underline{728.1}$ $\underline{2.8(-1)}$ $np {}^{1}P_{1}^{0}$ $5p$	4p	<u>3p</u>
Trans ns nm Pop. Trans <i>np</i> nm	itions to: 8s 393.6 7.9(-3) itions to: 10p 323.1	$2p {}^{1}P_{1}^{0}$ 7s 402.4 1.7(-2) $2s {}^{1}S_{0}$ 9p 325.8	6s 416.9 1.4(-2) 8p 329.7	From Se 5s 443.8 2.5(-2) From Se 7p 335.5	eries: 4s 504.8 1.5(-1) eries: 6p 344.8	$ns {}^{1}S_{0}$ $\underline{3s}$ $\underline{728.1}$ $\underline{2.8(-1)}$ $np {}^{1}P_{1}^{0}$ $\underline{5p}$ 361.4	4p 396.5	<u>3p</u> 501.6
Trans ns nm Pop. Trans np nm Pop.	itions to: 8s 393.6 7.9(-3) itions to: 10p 323.1 1.3(-3)	$2p {}^{1}P_{1}^{0}$ 7s 402.4 1.7(-2) $2s {}^{1}S_{0}$ 9p 325.8 2.4(-3)	6s 416.9 1.4(-2) 8p 329.7 2.4(-3)	From Se 5s 443.8 2.5(-2) From Se 7p 335.5 1.4(-3)	eries: 4s 504.8 1.5(-1) eries: 6p 344.8 6.2(-3)	$ns {}^{1}S_{0}$ $\underline{3s}$ $\underline{728.1}$ $\underline{2.8(-1)}$ $np {}^{1}P_{1}^{0}$ $\underline{5p}$ 361.4 $9.8(-3)$	4p 396.5 2.6(-2)	$\frac{3p}{501.6}$ 4.2(-1)
Trans ns nm Pop. Trans np nm Pop.	itions to: 8s 393.6 7.9(-3) itions to: 10p 323.1 1.3(-3)	$\begin{array}{c} 2p \ ^{1}P_{1}^{0} \\ 7s \\ 402.4 \\ 1.7(-2) \\ \\ 2s \ ^{1}S_{0} \\ 9p \\ 325.8 \\ 2.4(-3) \end{array}$	6s 416.9 1.4(-2) 8p 329.7 2.4(-3)	From Se 5s 443.8 2.5(-2) From Se 7p 335.5 1.4(-3)	eries: 4s 504.8 1.5(-1) eries: 6p 344.8 6.2(-3)	$ns {}^{1}S_{0}$ $\underline{3s}$ $\underline{728.1}$ $\underline{2.8(-1)}$ $np {}^{1}P_{1}^{0}$ $\underline{5p}$ 361.4 $9.8(-3)$	4p 396.5 2.6(-2)	$\frac{3p}{501.6}$ <u>4.2(-1)</u>
Trans nm Pop. Trans np nm Pop. Trans	itions to: 8s 393.6 7.9(-3) itions to: 10p 323.1 1.3(-3) itions to:	$2p \ {}^{1}P_{1}^{0}$ 7s 402.4 1.7(-2) $2s \ {}^{1}S_{0}$ 9p 325.8 2.4(-3) $2p \ {}^{1}P_{1}^{0}$	6s 416.9 1.4(-2) 8p 329.7 2.4(-3)	From Se 5s 443.8 2.5(-2) From Se 7p 335.5 1.4(-3) From Se	eries: 4s 504.8 1.5(-1) eries: 6p 344.8 6.2(-3) eries:	$ns {}^{1}S_{0}$ $\underline{3s}$ $\underline{728.1}$ $\underline{2.8(-1)}$ $np {}^{1}P_{1}^{0}$ $\underline{5p}$ 361.4 $9.8(-3)$ $nd {}^{1}D_{2}$	4p 396.5 2.6(-2)	$\frac{3p}{501.6}$ <u>4.2(-1)</u>
Trans nm Pop. Trans np nm Pop. Trans nd	itions to: 8s 393.6 7.9(-3) itions to: 10p 323.1 1.3(-3) itions to: 10d	$2p {}^{1}P_{1}^{0}$ 7s 402.4 1.7(-2) $2s {}^{1}S_{0}$ 9p 325.8 2.4(-3) $2p {}^{1}P_{1}^{0}$ 9d	6s 416.9 1.4(-2) 8p 329.7 2.4(-3) 8d	From Se 5s 443.8 2.5(-2) From Se 7p 335.5 1.4(-3) From Se 7d	eries: 4s 504.8 1.5(-1) eries: 6p 344.8 6.2(-3) eries: 6d	$ns {}^{1}S_{0}$ $\underline{3s}$ $\underline{728.1}$ $\underline{2.8(-1)}$ $np {}^{1}P_{1}^{0}$ $\underline{5p}$ 361.4 $9.8(-3)$ $nd {}^{1}D_{2}$ $\underline{5d}$	4p 396.5 2.6(-2) <u>4d</u>	$\frac{3p}{501.6}$ <u>4.2(-1)</u> <u>3d</u>
Trans nm Pop. Trans np nm Pop. Trans nd nm	itions to: 8s 393.6 7.9(-3) itions to: 10p 323.1 1.3(-3) itions to: 10d 383.4	$\begin{array}{c} 2p\ ^{1}P_{1}^{0}\\ 7s\\ 402.4\\ 1.7(-2)\\\\ 2s\ ^{1}S_{0}\\ 9p\\ 325.8\\ 2.4(-3)\\\\ 2p\ ^{1}P_{1}^{0}\\ 9d\\ 387.2\\ \end{array}$	6s 416.9 1.4(-2) 8p 329.7 2.4(-3) 8d 392.7	From Se 5s 443.8 2.5(-2) From Se 7p 335.5 1.4(-3) From Se 7d 400.9	eries: 4s 504.8 1.5(-1) eries: 6p 344.8 6.2(-3) eries: 6d 414.4	$ns {}^{1}S_{0}$ $\underline{3s}$ $\underline{728.1}$ $\underline{2.8(-1)}$ $np {}^{1}P_{1}^{0}$ $\underline{5p}$ 361.4 $9.8(-3)$ $nd {}^{1}D_{2}$ $\underline{5d}$ 438.8	4p 396.5 2.6(-2) 4d 492.2	$3p \\ 501.6 \\ 4.2(-1) \\ 3d \\ 667.8 \\ 3p \\ 3p \\ 667.8 \\ 3p \\ 3p \\ 3p \\ 3p \\ 3p \\ 667.8 \\ 3p \\ 3$

See the description on the previous page.

<u>electronic simulation</u>, see Chapter 6). These are graphed and discussed below. Mass spectra for these plasmas are also included in Appendix B.

The presence of excited states of atomic helium in the μ -wave discharge is not surprising. It is, however, somewhat surprising to find so many excited states present in the flow downstream at RP3. Indeed, all singly excited states of He(I) [NIST 2001b] that are sufficiently intense and that fall within the range of the optical spectrometers are observed. The helium is excited by collisions with high energy electrons in the microwave discharge. Some of the photons, then, are carried down the flowtube by absorption and re-emission. There is also the possibility that some of the light is simply being reflected along the interior wall of the flowtube. But, considering the results presented in the next section (4-3.2), internal reflection seems an unlikely explanation for the observed radiation. Many of the observed emissions correspond to decay to one of the helium metastable states. One of them, the $2s^1S_0$ state, is metastable because transition to the ground state is forbidden under the selection rule $\Delta \ell = \pm 1.^{\dagger}$ The other, the $2s^3S_1$ state, is metastable for the same reason and also because the decay to the ground state would violate the somewhat less rigorous selection rule $\Delta S = 0.^{\dagger}$ A complete list of the observed atomic helium transitions is in Table 4-3.1 and also in Appendix B.

Included in the list of transitions in Table 4-3.1 are the relative populations of the upper states as implied by the observed transition intensities. In these cases, and throughout this document, observed state populations have been corrected for J-value statistics, where J is the overall angular momentum quantum number for a given electronic state. The degeneracy for a state in level J is 2J + 1. Observed relative populations are divided by the relevant degeneracy.

[†] ℓ is the quantum number describing the angular momentum of the orbital occupied by the electron that changes orbitals during the transition and S is the sum of the spin quantum numbers for all the electrons in the atom.

In addition to excited states of atomic helium, a number of excited states of neutral dihelium, He₂ [NIST 2001a, Radzig 1985], are observed. These are identified on the series of spectra and associated keys in Appendix B. The emissions involve both singlet and triplet states of the dihelium, but emissions involving the triplet states are by far the more intense. Since transition probabilities for dihelium are not generally available, it it not possible to make statements about relative populations of the states. That is to say, the singlet states might well be populated more than the triplet states, but the triplet states might simply radiate more readily. It is not known whether the He₂ is produced in or downstream of the μ -wave source.

It is likely that these molecules are produced by three–body association of electronically excited helium atoms and neutral helium atoms. Experimental studies [Ludlum 1967] have shown that the metastable triplet dihelium ground state is produced by such a mechanism:

$$2He + He(2s^{3}S_{1}) \xrightarrow{\sim 2 \times 10^{-34} \text{ cm}^{6}/\#^{2}s} He_{2}(2s^{3}\Sigma_{u}^{+}) + He + 1.96 \text{ eV} \quad 46$$

No studies have be conducted concerning similar production of electronically excited states of dihelium. However, it is certainly possible that similar processes might occur involving three–body interactions between some other excited state of helium and two other helium atoms that are likely to be in the ground state, but that might be excited as well. Such associations would be far more likely where the energy barrier is small. For example [Ginter 1970 & 1965b], two separated He atoms in states $1s2p^{3}P$ and $1s^{2}{}^{1}S$ correlate with the dihelium molecular states $2p\pi {}^{3}\Pi_{g}(b)$, $3d\sigma {}^{3}\Sigma_{u}^{+}(f)$ and $3d\pi {}^{3}\Pi_{u}(f)$. But, only the *b* state is likely to be populated significantly unless the activation energy necessary for the *f* states (~ 0.5 eV) is available:

$$2He + He(2p^{3}P) \xrightarrow{low E} He_2(2p\pi^{3}\Pi_g) + He + 2.51 \ eV \quad 47$$

Excited states that could not be produced in this manner could perhaps be produced by electron–impact excitation of existing dihelium molecules or by the radiative de– excitation of dihelium molecules in higher electronic states. When the excited states of dihelium were initially characterized [Brown 1971 & 1973, Ginter 1965a,b, 1966 & 1969, Gloersen 1965, Orth 1976], the states were produced by passing helium through a discharge, a procedure similar to that used to produce ionization in these studies. A third production mechanism, which is discussed in more detail in the next section (4-3.2) involves the bimolecular reaction of a helium atom in its ground state with another He atom in a singly excited state with $n \geq 3$ [Lichten 1974]:

$$He + He(n \ge 3) \to He_2^+ + e^- \tag{48}$$

It is very likely (see next section) that this mechanism is significant.

In situations where argon was added, one class of species found in the plasma, excited states of Ar^+ , was not expected. Table 4-3.2 lists the emissions observed as well as the apparent relative populations of the upper states. Also listed are maximum populations of states that, if present, corresponded to transitions too faint to be considered significant. Only a narrow range of the possible excited states of Ar^+ [Bashkin 1975, NIST 2001b] are observed to be present in sufficient amounts for positive identification. Given the narrow range of states observed, it seems likely that the excitation is being caused by a reaction rather than by collisions with energetic electrons. Since argon is a noble gas, there are few species present in the tube that will excite an argon ion rather than neutralize it. But excited states of helium and dihelium are in abundant supply in the flowtube and are the likely sources of the excitation.

Which helium species, atomic or diatomic, is (or are) causing the excitation of the Ar⁺ is uncertain. Energetically speaking, it is possible that metastable states of atomic helium are reacting with the Ar⁺ in its ground state $(3s^23p^{5\,2}P^0)$, exciting the Ar⁺ and deexciting the helium. The energies are (see Figure 4-3.1): 20.616 eV and 19.82 eV for the singlet and triplet He metastables and a range of 19.22–19.76 eV for the excitation above ground state observed in the Ar⁺. The main problem with this _____ Table 4-3.2 ______

Configuration and Term	Level Energy	Relative Population*
$3s^2 3p^4 [^3P] 4p^1 \ ^4P^0_{5/2}$	19.22	0.9
$3s^2 3p^4 [^3P] 4p^1 \ ^4P^0_{3/2}$	19.26	1.0
$3s^2 3p^4 [^3P] 4p^1 \ ^4P^0_{1/2}$	19.31	0.3
$3s^2 3p^4 [^3P] 4p^1 \ ^4D^0_{7/2}$	19.49	0.7
$3s^2 3p^4 [{}^3P] 4p^1 {}^4D^0_{5/2}$	19.55	0.4
$3s^2 3p^4 [{}^3P] 4p^1 {}^4D^0_{3/2}$	19.61	0.2
$3s^2 3p^4 [^3P] 4p^1 \ ^4D^0_{1/2}$	19.64	0.1
$3s^2 3p^4 [{}^3P] 4p^1 {}^2D^0_{5/2}$	19.68	0.2
$3s^2 3p^4 [^3P] 4p^{1\ 2} D^0_{3/2}$	19.76	0.1
$3s^2 3p^4 [^3P] 4p^{1\ 2} P^0_{1/2}$	19.80	(0.02)
$3s^2 3p^4 [^3P] 4p^{1\ 2} P^0_{3/2}$	19.87	(0.003)
$3s^2 3p^4 [^3P] 4p^1 \ ^4S^0_{3/2}$	19.97	(0.002)
$3s^2 3p^4 [^3P] 4p^{1\ 2} S^0_{1/2}$	19.97	(0.02)
Other states through energy:	24.83	(< 0.005)

Relative Upper State Populations for Observed Ar^+ Transitions

*Relative populations are corrected for J-value statistics (see Section 4-2.1). () Populations in parentheses are maximum values possible. Their inclusion does not necessarily imply that those states are present; the intensities are too weak for more certain quantification.

mechanism is that, while the energies are certainly similar, they are hardly resonant. So, it would be necessary that the substantial 0.06-1.40 eV excess of translational energy be carried away. The Ar⁺ and the He could become translationally excited or



Figure 4-3.1: Comparison of upper–state energy levels for the observed transitions of Ar^+ to energies of species that could excite Ar^+ to the observed energies. Numbers beside diatomic levels are vibrational quanta. Vibrational energies assume Morse–like potentials and are derived from tabulated constants [NIST, 2001].

a third body could be involved, e. g.:

$$He(2s^{1}S_{0}, 2s^{3}S_{1}) + Ar^{+}(3s^{2}3p^{5\,2}P^{0}) + M \xrightarrow{possible, unlikely} \longrightarrow He(1s^{2\,1}S_{0}) + Ar(3s^{2}3p^{4}[^{3}P]4p: {}^{4}P^{0}, {}^{4}D^{0}, {}^{2}D^{0}) + M^{*}$$

$$49$$

where M represents the third body. Without more detailed experimental or computational information, it is impossible to predict the probability of such a reaction. If, for example, the energy transfer occurs at a set of internuclear separations corresponding to a position on the repulsive curve between two ground state helium atoms (one of them having just entered the ground state as a result of the reaction; this is the ground state of He₂), then the reaction, and the large amount of translational excitation would be possible.

However, comparisons of the spectra taken before and after the addition of argon do not readily support Reaction 8. Intensities of emissions from atomic helium do not change significantly after argon is added to the flow. Instead, intensities of the dihelium emissions change (see Figure 4-3.2). So it is likely that He_2 is the source of the excitation in the argon ions:

$$He_{2}(excited) + Ar^{+}(3s^{2}3p^{5\,2}P^{0}) \xrightarrow{possible} \rightarrow 2He(1s^{2\,1}S_{0})^{*} + Ar(3s^{2}3p^{4}[^{3}P]4p: {}^{4}P^{0}, {}^{4}D^{0}, {}^{2}D^{0})^{*} 50$$

where the asterisk (*) indicates possible translational excitation. It is necessary, for the emissions observed here, that the dihelium be in some sort of excited state. The lowest vibrational levels of the $a 2s {}^{3}\Sigma_{u}^{+}$, $b 2p {}^{3}\Pi_{g}$, $A 2s {}^{1}\Sigma_{u}^{+}$ and $B 2p {}^{1}\Pi_{g}$ states, the observed destination states for dihelium emissions, are not energetic enough to excite the argon ion to the observed upper states. The minimum vibrational levels with sufficient energy, assuming Morse-potential behavior, are: a, 7; b, 4; A, 5; and B, 3. A non-thermal population would be required for population of these vibrational levels. But in the plasma environment, with excitation by energetic electrons, non-thermal



Figure 4-3.2: Comparison of spectra before (solid, red) and after (dashed, green) the addition of Ar. The wavelength regions were chosen because emissions from He, He₂ and Ar⁺ are prominent features in them. Note that the intensities of the atomic He emissions (upper-case, un-rotated, alpha-numeric labels) do not change significantly while the intensities of the dihelium emissions (rotated labels with lower-case Greek and Roman letters) decrease, and, of course, the Ar⁺ emissions appear. Identifications refer to the legend key found in Appendix B.

			Transition Wavelengths (nm)						
$ Ar^+$ Upper State $$			—— Gro	$[3/2]^{\dagger}$ —	– — Grou	und $[1/2]^{\ddagger}$ —			
Configuration	Term	Energy	nm	$A_{(}k,i)$	nm	$A_{(}k,i)$			
$3s^2 3p^4 (^3P) 4s^1$	${}^{2}P_{3/2}$	17.140	72.336	$2.3 \times 10^{+01}$	73.093	$4.5 \times 10^{+00}$			
$3s^2 3p^4 (^3P) 4s^1$	${}^{2}P_{1/2}$	17.266	71.809	$9.5 \times 10^{+00}$	72.555	$1.9 \times 10^{+01}$			
$3s^23p^4 (^3P) 3d^1$	${}^{2}P_{1/2}$	17.942	69.104		69.794				
$3s^23p^4 (^3P) 3d^1$	${}^{2}P_{3/2}$	18.061	68.649		69.330				
$3s^2 3p^4 \ (^1D) \ 4s^1$	${}^{2}D_{3/2}$	18.427	67.286		67.940	*			
$3s^2 3p^4 \ (^1D) \ 4s^1$	${}^{2}D_{5/2}$	18.454	67.185	*					
$3s^23p^4 (^3P) 3d^1$	${}^{2}D_{3/2}$	18.657	66.456	*	67.095	*			
$3s^23p^4 (^3P) 3d^1$	${}^{2}D_{5/2}$	18.733	66.187	*					
ť	$3s^23p^5$	${}^{2}P_{3/2}^{0}$ [0.	$00 \mathrm{eV}];$	$\ddagger 3s^2 3p^5 \ ^2P_{1/2}^0$	$_{2} [0.18 \text{ eV}]$				

Ar^+	Far	VUV	Emissions	Expected	if He_2	Is Source	of Ar^+	Excitation
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Table 4-3.3: List of emissions not observable with the current experimental apparatus that are expected when the Ar⁺ is being excited by He₂ in the *a*, *b*, *A* and *B* states. Where transition probabilities $(A_{k,i})$ are reported by NIST, they are included here. Transitions without transition probabilites but that are reported by NIST are indicated by an asterisk (*). Transitions with neither $A_{k,i}$ nor an asterisk were calculated from Ar⁺ energy levels as reported by NIST. Only transitions that satisfy the following selection rules are included: $\Delta \ell = \pm 1$, $\Delta L = 0, \pm 1$, $\Delta J = 0, \pm 1$, $\Delta S = 0$.

vibrational populations are often observed, usually being produced as the result of decay from one or more higher electronic states. Any of the higher electronically excited states, themselves, have sufficient energy to excite the argon to the observed levels. In the case that any of these states is the reactive species, the excess energy could be carried away by translational motion in the three bodies: the two ground state, neutral helium atoms and one excited state argon ion.

A comparison of the relevant energy levels (Figure 4-3.1) shows that the most isoergic species are the c and C states of He₂. Since transitions to these states are not observed in the pure He spectrum, it is not likely that they are the source. Of course, as stated earlier, the transition probabilities are not known, so the states could certainly be present if the transition probabilities are low. But, since emissions involving the a, b, A and B states of He₂ change so significantly upon addition of Ar, it seems likely that these states, perhaps in addition to others, are participants in Reaction 9.

If this is the case, then the population of Ar^+ states with energies less than 19.22 eV but greater than the T_0 's for the a, b, A and B states of He₂ (17.97, 18.56, 18.26 and 18.70 eV, respectively) is expected. All of the electronically excited states of Ar^+ in this energy range radiate at wavelengths less than 100 nm, which is outside the range accessible to the equipment used in this study. Table 4-3.3 lists the wavelengths of transitions from Ar^+ states with the relevant energies that could be observed by the appropriate equipment if the ion is being excited by lower vibrational levels of the a, b, A and B states of He₂. Only those transitions with favorable selection rules are included in the table. Transition probabilities are given where available. Unless further information proves otherwise, it appears that the excited states of Ar^+ are being produced by reaction with neutral dihelium molecules.

4-3.2 Behavior of the Plasma with Attaching Gas Added

Although a spectrum of the base plasma (i. e., He or He with Ar added) after the addition of an attaching gas was not taken, the effect of an attaching gas on the base plasma can still be determined. Many other spectra were taken with and without the addition of an attaching gas, including spectra of reactive mixtures in _Table 4-3.4_

Spectrum	Reagent	Attaching	Spectral	Wavelength	Recombinatio
Label	Gas	Gas	Resolution	Range	Expected?
А	H_2	CH_3I	0.4 nm	280-400	Ν
					550-600
					700-750
В	H_2	CCl_4	0.4 nm	250-300	Ν
					625-675
\mathbf{C}	CO	SF_6	1.2 nm	180-800	Ν
D	H_2 , NH_3	SF_6	1.2 nm	180-800	Υ

Experimental Conditions for Discussion in Section 4-3.2

Legend: Spectrum Label: A convenient label that applies to figures in this subsection. Reagent Gas: The reagent(s) added at RP3. Attaching Gas: The attaching gas used (added at RP2). Spectral Resolution: Approximate spectral resolution (full width at half maximum). Wavelength Range: The spectral range(s) that were used for this discussion (other ranges might be available). Recombination Expected?: If emissions due to dissociative recombination were expected to be observed in these spectra, 'Y,' else 'N.'

which recombination is not expected to occur. In any case, the addition of gases at reactant port 3 (RP3) has little effect on the spectrum of the base plasma except in cases where the injected reagent produces emissions that coincide with the base emissions (see Figure 4-3.3 or the series in Appendix B. It is likely that species injected at RP3 react with species in the base plasma, but where this is the case, the relevant emissions will be affected in the origin spectrum as well as in the background spectrum. Since the concern here is the effect of the attaching gas, such reactions only cause a problem to the extent that they may quench emissions that can provide useful information about processes occurring in the plasma. the $A(4) \rightarrow X(0)$ transition of CO⁺. spectra are He (4E and 4L in Appendix B). The molecular emission at 380 in (c) is are reactant gases and attaching gases. the experimental conditions are detailed. Molecular species indicated on the graphs attaching gas added. Letters (A, B, C, D) correspond to those in Table 4-3.4, where Figure 4-3.3: Comparison of spectra without (red, solid) and with (green, dashed) an The two dominant atomic peaks in all four



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Four spectra, in particular, are useful for determining the effect of an attaching gas. The experimental conditions under which they were taken are given in Table 4-3.4. They were taken at different times and using three different attaching gases. The two at low resolution cover larger spectral regions than the high resolution spectra. But comparisons between the low and high resolution spectra show that the two taken at lower resolution, despite the lower resolution, are reliable sources of information concerning the behavior of plasma emissions upon addition of an attaching gas. Figure 4-3.3 compares the four data sets over a small wavelength range. The small range was chosen for clarity within a single figure; the data shown there are typical for regions where none of the fours sets contain emissions due to the addition of reagents at RP3.

Somewhat surprisingly, the addition of an attaching gas was found to quench nearly all of the emissions in the base plasma. This is in contradiction to what was previously thought [Foley 1993]. The explanation given in the paper in 1993 was based on a more limited set of data than is available here. In the data published in 1993, it was noted that an atomic helium emission $(3p^3P_{0,1,2}^0 \rightarrow 2s^3S_1, \text{ at } 388.86$ nm) was quenched upon addition of the attaching gas, SF₆. The explanation given went as follows. Both singlet He metastables $(2s^1S_0)$ and triplet metastables $(2s^3S_1)$ were present in the flow. Photons corresponding to transitions between both of those states and higher electronic states of He were generated in the microwave discharge and carried down the flowtube by absorption and re-emission by metastable He atoms in the flow. But, the photons involving the triplet metastable were carried more efficiently because singlet metastables were being converted to triplet metastables via collisions with ambient electrons as they flowed down the tube. When the attaching gas was added, the singlet metastables were no longer converted to triplet metastables and, so, the intensity of the helium transition at 388.86 nm decreased.

Subsequent experiments have shown that the process described in the preceding argument cannot be the dominant process, although it certainly might be occurring.

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$\operatorname{Term}(\operatorname{Hi})$	$\operatorname{Term}(\operatorname{Lo})$	nm	Label	$\%_f$ (A)	$\%_f$ (B)	$\%_f$ (C)	$\mathcal{H}_f(D)$
				(I_i)	(I_i)	(I_i)	(I_i)
$3p{}^{3}P_{1}^{0}$	$2s{}^{3}S_{0,1,2}$	388.86	4L	3.9	2.3	5.2	5.9
				(25871)	(23474)	(15890)	(13097)
$4d^{3}D_{1,2,3}$	$2p^{3}P_{0,1,2}^{0}$	447.15	6BB			5.6	6.7
						(6499)	(5232)
$4d{}^{1}D_{2}$	$2p {}^1P_1^0$	492.19	8N			14.4	7.0
						(3925)	(2633)
$3p {}^1P_1^0$	$2s {}^1S_0$	501.57	9B			13.8	14.7
						(3579)	(3248)
$3d{}^{3}D_{1,2,3}$	$2p^{3}P_{0,1,2}^{0}$	587.56	12O	31.0		25.0	29.9
				(24654)		(13917)	(12529)
$3d{}^{1}D_{2}$	$2p {}^1P_1^0$	667.82	17P		34.0	30.9	35.4
					(2038)	(2613)	(2589)
$3s{}^{3}S_{1}$	$2p^{3}P_{0,1,2}^{0}$	706.53	19B	60.6		39.6	48.6
				(6711)		(3497)	(3081)
$3s {}^1S_0$	$2p {}^1P_1^0$	728.14	20D	71.3		54.1	61.4
				(923)		(355)	(345)

Atomic Helium Emissions Remaining After Addition of an Attaching Gas

Legend: Label: These labels correspond to the key in Appendix B. Letters A, B, C and D have the same meanings as in Table 4-3.4 and Figure 4-3.3. I_i : The intensity (photon counts not corrected for optical system transmission intensity) of the peak before addition of the attaching gas. $\%_f$: Percent of I_i remaining after the addition of the attaching gas.

If the previous argument were correct, intensities of photons from transitions to the singlet He metastable should increase upon the addition of the attaching gas (since they are no longer being converted to triplet metastables). This is not the case. The intensities of all He emissions are reduced upon addition of an attaching gas; most are quenched entirely. Since the attaching gas, which is added in very small quantities, quenches the emissions, a few statements about the emissions can be made. One, the emissions are probably not being carried down the flowtube by internal reflection along the walls: it is unlikely that the attaching gas is absorbing the radiation so uniformly across the spectrum, especially since several different attaching gases quench the emissions so similarly as to be indistinguishable from each other. Two, since three different attaching gases affect the emissions similarly, it is unlikely that the changes are due, in a significant manner, to reactions involving the attaching gas (this is expected due to the relative reaction rates of neutrals with neutrals compared to that of electrons with neutrals or other species). Therefore, the presence of electrons in the tube is somehow crucial to the propagation of the emissions. This conclusion is unexpected, initially, since the emissions all correspond to neutral states of helium and dihelium.

A possible explanation can be deduced from the curious fact that some of the atomic helium emissions are not completely quenched upon addition of the attaching gas (Table 4-3.5). Different transitions survive by different amounts, ranging from about 70% down to around 5% (see table). The destination (lower) states for the surviving transitions are also the destination states for transitions that do not survive addition of the attaching gas. So, it is not likely that the destination state makes the difference. Instead, the upper state seems to determine whether a peak is still present after addition of the attaching gas, with the tendency for a peak to survive having the following trend:

It is possible that the transition wavelength is important, but it cannot be the only important characteristic of the transitions. If it were, then all atomic helium transitions in those wavelength ranges would survive with similar percentages of initial peak intensity. This is not observed. Neither is initial peak intensity the deciding factor, as inspection of Table 4-3.5 indicates. Figure 4-3.4 _____

Figure 4-3.4: Partial Grotrian diagram showing the atomic helium lines observed in these experiments. Also shown (and so noted) are transitions to the lower state that are certainly present but that are not observable with the equipment used in these studies. The heavy (blue) lines indicate transitions that survived addition of the attaching gas. Data contained here is from NIST [2001].

See the caption on the previous page.



Grotrian Diagram Showing Observed Transitions

Figure 4-3.4

A likely explanation is that the atomic He emissions are propagated down the tube by the following equilibrium process:

$$He(1s^2) + He(1s^1ns^1; n \ge 3) \rightleftharpoons He_2^+(excited) + e^-$$
 51

The forward and reverse reactions are, generally, studied separately [Berlande 1970, Collins 1972a,b, Ferguson 1965, Johnson 1972a,b, Lichten 1974]. But under the experimental conditions used in this study (high densities and pressures of the relevant species), both forward and reverse reactions are possible. The only requirement, and it is a requirement that should cause concern, is that the exited states of He⁺₂ do not react with Ar. The forward reaction has been studied for n = 5 [Collins 1972a] and the reaction rate reported as $8 \times 10^{-11} cm^3/s$. Rate coefficients for other values of n are not available. There is disagreement over the rate of the reverse reaction [references this paragraph and Bardsley 1970], and data as a function of initial state of He⁺₂ are not available. The reverse reaction for ground state He⁺₂ ions is known to be slow [Berlande 1970]. But, that might not be the case when the He⁺₂ is created via the forward Reaction in 10. In that case, the product He⁺₂ is likely to be in a high vibrationally and/or electronically excited state: not at all the He⁺₂ expected from the three body route:

$$He^+ + 2He \to He_2^+ + He^* \tag{52}$$

The equilibrium described in Reaction 10 is consistent with the data if the forward (and possibly also reverse) rates are much slower for the lowest values of n. If this is the case, then the addition of the attaching gas quenches the emissions by limiting production of the upper state rather than by removing the lower state from the plasma. In other words, the atomic helium emissions are emissions resulting from dissociative recombination. After the attaching gas is added, only the forward reaction in 10 can occur and, eventually, all the excited state helium atoms react away, producing He_2^+ ions. If the forward rates (and, possibly, but not necessarily, the corresponding reverse rates) are small for the 3s, 3p, 3d and 4d states, then addition of the attaching gas will have less effect on those emissions.

It is likely that the diatomic helium emissions are also products of the reverse of Reaction 10. Lichten, et. al [1974], reported such a recombination as the source of the dihelium in their study. The fact that the dihelium emissions are quenched by the addition of the attaching gas supports this argument as well. Since the Ar^+ peaks are also quenched upon addition of the attaching gas, their presence can be tied to the reaction in 4-10 as well.

If Reaction 10 is occurring, then the unexpected behavior of the CO^+ emissions (Section 4-1) is explained, and steps can be made to reduce it's influence on the chemistry in the plasma. So long as energetic species that depend on the electron concentration are present, it will be difficult to confidently identify photoproducts of recombination.

CHAPTER 5

THE FLOW OF GASES IN THE REACTION REGION

In this chapter a number of issues surrounding the injection of reactant gases at RP3 are discussed. In particular, how spatial and temporal characteristics of the injection plume affect the data presented in Chapter 4. In some cases, these characteristics limit the precision with which relative populations of observed electronic states can be determined. Since this is most important, it will be presented first.

5-1 The Size and Temporal Characteristics of the Injection Plume

The relative populations of observed electronic states, given in Tables 4-2.1 – 4-2.9, were calculated from the observed number of counts, taking into account the radiative lifetime for that state. Photons resulting from various processes in the flowtube are only collected for the time that the emitting species are within the viewing region of the optical spectrometers. If A is an electronically excited atomic or molecular species, the total number of photons, I_t , observed from an initial population, A_0 , within a given time, t is:

$$I_t \propto A_0 \left(1 - \mathrm{e}^{-t/\tau} \right)$$
 53

where τ is the radiative lifetime of the emitting species. This equation can be derived by recognizing the radiative lifetime as the inverse of a unimolecular decay rate constant. In that case, the number of A left after time, t, is:

$$A = A_0 e^{-t/\tau}$$

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$$54$$

That implies that the number (or number density, as appropriate) of photons, $A_{h\nu}$, emitted by time t is:

$$A_{h\nu} = f_{h\nu} A_0 (1 - e^{-t/\tau})$$
 55

where $f_{h\nu}$ is the probability that A will radiate via the channel of interest: if A decays to more than one lower electronic (or other) state, either all emissions must be considered or the fraction of decays to a single lower state must be known. Then the number, I_t , of photons observed will be proportional to the number emitted (the proportionality constant will depend on specific experimental circumstances).

It is important to know the overall probability that a state will radiate: an Einstein A coefficient, while useful, does not give sufficient information. Put more simply, the inverse of the radiative lifetime gives the frequency with which the upper state is likely to radiate. The Einstein A coefficient gives the probability that the radiation will decay into a particular lower state. So, the radiative lifetime available is used to determine the overall number of transitions. Where probabilities for individual channels are known (for instance, where Franck–Condon factors are known), they are used to predict relative importance of individual channels.

Consider making a comparison between emissions from the decay of a several different electronic states in order to determine their relative populations. The period of time over which the radiating states are viewed is very important, and is the central point of this section. In two cases, Equation 1 can be simplified. If the ratio of t to τ is large for all excited states, then the relative population of each state can be determined by finding the relative number of photons emitted from each state. This can be verified by substituting $t = \infty$ into Equation 1. If the ratio of t to τ is very small for all species, then the relative populations can be determined by multiplying the observed number of photons by τ . This can be verified by taking a truncated
expansion of the exponent in Equation 1:

$$\begin{aligned} I_t &\propto A_0 \left(1 - e^{-t/\tau} \right) \\ &\propto A_0 (1 - \left(1 + \frac{-t/\tau}{1!} \right)) \quad small \ t/\tau \\ &\propto A_0 t/\tau \end{aligned}$$
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This is not straightforward since the different emitting states in a given data set often do not have radiative lifetimes that are of similar magnitude, let alone radiative lifetimes that fall neatly into one of the two extremes presented in the last paragraph. In those cases, it is necessary to know the amount of time that the collection of emitting species is in viewing range of the observation device. Note that this is a different time from the counting period of the observation device. In flowing studies in steady state, the latter is relevant only in terms of enhancing signal to noise ratios.

The time the species spend in the viewing region can often be ignored because many electronic transitions have short radiative lifetimes, but, exceptions to this exist, for example, the $a^3\Pi_r$ state of CO. The radiative lifetimes of the a and $A^1\Pi$ states of CO are 8 ms and 11 ns, respectively [Radzig 1985]. 99% of molecules in the A state will have radiated within about 50 ns. It will take about 40 ms for 99% of the a state to have decayed, a time roughly the same as the travel time to the end of the flowtube (~100 cm). An upper–limit estimate of the time the gases are within view of the spectrometers is 2 ms. In that time, all of the A state is expected to have completely radiated, but only about 22% of the a state will have. A similar lower– limit estimate of the time the species spend in viewing range of the spectrometers is 0.5 ms (the basis of these estimates is discussed shortly). To illustrate the significance of this, let us assume that equal numbers of photons are observed from the two states. If a viewing–region time of 0.5 ms is assumed, then the relative populations are 0.22 to 1.



 $Q \approx 0.04 \ Tls^{-1}$ $Q \approx 0.5 \ Tls^{-1}$ $Q \approx 2 \ Tls^{-1}$

Figure 5-1.1: Photographs of the reaction region at three throughputs, Q, of CO₂. The CO₂ is injected into the typical reactive plasma described in Chapters 2 and 4. In all three photos, the plasma is flowing from left to right, and the reagent gas, CO₂, is being injected through RP3 into and against the flow of the plasma. RP3 is the small tube that begins near the top of the photographs, curves around and ends approximately in the center of each photograph. The He throughput is 220 Tls⁻¹. The first two photographs represent conditions similar to those, respectively, in the top and bottom graphs in Figure 5-1.2. In the third photo, sufficient CO₂ is being injected that the gas travels upstream beyond the viewing region. The distance traveled upstream is unknown, but an estimate is made in the text. Photographs by Aaron Powell.

In the experiments being described here, the amount of time the reagents spend in view of the spectrometers also depends on the throughput with which they are injected through RP3. This time difference is illustrated fairly plainly in Figure 5-1.1. The three pictures are photographs of the region around RP3 under typical experimental conditions, but varying the throughput of the gas being injected at RP3. The photographs in this figure were taken, using standard photographic techniques, through a viewport perpendicular to the flow, situated on top of the flowtube. The circular boundary, outside which the photographs are black, is the edge of the viewport. The throughputs given in the figure correspond to number densities of, left to right, 9.2×10^{12} , 1.2×10^{14} and 4.8×10^{14} cm⁻³ once the CO₂ has expanded to fill the flowtube.

The time estimates used earlier come from assuming that once the plume has been turned back it will have the same velocity as the bulk gases. The distance across the viewport is about 5 cm. If one assumes the slower, neutral particle velocity, 3000 cm/s, then the viewing time is about 1.7 ms or ≈ 2 ms. Similarly, if the gas exits the tube, turns back immediately and travels half that distance with the higher speed of the ions in the flow, 4500 cm/s, it will have spent about 0.5 ms traversing the window.

Spectra from the recombination of CO_2^+ taken under different injection conditions illustrate the combined effects of injection throughput and product radiative lifetime (Figure 5-1.2). The throughputs for the upper and lower spectra are similar to those in the left and middle photographs, respectively, in Figure 5-1.1. Note that the intensity of the CO $a \to X$ transitions change relative to the constant intensities of the CO $A \to X$ and $\operatorname{CO}_2^+ \tilde{B} \to \tilde{X}$ emissions. The radiative lifetime of the $\operatorname{CO}_2^+ \tilde{B}$ state is not known, but since the transition is not spin forbidden, it is expected to be more similar to that for the CO A state than to the a state. Indeed, conversely, if the time the species spent within range of the spectrometers were known, and it were sufficiently short, a radiative lifetime could be assigned to the CO_2^+ emissions.

The values reported for the relative populations of the a and A states of CO in the recombination of CO_2^+ (see Table 4-2.3) are based on experimental conditions similar to those in the center photograph in Figure 5-1.1. This set of conditions was chosen because the time spent in the viewing region is maximized, but none of the reagents have traveled upstream, out of range of the optical spectrometers. Uncertainty regarding the time the radiating species are in view of the spectrometer



Figure 5-1.2: Comparison of intensities of spectral features observed in a plasma containing CO_2^+ ions for different reagent gas flows (CO_2 , here). The upper graph has been offset on the abscissa by 1×10^6 for ease of comparison. The throughputs indicated correspond, once the CO_2 has expanded to fill the tube, to number densities of (a) 3.5×10^{12} and (b) 1.7×10^{14} cm⁻³. The conditions under which the spectra were taken are similar to those for the first two photographs in Figure 5-1.1. The resolutions (FWHM) and count periods are approximately (a) 1.5 nm, 2 s and (b) 0.5 nm, 4 s. The difference in resolution does not account for the difference in relative heights between the CO $A \to X$ and $a \to X$. See accompanying text for further details.

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limits the precision of the results. This is a difficult problem, but if a good number for the injection velocity and the time variation of the velocity were known for a known average travel distance, a better estimate of this time could be made.

An estimate of the injection velocity can be made, but the estimate is not very reliable. A throughput, essentially, measures the number of a given species that pass a certain point in a given time. If the pressure, p of the gas is known, the throughput, Q, can be converted to a velocity using the relationship:

$$Q = pav 57$$

where a is the cross-sectional area of the tube where the pressure is measured and v is the velocity of the gas. The only point at which the throughput and the pressure are known simultaneously is at the measurement of pressure drop across the capillary (see Chapter 2). The capillary tube exit velocity is not necessarily the same as the velocity with which the molecules exit RP3; only the throughput is a constant. The velocity of the gas will not necessarily remain constant since it must pass through a considerable length (decimeters, at least) of tubing with diameter changes. For the central photograph in Figure 5-1.1, the throughput is about 0.5 Tls⁻¹ and the pressure at the exit point from the capillary tube is 53 Torr. Assuming an inner diameter for the capillary tube of 0.05 cm, the velocity of the gas is about 1200 cm/s. For the lower flow shown in Figure 5-1.1, the injection velocity, by this estimation, is around 270 cm/s.

To make a calculation of residence time within viewing region of the optical spectrometers is not trivial. The problem is that the distance traveled by the injected gas depends on the injection velocity, the mass of the injected species and the frequency of collision with the oncoming He/Ar mixture. The latter, of course, depends on the number density, temperature and collisional cross sections of all species in the flow. Two of those (temperature and cross section) can be assumed to be constant when the gas is first injected, but the number density decreases due to expansion as soon as the gas exits RP3. Very soon, all of these variables change. As the CO_2 reacts, it not only changes size, but becomes an ion. Since a head–on collision is not necessary for charge transfer, a number of CO_2 molecules will become ions while still moving into the plasma. An ion interacts with an oncoming plasma in a very different manner than a neutral species. After the ion recombines, it becomes two or more different particles with different masses and collisional cross sections and temperatures. After that, the cross sectional areas of some of the product neutrals will change as excited species radiate.

A typical distance traveled by an injected particle can be determined empirically. The apparent size of the plume can be measured in a series of photographs similar to those shown in Figure 5-1.1. The distance from the terminus of RP3 to the visible edge of the plume has been measured relative to the size of the viewport in each photograph. A plot of the distance traveled upstream as a function of throughput is fairly linear (see Figure 5-1.3). This is true both for injection of a species likely to be involved in ion chemistry (CO₂) and for the injection of a gas likely to react only as a neutral (Ne injected into a He–only plasma). So, even if it is difficult to determine the amount of time the species spend in front of the viewing region, it is possible to estimate the volume of the reaction plume and to predict the distance upstream that an injected gas will travel. From the linear fits in Figure 5-1.3, the injected gas in the rightmost photograph in Figure 5-1.1, which has traveled upstream past the edge of the viewing window, traveled about 10 cm upstream.

A plot of the capillary tube exit velocity versus upstream distance is, as expected, non-linear. However, if a throughput is considered to be an energy, then it makes sense that the distance traveled upstream would be linear in the square of the particle velocity. This is indeed the case (Figure 5-1.4). If the kinetic energy were the sole concern, then the ratio of the slopes for CO_2 injection and Ne injection should be



Figure 5-1.3: Upstream distance traveled by parent gas injected through an upstream facing port as a function of throughput for CO_2 injected into a He and Ar plasma (red +'s) and for Ne injected into a He-only plasma (green \times 's). Linear best-fit lines with their equations are also displayed.



Figure 5-1.4: Upstream distance traveled by parent gas injected through an upstream facing port as a function of the square of capillary tube exit velocity for CO_2 injected into a He and Ar plasma (red +'s) and for Ne injected into a He-only plasma (green \times 's). Best-fit curves and equations are also displayed on the plot. In the equations, x is the square of the velocity.

the ratio of their masses (2.2), but the exact value is actually 4.3. The difference in collisional cross section for the two primary collision pairs (0.34 nm² for CO₂/He and 0.22 nm² for Ne/He [Spartan '02 calculation]) will make a difference in the distance traveled, too. But, the distance traveled will decrease with an increase in collisional cross section, so its inclusion will only serve to make the numbers even less alike. The additional presence of Ar in the plasma will also make a difference. But, since the argon number density is about one thousandth that of He, its effect is expected to be small. What is more likely is that the assumption about the equivalence of the injection velocity and the capillary tube exit velocity is erroneous, and the injection velocity is higher.

Despite the capillary tube exit velocity not being equal to the injection velocity, it is still a valuable assumption. If the injection velocity is known, then the time between exiting RP3 and turning back can be estimated. At the point at which the injected gas turns back, its velocity is zero. That makes the average velocity, assuming constant deceleration, equal to half the injection velocity. For the central photograph in Figure 5-1.1, the average capillary tube exit velocity is about 600 cm/s. So, given these assumptions, the time it takes for the oncoming plasma to stop the CO_2 is about 2 ms.

The slopes of the lines describing distance traveled upstream as a function of capillary tube exit velocity are not in the ratio of the masses of CO_2 and Ne. However, the slopes for the distance as a function of throughput are nearly in that ratio (2.6 slope ratio versus 2.2 mass ratio). If a good predictive model for the exit velocity as a function of throughput could be made, then the relative populations of electronic states with differing radiative lifetimes could be determined much more accurately.

5-2 The Shape and Spectral Characteristics of the Injection Plume

One interesting characteristic of the injection plume is the dependence of its shape on the reaction conditions. This difference is illustrated in Figure 5-2.1. The figure compares the injection plumes of two reactive systems. The photographs were chosen for comparison because the distance the injected gas travels upstream is similar. The photograph on the right is somewhat difficult to interpret: the light from the reaction between metastable helium atoms the injected neon (the He/Ne laser reaction) is bright and reflects off the port on the other side of RP3 from the camera. But, even with the difficulty, it is fairly clear that the two plumes are different. The most striking difference is that the plume on the left has a very sharply defined front, while the plume on the right has less of a "front" than a "leading diffusion zone." The difference between the shapes lies in the nature of the species emitting light.

In the photograph on the right, the injected Ne is reacting with neutral helium atoms to produce neutral neon atoms. The neutral neon atoms then radiate in the red. Since all the species involved in the production of the photons are neutral, then the positions at which the species react and then radiate should be controlled, in some sense, by diffusion. When mixing is diffusion controlled, the distribution of species is random–kinetic: a few should diffuse very quickly away, while others diffuse more slowly. Here, the "tag" for the presence of neon atoms is the red glow. The glow is of the form expected for a diffusing species, i. e., brighter near the center from which the species diffuse (RP3) and fading as the distance from RP3 grows (the yellow–ish feature near the center of the plume is discussed later). The purplish glow to the left of the plume (faintly visible in the photograph) is the combined effect of a number of mainly He but also He₂ emissions (see Section 4-2 for details).

In the photograph on the left, all of the dominant emissions depend on the presence of the CO_2^+ ion. The visible emissions (from about 400 to about 700 nm) are produced by the $CO_2^+ \tilde{A} \rightarrow \tilde{X}$, $CO^+ A \rightarrow X$ and the CO $d \rightarrow a$ transitions. The



Figure 5-2.1: Comparison of the plume shape when the emitting species is a product of reactions involving ions (left) and reactions involving neutrals (right). In the reaction on the left, CO_2 (the gas injected through RP3) is ionized by the oncoming plasma and then rapidly recombines with ambient electrons. In the reaction on the right, Neon, injected through RP3, reacts primarily with neutral He metastable atoms in the plasma, producing, among other emissions, the red glow characteristic of common He/Ne lasers. See text.

only neutral in that list, the CO, results from the recombination of CO_2^+ ions and is, therefore, the result of an ion-related process. The greenish glow to the left of the plume (faintly visible in the photograph), is produced by the combination of He, Ar and Ar⁺ and, to a small extent, He₂ emissions (see Section 4-2 for details).

Unlike the emissions in He/Ne photograph, the emissions in the $CO_2/He/Ar$ photograph are brightest at the sharply defined outer edge of the plume. If the situation were diffusion controlled, this would not be the case. Two mechanisms give rise to the distinctive appearance of the plume. The first is that charges that were moving from left to right before the CO_2 was injected are being transferred to the

 CO_2 . Charge transfer does not require a head-on collision. Indeed, according to the harpooning mechanisms used to describe a number of reactions [e. g., Atkins 1998] the electron frequently changes host (via a long-range electron transfer) without any close collision at all. When the charges transfer, then, they are, to some extent, being transferred to very massive objects that are moving in a direction opposite to the original motion of the charge. Now there is the situation of a charged particle moving into a plasma. While the plasma, overall, is neutral, it is not neutral in a local sense. The newly-charged CO_2^+ ions will be repelled by the oncoming plasma by long-distance (\sim Debye length) interactions, which are Coulomb-like, without having to undergo collisions. The second mechanism responsible for the appearance of the plume concerns the recombination of the CO_2^+ ions. The area behind the front, after the ions have recombined, will be ionization-poor and neutral CO₂ molecules will continue to diffuse to the point where the oncoming plasma meets the advancing front. The effect of these circumstances is to concentrate the CO_2^+ molecules, whose positions are recorded in the photograph. The light is brightest, and whitest, near the front because many of the species formed by reactions between CO_2 and the plasma have very short radiative lifetimes.

The glow not only dims but appears also to redden or become browner as the flow continues downstream. It is difficult to be certain from a photograph, but if the effect is real, then it might be due to diminishing populations of the CO_2^+ Å and CO^+ A states. The CO_2^+ Å radiates at the blue end of the spectrum (up to about 500 nm) and the CO^+ radiates all the way across the visible spectrum. But, the $CO \ d \rightarrow a$ transition has three broad peaks near 600, 650 and 700 nm, with the brightest being around 650.

The yellow–ish feature in the He/Ne plume

The observant reader [Ferrenberg 1996] will probably have noticed a yellow-ish band of color just to the left of RP3 in the photograph on the right in Figure 5-2.1. The



Figure 5-2.3: Mass spectra taken prior to taking the most recent optical spectra and pictures of the He/Ne reaction. The top spectrum was taken before neon was injected and is dominated by the presence of the He_2^+ ion. The bottom mass spectrum clearly shows a dominant peak at 20 amu without the expected 22 amu isotope at about 10% of the intensity of the 20 amu peak. At this resolution, the two masses, if both present, would be well resolved.



Figure 5-2.4: Photograph of the region around RP3 using the isotopically pure neon. The photograph is at much better resolution than is shown here. An additional ringshaped port was added prior to the time this photo was taken. The ring-shaped port encircles RP3. It confuses the photograph, but does not significantly alter the shape of the plume. Even with a better copy of the photo, there is no apparent yellow band. An obstructing piece of permanently-placed equipment prevented exact duplication of the previous photographs.

concentration of the yellow into a narrow band is reminiscent of the shape of the front in the CO_2 system where the emissions are primarily due to ion-related processes. A set of spectral data taken at the time of the photographs seemed to show a couple transitions that were affected significantly by the addition of an attaching gas. So, the experiments were repeated with a new bottle of neon to confirm the presence of the yellow band was not a photographic artifact. According to the mass spectrum, the new sample of neon was isotopically pure (20 amu, Figure 5-2.2). Another mass spectrum taken prior to the addition of the neon (same figure) indicates that the system was very clean. Photographs taken using neon from the new bottle (Figure 5-2.3) do not contain the yellow band. The spectra, also, do not indicate electron dependent emissions that would be perceived as yellow. The bottle of neon used in the earlier photographs was not isotopically pure. So, it is possible that the yellow feature in the previous photograph was real. If so, then it was produced either by an impurity in the neon or possibly by some isotopic effect, though the latter is not as likely as the former.

5-3 Simulation of the Injection Plume at RP3

Empirical investigations of flow characteristics are certainly useful. But, given the complexity of the interactions near RP3, a more complete understanding of the reactive flow can only come from building models and testing them for consistency with experimental findings. To that end, the first phase of a computational model of the flow has been developed. The details have been described elsewhere [Foley 1997], so only a synopsis will be presented here.

A computer program was developed that models the injection of neutral particles from an orifice into a larger opposing gas flow. The earliest models were full molecular dynamics simulations assuming hard walled collisions between spheres of finite size. The flows that could be simulated using these methods occurred in boxes that were, at most, a few thousand Å on a side: particles injected through the virtual RP3 were rarely turned around in the simulations. These simulations were event–driven: that is, the simulation determined the next pair of particles (or particle and wall) that would collide and moved all other particles to their new positions at the time of that collision. The collision was allowed to occur, and the colliding particle(s) were assigned new trajectories and velocities. Then the next collision was found and the process repeated. Although the simulation size was limited, the results were realistic (Figure 5-3.1).

The simulation of flows within boxes of somewhat more realistic size and flow characteristics became possible by treating the oncoming flow statistically, with the



Figure 5-3.1: Simulated injection plume from an event-driven simulation of 1000 CO₂ particles injected into counterpropagating neutral helium (the helium atoms are not displayed in the graphs). Particles are injected through a virtual port located centrally along X and Y (upper right), and at 10,000 Å from zero along Z (top left and bottom). They exit the port in the positive Z direction and encounter He atoms flowing in the negative Z direction. Upper left: Side view of the simulated plume. Upper right: View along the z direction showing the symmetry of the simulated plume. Lower graph: A plot of the velocity in the z direction, V_z , as a function of position along z. There are no positive values of V_z for positions behind the injection port.

event-driven algorithm being replaced by a temporally controlled simulation. In the current simulation, a single particle is assigned an initial trajectory and velocity according to a Maxwell-Boltzmann distribution. Taking account of the distance the particle is likely to travel within a constant timestep, a collision probability is assigned. A random number is chosen, and if the collisions probability is greater than the random number, the collision occurs; otherwise, the particle completes its trajectory. Using this algorithm, the trajectories of many particles can be traced. A relatively small collection of these single particles, collectively, represent the statistical distributions of a much larger set of particles. Using this algorithm, the basic shape of a diffusion controlled injection plume was generated.

As was stated earlier, this is merely the first phase in a more complete simulation. A more complete simulation would also take account of charge distributions, collisions between injected particles and reactions. The final simulation will probably not be limited to stochastic methods like that described in the last paragraph. Where statistical distributions could not be predicted, the simulation would need to include more familiar techniques such as molecular mechanics and dynamics and the numerical treatment of equations (such as reaction rate laws) known to describe certain processes. The simulation will also need to reproduce photoemissions from the flow, the subject of the next chapter.

CHAPTER 6 SIMULATOR FOR ROVIBRONIC SPECTRA

A computer program that simulates rovibronic spectra is described. A brief rationale for the program (Section 6-1) will be followed by a list of features available in the current version (Section 6-2) and a description of input and output files (Section 6-3). Section 6-4 summarizes the theoretical descriptions on which the simulation is based. Section 6-5 describes the storage and retrieval of data within the program. Since the program was written with the intent that it should be modified and expanded, Section 6-6 contains a list of suggested changes and additions. Finally, Section 6-7 contains a comparison of spectra simulated by the program to experimental spectra observed in this study and collected from the literature. There are numerous other comparisons to experimental data from the studies presented here in Section 4-2.

The source code for the program is written in the programming language C and is contained in Appendix C. The name of the program is specified by the user when the program is compiled and within an input file. But, within this dissertation, the program is referred to as "RVESIM" which stands for <u>rotational vibrational electronic</u> <u>simulation</u>.

6-1 Spectral Simulation

There are many reasons why one might wish to simulate a spectrum. An obvious reason is to facilitate identification of spectral features. Even if feature identification is not a concern, simulation can simplify quantification of properties such as temperature or relative population. The simulation can also be used for design: the necessary or optimum spectral range for an application can be determined based on simulations of the frequencies of light absorbed or emitted.

Relatively simple rovibronic (rotational, vibrational, electronic) spectra can be easily simulated. A great deal of information exists regarding atomic and molecular spectra of stable diatomic molecules. References such as Huber and Herzberg's Constants of Diatomic Molecules [Herzberg 1997] or collections of data like Radzig and Smirnov's Reference Data on Atoms, Molecules and Ions [Radzig 1985] contain detailed information concerning the spectroscopic behavior of a large number of molecules. The National Institute for Standards and Technology (NIST) provides a variety of spectral resources online [NIST 2001a,b], including an updated version of Herzberg's reference. There is less information available on small polyatomics, but a few texts contain information. Herzberg [1991] included a table of spectral information in the back of his book Molecular Spectra and Molecular Structure, V III: Electronic Spectra and Electronic Structure of Polyatomic Molecules. More recently, Marilyn Jacox [1994] published spectral information for a number of species in a monograph for the Journal of Physical and Chemical Reference Data entitled Vibrational and Electronic Energy Levels of Polyatomic Transient Molecules. The collection was supplemented in 1998 [Jacox 1998], and the entire collection is also available online [Jacox 2002]. Other spectroscopic data are spread throughout the literature.

Despite the availability of information, there are few computer programs available that simulate spectra of diatomic molecules. Two programs that simulate rovibronic spectra exist, but they only simulate rotational structure within one vibronic transition at a time and do not allow for the inclusion of other spectral features (atomic transitions, for example) [Western 2002, Robinson 1994].

The reason why there are so few simulation programs becomes apparent once one begins preparation for writing such a program. The rules governing the transitions are complex and deviations from the most common simplifications are frequent (although such deviations are usually relatively small). Even the simplest system, the diatomic molecule, is quite complex (as will be discussed below).

In it's current form, RVESIM can simulate two of the main types of rovibronic spectra (see below) based on generalized energy, population and intensity formulae. However, it was written so that it will be relatively simple to alter and expand. It is well-documented, open-source (there is no cost for use or redistribution) and easily available (can be downloaded from the internet or obtained from the author for copying and shipment costs). Because of this, changes could be made or additions incorporated as needed. Details of its current capabilities and limitations are given in the next section.

6-2 Program Features

In its current form, the program calculates positions and intensities for rovibronic transitions in diatomic molecules. At present, it can only handle transitions from Hund's Case (a) to (a) and Case (b) to (b) [e. g., Atkins 1998, Herzberg 1989, Steinfeld 1985]. It does not yet simulate Hund's Cases (c) or (d). If the rotational distribution is thermal, the program will calculate relative rotational-level populations and transition intensities automatically. If the distribution is not thermal, it must be entered from an input file (see Section 6-3). Details concerning calculations of energy-levels, populations and transition intensities are given below in Section 6-4.

Any number of states of any number of diatomics can be simulated at the same time. The limit to the number of molecules and states is determined only by computational resources, primarily the amount of random access memory (RAM) available. Each electronic state can be assigned a separate temperature (currently, individual vibrational levels cannot be assigned separate temperatures). Alternatively, overall temperatures can be assigned to each diatomic molecule or for all diatomic species.

Current Program Capabilities

Diatomic Molecules — States

Number of molecules and states is unlimited in program.

States must be Hund's Case a or Case b.

Any values of Λ , Ω and S may be used

Thermal rotational population distributions are calculated internally.

Alternate rotational distributions can be entered from file**.

Temperatures can be specified at global, molecule or state level.

Diatomic Molecules — Transitions

Hund's Case $a \rightarrow a$ and $b \rightarrow b$ for emission only.

Satellite bands can be assigned a constant intensity level

(level set to zero by default).

Hönl–London factors for rotational transition intensities can be turned on or off.

Electronic cascade is accounted for automatically.

Transitions calculated elsewhere can be included by input file.

Other Atoms or Molecules

Transition lines must be determined externally and included by input file.

Equipment-Specificity

Adjusts for photon–counting or calorimetric ** detection methods.

Adjusts for detectors that scan or that step^{**} from point to point.

Mimics apparatus resolution (triangular peak shape).

** Indicates features that have not yet been adequately tested.

Since the program was initially written to facilitate data analysis in studies of the photoproducts of dissociative recombination (which are not necessarily thermal), relative vibrational populations must be entered by the user, and are not assigned thermal distributions within the program. Each electronic and vibrational state of each molecule must also be assigned a relative population.

Atomic or other single–peak transitions can be entered from a file and included in the simulation. This feature allows easy import of positions and intensities calculated by other programs or obtained from the literature.

A program like this, ideally, should be capable of much more than the current program can do. Many additional features were considered at the design stage for inclusion later. Others are nearly complete but have not been activated or debugged. Table 6-6.1 lists these features and the relative ease with which they could be included. Table 6-2.1 lists the features already present and working.

6-3 Input and Output Files

The program requires a number of input files and creates a selection of output files. Details regarding the input and output files can be determined with a small amount of effort by inspection of the source code (see Appendix C-c). More extensive documentation will be available on the internet so long as web-space is available. A listing of the files and their contents is also given here.

Input Files:

Names of required files appear in **boldface**. Files that might become necessary if certain input values are used appear in *italics*. Files relating to features that are not yet working in the program appear in regular type. Input file formats are described in Appendix C-b.

- Main: This is the master file for the simulation. It tells the program what sort of simulation to do and how to do it.
- *.rvesimconfig*: This is an optional configuration file. If the program does not find this file in the directory from which it is called, it will write a brief message to that effect and continue to run. The file is mainly used during debugging after additions or changes have been made to the program.
- State File: This file is necessary if the user requests a rovibronic simulation. It contains information about the states involved in the transitions to be simulated.
- Transition File: This file is necessary if the user requests a rovibronic simulation. It contains information about the transitions the user wants the program to include.
- Franck-Condon Factor File: There must be one of these files for each transition listed in the Transition File. The format is based on output from a Franck-Condon factor program written by Kent Ervin [Ervin 1993]. The file contains Franck-Condon factors for the transitions.
- Rotational Distribution File: This file becomes necessary if the user specifies that the rotational populations are to be input from a file. It contains energy levels and relative populations for rotational levels in a given vibronic state.
- Efficiency File: This file becomes required if the EFFICIENCY entry is set to any value other than 1. This file contains the efficiency curve for the experimental detection system that is used to obtain spectra to which simulation output will be compared.

Currently, this feature is not working and the only useful value for EFFICIENCY is 1.

- Atomic File: This file becomes necessary if the user specifies inclusion of one or more files containing positions of discrete transitions. The file must contain transition wavelengths, relative populations and transition probabilities.
- External Spectrum ("Other") File: This file is called "other" within the program. This file becomes necessary if the user specifies inclusion of external spectral features. The spectral features in this file will be added to the final simulation without modification for spectral resolution, intensity or optical system efficiency.
- Experimental File: This file becomes necessary if the user requests the display of a graphical comparison between the simulation and the user's experimental data. The file contains the experimental spectrum to use for comparison.

Output Files:

Since the number of output files is potentially very large, the program creates subdirectories within the directory from which the program is called and places output files within those directories. In some cases, the directories, themselves, contain subdirectories. The following list of output files is categorized by the directory, and sub-directory if appropriate, where the output file is located.

In the main input file, the user must specify an OUTPREF, a prefix for all files and all first–level directories created by the program. The prefix may contain any characters that the computer's operating system will allow within file names. In the list that follows, OUTPREF is abbreviated to "PREF." Directories within program-created directories (sub-directories) are not prefixed. Some files within directories created by the program contain the prefix and others do not. In the following, MOL is a variable for the name of a diatomic molecule, s is the variable representing a state and v represents a vibrational level.

Files placed within the directory from which the program is called:

- PREF_parameter.txt: This file contains the parameters used by the program. It also contains a number of messages written by the program. For example, if a transition is omitted from the simulation, the omission is declared and briefly explained in the parameter file.
- PREF_debug.txt: The purpose of this file is to assist in debugging and checking the program. This file is only written if the value of DEBUG in the configuration file, .rvesimconfig, is set to an integer value greater than -1. It will be an empty file unless one or more of the other debugflag values is less than the value of DEBUG. If all debugflag values are less than DEBUG, copious quantities of detailed statements regarding the program's progress will be written to this file. "Copious," in this instance, means a file with a size on the order of megabytes or gigabytes.

Files placed within the PREF_molecules/MOL directories:

- $MOL_s_rot.dat$: This file contains energies (in wavenumbers) and relative populations, categorized by value of J or K (rotational quantum numbers) for each rotational level in each vibrational level in the thermal rotational distribution calculated for state s.
- $si-sj_vk-vl_NAT.dat$: Transition frequencies and intensities calculated for each $J' \rightarrow J$ transition from vibrational level k of electronic state i to vibrational level l of electronic state j. These positions and intensities are sep-

arated into P, Q (as applicable) and R branches, with values of J and/or K indicated. The NAT stands for "native." These are the intensities for transitions arising from user–specified parameters (see the next entry).

 $si-sj_vk-vl_CAS.dat$: The contents of this file are similar to the contents of the file above, but the intensities are due to electronic cascade. For example, if a user specifies to simulate the a'-a, d-a and e-a and a-X transitions of CO, a certain portion of the light observed for the a-X transition will be due to cascade from the a', d and e states. In that case, the a-X_vk-vl_CAS.dat files will contains only those portions of the a-X transition determined by the program to be due to transitions from the higher states.

Files placed within the PREF_simulations directory:

PREF_Sim_All: This file contains the final output from the entire simulation.

- *Atomic_lines*: This file contains the portion of the final simulation due to atomic lines.
- *Mol_native_pop*: This file contains the portion of the final simulation due to "native," or user–defined, diatomic molecular populations.
- *Mol_cascade_pop*: This file contains the portion of the final simulation due diatomic molecular populations arising from transitions from higher states.

6-4 State Energies, Relative Intensities and Populations, and Selection Rules

The program was designed to balance precision with ease of use. Greater precision than what is currently available in the program is certainly possible. For example, Kovács [1969] has published a book containing energy levels and transition intensities for almost every imaginable type of transition. However, not only are there hundreds of formulae, but the formulae also often require parameters that are not routinely available in tabulations of spectroscopic data. For example, many of his formulae require knowledge of a spin-orbit interaction coupling constant. While such information must certainly exist for a large number of diatomics, it is not generally available in convenient form. So, his formulae are not used in the program. Rather, the program is written so that the user needs only have a standard spectroscopic reference at hand [e. g., Herzberg 1989, NIST 2001a,b or Radzig 1985].

The equations used in the simulation come primarily from Herzberg [1989] with occasional augmentation or modification using information in Steinfeld's text [1985]. Only Hund's Cases a and b are modeled, for two reasons. Cases a and b are the two simplest cases: they do not require knowledge of the extent to which the electronic configuration of the molecule will couple to the rotational axis. Additionally, since cases c and d involve coupling to the axis of rotation, modeling them properly would require transition from case a or b as the rotational quantum numbers increase, which would involve the difficulties mentioned above regarding Kovács.

Obviously, the simulation can only be as good as the model upon which it is based, so, results from the simulation should be interpreted with care, especially if the molecules or states are unusual in some manner. For example, some electronic states of He₂, begin to transition to or toward Hund's Cases c or d as soon as there is rotational excitation. For these molecules the simulation produced by this program cannot be better than a good approximation. See Section 6-7 for further discussion on this.

The model is also only as good as the data used as input. For example, if Franck– Condon factors are calculated for high vibrational levels using Morse potentials, as is common, one should expect there to be errors in the simulated intensities and positions for those vibronic transitions. In the program, for example, the rotational constant, D_e , is calculated using an ideal–case equation (Eq. 2, below). Since this factor is usually very small, the error will be small, but could become significant for some cases. The program uses standard spectroscopic constants for electronic states of diatomic molecules. For convenience, they are defined here, but definitions of them can be found in any spectroscopy text that deals with electronic transitions in small molecules.

 ω_e : The fundamental vibrational frequency for the state.

 $\omega_e \chi_e$: The vibrational anharmonicity for the state.

- B_e : The principle rotational constant.
- α_e : The constant describing the interaction between vibration and rotation in the molecule.
- B_v : The rotational constant modified for vibrational interaction:

$$B_v = B_e - \alpha_e (v + \frac{1}{2}) \tag{58}$$

 D_e : Rotational constant describing cetrifugal effects:

$$D_e = \frac{4B_e^3}{we^2} \tag{59}$$

- β_e : A correction term for the vibrational interaction with the centrifugal distortion (see below). Herzberg [1989, p 108] offers an expression for β_e , but currently, the program always assumes β_e to be zero. It could be included quite easily, except that it is not widely tabulated and the correction is also generally very small.
- D_v Correction for the centrifugal distortion due to the rotation of the molecule:

$$D_v = D_e + \beta_e (v + \frac{1}{2}) \tag{60}$$

- J: The final rotational quantum number. This is the quantum number that has taken account of all relevant angular momenta.
- K: The rotational quantum number that takes account of all relevant angular momenta except for electron spin.

Energy Levels (all energies are entered in cm^{-1}):

- T_e : The term energy for the state. This is the energy at the bottom of the attractive potential well between the two atoms in the molecule.
- T_0 : The energy of the zeroth vibrational level.
- G_v : The energy associated with vibrational level v in the molecule:

$$G_v = \omega_e (v + \frac{1}{2}) - \omega_e \chi_e (v + \frac{1}{2})^2$$
 61

 $F_v(J)$: For Hund's Case a:

$$F_v(J) = B_v(J(J+1) - \Omega^2) - D_v J^2 (J+1)^2$$
⁶²

For Hund's Case b:

$$F_v(J) = B_v K(K+1) - D_v K^2 (K+1)^2$$
63

Note that J is not included explicitly in the right-hand side of the equation. This is accurate. The program does not account for splitting between the various J's for each K. So, each J is assigned the energy associated with its parent value of K. The splitting between those levels could be added in later, but the effect is small (on the order of a few cm⁻¹ for a large effect) and the equations needed change according to the type of electronic state.

 $T_v(J)$ The energy level associated with rotational quantum J of vibrational state v of the relevant electronic state relative to the bottom of the potential well for the electronic ground state:

$$T_v(J) = T_e + G_v + F_v(J) \tag{64}$$

Thermal Rotational Populations

Populations in the program are all assigned values relative to one. The program is designed to stop including rotational states in the simulation after the state populations fall below a cutoff fraction of the most populated rotational state. The cutoff fraction is input by the user. To make the initial estimate of the number of rotational levels to include, the program uses a simple equation for the rotational energy levels. It is taken at v = 0 and centrifugal effects on the energy are neglected $(D_v = 0)$:

$$Population_{estimate} \propto (2J+1) \exp\left(-\frac{F_0'(J)}{k_B T}\right)$$

$$65$$

where the form of $F'_0(J)$ depends on Hund's case (see Equations 5 and 6, above).

When the actual population for a given rotational level is calculated, the full form of the appropriate $F_v(J)$ is used:

$$Population \propto (2J+1) \exp\left(-\frac{F_v(J)}{k_B T}\right)$$
66

Note that since the pre–exponential factor is a statistical description of available orientations in space, it depends on whatever quantum number represents the total angular momentum in the system. So, for Hund's Cases (a) and (b), the important quantum number is J in the pre–exponential factor. Even when the value of F_v is calculated as an approximation based on K, as for Hund's Case (b) in this program, the exponential is multiplied by (2J + 1).

Selection Rules:

The relevant selection rules are widely available [for example, Herzberg 1989]. But, again, for convenience, they are summarized and included here.

Global Selection Rules:

- $\Delta J = 0, \pm 1$ except that $J = 0 \not\leftrightarrow J = 0$
- + ↔ − only (the ± here refers to overall symmetry of the wavefunction and not the ± value assigned to Σ electronic states)

- For homonuclear diatomics:
 - $\cdot g \leftrightarrow u$ only
 - $\cdot \ s \leftrightarrow s \text{ and } a \leftrightarrow a \text{ only}$

Rules that apply to both Hund's Case (a) and Hund's Case (b):

- $\Delta \Lambda = 0, \pm 1$
- $\Delta S = 0$ (this rule often broken)
- For $\Lambda = 0 \leftrightarrow \Lambda = 0$, $+ \leftrightarrow +$ and $\leftrightarrow -$ only (\pm here refers to reflection symmetry through internuclear axis)

Rules applying only to Case a–a transitions:

- $\Delta \Sigma(spin) = 0$ only
- $\Delta\Omega = 0, \pm 1$
- For $\Omega = 0 \leftrightarrow \Omega = 0$, $\Delta J = \pm 1$ only
- Bands with $\Delta J = 0$ and $\Delta \Lambda = 0$ (but not for $\Lambda = 0 \leftrightarrow \Lambda = 0$):
 - · Intensities for $\Delta J = 0$ fall off rapidly, with intensities decreasing approximately as $(1/J)e^{-E_r/k_BT}$.

Rules applying only to Case b-b transitions:

- For $\Lambda = 0 \leftrightarrow \Lambda = 0$:
 - · $\Delta K = \pm 1$ only.

Else:

- $\Delta K = 0. \pm 1$
- Bands with $\Delta K = 0$ and $\Delta \Lambda = 0$ (but not for $\Lambda = 0 \leftrightarrow \Lambda = 0$):
 - · Intensities for $\Delta K = 0$ fall off rapidly as the value of K increases, with intensities decreasing approximately as $(1/K)e^{-E_r/kT}$.
- Intensities for bands where $(\Delta J \neq \Delta K)$ also have intensities that drop off very rapidly with increasing K. The bands are called 'satellite bands.' In this program, their intensities are assigned a value of zero unless the user specifies some other value.



Figure 6-4.1: Flowchart for determining symmetry properties of rotational states. Chart shows nuclear symmetry for bosons only. For fermions, interchange the 'a' and 's' designations, but not the '+' and '-' designations. A refers to the electronic orbital angular momentum for the state. J and K are rotational quantum numbers. Encircled + or - signs refer to the overall symmetry of a given rotational state. g and u refer to gerade and ungerade states. s and a stand for symmetric and antisymmetric.

Determination of symmetry and nuclear effects:

In some cases, the overall symmetry of a given state must be determined (the selection rules will not always account for this automatically). The task is complicated further if the diatomic is homonuclear and nuclear spin statistics must also be considered. The necessary steps are outlined in the flowchart in Figure 6-4.1. Note that the flowchart only specifies symmetries for bosons (nuclei with integral spins). In the case of fermions (nuclei with half–integral spins), 's' and 'a' designations, but not any others, should be interchanged.

Transition Intensities:

All factors associated with transition intensities: transition probabilities, Franck– Condon Factors, Hönl–London Factors and species population are assigned values relative to one. It is up to the user to determine how to scale the overall simulation to match experimental observation.

The relative populations of each portion of the simulation are given in the input file. Populations of individual diatomic species, i, are given by a simple statistical formula:

$$Pop_i = f_{rve} * f_{mol} * f_{st} * f_{vib} * f_{rot}$$

$$67$$

 f_{rve} represents the relative weight of the rovibronic portion of the simulation compared to other parts of the simulation; f_{mol} , is the relative population of the molecule; f_{st} is the relative population of each electronic state for a given molecule; f_{vib} is the population of one vibrational level relative to other vibrational levels within its electronic state; and, f_{rot} is the relative population of the rotational level to other rotational levels in that vibrational level. All but the relative rotational level must be included in the input file. If desired, the relative rotational levels can be input as well. Relative populations of other species included in the simulation are calculated in an analogous and obvious fashion. _ Table 6-4.1 _

Relative Hönl–London Factors for Emission

$\Lambda' =$	J' =	Relative Hönl–London Factor
$\Lambda'' + 1$	J'' - 1(P)	$\tfrac{(J+1-\Lambda)(J+2-\Lambda)}{2(2J^2+3J+1)}$
	J''(Q)	$rac{(J+\Lambda)(J+1-\Lambda)}{2J(2J+1)}$
	J'' + 1(R)	$rac{(J+\Lambda)(J-1+\Lambda)}{2J(2J+1)}$
Λ''	J'' - 1(P)	$\tfrac{(J+1+\Lambda)(J+1-\Lambda)}{2J^2+3J+1}$
	J''(Q)	$rac{\Lambda^2}{J(J{+}1)}$
	J'' + 1(R)	$rac{(J+\Lambda)(J-\Lambda)}{J(2J+1)}$
$\Lambda'' - 1$	J'' - 1(P)	$rac{(J+1+\Lambda)(J+2+\Lambda)}{2(2J^2+3J+1)}$
	J''(Q)	$rac{(J-\Lambda)(J+1+\Lambda)}{2J(J+1)}$
	J'' + 1(R)	$rac{(J-\Lambda)(J-1-\Lambda)}{2J(2J+1)}$

Table 6-4.1: Hönl-London factors [Herzberg 1989] scaled so that each represents a probability, out of one, that the upper state will decay to each of the possible lower states. A is the electronic orbital angular momentum quantum number and J is the rotational quantum number. A single prime (') designates an upper state and a double prime (''), a lower state.

The relative transition intensity, $Irel_{i,j}$, then, from any rotational level *i* to another rotational level *j* is given by:

$$Irel_{i,j} = Pop_i * TFrel * FCFrel * HLrel_{i,j}$$

$$68$$

where TFrel is the fraction of the upper electronic state that is expected to radiate, FCFrel is the relative Franck–Condon factor and $HLrel_{i,j}$ is the relative Hönl– London factor for the transition. The relative Hönl–London factors (see Table 6-4.1) are derived from the general–case Hönl–London factors found in Herzberg [Herzberg 1989, p208-209]. The relative Franck–Condon factor, FCFrel, contains the effects due to the transition frequency (raised to either the third or fourth power as required by the detection technique) at the band origin. The program is currently being rewritten so that the effect of transition frequency is included at the level of each rotation \rightarrow rotation transition, which is more accurate.

6-5 Data Structures

Data in this program are stored in arrays, structures or combinations of arrays and structures. An array is an addressed list of data storage locations within a computer's memory. Structures are named collections of specified types of storage location. Arrays only contain one type of information — integer, float, character, etc. Structures can contain any number of different types of data. For example, a structure might contain a string, two float values, and an array of integers (or any other combination possible within the programming language). Structures can also contain other structures or arrays of other structures, a capability often exploited in this program. In this section, the more complex data structures employed in the program are described.

Arrays of data in this program frequently occupy 3, 4 or more dimensions. Regardless the number of dimensions required for convenient organization of the stored data, data in this program are physically stored linearly, in a 1D array of memory addresses. In order to access the information in a manner convenient to the needs of programming, the data is indexed in a regular fashion

Figure 6-5.1 graphically illustrates the indexing for a four-dimensional array. This particular 4D array stores Franck–Condon factors for a series of $v' \rightarrow v''$ transitions. A 4D array is necessary when the upper and lower electronic states are Hund's Case a and where one or both states can exist with multiple values of Ω , and where the Franck–Condon factors are different for each $\Omega' \rightarrow \Omega''$ transition. In this case, it is necessary to generate indexing such that the Franck–Condon factor for each $v' \rightarrow v''$ transition of each $\Omega' \rightarrow \Omega''$ transition occupies a unique address in the array. That makes 4 dimensions. The following equation exemplifies the manner in which individual storage locations within multi–dimensional arrays are addressed within the program.

$$Address = \Omega'_{i} * N_{\Omega''} * N_{v'} * N_{v''} + \Omega''_{j} * N_{v'} * N_{v''} + v'_{k} * N_{v''} + v'_{\ell}$$

$$69$$

where Ω'_i , Ω''_j , v'_k and v''_ℓ are the indexes (integers starting with zero) corresponding to the current values of the high-state and low-state values of Ω and v, respectively, and $N_{\Omega''}$, $N_{v'}$ and $N_{v''}$ are the total number of low state Ω 's and high and low state vibrational quanta. The equation above can be simplified algebraicly, but the current form makes its meaning more readily understood.

Sometimes, because of the greater flexibility, structures are used to store multidimensional arrays rather than the linear addressing described in the last paragraph. As an illustrative example, consider the way the program keeps track of states and transitions for a certain molecule. Here is the 'Molecule' structure used in the program (with comments):

```
typedef struct{
    int cp, cT; /* change flags for relative population
        and temperature */
    char Mol[41]; /* name of molecule */
    double pop; /* relative population for molecule */
    int states; /* number of electronic states for
        this molecule */
    State *s; /* array of electronic transitions for
        this molecule */
    Trans *t; /* array of electronic transition information */
    double T; /* temperature if specified at molecule level */
}Molecule;
```

After this declaration is made, "Molecule" is now a data type, (e. g., integer, character, etc.) to be used as needed in the program.
Each of these boxes contains 30 Franck-Condon Factors (2 Dimensions)



If there are several Low-State Omegas, the data is structured like this (3 Dimensions):



If there are also several High-State Omegas, the data is structured like this (4 Dimensions):



Each address above is given by: (current high Omega number)*(number low omegas)*30*30 + (current low Omega number)*30*30 + (high state vibrational quantum number index)*30

+ (low state vibrational quantum number index)

Figure 6-5.1: Graphical representation of the indexing used in multi-dimensional arrays in the program. Each of the boxes is, itself, a one-dimensional array (the 30 Franck-Condon factors). So, the row of boxes at the top is two dimesions and so forth. Dimensionalities higher than 4 can be visualized by considering each box to be a multi-dimensional array, itself.

The Molecule structure, itself, contains two structures. Each molecule considered in the simulation can be expected to exist in a number of electronic states — at least two if there is one transition — and might also undergo a number of transitions. The stars next to the s and the t indicate that those variables are "pointers." A pointer is simply a marker — an address within the computer's memory. Once the program is running and it reads the number of states to assign to a given molecule, it will allocate exactly the amount of memory needed to store the information. After it allocates that memory, the pointer will be pointing to an array. The data types State and Trans are structures similar to the Molecule structure except that they contain, not surprisingly, information pertaining to the states for that molecule and the transitions it should undergo. A portion of the State structure is:

```
typedef struct {
    char Name[21]; /* The letter designation for
        the state (a', B, c, etc.). */
    double pop; /* relative population for this state */
    char Case[11]; /* Hund's Case: a or b */
    ...
    rotset *r; /* pointer to set of rotational
        distribution info.
}State;
```

Note that the State structure also contains a pointer, *r. There will be one "rotset" for each $v' \rightarrow v''$ transition. Each rotset, itself, contains arrays corresponding to rotational energy levels and relative populations.

Accessing information in this sort of structure is quite straightforward. Let us expand upon an example from before. Assume that the molecules He₂, N₂ and CO are being simulated, and that they appear in the state file in that order. If the variable name 'MOL' is assigned to the Molecule structure, then the name "He2" would be assigned to MOL[0].Mol, "N2" would be assigned to MOL[1].Mol, and "CO", to MOL[2].Mol. Further, assume that the a', d, e, a, A and X states of the CO molecule are part of the simulation, and that they appear in that order in the transition file. In this case state a' would be assigned position 0 in the array of states, state d would be assigned position 1, and so on. Thus, the value assigned to MOL[2].s[2].Name would be "e." Since the chain of square–braces and periods can become lengthy, short names for pointers (e. g., "s" and "r") are recommended.

These structures are also explained in the supporting documentation for the program and are well documented within the code. Any given piece of data can be located with just a little effort and modified if necessary.

6-6 Possible Changes and Additions

As was mentioned in earlier sections, the program, in its current form, can only perform a limited number of tasks. But, it was designed to be changed and to be somewhat easy to change. Table 6-6.1 lists a number of proposed changes and additions.

6-7 Comparisons of Program Output with Experimental Data

The calculations that the program does have been tested thoroughly. Several small test systems were run and the results compared to equivalent calculations performed in Microsoft Excel. The instructions in the program or, if necessary, the spreadsheet, were adjusted until the two agreed. At this point, it was assumed that the program was performing the calculations it was intended to perform. Obviously, having performed the intended calculations doesn't mean that the intended calculations were appropriate.

Output from the program has also been compared to experimental data acquired for this study and to data acquired elsewhere [Brown 1971 & 1973]. Results of these comparisons are summarized in a series of tables and figures in this section. Captions on the figures and tables are detailed and will not be repeated here. A number of other comparisons can also be found in Chapter 4 of this manuscript.

The comparisons show that the program performs its assigned tasks. As is expected, though, when reality deviates from the model used, the simulation only approximates the experimental data.

Suggested Program Additions

See below for key to difficulty levels

Capability

Difficulty

Level

$Diatomic \ Molecules - States$	
Hund's Case's c & d	3
Temperature specification at vibrational level	4
Addition of higher-precision spectroscopic constants	2
Energy level splitting — simple equations	4
Energy level splitting — complex equations	5
Energy levels and populations by user-defined equations	6(5)
Energy levels by ab-initio calculation	6(5)
Diatomic Molecules — Transitions	
Hund's Case $a \leftrightarrow b$	3
Other transitions ($c \leftrightarrow c, b \leftrightarrow d, etc.$)	4
Variable intensity for satellite bands	4
Additional options for Hönl–London Factors	2
Cascade between vibrational or rotational levels	5
Add absorption as well as emission	4
Bound \leftrightarrow unbound transitions	4
Raman transitions	6(5)
Transitions by ab-initio calculations	6(5)
Polyatomic Molecules	
Energy levels and populations	6(6)
Transitions	6(6)

Equipment- and Experiment- Specificity

Transmission Efficiency curve from values in file	1
Transmission Efficiency curve from standard equation	3
Transmission Efficiency curve from user–defined equation	6(5)
Alternate line shapes	3
Doppler bradening, natural linewidth, etc.	2
Other Transitions	
Include spectral features from external sources	2
User-Friendliness	
Inclusion of interactive mode	5
Addition of graphical–user–interface (GUI)	6(6)
Inclusion of graphical display of results	5
Addition of experimental data to graphical display	3

Key to difficulty levels. Each item is followed by an approximate description of the work needed to accomplish that task.

Level Sample set of tasks.

- 0 Values that are already present in the program must be included in calculations or outputs that are already written into the program.
- 1 Existing code must be called or simple new code written and called. The result will be used in calculations or outputs that already exist or are very simple to write or to copy and modify.
- 2 Existing code must be copied and modified for a new task. Decision-making statements (e. g., "if" or "switch") must be augmented or written anew, with the result included in a simple calculation or output that might or might not already exist.
- 3 Existing code must be copied and modified in a complex manner. Some of the modifications might be subtle. Significant debugging is expected. Decision–

making statements must be written or augmented, with results included in calculations or output.

- 4 This level describes two situations. In the first, the necessary modification is level 2 or 3, but there are other level 2 or 3 modifications that must be completed first. In the second, this modification is non-trivial and changes must be made in several of the existing functions (which generally complicates debugging).
- 5 This level is similar to 3 or 4 except that the amount of work needed is greatly increased. For example, a complex function must be written from scratch or an existing function greatly expanded or modified.
- 6 This number indicates that this feature has not been designed or is in the earliest stages of design. The number in parentheses is an estimate of the difficulty level. If the number in parentheses is 6, the amount of work required is uncertain.

Table 6-7.1 _____

Example Comparison of Simulated Transition Frequencies to Experimental Data *

He ₂ : $e^{s}\Pi_{g}(v=0) \rightarrow a^{s}\Sigma_{u}^{*}(v=0)$						
	P		Q		R	
K''	$ u_{sim}$	$\nu_{sim-exp}$	$ u_{sim}$	$\nu_{sim-exp}$	$ u_{sim}$	$\nu_{sim-exp}$
1			21506.31	-0.12	21534.98	0.31
3	21459.17	0.31	21502.15	-0.13	21559.40	1.30
5	21423.21	1.36	21494.68	-0.11	21580.30	2.88
7	21384.23	2.89	21483.93	-0.14	21597.63	5.03
9	21342.36	4.99	21469.96	-0.14	21611.33	7.61
11	21297.78	7.60	21452.81	-0.15	21621.36	10.64
13	21250.66	10.74	21432.57	-0.20	21627.69	14.23
15	21201.18	14.38	21409.33	-0.22	21630.32	18.14
17	21149.56	18.50	21383.19	-0.26	21629.25	22.37
19	21096.00	23.02	21354.26	-0.32	21624.49	26.85
21	21040.75	27.97	21322.69	-0.24	21616.08	31.53
23	20984.04	33.32	21288.61	-0.44	21604.06	36.30
25	20926.15	39.11	21252.19	-0.49	21588.51	41.18
27	20867.34	45.30	21213.60	-0.60		
*[Brown	1971]					

He₂: $e^{3}\Pi_{q}(v=0) \to a^{3}\Sigma_{u}^{+}(v=0)$

Example Comparison of Simulated Transition Frequencies to Experimental Data^*

He ₂ : $e^{3}\Pi_{g}(v=2) \to a^{3}\Sigma_{u}^{+}(v=1)$						
	Р		ζ	2	R	
K''	$ u_{sim}$	$\nu_{sim-exp}$	$ u_{sim}$	$\nu_{sim-exp}$	$ u_{sim}$	$\nu_{sim-exp}$
1			23006.36	0.03	23033.26	0.47
3	22959.72	0.28	23000.05	-0.04	23053.76	1.44
5	22921.67	1.22	22988.71	-0.11	23069.02	2.89
7	22878.87	2.56	22972.38	-0.21	23078.99	4.86
9	22831.48	4.43	22951.10	-0.36	23083.61	7.31
11	22779.64		22924.93	-0.55	23082.84	10.11
13	22723.55	9.50	22893.94	-0.80	23076.66	13.29
15	22663.38	12.59	22858.23	-1.15	23065.05	16.80
17	22599.34		22817.91	-1.48	23048.02	20.53
19	22531.65		22773.08		23025.58	24.51
21	22460.55		22723.88		22997.78	28.43
23	22386.27		22670.46		22964.65	32.47
25	22309.09		22612.98		22926.26	36.50

*[Brown 1971], "—" indicate unreported values.

Example Comparison of Simulated Transition Frequencies to Experimental Data*

He ₂ : $J^1 \Delta_u (v=0) \rightarrow B^1 \Pi_g (v=0)$							
	Р		Q	5	1	R	
K''	$ u_{sim}$	$\nu_{sim-exp}$	$ u_{sim}$	$\nu_{sim-exp}$	$ u_{sim}$	$\nu_{sim-exp}$	
1					21655.71	-5.89	
2			21626.55	-6.00	21669.13	-17.94	
3	21582.83	-5.91	21625.42	-17.83	21682.19	-23.64	
4	21567.19	-18.19	21623.97	-23.96	21694.94	-51.63	
5	21551.28	-23.61	21622.25	-51.27	21707.41	-45.00	
6	21535.16	-52.03	21620.32	-45.71	21719.68	-94.55	
7	21518.90	-44.97	21618.26	-93.77	21731.81	-67.12	
8	21502.61	-95.03	21616.16	-68.39	21743.91	-140.11	
9	21486.37	-66.91	21614.11	-138.77	21756.05	-88.20	
10	21470.30	-140.66	21612.24	-90.07	21768.37	-184.61	
11	21454.52	-88.12	21610.65	-182.61	21780.98	-106.60	
12	21439.17	-185.23	21609.50	-109.20	21794.02	-225.65	
13	21424.40	-106.46	21608.92	-222.85	21807.64		
14	21410.38	-226.32	21609.09	-124.31	21822.00		
15	21397.27	-120.56	21610.18		21837.28		
16	21385.27	-261.95	21612.37	-133.79	21853.67		
17	21374.57	-128.85	21615.87		21871.36		
18	21365.39	-290.22	21620.88	-135.82	21890.57		
19	21357.95	-129.64	21627.64		21911.52		
20	21352.49		21636.37	-128.60	21934.45		

*[Brown 1973], "—" indicate unreported values. See Figure 6-7.3 and caption.



Figure 6-7.1: Graphical comparison of simulated line positions (red and blue lines) with experimental positions (green, magenta) [Brown 1971] for the $e^3\Pi_g(v=0) \rightarrow a^3\Sigma_u^+(v=0)$ transition of He₂. The x-axis is wavelength in nm. Y-axes are scaled similarly, but the intensity is arbitrary. Since Brown and Ginter do not report detailed line intensities, the relative intensities are those determined by the simulation. Most of the positions for the Q branch are nearly coincident, and the differences are not resolved on this graph. See also Figure 6-7.4.



Figure 6-7.2: Graphical comparison of simulated line positions (red and blue lines) with experimental positions (green and magenta) [Brown 1971] for the $e^3\Pi_g(v=2) \rightarrow a^3\Sigma_u^+(v=1)$ transition of He₂. The x-axis is wavelength in nm. Y-axes are scaled similarly, but the intensity is arbitrary. Since Brown and Ginter do not report detailed line intensities, the relative intensities are those determined by the simulation. Some of the positions for the Q branch are nearly coincident, and the differences are not resolved on this graph.



Figure 6-7.3: Graphical comparison of simulated line positions (red and blue lines) with experimental positions (green, magenta) [Brown 1973] for the $J^1\Delta_u(v=0) \rightarrow B^1\Pi_g(v=0)$ transition of He₂. Values for ω_e , $\omega_e\chi_e$ and α_e , not reported for this transition, were set to zero in the simulation; this accounts for most of the poor agreement. The x-axis is wavelength in nm. Y-axes are scaled similarly, but the intensity is arbitrary. Since Brown and Ginter do not report detailed line intensities, the relative intensities are those determined by the simulation.

Figure 6-7.3 _





Figure 6-7.4: Comparison of simulation (red, solid) to experimental data obtained during this study (green, dashed). Transitions included in the simulation are $h^{3}\Sigma_{u}^{+}$ $(v = 0) \rightarrow b^{3}\Pi_{g}(v = 0)$ and $e^{3}\Pi_{g}(v = 0) \rightarrow a^{3}\Sigma_{u}^{+}(v = 0)$ of He₂ and $4s^{3}S_{1} \rightarrow 2p^{3}P_{0,1,2}^{0}$ of atomic He. Emissions from He₂ transitions other than $e \rightarrow a$ and $h \rightarrow b$ are present in the experimental spectrum, but have not been included in this simulation. But, inclusion of these states in the simulation is problematic since spectroscopic constants ω_{e} , $\omega_{e}\chi_{e}$ and α_{e} are not reported for the J states (see also Figure 6-7.3). The difference in intensity between the simulated and the experimental spectrum is due to an indexing error within the program. The intensity should be higher in the simulation (see Figure 6-7.1). The simulation resolution is 0.5 nm FWHM, which is approximately the same as the experimental resolution.

CHAPTER 7

SUMMARY AND FUTURE DIRECTIONS

The work presented in this dissertation is summarized, and suggestions for continuations of the work are made.

7-1 Summary

A detailed study of the standard experimental procedure for producing and classifying optical emissions resulting from dissociative electron ion recombination (DR) has produced unexpected results. Of primary importance among these results is the observation that emissions which cannot result solely from DR are quenched by the addition of an electron–attaching gas. Investigation of the plasma in which the recombinations occur has revealed emissions from excited states of He, He₂, Ar and Ar⁺ that are also quenched in this way. A satisfactory mechanism for this behavior has not been found, but several hypotheses, and means for testing some of the hypotheses, are suggested. Means for identifying recombination emissions in the absence of a satisfactory mechanism are also discussed. In order to facilitate future studies, a survey of spectra containing emissions that are likely to be due to recombination is presented.

Emissions from the recombination of CO_2^+ were observed according to the protocol suggested by the studies mentioned above. Rotational temperatures and relative vibrational and electronic populations have been determined for a number of products of that recombination. These results indicate that photoproducts of DR can be positively identified, and that other systems should be treated similarly. A computer program, RVESIM (rotational vibrational electronic simulation), has been written that simulates rovibronic (rotational, vibrational, electronic) spectra. This makes identification and quantification of emissions simpler and more reliable. The inclusion of effects due to cascade from higher electronic states allows nascent populations of lower–lying electronic states to be determined. The program can be altered, and users of the program are encouraged to make changes and additions as needed or desired.

A photographic and spectroscopic study of the flow characteristics near the reactant gas inlet port, where emissions are detected, has also been made. The determination of relative electronic state populations is dependent on the time the species spend in viewing range of the spectrometers and, therefore, on the throughput of the injected reagent gas. An empirical dependence of injection plume size as a function of reagent gas throughput is given, but the relationship of plume size to observation time is neither obvious nor trivial. A computer program that simulates the mixing of neutral gases in the injection region has been developed, and suggestions for additions to the program are made.

7-2 Future Directions

The mechanism by which the plasma emissions (and also the CO^+ emissions) are affected by the attaching gas needs to be determined in more detail. Inherent in determining this mechanism will be determining the mechanism by which the emissions are maintained within the plasma. When these mechanisms are identified, it will be possible for the presence of unwanted species (excited states of He, He₂, Ar and Ar⁺) in the afterglow to be diminished or eliminated. This will make recombination studies more straightforward. The populations of these species could also be lessened by enhancing the creation of cold He⁺ ions at the ionization source (see the end of Section 4-1). In either case, the survey of recombination experiments presented in

Section 4-2 should be repeated in more detail, making use of the information presented in Chapter 4.

The computer program, RVESIM, needs to be expanded to make it easier to use, include many other types of transition and to make it more generally applicable. A list of suggested changes and additions to the program is given in Chapter 6.

A means for more accurately determining the time emitting species spend in the viewing region should be devised. This will need to be done empirically, but general models should be developed (for example, those independent of reagent type). These models can include or be independent of the program presented in Section 5-3. A camera of some sort, e. g., with a charge coupled device (CCD) array, which can record spectra at each position in the flow, might prove useful for such studies.

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APPENDIX A

REFERENCES CATEGORIZED BY CONTENT

Computational and Theoretical — $D {\rm R}$

Theory and/or	summaries of comput	ational techniques:		
0 /	Adams, 1975	Bates, 1992	Bates, 1993a	
	Bates, 1993b	Bates, 1994	Burke, 1988	
	Dalgarno, 2000	Golubkov, 2000	Halkier, 1998	
	Hardy, 1998	Harland, 1998	Larson, 2000	
	Pichl 2000	Schneider 2000b	Tachikawa 1999	
	Talbi 2000	Tennyson 2000	Tomashevsky 1998	
	Urbain 2000	van der Zande 2000		
Description or	use of a computation	nal technique (compu	itations involving any	
mechanism of l	DR any any type of pr	roduct):		
	Bates, 1992	Carata, 1999	Carata, 2000a	
	Carata, 2000b	Golubkov, 2000	Guberman, 1991	
	Hardy, 1998	Jursic, 1999	Jursic, 2000	
	Ketvirtis, 1999	Kraemer, 1998	Müller, 2000b	
	Mulliken, 1964	Orel, 2000	Osamura, 1999	
	Schneider, 2000a	Tachikawa, 1999	Tagaki, 2000	
	Tennyson, 2000	Tomashevsky, 1998	0	
Comparison of theory or computation to experimental data:				
1	Adams, 1994	Guberman, 1991	Lange, 1999	
	Schneider, 2000a	,	0 /	
Computational and	d Theoretical — Flow	or Reactive Flow Sim	nultation	
Theory and/or	summaries of comput	ational techniques:		
	Abdallah, 1999	Callear, 1978	Cornubert, 1991	
	Dubrulle, 1991	Ernst. 1991	Frisch, 1991	
	Gerling, 1991	Hasslacher, 1991	Higuera, 1993	
	Jenny, 1950	Kong. 1991	Landau, 2000	
	Monnery 1995	Petravic 1995	Shukla 1994	
	van der Berg 1993	10010010, 1000	Siraina, 100 I	
Description or	use of a computational	l technique [.]		
Description of	Banavar 1991	Baras 1995	Bernardin 1991	
	Brieger 1991	Brosa 1989	Brosa 1990	
	Brosa 1991	Chenoweth 1972	Cliffe 1991	
	Foley 1997	Frisch 1986	Green 1995	
	Kohring 1991a	Kohring 1991b	Kohring 1991c	
	Kohring, 1991a	Landau 2000	$L_{O}V_{2}$	
	Lawniczak 1001	Macagno 1967	Miyazaki 1005	
	NATO 1001	Noulloz 1001	O_{ran} 1002	
	Rapport 1088	Riccardi 1001	Society 1006	
	Singh 1004	Succi 1001	Uchigachi 1002	
	uan der Hoof 1001	Vilongly 1004	7 anotti 1001	
Companian of	theory on computation	v nensky, 1994	Zanetti, 1991	
Comparison of	Macagna 1067	$r_{\rm constraint} = 100 c_{\rm c} (2)$	a. Shultla 1004	
	macagno, 1907	Segatz, 1990 (?)	Shukia, 1994	

Computational and	Theoretical — Other		
Atmospheric an	ad Interstellar:	Duloy 1002	$F_{\rm OV}$ 1000
	For 2000	O_{samura} 1992	FOX, 1999
Spacecraft ·	POX, 2000	Osamura, 1999	
spaceciant.	Caledonia, 1993	Murad. 1986	Swenson, 1991
Spectroscopic (i	including structural ca	alculations):	, , , , , , , , , , , , , , , , , , , ,
1 1 (Blöcker, 1990	Castaño, 1983	Dunning, 1978
	Engler, 1984	Ginter, 1970	Guberman, 1972
	Guberman, 1975	Hardy, 1998	Herzberg, 1971
	Herzberg, 1987	Herzberg, 1988	Herzberg, 1989
	Kraemer, 1998	Lefebvre–Brion, 198	6
	LeRoy, 1993	LeRoy, 1988	Lo, 1994
	Luo, 1999	Mies, 1974	Morse, 1929
	Ortenberg, 1963	Read, 1980	Resende, 2001
	Sawaryn, 1989	Wilson, 1935	Yarkony, 1989
Decetiene (in ele	Zhirnov, 1968	.]] /	
Reactions (inclu	iaing those involving e	electrons and/or phot	ons, collisions, scatter
ing and relaxati	ion processes):	$\mathbf{D} = 144^{\circ} = 1004$	CL:11 1009
	Allison, 1900	Dursntein, 1994	Cm10, 1983 Dumming 1079
	Errop 1004	Cienturco 1088	Harland 1008
	Herbst 2000	Lambert 1977	Laudenschlager 105
	Lengvel 1992	Marci 1998	McCarthy 1995
	Miller 1994	Miller 1968	Miller 1979
	Mistrik. 2000	Rabadan, 1999	Rapp. 1965
	Resende, 2001	Schattschneider, 198	36
	Zhou, 1998	7	
Experimental Techi Experimental techn nation:	nique and Apparatus iques and apparatus o	descriptions for study	involving e–i recomb
	Adams, XXXX	Habs, 1989	Hardy, 2000
	Janev, 2000	Jensen, 1999	Krohn, 2000
	Lange, 2000 Zong, 1999	Mitchell, 2000	Tanabe, 2000
Other experime	ntal technique (inclue	les fluid flow):	
	Adams, 1975	Bastian, 1968	Dudeck, 1983
	Ferguson, 1969	Hardalupas, 1992	Harland, 1998
	Hiller, 1983	Hollo, 1994	McDaniel, 1983
	Mitchell, 2000	Schmeltekopf, 1963	Smith, 1972
Experimental Decui	SIIIIII, 1975		
Kinetics	$\mu \sigma = D \Pi$		
111100105.	Adams. XXXX	Adams. 1984	Amitav. 1999
	Glosik 2000	Jensen 1000	Johnsen 1087
	Johnsen 2000a	Lange 1999	Larsson 1996
	Larsson, 1998	Laubé, 1998 a b	LePadellec 1997
	Mostefaoui. 2000	Rebrion–Rowe. 2000)a
	Rebrion–Rowe, 2000)b	Schneider, 2000 a
	Semaniak, 1998	Strömholm, 1996	Torr, 1981
		,	
	Weller, 1967	Zipf, 1980 a	Zipf, 1980 b

Products, ge	eneral (see also Products,	$spectroscopic^{\ddagger}$ and F	Products, RIP^{\dagger}):
	Adams, 1991	Adams, 2000	Amitay, 1999
	Datz, 2000	Gougousi, 1997a	Gougousi, 1997b
	Guna, 1999	Herd, 1990	Jensen, 1999
	Kley, 1977	Larson, 1998	Larsson, 1996
	LePaddellec, 1999		Mostefaoui, 2000
	Neau, 2000	Rebrion–Rowe, 2000	a
	Rebrion–Rowe, 2000	b	Rosen, 1998
	Rosen, 2000	Semaniak, 1998	Sheehan, 1999
	Strömholm, 1996 Zong, 1999	Vikor, 1999	Zaiffman, 2000
Products R	IP^{\dagger} .		
11000000, 10	Diurić 2000	Lange 1999	Larson 1999
	Zong, 1999	1000	
Products, sp	$ectroscopic^{\ddagger}:$		
7 1	Adams, 1994a	Adams, 1994b	Adams, 2000
	Butler, XXXX	Foley, 1993	Johnsen, 2000b
	Skrzypkowski, 1998	Sonnenfroh, 1993 b	,
	Taieb, 1977	Tsuji, 1990	Tsuji, 1991
	Tsuji, 1995	Tsuji. 2000	Valée, 1986
	Zipf, 1979	Zipf, 1980 a	Zipf. 1980 b
Experimental Re	esults - non - DR	F)	F) F = F
¹ Kinetics (inc	cludes vibrational relaxati	ion):	
(Adams, XXXX	Ádams. 1988	Bailey, 1978
	Boffard, 1999	Bohme, 1970	Capelle, 1973
	Federer, 1983	Ferguson, 1969	Fernando, 1981
	Golde 1989	Gundel 1976	Harland 1998
	Howard 1983a	Howard 1983b	Katayama 1984
	Katayama 1985	Klots 1976	Kolts 1978
	Kriegl 1986	Lambert 1977	Laudenschlager 1974
	Lawrence 1971	Lee 1977	Marinelli 1989
	McEwan 1992	Moore 1973	Morgan 1962
	Morrison 1985	Orr 1987	Schmeltekonf 1967
	Schmeltekopf 1968	Smith 1986	Sobczynski 1989
	Stedman 1970	Tichy 1988	Torr 1981
	Tsuji 1002	Tsuii 1003	V_{elazco} 1976
	$V_{11} = 1000$	7_{i+1} 1088	Velazco, 1970
Reaction pro	ducts (includes spectrose	conic products)	
neaction pro	Arfs 1008	Bartschat 1008	Rohmo 1070
	D_{iurid} 2000	Datan 1002	Fland 1077
	Earginger 1060	$E_{out} = 1070$	C_{oldo} 1977
	$\frac{1009}{100}$	10X, 1979 Lombort 1077	Landonschlager 1074
	Leber 2000	Lampert, 1977 McFuon 1000	Mitaula 1090
	Level, 2000	Roleino 1092	NIIISUKE, 1989
	Sauter, 1998	Seкiya, 1985 Таліі 1080	Somemiron, 1993 a T_{max} : 1000
	SUZUKI, 1978	1 SUJ1, 1980	1 supp. 1992
	1 Suji, 1993	Williams, 1999	WIOdek, 1987
	Wu, 1998	ru, 1990	Lare, 1980

[†] These are the papers that focus on RIP formation. Other papers in this section might also mention the process. [‡] Although spectroscopic products of DR also imply particulate products, these entries are not duplicated in the "Products, general" section.

Spectroscopic d	lata (includes photoele	ectron and bound–un	bound processes):
	Baer, 1986	Baruch, 1992	Bhushan, 2000
	Birge, 1926	Brau, 1975	Brown, 1971
	Brown, 1973	Carrington, 1993	Carroll, 1962
	Chow, 1971	Dixon, 1963	Ewing, 1975
	Fairbairn, 1970	Ginter, 1965 a	Ginter, 1965 b
	Ginter, 1966	Gloersen, 1965	Golde, 1975
	Headrick, 1930	Hearn. 1991	Heidner, 1969
	Hoffman, 1976	Jacox, 2001	Jones, 1980
	Judge, 1973	Kolts, 1978	Komatsu, 1992
	Lawrence, 1971	Lawrence, 1972	Lichten, 1974
	Loginov. 2000	Mies. 1966	Miller, 1975
	Moazzen–Ahmadi, 1	1989	Müller, 2000 a
	Orient, 1992	Orient, 1993	Orr. 1987
	Orth. 1976	Pubanz, 1985	Ray, 1986
	Read. 1934	Schloss, 1992	Sekiva, 1983
	Slanger 1976	Smith 1967	Stark 1987
	Suzuki 1978	Valée 1986	Velazco 1975
	Wang 1988	Willey 1992	Wyttenbach 1989
	Y_{11} 1990	Zittel 1988	, you want to be
Other physical	data (atmospheric co	nstituents reactions	in the ISM spacecraft
alows etc.).	data (atmospheric co		in the Isin, spacecial
giows, coc.).	Banks 1083	Chakrabarti 1003	Chauvrin 1002
	Duplop 1005	Duprog 1070	Grobowsky 1987
	$\begin{array}{c} \text{Dufflop, 1995} \\ \text{Crear, 1003} \end{array}$	Hornondoz 1071	Hunton 1088
	Koch 1088	Kofely 1086	Krassovsky 1062
	Machuzak 1003	$M_{c}C_{ov}$ 1078	Mondo 1083
	Murad 1000	Murad 1086	Olvo 2000
	Rind 1003	Swonson 1085	$T_{\rm orr} = 1077$
	$T_{orr} = 1081$	Vierock 1002	Wulf 1086
	V_{00} 1083	$V_{100} = 1085$	Wull, 1980
Other references	166, 1900	166, 1909	
Mathematical t	ochniques.		
	$\Delta \text{ bramowitz } 1065$	Δ iry 1873	Zwillinger 1992
Physical data c	ollections:	Ally, 1075	Zwinniger, 1992
i nysicai data c	Adams 1988	Huber 2001	I_{acov} 2001
	NIST 2001	Radzig 1985	5acox, 2001
Handbooks and	l other general collect	ions.	
	Drake 1996	Eisberg 1967	Graedel 1989
	Lang 1978	Larsson 2000	Badzig 1985
Textbooks [.]	Lang, 1910	Laibboll, 2000	100218, 1909
TOAUDOOND.	Atkins 1998	Bueche 1986	Hanly 1996
	Hazeltine 1998	Herzberg 1988	Herzberg 1989
	Knuth 1986	Landau 2000	Levine 1983
	McQuarrie 1976	McQuarrie 1983	Oran 1987
	Read, 1980	Steinfeld, 1985	

APPENDIX B:

CHARACTERIZATION OF THE HELIUM-ARGON PLASMA

This appendix contains the spectra taken of the base plasma when only helium had been added and when both helium and argon had been added. Graphs of the spectra are grouped by wavelength range and numbered. Each number corresponds to two or three graphs: (a) the He–only spectrum; (b) the spectrum with Ar added; (c) for certain spectral ranges, the first two spectra plotted together. Appendix B-b is a key to the graphs in B-a and contains detailed spectral information regarding each of the labeled emissions.

Atomic emissions are labeled with the graph number and a letter from the English alphabet. Below each atomic emission is the identity of the atom responsible for that emission, e. g.: $\frac{2D}{He}$ signifies label D on graph 2 and that the emission is atomic helium emission.

All molecular species that are not explicitly identified on a graph are He₂. These emissions are labeled with the graph number, a letter from the Greek alphabet, and a short-hand notation for the electronic transition corresponding to the emission, e. g.: 2γ : $n \rightarrow a$ signifies label γ on graph 2 and that the emission is the $n \rightarrow a$ emission of diatomic neutral helium.

B-a Graphs

The first two graphs (i & ii) are mass spectra taken prior to taking the spectra. The graphs immediately following the mass spectra (iii & iv) contain emissions that were difficult to classify. No emissions from any know helium or argon species are present in those spectra. The other spectra are as described above.



Graph B-a.i: Mass spectrum taken before the spectra were taken. The mass indicated by a peak is the number at the right of the peak. Only helium had been added when this spectrum was taken.



Graph B-a.ii: Mass spectrum taken before the spectra were taken. The mass indicated by a peak is the number at the right of the peak. This spectrum was taken after the addition of argon.



tentative. See Appendix B-b for assignments. Graph B-a.iii (a): Spectrum of the helium plasma. All assignments on this plot are



are tentative. See Appendix B-b for assignments. Graph B-a.iii (b): Spectrum of the helium-argon plasma. All assignments on this plot

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Graph B-a.iv (a)







Graph B-a.1a: Emissions from the helium-only plasma with atomic and molecular species labeled at approximate positions. See Appendix B-b for assignments. Some low intensity peaks may be obscured by background or molecular emissions.



Graph B-a.1b: Emissions from the helium-argon plasma with atomic species labeled at approximate positions. See Appendix B-b for assignments. Molecular species are identified on graphs in this series labeled a and c. Some low intensity peaks may be obscured by background or molecular emissions.



species labeled at approximate positions. See Appendix B-b for assignments. low intensity peaks may be obscured by background or molecular emissions. Graph B-a.2a: Emissions from the helium-only plasma with atomic and molecular . Some



Graph B-a.2b: Emissions from the helium-argon plasma with atomic species labeled at approximate positions. See Appendix B-b for assignments. Molecular species are identified on graphs in this series labeled a and c. Some low intensity peaks may be obscured by background or molecular emissions.



Graph B-a.2c: Direct comparison of spectra taken before (solid line) and after (dashed line) the addition of argon. The emissions are labeled at approximate positions. See Appendix B-b for assignments. Some low intensity peaks may be obscured by background or molecular emissions.



species labeled at approximate positions. See Appendix B-b for assignments. low intensity peaks may be obscured by background or molecular emissions. Graph B-a.3a: Emissions from the helium-only plasma with atomic and molecular . Some



obscured by background or molecular emissions. identified on graphs in this series labeled a and c. at approximate positions. Graph B-a.3b: Emissions from the helium-argon plasma with atomic species labeled See Appendix B-b for assignments. Molecular species are Some low intensity peaks may be



background or molecular emissions. See Appendix B-b for assignments. line) the addition of argon. Graph B-a.3c: Direct comparison of spectra taken before (solid line) and after (dashed The emissions are labeled at approximate positions. Some low intensity peaks may be obscured by

species labeled at approximate positions. See Appendix B-b for assignments. low intensity peaks may be obscured by background or molecular emissions Graph B-a.4a: Emissions from the helium-only plasma with atomic and molecular Some





obscured by background or molecular emissions identified on graphs in this series labeled a and c. at approximate positions. See Appendix B-b for assignments. Molecular species are Graph B-a.4b: Emissions from the helium-argon plasma with atomic species labeled Some low intensity peaks may be



background or molecular emissions. See Appendix B-b for assignments. line) the addition of argon. Graph B-a.4c: Direct comparison of spectra taken before (solid line) and after (dashed The emissions are labeled at approximate positions. Some low intensity peaks may be obscured by



Graph B-a.5a: Emissions from the helium-only plasma with atomic and molecular species labeled at approximate positions. See Appendix B-b for assignments. Some low intensity peaks may be obscured by background or molecular emissions.







background or molecular emissions. See Appendix B-b for assignments. line) the addition of argon. Graph B-a.5c: Direct comparison of spectra taken before (solid line) and after (dashed The emissions are labeled at approximate positions. Some low intensity peaks may be obscured by



Graph B-a.6a: Emissions from the helium-only plasma with atomic and molecular species labeled at approximate positions. See Appendix B-b for assignments. Some low intensity peaks may be obscured by background or molecular emissions.



obscured by background or molecular emissions identified on graphs in this series labeled a and c. at approximate positions. Graph B-a.6b: Emissions from the helium-argon plasma with atomic species labeled See Appendix B-b for assignments. Molecular species are Some low intensity peaks may be



background or molecular emissions See Appendix B-b for assignments. line) the addition of argon. Graph B-a.6c: Direct comparison of spectra taken before (solid line) and after (dashed The emissions are labeled at approximate positions. Some low intensity peaks may be obscured by



Graph B-a.7a: Emissions from the helium-only plasma with atomic and molecular species labeled at approximate positions. See Appendix B-b for assignments. Some low intensity peaks may be obscured by background or molecular emissions.



obscured by background or molecular emissions. identified on graphs in this series labeled a and c. at approximate positions. Graph B-a.7b: Emissions from the helium-argon plasma with atomic species labeled See Appendix B-b for assignments. Molecular species are Some low intensity peaks may be



Graph B-a.8a: Emissions from the helium-only plasma with atomic and molecular species labeled at approximate positions. See Appendix B-b for assignments. Some low intensity peaks may be obscured by background or molecular emissions.



obscured by background or molecular emissions. identified on graphs in this series labeled a and c. at approximate positions. Graph B-a.8b: Emissions from the helium-argon plasma with atomic species labeled See Appendix B-b for assignments. Molecular species are Some low intensity peaks may be


Graph B-a.9a: Emissions from the helium-only plasma with atomic and molecular species labeled at approximate positions. See Appendix B-b for assignments. Some low intensity peaks may be obscured by background or molecular emissions.



obscured by background or molecular emissions. identified on graphs in this series labeled a and c. at approximate positions. Graph B-a.9b: Emissions from the helium-argon plasma with atomic species labeled See Appendix B-b for assignments. Molecular species are Some low intensity peaks may be

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Graph B-a.10a: Emissions from the helium-only plasma with atomic and molecular species labeled at approximate positions. See Appendix B-b for assignments. Some low intensity peaks may be obscured by background or molecular emissions.



obscured by background or molecular emissions identified on graphs in this series labeled a and c. at approximate positions. Graph B-a.10b: Emissions from the helium-argon plasma with atomic species labeled See Appendix B-b for assignments. Molecular species are Some low intensity peaks may be



Graph B-a.11a: Emissions from the helium-only plasma with atomic and molecular species labeled at approximate positions. See Appendix B-b for assignments. Some low intensity peaks may be obscured by background or molecular emissions.



obscured by background or molecular emissions identified on graphs in this series labeled a and c. at approximate positions. See Appendix B-b for assignments. Molecular species are Graph B-a.11b: Emissions from the helium-argon plasma with atomic species labeled Some low intensity peaks may be



Graph B-a.12a: Emissions from the helium-only plasma with atomic and molecular species labeled at approximate positions. See Appendix B-b for assignments. Some low intensity peaks may be obscured by background or molecular emissions.



obscured by background or molecular emissions. identified on graphs in this series labeled a and c. at approximate positions. See Appendix B-b for assignments. Molecular species are Graph B-a.12b: Emissions from the helium-argon plasma with atomic species labeled Some low intensity peaks may be



Graph B-a.13a: Emissions from the helium-only plasma with atomic and molecular species labeled at approximate positions. See Appendix B-b for assignments. Some low intensity peaks may be obscured by background or molecular emissions.



obscured by background or molecular emissions. identified on graphs in this series labeled a and c. at approximate positions. See Appendix B-b for assignments. Molecular species are Graph B-a.13b: Emissions from the helium-argon plasma with atomic species labeled Some low intensity peaks may be

Graph B-a.14a



Graph B-a.14a: Emissions from the helium-only plasma with atomic and molecular species labeled at approximate positions. See Appendix B-b for assignments. Some low intensity peaks may be obscured by background or molecular emissions.



obscured by background or molecular emissions identified on graphs in this series labeled a and c. at approximate positions. See Appendix B-b for assignments. Molecular species are Graph B-a.14b: Emissions from the helium-argon plasma with atomic species labeled Some low intensity peaks may be



Graph B-a.15a: Emissions from the helium-only plasma with atomic and molecular species labeled at approximate positions. See Appendix B-b for assignments. Some low intensity peaks may be obscured by background or molecular emissions.



obscured by background or molecular emissions. identified on graphs in this series labeled a and c. at approximate positions. Graph B-a.15b: Emissions from the helium-argon plasma with atomic species labeled See Appendix B-b for assignments. Molecular species are Some low intensity peaks may be



Graph B-a.16a: Emissions from the helium-only plasma with atomic and molecular species labeled at approximate positions. See Appendix B-b for assignments. Some low intensity peaks may be obscured by background or molecular emissions.



obscured by background or molecular emissions. identified on graphs in this series labeled a and c. at approximate positions. See Appendix B-b for assignments. Molecular species are Graph B-a.16b: Emissions from the helium-argon plasma with atomic species labeled Some low intensity peaks may be



Graph B-a.17a: Emissions from the helium-only plasma with atomic and molecular species labeled at approximate positions. See Appendix B-b for assignments. Some low intensity peaks may be obscured by background or molecular emissions.



obscured by background or molecular emissions. identified on graphs in this series labeled a and c. at approximate positions. Graph B-a.17b: Emissions from the helium-argon plasma with atomic species labeled See Appendix B-b for assignments. Molecular species are Some low intensity peaks may be



Graph B-a.18a: Emissions from the helium-only plasma with atomic and molecular species labeled at approximate positions. See Appendix B-b for assignments. Some low intensity peaks may be obscured by background or molecular emissions.



obscured by background or molecular emissions. identified on graphs in this series labeled a and c. at approximate positions. See Appendix B-b for assignments. Molecular species are Graph B-a.18b: Emissions from the helium-argon plasma with atomic species labeled Some low intensity peaks may be

 $\rightarrow C$ Wavelength, nm Э← ПІ :βеі -19B He ---- 19α : $1\Delta \rightarrow C$ Photon counts

Graph B-a.19a

Graph B-a.19a: Emissions from the helium-only plasma with atomic and molecular species labeled at approximate positions. See Appendix B-b for assignments. Some low intensity peaks may be obscured by background or molecular emissions.



obscured by background or molecular emissions identified on graphs in this series labeled a and c. at approximate positions. Graph B-a.19b: Emissions from the helium-argon plasma with atomic species labeled See Appendix B-b for assignments. Molecular species are Some low intensity peaks may be



Graph B-a.20a: Emissions from the helium-only plasma with atomic and molecular species labeled at approximate positions. See Appendix B-b for assignments. Some low intensity peaks may be obscured by background or molecular emissions.



obscured by background or molecular emissions. identified on graphs in this series labeled a and c. at approximate positions. Graph B-a.20b: Emissions from the helium-argon plasma with atomic species labeled See Appendix B-b for assignments. Molecular species are Some low intensity peaks may be

B-b Key

This appendix contains the key to the alpha–numeric labels used on the graphs in Appendix B-a. See the beginning of that appendix for further information.

_Key to Graphs iii & iv _____

-		,			
Label	Position	Energy	Term	Energy	Term
	(nm)	Low (eV)	Low	High (eV)	High
A (H)	121.6	0	$1s \ ^2S_{1/2}$	10.199	$2p \ ^2P^0_{1/2,3/2}$
B (O)	130.5	0	$2p^4 {}^3P_{0,1,2}$	9.52	$2p^33s \ {}^3S_1^0$

C (-) A collection of small unidentified peaks.

D (C) Several local peaks; the one with the largest transition probability is:

136.01.26
$$2p^{2\ 1}D_2$$
10.41 $2p4d\ {}^1F_3^0$ E (C)156.10 $2s^22p^2\ {}^3P_{0,1,2}$ 7.95 $2s2p^3\ {}^3D_{1,2,3}^0$

Graphs iv (a) & iv (b): 160-260 nm

Graphs iii (a) & iii (b): 100-160 nm

Label	Position	Energy	Term	Energy	Term
	(nm)	Low (eV)	Low	High (eV)	High
A (C)	165.7	0	$2p^2 {}^3P_{0,1,2}$	7.48	$2p3s \ ^{3}P_{0,1,2}^{0}$
$B~(CO^+)$	219.14	0	X $^{2}\Sigma^{+}$	5.688	B $^{2}\Sigma^{+}$

Labels for CO⁺ are $v_{Hi} \rightarrow v_{Lo}$.

Graphs iii & iv: Assignments for lines in plots of spectra in the range 100-260 nm. All atomic assignments in this table are tentative. Molecular assignments give position at $v = 0 \rightarrow v = 0$ and energies at T_e .

Key to Graphs 1-20							
Posiition	Energy	Term	Energy	Term			
(nm)	Low (eV)	Low	High (eV)	High			
0-300 nm							
Transitions t	to $2s \ ^3S_1$ from	n 11 p , 12 p , et	cc., of ${}^{3}P_{0,1,2}^{0}$				
267.71	19.820	$2s \ ^{3}S_{1}$	24.450	$10p \ ^{3}P_{0,1,2}^{0}$			
269.61	19.820	$2s$ 3S_1	24.417	$9p \ ^{3}P_{0,1,2}^{0}$			
272.32	19.820	$2s$ $^{3}S_{1}$	24.371	$8p \ ^{3}P_{0,1,2}^{0}$			
276.38	19.820	$2s$ 3S_1	24.304	$7p \ ^{3}P_{0,1,2}^{0}$			
282.91	19.820	$2s$ 3S_1	24.201	$6p \ ^{3}P_{0,1,2}^{0}$			
294.51	19.820	$2s \ ^{3}S_{1}$	24.028	$5p \ ^{3}P_{0,1,2}^{0}$			
$0-350 \mathrm{~nm}$							
301.3	17.86	a ${}^{3}\Sigma_{u}^{+}$	21.98	u ${}^3\Pi_g$			
303.71	17.86	a ${}^{3}\Sigma_{u}^{+}$	21.95	t ${}^3\Pi_g$			
307.16	17.86	a ${}^{3}\Sigma_{u}^{+}$	21.9	s ${}^3\Pi_g$			
312.34	17.86	a ${}^{3}\Sigma_{u}^{+}$	21.84	r ${}^3\Pi_g$			
318.77	19.820	$2s$ $^{3}S_{1}$	23.708	$4p \ ^{3}P_{0,1,2}^{0}$			
318.77	19.820	$2s$ $^{3}S_{1}$	23.708	$4p \ ^{3}P_{0,1,2}^{0}$			
320.72	17.86	a ${}^{3}\Sigma_{u}^{+}$	21.73	p ${}^3\Pi_g$			
323.13	20.616	$2s \ ^{1}S_{0}$	24.452	$10p \ ^1P_1^0$			
325.83	20.616	$2s \ ^{1}S_{0}$	24.420	$9p \ ^1P_1^0$			
329.68	20.616	$2s \ ^{1}S_{0}$	24.376	$8p \ ^1P_1^0$			
330.22	17.86	a ${}^{3}\Sigma_{u}^{+}$	21.62	n ${}^{3}\Sigma_{g}^{+}$			
330.81	18.15	A ${}^{1}\Sigma_{u}^{+}$	22.01	S $^{1}\Pi_{g}$			
335.46	20.616	$2s \ ^{1}S_{0}$	24.311	$7p \ ^1P_1^0$			
	Posiition (nm) 0-300 nm Transitions t 267.71 269.61 272.32 276.38 282.91 294.51 0-350 nm 301.3 303.71 307.16 312.34 318.77 318.77 318.77 320.72 323.13 325.83 329.68 330.22 330.81 335.46	Key to GPosiitionEnergy (nm)Low (eV) (nm) Low (eV) $0-300$ nmTransitions to $2s$ 3S_1 from 269.61269.6119.820272.3219.820276.3819.820282.9119.820294.5119.820294.5119.820 301.3 17.86 307.16 17.86 312.34 17.86 318.77 19.820 318.77 19.820 318.77 19.820 320.72 17.86 323.13 20.616 329.68 20.616 330.22 17.86 330.81 18.15 335.46 20.616	Key to Graphs 1-20PosiitionEnergyTerm(nm)Low (eV)Low0-300 nm11p, 12p, etTransitions to $2s$ 3S_1 from11p, 12p, et267.7119.820 $2s$ 3S_1 269.6119.820 $2s$ 3S_1 272.3219.820 $2s$ 3S_1 276.3819.820 $2s$ 3S_1 282.9119.820 $2s$ 3S_1 294.5119.820 $2s$ 3S_1 301.317.86 a ${}^3\Sigma_u^+$ 307.1617.86 a ${}^3\Sigma_u^+$ 318.7719.820 $2s$ 3S_1 318.7719.820 $2s$ 3S_1 320.7217.86 a ${}^3\Sigma_u^+$ 323.1320.616 $2s$ 1S_0 325.8320.616 $2s$ 1S_0 330.2217.86 a ${}^3\Sigma_u^+$ 330.8118.15 A ${}^1\Sigma_u^+$ 335.4620.616 $2s$ 1S_0	Key to Graph 1-20PosiitionEnergyTermEnergy(nm)Low (eV)LowHigh (eV)0-300 nm $$			

2ι (He ₂)	336.74	18.15	A ${}^{1}\Sigma_{u}^{+}$	21.94	R $^{1}\Pi_{g}$
2F (Ar)	340.62	11.828	$4s' [1/2]_1^0$	15.467	$7p' \ [1/2]_0$
2G (He)	344.76	20.616	$2s$ 1S_0	24.211	$6p \ ^1P_1^0$
2H (Ar)	346.11	11.624	$4s \ [3/2]_1^0$	15.205	$6p' [3/2]_2$
2κ (He ₂)	346.33	18.15	A ${}^{1}\Sigma_{u}^{+}$	21.84	P $^{1}\Pi_{g}$
2λ	Unidentified				

Graphs 3: 350-375 nm

3A (Ar)	355.43	11.548	$4s \ [3/2]_2^0$	15.036	$6p \ [3/2]_2$
3B (He)	355.44	20.964	$2p \ ^{3}P_{0,1,2}^{0}$	24.451	$10d \ ^{3}D_{1,2,3}$
3α (He ₂)	355.52	17.86	a ${}^3\Sigma_u^+$	21.35	k' ${}^{3}\Sigma_{g}^{+}$
3C (He)	356.30	20.964	$2p \ ^{3}P_{0,1,2}^{0}$	24.443	$10s \ ^{3}S_{1}$
3D (Ar)	356.33	11.723	$4s' [1/2]_0^0$	15.202	$6p' [3/2]_1$
3E (Ar)	356.77	11.548	$4s \ [3/2]_2^0$	15.023	$6p \ [5/2]_3$
3F(Ar)	357.23	11.828	$4s' [1/2]_1^0$	15.298	$7p \ [1/2]_0$
3G (He)	358.73	20.964	$2p \ ^{3}P_{0,1,2}^{0}$	24.419	$9d \ ^{3}D_{1,2,3}$
3eta	Unidentified				
3H (Ar)	360.65	11.624	$4s \ [3/2]_1^0$	15.060	$6p \ [1/2]_0$
3I (He)	361.36	20.616	$2s \ ^1S_0$	24.046	$5p \ ^1P_1^0$
3J (Ar)	363.27	11.624	$4s \ [3/2]_1^0$	15.036	$6p \ [3/2]_2$
3K (He)	363.42	20.964	$2p \ ^{3}P_{0,1,2}^{0}$	24.375	$8d \ ^{3}D_{1,2,3}$
3L (Ar)	363.45	11.624	$4s \ [3/2]_1^0$	15.034	$6p \ [3/2]_1$
3χ (He ₂)	363.53	18.15	A ${}^{1}\Sigma_{u}^{+}$	21.67	L $^{1}\Pi_{g}$
3M (Ar)	364.31	11.624	$4s \ [3/2]_1^0$	15.026	$6p \ [5/2]_2$
3N (Ar)	364.98	11.828	$4s' [1/2]_1^0$	15.224	$6p' \ [1/2]_0$
3O (He)	365.20	20.964	$2p \ ^{3}P_{0,1,2}^{0}$	24.358	$8s$ 3S_1
3P(Ar)	365.95	11.624	$4s \ [3/2]_1^0$	15.011	$6p \ [1/2]_1$

3Q (Ar)	367.07	11.828	$4s' \ [1/2]_1^0$	15.205	$6p' [3/2]_2$
3R (Ar)	367.52	11.828	$4s' \ [1/2]_1^0$	15.201	$6p' \ [1/2]_1$
3δ (He ₂)	367.74	17.86	a ${}^{3}\Sigma_{u}^{+}$	21.24	i ${}^3\Pi_g$
3S (He)	370.50	20.964	$2p \ ^{3}P_{0,1,2}^{0}$	24.310	$7d \ ^{3}D_{1,2,3}$
$3T (Ar^+)$	371.47	16.43	$^{3}P3d$ $^{4}D_{5/2}$	19.76	${}^{3}P4p \; {}^{2}D_{3/2}^{0}$
$3U (Ar^+)$	373.55	16.44	$^{3}P3d$ $^{4}D_{3/2}$	19.76	${}^{3}P4p \; {}^{2}D_{3/2}^{0}$
aphs 4: 375-	400 nm				
$4A (Ar^+)$	375.05	16.46	$^{3}P3d \ ^{4}D_{1/2}$	19.76	${}^{3}P4p \; {}^{2}D_{3/2}^{0}$
4B (Ar)	377.04	11.723	$4s' [1/2]_0^0$	15.011	$6p \ [1/2]_1$
4α (He ₂)	377.6	18.45	b ${}^{3}\Pi_{g}$	21.85	q $^{3}\Delta_{u}$
4β (He ₂)	377.84	18.45	b ${}^{3}\Pi_{g}$	21.84	q ${}^{3}\Pi_{u}$
$4C (Ar^+)$	378.64	16.41	$^{3}P3d \ ^{4}D_{7/2}$	19.68	${}^{3}P4p \; {}^{2}D_{5/2}^{0}$
4χ (He ₂)	378.66	18.45	b ${}^{3}\Pi_{g}$	21.84	q ${}^{3}\Sigma_{u}^{+}$
4δ (He ₂)	380.37	18.45	b ${}^{3}\Pi_{g}$	21.82	o ${}^3\Sigma_u^+$
$4D (Ar^+)$	380.86	16.43	$^{3}P3d \ ^{4}D_{5/2}$	19.68	${}^{3}P4p \; {}^{2}D_{5/2}^{0}$
4E (He)	381.96	20.964	$2p \ ^{3}P_{0,1,2}^{0}$	24.209	$6d \ ^{3}D_{1,2,3}$

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$4A (Ar^+)$	375.05	16.46	${}^{3}P3d \; {}^{4}D_{1/2}$	19.76	${}^{3}P4p \; {}^{2}D_{3/2}^{0}$
4B (Ar)	377.04	11.723	$4s' \ [1/2]_0^0$	15.011	$6p \ [1/2]_1$
4α (He ₂)	377.6	18.45	b ${}^{3}\Pi_{g}$	21.85	q $^{3}\Delta_{u}$
4β (He ₂)	377.84	18.45	b ${}^{3}\Pi_{g}$	21.84	q ${}^{3}\Pi_{u}$
$4C (Ar^+)$	378.64	16.41	$^{3}P3d \ ^{4}D_{7/2}$	19.68	${}^{3}P4p \; {}^{2}D_{5/2}^{0}$
4χ (He ₂)	378.66	18.45	b ${}^{3}\Pi_{g}$	21.84	q ${}^{3}\Sigma_{u}^{+}$
4δ (He ₂)	380.37	18.45	b ${}^{3}\Pi_{g}$	21.82	o ${}^{3}\Sigma_{u}^{+}$
$4D (Ar^+)$	380.86	16.43	$^{3}P3d \ ^{4}D_{5/2}$	19.68	${}^{3}P4p \; {}^{2}D_{5/2}^{0}$
4E (He)	381.96	20.964	$2p \ ^{3}P_{0,1,2}^{0}$	24.209	$6d \ ^{3}D_{1,2,3}$
$4F (Ar^+)$	383.04	16.44	$^{3}P3d \ ^{4}D_{3/2}$	19.68	${}^{3}P4p \; {}^{2}D_{5/2}^{0}$
4G (He)	383.37	21.218	$2p \ ^1P_1^0$	24.451	$10d \ ^1D_2$
4H (Ar)	383.47	11.828	$4s' \ [1/2]_1^0$	15.060	$6p \ [1/2]_0$
4I (He)	386.75	20.964	$2p \ ^{3}P_{0,1,2}^{0}$	24.169	$6s \ ^{3}S_{1}$
4J (He)	387.18	21.218	$2p \ ^1P_1^0$	24.420	$9d \ ^1D_2$
$4K (Ar^+)$	387.53	16.44	$^{3}P3d \ ^{4}D_{3/2}$	19.64	${}^{3}P4p \ 4D^{0}_{1/2}$
4ε (He ₂)	397.58	18.45	b ${}^{3}\Pi_{g}$	21.68	m $^{3}\Delta_{u}$
4L (He)	388.86	19.820	$2s \ ^3S_{0,1,2}$	23.007	$3p \ ^{3}P_{1}^{0}$
$4M (Ar^+)$	389.14	16.46	${}^{3}P3d \; {}^{4}D_{1/2}$	19.64	${}^{3}P4p \ 4D_{1/2}^{0}$
$4N (Ar^+)$	389.20	16.43	$^{3}P3d \ ^{4}D_{5/2}$	19.61	${}^{3}P4p \ 4D^{0}_{3/2}$

$4P(Ar^+)$	301 /8		[/]]		1 [/]1
	091.40	16.44	$^{3}P3d \ ^{4}D_{3/2}$	19.61	${}^{3}P4p \ 4D_{2/2}^{0}$
4Q (He)	392.65	21.218	$2p \ ^{1}P_{1}^{0}$	24.375	3/2 8d 1D_2
$4 R (Ar^+)$	393.12	16.46	$^{3}P3d \ ^{4}D_{1/2}$	19.61	${}^{3}P4p \ 4D_{3/2}^{0}$
4S (He)	393.59	21.218	$2p \ ^{1}P_{1}^{0}$	24.367	$8s {}^{1}S_{0}$
$4T (Ar^+)$	394.43	16.41	$^{3}P3d \ ^{4}D_{7/2}$	19.55	${}^{3}P4p \ 4D_{5/2}^{0}$
4U (Ar)	394.75	11.548	$4s \; [3/2]_2^0$	14.688	$5p' [3/2]_2$
4V (Ar)	394.90	11.548	$4s \; [3/2]_2^0$	14.687	$5p' \ [1/2]_1$
4W (He)	396.47	20.616	$2s \ ^{1}S_{0}$	23.742	$4p \ ^1P_1^0$
$4X (Ar^+)$	396.84	16.43	${}^{3}P3d \; {}^{4}D_{5/2}$	19.55	${}^{3}P4p \; {}^{4}D_{5/2}^{0}$
$4Y (Ar^+)$	397.48	16.64	${}^{3}P4s \; {}^{4}P_{5/2}$	19.76	${}^{3}P4p \; {}^{2}D_{3/2}^{0}$
4φ (He ₂)	398.88	18.45	b ${}^{3}\Pi_{g}$	21.67	m ${}^{3}\Pi_{u}$
$4Z (Ar^+)$	399.21	16.44	$^{3}P3d \ ^{4}D_{3/2}$	19.55	${}^{3}P4p \; {}^{4}D_{5/2}^{0}$
4γ (He ₂)	399.7	18.45	b ${}^{3}\Pi_{g}$	21.66	m ${}^{3}\Sigma_{u}^{+}$
aphs 5: 400-4	25 nm				
5α (He ₂)	400.33	18.15	A ${}^{1}\Sigma_{u}^{+}$	21.36	I $^{1}\Pi_{g}$
5A (He)	400.93	21.218	$2p \ ^1P_1^0$	24.310	$7d \ ^1D_2$
$5B (Ar^+)$	401.39	16.41	$^{3}P3d \ ^{4}D_{7/2}$	19.49	${}^{3}P4p \; {}^{4}D_{7/2}^{0}$
5C (He)	402.40	21.218	$2p \ ^1P_1^0$	24.298	$7s$ 1S_0
5D (He)	402.62	20.964	$2p \ ^{3}P_{0,1,2}^{0}$	24.043	$5d \ ^{3}D_{1,2,3}$
5β (He ₂)	403.15	18.45	b ${}^{3}\Pi_{g}$	21.54	k ${}^3\Sigma_u^+$
$5E (Ar^+)$	403.88	16.43	$^{3}P3d \ ^{4}D_{5/2}$	19.49	${}^{3}P4p \; {}^{4}D_{7/2}^{0}$
5F(Ar)	404.44	11.624	$4s \; [3/2]_1^0$	14.688	$5p' [3/2]_2$
5G (Ar)	404.60	11.624	$4s \; [3/2]_1^0$	14.687	$5p' \ [1/2]_1$
5H (Ar)	405.45	11.624	$4s \; [3/2]_1^0$	14.681	$5p' [3/2]_1$
$5I (Ar^+)$	408.24	16.64	${}^{3}P4s \; {}^{4}P_{5/2}$	19.68	${}^{3}P4p \; {}^{2}D_{5/2}^{0}$
	4S (He) 4T (Ar ⁺) 4U (Ar) 4V (Ar) 4W (He) 4X (Ar ⁺) 4Y (Ar ⁺) 4Y (Ar ⁺) 4Y (Ar ⁺) 4 φ (He ₂) 4Z (Ar ⁺) 4 γ (He ₂) aphs 5: 400-4 5 α (He ₂) 5A (He) 5B (Ar ⁺) 5C (He) 5D (He) 5 β (He ₂) 5E (Ar ⁺) 5F (Ar) 5G (Ar) 5H (Ar) 5I (Ar ⁺)	AS (He)393.594T (Ar ⁺)394.434U (Ar)394.754V (Ar)394.904W (He)396.474X (Ar ⁺)396.844Y (Ar ⁺)397.484 φ (He ₂)398.884Z (Ar ⁺)399.214 γ (He ₂)399.7aphs 5: 400-425 nm5 α (He ₂)400.335A (He)400.935B (Ar ⁺)401.395C (He)402.405D (He)402.625 β (He ₂)403.155E (Ar ⁺)403.885F (Ar)404.445G (Ar)404.605H (Ar)405.455I (Ar ⁺)408.24	AS (AP)JUSTALJUSTAL4S (He) 393.59 21.218 4T (Ar ⁺) 394.43 16.41 4U (Ar) 394.75 11.548 4V (Ar) 394.90 11.548 4W (He) 396.47 20.616 4X (Ar ⁺) 396.84 16.43 4Y (Ar ⁺) 397.48 16.64 4 φ (He ₂) 398.88 18.45 4Z (Ar ⁺) 399.21 16.44 4γ (He ₂) 399.7 18.45 aphs 5: $400-425$ nm 5α (He ₂) 400.33 18.15 $5A$ (He) 400.93 21.218 $5B$ (Ar ⁺) 401.39 16.41 $5C$ (He) 402.40 21.218 $5D$ (He) 402.62 20.964 5β (He ₂) 403.15 18.45 $5E$ (Ar ⁺) 403.88 16.43 $5F$ (Ar) 404.44 11.624 $5G$ (Ar) 404.60 11.624 $5H$ (Ar) 405.45 11.624 $5H$ (Ar ⁺) 408.24 16.64	AN (A)JOLLL<	Int (III)John 2John 2

	$5J (Ar^+)$	411.28	16.75	${}^{3}P4s \; {}^{4}P_{3/2}$	19.76	${}^{3}P4p \; {}^{2}D_{3/2}^{0}$
	5K (He)	412.08	20.964	$2p \ ^{3}P_{0,1,2}^{0}$	23.972	$5s \ ^{3}S_{1}$
	5L (He)	414.38	21.218	$2p \ ^1P_1^0$	24.209	$6d \ ^1D_2$
	5χ (He ₂)	415.8	18.59	B $^{1}\Pi_{g}$	21.68	M $^{1}\Delta_{u}$
	5M (Ar)	415.86	11.548	$4s \ [3/2]_2^0$	14.529	$5p \ [3/2]_2$
	5N (Ar)	416.42	11.548	$4s \ [3/2]_2^0$	14.525	$5p \ [3/2]_1$
	5δ (He ₂)	416.67	18.59	B $^{1}\Pi_{g}$	21.67	M $^{1}\Pi_{u}$
	50 (He)	416.90	21.218	$2p \ ^1P_1^0$	24.191	$6s \ ^1S_0$
	5ε (He ₂)	417.36	18.59	B $^{1}\Pi_{g}$	Not Avail.	M $^{1}\Sigma_{u}^{+}$
	$5P(Ar^+)$	417.84	16.64	${}^{3}P4s \; {}^{4}P_{5/2}$	19.61	${}^{3}P4p \; {}^{4}D^{0}_{3/2}$
	5Q (Ar)	418.19	11.723	$4s' [1/2]_0^0$	14.687	$5p' \ [1/2]_1$
	5R (Ar)	419.07	11.548	$4s \ [3/2]_2^0$	14.506	$5p \ [5/2]_2$
	5S (Ar)	419.10	11.723	$4s' [1/2]_0^0$	14.681	$5p' [3/2]_1$
	5T (Ar)	419.83	11.624	$4s \ [3/2]_1^0$	14.576	$5p \ [1/2]_0$
	5U (Ar)	420.07	11.548	$4s \ [3/2]_2^0$	14.499	$5p \ [5/2]_3$
	$5V (Ar^+)$	420.20	16.81	${}^{3}P4s \; {}^{4}P_{1/2}$	19.76	${}^{3}P4p \; {}^{2}D^{0}_{3/2}$
	$5W (Ar^+)$	422.82	16.75	${}^{3}P4s \; {}^{4}P_{3/2}$	19.68	${}^{3}P4p \; {}^{2}D^{0}_{5/2}$
	5φ (He ₂)	423.78	17.86	a ${}^{3}\Sigma_{u}^{+}$	20.79	g ${}^3\Sigma_g^+$
G	raphs 6: 425-4	450 nm				
	6A (Ar)	425.12	11.548	$4s \ [3/2]_2^0$	14.464	$5p \ [1/2]_1$
	6B (Ar)	425.94	11.828	$4s' \ [1/2]_1^0$	14.738	$5p' \ [1/2]_0$
	6C (Ar)	426.63	11.624	$4s \ [3/2]_1^0$	14.529	$5p \ [3/2]_2$
	$6D (Ar^+)$	426.65	16.64	${}^{3}P4s \; {}^{4}P_{5/2}$	19.55	${}^{3}P4p \; {}^{4}D^{0}_{5/2}$
	6E (Ar)	427.22	11.624	$4s \ [3/2]_1^0$	14.525	$5p \ [3/2]_1$
	$6F(Ar^+)$	428.29	16.75	${}^{3}P4s \; {}^{4}P_{3/2}$	19.64	${}^{3}P4p \; {}^{4}D_{1/2}^{0}$
	6G (Ar)	430.01	11.624	$4s \ [3/2]_1^0$	14.506	$5p \ [5/2]_2$

$6 H (Ar^+)$	433.12	16.75	${}^{3}P4s \; {}^{4}P_{3/2}$	19.61	${}^{3}P4p \; {}^{4}D^{0}_{3/2}$
$6I (Ar^+)$	433.20	16.44	$^{3}P3d$ $^{4}D_{3/2}$	19.31	${}^{3}P4p \; {}^{4}P_{1/2}^{0}$
6J (Ar)	433.36	11.828	$4s' [1/2]_1^0$	14.688	$5p' [3/2]_2$
6K (Ar)	433.53	11.828	$4s' [1/2]_1^0$	14.687	$5p' \ [1/2]_1$
6L (Ar)	434.52	11.828	$4s' [1/2]_1^0$	14.681	$5p' [3/2]_1$
$6M (Ar^+)$	434.81	16.64	${}^{3}P4s \; {}^{4}P_{5/2}$	19.49	${}^{3}P4p \; {}^{4}D_{7/2}^{0}$
$6N (Ar^+)$	435.22	16.46	$^{3}P3d$ $^{4}D_{1/2}$	19.31	${}^{3}P4p \; {}^{4}P_{1/2}^{0}$
60 (Ar)	436.38	11.624	$4s \ [3/2]_1^0$	14.464	$5p \ [1/2]_1$
$6P (Ar^+)$	437.13	16.43	${}^{3}P3d \; {}^{4}D_{5/2}$	19.26	${}^{3}P4p \; {}^{4}P^{0}_{3/2}$
$6Q (Ar^+)$	437.97	16.81	${}^{3}P4s \; {}^{4}P_{1/2}$	19.64	${}^{3}P4p \; {}^{4}D_{1/2}^{0}$
6R (He)	438.79	21.218	$2p \ ^1P_1^0$	24.043	$5d \ ^1D_2$
$6S (Ar^+)$	440.01	16.44	$^{3}P3d$ $^{4}D_{3/2}$	19.26	${}^{3}P4p \; {}^{4}P^{0}_{3/2}$
$6T (Ar^+)$	440.10	16.41	$^{3}P3d$ $^{4}D_{7/2}$	19.22	${}^{3}P4p \; {}^{4}P^{0}_{5/2}$
$6\alpha \ (\mathrm{He}_2)$	440.44	18.45	b ${}^{3}\Pi_{g}$	21.27	j $^{3}\Delta_{u}$
$6U (Ar^+)$	442.09	16.46	$^{3}P3d$ $^{4}D_{1/2}$	19.26	${}^{3}P4p \; {}^{4}P^{0}_{3/2}$
6V (Ar)	442.40	11.723	$4s' [1/2]_0^0$	14.525	$5p \ [3/2]_1$
$6W (Ar^+)$	442.60	16.75	${}^{3}P4s \; {}^{4}P_{3/2}$	19.55	${}^{3}P4p \; {}^{4}D^{0}_{5/2}$
$6X (Ar^+)$	443.02	16.81	${}^{3}P4s \; {}^{4}P_{1/2}$	19.61	${}^{3}P4p \; {}^{4}D^{0}_{3/2}$
$6Y (Ar^+)$	443.10	16.43	$^{3}P3d$ $^{4}D_{5/2}$	19.22	${}^{3}P4p \; {}^{4}P_{5/2}^{0}$
6Z (He)	443.76	21.218	$2p \ ^1P_1^0$	24.011	$5s \ ^1S_0$
6β (He ₂)	444.01	18.45	b ${}^{3}\Pi_{g}$	21.25	j ${}^3\Pi_u$
6χ (He ₂)	445.68	18.45	b ${}^{3}\Pi_{g}$	21.24	j ${}^3\Sigma^+_u$
$6AA (Ar^+)$	446.06	16.44	$^{3}P3d \ ^{4}D_{3/2}$	19.22	${}^{3}P4p \; {}^{4}P_{5/2}^{0}$
6BB (He)	447.15	20.964	$2p \ ^{3}P_{0,1,2}^{0}$	23.736	$4d \ ^{3}D_{1,2,3}$

Graphs 7: 450-475 nm

7A (Ar)	451.07	11.828	$4s' [1/2]_1^0$	14.576	$5p \ [1/2]_0$
7B (Ar)	452.23	11.723	$4s' [1/2]_0^0$	14.464	$5p \ [1/2]_1$
7C (Ar)	454.47	12.907	$4p \ [1/2]_1$	15.634	$11d \ [1/2]_1^0$
$7\alpha \ (\mathrm{He}_2)$	454.71	18.45	b ${}^{3}\Pi_{g}$	21.19	h ${}^{3}\Sigma_{u}^{+}$
7D (Ar)	455.43	12.907	$4p \ [1/2]_1$	15.629	$7d' [3/2]_2^0$
7E (Ar)	458.50	12.907	$4p \ [1/2]_1$	15.610	$10d \ [3/2]_2^0$
7F (Ar)	458.66	12.907	$4p \ [1/2]_1$	15.610	$10d \ [1/2]_1^0$
7G (Ar)	458.72	12.907	$4p \ [1/2]_1$	15.609	$10d \ [1/2]_0^0$
7H (Ar)	458.93	11.828	$4s' [1/2]_1^0$	14.529	$5p \ [3/2]_2$
7I (Ar)	459.61	11.828	$4s' [1/2]_1^0$	14.525	$5p \ [3/2]_1$
7β (He ₂)	462.37	18.59	B ${}^{1}\Pi_{g}$	21.38	J $^{1}\Delta_{u}$
7J (Ar)	462.84	11.828	$4s' [1/2]_1^0$	14.506	$5p \ [5/2]_2$
7K (Ar)	464.21	12.907	$4p \ [1/2]_1$	15.577	$9d \ [3/2]_2^0$
7L (Ar)	464.75	12.907	$4p \ [1/2]_1$	15.574	$9d \ [1/2]_1^0$
7χ (He ₂)	464.96	17.86	a ${}^{3}\Sigma_{u}^{+}$	20.53	e ${}^{3}\Pi_{g}$
7δ (He ₂)	465.06	18.59	B $^{1}\Pi_{g}$	21.36	J $^{1}\Pi_{u}$
7ε (He ₂)	466.54	18.59	B $^{1}\Pi_{g}$	21.35	J $^{1}\Sigma_{u}^{+}$
7M (Ar)	470.23	11.828	$4s' [1/2]_1^0$	14.464	$5p \ [1/2]_1$
7N (He)	471.32	20.964	$2p \ ^{3}P_{0,1,2}^{0}$	23.594	$4s \ ^3S_1$
7φ (He ₂)	472.51	18.59	B ${}^{1}\Pi_{g}$	21.32	H $^{1}\Sigma_{u}^{+}$
$70 (Ar^+)$	472.69	17.14	${}^{3}P4s \; {}^{2}P3/2$	19.76	${}^{3}P4p \; {}^{2}D^{0}_{3/2}$
$7P(Ar^+)$	473.59	16.64	${}^{3}P4s \; {}^{4}P5/2$	19.26	${}^{3}P4p \; {}^{4}P^{0}_{3/2}$
7Q (Ar)	474.68	12.907	$4p \ [1/2]_1$	15.518	$8d \ [1/2]_0^0$

Graphs 8: 475-500 nm

8U (Ar)

8A (Ar)	475.29	12.907	$4p \ [1/2]_1$	15.515	$8d \ [1/2]_1^0$
8B (Ar)	476.87	12.907	$4p \ [1/2]_1$	15.506	$6d' [3/2]_2^0$
8C (Ar)	479.87	13.076	$4p \ [5/2]_3$	15.659	$12d \ [7/2]_4^0$
$8D (Ar^+)$	480.60	16.64	${}^{3}P4s \; {}^{4}P_{5/2}$	19.22	${}^{3}P4p \; {}^{4}P^{0}_{5/2}$
8α	Unidentified				
8E(Ar)	483.60	13.076	$4p \ [5/2]_3$	15.639	$11d \ [7/2]_4^0$
8F(Ar)	483.67	12.907	$4p \ [1/2]_1$	15.470	$9s \; [3/2]_2^0$
$8 G (Ar^+)$	484.78	16.75	${}^{3}P4s \; {}^{4}P_{3/2}$	19.31	${}^{3}P4p \; {}^{4}P_{1/2}^{0}$
8H (Ar)	487.63	12.907	$4p \ [1/2]_1$	15.449	$7d \ [3/2]_2^0$
$8I (Ar^+)$	487.99	17.14	${}^{3}P4s \; {}^{2}P_{3/2}$	19.68	${}^{3}P4p \; {}^{2}D_{5/2}^{0}$
8J (Ar)	488.63	13.076	$4p \ [5/2]_3$	15.612	$10d \ [7/2]_4^0$
8K (Ar)	488.79	12.907	$4p \ [1/2]_1$	15.443	$7d \ [1/2]_1^0$
8L (Ar)	489.47	12.907	$4p \ [1/2]_1$	15.439	$7d \ [1/2]_0^0$
8β (He ₂)	491.04	19.22	c ${}^{3}\Sigma_{g}^{+}$	21.85	q $^{3}\Delta_{u}$
8χ (He ₂)	491.88	19.22	c ${}^{3}\Sigma_{g}^{+}$	21.84	q ${}^{3}\Pi_{u}$
8M (Ar)	492.10	13.095	$4p \ [5/2]_2$	15.614	$10d \ [7/2]_3^0$
8N (He)	492.19	21.218	$2p \ ^1P_1^0$	23.736	$4d \ ^1D_2$
8δ (He ₂)	492.9	19.22	c ${}^{3}\Sigma_{g}^{+}$	21.84	q ${}^{3}\Sigma_{u}^{+}$
$80 (Ar^+)$	493.32	16.75	${}^{3}P4s \; {}^{4}P_{3/2}$	19.26	${}^{3}P4p \; {}^{4}P^{0}_{3/2}$
8P(Ar)	493.77	13.076	$4p \ [5/2]_3$	15.586	$11s \ [3/2]_2^0$
$8Q (Ar^+)$	495.29	17.14	${}^{3}P4s \; {}^{2}P_{3/2}$	19.64	${}^{3}P4p \; {}^{4}D_{1/2}^{0}$
8R (Ar)	495.68	13.076	$4p \ [5/2]_3$	15.576	$9d \ [7/2]_4^0$
8ε (He ₂)	495.82	19.22	c ${}^{3}\Sigma_{g}^{+}$	21.82	o ${}^3\Sigma_u^+$
$8S (Ar^+)$	496.51	17.27	${}^{3}P4s \; {}^{2}P_{1/2}$	19.76	${}^{3}P4p \; {}^{2}D_{3/2}^{0}$
$8T (Ar^+)$	497.22	16.81	${}^{3}P4s \; {}^{4}P_{1/2}$	19.31	${}^{3}P4p \; {}^{4}P_{1/2}^{0}$

 $4p \ [5/2]_2$

15.579

13.095

498.99

 $9d \ [7/2]_3^0$

Graphs 9: 500-525 nm

$9A (Ar^+)$	500.93	16.75	${}^{3}P4s \; {}^{4}P_{3/2}$	19.22	${}^{3}P4p \; {}^{4}P_{5/2}^{0}$
9B (He)	501.57	20.616	$2s \ ^{1}S_{0}$	23.087	$3p \ ^1P_1^0$
$9C (Ar^+)$	501.76	17.14	${}^{3}P4s \; {}^{2}P_{3/2}$	19.61	${}^{3}P4p \; {}^{4}D_{3/2}^{0}$
9D (Ar)	503.20	13.076	$4p \ [5/2]_3$	15.539	$10s \ [3/2]_2^0$
9E (He)	504.77	21.218	$2p \ ^1P_1^0$	23.674	$4s \ ^1S_0$
9F (Ar)	504.88	12.907	$4p \ [1/2]_1$	15.362	$8s \ [3/2]_2^0$
9G (Ar)	505.42	12.907	$4p \ [1/2]_1$	15.360	$7s' \ [1/2]_1^0$
9H (Ar)	505.65	12.907	$4p \ [1/2]_1$	15.358	$7s' \ [1/2]_0^0$
9I (Ar)	506.01	13.076	$4p \ [5/2]_3$	15.525	$8d \ [7/2]_4^0$
9J (Ar^+)	506.20	16.81	${}^{3}P4s \; {}^{4}P_{1/2}$	19.26	${}^{3}P4p \; {}^{4}P_{3/2}^{0}$
9K (Ar)	507.10	13.095	$4p \ [5/2]_2$	15.539	$10s \ [3/2]_1^0$
9L (Ar)	507.31	12.907	$4p \ [1/2]_1$	15.350	$6d \ [3/2]_2^0$
9M (Ar)	507.80	13.076	$4p \ [5/2]_3$	15.517	$6d' [5/2]_3^0$
9N (Ar)	508.71	13.095	$4p \ [5/2]_2$	15.532	$8d \ [7/2]_3^0$
90 (Ar)	510.47	13.153	$4p \ [3/2]_1$	15.581	$9d \ [5/2]_2^0$
9P(Ar)	511.82	13.095	$4p \ [5/2]_2$	15.517	$6d' [5/2]_3^0$
9Q (Ar)	512.78	13.095	$4p \ [5/2]_2$	15.512	$6d' [5/2]_2^0$
9α (He ₂)	513.44	18.15	A ${}^{1}\Sigma_{u}^{+}$	20.57	E $^{1}\Pi_{g}$
$9R (Ar^+)$	514.53	17.14	${}^{3}P4s \; {}^{2}P_{3/2}$	19.55	${}^{3}P4p \; {}^{4}D_{5/2}^{0}$
9S (Ar)	515.14	12.907	$4p \ [1/2]_1$	15.313	$6d \ [1/2]_0^0$
9T (Ar)	515.23	12.907	$4p \ [1/2]_1$	15.313	$5d' [5/2]_2^0$
9U (Ar)	516.23	12.907	$4p \ [1/2]_1$	15.308	$6d \ [1/2]_1^0$
9V (Ar)	517.75	13.076	$4p \ [5/2]_3$	15.470	$9s \ [3/2]_2^0$
9W (Ar)	518.77	12.907	$4p \ [1/2]_1$	15.296	$5d' [3/2]_2^0$
9X (Ar)	519.27	13.076	$4p \ [5/2]_3$	15.463	$7d \ [5/2]_3^0$
9Y (Ar)	519.41	13.153	$4p \ [3/2]_1$	15.540	$8s' \ [1/2]_0^0$

9Z (Ar)	521.05	13.076	$4p \ [5/2]_3$	15.455	$7d \ [7/2]_3^0$
9AA (Ar)	521.48	13.095	$4p \ [5/2]_2$	15.472	$7d \ [3/2]_1^0$
$9BB (Ar^+)$	521.51	17.27	${}^{3}P4s \; {}^{2}P_{1/2}$	19.64	${}^{3}P4p \; {}^{4}D_{1/2}^{0}$
9CC (Ar)	521.63	13.095	$4p \ [5/2]_2$	15.471	$9s \; [3/2]_1^0$
9DD (Ar)	522.13	13.076	$4p \ [5/2]_3$	15.450	$7d \ [7/2]_4^0$
9 EE (Ar)	524.11	13.095	$4p \ [5/2]_2$	15.460	$7d \ [5/2]_2^0$
9FF(Ar)	524.62	13.172	$4p \ [3/2]_2$	15.535	$8d \ [5/2]_3^0$
9GG (Ar)	524.92	13.172	$4p \ [3/2]_2$	15.533	$8d \ [3/2]_2^0$
Graphs 10: 52	5-550 nm				
10α (He ₂)	525.24	19.22	c ${}^{3}\Sigma_{g}^{+}$	21.68	m $^{3}\Delta_{u}$
10A (Ar)	525.28	13.095	$4p \ [5/2]_2$	15.455	$7d \ [7/2]_3^0$
10B (Ar)	525.45	13.153	$4p \ [3/2]_1$	15.512	$6d' [5/2]_2^0$
10β (He ₂)	527.87	19.22	$c^{3}\Sigma_{g}^{+}$	21.67	m ${}^3\Pi_u$
10C (Ar)	528.61	13.172	$4p \ [3/2]_2$	15.517	$6d' \ [5/2]_3^0$
$10D (Ar^+)$	528.69	17.27	${}^{3}P4s \; {}^{2}P_{1/2}$	19.61	${}^{3}P4p \; {}^{4}D_{3/2}^{0}$
10E (Ar)	529.00	13.172	$4p \ [3/2]_2$	15.515	$8d \ [1/2]_1^0$
10χ (He ₂)	529.13	19.22	c ${}^{3}\Sigma_{g}^{+}$	21.66	m ${}^{3}\Sigma_{u}^{+}$
10F (Ar)	530.95	13.172	$4p \ [3/2]_2$	15.506	$6d' [3/2]_2^0$
10G (Ar)	531.77	13.302	$4p' [3/2]_2$	15.633	$7d' [5/2]_3^0$
$10\delta \ (\mathrm{He}_2)$	535.23	19.22	c ${}^3\Sigma_g^+$	21.54	k ${}^{3}\Sigma_{u}^{+}$
10H (Ar)	537.35	13.153	$4p \ [3/2]_1$	15.460	$7d \ [5/2]_2^0$
10I (Ar)	539.40	13.172	$4p \ [3/2]_2$	15.470	$9s \; [3/2]_2^0$
10J (Ar)	541.05	13.172	$4p \; [3/2]_2$	15.463	$7d \ [5/2]_3^0$
10K (Ar)	542.14	13.076	$4p \ [5/2]_3$	15.362	$8s \ [3/2]_2^0$
10L (Ar)	544.00	12.907	$4p \ [1/2]_1$	15.186	$7s \ [3/2]_1^0$
10M (Ar)	544.22	13.076	$4p \ [5/2]_3$	15.353	$6d \ [5/2]_3^0$

10N (Ar)	545.17	12.907	$4p \ [1/2]_1$	15.181	$7s \ [3/2]_2^0$	
100 (Ar)	545.74	13.095	$4p \ [5/2]_2$	15.366	$8s \ [3/2]_1^0$	
10P (Ar)	545.97	13.076	$4p \ [5/2]_3$	15.346	$6d \ [7/2]_3^0$	
10Q (Ar)	546.72	13.095	$4p \ [5/2]_2$	15.362	$8s \ [3/2]_2^0$	
10R (Ar)	547.35	13.095	$4p \ [5/2]_2$	15.360	$7s' \ [1/2]_1^0$	
10S (Ar)	549.01	13.095	$4p \ [5/2]_2$	15.353	$6d \ [5/2]_2^0$	
10T (Ar)	549.21	13.283	$4p' \ [3/2]_1$	15.540	$8s' \ [1/2]_0^0$	
10U (Ar)	549.59	13.076	$4p \ [5/2]_3$	15.331	$6d \ [7/2]_4^0$	
Graphs 11: 55	50-570 nm					
11A (Ar)	550.61	13.095	$4p \ [5/2]_2$	15.346	$6d \ [7/2]_3^0$	
11B (Ar)	552.50	13.076	$4p \ [5/2]_3$	15.319	$5d' [5/2]_3^0$	
11C (Ar)	552.90	13.273	$4p \ [1/2]_0$	15.515	$8d \ [1/2]_1^0$	
11D (Ar)	553.45	13.302	$4p' [3/2]_2$	15.542	$8s' [1/2]_1^0$	
11E (Ar)	554.09	13.076	$4p \ [5/2]_3$	15.313	$5d' [5/2]_2^0$	
11F (Ar)	555.27	13.283	$4p' \ [3/2]_1$	15.515	$8d \ [1/2]_1^0$	
11G (Ar)	555.87	12.907	$4p \ [1/2]_1$	15.137	$5d \ [3/2]_2^0$	
11H (Ar)	555.97	13.283	$4p' [3/2]_1$	15.512	$6d' [5/2]_2^0$	
11I (Ar)	557.25	13.095	$4p \ [5/2]_2$	15.319	$5d' [5/2]_3^0$	
11J (Ar)	557.42	13.283	$4p' [3/2]_1$	15.506	$6d' [3/2]_2^0$	
11K (Ar)	558.19	13.076	$4p \ [5/2]_3$	15.296	$5d' [3/2]_2^0$	
11L (Ar)	558.87	13.095	$4p \ [5/2]_2$	15.313	$5d' [5/2]_2^0$	
11M (Ar)	559.75	13.302	$4p' [3/2]_2$	15.517	$6d' [5/2]_3^0$	
11N (Ar)	560.67	12.907	$4p \ [1/2]_1$	15.118	$5d \ [1/2]_1^0$	
110 (Ar)	561.80	13.153	$4p \; [3/2]_1$	15.360	$7s' [1/2]_1^0$	
11P (Ar)	562.09	13.153	$4p \; [3/2]_1$	15.358	$7s' [1/2]_0^0$	
11Q (Ar)	562.38	13.302	$4p' [3/2]_2$	15.506	$6d' [3/2]_2^0$	
	11R (Ar)	563.56	13.153	$4p \ [3/2]_1$	15.353	$6d \ [5/2]_2^0$
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	11S (Ar)	563.73	13.273	$4p \ [1/2]_0$	15.472	$7d \ [3/2]_1^0$
	11T (Ar)	563.91	13.273	$4p \ [1/2]_0$	15.471	$9s \; [3/2]_1^0$
	11U (Ar)	564.14	13.153	$4p \ [3/2]_1$	15.350	$6d \ [3/2]_2^0$
	11V (Ar)	564.87	13.172	$4p \ [3/2]_2$	15.366	$8s \ [3/2]_1^0$
	11W (Ar)	565.07	12.907	$4p \ [1/2]_1$	15.101	$5d \ [1/2]_0^0$
	11X (Ar)	565.91	13.172	$4p \ [3/2]_2$	15.362	$8s \; [3/2]_2^0$
	11Y (Ar)	568.19	13.172	$4p \ [3/2]_2$	15.353	$6d \ [5/2]_3^0$
	11Z (Ar)	568.37	13.172	$4p \ [3/2]_2$	15.353	$6d \ [5/2]_2^0$
G	raphs 12: 570)-590 nm				
	12A (Ar)	570.09	13.172	$4p \ [3/2]_2$	15.346	$6d \ [7/2]_3^0$
	12B (Ar)	571.25	13.273	$4p \ [1/2]_0$	15.443	$7d \ [1/2]_1^0$
	$12C (Ar^+)$	572.43	17.14	${}^{3}P4s \; {}^{2}P_{3/2}$	19.31	${}^{3}P4p \; {}^{4}P_{1/2}^{0}$
	12α (He ₂)	573.48	18.45	b ${}^{3}\Pi_{g}$	20.62	f $^{3}\Delta_{u}$
	12D (Ar)	573.95	13.153	$4p \ [3/2]_1$	15.313	$5d' [5/2]_2^0$
	12E (Ar)	577.21	13.172	$4p \ [3/2]_2$	15.319	$5d' [5/2]_3^0$
	12F (Ar)	577.40	13.302	$4p' [3/2]_2$	15.449	$7d \ [3/2]_2^0$
	12G (Ar)	578.35	13.153	$4p \ [3/2]_1$	15.296	$5d' [3/2]_2^0$
	12H (Ar)	578.95	13.172	$4p \ [3/2]_2$	15.313	$5d' [5/2]_2^0$
	12I (Ar)	579.04	13.302	$4p' [3/2]_2$	15.443	$7d \ [1/2]_1^0$
	12J (Ar)	580.21	13.172	$4p \ [3/2]_2$	15.308	$6d \ [1/2]_1^0$
	12K (Ar)	583.43	13.172	$4p \ [3/2]_2$	15.296	$5d' [3/2]_2^0$
	12L (Ar)	584.38	13.328	$4p' \ [1/2]_1$	15.449	$7d \ [3/2]_2^0$
	$12M~(\mathrm{Ar^+})$	584.38	17.14	${}^{3}P4s \; {}^{2}P_{3/2}$	19.26	${}^{3}P4p \; {}^{4}P_{3/2}^{0}$
	12N (Ar)	586.03	12.907	$4p \ [1/2]_1$	15.022	$6s' \ [1/2]_1^0$
	12O (He)	587.56	20.964	$2p \ ^{3}P_{0,1,2}^{0}$	23.074	$3d \ ^{3}D_{1,2,3}$

12P(Ar)	588.26	12.907	$4p \ [1/2]_1$	15.014	$6s' \ [1/2]_0^0$
12β (He ₂)	588.73	18.45	b ${}^{3}\Pi_{g}$	20.57	f ${}^{3}\Pi_{u}$
12Q (Ar)	588.86	13.076	$4p \ [5/2]_3$	15.181	$7s \ [3/2]_2^0$
Graphs 13: 59	0-600 nm				
13A (Ar)	591.21	12.907	$4p \ [1/2]_1$	15.004	$4d' [3/2]_1^0$
13B (Ar)	591.66	13.095	$4p \ [5/2]_2$	15.190	$5d \ [3/2]_1^0$
13C (Ar)	592.71	13.076	$4p \ [5/2]_3$	15.167	$5d \ [5/2]_3^0$
13D (Ar)	592.88	13.095	$4p \ [5/2]_2$	15.186	$7s \; [3/2]_1^0$
13E (Ar)	594.09	13.273	$4p \ [1/2]_0$	15.360	$7s' \ [1/2]_1^0$
13F (Ar)	594.27	13.095	$4p \ [5/2]_2$	15.181	$7s \; [3/2]_2^0$
13G (Ar)	594.39	13.076	$4p \ [5/2]_3$	15.161	$5d \ [5/2]_2^0$
13H (Ar)	594.93	13.283	$4p' [3/2]_1$	15.366	$8s \ [3/2]_1^0$
$13I (Ar^{+})$	595.09	17.14	${}^{3}P4s \; {}^{2}P_{3/2}$	19.22	${}^{3}P4p \; {}^{4}P_{5/2}^{0}$
13J (Ar)	596.45	13.273	$4p \ [1/2]_0$	15.351	$5d' [3/2]_1^0$
13K (Ar)	596.83	13.283	$4p' [3/2]_1$	15.360	$7s' \ [1/2]_1^0$
13L (Ar)	597.16	13.283	$4p' [3/2]_1$	15.358	$7s' \ [1/2]_0^0$
13M (Ar)	598.19	13.095	$4p \ [5/2]_2$	15.167	$5d \ [5/2]_3^0$
13N (Ar)	598.73	13.076	$4p \ [5/2]_3$	15.146	$5d \ [7/2]_3^0$
13O (Ar)	598.81	13.283	$4p' \ [3/2]_1$	15.353	$6d \ [5/2]_2^0$
13P (Ar)	599.47	13.283	$4p' [3/2]_1$	15.350	$6d \ [3/2]_2^0$
13Q(Ar)	599.90	13.095	$4p \ [5/2]_2$	15.161	$5d \ [5/2]_2^0$
Graphs 14: 60	0-615 nm				
14A (Ar)	600.57	13.302	$4p' [3/2]_2$	15.366	$8s \; [3/2]_1^0$
14B (Ar)	601.37	13.076	$4p \ [5/2]_3$	15.137	$5d \ [3/2]_2^0$
14C (Ar)	602.52	13.302	$4p' \ [3/2]_2$	15.360	$7s' \ [1/2]_1^0$
14α (He ₂)	603.02	19.22	c ${}^{3}\Sigma_{g}^{+}$	21.27	j $^{3}\Delta_{u}$

14D (Ar)	603.21	13.076	$4p \ [5/2]_3$	15.131	$5d \ [7/2]_4^0$
14E (Ar)	604.32	13.095	$4p \ [5/2]_2$	15.146	$5d \ [7/2]_3^0$
14F (Ar)	605.27	12.907	$4p \ [1/2]_1$	14.955	$4d' [5/2]_2^0$
14G (Ar)	605.94	12.907	$4p \ [1/2]_1$	14.953	$4d' [3/2]_2^0$
14H (Ar)	606.48	13.302	$4p' \ [3/2]_2$	15.346	$6d \ [7/2]_3^0$
$14I (Ar^{+})$	607.74	17.27	${}^{3}P4s \; {}^{2}P_{1/2}$	19.31	${}^{3}P4p \; {}^{4}P_{1/2}^{0}$
14J (Ar)	608.12	13.328	$4p' \ [1/2]_1$	15.366	$8s \ [3/2]_1^0$
14K (Ar)	608.59	13.153	$4p \ [3/2]_1$	15.190	$5d \ [3/2]_1^0$
14L (Ar)	609.08	13.273	$4p \ [1/2]_0$	15.308	$6d \ [1/2]_1^0$
14β (He ₂)	609.73	19.22	c ${}^3\Sigma_g^+$	21.25	j ${}^{3}\Pi_{u}$
14M (Ar)	609.88	13.153	$4p \ [3/2]_1$	15.186	$7s \ [3/2]_1^0$
14N (Ar)	610.12	13.328	$4p' \ [1/2]_1$	15.360	$7s' \ [1/2]_1^0$
14O (Ar)	610.46	13.328	$4p' \ [1/2]_1$	15.358	$7s' \ [1/2]_0^0$
14P (Ar)	610.56	13.283	$4p' [3/2]_1$	15.313	$5d' \ [5/2]_2^0$
14χ (He ₂)	611.21	18.59	B ${}^{1}\Pi_{g}$	20.62	F $^{1}\Delta_{u}$
14Q (Ar)	611.35	13.153	$4p \ [3/2]_1$	15.181	$7s \ [3/2]_2^0$
14R (Ar)	611.97	13.283	$4p' [3/2]_1$	15.308	$6d \ [1/2]_1^0$
14S (Ar)	612.19	13.328	$4p' \ [1/2]_1$	15.353	$6d \ [5/2]_2^0$
14T (Ar)	612.74	13.095	$4p \ [5/2]_2$	15.118	$5d \ [1/2]_1^0$
14U (Ar)	612.87	13.328	$4p' \ [1/2]_1$	15.350	$6d \ [3/2]_2^0$
14δ (He ₂)	612.88	19.22	c ${}^3\Sigma_g^+$	21.24	j $^{3}\Sigma_{u}^{+}$
$14V (Ar^+)$	613.87	17.74	$^{3}P3d \ ^{4}F_{5/2}$	19.76	${}^{3}P4p \; {}^{2}D_{3/2}^{0}$
14W (Ar)	614.54	13.302	$4p' [3/2]_2$	15.319	$5d' [5/2]_3^0$
Graphs 15: 61	5-630 nm				
15A (Ar)	615.52	13.172	$4p \ [3/2]_2$	15.186	$7s \ [3/2]_1^0$
15B (Ar)	616.51	13.302	$4p' \ [3/2]_2$	15.313	$5d' \ [5/2]_2^0$

	15C (Ar)	617.02	13.172	$4p \ [3/2]_2$	15.181	$7s \ [3/2]_2^0$
	15D (Ar)	617.31	13.153	$4p \ [3/2]_1$	15.161	$5d \ [5/2]_2^0$
	15E (Ar)	617.94	13.302	$4p' \ [3/2]_2$	15.308	$6d \ [1/2]_1^0$
	$15F (Ar^+)$	621.22	17.27	${}^{3}P4s \; {}^{2}P_{1/2}$	19.26	${}^{3}P4p \; {}^{4}P_{3/2}^{0}$
	15G (Ar)	621.25	13.172	$4p \; [3/2]_2$	15.167	$5d \ [5/2]_3^0$
	15H (Ar)	621.59	13.302	$4p' [3/2]_2$	15.296	$5d' [3/2]_2^0$
	15I (Ar)	623.09	13.172	$4p \; [3/2]_2$	15.161	$5d \ [5/2]_2^0$
	$15J (Ar^+)$	623.97	17.78	$^{3}P3d$ $^{4}F_{3/2}$	19.76	${}^{3}P4p \; {}^{2}D_{3/2}^{0}$
	$15K (Ar^+)$	624.31	17.69	$^{3}P3d \ ^{4}F_{7/2}$	19.68	${}^{3}P4p \; {}^{2}D^{0}_{5/2}$
	15L (Ar)	624.34	13.328	$4p' \ [1/2]_1$	15.313	$6d \ [1/2]_0^0$
	15M (Ar)	624.47	13.328	$4p' \ [1/2]_1$	15.313	$5d' [5/2]_2^0$
	15α (He ₂)	624.68	18.59	B $^{1}\Pi_{g}$	20.58	F $^{1}\Pi_{u}$
	15N (Ar)	624.84	13.153	$4p \; [3/2]_1$	15.137	$5d \ [3/2]_2^0$
	15O (Ar)	627.86	13.172	$4p \; [3/2]_2$	15.146	$5d \ [7/2]_3^0$
	15P (Ar)	629.69	13.328	$4p' \ [1/2]_1$	15.296	$5d' [3/2]_2^0$
Graphs 16: 630-650 nm						
	$16\alpha \ (\mathrm{He}_2)$	630.09	19.22	$c^{3}\Sigma_{g}^{+}$	21.19	h ${}^{3}\Sigma_{u}^{+}$
	16A (Ar)	630.77	13.172	$4p \ [3/2]_2$	15.137	$5d \ [3/2]_2^0$
	16B (Ar)	630.92	13.153	$4p \; [3/2]_1$	15.118	$5d \ [1/2]_1^0$
	16β (He ₂)	631.41	18.59	B $^{1}\Pi_{g}$	20.56	F ${}^{1}\Sigma_{u}^{+}$
	16C (Ar)	636.49	13.153	$4p \; [3/2]_1$	15.101	$5d \ [1/2]_0^0$
	16D (Ar)	636.96	13.172	$4p \; [3/2]_2$	15.118	$5d \ [1/2]_1^0$
	16E (Ar)	638.47	12.907	$4p \ [1/2]_1$	14.848	$6s \ [3/2]_1^0$
	$16F (Ar^+)$	639.92	17.74	${}^{3}P3d \; {}^{4}F_{5/2}$	19.68	${}^{3}P4p \; {}^{2}D_{5/2}^{0}$
	16χ (He ₂)	640.08	18.45	b ${}^{3}\Pi_{g}$	20.39	d ${}^{3}\Sigma_{u}^{+}$
	16G (Ar)	641.63	12.907	$4p \ [1/2]_1$	14.839	$6s \ [3/2]_2^0$

	16H (Ar)	643.16	13.095	$4p [5/2]_2$	15.022	$6s' [1/2]_1^0$
	16I (Ar)	646.66	13.273	$4p [1/2]_0$	15.190	$5d [3/2]_1^0$
	16J (Ar)	648.11	13.273	$4p \ [1/2]_0$	15.186	$7s [3/2]_1^0$
	16K (Ar)	649.40	13.095	$4p \ [5/2]_2$	15.004	$4d' [3/2]_1^0$
G	raphs 17: 650)-675 nm				
	$17A (Ar^+)$	650.91	17.78	$^{3}P3d$ $^{4}F_{3/2}$	19.68	${}^{3}P4p \; {}^{2}D_{5/2}^{0}$
	17B (Ar)	651.38	13.283	$4p' [3/2]_1$	15.186	$7s \ [3/2]_1^0$
	17C (Ar)	653.81	13.076	$4p \ [5/2]_3$	14.972	$4d' [5/2]_3^0$
	17α (He ₂)	659.55	18.59	B ${}^{1}\Pi_{g}$	20.47	D $^{1}\Sigma_{u}^{+}$
	17D (Ar)	659.61	13.076	$4p \ [5/2]_3$	14.955	$4d' [5/2]_2^0$
	17E (Ar)	659.87	13.302	$4p' [3/2]_2$	15.181	$7s \ [3/2]_2^0$
	17F (Ar)	660.40	13.076	$4p \ [5/2]_3$	14.953	$4d' [3/2]_2^0$
	17G (Ar)	660.49	13.095	$4p \ [5/2]_2$	14.972	$4d' [5/2]_3^0$
	17H (Ar)	663.21	13.153	$4p \ [3/2]_1$	15.022	$6s' \ [1/2]_1^0$
	$17I (Ar^+)$	663.82	17.74	${}^{3}P3d \; {}^{4}F_{5/2}$	19.61	${}^{3}P4p \; {}^{4}D_{3/2}^{0}$
	$17J (Ar^+)$	663.97	17.78	$^{3}P3d \ ^{4}F_{3/2}$	19.64	${}^{3}P4p \; {}^{4}D_{1/2}^{0}$
	$17 \mathrm{K} (\mathrm{Ar^+})$	664.37	17.63	${}^{3}P3d \; {}^{4}F_{9/2}$	19.49	${}^{3}P4p \; {}^{4}D_{7/2}^{0}$
	17L (Ar)	665.69	13.328	$4p' \ [1/2]_1$	15.190	$5d \ [3/2]_1^0$
	17M (Ar)	666.07	13.153	$4p \; [3/2]_1$	15.014	$6s' \ [1/2]_0^0$
	17N (Ar)	666.41	13.095	$4p \ [5/2]_2$	14.955	$4d' [5/2]_2^0$
	170 (Ar)	667.73	11.624	$4s \ [3/2]_1^0$	13.480	$4p' \ [1/2]_0$
	17P (He)	667.82	21.218	$2p \ ^1P_1^0$	23.074	$3d \ ^1D_2$
	$17Q (Ar^+)$	668.43	17.69	${}^{3}P3d \; {}^{4}F_{7/2}$	19.55	${}^{3}P4p \; {}^{4}D_{5/2}^{0}$
	17R (Ar)	668.48	13.283	$4p' [3/2]_1$	15.137	$5d \ [3/2]_2^0$
	17S (Ar)	669.85	13.153	$4p \; [3/2]_1$	15.004	$4d' [3/2]_1^0$
	17T (Ar)	669.89	13.172	$4p \; [3/2]_2$	15.022	$6s' \ [1/2]_1^0$

17U (Ar)	671.92	13.273	$4p \ [1/2]_0$	15.118	$5d \ [1/2]_1^0$
17V (Ar)	672.29	13.302	$4p' [3/2]_2$	15.146	$5d \ [7/2]_3^0$
Graphs 18: 67	5-700 nm				
18A (Ar)	675.28	12.907	$4p \ [1/2]_1$	14.743	$4d \ [3/2]_2^0$
18B (Ar)	675.44	13.283	$4p' [3/2]_1$	15.118	$5d \ [1/2]_1^0$
18C (Ar)	675.62	13.302	$4p' \ [3/2]_2$	15.137	$5d \ [3/2]_2^0$
$18D (Ar^+)$	675.66	17.78	$^{3}P3d\ ^{4}F_{3/2}$	19.61	${}^{3}P4p \; {}^{4}D_{3/2}^{0}$
18E (Ar)	676.66	13.172	$4p \ [3/2]_2$	15.004	$4d' [3/2]_1^0$
18F (Ar)	677.99	13.480	$4p' \ [1/2]_0$	15.308	$6d \ [1/2]_1^0$
$18G (Ar^+)$	680.85	17.94	$^{3}P3d$ $^{2}P_{1/2}$	19.76	${}^{3}P4p \; {}^{2}D_{3/2}^{0}$
18H (Ar)	681.83	13.283	$4p' [3/2]_1$	15.101	$5d \ [1/2]_0^0$
18I (Ar)	682.72	13.302	$4p' [3/2]_2$	15.118	$5d \ [1/2]_1^0$
18J (Ar)	685.19	13.328	$4p' \ [1/2]_1$	15.137	$5d \ [3/2]_2^0$
$18 \mathrm{K} (\mathrm{Ar^+})$	686.35	17.74	$^{3}P3d$ $^{4}F_{5/2}$	19.55	${}^{3}P4p \; {}^{4}D_{5/2}^{0}$
18L (Ar)	687.13	12.907	$4p \ [1/2]_1$	14.711	$4d \ [1/2]_1^0$
18M (Ar)	687.96	13.153	$4p \; [3/2]_1$	14.955	$4d' [5/2]_2^0$
$18N (Ar^+)$	688.66	17.69	$^{3}P3d \ ^{4}F_{7/2}$	19.49	${}^{3}P4p \; {}^{4}D_{7/2}^{0}$
18O (Ar)	688.71	13.172	$4p \ [3/2]_2$	14.972	$4d' [5/2]_3^0$
18P (Ar)	688.82	13.153	$4p \; [3/2]_1$	14.953	$4d' [3/2]_2^0$
18Q (Ar)	692.50	13.328	$4p' \ [1/2]_1$	15.118	$5d \ [1/2]_1^0$
18R (Ar)	693.77	12.907	$4p \ [1/2]_1$	14.694	$4d \ [1/2]_0^0$
18S (Ar)	695.15	13.172	$4p \ [3/2]_2$	14.955	$4d' [5/2]_2^0$
18T (Ar)	696.03	13.172	$4p \ [3/2]_2$	14.953	$4d' [3/2]_2^0$
18U (Ar)	696.54	11.548	$4s \; [3/2]_2^0$	13.328	$4p' \ [1/2]_1$
$18V (Ar^+)$	699.01	17.78	$^{3}P3d$ $^{4}F_{3/2}$	19.55	${}^{3}P4p \; {}^{4}D_{5/2}^{0}$
18W (Ar)	699.22	13.328	$4p' \ [1/2]_1$	15.101	$5d \ [1/2]_0^0$

Graphs 19: 700-725 nm

	19A (Ar)	703.03	13.076	$4p \ [5/2]_3$	14.839	$6s \ [3/2]_2^0$
	19α (He ₂)	705.02	19.52	C $^{1}\Sigma_{g}^{+}$	21.38	J $^{1}\Delta_{u}$
	19B (He)	706.53	20.964	$2p \ ^{3}P_{0,1,2}^{0}$	22.719	$3s \ {}^3S_1$
	19C (Ar)	706.72	11.548	$4s \ [3/2]_2^0$	13.302	$4p' [3/2]_2$
	19D (Ar)	706.87	13.095	$4p \ [5/2]_2$	14.848	$6s \ [3/2]_1^0$
	$19E (Ar^+)$	707.70	17.74	$^{3}P3d$ $^{4}F_{5/2}$	19.49	${}^{3}P4p \; {}^{4}D_{7/2}^{0}$
	19F (Ar)	708.67	13.273	$4p \ [1/2]_0$	15.022	$6s' \ [1/2]_1^0$
	19G (Ar)	710.75	13.095	$4p \ [5/2]_2$	14.839	$6s \ [3/2]_2^0$
	19β (He ₂)	711.32	19.52	C $^{1}\Sigma_{g}^{+}$	21.36	J $^{1}\Pi_{u}$
	19H (Ar)	712.58	13.283	$4p' [3/2]_1$	15.022	$6s' \ [1/2]_1^0$
	19I (Ar)	714.70	11.548	$4s \ [3/2]_2^0$	13.283	$4p' [3/2]_1$
	19χ (He ₂)	714.78	19.52	C $^{1}\Sigma_{g}^{+}$	21.35	J $^{1}\Sigma_{u}^{+}$
	19J (Ar)	715.88	13.283	$4p' [3/2]_1$	15.014	$6s' \ [1/2]_0^0$
	19K (Ar)	716.26	13.273	$4p \ [1/2]_0$	15.004	$4d' [3/2]_1^0$
	19L (Ar)	720.70	13.302	$4p' [3/2]_2$	15.022	$6s' \ [1/2]_1^0$
	19M (Ar)	722.99	13.095	$4p \ [5/2]_2$	14.809	$4d \ [5/2]_2^0$
G	raphs 20: 725	5-750 nm				
	20A (Ar)	726.52	13.153	$4p \ [3/2]_1$	14.859	$4d \; [3/2]_1^0$
	20B (Ar)	727.07	13.076	$4p \ [5/2]_3$	14.781	$4d \ [7/2]_3^0$
	20C (Ar)	727.29	11.624	$4s \ [3/2]_1^0$	13.328	$4p' \ [1/2]_1$
	20D (He)	728.14	21.218	$2p \ ^1P_1^0$	22.920	$3s \ ^1S_0$
	20E (Ar)	728.54	13.302	$4p' [3/2]_2$	15.004	$4d' [3/2]_1^0$
	20α (He ₂)	728.89	19.52	C $^{1}\Sigma_{g}^{+}$	21.32	H $^{1}\Sigma_{u}^{+}$
	20F (Ar)	731.17	13.153	$4p \ [3/2]_1$	14.848	$6s \ [3/2]_1^0$
	20G (Ar)	731.60	13.328	$4p' [1/2]_1$	15.022	$6s' \ [1/2]_1^0$

20 H (Ar)	735.08	13.328	$4p' \ [1/2]_1$	15.014	$6s' \ [1/2]_0^0$
20I (Ar)	735.32	13.153	$4p \; [3/2]_1$	14.839	$6s \ [3/2]_2^0$
20J (Ar)	735.33	13.095	$4p \ [5/2]_2$	14.781	$4d \ [7/2]_3^0$
$20 \mathrm{K} (\mathrm{Ar})$	737.21	13.076	$4p \ [5/2]_3$	14.757	$4d \ [7/2]_4^0$
20L (Ar)	738.40	11.624	$4s \ [3/2]_1^0$	13.302	$4p' [3/2]_2$
20M (Ar)	739.30	13.172	$4p \; [3/2]_2$	14.848	$6s \ [3/2]_1^0$
20N (Ar)	741.23	13.283	$4p' [3/2]_1$	14.955	$4d' [5/2]_2^0$
200 (Ar)	742.23	13.283	$4p' [3/2]_1$	14.953	$4d' [3/2]_2^0$
20P (Ar)	742.53	13.302	$4p' [3/2]_2$	14.972	$4d' [5/2]_3^0$
20Q (Ar)	743.54	13.172	$4p \; [3/2]_2$	14.839	$6s \ [3/2]_2^0$
20R (Ar)	743.63	13.076	$4p \ [5/2]_3$	14.743	$4d \; [3/2]_2^0$
20S (Ar)	747.12	11.624	$4s \ [3/2]_1^0$	13.283	$4p' [3/2]_1$
20T (Ar)	748.43	13.153	$4p \; [3/2]_1$	14.809	$4d \ [5/2]_2^0$

APPENDIX C

THE RVESIM PROGRAM

The pages that follow contain:

- a A minimal set of instructions for compiling and running the program.
- b Instructions for creating the input files, with samples.
- c A formatted printout of the program.

A text-only, compilable version of the program and a set of sample input files are available in electronic versions of this document by clicking on the hyperlinks below. The documents linked here are "works in progress." Their appearance will reflect that status, but they can be used to run simulations. The hyperlinked files are:

- A <u>plain-text version</u> of the program
- A set of sample input files: <u>main</u>, <u>configuration</u>, <u>state</u>, <u>transition</u>, Franck–Condon factor (4 files: <u>FCF1</u>, <u>FCF2</u>, <u>FCF3</u>, <u>FCF4</u>) and <u>atomic</u>
- A "<u>tar-ball</u>" (archive made with the program "tar") containing all of the files.

The program will probably be modified after this document is complete. More recent versions of the program should be accessible by searching the internet on "RVESIM" (as of this date, this term is not used on the internet in any other context). In addition to being more up-to-date, the documentation at the internet location will be more extensive than what is contained here. At present, the universal resource locator (URL) for the most recent version of the program is:

• <u>http://cathubodva.agnesscott.edu/rvesim/</u>

The site can be accessed from electronic versions of this document by clicking on the URL for the site.

C-a Minimal Instructions for Compilation and Execution

C-a.1 System requirements

- The program will run under Linux. It will probably work for most UNIX and UNIX-like systems (e. g., Linux). It should work under other operating systems with minimal changes to the source code: editing the strings used to create directories and files so that they are compatible with the operating system might be sufficient.
- The program requires a compiler for the computer language C.
- The amount of disk space and random-access memory (RAM) required will, of course, depend on the size of the simulation. To run the sample simulation (hyperlinked files available in electronic versions of the document only) used about 4 megabytes of RAM and required a total of about 10 megabytes of disk space (including source code, executable file and all input and output files).
- The program was written and tested under Linux, kernel 2.2.13, Slackware 7.0.0 distribution, using gcc version egcs-2.91.66 19990314/Linux (egcs-1.1.2 release).

C-a.2 Compiling the program

- You must compile the program. Using the gcc compiler, the command is:

```
gcc RVESIM.c -lm -Wall -o RVESIM
```

If all goes well, you will probably see this warning:

```
RVESIM.c: In function 'new_mol_ck':
RVESIM.c:8666: warning: function returns address of local variable
```

Do not be concerned by the warning; the return of the local variable's address will not cause problems.

C-a.3 Running the program

- Make sure that the input files are in the proper format and that they are in the directory from which the program is called. Then, use the following command:

RVESIM input_file

where "input_file" is the name of your main input file (see below).

- As the program runs, you will probably see statements such as:

mkdir: cannot make directory 'sample_molecules/NH': File exists
mkdir: cannot make directory sample_simulations': File exists
rm: cannot remove '.rvesim_temp': No such file or directory

These statements are expected and do not indicate a problem.

C-b Input and Output Files

See Section 6-3 for a description of the usage of the input files. Only the formats for the files will be included here. The files are listed in the order in which they are accessed by the program.

C-b.1 The main input file:

The main input file contains a list of keywords and values. The keywords are required as a form of safety-check: the program checks that the input file is in the expected form and will inform the user (and stop running) if that form is not followed. Each keyword and its corresponding entry may be entered on a separate line or not, as suits the user; "whitespaces" (tabs, new-line characters and spaces) are ignored by the program. A sample main input file is given in Figure C-b.1. The required entries are listed below in the following format:

KEYWORD acceptable value(s) A brief description of the entry.

- OUTPREF string that does not contain spaces and contains only characters used in filenames with a maximum length of 100 characters This is the prefix for the names of most output files and all first–level directories created by the program.
- UNITS "cm" or "nm" Enter "nm" for nanometers or "cm" for wavenumbers. Note: this unit choice applies to all output from the program and to the keywords RES-

		Figure C-b.1	
OUTPREF UNITS BESOLUTION	sample nm 0 5	Figure C-D.1	
EFFICIENCY	1		
DETECTION	p		
SCAN	S		
CUTOFF	0.001		
INTERACTIVE	n		
MINPOINT	400		
MAXPOINT	600		
POINTSTEP	0.1		
MAXIMUM	1.1e6		
ROVIBSIM	Y	<pre>state_file.txt</pre>	transition_file.txt
NUMAT	3	Ar-Lines.txt 0.5 He-Lines.txt 1.0 ArII-Lines.txt 0.8	
NUMOT	0	MIII HINOS. UKU U.U	
NUMEX	Õ		

Figure C-b.1: A sample main input file.

OLUTION, MINPOINT, MAXPOINT and POINTSTEP. Caution: the program has only been thoroughly tested for nanometers.

- RESOLUTION *positive number* This is the base, in the unit specified for "UNITS," of a triangle describing a single atomic emission in the experimental spectrum being simulated.
- EFFICIENCY "1" Currently, the only acceptable value for this keyword is "1" (one).
- DETECTION "p" or "c" This entry specifies the detection method for the experiment being simulated: enter "p" for photon–counting or "c" for calorimetric.
- SCAN "s" or "j" This entry specifies the manner in which data points are taken in the experiment being simulated: enter "s" (scan) for systems that collect data continuously while scanning a series of wavelengths; enter "j" (jump) for systems

that take data while stopped at one wavelength then move to the next wavelength to collect more data and so on.

- CUTOFF number between 0 and 1 This is the low-intensity cut-off fraction. When the program calculates a rotational state distribution, it will ignore states with relative populations less than this number (relative to the most populated rotational level for that vibrational state). The program will also ignore vibration \rightarrow vibration transitions with Franck-Condon factors less than this number.
- INTERACTIVE "n" Currently, the only acceptable value for this keyword is "n" (for "no").
- MINPOINT *positive number* The lowest wavelength or frequency to include in your simulation. Be sure to use the units specified for "UNITS."
- MAXPOINT *positive number* The highest wavelength or frequency to include in your simulation. Be sure to use the units specified for "UNITS."
- POINTSTEP positive number less than the difference between MINPOINT and MAXPOINT This is the size of the steps between data points in the experiment being simulated. Ideally, this number is at least a third of RESOLUTION, as defined above, but should be chosen to match the experimental conditions.
- MAXIMUM any number This number scales the overall intensity of the final simulation: the maximum intensity in the simulated spectrum will be this value. This number can be negative if negative values for intensity are desired.
- ROVIBSIM "Y" or "N" Enter "Y" if program should perform a rovibronic simulation and "N" if it should not (this is useful, for example, if only atomic transitions will be included). If "Y" is entered, also include, with no additional keywords, the names of the state file and the transition file (in that order). These filenames cannot contain spaces.
- NUMAT zero or a positive integer The number of atomic files to be included. For each atomic file, include, with no additional keywords, the name of each atomic

PROGRAM_NAME	RVESIM
DEBUG	-1
mdebugflag	0
tdebugflag	0
mrdebugflag	0
mnadebugflag	0
mnbdebugflag	0
msdebugflag	0
sdebugflag	0
mtdebugflag	0
cacdebugflag	0
cbcdebugflag	0
aadebugflag	0
bbdebugflag	0
bbSSdebugflag	0
bbSOdebugflag	0
bbOOdebugflag	0
ddebugflag	0
rpdebugflag	0
radebugflag	0
rddebugflag	0
XYdebugflag	0
HLswitch	0
bbSSSATT	0
bbSOSATT	0
bbOOSATT	0

Figure C-b.2: Sample configuration file (.rvesimconfig).

file immediately followed by the relative weight for transitions in that file. These filenames cannot contain spaces.

Currently, the only acceptable value for this keyword is "0" (zero). NUMOT "0"

NUMEX "0" Currently, the only acceptable value for this keyword is "0" (zero).

C-b.2 The configuration file:

Keywords must be entered exactly as they appear here and in the order given here, but need not each be on a separate line. The name of this file must be ".rvesimconfig"

Figure C-b.2 _____

(the leading period is required). A sample configuration file is given in Figure C-b.2. The format for the descriptions below is:

KEYWORD appropriate values default value Use of value in program

PROGRAM_NAME String with no spaces containing a maximum of 199 characters RVESIM This is the name the program calls itself in many of the output files created by the program. These files begin with some variation on the comment "File generated by PROGRAM_NAME." The name does not have to be the same as the name given to the program's executable file. This name can be changed, for example, to identify a user, e. g., "BLF_RVESIM."

The following 21 entries are intended for debugging purposes and can cause enormous files (gigabytes large) to be written to the disk. The casual user is encouraged to enter the values as they appear here.

DEBUG -1	mdebugflag 0	tdebugflag 0
mrdebugflag 0	mnadebugflag 0	mnbdebugflag 0
msdebugflag 0	sdebugflag 0	mtdebugflag 0
cacdebugflag 0	cbcdebugflag 0	aadebugflag 0
bbdebugflag 0	bbSSdebugflag 0	bbSOdebugflag 0
bbOOdebugflag 0	ddebugflag 0	rpdebugflag 0
radebugflag 0	rddebugflag 0	XYdebugflag 0

The remaining entries allow the user to alter certain calculations involving transition intensities. The default values follow the rules (such as they exist). Only a small number of such modifications are available in the current version of the program.

HLswitch 0 or 1 0 Switch to turn off the use of Hönl-London factors. If set to 0 (zero), Hönl-London factors are used; if set to 1 (one), they are not used.

The next three entries specify the extent to which satellite bands are to be included in the simulation. Ideally, satellite intensities should vary with K or J, but at present, they are all included with equal weight. This modification is only available for transitions between two states described by Hund's Case (b).

- bbSSSATT number between 0 and 1 0 Weight for satellite bands between two Σ electronic states that are both Hund's Case (b).
- bbSOSATT number between 0 and 1 0 Weight for satellite bands between one Σ and one non- Σ electronic state; both are Hund's Case (b).
- bbOOSATT number between 0 and 1 0 Weight for satellite bands between two non- Σ electronic states that are both Hund's Case (b).

C-b.3 The state file

This file may contain more entries than are used in any given simulation, allowing one state file to be prepared and used repeatedly. But, each molecule/state pair must be unique. Lines that do not contain data may be included in the file (for comments). Each data-containing line must begin with an entry for MOLECULE and STATE separated by a single space, only. All data for a given state must be contained in one line. Keywords ("MOLECULE," "WEXE," etc.) should not be included. Each line beginning with a molecule/state pair should contain:

MOLECULE STATE CASE LAMBDA (p) MULTIPLICITY

HOMONUCLEAR? (g) (i) TE WE WEXE BE AE REQ

A sample state file is given in Figure C-b.3. Descriptions of each entry are listed below in the following format:

usable by the program.

All information contained in this file from: Reference Data on

0

43740

29807

12570

32684

126.2

0

0

wexe Be

2169.81 13.29 1.93128 0.0175

14.54

16.44

16.7

17.36

16.674 0.745

65075.8 1518.2 19.4 1.6115 0.0232

48686.7 1743.4 14.4 1.6912 0.019

214

99

70

78.3

92.9

3737.8 84.9 18.91

3737.8 84.9 18.91

ae

0.0181

0.018

0.593

0.66

0.649

re

1.235

1.2057

1.1283

1.212

1.287

1.111

1.037

1.034

1.036

0.00079 1.012

0.000724 0.97

0.000724 0.97

we

1 1 59618.7 1733.98 14.39 1.6379

-1 1 50203.6 1460.6 13.87 1.455

2551

3231

3320

3282

3178.9

Atoms, Molecules, and Ions by Radzig and Smirnov. Springer-Verlag. 1985. Unles otherwise indicated

case Lamb p Mult Hom? g I Te

Ν

Ν

Ν

Y

Y

Ν

Ν

Ν

Ν

Ν

Ν

Ν

1

3

З

1

3

1

2

2

-1 3

1 2

1 1

1 3

1

1

0

1

0

1

1

2

0

0

1

2

b

b

b

b

b

b

b

b

b

b

Figure
C-b.3:
Sample
state file
. Hund's ca
ases are
assigned
the
closest
value
currently

Mol St

CO A

CO a

CO X

N2 B

N2 A

NH c

NH A

NH a

NH X

OH A

OH X-0.5 b

OH X-1.5 b

Figur	
e C-b	
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ENTRY_NAME acceptable values Brief description of entry.

- MOLECULE string that does not contain spaces and with a maximum length of 39 characters This is the name of the molecule. It must match exactly corresponding entries in the transition file.
- STATE string that does not contain spaces and with a maximum length of 20 characters. This is the name of the electronic state. It must match exactly corresponding entries in the transition file.
- CASE "a" or "b" Hund's Case for this state. Note that transitions between different Hund's Cases are not yet treated by the program. For example, if one state in a transition is a Σ state then both states must be specified as Case (b) (regardless whether this is the truth).
- LAMBDA zero or positive integer This is the total orbital angular momentum quantum number for the electronic state (Σ states have $\Lambda = 0$, for example).
- (p) none, "1" or "-1" If the entry for LAMBDA is zero, then the symmetry of the wavefunction upon reflection through the internuclear axis must be specified. In typical notation, this is the "+" or "-" superscript for Σ electronic states. If the entry for LAMBDA is non-zero, this field should be left blank (a tab or other whitespace, except new-line, is acceptable).
- MULTIPLICITY positive integer This is 2S + 1 where S is the vector-sum of all electron spins in the molecule.
- HOMONUCLEAR? "Y" or "N" Enter "Y" if the molecule is homonuclear and "N" if not.
- (g) none, "1" or "-1" If the entry for HOMONUCLEAR? is "Y," then the inversion symmetry of the wavefunction must be specified. In typical notation, this is the "g" or "u" subscript given to electronic states for homonuclear molecules. If the entry for HOMONUCLEAR? is "N," this field should be left blank (a tab or other

whitespace, except new-line, is acceptable). "1" indicates a symmetric (gerade) wavefunction; "-1" indicates an antisymmetric (ungerade) wavefunction.

- (i) none or decimal number (no fractions) If the entry for HOMONUCLEAR? is "Y," then the nuclear spin of the atoms must be specified. This is the spin for only one of the atoms (do not attempt to take a vector sum of both). If the entry for HOMONUCLEAR? is "N," this field should be left blank (a tab or other whitespace, except new-line, is acceptable). Enter the nuclear spin as a decimal; for example, enter 1.5 rather than 3/2.
- TE zero or positive number This is the term energy for the electronic state in wavenumbers.
- WE *positive number* This is the fundamental vibration frequency for the electronic state in wavenumbers.
- WEXE *positive number* This is the vibration anharmonicity for the electronic state in wavenumbers.
- BE *positive number* This is the rotational constant for the electronic state in wavenumbers.
- AE positive number This is the vibration–rotation interaction constant for the electronic state in wavenumbers.
- REQ positive number This is the equilibrium bond length for the molecule. Currently, this number is not used in the program.

C-b.4 The transition file

The structure of the transition file is somewhat complex, but the file is easy to read and change once the structure is learned. White–spaces are ignored, so the user is free to indent or merge and break lines as desired in order to make the file easier to read. The structure of the file is illustrated and a sample file is given in Figure C-b.4. The required entries are described below using the format:

TEMPERATURE NUMBER_OF_MOLECULES



Figure C-b.4a: Graphical illustration of the structure of the transition file. See text for a description of the file and Figure C-b.4b for a sample.

ENTRY_NAME acceptable values Brief description of entry.

TEMPERATURE zero or positive number, degrees Kelvin This number represents the default rotational temperature for any species in the simulation. Temperatures for molecules or states that are specified later override this entry. This number should be non-zero unless either a temperature is specified at either the molecule or the state level for each state entered in the file. The program will not produce a meaningful simulation if the temperature is set to zero.

	Figure C-b.4b								
300 3 MOL	CO	1	300	3					
a A X	1.00 .2 0.00	N N N	0 800 0	2 3 1	0 5 0	1.0 .92 1.0	.6 1	.3	
2									
a-X A-X	1 1	CO_sa_X.dat CO_A_X.dat							
MOL	ОН	.06	1000	3					
A X-0.5 X-1.5	1.0 0 0	N N N	0 0 0	3 1 1	0 0 0	.7 1.0 1.0	1.0	.2	
2									
A-X-1.5 A-X-0.5	1 1	OH_A_X.dat OH_A_X.dat							
MOL c a	NH 1 O	.35 N N	1000 0 0	2 1 1	0 0	1 1			
1									
c-a	1	NH_c_a.dat							

Figure C-b.4b: Sample transition file.

_

NUMBER_OF_MOLECULES *positive integer* This is the number of molecules to be included in the simulation, and it must be less than or equal to the number of molecules in the file. If there are more molecules, the program will read the file until it has read the specified number of molecules, then stop. The program will terminate if the file ends before this number of molecules is read.

- MOL "MOL" This is a safety-check. At the beginning of the set of information for each molecule, type "MOL" (exactly like that, without quotation marks and in all-capital letters). The program continually scans for this entry. If the entry is found before a molecule is finished, the program will write a descriptive error message and terminate.
- MOL_NAME string that does not include spaces and has a maximum length of 39 characters This string must match exactly the corresponding entry for MOL-ECULE in the state file.
- REL-POP zero or positive number This is the relative population for this molecule. Ideally, it should be a number between 0 and 1, numbers greater than one are permissible.
- TEMP zero or positive number, degrees Kelvin This is the default rotational temperature assigned to this molecule. If this entry is zero, then the previously defined temperature is the default.
- NUM_STATES *positive integer* This is the number of states to be considered for the current molecule. This number must exactly match the number of states described below.
- STATE string that does not include spaces and has a maximum length of 20 characters This is the name given to the electronic state to be considered. This string must match exactly the corresponding entry in the state file.
- REL-POP zero or positive number This is the relative population for this state.
- Ω -REST? for this description "N" The program is written so that electronic states with multiple possible values of Ω (the total angular momentum quantum number, including S, the electronic spin vector) can be treated as separate states. But, the description of this feature is complex, and it has not been thoroughly tested, so the only value for this entry that will be considered here is "N."

- TEMP/FILE zero, positive number (degrees, Kelvin) or file-name This is the rotational temperature to use for this state. If this number is zero, then the temperature specified for the molecule is used. If the temperature for the molecule is also zero, then the default temperature for the simulation is used. If all three numbers are zero, the program will not produce a meaningful simulation. If a file name is entered here, the program will attempt to read a distribution of rotational populations from the indicated file. Caution: reading rotational distributions from a file has been only minimally tested. A description of the contents of the rotational distribution file will not be included here; details of its structure can be determined by inspecting the source code (Section C-c).
- NUM_VIB positive integer This is the total number of vibrational levels to consider for this state. It is not permissible to skip vibrational levels in the transition file. To omit a vibrational level in the middle of a range of levels, assign that level a relative population of zero (see REL_POP, below).
- VIB_LO zero or positive integer This is the lowest vibrational level to consider.
- REL_POP zero or positive number The number of REL_POP entries must match exactly the number given for NUM_VIB. Each REL_POP describes the relative population of a vibrational level, beginning with the level specified in VIB_LO.
- NUMTRANS *positive integer* The number of transitions to be considered in the simulation. This number must match exactly the number of transitions listed below.
- TRANSITION valid string representing a STATE for the current MOLECULE followed by a single dash and the followed by a valid string representing some other STATE for the current MOLECULE; both states must be properly entered in the state file The transitions listed here must involve states listed for this molecule. If a requested transition contains a state not already described (or not

described for the current molecule), the program will issue a message similar to the following and terminate:

Missing definition for at least one state in transition b-X. Exiting. Please edit transition file and restart program

- TRANS-FRACT zero or positive number This number describes the fraction of the upper state whose emissions are observed. For example, if an upper state has a radiative lifetime of 8 ms, and data will be collected for the first 2 ms after the state is produced, then only about 0.22 of the states present will have radiated during the data-collection period. In this case, the entry here should be 0.22. See Chapter 5 for a more detailed discussion of radiative lifetimes and fraction of emissions observed.
- FCF-FILE name of the Franck-Condon file for the transition (maximum of 200 characters) This string must exactly match the name of the file containing Franck-Condon factors for this transition. See below for the structure of the Franck-Condon factor file.

C-b.5 Franck-Condon factor files

The file containing Franck–Condon factors can contain lines that do not contain data (for comments, etc.). Lines that contain data must begin with an integer followed by a single space, a dash and a greater–than sign (>); leading whitespace is permissible in these lines. If other lines in this file contain this combination of characters, the program might behave unexpectedly. A sample Franck–Condon factor file is given in Figure C-b.5. The format for a line containing data is:

VLO -> VHI , WAVENUMBERS , FCF , NM , PEC

Only VLO, VHI and FCF are used by the program. The entries are described below using the format:

```
Morse potential parameters:
De = 10.981 eV
alpha = 2.3256 /Angst
Morse potential parameters:
De = 3.6827 eV
alpha = 2.8098 /Angst
Beta:
       2.32562416 2.80981623 /Angst
  163.266371 78.257731
     1.12829995 1.23500001 Angst
Re:
Nmax = 19 19
       0
          ->
               0
                     64748.47
                                  0.11172
                                                               3.03273E+13
                                                   154.44
                  ,
       0
         ->
               1
                     66227.87
                                  0.21104
                                                   150.99
                                                               6.13047E+13
                  ,
                               ,
         ->
               2
       0
                     67668.47
                                  0.22453
                                                   147.78
                                                               6.95717E+13
                  ,
                                ,
       0
          ->
               3
                     69070.27
                                  0.17888
                                                   144.78
                                                               5.89430E+13
                                                            ,
                                ,
       0
          ->
               4
                     70433.27
                                  0.11972
                                                   141.98
                                                               4.18321E+13
                  ,
       0
          ->
               5
                     71757.47
                                  7.16097E-02
                                                   139.36
                                                               2.64590E+13
       0
          ->
               6
                     73042.87
                                  3.97653E-02
                                                   136.91
                                                               1.54967E+13
               7
       0
          ->
                     74289.47
                                  2.10304E-02
                                                   134.61
                                                               8.62243E+12
                  ,
                                ,
               8
       0
         ->
                     75497.27
                                  1.07845E-02
                                                   132.46
                                                               4.64081E+12
                  ,
                                ,
       0
         ->
               9
                     76666.27
                                                   130.44
                                                               2.44828E+12
                                  5.43310E-03
                  ,
                                ,
                                                            ,
       0
          ->
              10
                     77796.47
                                  2.71544E-03
                                                   128.54
                                                               1.27856E+12
                                                            ,
       0
         ->
              11
                     78887.87
                                  1.35644E-03
                                                   126.76
                                                               6.65936E+11
                  ,
              12
       0
          ->
                     79940.47
                                  6.81096E-04
                                                   125.09
                                                               3.47943E+11
                                ,
       0
         ->
              13
                     80954.27
                                  3.45278E-04
                                                   123.53
                                                               1.83184E+11
```

Figure C-b.5: Portion of a Franck–Condon factor file. This file was generated using the modified version of Kent Ervin's program [Ervin 1993] that is used with CASI (computer assisted spectral identification, see Section 3-2).

ENTRY_NAME acceptable values Brief description of entry.

- VLO zero or positive integer This is the vibrational quantum number for the lower electronic state.
- -> "->" This combination of characters must be entered between vibrational quantum numbers. Spaces must surround this character combination.
- VHI zero or positive integer This is the vibrational quantum number for the higher electronic state.

3554 413	3 64E-04	8
3554,413	3.27E-03	.8
3554,413	1.31E-02	.8
3554,422	5.46E-03	.8
3554.422	9.83E-03	.8
3554.547	7.28E-03	.8
3587.268	5.69E-04	.5
3587.268	5.13E-03	.5
3587.268	2.05E-02	.5
3587.278	8.54E-03	.5
3587.278	1.54E-02	.5
3587.405	1.14E-02	.5
3634.2308	7.25E-04	.7
3634.2311	2.61E-02	.7
3634.2311	6.52E-03	.7
3634.2409	1.09E-02	.7
3634.2412	1.96E-02	.7
3634.3714	1.45E-02	.7

Figure C-b.6: Sample atomic file. Here, transitions from a common upper electronic state (of helium) are grouped together and assigned a common relative population (RELATIVE-WEIGHT).

, "," Commas must appear, separated by spaces, in the locations indicated above.
WAVENUMBERS any positive number or zero This value is not used by the program, but a number must be entered here. The recommended value is either the frequency, in wavenumbers, for this transition, or zero. If this number is negative, the program will assign a value of zero to the Franck–Condon factor for the current transition.

FCF positive number between 0 and 1 This is the Franck–Condon factor for this transition. The program will continue to run if this number is larger than one, but the results will not have a predictable meaning.

- NM any number The program ignores this entry, but it must be a number. The recommended value is either the wavelength, in nanometers, for the current transition, or zero.
- PEC any number The program ignores this entry, but it must be a number. The recommended value is either a variation of the Einstein–A coefficient for the current transition, or zero.

C-b.6 Atomic files

All lines in atomic files must either be blank or contain only information for a single transition. Although the file is called "atomic," this file can be used to include any single–line transition. For example, if frequencies and intensities for a series of rotational transitions are available from an external source (experiment or calculation, for example), they can be entered using this file. The format for non–blank lines is:

TRANSITION–POSITION TRANSITION–PROBABILITY RELATIVE–WEIGHT

The TRANSITION–POSITION must be entered in Ångstroms. This unit was chosen because it is the wavelength unit used in many references for atomic transitions. The units used for the TRANSITION–PROBABILITY can be any that are convenient to the user, but should be uniform. This entry can be used in a manner similar to TRANS_FRACT in the transition file. If the transition probability is not useful in the simulation, set all values equal to one. The RELATIVE–WEIGHT is the relative population for that state. /***********************************/
/* These are the headers for the RVESIM.c program */

- 1 #include <stdio.h>
- 2 #include <math.h>
- 3 #include <stdlib.h>
- 4 #include <string.h>
- 5 #include <ctype.h>
- 6 #define SUB (double)0.5
- 7 #define PI 3.14159265358979323846264338
- 8 #define JKm 0.0504507857956213 /* constant for an equation trick */
- 9 #define JKb 3.04614091081434 /* another constant for an equation trick */
- 10 #define kB 1.38066e-23/1.9864e-23 /* Boltzmann's constant in wavenumbers per kelvin. The first number is Boltzmann's constant in J/K (joules per kelvin). The second number is the conversion from joules to wavenumbers. */

- 11 typedef struct {
- 12 char f[201]; /* filename */
- 13 FILE *F; /* file pointer */
- 14 } fileset;
- 15 typedef struct{
- 16 int vlo, vnum; /* starting vibrational quantum number and number of quantum numbers to consider */
- 17 int vclo, vcnum; /* starting vib quant number for cascade population and number of quanta to consider -- the population will all be contained in the rotset, but need to know about it */
- 18 double *p; /* relative populations for each of the vnum levels */
- 19 int *c; /* change flag for the relative population: (0) not calculated, (1) calculated (-1) re-calculated or (-2) is awaiting recalculation. */
- 20 } vset;
- 21 typedef struct{
- 22 int c; /* change flag for this set */
- 23 int j,k,jc,kc; /* number of J and/or K values in this set jc and kc are there because there might be more E entries than there are P entries -- there will also be more CJ/CK entries.*/
- 24 double *J, *K; /* values of J and/or K for each level */
- 25 double Jdissoc, Kdissoc; /* values of J/K where the molecule dissociates, according to the ratio of Bv to Dv. */
- 26 double *EJ, *EK; /* the energies of this level (wavenumbers) */
- 27 double *PJ, *PK, Jmaxp; /* relative populations of this level, not including any contribution from cascade and the value of J that was found to be the true maximum value -- 10 June 02: I just commented out all use of Jmaxp */
- 28 double *CJ, *CK; /* cascade population of this level */
- 29 } rotset;

/*** The 'State' structure ***/

- 30 typedef struct {
- 32 double pop; /* relative population for this state */
- 33 int cp, cC, cD, co, cT, cS, cr, cv; /* change flags for population (cp), Case (cC), presence of rotational input file (cD), number omegas (co), temperature (cT), spectroscopic information (cS), rotation (cr) and vibration (cv) info */
- 34 char Case[11]; /* Hund's Case. a or b */
- 35 int Ca; /* numerical position in stateinfo array if Case a */
- 36 int Cb; /* numerical position in stateinfo array if Case b */
- 37 int Cc, Cd; /* similar to Ca and Cb */
- 38 int Dist; /* is the distribution of states is from a file (-1), from the temperature (1), or not relevant (0). */
- 39 vset *v; /* pointer to set of vibrational information MEMORY AL-LOCATED in read_trans.c */
- 40 rotset *r; /* pointer to set of rotational distribution info MEMORY ALLOCATED in rotation-distribution functions (e.g., multi_nonzero_JKb.c) */
- 41 int nr,n0,nV; /* number of rotsets, number Omegas and vnum (this will change if different Omegas get different vnums...) */
- 42 rotset *rc; /* pointer to rotsets for additional vibrational levels that are populated only by cascade -- the number of these sets is 30 (or Onum*30) because it's hard to know which levels will get populated from which states, and I'm too lazy to shuffle all the array entries. */
- 43 int pmsymm, Isymm; /* if Lambda==0: Are even numbered K's + or (pmsymm); and, if this set is homonuclear, are even K's symmetric
 or antisymmetric (Isymm). */
- 44 int no; /* How many times is this state an origination state? */
- 45 int *o; /* the list of positions in the transition array where this state is the origination state. MEMORY ALLOCATED in read_trans.c */
- 46 int nd; /* How many times is this state a destination state? */
- 47 int *d; /* the list of positions in the transition array where this state is the destination state. MEMORY ALLOCATED in read_trans.c */
- 48 fileset *f; /* file name and pointer for J/k distribution file(s)
 if there are any for this state MEMORY ALLOCATED in read_trans.c
 */
- 49 double *T; /* Temperature of state. Leave zero if this is only a destination state or if temp is defined at a higher level. There is one of these for each omega. MEMORY ALLOCATED in read_trans.c */
- 50 } State;

/*** The 'caseinfo' structures ***/
/* For now, only cases (a) and (b) are defined here. */

- 51 typedef struct {
- 52 int cTe, cwe, cwexe, cBe, cae, cbeta, cO; /* change flags for the term energy (cTe), we and wexe (cwe, cwexe), the rotational constant (cBe), the vibration-rotation interaction constant (cae),

the centrifugal distortion constant (cbeta), anything concerning Omegas (cO) $\ast/$

- 53 double Te, we, wexe, Be, ae, beta; /* all units wavenumbers -beta currently not used in the program */
- 54 int L, O, g; /* Lambda (L). The number of Omegas to consider; use 0 (zero) to have the program use all possible. If applicable (g), gerade (1), ungerade (-1); if not homonuclear, use 0 (zero). */
- double *10, I, S, sflag; /* if the user specifies certain Omegas to use, this is the list of desired Omegas (10). It has to be float since I don't want to work out some other way to have halfintegral values for Omega. Also, if homonuclear, the nuclear spin (I). The electronic spin, S, and a flag for looking up whether the spin is integral (=0) or half-integral (=0.5). MEMORY ALLOCATED in read_trans.c */
- 56 double *pO; /* If the user specifies populations for each Omega, they go here. MEMORY ALLOCATED in read_trans.c */
- 57 int symm; /* If homonuclear: are even-plus (+1) or even-minus (1) (even J-values) symmetric (default value 0)? -- This variable
 will only be useful if someone includes the +/- splitting in the
 program one day -- SEE PROGRAM_CHANGES if you are the person wanting to do that */
- 58 double Jmin, Jmax; /* Minimum and maximum values for J. */
- 59 double *Jpop; /* pointer to the array of J-state populations if they are entered from a file MEMORY ALLOCATED in read_rot.c */
- 60 int a; /* how many J-values long is the array? */
- 61 } Case_a_stateinfo;
- 62 typedef struct {
- 63 int cTe, cwe, cwexe, cBe, cae, cbeta; /* change flags for the term energy (cTe), we and wexe (cwe, cwexe), the rotational constant (cBe), the vibration-rotation interaction constant (cae), the centrifugal distortion constant (cbeta) */
- 64 double Te, we, wexe, Be, ae, beta; /* all units wavenumbers -beta is currently included in some calculations in the program, but since it isn't read in, the value is always zero. */
- 65 int L, p, g; /* Lambda (L). If L=0, indicate (p) plus (+1) or minus (-1); if L!=0, use zero (0). If homonuclear, indicate (g) gerade (+1), ungerade (-1); if not homonuclear, use zero (0). */
- 66 double I, S, sflag; /* If homonuclear, the nuclear spin. The electronic spin, S and a flag for looking up whether the spin is integral (=0) or half-integral (=0.5). */
- 67 /*int symm; [1] If L=0 and homonuclear: are even (+1) or odd (1)
 K-values symmetric? [2] If Lambda>0 and homonuclear are even plus states (+1) or even-minus states (-1) symmetric? (default
 0) */
- 68 double Kmin, Kmax, Jnum, *K, *J; /* Minimum and maximum values for K, the number of J's, and the actual values of J and K */
- 69 double *Jpop; /* pointer to the array of J-state populations if they are entered from a file MEMORY ALLOCATED in read_rot.c */
- 70 int a; /* how many K-values long is the array? */
- 71 } Case_b_stateinfo;

/*** General structures for simulation parts ***/

- 72 typedef struct{
- 73 int n; /* number of transitions here */
- 74 double pop; /* relative population for this set */
- 75 double *f; /* frequency of transition */
- 76 double *ni; /* native intensity at that transition */
- 77 double *ci; /* cascade intensity at that transition if needed */
- 78 } simset; /* set of information needed to make the simulation */
- 79 typedef struct{
- 80 int n; /* number of points */
- 81 double *x; /* position */
- 82 double *y; /* relative intensity */
- 83 } sim; /* a simulation */

/*** A structure for Franck-Condon Factors ***/

- 84 typedef struct {
- 85 double fcfn[30]; /* An array of frequency-adjusted franck-condon factors from one vibrational level to a series of lower levels, for observed transitions. */
- 86 double fcfc[30]; /* An array of frequency-adjusted franck-condon factors from one vibrational level to a series of lower levels for transitions that contribute to cascade transitions. */
- 88 int vqn[30]; /* redundant, but just in case the vib quantum number isn't what's expected from the file -- these are the lower state quantum numbers. */
- 89 } vfcf;

/*** The 'Transition' structure ***/

- 90 typedef struct {
- 91 char Nhi[21], Nlo[21]; /* The letter designations for the higher state (Nhi -- e.g., a', B, c, etc.), and the lower state (Nlo). */
- 92 int Hi, Lo; /* Numerical position in states array for info about the high state and the low state. */
- 93 int Ohi,Olo; /* Number of Omegas specified for the high and low states. */
- 94 int vs,vnh,vnl,vhlo,vllo; /* the actual number of v's found in the file, the number of high and low v's simulated and the lowest values for those sets of v's */
- 95 int cv,*cP; /* change flag for FCF info and transition probability MEMORY ALLOCATED in read_trans.c */
- 96 vfcf *v; /* pointer to the arrays of franck-condon factors. The declaration of 30 states is based on the maximum number output from Ervin's FCF program. These array spots are indexed by the upper vibrational q#. MEMORY ALLOCATED in read_FCF.c*/
- 97 int nS, *fS; /* number of simulations for this transition and flags to tell if the simulations should be included in the overall simulation (won't be if spin-Sigma forbidden) MEMORY ALLOCATED in transition functions (e.g., a-a.c)*/
- 98 simset *S; /* pointer to simulations for this transition MEMORY ALLOCATED in transition functions (e.g., a-a.c)*/

```
99
      double *P; /* overall electronic transition probability MEMORY
       ALLOCATED in read_trans.c */
      fileset *f; /* filenames and pointers for FCF files MEMORY ALLO-
100
       CATED in read_trans.c */
101
      } Trans;
    /* This is a structure made solely for the purpose of transmitting
       information between b_b() and the various sub-functions it calls
       */
102 typedef struct {
      int hvnlo,hvnnum,hvclo,hvcnum,hivlo,hivnum; /* Re high state:
103
       native low vib num, number vib levels; same, but for cascade;
       overall lowest vib num and overall number vib levels */
104
      int lvnlo, lvnnum, lvclo, lvcnum, lovlo, lovnum; /* like above, low
      state */
105
      int nT; /* maximum number transitions per K level */
106
      int nhJ,nlJ; /* 2S+1 for high and low states */
107
      int hiK; /* maximum number hi K might be */
      int m; /* position in MOL array */
108
109
      Trans *T; /* pointer to this transition structure */
110
      Case_b_stateinfo *Ch,*Cl; /* to high and low Case_b_info struc-
      tures */
111
      rotset *Rh,*Rl; /* to high and low rotsets */
112
      State *Sh,*Sl; /* to high and low State structures */
      vset *Vh; /* high-state vib set */
113
114
      } BBTinfo;
    /*** Included Atomic Transitions ***/
115 typedef struct {
      double p; /* relative population for this file */
116
      fileset f; /* name and pointer for this file */
117
118
      double *x; /* position of the transition */
119
      double *A; /* Einstein A */
      double *pop; /* relative population for this transition */
120
121
      int M; /* multiplicity for the origination state -- not used now
       */
122
      simset S; /* the part of the simulation due to this set */
123
      int c, n; /* change flag for this set of atomic transitions, num-
      ber of sets of information */
124
      } Ainfo;
    /*** Included Transitions, 'Other' 'experimental', etc. ***/
125 typedef struct {
126
      double p; /* relative population for this set */
127
      double *x; /* position of transition */
      double *y; /* relative intensity at that position */
128
129
      int c, n; /* change flag for this set of data and number of x,y
      pairs in this set. */
130
      fileset f; /* file where this info was found */
131
      } XYlist;
    /* Structure for keeping up with molecule information */
132 typedef struct{
```

133 int cp, cT; /* change flags for relative population and temperature */

- 134 char Mol[41]; /* name of molecule */
- 135 double pop; /* relative population for molecule */
- 136 int states ; /* number of states for this molecule */
- 137 State *s; /* state array MEMORY ALLOCATED in read_trans.c */
- 138 int trans; /* number of transitions for this molecule */
- 139 Trans *t; /* transition array MEMORY ALLOCATED in read_trans.c */
- 140 double T; /* temperature if specified at molecule level */
- 141 } Molecule;

/* these are the names for files containing information about the
 run */

- 142 char PREF[101], TMPFILE[300];
- 143 FILE *INMAIN, *DBG, *OUT, *PAR, *SCR, *SYS;
- 144 fileset *INOT, *INV, *OTR, *INEX, *INAT, INST, INTR;

/* these functions read in the various input files */

- 145 void read_state_and_transition_files(), read_FCF_file(),
 read_atomic_files();
- 146 void read_XY_file(XYlist*),read_rot_dist_files();
 /* these are managerial and graphical functions */
 /*void get_energies_intensities();*/
- 147 void manage_transitions(),manage_rotations();
- 148 void do_simulation(), graph_results(), ask_for_changes();
 /* these functions calculate spectra for different transition types
 */
- 149 void
- a_a(int,int),a_b(int,int),a_c(int,int),a_d(int,int),b_b(int,int);
 150 void

b_c(int,int),b_d(int,int),c_c(int,int),c_d(int,int),d_d(int,int);
 /* these functions calculate rotational levels and populations */

- 151 void singlet_JK(int, int), multiplet_zeroL_JK(int, int);
- 152 void

```
multiplet_nonzeroL_JK_a(int,int),multiplet_nonzeroL_JK_b(int,int);
```

- 153 void case_a_cascade(rotset*,int,double,int,int,int); 154 void case_b_cascade(rotset*,int,int,int,int);
- 155 void
- bb_SigmaSigma(BBTinfo), bb_SigmaOther(BBTinfo), bb_Other(BBTinfo);
- 156 double HL(int, double, int, int);
- 157 char *new_mol_ck(char*,char*);
- 158 int DEBUG=0,NUMTR=0,NUMAT=0,NUMOT=0,NUMEX=0,NUMMOL=0,NUMST=0; /* A note on the DEBUG variable. If this is equal to -1, no functions will print any messages. Adjusting values in .rvesimconfig can cause messages about the execution of functions to print. Use this feature cautiously as it can produce enormous files. */
- 159 int Case_a_num=0, Case_b_num=0, SCANTYPE=0, DETECTTYPE=3, UNITTYPE=0;
- 160 int EFFTYPE=1, INTERACT=1, ROVIB=0;
- 161 double SIMMAX=1,*ATPOP,*OTINT,*EXINT,TEMP=0,JKCUT=0.001;
- 162 double MINV=100, MAXV=3500, PSTEP=0.5, MAXINT=5000, RESN=2.0;
- 163 Case_a_stateinfo *CA;
- 164 Case_b_stateinfo *CB;
- 165 Molecule *MOL;
- 166 Ainfo *AT;
- 167 XYlist *OT,*EX,*EF;

```
168 char PROGRAM_NAME [200] = "RVESIM";
    /* debugging-level flags */
    /* Functions that affect many functions */
169 int mdebugflag=0; /* main */
170 int tdebugflag=0; /* transition file */
    /* Functions for calculating rotational populations and energies */
171 int mrdebugflag=0; /* manage rotations */
172 int mnadebugflag=0; /* multiplet non-zero-L Case a */
173 int mnbdebugflag=0; /* multiplet non-zero-L Case b */
174 int msdebugflag=0; /* multiplet sigma */
175 int sdebugflag=0; /* singlet sigma */
    /* Functions involved in calculating transitions */
176 int mtdebugflag=0; /* manage transitions */
177 int aadebugflag=0; /* Case a <-> case a transition */
178 int cacdebugflag=0; /* calculate energy levels in destination Case
      a state */
179 int bbdebugflag=0; /* manages case b <-> case b transitions */
180 int cbcdebugflag=0; /* calculate energy levels in destination Case
      b state */
181 int bbSSdebugflag=0; /* Case b Sigma<->Sigma transitions */
182 int bbSOdebugflag=0; /* Case b Sigma<->Non-Sigma transitions */
183 int bb00debugflag=0; /* Case b Non-Sigma<->Non-Sigma transitions
      */
    /* The function that turns lines into spectra */
184 int ddebugflag=0; /* do_simulation */
    /* Functions that read contents of files */
185 int rpdebugflag=0; /* read FCF files */
186 int radebugflag=0; /* read atomic files */
187 int rddebugflag=0; /* read rotational distribution files */
188 int XYdebugflag=0; /* read files in x-y format */
189 int HLswitch=0; /* use Honl-London factors? 1=no 0=yes */
190 double bbSSSATT=0,bbSOSATT=0,bbOOSATT=0;
    /* main opens and reads the input file, assigning values to vari-
      ables as needed and handles other file opening/closing and func-
      tion calls */
191 int main(int argc, char *argv[]){
    /* generic counters */
192 int ma=0,mb=0,mc=0,mOnuma=0,mOnumb=0;
    /* strings for various things */
193 char mstrdum[1000],mconf[100]=".rvesimconfig",mtmp[200];
194 FILE *MCONF;
    /* for scaling the transition probabilites to one */
195 double mtrprobmax=0;
196 MCONF=fopen(mconf,"r");
197 if (MCONF==NULL) {
      printf("Configuration file .rvesimconfig not found.\n");
198
199
      printf("Using internal defaults.\n");
200
```

```
201 else{
      fscanf(MCONF,"%s %s",mstrdum,PROGRAM_NAME);
202
      fscanf(MCONF,"%s %d",mstrdum,&DEBUG);
203
      fscanf(MCONF,"%s %d",mstrdum,&mdebugflag);
204
      fscanf(MCONF, "%s %d", mstrdum, &tdebugflag);
205
      fscanf(MCONF,"%s %d",mstrdum,&mrdebugflag);
206
      fscanf(MCONF, "%s %d", mstrdum, &mnadebugflag);
207
      fscanf(MCONF,"%s %d",mstrdum,&mnbdebugflag);
208
209
      fscanf(MCONF,"%s %d",mstrdum,&msdebugflag);
      fscanf(MCONF,"%s %d",mstrdum,&sdebugflag);
210
      fscanf(MCONF,"%s %d",mstrdum,&mtdebugflag);
fscanf(MCONF,"%s %d",mstrdum,&cacdebugflag);
211
212
      fscanf(MCONF, "%s %d", mstrdum, & cbcdebugflag);
213
      fscanf(MCONF, "%s %d", mstrdum, &aadebugflag);
214
      fscanf(MCONF,"%s %d",mstrdum,&bbdebugflag);
215
      fscanf(MCONF,"%s %d",mstrdum,&bbSSdebugflag);
216
      fscanf(MCONF,"%s %d",mstrdum,&bbSOdebugflag);
217
      fscanf(MCONF,"%s %d",mstrdum,&bb00debugflag);
fscanf(MCONF,"%s %d",mstrdum,&ddebugflag);
218
219
      fscanf(MCONF,"%s %d",mstrdum,&rpdebugflag);
220
      fscanf(MCONF,"%s %d",mstrdum,&radebugflag);
221
      fscanf(MCONF, "%s %d", mstrdum, &rddebugflag);
222
223
      fscanf(MCONF, "%s %d", mstrdum, &XYdebugflag);
224
      fscanf(MCONF, "%s %d", mstrdum, &HLswitch);
      fscanf(MCONF,"%s %lf",mstrdum,&bbSSSATT);
fscanf(MCONF,"%s %lf",mstrdum,&bbSOSATT);
225
226
      fscanf(MCONF,"%s %lf",mstrdum,&bbOOSATT);
227
228
      }
     /* inform user of usage if there is no input file on the command line
       */
229 if(argv[1]==NULL){
230
      printf("Usage: %s input_file\n", PROGRAM_NAME);
231
      printf("See the documentation files for more info.\n");
232
      exit(1);
233
      }
     /* otherwise, open the file from the command line */
234 else{
235
      INMAIN=fopen(argv[1], "r");
236
      if(INMAIN==NULL){
237
         printf("Input file open error. Exiting. \n");
238
         exit(1);
239
         }
      }
240
     /* read the contents of the main input file */
241 fscanf(INMAIN, "%s %s", mstrdum, PREF);
242 if(strcmp(mstrdum,"OUTPREF")!=0){
243
      printf("Input file error.\n");
244
      printf("Entry %s should say \"OUTPREF\". Exiting.\n",mstrdum);
245
      exit(1);
      }
246
247 if(DEBUG>-1){
248
      sprintf(mstrdum, "%s_debug.txt", PREF);
249
      DBG=fopen(mstrdum,"w");
```

```
250
      if(DBG==NULL){
251
        printf("Error opening debugging output file. Exiting.\n");
252
        exit(1);
253
        }
      }
254
255 sprintf(mstrdum,"%s_parameter.txt",PREF);
256 PAR=fopen(mstrdum,"w");
257 if(PAR==NULL){
258
      printf("Error opening parameter file. Exiting.\n");
259
      exit(1);
260
      }
261 strcpy(TMPFILE,".rvesim_temp");
262 fscanf(INMAIN, "%s %s", mstrdum, mtmp);
263 if(strcmp(mstrdum,"UNITS")!=0){
264
      printf("Input file error.\n");
265
      printf("Entry %s should say \"UNITS\". Exiting.\n",mstrdum);
266
      exit(1);
      }
267
268 else{
269
      switch (mtmp[0]){
270
        case 'c':
271
          UNITTYPE=1;
272
          break;
273
        case 'n':
274
          UNITTYPE=0;
275
          break;
276
        default:
          printf("Unexpected entry for \"Units\". Exiting.\n");
277
278
          exit(1);
279
        }
280
      }
281 fscanf(INMAIN, "%s %lf", mstrdum, &RESN);
282 if(strcmp(mstrdum,"RESOLUTION")!=0){
283
      printf("Input file error.\n");
284
      printf("Entry %s should say \"RESOLUTION\". Exit-
    ing.\n",mstrdum);
285
      exit(1);
286
      }
287 else RESN/=2;
288 fscanf(INMAIN,"%s %s",mstrdum,mtmp);
289 if(strcmp(mstrdum,"EFFICIENCY")!=0){
290
      printf("Input file error.\n");
291
      printf("Entry %s should say \"EFFICIENCY\". Exit-
    ing.\n",mstrdum);
292
      exit(1);
293
      }
294 else{
295
      switch (mtmp[0]){
296
        case '1':
297
          EFFTYPE=1;
298
          break;
299
        default:
300
          EFFTYPE=0;
301
          EF=(XYlist*)calloc(1,sizeof(XYlist));
```
```
302
          strcpy(EF[0].f.f,mtmp);
303
          read_XY_file(EF);
        }
304
305
      }
306 fscanf(INMAIN, "%s %s", mstrdum, mtmp);
307 if(strcmp(mstrdum,"DETECTION")!=0){
308
      printf("Input file error.\n");
309
      printf("Entry %s should say \"DETECTION\". Exiting.\n",mstrdum);
310
      exit(1);
311
      }
312 else{
313
      switch (mtmp[0]){
314
        case 'c':
          DETECTTYPE=4;
315
316
          break;
317
        case 'p':
318
          DETECTTYPE=3;
319
          break;
320
        default:
321
        printf("Unexpected entry for \"DETECTION\". Exiting.\n");
322
          exit(1);
323
        }
      }
324
325 fscanf(INMAIN, "%s %s", mstrdum, mtmp);
326 if(strcmp(mstrdum,"SCAN")!=0){
327
      printf("Input file error.\n");
      printf("Entry %s should say \"SCAN\". Exiting.\n",mstrdum);
328
329
      exit(1);
330
      }
331 else{
332
      switch (mtmp[0]){
333
        case 's':
334
          SCANTYPE=0;
335
          break;
336
        case 'j':
          SCANTYPE=1;
337
338
          break;
339
        default:
340
      printf("Unexpected entry for \"SCAN\". Exiting.\n");
341
          exit(1);
342
        }
343
      }
344 fscanf(INMAIN, "%s %lf", mstrdum, & JKCUT);
345 if(strcmp(mstrdum,"CUTOFF")!=0){
346
      printf("Input file error.\n");
347
      printf("Entry %s should say \"CUTOFF\". Exiting.\n",mstrdum);
348
      exit(1);
349
      }
350 if(JKCUT<=0){
351 fprintf(PAR, "The low intensity cutoff was set to a value too low
    for\n");
352 fprintf(PAR,"\tthis program to understand. Resetting to default
    0.001.\n");
353
      JKCUT=0.001;
```

```
t-
```

```
356 if(strcmp(mstrdum,"INTERACTIVE")!=0){
      printf("Input file error.\n");
357
358
      printf("Entry %s should say \"INTERACTIVE\". Exit-
    ing.\n",mstrdum);
359
      exit(1);
      }
360
361 else{
      switch (mtmp[0]){
362
363
        case 'i':
364
          INTERACT=0;
365
          break;
366
        case 'n':
367
          INTERACT=1;
368
          break;
369
        default:
      printf("Unexpected entry for \"INTERACTIVE\". Exiting.\n");
370
371
          exit(1);
372
        }
      }
373
374 fscanf(INMAIN, "%s %lf", mstrdum, &MINV);
375 if(strcmp(mstrdum,"MINPOINT")!=0){
376
      printf("Input file error.\n");
377
      printf("Entry %s should say \"MINPOINT\". Exiting.\n",mstrdum);
378
      exit(1);
379
      }
380 fscanf(INMAIN, "%s %lf", mstrdum, &MAXV);
381 if(strcmp(mstrdum,"MAXPOINT")!=0){
382
      printf("Input file error.\n");
      printf("Entry %s should say \"MAXPOINT\". Exiting.\n",mstrdum);
383
384
      exit(1);
385
      }
386 fscanf(INMAIN, "%s %lf", mstrdum, &PSTEP);
387 if(strcmp(mstrdum, "POINTSTEP")!=0){
388
      printf("Input file error.\n");
      printf("Entry %s should say \"POINTSTEP\". Exiting.\n",mstrdum);
389
390
      exit(1);
391
      }
392 MINV-=0.5*PSTEP;
393 MAXV-=0.5*PSTEP;
394 fscanf(INMAIN, "%s %lf", mstrdum, &MAXINT);
395 if(strcmp(mstrdum, "MAXIMUM")!=0){
396
      printf("Input file error.\n");
397
      printf("Entry %s should say \"MAXIMUM\". Exiting.\n",mstrdum);
398
      exit(1);
      }
399
400 fscanf(INMAIN, "%s %s", mstrdum, mtmp);
401 if(strcmp(mstrdum,"ROVIBSIM")!=0){
402
      printf("Input file error.\n");
403
      printf("Entry %s should say \"ROVIBSIM\". Exiting.\n",mstrdum);
404
      exit(1);
405
      }
406 else{
```

354

}

355 fscanf(INMAIN, "%s %s", mstrdum, mtmp);

```
407
      switch (mtmp[0]){
408
        case 'Y':
409
          ROVIB=0;
410
          break;
411
        case 'N':
412
          ROVIB=1;
413
          break;
414
        case 'y':
415
          ROVIB=0;
416
          break;
417
        case 'n':
418
          ROVIB=1;
419
          break;
420
        default:
421
      printf("Unexpected entry for \"ROVIBSIM\". Exiting.\n");
422
          exit(1);
423
        }
      }
424
425 if(ROVIB==0){
426
      fscanf(INMAIN,"%s %s",INST.f,INTR.f);
427
      INST.F=fopen(INST.f,"r");
428
      if(INST.F==NULL){
429
        printf("Error opening state file. Exiting.\n");
430
        exit(1);
431
        }
432
      fclose(INST.F);
433
      INTR.F=fopen(INTR.f,"r");
434
      if(INTR.F==NULL){
435
        printf("Error opening transition file. Exiting.\n");
436
        exit(1);
437
        }
438
      fclose(INTR.F);
439
      }
440 fscanf(INMAIN, "%s %d", mstrdum, &NUMAT);
441 if(strcmp(mstrdum,"NUMAT")!=0){
442
      printf("Input file error.\n");
443
      printf("Entry %s should say \"NUMAT\". Exiting.\n",mstrdum);
444
      exit(1);
445
      }
446 if(NUMAT!=0){
      AT=(Ainfo*)calloc(NUMAT,sizeof(Ainfo));
447
448
      for(ma=0;ma<NUMAT;ma++){</pre>
        fscanf(INMAIN,"%s %lf",AT[ma].f.f,&AT[ma].p);
449
450
        AT[ma].f.F=fopen(AT[ma].f.f,"r");
451
        if(AT[ma].f.F==NULL){
452
          printf("Error opening %s. Exiting.\n",AT[ma].f.f);
453
          exit(1);
454
          }
455
        fclose(AT[ma].f.F);
456
        }
      }
457
458 fscanf(INMAIN, "%s %d", mstrdum, &NUMOT);
459 if(strcmp(mstrdum,"NUMOT")!=0){
      printf("Input file error.\n");
460
```

```
461
      printf("Entry %s should say \"NUMOT\". Exiting.\n",mstrdum);
462
      exit(1);
463
      }
464 if(NUMOT!=0){
465
      OT=(XYlist*)calloc(NUMOT,sizeof(XYlist));
466
      for(ma=0;ma<NUMOT;ma++){</pre>
        fscanf(INMAIN,"%s %lf",OT[ma].f.f,&OT[ma].p);
467
468
        read_XY_file(&OT[ma]);
469
        }
470
      }
471 fscanf(INMAIN, "%s %d", mstrdum, &NUMEX);
472 if(strcmp(mstrdum,"NUMEX")!=0){
473
      printf("Input file error.\n");
474
      printf("Entry %s should say \"NUMEX\". Exiting.\n",mstrdum);
475
      exit(1);
476
      }
477 if(NUMEX!=0){
478
      EX=(XYlist*)calloc(NUMEX,sizeof(XYlist));
479
      for(ma=0;ma<NUMEX;ma++){</pre>
480
        fscanf(INMAIN,"%s %lf",EX[ma].f.f,&EX[ma].p);
481
        read_XY_file(&EX[ma]);
482
        }
483
      }
484 fclose(INMAIN);
    /* Create directory for output */
485 sprintf(mstrdum,"mkdir %s_molecules",PREF);
486 system(mstrdum);
    /* FUNCTIONS for reading some of the input files */
487 if(ROVIB==0) read_state_and_transition_files();
488 if(ROVIB==0) read_FCF_file();
489 if(NUMAT>0) read_atomic_files();
     /* Loop through all the transition probabilities and make sure that
       they are all expressed in terms of fractions of one. The only
       place where this is really necessary is in the calculation of cas-
       cade intensities. But, it won't hurt elsewhere, either. If other
       files containing transition probabilites are added to the pro-
       gram, don't forget to put them in these loops, too. First: find
       the maximum transition probability */
490 if (mdebugflag<DEBUG) {
491 fprintf(DBG,"NUMMOL=%d, NUMAT=%d\n",NUMMOL,NUMTR);
492 fflush(DBG);
493
      }
494 for(ma=0;ma<NUMMOL;ma++){
495
      for(mb=0;mb<MOL[ma].trans;mb++){</pre>
496
        mOnuma=MOL[ma].t[mb].Ohi;
497
        if(mOnuma==0) mOnuma=1;
498
        mOnumb=MOL[ma].t[mb].Olo;
499
        if(mOnumb==0) mOnumb=1;
```

```
500 mOnuma*=mOnumb;
```

```
501 if(mdebugflag<DEBUG){
```

```
502 fprintf(DBG,"First trprob scan: ma=%d, mb=%d, mOnumb=%d, mOn-
uma=%d\n",\
```

```
503 ma, mb, mOnumb, mOnuma);
```

```
504 fflush(DBG);
505
      }
506
        for(mc=0;mc<mOnuma;mc++){</pre>
507
           if(MOL[ma].t[mb].P[mc]>mtrprobmax){
508
             mtrprobmax=MOL[ma].t[mb].P[mc];
509 if (mdebugflag<DEBUG) {
510 fprintf(DBG, "MOL[%d].t[%d].P[%d]=mtrprobmax=%f\n", ma, mb, mc,
    mtrprobmax);
511 fflush(DBG);
512
      }
513
             }
          }
514
        }
515
516
      }
517 for(ma=0;ma<NUMAT;ma++){</pre>
      for(mb=0;mb<AT[ma].n;mb++){</pre>
518
519
        if(AT[ma].A[mb]>mtrprobmax) mtrprobmax=AT[ma].A[mb];
520 if (mdebugflag<DEBUG) {
521 fprintf(DBG,"AT[%d].A[%d]=%f;
    mtrprobmax=%f\n",ma,mb,AT[ma].A[mb],mtrprobmax);
522 fflush(DBG);
523
      }
524
        }
      }
525
     /* Now, scale all the transition probabilites to that one */
526 for(ma=0;ma<NUMMOL;ma++){
      for(mb=0;mb<MOL[ma].trans;mb++){</pre>
527
528
        mOnuma=MOL[ma].t[mb].Ohi;
        if(mOnuma==0) mOnuma=1;
529
530
        mOnumb=MOL[ma].t[mb].0lo;
531
        if(mOnumb==0) mOnumb=1;
532
        mOnuma*=mOnumb;
533 if(mdebugflag<DEBUG){
534 fprintf(DBG, "Second trprob scan: ma=%d, mb=%d, mOnumb=%d, mOn-
    uma=%d\n",\
535
        ma,mb,mOnumb,mOnuma);
536 fflush(DBG);
537
      }
538
        for(mc=0;mc<mOnuma;mc++){</pre>
539 if(mdebugflag<DEBUG){
540 fprintf(DBG, "MOL[%d].t[%d].P[%d]=%f\t", ma, mb, mc,
    MOL[ma].t[mb].P[mc]);
541 fflush(DBG);
542
      }
543
           MOL[ma].t[mb].P[mc]/=mtrprobmax;
544 if(mdebugflag<DEBUG){
545 fprintf(DBG, "MOL[%d].t[%d].P[%d]=%f\n", ma, mb, mc,
    MOL[ma].t[mb].P[mc]);
546 fflush(DBG);
547
      }
548
             }
           }
549
550
        }
551 for(ma=0;ma<NUMAT;ma++){</pre>
```

```
355
```

```
552
      for(mb=0;mb<AT[ma].n;mb++){</pre>
553 if(mdebugflag<DEBUG){
554 fprintf(DBG,"AT[%d].A[%d]=%f\t",ma,mb,AT[ma].A[mb]);
555 fflush(DBG);
556
      }
557
        AT[ma].A[mb]/=mtrprobmax;
558 if(mdebugflag<DEBUG){
559 fprintf(DBG, "AT[%d].A[%d]=%f\n", ma, mb, AT[ma].A[mb]);
560 fflush(DBG);
561
      }
562
        }
      }
563
    /* FUNCTION to calculate energies and relative intensities for ro-
      tational states */
564 if(ROVIB==0) manage_rotations();
    /* FUNCTION to step through transitions, figure out what sort of
      transitions they are and then call the right functions to simu-
      late them */
565 if(ROVIB==0) manage_transitions();
    /* FUNCTION to add together all the individual pieces and make the
       simulation -- this function will call others that write the data
      */
566 do_simulation();
    /* FUNCTION to graph the simulated spectrum, with experimental if
      requested */
    /* graph_results(); */
    /* FUNCTION to ask user if something should be changed and to make
      the change as needed */
    /* ask_for_changes(); */
567 if(ROVIB==0) fclose(INTR.F);
568 if(NUMMOL>0) free(MOL);
569 if(Case_a_num>0) free(CA);
570 if(Case_b_num>0) free(CB);
571 if(NUMAT>0) free(AT);
572 if(NUMEX>0) free(EX);
573 if(NUMOT>0) free(OT);
574 if(EFFTYPE==0) free(EF);
575 sprintf(mstrdum,"rm %s",TMPFILE);
576 system(mstrdum);
577 if(DEBUG>-1) fclose(DBG);
578 fclose(PAR);
579 return 0;
580 }
    /* This function identifies each transition's type and calls the
      correct function to do the transition. */
581 void manage_transitions(){
582 int mta=0,mtb=0,mtc=0,mtd=0,mte=0,mtdone=1,mtcasesum=0,*mtz;
```

```
583 double *mtTeH,*mtTeL,mtEmax=0;
```

```
584 int mtcounter=0, mtsorth=0, mtsortdum=0;
585 if (DEBUG>mtdebugflag) {
586 fprintf(DBG, "NUMMOL is %d\n", NUMMOL);
587 fflush(DBG);
588 }
    /* begin loop over molecules */
589 for(mta=0;mta<NUMMOL;mta++){
    /* begin loop over transitions */
      mtz=(int*)calloc(MOL[mta].trans,sizeof(int));
590
591
      mtTeH=(double*)calloc(MOL[mta].trans,sizeof(double));
592
      mtTeL=(double*)calloc(MOL[mta].trans,sizeof(double));
    /* the following is a mechanism for sorting the transitions from
      highest energy to lowest energy -- this is necessary to get the
       cascade right. The algorithm is probably primitive and ineffi-
       cient, so if you want to improve it, go right ahead ... */
593
      for(mtb=0;mtb<MOL[mta].trans;mtb++){ /* save Te's to temporary</pre>
       arrays */
594
        mtz[mtb]=mtb;
595
        if(MOL[mta].s[MOL[mta].t[mtb].Hi].Ca>-1){
          mtTeH[mtb]=CA[MOL[mta].s[MOL[mta].t[mtb].Hi].Ca].Te;}
596
597
        if(MOL[mta].s[MOL[mta].t[mtb].Hi].Cb>-1){
598
          mtTeH[mtb]=CB[MOL[mta].s[MOL[mta].t[mtb].Hi].Cb].Te;}
599
        if (MOL[mta].s[MOL[mta].t[mtb].Lo].Ca>-1){
600
          mtTeL[mtb]=CA[MOL[mta].s[MOL[mta].t[mtb].Lo].Ca].Te;}
601
        if(MOL[mta].s[MOL[mta].t[mtb].Lo].Cb>-1){
602
          mtTeL[mtb]=CB[MOL[mta].s[MOL[mta].t[mtb].Lo].Cb].Te;}
603 if (DEBUG>mtdebugflag) {
604 fprintf(DBG,"MOL[%d].s[%d].Ca (Hi) is %d",mta,MOL[mta].t[mtb].Hi,\
        MOL[mta].s[MOL[mta].t[mtb].Hi].Ca);
605
606 fprintf(DBG,"MOL[%d].s[%d].Cb (Hi) is
    %d\n",mta,MOL[mta].t[mtb].Hi,\
        MOL[mta].s[MOL[mta].t[mtb].Hi].Cb);
607
608 fprintf(DBG,"MOL[%d].s[%d].Ca (Lo) is %d",mta,MOL[mta].t[mtb].Lo,\
609
        MOL[mta].s[MOL[mta].t[mtb].Lo].Ca);
610 fprintf(DBG,"MOL[%d].s[%d].Cb (Lo) is
    %d\n",mta,MOL[mta].t[mtb].Lo,\
611
        MOL[mta].s[MOL[mta].t[mtb].Lo].Cb);
612 fprintf(DBG,"mtTeH[%d] is %f; mtTeL[%d} is %f\n",\
        mtb,mtTeH[mtb],mtb,mtTeL[mtb]);
613
614 fflush(DBG);
615 }
616
        }
617
      mtdone=1;
618
      if (MOL[mta].trans==1) {mtdone=0;}
619 if (DEBUG>mtdebugflag) {
620 fprintf(DBG, "Before sort. mtdone is %d\n ", mtdone);
621 fflush(DBG);
622 }
623 mtcounter=0;
624
      while(mtdone!=0){ /* this first loop orders the term energy for
       the high state */
625
        for(mtb=0;mtb<(MOL[mta].trans-1);mtb++){</pre>
626 if (DEBUG>mtdebugflag) {
```

```
627 fprintf(DBG,"First sort for-loop: mtb=%d, mtz[mtb]=%d, mt-
    TeH[%d] = %f n'', \
628
        mtb,mtz[mtb],mtb,mtTeH[mtb]);
629 fflush(DBG);
630 }
631
          mtsorth=mtsortdum=mtz[mtb];
632
          mtEmax=mtTeH[mtz[mtb]];
          for(mtc=mtb;mtc<(MOL[mta].trans);mtc++){</pre>
633
634
             if(mtTeH[mtz[mtc]]>mtEmax) {
               mtsorth=mtz[mtc];
635
               mtEmax=mtTeH[mtz[mtc]];
636
637
               }
638 if(DEBUG>mtdebugflag){
639 fprintf(DBG,"scan mtb=%d, mtc=%d, mtz[mtc]=%d, mtTeH[%d]=%f\n",\
        mtb,mtc,mtz[mtc],mtz[mtc],mtTeH[mtz[mtc]]);
640
641 fprintf(DBG,"\t\t mtsorth=%d, mtEmax=%f\n",mtsorth,mtEmax);
642 fflush(DBG);
643 }
644
             }
          mtz[mtb]=mtsorth;
645
646 if (DEBUG>mtdebugflag) {
647
      for(mtc=0;mtc<mtb+2;mtc++){</pre>
648 fprintf(DBG,"mtc=%d, mtz[mtc]=%d, mtTeH[%d]=%f\n",\
649
        mtc,mtz[mtc],mtz[mtc],mtTeH[mtz[mtc]]);
      }
650
651 fflush(DBG);
652 }
          for(mtc=(mtb+1);mtc<(MOL[mta].trans);mtc++){</pre>
653
654
             if(mtz[mtc]==mtsorth) {
655
               mtz[mtc]=mtsortdum;
656
               }
657 if (DEBUG>mtdebugflag) {
658 fprintf(DBG,"assign loop: mtb=%d, mtc=%d, mtz[mtb]=%d,
    mtz[mtc] = %d n'', \
659
        mtb,mtc,mtz[mtb],mtz[mtc]);
660 fflush(DBG);
661 }
662
             }
          }
663
664
        mtdone=0;
        for(mtb=0;mtb<(MOL[mta].trans-1);mtb++){</pre>
665
          if(mtTeH[mtz[mtb]]<mtTeH[mtz[mtb+1]]){</pre>
666
667
            mtdone=1;
668
             }
669 if (DEBUG>mtdebugflag) {
670 fprintf(DBG, "sort check: mtz[%d]=%d, mtTeH[%d]=%f,
    mtTeH[%d] = \%f n'', \
671
      mtb, mtz[mtb], mtz[mtb], mtTeH[mtz[mtb]], mtz[mtb+1], mt-
    TeH[mtz[mtb+1]]);
672 fflush(DBG);
673 }
674
          }
```

```
675 if(DEBUG>mtdebugflag){
676 fprintf(DBG,"sort check: mtz[%d]=%d, mtTeH[%d]=%f\n",\
677
      mtb,mtz[mtb],mtz[mtb],mtTeH[mtz[mtb]]);
678 fflush(DBG);
679 }
        }
680
681
      for(mtd=0;mtd<MOL[mta].trans-1;mtd++){ /* this loop orders the</pre>
       term energy for the low state */
682
        mtdone=1;
683
        mte=mtd;
684
        while(mtdone!=0){
          if(mtTeH[mtz[mte]]!=mtTeH[mtz[mte+1]]){mtdone=0;}
685
686
          else mte++;
687
          }
        for(mtb=mtd;mtb<mte;mtb++){</pre>
688
689 if(DEBUG>mtdebugflag){
690 fprintf(DBG,"low sort mtb=%d, mtz[mtb]=%d, mtTeL[%d]=%f\n",\
        mtb,mtz[mtb],mtb,mtTeL[mtb]);
691
692 fprintf(DBG,"\t\t mtz[mtb+1]=%d, mtTeL[%d]=%f\n",\
693
        mtz[mtb+1],mtb+1,mtTeL[mtb+1]);
694 fflush(DBG);
695 }
696
          mtsorth=mtsortdum=mtz[mtb];
697
          mtEmax=mtTeL[mtz[mtb]];
698
          for(mtc=mtb;mtc<=mte;mtc++){</pre>
            if(mtTeL[mtz[mtc]]>mtEmax) {
699
700
               mtsorth=mtz[mtc];
701
              mtEmax=mtTeL[mtz[mtc]];
702
               }
703 if (DEBUG>mtdebugflag) {
704 fprintf(DBG,"scan mtb=%d, mtc=%d, mtz[mtc]=%d, mtTeL[%d]=%f\n",\
        mtb,mtc,mtz[mtc],mtz[mtc],mtTeL[mtz[mtc]]);
705
706 fprintf(DBG,"\t\t mtsorth=%d, mtEmax=%f\n",mtsorth,mtEmax);
707 fflush(DBG);
708 }
             }
709
710
          mtz[mtb]=mtsorth;
711 if(DEBUG>mtdebugflag){
      for(mtc=mtd;mtc<mtb+2;mtc++){</pre>
712
713 fprintf(DBG,"mtc=%d, mtz[mtc]=%d, mtTeL[%d]=%f\n",\
714
        mtc,mtz[mtc],mtz[mtc],mtTeL[mtz[mtc]]);
      }
715
716 fflush(DBG);
717 }
718
          for(mtc=(mtb+1);mtc<=mte;mtc++){</pre>
719
            if(mtz[mtc]==mtsorth) {
720
              mtz[mtc]=mtsortdum;
721
               }
722 if(DEBUG>mtdebugflag){
723 fprintf(DBG, "assign loop: mtb=%d, mtc=%d, mtz[mtb]=%d,
    mtz[mtc] = %d n'', \
724
        mtb,mtc,mtz[mtb],mtz[mtc]);
```

```
725 fflush(DBG);
726 }
            }
727
728
          }
729
        mtdone=0;
        for(mtb=mtd;mtb<(mte);mtb++){</pre>
730
          if((mtTeH[mtz[mtb]]==mtTeH[mtz[mtb+1]])&&\
731
             (mtTeL[mtz[mtb]]<mtTeL[mtz[mtb+1]])){</pre>
732
            mtdone=1;
733
734
            }
735 if(DEBUG>mtdebugflag){
736 fprintf(DBG,"sort check low mtb=%d, mtz[mtb]=%d, mtTeH[%d]=%f, ",
        mtb,mtz[mtb],mtz[mtb],mtTeH[mtz[mtb]]);
737
738 fprintf(DBG,"mtTeL[%d]=%f\n",mtz[mtb],mtTeL[mtz[mtb]]);
739 fprintf(DBG,"\t\t mtz[mtb+1]=%d, mtTeL[%d]=%f\n",\
        mtz[mtb+1],mtz[mtb+1],mtTeL[mtz[mtb+1]]);
740
741 fflush(DBG);
742 }
743
          }
744 if(DEBUG>mtdebugflag){
745 fprintf(DBG,"sort check low mtb=%d, mtz[mtb]=%d, mtTeH[%d]=%f, ",
        mtb,mtz[mtb],mtz[mtb],mtTeH[mtz[mtb]]);
746
747 fprintf(DBG,"mtTeL[%d]=%f\n",mtz[mtb],mtTeL[mtz[mtb]]);
748 fflush(DBG);
749 }
750
        mtd=mte;
751
        }
752
      for(mtc=0;mtc<MOL[mta].trans;mtc++){</pre>
753
        mtb=mtz[mtc]; /* do transitions in order determined in the last
       100p */
     /* decide which type of transition it is and call that one */
     /* note: lines for transitions involving Case c and d are included
       here for "forward compatibility" -- they can't be used yet. But,
       having them in the code shouldn't cause a problem. */
754
        if(MOL[mta].s[MOL[mta].t[mtb].Hi].Ca>-1) mtcasesum=1;
755
        if(MOL[mta].s[MOL[mta].t[mtb].Hi].Cb>-1) mtcasesum=2;
        if(MOL[mta].s[MOL[mta].t[mtb].Hi].Cc>-1) mtcasesum=4;
756
        if(MOL[mta].s[MOL[mta].t[mtb].Hi].Cd>-1) mtcasesum=8;
757
758 if (DEBUG>mtdebugflag) {
759 fprintf(DBG,"mtcasenum for mtb=%d (mtz[%d]=%d) is %d\n",\
        mtb,mtc,mtz[mtc],mtcasesum);
760
761 fflush(DBG);
762 }
763
        if(MOL[mta].s[MOL[mta].t[mtb].Lo].Ca>-1) mtcasesum+=1;
        if(MOL[mta].s[MOL[mta].t[mtb].Lo].Cb>-1) mtcasesum+=2;
764
765
        if(MOL[mta].s[MOL[mta].t[mtb].Lo].Cc>-1) mtcasesum+=4;
        if(MOL[mta].s[MOL[mta].t[mtb].Lo].Cd>-1) mtcasesum+=8;
766
767 if(DEBUG>mtdebugflag){
768 fprintf(DBG,"mtcasenum for mtb=%d (mtz[%d]=%d) is %d\n",\
        mtb,mtc,mtz[mtc],mtcasesum);
769
770 fflush(DBG);
771 }
```

```
772
        switch(mtcasesum){
773
          case 2:
774 if (DEBUG>mtdebugflag) {
775 fprintf(DBG, "a_a transition called for\n\t MOL[%d].s[%d].Name = %s
    to ",\
776
      mta,(MOL[mta].t[mtb].Hi),MOL[mta].s[MOL[mta].t[mtb].Hi].Name);
777 fprintf(DBG,"MOL[%d].s[%d].Name = s\n'',\
      mta, (MOL[mta].t[mtb].Lo), MOL[mta].s[MOL[mta].t[mtb].Lo].Name);
778
779 fflush(DBG);
780 }
781
            a_a(mta,mtb);
782
            break:
783
          case 3:
784 if(DEBUG>mtdebugflag){
785 fprintf(DBG,"a_b transition called for\n\t MOL[%d].s[%d].Name = %s
    to ",\
      mta,(MOL[mta].t[mtb].Hi),MOL[mta].s[MOL[mta].t[mtb].Hi].Name);
786
787 fprintf(DBG,"MOL[%d].s[%d].Name = %s\n",\
788
      mta,(MOL[mta].t[mtb].Lo),MOL[mta].s[MOL[mta].t[mtb].Lo].Name);
789 fflush(DBG);
790 }
791
             /*a_b(mta,mtb);*/
792
            break;
793
          case 5:
794 if (DEBUG>mtdebugflag) {
795 fprintf(DBG,"a_c transition called for\n\t MOL[%d].s[%d].Name = %s
    to ",\
      mta,(MOL[mta].t[mtb].Hi),MOL[mta].s[MOL[mta].t[mtb].Hi].Name);
796
797 fprintf(DBG,"MOL[%d].s[%d].Name = %s\n",\
798
      mta,(MOL[mta].t[mtb].Lo),MOL[mta].s[MOL[mta].t[mtb].Lo].Name);
799 fflush(DBG);
800 }
801
             /*a_c(mta,mtb);*/
802
            break;
803
          case 9:
804 if (DEBUG>mtdebugflag) {
805 fprintf(DBG,"a_d transition called for\n\t MOL[%d].s[%d].Name = %s
    to ",\
806
      mta,(MOL[mta].t[mtb].Hi),MOL[mta].s[MOL[mta].t[mtb].Hi].Name);
807 fprintf(DBG,"MOL[%d].s[%d].Name = %s\n",\
      mta,(MOL[mta].t[mtb].Lo),MOL[mta].s[MOL[mta].t[mtb].Lo].Name);
808
809 fflush(DBG);
810 }
             /*a_d(mta,mtb);*/
811
812
            break;
813
          case 4:
814 if (DEBUG>mtdebugflag) {
815 fprintf(DBG,"b_b transition called for\n\t MOL[%d].s[%d].Name = %s
    to ",\
      mta,(MOL[mta].t[mtb].Hi),MOL[mta].s[MOL[mta].t[mtb].Hi].Name);
816
817 fprintf(DBG,"MOL[%d].s[%d].Name = %s\n",\
      mta,(MOL[mta].t[mtb].Lo),MOL[mta].s[MOL[mta].t[mtb].Lo].Name);
818
819 fprintf(DBG,"b_b transition called for\n\t MOL[%d].t[%d].Nhi = %s
    to ",\
```

mta,mtb,MOL[mta].t[mtb].Nhi); 820 821 fprintf(DBG,"b_b transition called for\n\t MOL[%d].t[%d].Nlo = %s \n",\ 822 mta,mtb,MOL[mta].t[mtb].Nlo); 823 fflush(DBG); 824 } 825 b_b(mta,mtb); 826 break; 827 case 6: 828 if(DEBUG>mtdebugflag){ 829 fprintf(DBG,"b_c transition called for\n\t MOL[%d].s[%d].Name = %s to ",\ mta,(MOL[mta].t[mtb].Hi),MOL[mta].s[MOL[mta].t[mtb].Hi].Name); 830 831 fprintf(DBG,"MOL[%d].s[%d].Name = %s\n",\ mta,(MOL[mta].t[mtb].Lo),MOL[mta].s[MOL[mta].t[mtb].Lo].Name); 832 833 fflush(DBG); 834 } 835 /*b_c(mta,mtb);*/ 836 break; 837 case 10: 838 if(DEBUG>mtdebugflag){ 839 fprintf(DBG,"b_d transition called for\n\t MOL[%d].s[%d].Name = %s to ",\ 840 mta,(MOL[mta].t[mtb].Hi),MOL[mta].s[MOL[mta].t[mtb].Hi].Name); 841 fprintf(DBG,"MOL[%d].s[%d].Name = $s\n",\$ mta,(MOL[mta].t[mtb].Lo),MOL[mta].s[MOL[mta].t[mtb].Lo].Name); 842 843 fflush(DBG); 844 } 845 /*b_d(mta,mtb);*/ 846 break; 847 case 8: 848 if(DEBUG>mtdebugflag){ 849 fprintf(DBG,"c_c transition called for\n\t MOL[%d].s[%d].Name = %s to ",\ 850 mta,(MOL[mta].t[mtb].Hi),MOL[mta].s[MOL[mta].t[mtb].Hi].Name); 851 fprintf(DBG,"MOL[%d].s[%d].Name = %s\n",\ 852 mta,(MOL[mta].t[mtb].Lo),MOL[mta].s[MOL[mta].t[mtb].Lo].Name); 853 fflush(DBG); 854 } 855 /*c_c(mta,mtb);*/ 856 break; 857 case 12: 858 if(DEBUG>mtdebugflag){ 859 fprintf(DBG,"c_d transition called for\n\t MOL[%d].s[%d].Name = %s to ",\ 860 mta,(MOL[mta].t[mtb].Hi),MOL[mta].s[MOL[mta].t[mtb].Hi].Name); 861 fprintf(DBG,"MOL[%d].s[%d].Name = %s\n",\ 862 mta, (MOL[mta].t[mtb].Lo), MOL[mta].s[MOL[mta].t[mtb].Lo].Name); 863 fflush(DBG); 864 } 865 /*c_d(mta,mtb);*/ 866 break; 867 case 16: 868 if (DEBUG>mtdebugflag) {

```
869 fprintf(DBG,"d_d transition called for\n\t MOL[%d].s[%d].Name = %s
     to ",\
       mta,(MOL[mta].t[mtb].Hi),MOL[mta].s[MOL[mta].t[mtb].Hi].Name);
 870
 871 fprintf(DBG,"MOL[%d].s[%d].Name = %s\n",\
 872
       mta,(MOL[mta].t[mtb].Lo),MOL[mta].s[MOL[mta].t[mtb].Lo].Name);
 873 fflush(DBG);
 874 }
 875
              /*d_d(mta,mtb);*/
 876
             break:
 877
           default:
 878 printf("Error in manage_transitions at mta=%d, mtb=%d. Exit-
     ing.\n",mta,mtb);
 879
             exit(1);
 880
           } /* close switch case */
 881
         } /* close loop over transitions */
 882
       free(mtz);
 883
       } /* close loop over molecules */
 884 return;
 885 }
      886
      /* This function calculates the RELATIVE Holn-London factor for all
        transitions (called from all transition functions). The equa-
        tions here are from Herzberg and expressed conveniently for emis-
        sion.
     For consistency with the currently written transition functions,
the integer for P is +1, for Q is 0 and for R is -1. Since Delta-Lambda
isn't used in those functions, they will be counted from the lower
state....*/
 887 double HL(int HB, double HJ, int HL, int HdL){
 888 double Hfac=0;
 889 if(HdL==0){ /* if Delta-Lambda =0 */
 890
       if(HB==+1){ /* P-branch */
 891
         Hfac=(HJ+1+HL)*(HJ+1-HL)/(2*HJ*HJ+3*HJ+1);
 892
         ł
 893
       if(HB==0){ /* Q-branch */
         if(HJ==0) Hfac=0;
 894
 895
         else Hfac=HL*HL/(HJ*(HJ+1));
 896
         }
 897
       if(HB==-1){ /* R-branch */
 898
         if(HJ==0) Hfac=0;
 899
         else Hfac=(HJ+HL)*(HJ-HL)/(HJ*(2*HJ+1));
 900
         }
       }
 901
 902 if (HdL==+1) { /* if the low state is one less than the high state */
       if(HB==+1){ /* P-branch */
 903
         Hfac=0.5*(HJ+1-HL)*(HJ+2-HL)/(2*HJ*HJ+3*HJ+1);
 904
 905
         }
 906
       if(HB==0){ /* Q-branch */
 907
         if(HJ==0) Hfac=0;
 908
         else Hfac=0.5*(HJ+HL)*(HJ+1-HL)/(HJ*(HJ+1));
```

```
}
909
910
      if(HB==-1){ /* R-branch */
911
        if(HJ==0) Hfac=0;
912
        else Hfac=0.5*(HJ+HL)*(HJ-1+HL)/(HJ*(2*HJ+1));
913
        }
      }
914
915 if (HdL==-1) { /* if the low state is one more than the high state */
      if(HB==+1){ /* P-branch */
916
917
        Hfac=0.5*(HJ+1+HL)*(HJ+2+HL)/(2*HJ*HJ+3*HJ+1);
918
        }
919
      if(HB==0){ /* Q-branch */
920
        if(HJ==0) Hfac=0;
        else Hfac=0.5*(HJ-HL)*(HJ+1+HL)/(HJ*(HJ+1));
921
922
        }
923
      if(HB==-1){ /* R-branch */
924
        if(HJ==0) Hfac=0;
925
        else Hfac=0.5*(HJ-HL)*(HJ-1-HL)/(HJ*(2*HJ+1));
926
        }
      }
927
928 if(HLswitch==0) return Hfac;
929 else return 1;
930 }
    931
    /* This function calculates transitions between Hund's Cases (a)
       and (a) */
932 void a_a(int aaa, int aab){
    /* indexes and dummy variables: */
933 int aac=0,aacc=0,aad=0,aadd=0,aae=0,aae=0,aaf=0,aaff=0,aag=0;
934 int aah=0,aaj=0,aafvl=0,aafvh=0,aafrnh=0,aafrcl=0,aafrch=0;
935 int aadum=0;
    /* for variables below: n="native"; c="cascade"; St="state";
       Ca="Case a"; v="vibrational"; num="number"; des="designation";
       hi="high"; lo="low"; O="Omega"; max="maximum"; pec="pseudo-
       Einstein coefficient"; comp="comparison"; a,b,<etc> are indexes
       */
    /* variables about vibrational levels */
936 int aahvnlo=0, aahvnnum=0, aahvclo=0, aahvcnum=0, aahivlo=0,
    aahivnum=0, aaHV=0;
937 int aalvnlo=0, aalvnnum=0, aalvclo=0, aalvcnum=0, aalovlo=0,
    aalovnum=0, aaLV=0;
    /* variables for info about the two states */
938 int aaStlo=0, aaSthi=0, aaStnlovlo=30, aaStnlovhi=0, aaSt-
    clovlo=30, aaStclovhi=0;
939 int aaCahi=0,aaCalo=0,aaJsh=0;
940 double aahipop=0, aatrprob=0, aavhpop=0, aaBvDv=0, aaDe=0,
    aavfcf=0, aavfcfr=0;
    /* variables about Omegas and J-values */
941 int aaOhnum=0, aaOlnum=0, aaOvhnum=0, aaOvlnum=0, aamaxhiJ=0;
942 double aahiOlo=0, aaloOlo=0, aamaxOmJ=0, aaOmJ=0, aaOlocurr=0, aaO-
    hicurr=0;
```

```
/* variables related to which v-v transitions need to be included */
943 double aapecnmax=0, aapecncompb=0, aapeccmax=0, aapecccompb=0;
    /* variables for the spectroscopic constants */
944 double aawexehi=0, aawexelo=0, aaTehi=0, aaTelo=0, aawehi=0,
    aawelo=0;
    /* some local pointers to use as abbreviations for the longer ad-
       dresses */
945 Case_a_stateinfo *aaHI, *aaLO;
946 Trans *aaT;
947 rotset *aaRh,*aaRl;
948 vset *aaVh;
    /* a few flags for various purposes */
949 int aaflg=0, aafrnhf=0, aafrchf=0;
    /* variables for creating and writing to output files */
950 char aafile[1000];
951 FILE *AAFILE;
    /* variables for calculating Holn-London factors */
952 int aaL=0, aaB=0, aadL=0;
953 double aaJ=0;
    /* Check FCF's for lower-state vibrational levels. Find highest and
       lowest lower-state levels that wil be populated (within the user-
       set lower precision limit). Check to see that there are energies
       for all those levels. If not, reallocate the state info to have
       room for the new levels. Don't add "native" population -- only
       cascade. (the added population will be ignored if it's a destina-
       tion state only) */
954 aaSthi=MOL[aaa].t[aab].Hi;
955 aaStlo=MOL[aaa].t[aab].Lo;
956 aaCahi=MOL[aaa].s[aaSthi].Ca;
957 aaCalo=MOL[aaa].s[aaStlo].Ca;
958 aaLO=&CA[aaCalo];
959 aaHI=&CA[aaCahi];
960 aahipop=MOL[aaa].s[aaSthi].pop; /* upper state relative population
       */
961 aahvnlo=MOL[aaa].s[aaSthi].v[0].vlo; /* user-specified low vib
       number */
962 aahvnnum=MOL[aaa].s[aaSthi].v[0].vnum; /* user-specified number
       of vib levels */
963 aahvclo=MOL[aaa].s[aaSthi].v[0].vclo; /* low vib level from cas-
       cade */
964 aahvcnum=MOL[aaa].s[aaSthi].v[0].vcnum; /* number of vib levels
       from cascade */
965 aalvnlo=MOL[aaa].s[aaStlo].v[0].vlo; /* user-specified low vib
       number */
966 aalvnnum=MOL[aaa].s[aaStlo].v[0].vnum; /* user-specified number
       of vib levels */
967 aalvclo=MOL[aaa].s[aaStlo].v[0].vclo; /* low vib level from cas-
       cade */
968 aalvcnum=MOL[aaa].s[aaStlo].v[0].vcnum; /* number of vib levels
       from cascade */
969 aaOhnum=CA[aaCahi].0;
970 aaOlnum=CA[aaCalo].0;
```

```
971 aaOvhnum=CA[aaCahi].0; /* these because the number of sets of v-v
        transitions */
 972 aaOvlnum=CA[aaCalo].0; /* might not be the same as the number of O-O
        trans's */
 973 aawexehi=aaHI[0].wexe;
 974 aawexelo=aaLO[0].wexe;
 975 aaTehi=aaHI[0].Te;
 976 aaTelo=aaLO[0].Te;
 977 aawehi=aaHI[0].we;
 978 aawelo=aaLO[0].we;
 979 if((aaHI[0].L-aaLO[0].L)==+1) aadL=+1;
 980 if((aaHI[0].L==aaLO[0].L)) aadL=+0;
 981 if((aaHI[0].L-aaLO[0].L)==-1) aadL=-1;
 982 aaL=aaHI[0].L;
 983 if(aadebugflag<DEBUG){
 984 fprintf(DBG,"aaSthi=%d, aaStlo=%d, aaCahi=%d, aaCalo=%d,
     aahipop=%f\n",\
 985
         aaSthi,aaStlo,aaCahi,aaCalo,aahipop);
 986 fprintf(DBG,"aahvnlo=%d, aahvnnum=%d, aahvclo=%d, aahvcnum=%d\n",\
 987
         aahvnlo,aahvnnum,aahvclo,aahvcnum);
 988 fprintf(DBG,"aalvnlo=%d, aalvnnum=%d, aalvclo=%d, aalvcnum=%d\n",\
         aalvnlo,aalvnnum,aalvclo,aalvcnum);
 989
 990 fprintf(DBG,"aaOhnum=%d, aaOlnum=%d, aaOvhnum=%d, aaOvlnum=%d\n",\
 991
         aaOhnum,aaOlnum,aaOvhnum,aaOvlnum);
 992 fflush(DBG);
 993 }
     /* There needs to be either (a) all specified Omegas or (b) all pos-
        sible Omegas. Find all possible if they weren't specified. Also,
        if they weren't specified, there will only be one set of v-v tran-
        sitions */
 994 if(aaOhnum==0){
 995
       aaOvhnum=1;
 996
       aaOhnum=(int)(2*CA[aaCahi].S+1.000000001); /* hail, hail, o
        great Numera / may we not have a truncation error :-) */
 997
       aahiOlo=(double)CA[aaCahi].L-CA[aaCahi].S;
 998 if(aadebugflag<DEBUG){
 999 fprintf(DBG,"aaOhnum is zero and aaOvhnum=%d, aaOhnum=%d, aahi-
     0lo=%f\n",\
1000
       aaOvhnum,aaOhnum,aahiOlo);
1001 fflush(DBG);
1002 }
1003
       if(aahiOlo<0){
1004
         aahiOlo*=-1; /* make a positive number for clarity */
         aahiOlo-=0.0000001; /* avoid truncation mishaps */
1005
1006
         aahiOlo=ceil(aaloOlo); /* get the next largest integer */
1007
         aaOhnum-=(int)aaloOlo; /* subtract that from 2S+1 */
         aahiOlo+=(double)CA[aaCahi].L-CA[aaCahi].S;
1008
1009 if(aadebugflag<DEBUG){
1010 fprintf(DBG, "aahiOlo<0 and aaOhnum=%d,
     aahiOlo=%f\n",aaOhnum,aahiOlo);
1011 fflush(DBG);
1012 }
1013
         }
```

```
1014
       }
1015 if(aaOlnum==0){
       aaOvlnum=1:
1016
1017
       aaOlnum=(int)(2*CA[aaCalo].S+1.000000001);
1018
       aaloOlo=(double)CA[aaCalo].L-CA[aaCalo].S;
1019 if(aadebugflag<DEBUG){
1020 fprintf(DBG,"aaOlnum is zero and aaOvlnum=%d, aaOlnum=%d,
     aaloOlo=%f\n",\
1021
        aaOvlnum,aaOlnum,aaloOlo);
1022 fflush(DBG);
1023 }
1024
      if(aaloOlo<0){
1025
         aaloOlo*=-1; /* make a positive number for clarity */
1026
         aaloOlo-=0.0000001; /* avoid truncation mishaps */
         aaloOlo=ceil(aaloOlo); /* get the next largest integer */
1027
1028
         aaOlnum-=(int)aaloOlo; /* subtract that from 2S+1 */
1029
         aaloOlo+=(double)CA[aaCalo].L-CA[aaCalo].S;
1030 if(aadebugflag<DEBUG){</pre>
1031 fprintf(DBG,"aaloOlo<0 and aaOlnum=%d,
     aaloOlo=%f\n",aaOlnum,aaloOlo);
1032 fflush(DBG);
1033 }
1034
         }
       }
1035
     /* find total number of sub-transitions (per v-v and also Omega-
        Omega) for this transition, then allocate memory for them */
1036 if((aahvnlo<aahvclo)||(aahvcnum==0)) aahivlo=aahvnlo;
1037 else aahivlo=aahvclo;
1038 if((aahvnlo+aahvnnum)>(aahvclo+aahvcnum)){
1039
       aahivnum=aahvnlo+aahvnnum-aahivlo;
1040
       }
1041 else{
       aahivnum=aahvclo+aahvcnum-aahivlo;
1042
1043
       }
1044 MOL[aaa].t[aab].vnh=aahivnum;
1045 MOL[aaa].t[aab].vhlo=aahivlo;
1046 if(aadebugflag<DEBUG){
1047 fprintf(DBG,"aahvnlo=%d, aahvclo=%d ",aahvnlo,aahvclo);
1048 fprintf(DBG,"(aahvnlo+aahvnnum)=%d, (aahvclo+aahvcnum)=%d\n",\
1049
         (aahvnlo+aahvnnum),(aahvclo+aahvcnum));
1050 fprintf(DBG,"aahivnum=%d, aahivlo=%d\n",aahivnum,aahivlo);
1051 fprintf(DBG, "aahivnum is %d, aahivlo is
     %d\n",MOL[aaa].t[aab].vnh,\
1052
         MOL[aaa].t[aab].vhlo);
1053 fflush(DBG);
1054 }
     /* loop to find maximum PEC (=FCF times FREQ^DETECTTYPE) */
1055 for(aac=0;aac<aaOvhnum;aac++){
1056 for(aad=0;aad<aaOvlnum;aad++){ /* for user-specified populations
        */
1057
       aaHV=aahvnnum+aahvnlo;
1058 if(aadebugflag<DEBUG){
```

1059 fprintf(DBG,"aac=%d, aad=%d, aaHV=%d\n",aac,aad,aaHV); 1060 fflush(DBG); 1061 } 1062 for(aae=aahvnlo;aae<aaHV;aae++){ /* find max pec for native v's</pre> */ 1063 for(aaf=0;aaf<30;aaf++){</pre> 1064 if(MOL[aaa].t[aab].v[aaee].fcfn[aaf]>aapecnmax){ aapecnmax=MOL[aaa].t[aab].v[aaee].fcfn[aaf]; 1065 1066 } 1067 if(aadebugflag<(DEBUG-1)){</pre> 1068 fprintf(DBG,"aapecnmax=%11.4e\n",aapecnmax); 1069 fflush(DBG); 1070 } 1071 } 1072 } 1073 aaHV=aahvcnum+aahvclo; 1074 if(aadebugflag<(DEBUG-1)){</pre> 1075 fprintf(DBG,"Out of find-max-pec for native v's. aaHV=%d\n",aaHV); 1076 fflush(DBG); 1077 } for(aae=aahvclo;aae<aaHV;aae++){ /* find max pec for cascade v's</pre> 1078 */ 1079 for(aaf=0;aaf<30;aaf++){</pre> 1080 if(MOL[aaa].t[aab].v[aaee].fcfc[aaf]>aapeccmax){ 1081 aapeccmax=MOL[aaa].t[aab].v[aaee].fcfc[aaf]; } 1082 1083 if(aadebugflag<(DEBUG-1)){</pre> 1084 fprintf(DBG, "aapeccmax=%11.4e\n", aapeccmax); 1085 fflush(DBG); 1086 } 1087 } } 1088 } 1089 1090 } /* find minimum and maximum lower-state v's with PEC's that are above the low-intensity cutoff (JKCUT) */ 1091 for(aac=0;aac<aaOvhnum;aac++){</pre> 1092 for(aad=0;aad<aa0vlnum;aad++){ /* for user-specified populations */ 1093 aaHV=aahvnnum+aahvnlo; 1094 if(aadebugflag<DEBUG){ 1095 fprintf(DBG,"In cut-off loop: aac=%d, aad=%d, aaHV=%d\n",aac,aad,aaHV); 1096 fflush(DBG); 1097 } 1098 for(aae=aahvnlo;aae<aaHV;aae++){ /* for native populations */</pre> 1099 aaee=aac*aaOvlnum*30+aad*30+aae; 1100 aaf=0; 1101 if(aadebugflag<(DEBUG-1)){</pre> 1102 fprintf(DBG,"aaee=%d\n",aaee); 1103 fflush(DBG); 1104 } 1105 while(aaflg==0){ 1106 aapecncompb=MOL[aaa].t[aab].v[aaee].fcfn[aaf]/JKCUT;

```
1107
            if(aapecncompb<aapecnmax) aadum=aaf;
1108
            else aaflg=1;
1109
            aaf++;
            }
1110
1111 if(aadebugflag<(DEBUG-1)){</pre>
1112 fprintf(DBG,"aapecncompb=%11.4e, aaf=%d\n",aapecncompb,aaf);
1113 fflush(DBG);
1114 }
1115
         if(aadum<aaStnlovlo) aaStnlovlo=aadum;</pre>
1116
         aaf=29;
1117
         aaflg=0;
1118 if(aadebugflag<(DEBUG-1)){</pre>
1119 fflush(DBG);
1120 }
1121
         while(aaflg==0){
            aapecncompb=MOL[aaa].t[aab].v[aaee].fcfn[aaf]/JKCUT;
1122
1123
            if(aapecncompb<aapecnmax) aadum=aaf;
1124
            else aaflg=1;
1125
            aaf--;
1126
            }
1127 if(aadebugflag<(DEBUG-1)){</pre>
1128 fprintf(DBG, "aapecncompb=%11.4e, aaf=%d,
     aadum=%d\n",aapecncompb,aaf,aadum);
1129 fflush(DBG);
1130 }
1131
         if(aadum>aaStnlovhi) aaStnlovhi=aadum;
1132
         }
1133
       aaHV=aahvcnum+aahvclo;
1134 if(aadebugflag<(DEBUG-1)){</pre>
1135 fprintf(DBG,"out of native population cutoff. aaHV=%d\n",aaHV);
1136 fflush(DBG);
1137 }
1138
       for(aae=aahvclo;aae<aaHV;aae++){ /* for cascade populations */</pre>
1139
         aaee=aac*aaOvlnum*30+aad*30+aae;
1140
         aaf=0;
1141 if(aadebugflag<(DEBUG-1)){</pre>
1142 fflush(DBG);
1143 }
1144
         while(aaflg==0){
            aapecccompb=MOL[aaa].t[aab].v[aaee].fcfc[aaf]/JKCUT;
1145
1146
            if(aapecccompb<aapeccmax) aadum=aaf;</pre>
1147
            else aaflg=1;
1148
            aaf++;
            }
1149
1150 if(aadebugflag<(DEBUG-1)){</pre>
1151 fprintf(DBG,"aapecccompb=%11.4e, aaf=%d,
     aadum=%d\n",aapecccompb,aaf,aadum);
1152 fflush(DBG);
1153 }
1154
         if(aadum<aaStclovlo) aaStclovlo=aadum;
1155
         aaf=29;
1156
         aaflg=0;
1157 if(aadebugflag<(DEBUG-1)){</pre>
1158 fflush(DBG);
```

```
1159 }
1160
         while(aaflg==0){
           aapecccompb=MOL[aaa].t[aab].v[aaee].fcfc[aaf]/JKCUT;
1161
1162
           if(aapecccompb<aapeccmax) aadum=aaf;
1163
           else aaflg=1;
1164
           aaf--;
           }
1165
1166 if(aadebugflag<(DEBUG-1)){</pre>
1167 fprintf(DBG,"aapecccompb=%11.4e, aaf=%d,
     aadum=%d\n",aapecccompb,aaf,aadum);
1168 fflush(DBG);
1169 }
1170
         if(aadum>aaStclovhi) aaStclovhi=aadum;
1171
         }
       }
1172
       }
1173
1174 if(aadebugflag<(DEBUG-1)){</pre>
1175 fprintf(DBG,"out of cutoff loop\n\n");
1176 fflush(DBG);
1177 }
     /* determine the lowest necessary destination-state vib level and
        the number of destination-state vibration levels */
1178 if((aaStnlovlo)<(aaStclovlo)) aalovlo=aaStnlovlo;
1179 else aalovlo=aaStclovlo;
1180 if((aaStnlovhi)>(aaStclovhi)) aalovnum=aaStnlovhi+1-aalovlo;
1181 else aalovnum=aaStclovhi+1-aalovlo;
1182 MOL[aaa].t[aab].vnl=aalovnum;
1183 MOL[aaa].t[aab].vllo=aalovlo;
     /* allocate memory for the simsets in the transition structure */
1184 MOL[aaa].t[aab].nS=aaOhnum*aaOlnum*aahivnum*aalovnum;
1185 MOL[aaa].t[aab].S = (simset*) calloc(MOL[aaa].t[aab].nS,
     sizeof(simset));
1186 MOL[aaa].t[aab].fS=(int*)calloc(MOL[aaa].t[aab].nS,sizeof(int));
1187 if(aadebugflag<DEBUG){</pre>
1188 fprintf(DBG,"MOL[%d].t[%d].vnl=%d, MOL[%d].t[%d].vllo=%d
     ",aaa,aab,\
1189
         MOL[aaa].t[aab].vnl,aaa,aab,MOL[aaa].t[aab].vllo);
1190 fprintf(DBG,"MOL[%d].t[%d].nS=%d\n",aaa,aab,MOL[aaa].t[aab].nS);
1191 fflush(DBG);
1192 }
     /* get maximum J value present in any of the high-state Omegas */
1193 for(aae=0;aae<aaOhnum;aae++){
1194 if(aadebugflag<DEBUG){
1195 fprintf(DBG,"At top of J-value loop. aae=%d
     aaLO[0].0=%d\n",aae,aaLO[0].0);
1196 fflush(DBG);
1197 }
1198
       aaHV=aahvnnum+aahvnlo;
       if(aaLO[0].0!=0){ /* if Omegas are user-defined */
1199
         aaOlocurr=aaLO[0].10[aae];
1200
1201 if(aadebugflag<DEBUG){
1202 fprintf(DBG,"aaLO[0].0!=0; aaOlocurr=%f\n",aaLO[0].10[aae]);
```

```
1203 fflush(DBG);
1204 }
1205
         }
1206
       else{
1207
         aaOlocurr=aaloOlo + aae;
1208 if(aadebugflag<DEBUG){
1209 fprintf(DBG,"else, and aaOlocurr=%f\n",aaOlocurr);
1210 fflush(DBG);
1211 }
1212
         }
       for(aaf=aahvnlo;aaf<aaHV;aaf++){ /* check native populations */</pre>
1213
1214 if(aadebugflag<(DEBUG)){
1215 fprintf(DBG,"In native population loop \n");
1216 fflush(DBG);
1217 }
1218
         aaj=MOL[aaa].s[aaSthi].r[aaf-aahvnlo].j;
1219
         aaOmJ=aaOlocurr+aaj-1;
1220
         if(aaj>aamaxhiJ){
1221
           aamaxhiJ=aaj;
1222
           }
1223
         if(aaOmJ>aamaxOmJ){
1224
           aamaxOmJ=aaOmJ;
1225
           }
         }
1226
1227 if(aadebugflag<(DEBUG)){
1228 fprintf(DBG,"Native: aae=%d, aaf=%d,
     aamaxhiJ=%d\n",aae,aaf,aamaxhiJ);
1229 fflush(DBG);
1230 }
1231
       aaHV=aahvcnum+aahvclo;
1232
       for(aaf=aahvclo;aaf<aaHV;aaf++){ /* check cascade populations */</pre>
1233
         aaj=MOL[aaa].s[aaSthi].rc[aaf-aahvclo].j;
1234
         aaOmJ=aaOlocurr+aaj-1;
1235
         if(aaj>aamaxhiJ){
1236
           aamaxhiJ=aaj;
1237
           }
1238
         if(aaOmJ>aamaxOmJ){
1239
           aamaxOmJ=aaOmJ;
1240
           }
         }
1241
1242 if(aadebugflag<(DEBUG)){
1243 fprintf(DBG, "Cascade: aae=%d, aaf=%d,
     aamaxhiJ=%d\n",aae,aaf,aamaxhiJ);
1244 fflush(DBG);
1245 }
1246
       }
```

/* loop through the list of low-state Omegas first. See if all the needed destination-state v's are calculated. Check also that enough J's are calculated. Calculate any states that aren't already done. The following method isn't efficient. It will calculate more lower-state energy levels than are actually needed. But, this shouldn't be a problem other than having a few unnecessary calculations happen. */

1247 aamaxhiJ++; /* because of the Delta-J = +1 possibility */ 1248 aamaxOmJ++; /* '' */ 1249 if(aadebugflag<(DEBUG)){ 1250 fprintf(DBG, "Before new calculations loop aamaxhiJ=%d\n",aamaxhiJ); 1251 fflush(DBG); 1252 } /* Calculate any newly needed energy levels. */ /* loop through each lower Omega */ 1253 for(aad=0;aad<aa0lnum;aad++){ /* loop through each lower-state Omega */ 1254 if(aaOvlnum==1) aaee=0; /* Only one vset if auto-Omega */ 1255 else aaee=aad; if(aaLO[0].0!=0){ /* if Omegas are user-defined */ 1256 aaOlocurr=aaLO[0].10[aad]; 1257 1258 if(aadebugflag<(DEBUG)){</pre> 1259 fprintf(DBG, "Omegas User-defined and aaOlocurr=%15.8e.\n",aaOlocurr); 1260 fflush(DBG); 1261 } 1262 } 1263 else{ aaOlocurr=aaloOlo + aad; 1264 1265 if(aadebugflag<(DEBUG)){ 1266 fprintf(DBG,"Omegas Not user-defined and aaOlocurr=%15.8e.\n",aaOlocurr); 1267 fprintf(DBG,"aaloOlo=%15.8e; aaOlnum=%d\n",aaloOlo,aaOlnum); 1268 fflush(DBG); 1269 } 1270 } 1271 aaLV=aalovlo+aalovnum; 1272 if(aadebugflag<(DEBUG)){ 1273 fprintf(DBG,"aad=%d, aaee=%d, aaLV=%d\n",aad,aaee,aaLV); 1274 fflush(DBG); 1275 } 1276 for(aaf=aalovlo;aaf<aaLV;aaf++){ /* check low-state v-levels */</pre> 1277 aaff=aad*30+aaf; /* Index for the array of rc rotational sets */ 1278 if(aadebugflag<(DEBUG)){ 1279 fprintf(DBG,"aaf=%d, aaff=%d, aadum=%d, ",aaf,aaff,aadum); 1280 fflush(DBG); 1281 } 1282 if(MOL[aaa].s[aaStlo].rc[aaff].jc==0){ /* this v has never been calculated, so call a function to calculate it. */ if(aaLO[0].we!=0){ 1283 1284 aaDe=4*pow(aaLO[0].Be,3)/(aaLO[0].we*aaLO[0].we); 1285 aaBvDv=(aaLO[0].Be-aaLO[0].ae*(aaf+0.5))/\ 1286 (2*(aaDe+aaLO[0].beta*(aaf+0.5))); 1287 MOL[aaa].s[aaStlo].rc[aaff].Jdissoc=aaL0[0].sflag+\ 1288 floor((sqrt(1+4*aaBvDv)-1)/2); } 1289 1290 else MOL[aaa].s[aaStlo].rc[aaff].Jdissoc=RAND_MAX; 1291 if(aamaxhiJ<MOL[aaa].s[aaStlo].rc[aaff].Jdissoc){</pre> 1292 case_a_cascade(&MOL[aaa].s[aaStlo].rc[aaff],\

```
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```

```
1293
               aaCalo,aaOlocurr,aaf,0,aamaxhiJ);
             }
1294
1295
           else{
1296
             case_a_cascade(&MOL[aaa].s[aaStlo].rc[aaff],\
1297
               aaCalo,aaOlocurr,aaf,0,\
1298
           (int)(MOL[aaa].s[aaStlo].rc[aaff].Jdissoc+1));
1299
             }
1300 if(aadebugflag<(DEBUG)){
1301 fprintf(DBG,"just called case_a_cascade, v never calc'd\n");
1302 fprintf(DBG,"aaDe=%12.6e, aaBvDv=%12.6e, ",aaDe,aaBvDv);
1303 fprintf(DBG, "MOL[%d].s[%d].rc[%d].Jdissoc = %12.6e\n", aaa,
     aaStlo, aaff, \
1304
         MOL[aaa].s[aaStlo].rc[aaff].Jdissoc);
1305 fflush(DBG);
1306 fprintf(DBG,"jwas zero; just called cascade \n");
1307 fprintf(DBG, "MOL[%d].s[%d].rc[%d].jc=%d\n",aaa,aaStlo,aaff,\
         MOL[aaa].s[aaStlo].rc[aaff].jc);
1308
1309 fflush(DBG);
1310 }
1311
           }
1312
         else{
     /* this v has been calculated. See if enough J's are calculated */
           if(MOL[aaa].s[aaStlo].rc[aaff].jc<aamaxhiJ){</pre>
1313
1314 if(aadebugflag<(DEBUG)){
1315 fprintf(DBG,"j<maxJ; about to call cascade \n");
1316 fprintf(DBG,"MOL[%d].s[%d].rc[%d].jc=%d\n",aaa,aaStlo,aaff,\
         MOL[aaa].s[aaStlo].rc[aaff].jc);
1317
1318 fflush(DBG);
1319 }
1320
           if(aamaxhiJ<MOL[aaa].s[aaStlo].rc[aaff].Jdissoc){</pre>
1321
             case_a_cascade(&MOL[aaa].s[aaStlo].rc[aaff],\
1322
               aaCalo, aaOlocurr, aaf, \
1323
             MOL[aaa].s[aaStlo].rc[aaff].jc,aamaxhiJ);
1324
             }
1325
           else{
1326
             case_a_cascade(&MOL[aaa].s[aaStlo].rc[aaff],\
1327
         aaCalo,aaOlocurr,aaf,MOL[aaa].s[aaStlo].rc[aaff].jc,\
1328
           (int)(MOL[aaa].s[aaStlo].rc[aaff].Jdissoc+1));
1329
             }
1330 if(aadebugflag<(DEBUG)){
1331 fprintf(DBG,"j was <maxJ; just called cascade \n");</pre>
1332 fprintf(DBG,"MOL[%d].s[%d].rc[%d].jc=%d\n",aaa,aaStlo,aaff,\
         MOL[aaa].s[aaStlo].rc[aaff].jc);
1333
1334 fflush(DBG);
1335 fprintf(DBG,"just called case_a_cascade for cascade only\n");
1336 fflush(DBG);
1337 }
1338
             }
           }
1339
         }
1340
     /* Reset values of vclo and vcnum for the next transition */
1341
         MOL[aaa].s[aaStlo].v[aaee].vclo=aalovlo;
1342
         MOL[aaa].s[aaStlo].v[aaee].vcnum=aalovnum;
1343 if(aadebugflag<(DEBUG)){
```

```
1344 fprintf(DBG,"MOL[%d].s[%d].v[%d].vclo=%d ",aaa,aaStlo,aaee,\
1345
         MOL[aaa].s[aaStlo].v[aaee].vclo);
1346 fprintf(DBG,"MOL[%d].s[%d].v[%d].vcnum=%d\n",aaa,aaStlo,aaee,\
         MOL[aaa].s[aaStlo].v[aaee].vcnum);
1347
1348 fflush(DBG);
1349 }
1350
      }
1351
     /* Check whether larger selection rules (Lambda, S, +/- in Sigma
        states) are * violated. If they are, write a note to that effect
        to the DBG file. */
1352 if(aadebugflag<(DEBUG-1)){</pre>
1353 fprintf(DBG,"aaHI[0].L=%d, aaLO[0].L=%d\n",aaHI[0].L,aaLO[0].L);
1354 fflush(DBG);
1355 }
1356 if((abs(aaHI[0].L-aaLO[0].L))>1){
1357
       fprintf(PAR, "\nTRANSITION OMITTED!!! (see below)\n\n");
       fprintf(PAR, "Normal selection rule violated for Delta-");
1358
1359
       fprintf(PAR,"Lambda=0,+/-1 for\n\tTransition %s-->%s\n",\
1360
           MOL[aaa].t[aab].Nhi,MOL[aaa].t[aab].Nlo);
1361
       fprintf(PAR,"\tThis program doesn't understand that.\n\n");
1362 if(aadebugflag<(DEBUG)){
1363 fprintf(DBG, "Delta-L selection rule violated.\n");
1364 fflush(DBG);
1365 }
1366
      return;
1367
       ł
1368 if((fabs(aaHI[0].S-aaLO[0].S))>0.01){ /* <<< an overkill against
        round-off */
       fprintf(PAR, "WARNING!!! Normal selection rule violated for
1369
     Delta-");
1370
       fprintf(PAR,"S=0 for\n\tTransition %s-->%s\n",\
1371
           MOL[aaa].t[aab].Nhi,MOL[aaa].t[aab].Nlo);
1372
       fprintf(PAR,"\tThis is non-fatal; only a warning.\n");
1373 if(aadebugflag<(DEBUG)){
1374 fprintf(DBG, "Delta-S selection rule violated\n");
1375 fflush(DBG);
1376 }
1377
       }
     /* Start with the largest Omega of the high state (in case someone
```

writes in cascade between different Omegas). Check for presence of lower-state Omegas to which to transit. If present, transit, if not move on to the next higher Omega.

If Delta-spinSigma is not zero (true if, for example, a pi-pi transition occurs and one Omega is 2 and the other is 1), flag this set of transitions to be left out of simulation and placed in separate file. At the moment I don't recall whether that separate file actually gets written. */

```
1378 aaT=&MOL[aaa].t[aab]; /* an abbreviation */
```

```
1379 if(aadebugflag<DEBUG){</pre>
```

```
1380 fprintf(DBG,"aaT.Nhi=%s, aaT.Nlo=%s\n",aaT[0].Nhi,aaT[0].Nlo);
```

```
1381 fprintf(DBG,"High: MOL[%d].s[%d].v[0].vclo=%d ",aaa,aaSthi,
```

```
1382 MOL[aaa].s[aaSthi].v[0].vclo);
```

```
1383 fprintf(DBG,"High: MOL[%d].s[%d].v[0].vcnum=%d\n",aaa,aaSthi,\
         MOL[aaa].s[aaSthi].v[0].vcnum);
1384
1385 fprintf(DBG,"High: MOL[%d].s[%d].v[0].vlo=%d ",aaa,aaSthi,\
         MOL[aaa].s[aaSthi].v[0].vlo);
1386
1387 fprintf(DBG,"High: MOL[%d].s[%d].v[0].vnum=%d\n",aaa,aaSthi,\
         MOL[aaa].s[aaSthi].v[0].vnum);
1388
1389 fprintf(DBG,"aahivnum=%d; aalovnum=%d; aaOhnum=%d, aaOlnum=%d\n",\
1390
         aahivnum,aalovnum,aaOhnum,aaOlnum);
1391 fflush(DBG);
1392 }
1393 for(aac=(aaOhnum-1);aac>=0;aac--){ /* down through high-state
        Omegas */
1394
       if(aaHI[0].0!=0){ /* if Omegas are user-defined */
         aaOhicurr=aaHI[0].10[aac];
1395
1396
         aafvh=aac*aahivnum;
         aaVh=&MOL[aaa].s[aaSthi].v[aac];
1397
1398
         aatrprob=aaT[0].P[aac];
1399
         }
       else{
1400
1401
         aaOhicurr=aahiOlo + aac;
1402
         aafvh=0;
         aaVh=&MOL[aaa].s[aaSthi].v[0];
1403
1404
         aatrprob=aaT[0].P[0];
1405
         }
1406
       aafrnh=aac*aahvnnum; /* indexes for high state rotsets */
       aacc=aac*aaOlnum*aahivnum*aalovnum; /* posn. in 4 dimensions */
1407
1408 if(aadebugflag<DEBUG){
1409 fprintf(DBG,"aac=%d, aafvh=%d, aatrprob=%f ",\
1410
         aac,aafvh,aatrprob);
1411 fprintf(DBG,"aafrnh=%d, aafrch=%d,
     aacc=%d\n",aafrnh,aafrch,aacc);
1412 fprintf(DBG,"aaOhicurr=%11.4e\n",aaOhicurr);
1413 fflush(DBG);
1414 }
1415 for(aad=(aaOlnum-1);aad>=0;aad--){ /* down through low-state
        Omegas */
1416
       aafrnh+=aahivnum;
1417
       if(aaLO[0].0!=0){ /* if Omegas are user-defined */
1418
         aaOlocurr=aaLO[0].10[aad];
1419
         aafvl=aad*aalovnum;
1420
         }
1421
       else{
1422
         aaOlocurr=aaloOlo + aad;
1423
         aafvl=0;
1424
         }
1425
       aaJsh=(int)(aaOhicurr-aaOlocurr+0.0000001); /* shift in J index-
        ing due to difference in Omegas */
1426
       if((fabs(aaOhicurr-aaOlocurr))>1.000000001) aaflg=1;
1427
       else aaflg=0;
       aadd=aacc+aad*aahivnum*aalovnum; /* posn. in remaining 3 dimen-
1428
        sions */
1429 if(aadebugflag<DEBUG){
1430 fprintf(DBG,"aad=%d, aafrcl=%d, aadd=%d\n",aad,aafrcl,aadd);
1431 fprintf(DBG,"aaOlocurr=%11.3e\n",aaOlocurr);
```

```
1432 fflush(DBG);
1433 }
1434
       for(aae=(aahivlo+aahivnum-1);aae>=aahivlo;aae--){ /*high-state
        viblev*/
1435
         aaee=aadd+(aae-aahivlo)*aalovnum; /* posn. in remaining 2 di-
        mensions */
1436
         aafrnh--;
     /* these flags (aafrnhf and aafrchf) tell if this high vib state is
        natively populated, populated by cascade, or both. They will be
        used later */
1437
         if((aae>=aahvnlo)&&(aae<(aahvnlo+aahvnnum))){
1438
           aafrnhf=0:
1439
           aavhpop=aaVh[0].p[aae-aahvnlo];
1440
           }
1441
         else aafrnhf=-1;
1442
         if((aae>=aahvclo)&&(aae<(aahvclo+aahvcnum))){
1443
           aafrchf=0;
1444
           }
1445
         else aafrchf=-1;
1446 if(aadebugflag<DEBUG){
1447 fprintf(DBG,"aafrnhf=%d, aafrnh=%d, aavhpop=%f, aafrchf=%d\n",\
1448
         aafrnhf,aafrnh,aavhpop,aafrchf);
1449 fprintf(DBG,"aae=%d, aaee=%d\n",aae,aaee);
1450 fprintf(DBG,"aahivlo=%d, aahivnum=%d, aafrnh=%d, aafrch=%d\n",\
1451
         aahivlo,aahivnum,aafrnh,aafrch);
1452 fflush(DBG);
1453 }
1454
       aafrcl=aad*30+aalovnum; /* indexes for low state rotsets */
1455
       for(aaf=(aalovlo+aalovnum-1);aaf>=aalovlo;aaf--){ /*low-state
        viblev*/
1456 if(aadebugflag<DEBUG){
1457 fprintf(DBG,"aaf=%d, aalovlo=%d, aalovnum=%d
     \n",aaf,aalovlo,aalovnum);
1458 fflush(DBG);
1459 }
     /* Right now, all Omegas get the same set of FCF's. */
         aaff=aaee+aaf-aalovlo; /* posn. in final dimension */
1460
1461
         aafrcl--; /* position in low-state cascade rotset */
1462
         aaT[0].fS[aaff]=aaflg;
         aavfcf=aaT[0].v[aae].fcfn[aaf];
1463
1464
         if(aavfcf!=0){aavfcfr=aaT[0].v[aae].fcfc[aaf]/aavfcf;}
1465
         if((aaOhicurr==0)&&(aaOlocurr==0))
     aaT[0].S[aaff].n=2*aamaxhiJ;
1466
         else aaT[0].S[aaff].n=3*aamaxhiJ;
1467
         aaT[0].S[aaff].f=\
1468
           (double*)calloc(aaT[0].S[aaff].n,sizeof(double));
1469
         aaT[0].S[aaff].ni=\
1470
           (double*)calloc(aaT[0].S[aaff].n,sizeof(double));
1471
         aaT[0].S[aaff].ci=\
           (double*)calloc(aaT[0].S[aaff].n,sizeof(double));
1472
         aaRl=&MOL[aaa].s[aaStlo].rc[aafrcl];
1473
1474 if(aadebugflag<DEBUG){
1475 fprintf(DBG,"aaff=%d, aafrcl=%d, aaT[0].S[aaff].n=%d\n",\
1476
         aaff,aafrcl,aaT[0].S[aaff].n);
```

- 1477 fflush(DBG); 1478 } /* start with highest J value (same reason as before), and loop down looking for lower J's to which to transit. assign intensities. If both states are Omega=0, then assign zero intensity to transitions for J=0<->J=0. */if(aafrnhf==0){ /* if this v is natively populated.*/ 1479 1480 sprintf(aafile,"%s_molecules/%s/%s-%.1f--%s-%.1f_v%d-v%d_NAT.dat",\ 1481 PREF, MOL[aaa].Mol, aaT[0].Nhi, aaOhicurr, \ 1482 aaT[0].Nlo,aaOlocurr,aae,aaf); 1483 AAFILE=fopen(aafile,"w"); 1484 if(AAFILE==NULL){ 1485 printf("Error opening transition sub-file %s. Exiting.\n",aafile); 1486 exit(1);1487 } 1488 fprintf(AAFILE,"# File created by %s.\n# File contains ",PRO-GRAM_NAME); 1489 if((aaOhicurr==O)&&(aaOlocurr==O)) fprintf(AAFILE,"P and R"); 1490 else fprintf(AAFILE, "P, Q and R"); 1491 fprintf(AAFILE," branches from the simulation titled $s\n", PREF$; 1492 fprintf(AAFILE, "# THESE INTENSITIES ARE DUE TO USER-SPECIFIED POPU-LATIONS"); 1493 fprintf(AAFILE," ONLY -- NO CASCADE\n"); 1494 fprintf(AAFILE, "# Transition is Hund's Case (a) to Hund's Case (a).\n"); 1495 fprintf(AAFILE,"# Molecule %s, \tHigh state: %s, Omega=%.1f, v=%d\n",\ 1496 MOL[aaa].Mol,aaT[0].Nhi,aaOhicurr,aae); 1497 fprintf(AAFILE,"#\t\tLow state: %s, Omega=%.1f, v=%d\n# Columns are: ",\ 1498 aaT[0].Nlo,aaOlocurr,aaf); 1499 if((aaOhicurr==0)&&(aaOlocurr==0)){ 1500 fprintf(AAFILE,"J_hi P(J_hi+1)_v P_i R(J_hi-1)_v R_i\n#\n"); 1501 } 1502 else fprintf(AAFILE,"J_hi P(Jhi+1)_v P_i Q(J_hi+0)_v Q_i R(J_hi-1)_v $R_i n\#(n");$ 1503 aaRh=&MOL[aaa].s[aaSthi].r[aafrnh]; 1504 if((aamaxhiJ)<MOL[aaa].s[aaSthi].r[aafrnh].j){</pre> 1505 aaj=aamaxhiJ-1; 1506 } 1507 else aaj=MOL[aaa].s[aaSthi].r[aafrnh].j-1; 1508 if((aaR1[0].Jdissoc-aaOlocurr)<(aaj-1)){ 1509 fprintf(PAR,"\nWARNING!! State %s(%.1f) of molecule %s has significant ",\ MOL[aaa].s[aaSthi].Name,aaOhicurr,MOL[aaa].Mol); 1510 1511 fprintf(PAR, "rotational population at level %.1f\n",aaRh[0].J[aaj-1]); 1512 fprintf(PAR,"\tBut lower state %s(%.1f) dissociates at level %.1f\n",\ MOL[aaa].s[aaStlo].Name,aaOlocurr,aaRl[0].Jdissoc); 1513
- 1514 fprintf(PAR,"It is likely that the bound upper state is transiting to (an)");

```
1515 fprintf(PAR," unbound lower state(s).\n");
1516 fprintf(PAR, "Look for continuum emissions trailing off to the low-
     energy ");
1517 fprintf(PAR, "end of the v(hi)=%d to v(lo)=%d\nband in the real
     ",aae,aaf);
1518 fprintf(PAR, "spectrum (not the simulated one)\nCurrently, this pro-
     gram will");
1519 fprintf(PAR, " not simulate bound-->unbound spectra.\n\n");
1520
             aaj=(int)(aaRl[0].Jdissoc-aaOlocurr);
1521
             }
1522 if(aadebugflag<DEBUG){
1523 fprintf(DBG,"aafrnh=%d, aaj=%d\n",aafrnh,aaj);
1524 fprintf(DBG,"MOL[%d].s[%d].r[%d].j=%d\n",aaa,aaSthi,aafrnh,\
1525
         MOL[aaa].s[aaSthi].r[aafrnh].j);
1526 fflush(DBG);
1527 }
1528
           for(aag=(aaj-1);aag>=0;aag--){
1529
             aah=aag+aaJsh;
1530
             aaJ=aaRh[0].J[aag];
1531 if(aadebugflag<DEBUG){</pre>
1532 fprintf(DBG,"aah=%d, aag=%d, aaJsh=%d, aaJ=%.1f
     \n",aah,aag,aaJsh,aaJ);
1533 fflush(DBG);
1534 }
1535
             if((aaOhicurr==0)&&(aaOlocurr==0)){
             if(((aah+1)>=0)&&((aah+1)<=aaj)){
1536
1537
               aaB=+1;
1538
               aaT[0].S[aaff].f[aag*2+1]=\
1539
                 aaRh[0].EJ[aag]-
1540
                 aaR1[0].EJ[aah+1];
               aaT[0].S[aaff].ni[aag*2+1]=\
1541
                 aahipop*aatrprob*aavhpop*\
1542
1543
                 aaRh[0].PJ[aag]*aavfcf*\
1544
                 HL(aaB,aaJ,aaL,aadL);
1545
               aaRl[0].CJ[aah+1]+=aavfcfr*\
1546
                 aaT[0].S[aaff].ni[aag*2+1];
1547 if(aadebugflag<DEBUG){
1548 fprintf(DBG,"aaRh[0].J[%d]=%.1f ",aag,aaRh[0].J[aag]);
1549 fprintf(DBG,"aaRh[0].EJ[%d]=%13.6e ",aag,aaRh[0].EJ[aag]);
1550 fprintf(DBG,"aaRl[0].J[%d]=%.1f ",aah+1,aaRl[0].J[aah+1]);
1551 fprintf(DBG,"aaRl[0].EJ[%d]=%13.6e\n",aah+1,aaRl[0].EJ[aah+1]);
1552 fprintf(DBG,"aaRh[0].PJ[%d]=%13.6e ",aag,aaRh[0].PJ[aag]);
1553 fprintf(DBG,"aaR1[0].CJ[%d]=%13.6e\n",aah+1,aaR1[0].CJ[aah+1]);
1554 fprintf(DBG,"aahipop=%13.6e aatrprob=%13.6e aavfcf=%13.6e aavh-
     pop=%13.6e\n",\
1555
         aahipop,aatrprob,aavfcf,aavhpop);
1556 fflush(DBG);
1557 }
1558
               }
1559
             if(((aah-1)>=0)&&((aah-1)<=aaj)){
1560
               aaB=-1;
               aaT[0].S[aaff].f[aaf*2+0]=\
1561
1562
                 aaRh[0].EJ[aag]-
                 aaR1[0].EJ[aah-1];
1563
```

```
aaT[0].S[aaff].ni[aag*2+0]=\
1564
                 aahipop*aatrprob*aavhpop*\
1565
1566
                 aaRh[0].PJ[aag]*aavfcf*\
1567
                 HL(aaB,aaJ,aaL,aadL);
1568
               aaRl[0].CJ[aah-1]+=aavfcfr*\
1569
                 aaT[0].S[aaff].ni[aag*2+0];
1570 if(aadebugflag<DEBUG){
1571 fprintf(DBG, "aaRh[0].J[%d]=%.1f ", aag, aaRh[0].J[aag]);
1572 fprintf(DBG,"aaRh[0].EJ[%d]=%13.6e ",aag,aaRh[0].EJ[aag]);
1573 fprintf(DBG,"aaRl[0].J[%d]=%.1f ",aah+1,aaRl[0].J[aah-1]);
1574 fprintf(DBG,"aaR1[0].EJ[%d]=%13.6e\n",aah-1,aaR1[0].EJ[aah-1]);
1575 fprintf(DBG,"aaRh[0].PJ[%d]=%13.6e ",aag,aaRh[0].PJ[aag]);
1576 fprintf(DBG,"aaR1[0].CJ[%d]=%13.6e\n",aah-1,aaR1[0].CJ[aah-1]);
1577 fprintf(DBG,"aahipop=%13.6e aatrprob=%13.6e aavfcf=%13.6e aavh-
     pop=%13.6e\n",\
1578
         aahipop,aatrprob,aavfcf,aavhpop);
1579 fflush(DBG);
1580 }
1581
               }
1582 if(aadebugflag<DEBUG){
1583 fprintf(DBG,"aag=%d, aaT[0].S[aaff].f[aag*2+1]=%13.6e, ",aag,\
         aaT[0].S[aaff].f[aag*2+1]);
1584
1585 fprintf(DBG, "aaT[0].S[aaff].f[aag*2+0] = %13.6e\n",
     aaT[0].S[aaff].f[aag*2+0]);
1586 fprintf(DBG, "aaT[0].S[aaff].ni[aag*2+1]=%13.6e, ",
     aaT[0].S[aaff].ni[aag*2+1]);
1587 fprintf(DBG, "aaRl[0].CJ[aah+1] =
     %13.6e\naaT[0].S[aaff].ni[aag*2+0] = %13.6e, ",\
1588
         aaR1[0].CJ[aah+1],aaT[0].S[aaff].ni[aag*2+0]);
1589 fprintf(DBG,"aaRl[0].CJ[aah-1]=%13.6e\n",aaRl[0].CJ[aah-1]);
1590 fflush(DBG);
1591 }
1592 fprintf(AAFILE, "%5.1f\t %18.10e\t %18.10e\t %18.10e\t %18.10e\n",
     aaRh[0].J[aag], \
1593
       aaT[0].S[aaff].f[aag*2+1],aaT[0].S[aaff].ni[aag*2+1],
1594
       aaT[0].S[aaff].f[aag*2+0],aaT[0].S[aaff].ni[aag*2+0]);
1595
               }
1596
             else{
1597
             if(((aah+1)>=0)&&((aah+1)<=aaj)){
1598
               aaB=+1;
               aaT[0].S[aaff].f[aag*3+2]=\
1599
1600
                 aaRh[0].EJ[aag]-
1601
                 aaR1[0].EJ[aah+1];
1602
               aaT[0].S[aaff].ni[aag*3+2]=\
1603
                 aahipop*aatrprob*aavhpop*\
1604
                 aaRh[0].PJ[aag]*aavfcf*\
1605
                 HL(aaB,aaJ,aaL,aadL);
1606
               aaRl[0].CJ[aah+1]+=aavfcfr*\
1607
                 aaT[0].S[aaff].ni[aag*3+2];
1608 if(aadebugflag<DEBUG){
1609 fprintf(DBG,"aaRh[0].J[%d]=%.1f ",aag,aaRh[0].J[aag]);
1610 fprintf(DBG,"aaRh[0].EJ[%d]=%13.6e ",aag,aaRh[0].EJ[aag]);
1611 fprintf(DBG,"aaRl[0].J[%d]=%.1f ",aah+1,aaRl[0].J[aah+1]);
1612 fprintf(DBG,"aaR1[0].EJ[%d]=%13.6e\n",aah+1,aaR1[0].EJ[aah+1]);
```

1613 fprintf(DBG,"aaRh[0].PJ[%d]=%13.6e ",aag,aaRh[0].PJ[aag]); 1614 fprintf(DBG,"aaR1[0].CJ[%d]=%13.6e\n",aah+1,aaR1[0].CJ[aah+1]); 1615 fprintf(DBG,"aahipop=%13.6e aatrprob=%13.6e aavfcf=%13.6e aavhpop=%13.6e\n",\ 1616 aahipop,aatrprob,aavfcf,aavhpop); 1617 fflush(DBG); 1618 } 1619 } 1620 if(((aah+0)>=0)&&((aah+0)<=aaj)){ 1621 aaB=0;aaT[0].S[aaff].f[aag*3+1]=\ 1622 1623 aaRh[0].EJ[aag]-1624 aaR1[0].EJ[aah+0]; 1625 aaT[0].S[aaff].ni[aag*3+1]=\ 1626 aahipop*aatrprob*aavhpop*\ 1627 aaRh[0].PJ[aag]*aavfcf*\ 1628 HL(aaB,aaJ,aaL,aadL); 1629 aaRl[0].CJ[aah+0]+=aavfcfr*\ 1630 aaT[0].S[aaff].ni[aag*3+1]; 1631 if(aadebugflag<DEBUG){</pre> 1632 fprintf(DBG,"aaRh[0].J[%d]=%.1f ",aag,aaRh[0].J[aag]); 1633 fprintf(DBG,"aaRh[0].EJ[%d]=%13.6e ",aag,aaRh[0].EJ[aag]); 1634 fprintf(DBG,"aaRl[0].J[%d]=%.1f ",aah,aaRl[0].J[aah+0]); 1635 fprintf(DBG,"aaRl[0].EJ[%d]=%13.6e\n",aah,aaRl[0].EJ[aah+0]); 1636 fprintf(DBG,"aaRh[0].PJ[%d]=%13.6e ",aag,aaRh[0].PJ[aag]); 1637 fprintf(DBG,"aaRl[0].CJ[%d]=%13.6e\n",aah,aaRl[0].CJ[aah+0]); 1638 fprintf(DBG,"aahipop=%13.6e aatrprob=%13.6e aavfcf=%13.6e aavhpop=%13.6e\n",\ 1639 aahipop,aatrprob,aavfcf,aavhpop); 1640 fflush(DBG); 1641 } 1642 } 1643 if(((aah-1)>=0)&&((aah-1)<=aaj)){ 1644 aaB=-1;1645 aaT[0].S[aaff].f[aag*3+0]=\ aaRh[0].EJ[aag]-1646 aaR1[0].EJ[aah-1]; 1647 aaT[0].S[aaff].ni[aag*3+0]=\ 1648 1649 aahipop*aatrprob*aavhpop*\ 1650 aaRh[0].PJ[aag]*aavfcf*\ 1651 HL(aaB,aaJ,aaL,aadL); 1652 aaRl[0].CJ[aah-1]+=aavfcfr*\ 1653 aaT[0].S[aaff].ni[aag*3+0]; 1654 if(aadebugflag<DEBUG){ 1655 fprintf(DBG,"aaRh[0].J[%d]=%.1f ",aag,aaRh[0].J[aag]); 1656 fprintf(DBG,"aaRh[0].EJ[%d]=%13.6e ",aag,aaRh[0].EJ[aag]); 1657 fprintf(DBG,"aaRl[0].J[%d]=%.1f ",aah-1,aaRl[0].J[aah-1]); 1658 fprintf(DBG,"aaR1[0].EJ[%d]=%13.6e\n",aah-1,aaR1[0].EJ[aah-1]); 1659 fprintf(DBG,"aaRh[0].PJ[%d]=%13.6e ",aag,aaRh[0].PJ[aag]); 1660 fprintf(DBG,"aaR1[0].CJ[%d]=%13.6e\n",aah-1,aaR1[0].CJ[aah-1]); 1661 fprintf(DBG,"aahipop=%13.6e aatrprob=%13.6e aavfcf=%13.6e aavhpop=%13.6e\n",\ 1662 aahipop,aatrprob,aavfcf,aavhpop); 1663 fflush(DBG);

```
1664 }
1665
1666 if(aadebugflag<DEBUG){
1667 fprintf(DBG, "aaT[0].S[aaff].f[aag*3+2]=%13.6e ",
     aaT[0].S[aaff].f[aag*3+2]);
1668 fprintf(DBG, "aaT[0].S[aaff].f[aag*3+1]=%13.6e ",
     aaT[0].S[aaff].f[aag*3+1]);
1669 fprintf(DBG, "aaT[0].S[aaff].f[aag*3+0]=%13.6e\n",
     aaT[0].S[aaff].f[aag*3+0]);
1670 fprintf(DBG, "aaT[0].S[aaff].ni[aag*3+2]=%13.6e ",
     aaT[0].S[aaff].ni[aag*3+2]);
1671 fprintf(DBG, "aaT[0].S[aaff].ni[aag*3+1]=%13.6e ",
     aaT[0].S[aaff].ni[aag*3+1]);
1672 fprintf(DBG, "aaT[0].S[aaff].ni[aag*3+0]=%13.6e\n",
     aaT[0].S[aaff].ni[aag*3+0]);
1673 fprintf(DBG,"aaRl[0].CJ[aah+1]=%13.6e ",aaRl[0].CJ[aah+1]);
1674 fprintf(DBG,"aaRl[0].CJ[aah+0]=%13.6e ",aaRl[0].CJ[aah+0]);
1675 fprintf(DBG,"aaRl[0].CJ[aah-1] =%13.6e\n",aaRl[0].CJ[aah-1]);
1676 fflush(DBG);
1677 }
1678 fprintf(AAFILE,\
1679
       "%5.1f\t %18.10e\t %18.10e\t %18.10e\t %18.10e\t %18.10e\t %18.10e\t
     %18.10e\n",\
1680
       aaRh[0].J[aag], \
       aaT[0].S[aaff].f[aag*3+2],aaT[0].S[aaff].ni[aag*3+2],\
1681
1682
       aaT[0].S[aaff].f[aag*3+1],aaT[0].S[aaff].ni[aag*3+1],
1683
       aaT[0].S[aaff].f[aag*3+0],aaT[0].S[aaff].ni[aag*3+0]);
1684
               }
1685
1686
           fclose(AAFILE);
1687
           }
1688
         if(aafrchf==0){ /* if this v is cascade populated */
1689 sprintf(aafile,"%s_molecules/%s/%s-%.1f--%s-%.1f_v%d--
     v%d_CAS.dat", \
1690
       PREF,MOL[aaa].Mol,aaT[0].Nhi,aaOhicurr,\
1691
         aaT[0].Nlo,aaOlocurr,aae,aaf);
1692
           AAFILE=fopen(aafile,"w");
1693
           if(AAFILE==NULL){
1694 printf("Error opening transition sub-file %s. Exiting.\n",aafile);
1695
             exit(1);
1696
1697 fprintf(AAFILE,"# File created by %s.\n# File contains ",PRO-
     GRAM_NAME);
1698 if((aaOhicurr==0)&&(aaOlocurr==0)) fprintf(AAFILE,"P and R");
1699 else fprintf(AAFILE, "P, Q and R");
1700 fprintf(AAFILE," branches from the simulation titled %s\n",PREF);
1701 fprintf(AAFILE, "# THESE INTENSITIES ARE DUE TO CASCADE ");
1702 fprintf(AAFILE," ONLY -- NO USER-SPECIFIED POPULATIONS\n");
1703 fprintf(AAFILE, "# Transition is Hund's Case (a) to Hund's Case
     (a).\n");
1704 fprintf(AAFILE,"# Molecule %s, \tHigh state: %s, Omega=%.1f,
     v=%d\n",\
1705
         MOL[aaa].Mol,aaT[0].Nhi,aaOhicurr,aae);
```

- 1706 fprintf(AAFILE,"#\t\tLow state: %s, Omega=%.1f, v=%d\n# Columns are: ",\
- aaT[0].Nlo,aaOlocurr,aaf); 1707
- 1708 if((aaOhicurr==0)&&(aaOlocurr==0)){
- 1709 fprintf(AAFILE, "J_hi P(J_hi+1)_v P_i R(J_hi-1)_v R_i n#\n");
- 1710 ł
- 1711 else fprintf(AAFILE,"J_hi P(Jhi+1)_v P_i Q(J_hi+0)_v Q_i R(J_hi-1)_v $R_i n#(n");$
- 1712 aaRh=&MOL[aaa].s[aaSthi].rc[aae];
- 1713 if((aamaxhiJ-1)<MOL[aaa].s[aaSthi].rc[aae].jc){
- 1714 aaj=aamaxhiJ-1; }
- 1715
- 1716 else aaj=MOL[aaa].s[aaSthi].rc[aae].jc;
- if((aaRl[0].Jdissoc-aaOlocurr)<(aaj-1)){</pre> 1717
- 1718 fprintf(PAR,"\nWARNING!! State %s(%.1f) of molecule %s has significant ",\
- 1719 MOL[aaa].s[aaSthi].Name,aaOhicurr,MOL[aaa].Mol);
- 1720 fprintf(PAR, "CASCADE rotational population at level %.1f\n",aaRh[0].J[aaj-1]);
- 1721 fprintf(PAR,"\tBut lower state %s(%.1f) dissociates at level %.1f\n",\
- 1722 MOL[aaa].s[aaStlo].Name,aaOlocurr,aaRl[0].Jdissoc);
- 1723 fprintf(PAR,"It is likely that the bound upper state is transiting to (an)");
- 1724 fprintf(PAR," unbound lower state(s).\n");
- 1725 fprintf(PAR, "Look for continuum emissions trailing off to the lowenergy ");
- 1726 fprintf(PAR, "end of the v(hi)=%d to v(lo)=%d\nband in the real ",aae,aaf);
- 1727 fprintf(PAR, "spectrum (not the simulated one)\nCurrently, this program will");

```
1728 fprintf(PAR," not simulate bound-->unbound spectra.\n\n");
```

```
1729
             aaj=(int)(aaRl[0].Jdissoc-aaOlocurr);
```

1730

```
1731
           for(aag=(aaj-1);aag>=0;aag--){
```

```
1732
              aah=aag+aaJsh;
```

1733 aaJ=aaRh[0].J[aag];

```
if((aaOhicurr==0)&&(aaOlocurr==0)){
1734
```

```
1735
             if(((aah+1)>=0)&&((aah+1)<=aaj)){
```

```
1736
                 aaB=+1;
```

```
1737
               aaT[0].S[aaff].f[aag*2+1]=\
```

```
1738
                 aaRh[0].EJ[aag]-
```

```
1739
                  aaR1[0].EJ[aah+1];
```

```
aaT[0].S[aaff].ci[aag*2+1]=aatrprob*\
1740
```

```
1741
                 aaRh[0].CJ[aag]*aavfcf*\
```

```
HL(aaB,aaJ,aaL,aadL);
1742
```

```
1743
               aaRl[0].CJ[aah+1]+=aavfcfr*\
                 aaT[0].S[aaff].ci[aag*2+1];
1744
```

```
1745 if(aadebugflag<DEBUG){
```

```
1746 fprintf(DBG,"aaRh[0].EJ[%d]=%13.6e ",aag,aaRh[0].EJ[aag]);
```

```
1747 fprintf(DBG,"aaRl[0].EJ[%d]=%13.6e ",aah+1,aaRl[0].EJ[aah+1]);
```

```
1748 fprintf(DBG,"aaRh[0].CJ[%d]=%13.6e ",aag,aaRh[0].CJ[aag]);
```

```
1749 fprintf(DBG,"aaR1[0].CJ[%d]=%13.6e\n",aah+1,aaR1[0].CJ[aah+1]);
```

```
1750 fprintf(DBG,"aavfcf=%13.6e aatrprob=%13.6e \n",\
```

```
1751
                  aavfcf,aatrprob);
1752 fflush(DBG);
1753 }
1754
                               }
1755
                           if(((aah-1)>=0)&&((aah-1)<=aaj)){
1756
                               aaB=-1;
                               aaT[0].S[aaff].f[aag*2+0]=\
1757
                                    aaRh[0].EJ[aag]-
1758
1759
                                    aaR1[0].EJ[aah-1];
1760
                               aaT[0].S[aaff].ci[aag*2+0]=aatrprob*\
1761
                                    aaRh[0].CJ[aag]*aavfcf*\
1762
                                   HL(aaB,aaJ,aaL,aadL);
1763
                               aaRl[0].CJ[aah-1]+=aavfcfr*\
1764
                                    aaT[0].S[aaff].ci[aag*2+0];
1765 if(aadebugflag<DEBUG){
1766 fprintf(DBG,"aaRh[0].EJ[%d]=%13.6e ",aag,aaRh[0].EJ[aag]);
1767 fprintf(DBG,"aaRl[0].EJ[%d]=%13.6e ",aah-1,aaRl[0].EJ[aah-1]);
1768 fprintf(DBG,"aaRh[0].CJ[%d]=%13.6e ",aag,aaRh[0].CJ[aag]);
1769 fprintf(DBG,"aaRl[0].CJ[%d]=%13.6e\n",aah-1,aaRl[0].CJ[aah-1]);
1770 fprintf(DBG,"aavfcf=%13.6e aatrprob=%13.6e \n",\
1771
                  aavfcf,aatrprob);
1772 fflush(DBG);
1773 }
1774
1775 if(aadebugflag<DEBUG){
1776 fprintf(DBG,"aag=%d, aaT[0].S[aaff].f[aag*2+1]=%13.6e, ",aag,\
                  aaT[0].S[aaff].f[aag*2+1]);
1777
1778 fprintf(DBG, "aaT[0].S[aaff].f[aag*2+0] = %13.6e\n",
          aaT[0].S[aaff].f[aag*2+0]);
1779 fprintf(DBG, "aaT[0].S[aaff].ci[aag*2+1] = %13.6e, ",
          aaT[0].S[aaff].ci[aag*2+1]);
1780 fprintf(DBG, "aaR1[0].CJ[aah+1] = %13.6e\n
          aaT[0].S[aaff].ci[aag*2+0] = %13.6e, ",\
1781
                  aaR1[0].CJ[aah+1],aaT[0].S[aaff].ci[aag*2+0]);
1782 fprintf(DBG,"aaRl[0].CJ[aah-1]=%13.6e\n",aaRl[0].CJ[aah-1]);
1783 fflush(DBG);
1784 }
1785 fprintf(AAFILE,"%5.1f\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%18.10e\t%1
              aaRh[0].J[aag], \
1786
              aaT[0].S[aaff].f[aag*2+1],aaT[0].S[aaff].ci[aag*2+1],\
1787
1788
              aaT[0].S[aaff].f[aag*2+0],aaT[0].S[aaff].ci[aag*2+0]);
1789
                               }
1790
                           else{
1791
                           if(((aah+1)>=0)&&((aah+1)<=aaj)){
                               aaB=+1;
1792
1793
                               aaT[0].S[aaff].f[aag*3+2]=\
1794
                               aaRh[0].EJ[aag]-aaR1[0].EJ[aah+1];
1795
                               aaT[0].S[aaff].ci[aag*3+2]=aatrprob*\
1796
                                    aaRh[0].CJ[aag]*aavfcf*\
1797
                                    HL(aaB,aaJ,aaL,aadL);
                               aaR1[0].CJ[aah+1]+=aavfcfr*\
1798
                                    aaT[0].S[aaff].ci[aag*3+2];
1799
1800 if(aadebugflag<DEBUG){
1801 fprintf(DBG,"aaRh[0].EJ[%d]=%13.6e ",aag,aaRh[0].EJ[aag]);
```

```
1802 fprintf(DBG,"aaRl[0].EJ[%d]=%13.6e ",aah+1,aaRl[0].EJ[aah+1]);
1803 fprintf(DBG,"aaRh[0].CJ[%d]=%13.6e ",aag,aaRh[0].CJ[aag]);
1804 fprintf(DBG,"aaR1[0].CJ[%d]=%13.6e\n",aah+1,aaR1[0].CJ[aah+1]);
1805 fprintf(DBG,"aavfcf=%13.6e aatrprob=%13.6e \n",\
1806
         aavfcf,aatrprob);
1807 fflush(DBG);
1808 }
1809
                }
1810
             if(((aah+0)>=0)&&((aah+0)<=aaj)){
1811
                aaB=0;
                aaT[0].S[aaff].f[aag*3+1]=\
1812
1813
                aaRh[0].EJ[aag]-aaR1[0].EJ[aah+0];
                aaT[0].S[aaff].ci[aag*3+1]=aatrprob\
1814
1815
                  *aavfcf*aaRh[0].CJ[aag]*\
1816
                  HL(aaB,aaJ,aaL,aadL);
1817
                aaRl[0].CJ[aah+0]+=aavfcfr*\
                  aaT[0].S[aaff].ci[aag*3+1];
1818
1819 if(aadebugflag<DEBUG){
1820 fprintf(DBG,"aaRh[0].EJ[%d]=%13.6e ",aag,aaRh[0].EJ[aag]);
1821 fprintf(DBG,"aaRl[0].EJ[%d]=%13.6e ",aah,aaRl[0].EJ[aah+0]);
1822 fprintf(DBG,"aaRh[0].CJ[%d]=%13.6e ",aag,aaRh[0].CJ[aag]);
1823 fprintf(DBG,"aaRl[0].CJ[%d]=%13.6e\n",aah,aaRl[0].CJ[aah+0]);
1824 fprintf(DBG,"Here 20\n");
1825 fprintf(DBG,"aavfcf=%13.6e aatrprob=%13.6e\n",\
1826
         aavfcf,aatrprob);
1827 fflush(DBG);
1828 }
1829
                }
1830
             if(((aah-1)>=0)&&((aah-1)<=aaj)){
                aaB=-1;
1831
1832
                aaT[0].S[aaff].f[aag*3+0]=\
1833
                aaRh[0].EJ[aag]-aaR1[0].EJ[aah-1];
                aaT[0].S[aaff].ci[aag*3+0]=aatrprob\
1834
1835
                  *aavfcf*aaRh[0].CJ[aag]*\
1836
                  HL(aaB,aaJ,aaL,aadL);
1837
                aaRl[0].CJ[aah-1]+=aavfcfr*\
1838
                  aaT[0].S[aaff].ci[aag*3+0];
1839 if(aadebugflag<DEBUG){
1840 fprintf(DBG,"aaRh[0].EJ[%d]=%13.6e ",aag,aaRh[0].EJ[aag]);
1841 fprintf(DBG,"aaRl[0].EJ[%d]=%13.6e ",aah-1,aaRl[0].EJ[aah-1]);
1842 fprintf(DBG,"aaRh[0].CJ[%d]=%13.6e ",aag,aaRh[0].CJ[aag]);
1843 fprintf(DBG,"aaRl[0].CJ[%d]=%13.6e\n",aah-1,aaRl[0].CJ[aah-1]);
1844 fprintf(DBG,"aavfcf=%13.6e aatrprob=%13.6e\n",\
1845
         aavfcf,aatrprob);
1846 fflush(DBG);
1847 }
1848
                }
1849 if(aadebugflag<DEBUG){
1850 fprintf(DBG, "aaT[0].S[aaff].f[aag*3+2] = %13.6e ",
     aaT[0].S[aaff].f[aag*3+2]);
1851 fprintf(DBG, "aaT[0].S[aaff].f[aag*3+1] = %13.6e ",
     aaT[0].S[aaff].f[aag*3+1]);
1852 fprintf(DBG, "aaT[0].S[aaff].f[aag*3+0] = %13.6e\n",
     aaT[0].S[aaff].f[aag*3+0]);
```

```
1853 fprintf(DBG, "aaT[0].S[aaff].ci[aag*3+2] = %13.6e ",
     aaT[0].S[aaff].ci[aag*3+2]);
1854 fprintf(DBG, "aaT[0].S[aaff].ci[aag*3+1] = %13.6e ",
     aaT[0].S[aaff].ci[aag*3+1]);
1855 fprintf(DBG, "aaT[0].S[aaff].ci[aag*3+0] = %13.6e\n",
     aaT[0].S[aaff].ci[aag*3+0]);
1856 fprintf(DBG,"aaRl[0].CJ[aah+1]=%13.6e ",aaRl[0].CJ[aah+1]);
1857 fprintf(DBG,"aaRl[0].CJ[aah+0]=%13.6e ",aaRl[0].CJ[aah+0]);
1858 fprintf(DBG,"aaRl[0].CJ[aah-1] =%13.6e\n",aaRl[0].CJ[aah-1]);
1859 fflush(DBG);
1860 }
1861 fprintf(AAFILE,\
1862
       "%5.1f\t %18.10e\t %18.10e\t %18.10e\t %18.10e\t %18.10e\t
     %18.10e\n",\
1863
       aaRh[0].J[aag], \
       aaT[0].S[aaff].f[aag*3+2],aaT[0].S[aaff].ci[aag*3+2],\
1864
1865
       aaT[0].S[aaff].f[aag*3+1],aaT[0].S[aaff].ci[aag*3+1],\
1866
       aaT[0].S[aaff].f[aag*3+0],aaT[0].S[aaff].ci[aag*3+0]);
1867
               }
             }
1868
           }
1869
         }
1870
         }
1871
       }
1872
       }
1873
1874 return;
1875 }
     1876
     /* This function calls other functions that calculate transitions
       between Hund's Case (b) and Hund's Case (b) */
1877 void b_b(int bba, int bbb){
     /* indexes and dummy variables: */
1878 int bbc=0, bbd=0, bbe=0, bbf=0, bbff=0, bbk=0, bbdum=0;
     /* for variables below: n="native"; c="cascade"; St="state";
       Cb="Case b"; v="vibrational"; num="number"; des="designation";
       hi="high"; lo="low"; max="maximum"; pec="pseudo-Einstein coef-
       ficient"; comp="comparison"; a,b,<etc> are indexes */
     /* variables about vibrational levels */
1879 int bbhvnlo=0, bbhvnnum=0, bbhvclo=0, bbhvcnum=0, bbhivlo=0, bb-
     hivnum=0, bbHV=0;
1880 int bblvnlo=0, bblvnnum=0, bblvclo=0, bblvcnum=0, bblovlo=0,
     bblovnum=0, bbLV=0;
     /* variables for info about the two states */
1881 int bbStlo=0, bbSthi=0, bbStnlovlo=30, bbStnlovhi=0, bbSt-
     clovlo=30, bbStclovhi=0;
1882 int bbCbhi=0,bbCblo=0;
1883 double bbhipop=0,bbDe=0,bbBvDv=0;
     /* variables related to which v-v transitions need to be included */
1884 double bbpecnmax=0,bbpecncompb=0,bbpecccmax=0,bbpecccompb=0;
     /* variables to use for relating J and K */
1885 int bbHiJnum=0,bbLoJnum=0,bbmaxhiK=0,bbtransperK=0;
```

1886 double bbSh=0,bbSl=0;

/* variables for the spectrscopic constants */

- 1887 double bbwexehi=0,bbwexelo=0,bbTehi=0,bbTelo=0,bbwehi=0,bbwelo=0;
 /* some local pointers to use as abbreviations for the longer ad dresses */
- 1888 Case_b_stateinfo *bbHI,*bbLO;
- 1889 Trans *bbT;
- /* a few flags for various purposes */
- 1890 int bbflg=0;

/* a set of info for transferring to the sub-transition functions */
1891 BBTinfo bbinfo;

- /* Check FCF's for lower-state vibrational levels. Find highest and lowest lower-state levels that wil be populated (within the userset lower precision limit). Check to see that there are energies for all those levels. If not, reallocate the state info to have room for the new levels. Don't add "native" population -- only cascade. (the added population will be ignored if it's a destination state only) */
- /* a whole lot of the stuff below is redundant. That's because I
 copied this function from a-a.c and it takes less time to be re dundant than to make sure I changed everything correctly */
- 1892 bbSthi=MOL[bba].t[bbb].Hi;
- 1893 bbStlo=MOL[bba].t[bbb].Lo;
- 1894 bbinfo.T=&MOL[bba].t[bbb];
- 1895 bbCbhi=MOL[bba].s[bbSthi].Cb;
- 1896 bbCblo=MOL[bba].s[bbStlo].Cb;
- 1897 bbinfo.Sh=&MOL[bba].s[bbSthi];
- 1898 bbinfo.Sl=&MOL[bba].s[bbStlo];
- 1899 bbLO=&CB[bbCblo];
- 1900 bbHI=&CB[bbCbhi];
- 1901 bbinfo.Cl=bbLO;
- 1902 bbinfo.Ch=bbHI;
- 1903 bbinfo.m=bba;

- 1907 bbhvclo=MOL[bba].s[bbSthi].v[0].vclo; /* low vib level from cascade */
- 1908 bbhvcnum=MOL[bba].s[bbSthi].v[0].vcnum; /* number of vib levels
 from cascade */

- 1911 bblvclo=MOL[bba].s[bbStlo].v[0].vclo; /* low vib level from cascade */
- 1912 bblvcnum=MOL[bba].s[bbStlo].v[0].vcnum; /* number of vib levels
 from cascade */
- 1913 bbinfo.Vh=MOL[bba].s[bbSthi].v;
```
1914 bbinfo.hvnlo=bbhvnlo;
1915 bbinfo.hvnnum=bbhvnnum;
1916 bbinfo.hvclo=bbhvclo;
1917 bbinfo.hvcnum=bbhvcnum;
1918 bbinfo.lvnlo=bblvnlo;
1919 bbinfo.lvnnum=bblvnnum;
1920 bbinfo.lvclo=bblvclo;
1921 bbinfo.lvcnum=bblvcnum;
1922 bbwexehi=bbHI[0].wexe;
1923 bbwexelo=bbL0[0].wexe;
1924 bbTehi=bbHI[0].Te;
1925 bbTelo=bbLO[0].Te;
1926 bbwehi=bbHI[0].we;
1927 bbwelo=bbL0[0].we;
1928 if(bbdebugflag<DEBUG){
1929 fprintf(DBG,"bbSthi=%d, bbStlo=%d, bbCbhi=%d, bbCblo=%d, bb-
    hipop=%f\n",bbSthi,\
         bbStlo,bbCbhi,bbCblo,bbhipop);
1930
1931 fprintf(DBG,"bbhvnlo=%d, bbhvnnum=%d, bbhvclo=%d, bbhvc-
     num=%d\n",bbhvnlo,\
1932
         bbhvnnum,bbhvclo,bbhvcnum);
1933 fprintf(DBG,"bblvnlo=%d, bblvnnum=%d, bblvclo=%d, bblvc-
     num=%d\n",bblvnlo,\
1934
         bblvnnum,bblvclo,bblvcnum);
1935 fprintf(DBG,"bbinfo.Sh[0].Cb=%d, bbinfo.Sl[0].Cb=%d\n",\
         bbinfo.Sh[0].Cb,bbinfo.Sl[0].Cb);
1936
1937 fprintf(DBG,"Molecule is %s; Transition %s --> %s\n",MOL[bba].Mol,\
1938
         MOL[bba].s[bbSthi].Name,MOL[bba].s[bbStlo].Name);
1939 fprintf(DBG, "MOL[%d].t[%d].Nhi=%s,
     MOL[%d].t[%d].Nlo=%s\n",bba,bbb,\
1940
         MOL[bba].t[bbb].Nhi,bba,bbb,MOL[bba].t[bbb].Nlo);
1941 fflush(DBG);
1942 }
     /* Find the number of J's per (most) K(s) */
1943 bbHiJnum=(int)(2*CB[bbCbhi].S+1.000000001); /* hail, hail, o great
       Numera / may we not have a truncation error :-) */
1944 bbLoJnum=(int)(2*CB[bbCblo].S+1.000000001);
1945 bbinfo.nhJ=bbHiJnum;
1946 bbinfo.nlJ=bbLoJnum;
1947 bbSh=CB[bbCbhi].S;
1948 bbSl=CB[bbCblo].S;
1949 if(bbdebugflag<DEBUG){
1950 fprintf(DBG,"bbSh=%.1f, bbsL=%.1f\n",bbSh,bbS1);
1951 fflush(DBG);
1952 }
     /* Find the maximum number of transitions to expect for each value
       of K. There must be some general form to use for this, but I spent
       20 minutes working on it and decided I could just let the program
       calculate it by brute force before I could work out the general
       form. This is necessary to get the relative intensities right,
       but will be crucial if anyone ever adds any fine splitting ef-
```

fects. See the documentation on transitions for more info. */

386

```
/* NOTE::: This is a neat idea, but I'm running low on time and need
       to get this done. So, I'll be being lazy a little bit further
       down. Scan for "Laziness:". */
1953 bbtransperK=0;
1954 for(bbc=0;bbc<bbHiJnum;bbc++){
     /* for K to K-1 transitions: */
1955
       if(((-1-bbSl)<(-bbSh+bbc))&&((bbSl-1)>(-bbSh+bbc))) bb-
     transperK+=3;
1956
       if(((-1-bbSl)==(-bbSh+bbc))&&((bbSl-1)>(-bbSh+bbc))) bb-
     transperK+=2;
       if(((-1-bbS1)<(-bbSh+bbc))\&\&((bbS1-1)=(-bbSh+bbc))) bb-
1957
     transperK+=2:
       if((bbS1==0)&&((-bbSh+bbc)>=-2)&&((-bbSh+bbc)<=0)) bb-
1958
     transperK+=1;
1959 if(bbdebugflag<DEBUG){
1960 fprintf(DBG, "after Delta-K=-1 for bbc=%d,
     bbtransperK=%d\n",bbc,bbtransperK);
1961 fflush(DBG);
1962 }
     /* for K to K transitions: */
1963 if((bbHI[0].L!=0)||(bbL0[0].L!=0)){ /* only if not Sigma-Sigma */
       if(((-bbS1)<(-bbSh+bbc))&&((bbS1)>(-bbSh+bbc))) bbtransperK+=3;
1964
1965
       if(((-bbSl)==(-bbSh+bbc))&&((bbSl)>(-bbSh+bbc))) bb-
     transperK+=2;
       if(((-bbSl)<(-bbSh+bbc))&&((bbSl)==(-bbSh+bbc))) bb-
1966
     transperK+=2;
1967
       if((bbS1==0)&&((-bbSh+bbc)>=-1)&&((-bbSh+bbc)<=1)) bb-
     transperK+=1;
1968
       }
1969 if(bbdebugflag<DEBUG){
1970 fprintf(DBG,"after Delta-K=0 for bbc=%d,
     bbtransperK=%d\n",bbc,bbtransperK);
1971 fflush(DBG);
1972 }
     /* for K to K+1 transitions: */
1973
       if((((+1-bbSl)<(-bbSh+bbc))&&((bbSl+1)>(-bbSh+bbc))) bb-
     transperK+=3;
       if(((+1-bbSl)==(-bbSh+bbc))&&((bbSl+1)>(-bbSh+bbc))) bb-
1974
     transperK+=2;
       if((((+1-bbS1)<(-bbSh+bbc))&&((bbS1+1)==(-bbSh+bbc))) bb-
1975
     transperK+=2;
       if((bbS1==0)&&((-bbSh+bbc)>=0)&&((-bbSh+bbc)<=2)) bb-
1976
     transperK+=1;
1977 if(bbdebugflag<DEBUG){
1978 fprintf(DBG,"after Delta-K=+1 for bbc=%d,
     bbtransperK=%d\n",bbc,bbtransperK);
1979 fflush(DBG);
1980 }
1981
       }
1982 bbinfo.nT=bbtransperK;
     /* Laziness: If the business above worked in all cases, the fol-
       lowing line wouldn't be necessary. But, this way, there is def-
       initely enough space in the array. In some cases, there will be
```

far too much. */

```
1983 bbinfo.nT=bbtransperK=(int)((2*bbSh+1)*3*(2*bbSl+1));
1984 if(bbdebugflag<DEBUG){
1985 fprintf(DBG, "The Lazy bbtransperK (bbinfo.nT) is
     %d\n",bbtransperK);
1986 fflush(DBG);
1987 }
      /* find total number of sub-transitions (v-v) for this transition.
        This will take some doing. After, allocate memory for them */
1988 if((bbhvnlo<bbhvclo)||(bbhvcnum==0)) bbhivlo=bbhvnlo;
1989 else bbhivlo=bbhvclo;
1990 if((bbhvnlo+bbhvnnum)>(bbhvclo+bbhvcnum)){
1991
       bbhivnum=bbhvnlo+bbhvnnum-bbhivlo;
1992
       }
1993 else{
1994
       bbhivnum=bbhvclo+bbhvcnum-bbhivlo;
1995
       }
1996 MOL[bba].t[bbb].vnh=bbhivnum;
1997 MOL[bba].t[bbb].vhlo=bbhivlo;
1998 bbinfo.hivnum=bbhivnum;
1999 bbinfo.hivlo=bbhivlo;
2000 if(bbdebugflag<DEBUG){
2001 fprintf(DBG,"bbhvnlo=%d, bbhvclo=%d ",bbhvnlo,bbhvclo);
2002 fprintf(DBG,"(bbhvnlo+bbhvnnum)=%d, (bbhvclo+bbhvcnum)=%d\n",\
2003
         (bbhvnlo+bbhvnnum),(bbhvclo+bbhvcnum));
2004 fprintf(DBG,"bbhivnum=%d, bbhivlo=%d\n",bbhivnum,bbhivlo);
2005 fprintf(DBG, "bbhivnum is %d, bbhivlo is
     %d\n",MOL[bba].t[bbb].vnh,\
2006
         MOL[bba].t[bbb].vhlo);
2007 fprintf(DBG,"MOL[%d].t[%d].Nhi=%s,
     MOL[%d].t[%d].Nlo=%s\n",bba,bbb,\
         MOL[bba].t[bbb].Nhi,bba,bbb,MOL[bba].t[bbb].Nlo);
2008
2009 fflush(DBG);
2010 }
      /* loop to find maximum PEC (=FCF times FREQ^DETECTTYPE) */
2011 bbHV=bbhvnnum+bbhvnlo;
2012 if(bbdebugflag<DEBUG){
2013 fprintf(DBG,"bbc=%d, bbd=%d, bbHV=%d\n",bbc,bbd,bbHV);
2014 fflush(DBG);
2015 }
2016 for(bbe=bbhvnlo;bbe<bbHV;bbe++){ /* find max pec for native v's */
       for(bbf=0;bbf<30;bbf++){</pre>
2017
2018
         if(MOL[bba].t[bbb].v[bbe].fcfn[bbf]>bbpecnmax){
2019
           bbpecnmax=MOL[bba].t[bbb].v[bbe].fcfn[bbf];
2020
           }
2021 if(bbdebugflag<(DEBUG-1)){
2022 fprintf(DBG,"bbpecnmax=%11.4e\n",bbpecnmax);
2023 fflush(DBG);
2024 }
2025
         }
       }
2026
2027 bbHV=bbhvcnum+bbhvclo;
2028 if(bbdebugflag<(DEBUG-1)){
2029 fprintf(DBG,"Out of find-max-pec for native v's. bbHV=%d\n",bbHV);
```

```
2030 fflush(DBG);
2031 }
2032 for(bbe=bbhvclo;bbe<bbHV;bbe++){ /* find max pec for cascade v's */
2033
       for(bbf=0;bbf<30;bbf++){</pre>
2034
         if(MOL[bba].t[bbb].v[bbe].fcfc[bbf]>bbpeccmax){
2035
           bbpeccmax=MOL[bba].t[bbb].v[bbe].fcfc[bbf];
2036
           }
2037 if(bbdebugflag<(DEBUG-1)){
2038 fprintf(DBG,"bbpeccmax=%11.4e\n",bbpeccmax);
2039 fflush(DBG);
2040 }
2041
         }
       }
2042
      /* find minimum and maximum lower-state v's with PEC's that are
        above the low-intensity cutoff (JKCUT) */
2043 bbHV=bbhvnnum+bbhvnlo;
2044 if (bbdebugflag<DEBUG) {
2045 fprintf(DBG,"In cut-off loop: bbc=%d, bbd=%d,
     bbHV=%d\n",bbc,bbd,bbHV);
2046 fprintf(DBG,"\tMOL[%d].t[%d].Nhi=%s,
     MOL[%d].t[%d].Nlo=%s\n",bba,bbb,\
2047
         MOL[bba].t[bbb].Nhi,bba,bbb,MOL[bba].t[bbb].Nlo);
2048 fflush(DBG);
2049 }
2050 for(bbe=bbhvnlo;bbe<bbHV;bbe++){ /* for native populations */
2051
       bbf=0;
2052 if(bbdebugflag<(DEBUG-1)){
2053 fprintf(DBG,"\tMOL[%d].t[%d].Nhi=%s,
     MOL[%d].t[%d].Nlo=%s\n",bba,bbb,\
2054
         MOL[bba].t[bbb].Nhi,bba,bbb,MOL[bba].t[bbb].Nlo);
2055 fflush(DBG);
2056 }
2057
       while(bbflg==0){
2058
         bbpecncompb=MOL[bba].t[bbb].v[bbe].fcfn[bbf]/JKCUT;
2059
         if(bbpecncompb<bbpecnmax) bbdum=bbf;</pre>
2060
         else bbflg=1;
2061
         bbf++;
2062
2063
       if(bbdum<bbStnlovlo) bbStnlovlo=bbdum;
2064 if(bbdebugflag<(DEBUG-1)){
2065 fprintf(DBG,"bbpecncompb=%11.4e, bbf=%d\n",bbpecncompb,bbf);
2066 fprintf(DBG,"bbStnlovlo=%d\n",bbStnlovlo);
2067 fflush(DBG);
2068 }
2069
       bbf=29;
2070
       bbflg=0;
2071 if(bbdebugflag<(DEBUG-1)){
2072 fflush(DBG);
2073 }
2074
       while(bbflg==0){
         bbpecncompb=MOL[bba].t[bbb].v[bbe].fcfn[bbf]/JKCUT;
2075
2076
         if(bbpecncompb<bbpecnmax) bbdum=bbf;</pre>
2077
         else bbflg=1;
2078 if(bbdebugflag<(DEBUG-1)){
```

```
2079 fprintf(DBG,"bbStnlovhi loop: bbpecncompb=%11.4e , ",bbpecncompb);
2080 fprintf(DBG,"bbf=%d, bbdum=%d, bbflg=%d\n",bbf,bbdum,bbflg);
2081 fflush(DBG);
2082 }
2083
         bbf--;
2084
         ł
2085
       if(bbdum>bbStnlovhi) bbStnlovhi=bbdum;
2086 if(bbdebugflag<(DEBUG-1)){
2087 fprintf(DBG,"bbpecncompb=%11.4e, bbf=%d,
     bbdum=%d\n", bbpecncompb, bbf, bbdum);
2088 fprintf(DBG,"bbStnlovhi=%d\n",bbStnlovhi);
2089 fflush(DBG);
2090 }
2091
       }
2092 bbHV=bbhvcnum+bbhvclo;
2093 if(bbdebugflag<(DEBUG-1)){
2094 fprintf(DBG,"out of native population cutoff. bbHV=%d\n",bbHV);
2095 fprintf(DBG,"\tMOL[%d].t[%d].Nhi=%s,
     MOL[%d].t[%d].Nlo=%s\n",bba,bbb,\
2096
         MOL[bba].t[bbb].Nhi,bba,bbb,MOL[bba].t[bbb].Nlo);
2097 fflush(DBG);
2098 }
2099 for(bbe=bbhvclo;bbe<bbHV;bbe++){ /* for cascade populations */
2100
       bbf=0;
2101 if(bbdebugflag<(DEBUG-1)){</pre>
2102 fflush(DBG);
2103 }
2104
       while(bbflg==0){
         bbpecccompb=MOL[bba].t[bbb].v[bbe].fcfc[bbf]/JKCUT;
2105
2106
         if(bbpecccompb<bbpeccmax) bbdum=bbf;</pre>
2107
         else bbflg=1;
2108
         bbf++;
2109
2110 if(bbdebugflag<(DEBUG-1)){</pre>
2111 fprintf(DBG,"bbpecccompb=%11.4e, bbf=%d,
     bbdum=%d\n",bbpecccompb,bbf,bbdum);
2112 fflush(DBG);
2113 }
2114
       if(bbdum<bbStclovlo) bbStclovlo=bbdum;
2115
       bbf=29;
2116
       bbflg=0;
2117
       while(bbflg==0){
2118
         bbpecccompb=MOL[bba].t[bbb].v[bbe].fcfc[bbf]/JKCUT;
2119
         if(bbpecccompb<bbpeccmax) bbdum=bbf;</pre>
2120
         else bbflg=1;
         bbf--;
2121
2122
         ł
2123 if(bbdebugflag<(DEBUG-1)){
2124 fprintf(DBG,"bbpecccompb=%11.4e, bbf=%d,
     bbdum=%d\n",bbpecccompb,bbf,bbdum);
2125 fflush(DBG);
2126 }
2127
       if(bbdum>bbStclovhi) bbStclovhi=bbdum;
```

```
2128
       }
2129 if(bbdebugflag<(DEBUG-1)){</pre>
2130 fprintf(DBG,"out of cutoff loop\n\n");
2131 fprintf(DBG, "MOL[%d].t[%d].Nhi=%s,
     MOL[%d].t[%d].Nlo=%s\n",bba,bbb, \
         MOL[bba].t[bbb].Nhi,bba,bbb,MOL[bba].t[bbb].Nlo);
2132
2133 fflush(DBG);
2134 }
      /* determine the lowest necessary destination-state vib level and
        the number of destination-state vibration levels */
2135 if((bbStnlovlo)<(bbStclovlo)) bblovlo=bbStnlovlo;</pre>
2136 else bblovlo=bbStclovlo;
2137 if((bbStnlovhi)>(bbStclovhi)) bblovnum=bbStnlovhi+1-bblovlo;
2138 else bblovnum=bbStclovhi+1-bblovlo;
2139 MOL[bba].t[bbb].vnl=bblovnum;
2140 MOL[bba].t[bbb].vllo=bblovlo;
2141 bbinfo.lovnum=bblovnum;
2142 bbinfo.lovlo=bblovlo;
      /* allocate memory for the simsets in the transition structure */
2143 MOL[bba].t[bbb].nS=bbhivnum*bblovnum;
2144 MOL[bba].t[bbb].S = (simset*) calloc(MOL[bba].t[bbb].nS,
     sizeof(simset));
2145 MOL[bba].t[bbb].fS=(int*)calloc(MOL[bba].t[bbb].nS,sizeof(int));
2146 if(bbdebugflag<DEBUG){
2147 fprintf(DBG,"MOL[%d].t[%d].vnl=%d, MOL[%d].t[%d].vllo=%d
     ",bba,bbb,\
         MOL[bba].t[bbb].vnl,bba,bbb,MOL[bba].t[bbb].vllo);
2148
2149 fprintf(DBG,"MOL[%d].t[%d].nS=%d\n",bba,bbb,MOL[bba].t[bbb].nS);
2150 fprintf(DBG,"\tMOL[%d].t[%d].Nhi=%s,
     MOL[%d].t[%d].Nlo=%s\n",bba,bbb,\
2151
         MOL[bba].t[bbb].Nhi,bba,bbb,MOL[bba].t[bbb].Nlo);
2152 fflush(DBG);
2153 }
2154 bbHV=bbhvnnum+bbhvnlo;
      /* get maximum K value present */
2155 for(bbf=bbhvnlo;bbf<bbHV;bbf++){ /* check native populations */
2156 if(bbdebugflag<(DEBUG)){</pre>
2157 fprintf(DBG,"In native population loop \n");
2158 fprintf(DBG,"\tMOL[%d].t[%d].Nhi=%s,
     MOL[%d].t[%d].Nlo=%s\n",bba,bbb,\
2159
         MOL[bba].t[bbb].Nhi,bba,bbb,MOL[bba].t[bbb].Nlo);
2160 fflush(DBG);
2161 }
2162
       bbk=MOL[bba].s[bbSthi].r[bbf-bbhvnlo].k;
2163
       if(bbk>bbmaxhiK){
2164
         bbmaxhiK=bbk;
2165
         }
       }
2166
2167 if(bbdebugflag<(DEBUG)){</pre>
2168 fprintf(DBG,"Native: bbe=%d, bbf=%d,
     bbmaxhiK=%d\n",bbe,bbf,bbmaxhiK);
```

```
2169 fprintf(DBG,"\tMOL[%d].t[%d].Nhi=%s,
     MOL[%d].t[%d].Nlo=%s\n",bba,bbb,\
         MOL[bba].t[bbb].Nhi,bba,bbb,MOL[bba].t[bbb].Nlo);
2170
2171 fflush(DBG);
2172 }
2173 bbHV=bbhvcnum+bbhvclo;
2174 for(bbf=bbhvclo;bbf<bbHV;bbf++){ /* check cascade populations */
2175
       bbk=MOL[bba].s[bbSthi].rc[bbf-bbhvclo].k;
2176
       if(bbk>bbmaxhiK){
2177
         bbmaxhiK=bbk;
2178
         }
       }
2179
2180 if(bbdebugflag<(DEBUG)){</pre>
2181 fprintf(DBG,"Cascade: bbe=%d, bbf=%d,
     bbmaxhiK=%d\n",bbe,bbf,bbmaxhiK);
2182 fprintf(DBG,"\tMOL[%d].t[%d].Nhi=%s,
     MOL[%d].t[%d].Nlo=%s\n",bba,bbb,\
2183
         MOL[bba].t[bbb].Nhi,bba,bbb,MOL[bba].t[bbb].Nlo);
2184 fflush(DBG);
2185 }
      /* See if all the needed destination-state v's are calculated.
        Check also that enough K/J's are calculated. Calculate any states
        that aren't already done. The following method isn't efficient.
        It will calculate more lower-state energy levels than are actu-
        ally needed. But, this shouldn't be a problem other than doing a
        few unnecessary calculations. */
2186 bbinfo.hiK=bbmaxhiK;
2187 bbmaxhiK++; /* because of the Delta-K = +1 possibility */
2188 if(bbdebugflag<(DEBUG)){
2189 fprintf(DBG, "Before new calculations loop
     bbmaxhiK=%d\n",bbmaxhiK);
2190 fprintf(DBG,"\tMOL[%d].t[%d].Nhi=%s,
     MOL[%d].t[%d].Nlo=%s\n",bba,bbb,\
2191
         MOL[bba].t[bbb].Nhi,bba,bbb,MOL[bba].t[bbb].Nlo);
2192 fflush(DBG);
2193 }
      /* Calculate any newly needed energy levels. */
      /* loop through each lower Omega */
2194 bbLV=bblovlo+bblovnum;
2195 if(bbdebugflag<(DEBUG)){</pre>
2196 fprintf(DBG,"bbd=%d, bbLV=%d\n",bbd,bbLV);
2197 fflush(DBG);
2198 }
2199 for(bbf=bblovlo;bbf<bbLV;bbf++){ /* check low-state v-levels */
2200
       bbff=bbd*30+bbf; /* Index for the array of rc rotational sets */
2201 if(bbdebugflag<(DEBUG)){</pre>
2202 fprintf(DBG,"bbf=%d, bbff=%d, bbdum=%d\n",bbf,bbff,bbdum);
2203 fprintf(DBG,"\tMOL[%d].t[%d].Nhi=%s,
     MOL[%d].t[%d].Nlo=%s\n",bba,bbb,\
2204
         MOL[bba].t[bbb].Nhi,bba,bbb,MOL[bba].t[bbb].Nlo);
2205 fflush(DBG);
2206 }
2207
       if(MOL[bba].s[bbStlo].rc[bbff].kc==0){
```

```
/* this v has never been calculated, so call a function to calculate
        it. */
       if(CB[bbCblo].we!=0){
2208
2209
         bbDe=4*pow(CB[bbCblo].Be,3)/(CB[bbCblo].we*CB[bbCblo].we);
2210
         bbBvDv=(CB[bbCblo].Be-CB[bbCblo].ae*(bbf+0.5))/\
2211
           (2*(bbDe+CB[bbCblo].beta*(bbf+0.5)));
2212
         MOL[bba].s[bbStlo].rc[bbff].Kdissoc=\
2213
           floor((sqrt(1+4*bbBvDv)-1)/2);
2214
         }
2215
       else MOL[bba].s[bbStlo].rc[bbff].Kdissoc=RAND_MAX;
2216
         if(bbmaxhiK<MOL[bba].s[bbStlo].rc[bbff].Kdissoc){</pre>
2217
           case_b_cascade(&MOL[bba].s[bbStlo].rc[bbff],
2218
             bbCblo,bbf,0,bbmaxhiK,bbinfo.nlJ);
2219
           }
2220
         else{
           case_b_cascade(&MOL[bba].s[bbStlo].rc[bbff],bbCblo,\
2221
2222
           bbf,0,(int)(MOL[bba].s[bbStlo].rc[bbff].Kdissoc+1),
2223
           bbinfo.nlJ);
2224
           }
2225 if(bbdebugflag<(DEBUG)){</pre>
2226 fprintf(DBG,"just called case_b_cascade, v never calc'd\n");
2227 fprintf(DBG,"CB[%d].Be=%12.6e; CB[%d].we=%12.6e;
     CB[%d].ae=%12.6e\n",\
2228
     bbCblo,CB[bbCblo].Be,bbCblo,CB[bbCblo].we,bbCblo,CB[bbCblo].ae);
2229 fprintf(DBG,"bbf=%d, bbDe=%12.6e, bbBvDv=%12.6e,
     ",bbf,bbDe,bbBvDv);
2230 fprintf(DBG, "MOL[%d].s[%d].rc[%d].Jdissoc = %12.6e\n", bba, bb-
     Stlo, bbff,\
2231
         MOL[bba].s[bbStlo].rc[bbff].Kdissoc);
2232 fflush(DBG);
2233 fprintf(DBG,"j was zero; just called cascade \n");
2234 fprintf(DBG,"MOL[%d].s[%d].rc[%d].kc=%d\n",bba,bbStlo,bbff,\
2235
         MOL[bba].s[bbStlo].rc[bbff].kc);
2236 fprintf(DBG,"\tMOL[%d].t[%d].Nhi=%s, MOL[%d].t[%d].Nlo = %s\n",
     bba, bbb,\
2237
         MOL[bba].t[bbb].Nhi,bba,bbb,MOL[bba].t[bbb].Nlo);
2238 fflush(DBG);
2239 }
2240
         }
2241
       else{
      /* This v has been calculated. See if enough J's are calculated */
2242
         if(MOL[bba].s[bbStlo].rc[bbff].kc<bbmaxhiK){
         if(bbmaxhiK<MOL[bba].s[bbStlo].rc[bbff].Kdissoc){</pre>
2243
2244 if(bbdebugflag<(DEBUG)){
2245 fprintf(DBG,"j<maxJ; bbmaxhiK < Kdissoc; about to call cascade
     \n");
2246 fprintf(DBG,"bbmaxhiK=%d;
     MOL[%d].s[%d].rc[%d].Kdissoc=%12.6e\n",\
       bbmaxhiK,bba,bbStlo,bbff,MOL[bba].s[bbStlo].rc[bbff].Kdissoc);
2247
2248 fprintf(DBG,"MOL[%d].s[%d].rc[%d].kc=%d\n",bba,bbStlo,bbff,\
         MOL[bba].s[bbStlo].rc[bbff].kc);
2249
2250 fprintf(DBG,"\tMOL[%d].t[%d].Nhi=%s,
     MOL[\%d].t[\%d].Nlo=\%s\n",bba,bbb,\
```

2251 MOL[bba].t[bbb].Nhi,bba,bbb,MOL[bba].t[bbb].Nlo); 2252 fflush(DBG); 2253 } 2254 case_b_cascade(&MOL[bba].s[bbStlo].rc[bbff],bbCblo,\ 2255 bbf,MOL[bba].s[bbStlo].rc[bbff].kc, 2256 bbmaxhiK,bbinfo.nlJ); } 2257 2258 else{ 2259 if(bbdebugflag<(DEBUG)){ 2260 fprintf(DBG, "j<maxJ; about to call cascade \n"); 2261 fprintf(DBG,"j<maxJ; bbmaxhiK > Kdissoc; about to call cascade \n"); 2262 fprintf(DBG,"bbmaxhiK=%d; MOL[%d].s[%d].rc[%d].Kdissoc=%12.6e\n",\ 2263 bbmaxhiK,bba,bbStlo,bbff,MOL[bba].s[bbStlo].rc[bbff].Kdissoc); 2264 fprintf(DBG,"MOL[%d].s[%d].rc[%d].kc=%d\n",bba,bbStlo,bbff,\ MOL[bba].s[bbStlo].rc[bbff].kc); 2265 2266 fprintf(DBG,"\tMOL[%d].t[%d].Nhi=%s, $MOL[%d].t[%d].Nlo=%s\n",bba,bbb,\$ 2267 MOL[bba].t[bbb].Nhi,bba,bbb,MOL[bba].t[bbb].Nlo); 2268 fflush(DBG); 2269 } 2270 case_b_cascade(&MOL[bba].s[bbStlo].rc[bbff],bbCblo, 2271 bbf,MOL[bba].s[bbStlo].rc[bbff].kc, 2272 (int)(MOL[bba].s[bbStlo].rc[bbff].Kdissoc+1),bbinfo.nlJ); 2273 } 2274 if(bbdebugflag<(DEBUG)){ 2275 fprintf(DBG, "j was <maxJ; just called cascade \n"); 2276 fprintf(DBG,"MOL[%d].s[%d].rc[%d].kc=%d\n",bba,bbStlo,bbff,\ 2277 MOL[bba].s[bbStlo].rc[bbff].kc); 2278 fprintf(DBG,"\tMOL[%d].t[%d].Nhi=%s, $MOL[%d].t[%d].Nlo=%s\n",bba,bbb,\$ 2279 MOL[bba].t[bbb].Nhi,bba,bbb,MOL[bba].t[bbb].Nlo); 2280 fflush(DBG); 2281 fprintf(DBG,"just called case_b_cascade for cascade only\n"); 2282 fflush(DBG); 2283 } 2284 } } 2285 } 2286 /* Reset values of vclo and vcnum for the next transition */ 2287 MOL[bba].s[bbStlo].v[0].vclo=bblovlo; 2288 MOL[bba].s[bbStlo].v[0].vcnum=bblovnum; 2289 if(bbdebugflag<(DEBUG)){</pre> 2290 fprintf(DBG,"MOL[%d].s[%d].v[%d].vclo=%d ",bba,bbStlo,0,\ 2291 MOL[bba].s[bbStlo].v[0].vclo); 2292 fprintf(DBG,"MOL[%d].s[%d].v[%d].vcnum=%d\n",bba,bbStlo,0,\ MOL[bba].s[bbStlo].v[0].vcnum); 2293 2294 fprintf(DBG,"\tMOL[%d].t[%d].Nhi=%s, $MOL[%d].t[%d].Nlo=%s\n",bba,bbb,\$ MOL[bba].t[bbb].Nhi,bba,bbb,MOL[bba].t[bbb].Nlo); 2295 2296 fflush(DBG);

```
/* Check whether larger selection rules (Lambda, S, +/- in Sigma
        states) are violated. If they are, write a note to that effect to
        the DBG file. */
2298 if(bbdebugflag<(DEBUG)){
2299 fprintf(DBG,"bbHI[0].L=%d, bbL0[0].L=%d\n",bbHI[0].L,bbL0[0].L);
2300 fflush(DBG);
2301 }
2302 if((abs(bbHI[0].L-bbL0[0].L))>1){
2303
       fprintf(PAR, "WARNING!!! Normal selection rule violated for
     Delta-");
2304
       fprintf(PAR, "Lambda=0,+/-1 for\n\tTransition %s-->%s\n",\
2305
           MOL[bba].t[bbb].Nhi,MOL[bba].t[bbb].Nlo);
       fprintf(PAR,"\tThis is non-fatal; only a warning.\n");
2306
2307 if(bbdebugflag<(DEBUG)){
2308 fprintf(DBG, "Delta-L selection rule violated.\n");
2309 fflush(DBG);
2310 }
2311
       }
2312 if((fabs(bbHI[0].S-bbL0[0].S))>0.01){ /* <<< an overkill against
        round-off */
2313
       fprintf(PAR, "WARNING!!! Normal selection rule violated for
     Delta-");
       fprintf(PAR,"S=0 for\n\tTransition %s-->%s\n",\
2314
2315
           MOL[bba].t[bbb].Nhi,MOL[bba].t[bbb].Nlo);
2316
       fprintf(PAR,"\tThis is non-fatal; only a warning.\n");
2317 if(bbdebugflag<(DEBUG)){
2318 fprintf(DBG, "Delta-S selection rule violated\n");
2319 fflush(DBG);
2320 }
2321
       }
     /* loop through vibration levels starting with the highest in
        case anyone wants to include cascade between v-levels one day.
        Same for J's and K's later. Certainly *someone* will want to do
        that... */
2322 bbT=&MOL[bba].t[bbb]; /* an abbreviation */
2323 if(bbdebugflag<DEBUG){
2324 fprintf(DBG,"bba=%d, bbb=%d,
     MOL[bba].t[bbb].Nlo=%s\n",bba,bbb,bbT[0].Nlo);
2325 fprintf(DBG,"bbT.Nhi=%s, bbT.Nlo=%s\n",bbT[0].Nhi,bbT[0].Nlo);
2326 fprintf(DBG,"High: MOL[%d].s[%d].v[0].vclo=%d ",bba,bbSthi,
2327
         MOL[bba].s[bbSthi].v[0].vclo);
2328 fprintf(DBG,"High: MOL[%d].s[%d].v[0].vcnum=%d\n",bba,bbSthi,\
2329
         MOL[bba].s[bbSthi].v[0].vcnum);
2330 fprintf(DBG,"High: MOL[%d].s[%d].v[0].vlo=%d ",bba,bbSthi,\
2331
         MOL[bba].s[bbSthi].v[0].vlo);
2332 fprintf(DBG,"High: MOL[%d].s[%d].v[0].vnum=%d\n",bba,bbSthi,\
         MOL[bba].s[bbSthi].v[0].vnum);
2333
2334 fprintf(DBG,"bbhivnum=%d; bblovnum=%d\n",bbhivnum,bblovnum);
2335 fprintf(DBG,"bbHI[0].L=%d, bbL0[0].L=%d\n",bbHI[0].L,bbL0[0].L);
2336 fflush(DBG);
2337 }
      /* call other functions to calculate transitions for various sce-
        narios */
2338 if((bbHI[0].L==0)&&(bbL0[0].L==0)){ /* If Sigma to Sigma */
```

```
2339
       if(bbHI[0].p!=bbL0[0].p){ /* For the +<->+, -<->- rule */
2340 fprintf(PAR,"\n\nTRANSITION OMITTED!!!!!!!! (see below)\n\n");
2341 fprintf(PAR, "Transition called for Sigma((d)-->Sigma((d).\n", \
         bbHI[0].p,bbL0[0].p);
2342
2343 fprintf(PAR, "Molecule is %s; Transition %s-->%s\n", MOL[bba].Mol, \
2344
         bbT[0].Nhi,bbT[0].Nlo);
2345 fprintf(PAR, "This program doesn't know how to break that selection
     rule.\n");
2346 fprintf(PAR,"The program will continue with this transition omit-
     ted.\n\n";
2347 fflush(PAR);
2348
         }
2349
       else{ /* check g-u rule if homonuclear and call function */
         if((bbHI[0].g!=0)&&(bbHI[0].g==bbL0[0].g)){
2350
2351 fprintf(PAR,"\n\nTRANSITION OMITTED!!!!!!!! (see below)\n\n");
2352 fprintf(PAR,"Transition called for two states that are both either
     ");
2353 fprintf(PAR,"gerade or ungerade.\n");
2354 fprintf(PAR, "Molecule is %s; Transition %s-->%s\n", MOL[bba].Mol, \
         bbT[0].Nhi,bbT[0].Nlo);
2355
2356 fprintf(PAR, "This program doesn't know how to break that selection
     rule.\n");
2357 fprintf(PAR, "The program will continue with this transition omit-
     ted.\n\n";
2358 fflush(PAR);
2359
           ł
2360
         else bb_SigmaSigma(bbinfo);
2361
         }
2362
       }
2363 else{
       if((bbHI[0].L==0)||(bbL0[0].L==0)) bb_SigmaOther(bbinfo); /* if
2364
       one or the other state is Sigma, but not both */
       else bb_Other(bbinfo); /* neither state is Sigma */
2365
2366
       }
2367 return;
2368 }
     2369
     /*This function calculates transitions between Hund's Cases (b) and
        (b) when both the upper and lower states are sigma states. */
2370 void bb_SigmaSigma(BBTinfo bbSS){
     /* see parent function and header file for key to variable names */
     /* indexes and dummy variables: */
2371 int bbSSe=0, bbSSee=0, bbSSf=0, bbSSff=0;
2372 int bbSSh=0,bbSSk=0,bbSSfrnh=0,bbSSfrcl=0,bbSSfrch=0;
2373 int bbSSeh=0,bbSSi=0,bbSSehh=0,bbSSel=0,bbSSel1=0,bbSSjii=0;
     /* variables for info about the two states */
2374 double
     bbSSJ=0,bbSSSh=0,bbSSS1=0,bbSStrprob=0,bbSSvhpop=0,bbSShipop=0;
     /* Intensity multiplier for satellite bands and FCF dummy variable
        */
2375 double bbSSSATT=0,bbSSfcf=0,bbSSfcfr=0;
```

```
/* variables for calculating Holn-London factors */
2376 int bbSSL=0, bbSSB=0, bbSSdL=0;
     /* variables for spin stats if the state is homonuclear */
2377 int bbSSg=0,bbSSisym=0,bbSSpsym=0;
2378 double bbSSIa=0,bbSScascadetemp=0;
      /* a few flags for various purposes */
2379 int bbSSflga=0,bbSSflgb=0,bbSSfrnhf=0,bbSSfrchf=0;
      /* variables for creating and writing to output files */
2380 char bbSSfile[1000];
2381 FILE *BBSSFILE;
2382 Case_b_stateinfo *bbSSHI,*bbSSLO;
2383 if(bbSSdebugflag<DEBUG){
2384 fprintf(DBG,"bbSS.hvnlo=%d, bbSS.hvnnum=%d\n",\
2385
         bbSS.hvnlo,bbSS.hvnnum);
2386 fprintf(DBG,"bbSS.hvclo=%d, bbSS.hvcnum=%d\n",\
2387
         bbSS.hvclo,bbSS.hvcnum);
2388 fprintf(DBG,"bbSS.lvnlo=%d, bbSS.lvnnum=%d,\n",\
         bbSS.lvnlo,bbSS.lvnnum);
2389
2390 fprintf(DBG,"bbSS.lvclo=%d, bbSS.lvcnum=%d\n",\
         bbSS.lvclo,bbSS.lvcnum);
2391
2392 fprintf(DBG,"bbSS.hivlo=%d, bbSS.hivnum=%d,\n",\
2393
         bbSS.hivlo,bbSS.hivnum);
2394 fprintf(DBG,"bbSS.lovlo=%d, bbSS.lovnum=%d\n",\
2395
         bbSS.lovlo,bbSS.lovnum);
2396 fflush(DBG);
2397 }
2398 bbSSHI=bbSS.Ch;
2399 bbSSLO=bbSS.Cl;
2400 bbSSSh=bbSSHI[0].S;
2401 bbSSS1=bbSSL0[0].S;
2402 bbSSisym=bbSS.Sh[0].Isymm;
2403 bbSSpsym=bbSS.Sh[0].pmsymm;
2404 bbSShipop=bbSS.Sh[0].pop;
2405 bbSStrprob=bbSS.T[0].P[0];
      /* check for homonuclear information */
2406 if(bbSSHI[0].g!=0){
2407
       bbSSg=bbSSHI[0].g;
2408
       bbSSIa=bbSSHI[0].I/(bbSSHI[0].I+1);
2409
       }
      /* Just to be explicit about it... */
2410 bbSSL=bbSSdL=0; /* Upper-state Lambda is zero and Delta-Lambda is
        zero. */
      /* start loop down through high vib levels */
2411 for(bbSSe=(bbSS.hivlo+bbSS.hivnum-1);bbSSe>=bbSS.hivlo;bbSSe--){
2412
       bbSSee=(bbSSe-bbSS.hivlo)*bbSS.lovnum; /* simset posn. in 2D */
2413
       bbSSfrnh=(bbSSe-bbSS.hvnlo); /* high state native vib position
        */
       bbSSfrch=bbSSe; /* high state cascade vib position */
2414
      /* these flags (bbSSfrnhf and bbSSfrchf) tell if this high vib state
        is populated natively, by cascade, or both. They will be used
        later */
```

```
2416
         bbSSfrnhf=0;
2417
         bbSSvhpop=bbSS.Vh[0].p[bbSSe-bbSS.hvnlo];
2418
         }
2419
       else bbSSfrnhf=-1;
2420
       if((bbSSe>=bbSS.hvclo)&&(bbSSe<(bbSS.hvclo+bbSS.hvcnum))){
2421
         bbSSfrchf=0;
2422
         }
2423
       else bbSSfrchf=-1;
2424 if(bbSSdebugflag<DEBUG){
2425 fprintf(DBG,"bbSSfrnhf=%d, bbSSvhpop=%f, bbSSfrchf=%d, ",
2426
         bbSSfrnhf, bbSSvhpop, bbSSfrchf);
2427 fprintf(DBG,"bbSSe=%d, bbSSee=%d\nbbSSfrnh=%d, bbSSfrch=%d, ",\
2428
         bbSSe, bbSSee, bbSSfrnh, bbSSfrch);
2429 fflush(DBG);
2430 }
     /* start loop down through low vib levels */
2431 for(bbSSf=(bbSS.lovlo+bbSS.lovnum-1);bbSSf>=bbSS.lovlo;bbSSf--){
2432
       bbSSfcf=bbSS.T[0].v[bbSSe].fcfn[bbSSf];
2433
     if(bbSSfcf!=0){bbSSfcfr=bbSS.T[0].v[bbSSe].fcfc[bbSSf]/bbSSfcf;}
2434
       bbSSff=bbSSee+bbSSf-bbSS.lovlo; /* position in last dimension */
2435
       bbSSfrcl=bbSSf;
2436 if(bbSSdebugflag<DEBUG){
2437 fprintf(DBG,"bbSSf=%d, bbSS.lovlo=%d, bbSS.lovnum=%d \n",\
2438
         bbSSf,bbSS.lovlo,bbSS.lovnum);
2439 fprintf(DBG,"bbSS.nT=%d, bbSS.hiK=%d \n",bbSS.nT,bbSS.hiK);
2440 fflush(DBG);
2441 }
2442
       bbSS.T[0].S[bbSSff].n=bbSS.nT*bbSS.hiK;
2443
       bbSS.T[0].S[bbSSff].f=\
         (double*)calloc(bbSS.T[0].S[bbSSff].n,sizeof(double));
2444
2445
       bbSS.T[0].S[bbSSff].ni=
2446
         (double*)calloc(bbSS.T[0].S[bbSSff].n,sizeof(double));
2447
       bbSS.T[0].S[bbSSff].ci=
2448
         (double*)calloc(bbSS.T[0].S[bbSSff].n,sizeof(double));
2449 bbSS.Rl=&bbSS.Sl[0].rc[bbSSfrcl];
2450 if(bbSSdebugflag<DEBUG){
2451 fprintf(DBG,"bbSSff=%d, bbSSfrcl=%d,
     bbSS.T[0].S[bbSSff].n=%d\n",\
2452
         bbSSff,bbSSfrcl,bbSS.T[0].S[bbSSff].n);
2453 fflush(DBG);
2454 }
     /* start with highest J value (same reason as before), and loop down
        looking for lower J's to which to transit. assign intensities.
        If both states are Omega=0, then assign zero intensity to transi-
        tions for J=O<->J=O. */
2455
       if (bbSSfrnhf==0) { /* if this v is natively populated.*/
2456 sprintf(bbSSfile,"%s_molecules/%s/%s--%s_v%d--v%d_NAT.dat",
       PREF,MOL[bbSS.m].Mol,bbSS.T[0].Nhi,bbSS.T[0].Nlo,bbSSe,bbSSf);
2457
2458
         BBSSFILE=fopen(bbSSfile,"w");
2459
         if(BBSSFILE==NULL){
2460 printf("Error opening transition sub-file %s. Exit-
     ing.\n",bbSSfile);
```

```
2461
           exit(1);
2462
           }
2463 fprintf(BBSSFILE,"# File created by %s.\n# File contains ",PRO-
     GRAM_NAME);
2464 fprintf(BBSSFILE,"P and R");
2465 fprintf(BBSSFILE," branches from the simulation titled s\n",PREF);
2466 fprintf(BBSSFILE, "# THESE INTENSITIES ARE DUE TO USER-SPECIFIED
     POPULATIONS");
2467 fprintf(BBSSFILE," ONLY -- NO CASCADE\n");
2468 fprintf(BBSSFILE, "# Transition is Hund's Case (b) to Hund's Case
     (b).\n");
2469 fprintf(BBSSFILE,"# Molecule %s, \tHigh state: %s, v=%d\n",\
2470
         MOL[bbSS.m].Mol,bbSS.T[0].Nhi,bbSSe);
2471 fprintf(BBSSFILE,"#\t\tLow state: %s, v=%d\n# Columns are: ",\
2472
         bbSS.T[0].Nlo,bbSSf);
2473 fprintf(BBSSFILE, "K_hi K_lo J_hi P(J_hi+1)_v P_i R(J_hi-1)_v
     R_i n#(n");
2474 fflush(BBSSFILE);
2475
         bbSS.Rh=&bbSS.Sh[0].r[bbSSfrnh];
2476
         if((bbSS.hiK)<bbSS.Sh[0].r[bbSSfrnh].k){</pre>
2477
           bbSSk=bbSS.hiK-1;
2478
           }
2479
         else bbSSk=bbSS.Sh[0].r[bbSSfrnh].k-1;
2480
         if(bbSS.R1[0].Kdissoc<(bbSSk-1)){
2481 fprintf(PAR,"\nWARNING!! State %s of molecule %s has significant
     ",\
2482
         bbSS.T[0].Nhi,MOL[bbSS.m].Mol);
2483 fprintf(PAR, "rotational population at level %d\n", bbSSk);
2484 fprintf(PAR,"\tBut lower state %s dissociates at level %.1f\n",\
2485
         bbSS.T[0].Nlo,bbSS.Rl[0].Kdissoc);
2486 fprintf(PAR,"It is likely that the bound upper state is transiting
     to (an)");
2487 fprintf(PAR, " unbound lower state(s).\n");
2488 fprintf(PAR,"Look for continuum emissions trailing off to the low-
     energy ");
2489 fprintf(PAR,"end of the v(hi)=%d to v(lo)=%d\nband in the real ",bb-
     SSe, bbSSf);
2490 fprintf(PAR,"spectrum (not the simulated one)\nCurrently, this pro-
     gram will");
2491 fprintf(PAR," not simulate bound-->unbound spectra.\n\n");
2492
           bbSSk=(int)(bbSS.R1[0].Kdissoc);
2493
           ł
2494 if(bbSSdebugflag<DEBUG){
2495 fprintf(DBG,"bbSSfrnh=%d, bbSSk=%d, ",bbSSfrnh,bbSSk);
2496 fprintf(DBG, "bbSS.Sh[0].r[%d].k = %dn", bbSSfrnh,
     bbSS.Sh[0].r[bbSSfrnh].k);
2497 fflush(DBG);
2498 }
      /* To make the output file easy to write, I'm cycling by high-state
        K first, then by high-state J. From that J/K(hi) pair, the pro-
        gram will look for a P transition and an R transition to K+1 then
```

to K-1. If all the necessary states exist, it will check to see if there are any symmetry or nuclear spin effects to be concerned

```
about. Taking these into account, it will calculate the transi-
        tion. */
      /* loop first by upper-state K-value */
2499 for(bbSSh=bbSSk;bbSSh>=0;bbSSh--){
2500
       bbSSjii=(bbSSh+1)*bbSS.nT-1; /* position in simset array */
2501
       bbSSeh=bbSSh*bbSS.nhJ; /* position in 2D for high EJ & PJ */
      /* then loop by upper-state J for this K */
2502
       for(bbSSi=(bbSS.nhJ-1);bbSSi>=0;bbSSi--){
2503
         bbSSJ=bbSSh+bbSSi-bbSSSh;
2504
         bbSSehh=bbSSeh+bbSSi;
2505
         bbSSflga=0;
2506
         if(bbSSh<bbSSHI[0].L) bbSSflga=1; /* if this K is less than
        Lambda for the high state, don't proceed */
         if(bbSSJ<0) bbSSflga=1; /* if J is less than zero, don't */
2507
2508 if (bbSSdebugflag<DEBUG) {
2509 fprintf(DBG,"bbSSh=%d, bbSSi=%d, bbSSSh=%.1f, bbSSHI[0].L=%d, bb-
     SSflga=%d\n",\
2510
         bbSSh, bbSSi, bbSSSh, bbSSHI[0].L, bbSSflga);
2511 fprintf(DBG,"bbSSjii=%d\n",bbSSjii);
2512 fflush(DBG);
2513 }
2514
         if(bbSSflga==0){
2515
           bbSSflgb=0;
      /* Check Delta-J=+1 (P) and then Delta-J=-1 (R) for Delta-K=+1.
        First, check to see if the target K exists: */
2516
           if((bbSSh+1)<(bbSSL0[0].L)) bbSSflgb=1;</pre>
      /* Relative position in the low state E/P array */
2517
           bbSSel=(bbSSh+1)*bbSS.nlJ + bbSS.nlJ-bbSS.nhJ + \
2518
             (int)(bbSSSh-bbSSSl) -1 + bbSSi;
2519 if(bbSSdebugflag<DEBUG){
2520 fprintf(DBG,"\t(bbSSh+1)*bbSS.nlJ=%d, bbSS.nlJ-bbSS.nhJ=%d\n",\
2521
         (bbSSh+1)*bbSS.nlJ,bbSS.nlJ-bbSS.nhJ);
2522 fprintf(DBG,"\t(int)(bbSSSh-bbSSS1)=%d, bbSSi=%d, bbSSel=%d\n",\
2523
         (int)(bbSSSh-bbSSS1),bbSSi,bbSSel);
2524 fflush(DBG);
2525 }
2526
           if((bbSSel+1)>=(bbSS.Rl[0].kc*bbSS.nlJ)) bbSSflgb=1;
      /* Then check if the target value for J+1 is less than or greater
        than the allowed J's for K+1. */
2527
           if((bbSSJ+1)>(bbSSh+1+bbSSS1)) bbSSflgb=1;
2528
           if((bbSSJ+1)<(bbSSh+1-bbSSS1)) bbSSflgb=1;
      /* Still OK? Calculate transition */
2529
           if(bbSSflgb==0){
2530
             bbSSB=+1;
2531
             bbSSell=bbSSel+1;
2532
             bbSS.T[0].S[bbSSff].f[bbSSjii]=\
2533
               bbSS.Rh[0].EJ[bbSSehh]-\
2534
               bbSS.R1[0].EJ[bbSSel1];
2535 if(bbSSdebugflag<DEBUG){
2536 fprintf(DBG,"bbSS.T[0].S[%d].f[%d]=%13.5e ",bbSSff,bbSSjii,\
2537
         bbSS.T[0].S[bbSSff].f[bbSSjii]);
2538 fprintf(DBG, "bbSS.Rh[0].EJ[%d] = %13.5e ", bbSSehh,
     bbSS.Rh[0].EJ[bbSSehh]);
```

```
2539 fprintf(DBG, "bbSS.R1[0].EJ[%d] = %13.5e\n", bbSSell,
     bbSS.R1[0].EJ[bbSSel1]);
2540 fflush(DBG);
2541 }
2542
             bbSS.T[0].S[bbSSff].ni[bbSSjii]=\
2543
               bbSShipop*bbSStrprob*bbSSvhpop*\
2544
               bbSS.Rh[0].PJ[bbSSehh]*bbSSfcf*\
2545
               HL(bbSSB,bbSSJ,bbSSL,bbSSdL);
2546 if(bbSSdebugflag<DEBUG){
2547 fprintf(DBG,"bbSShipop=%13.5e bbSStrprob=%13.5e ",bbS-
     Shipop, bbSStrprob);
2548 fprintf(DBG,"bbSSvhpop=%13.5e
     bbSSfcf=%13.6e\n",bbSSvhpop,bbSSfcf);
2549 fprintf(DBG,"bbSS.T[0].S[%d].ni[%d]=%13.5e ",\
2550
         bbSSff,bbSSjii,bbSS.T[0].S[bbSSff].ni[bbSSjii]);
2551 fprintf(DBG, "bbSS.Rh[0].PJ[%d] = %13.5e\n", bbSSehh,
     bbSS.Rh[0].PJ[bbSSehh]);
2552 fprintf(DBG, "HL(%d, %.1f, %d, %d) = %12.6e n", bbSSB, bbSSJ, bbSSL,
     bbSSdL,
2553
         HL(bbSSB,bbSSJ,bbSSL,bbSSdL));
2554 fflush(DBG);
2555 }
2556
             bbSS.R1[0].CJ[bbSSell]+=bbSSfcfr*\
               bbSS.T[0].S[bbSSff].ni[bbSSjii];
2557
2558 if(bbSSdebugflag<DEBUG){</pre>
2559 fprintf(DBG, "bbSS.Rl[0].CJ[%d] = %13.5e\n", bbSSell,
     bbSS.R1[0].CJ[bbSSel1]);
2560 fflush(DBG);
2561 }
2562
             bbSSjii--;
2563
             }
2564 if(bbSSdebugflag<DEBUG){
2565 fprintf(DBG,"%d",bbSSh);
2566 fflush(DBG);
2567 if(bbSSflgb!=0) fprintf(DBG," %d %.1f M M ",(bbSSh+1),bbSSJ);
2568 else{
2569 fprintf(DBG,"%d %.1f %18.12e %18.12e (1a)\n",(bbSSh+1),\
       bbSSJ,bbSS.T[0].S[bbSSff].f[bbSSjii+1],
2570
2571
       bbSS.T[0].S[bbSSff].ni[bbSSjii+1]);
2572
       }
2573 fflush(DBG);
2574 }
2575 fprintf(BBSSFILE,"%d ",bbSSh);
2576 if(bbSSflgb!=0) fprintf(BBSSFILE," %d %.1f M M ",(bbSSh+1),bbSSJ);
2577 else{
2578 fprintf(BBSSFILE, "%d %.1f %18.12e %18.12e ",(bbSSh+1),\
       bbSSJ,bbSS.T[0].S[bbSSff].f[bbSSjii+1],\
2579
2580
       bbSS.T[0].S[bbSSff].ni[bbSSjii+1]);
2581
       ł
2582 fflush(BBSSFILE);
      /* Now, Delta-J=-1 (R) for Delta-K=+1. */
2583
           bbSSflgb=0;
2584
           if((bbSSh+1)<(bbSSL0[0].L)) bbSSflgb=1;
2585
           if((bbSSJ-1)>(bbSSh+1+bbSSS1)) bbSSflgb=1;
```

```
2586
           if((bbSSJ-1)<(bbSSh+1-bbSSS1)) bbSSflgb=1;
2587
           if((bbSSJ-1)<0) bbSSflgb=1;
2588
           if((bbSSel-1)<0) bbSSflgb=1;
2589
           if(bbSSflgb==0){
2590
             bbSSB=-1;
2591
             bbSSell=bbSSel-1;
             bbSS.T[0].S[bbSSff].f[bbSSjii]=\
2592
               bbSS.Rh[0].EJ[bbSSehh]-\
2593
2594
               bbSS.R1[0].EJ[bbSSel1];
2595 if(bbSSdebugflag<DEBUG){
2596 fprintf(DBG,"bbSS.T[0].S[%d].f[%d]=%13.5e ",bbSSff,bbSSjii,\
         bbSS.T[0].S[bbSSff].f[bbSSjii]);
2597
2598 fprintf(DBG, "bbSS.Rh[0].EJ[%d] = %13.5e ", bbSSehh,
     bbSS.Rh[0].EJ[bbSSehh]);
2599 fprintf(DBG, "bbSS.R1[0].EJ[%d] = %13.5e\n", bbSSell,
     bbSS.R1[0].EJ[bbSSel1]);
2600 fflush(DBG);
2601 }
2602
             bbSS.T[0].S[bbSSff].ni[bbSSjii]=\
2603
               bbSShipop*bbSStrprob*bbSSvhpop*\
2604
               bbSS.Rh[0].PJ[bbSSehh]*bbSSSATT*\
2605
               HL(bbSSB,bbSSJ,bbSSL,bbSSdL)*bbSSfcf;
2606 if(bbSSdebugflag<DEBUG){
2607 fprintf(DBG,"bbSShipop=%13.5e bbSStrprob=%13.5e bbSSvhpop=%13.5e
     ",\
2608
         bbSShipop,bbSStrprob,bbSSvhpop);
2609 fprintf(DBG,"bbSSfcf=%13.6e\n",bbSSfcf);
2610 fprintf(DBG,"bbSS.T[0].S[%d].ni[%d]=%13.5e ",
2611
         bbSSff,bbSSjii,bbSS.T[0].S[bbSSff].ni[bbSSjii]);
2612 fprintf(DBG, "bbSS.Rh[0].PJ[%d] = %13.5e\n", bbSSehh,
     bbSS.Rh[0].PJ[bbSSehh]);
2613 fprintf(DBG, "HL(%d, %.1f, %d, %d) = %12.6e n", bbSSB, bbSSJ, bbSSL,
     bbSSdL,\
2614
         HL(bbSSB,bbSSJ,bbSSL,bbSSdL));
2615 fflush(DBG);
2616 }
2617
             bbSS.R1[0].CJ[bbSSel1]+=bbSSfcfr*\
               bbSS.T[0].S[bbSSff].ni[bbSSjii];
2618
2619 if(bbSSdebugflag<DEBUG){
2620 fprintf(DBG, "bbSS.R1[0].CJ[%d] = %13.5e\n", bbSSell,
     bbSS.R1[0].CJ[bbSSell]);
2621 }
2622
             bbSSjii--;
             }
2623
2624 if(bbSSdebugflag<DEBUG){
2625 if(bbSSflgb!=0) fprintf(DBG,"M M (Nat) (1b)\n");
2626 else{
2627 fprintf(DBG, "%18.12e (Z) %18.12e (1b)\n",
     bbSS.T[0].S[bbSSff].f[bbSSjii+1],
2628
       bbSS.T[0].S[bbSSff].ni[bbSSjii+1]);
2629
       }
2630 }
2631 if(bbSSflgb!=0) fprintf(BBSSFILE,"M M\n");
2632 else{
```

```
2633 fprintf(BBSSFILE, "%18.12e %18.12e\n",
     bbSS.T[0].S[bbSSff].f[bbSSjii+1],
2634
       bbSS.T[0].S[bbSSff].ni[bbSSjii+1]);
2635
       }
2636
           bbSSflgb=0;
      /* Check Delta-J=+1 (P) and then Delta-J=-1 (R) for Delta-K=-1.
        First, check to see if the target K exists: */
           if((bbSSh-1)<(bbSSL0[0].L)) bbSSflgb=1;</pre>
2637
      /* Relative position in the low state E/P array */
2638
           bbSSel=(bbSSh-1)*bbSS.nlJ + bbSS.nlJ-bbSS.nhJ + \
2639
             (int)(bbSSSh-bbSSS1) + 1 + bbSSi;
2640 if(bbSSdebugflag<DEBUG){
2641 fprintf(DBG, "\t(bbSSh+1)*bbSS.nlJ = %d, bbSS.nlJ-bbSS.nhJ=%d\n",\
         (bbSSh+1)*bbSS.nlJ,bbSS.nlJ-bbSS.nhJ);
2642
2643 fprintf(DBG,"\t(int)(bbSSSh-bbSSS1)=%d, bbSSi=%d, bbSSel=%d\n",\
2644
         (int)(bbSSSh-bbSSS1),bbSSi,bbSSel);
2645 fflush(DBG);
2646 }
      /* Then check if the target value for J+1 is less than or greater
        than the allowed J's for K-1. */
2647
           if((bbSSJ+1)>(bbSSh-1+bbSSS1)) bbSSflgb=1;
           if((bbSSJ+1)<(bbSSh-1-bbSSS1)) bbSSflgb=1;</pre>
2648
2649
           if((bbSSel+1)>=(bbSS.Rl[0].kc*bbSS.nlJ)) bbSSflgb=1;
      /* Still OK? Calculate transition */
2650
           if(bbSSflgb==0){
2651
             bbSSB=+1;
2652
             bbSSell=bbSSel+1;
2653
             bbSS.T[0].S[bbSSff].f[bbSSjii]=\
2654
               bbSS.Rh[0].EJ[bbSSehh]-
               bbSS.R1[0].EJ[bbSSel1];
2655
2656
             bbSS.T[0].S[bbSSff].ni[bbSSjii]=\
2657
               bbSShipop*bbSStrprob*bbSSvhpop*\
               bbSS.Rh[0].PJ[bbSSehh]*bbSSSATT*\
2658
2659
               HL(bbSSB,bbSSJ,bbSSL,bbSSdL)*bbSSfcf;
2660
             bbSS.R1[0].CJ[bbSSel1]+=bbSSfcfr*\
               bbSS.T[0].S[bbSSff].ni[bbSSjii];
2661
2662 if(bbSSdebugflag<DEBUG){
2663 fprintf(DBG,"bbSSel=%d, bbSSi-1=%d, bbSSel1=%d\n",bbSSel,bbSSi-
     1,bbSSell);
2664 fprintf(DBG,"\tbbSS.T[0].S[%d].f[%d]=%12.6e\n",\
2665
         bbSSff,bbSSjii,bbSS.T[0].S[bbSSff].f[bbSSjii]);
2666 fprintf(DBG, "\tbbSS.Rh[0].EJ[%d] = %12.6e\n", bbSSehh,
     bbSS.Rh[0].EJ[bbSSehh]);
2667 fprintf(DBG, "\tbbSS.R1[0].EJ[%d] = %12.6e\n", bbSSell,
     bbSS.R1[0].EJ[bbSSel1]);
2668 fprintf(DBG,"\tbbSS.T[0].S[%d].ni[%d]=%12.6e\n",\
         bbSSff,bbSSjii,bbSS.T[0].S[bbSSff].ni[bbSSjii]);
2669
2670 fprintf(DBG,"\tbbSShipop=%12.6e, bbSStrprob=%12.6e, bbSSvh-
     pop=%12.6e ",\
         bbSShipop, bbSStrprob, bbSSvhpop);
2671
2672 fprintf(DBG,"bbSSfcf=%13.6e\n",bbSSfcf);
2673 fprintf(DBG, "\tbbSS.Rh[0].PJ[%d] = %12.6e\n", bbSSehh,
     bbSS.Rh[0].PJ[bbSSehh]);
2674 fprintf(DBG,"\tHL(%d,%.1f,%d,%d)=%12.6e\n",bbSSB,bbSSJ,\
```

```
2675
         bbSSL, bbSSdL, HL(bbSSB, bbSSJ, bbSSL, bbSSdL));
2676 fprintf(DBG, "\tbbSS.R1[0].CJ[%d] = %12.6e\n", bbSSell,
     bbSS.R1[0].CJ[bbSSel1]);
2677 fprintf(DBG,"\tbbSS.T[0].S[%d].ni[%d]=%12.6e\n",\
2678
         bbSSff,bbSSjii,bbSS.T[0].S[bbSSff].ni[bbSSjii]);
2679 }
2680
             bbSSjii--;
             }
2681
2682 if(bbSSdebugflag<DEBUG){
2683 fprintf(DBG,"%d ",bbSSh);
2684 if(bbSSflgb!=0) fprintf(DBG," %d %.1f M M (here)",(bbSSh-1),bbSSJ);
2685 else{
2686 fprintf(DBG,"%d %.1f %18.12e %18.12e (here) ",(bbSSh-1),\
2687
       bbSSJ,bbSS.T[0].S[bbSSff].f[bbSSjii+1],
2688
       bbSS.T[0].S[bbSSff].ni[bbSSjii+1]);
       }
2689
2690 }
2691 fprintf(BBSSFILE,"%d ",bbSSh);
2692 if(bbSSflgb!=0) fprintf(BBSSFILE," %d %.1f M M ",(bbSSh-1),bbSSJ);
2693 else{
2694 fprintf(BBSSFILE, "%d %.1f %18.12e %18.12e ",(bbSSh-1),\
       bbSSJ,bbSS.T[0].S[bbSSff].f[bbSSjii+1],\
2695
2696
       bbSS.T[0].S[bbSSff].ni[bbSSjii+1]);
2697
       }
      /* Now, Delta-J=-1 (R) for Delta-K=+1. */
2698
           bbSSflgb=0;
2699
           if((bbSSh-1)<(bbSSL0[0].L)) bbSSflgb=1;</pre>
2700
           if((bbSSJ-1)>(bbSSh-1+bbSSS1)) bbSSflgb=1;
2701
           if((bbSSJ-1)<(bbSSh-1-bbSSS1)) bbSSflgb=1;
2702
           if((bbSSJ-1)<0) bbSSflgb=1;</pre>
2703
           if((bbSSel-1)<0) bbSSflgb=1;</pre>
2704 if(bbSSdebugflag<DEBUG){
2705 fprintf(DBG,"bbSSh-1=%d bbSSL0[0].L=%d\n",bbSSh-1,bbSSL0[0].L);
2706 fprintf(DBG,"bbSSh-1=%d, bbSS.nlJ-1=%d, bbSSel=%d\n",\
2707
         bbSSh-1,bbSS.nlJ-1,bbSSel);
2708 fprintf(DBG,"bbSSJ-1=%.1f bbSSh-1=%d, bbSSSl=%.1f\n",bbSSJ-
     1,bbSSh-1,bbSSS1);
2709 fprintf(DBG,"bbSSJ-1=%.1f, bbSSh-1=%d, bbSSSl=%.1f\n",bbSSJ-
     1,bbSSh-1,bbSSS1);
2710 fprintf(DBG,"bbSSflgb=%d\n",bbSSflgb);
2711 }
2712
           if(bbSSflgb==0){
2713
             bbSSB=-1;
             bbSSell=bbSSel-1;
2714
             bbSS.T[0].S[bbSSff].f[bbSSjii]=\
2715
2716
                bbSS.Rh[0].EJ[bbSSehh]-
               bbSS.R1[0].EJ[bbSSel1];
2717
2718
             bbSS.T[0].S[bbSSff].ni[bbSSjii]=\
2719
               bbSShipop*bbSStrprob*bbSSvhpop*\
2720
               bbSS.Rh[0].PJ[bbSSehh]*bbSSfcf*\
2721
               HL(bbSSB,bbSSJ,bbSSL,bbSSdL);
2722
             bbSS.R1[0].CJ[bbSSell]+=bbSSfcfr*\
2723
               bbSS.T[0].S[bbSSff].ni[bbSSjii];
2724 if(bbSSdebugflag<DEBUG){
```

```
2725 fprintf(DBG,"bbSSel=%d, bbSSi-1=%d, bbSSel1=%d\n",bbSSel,bbSSi-
     1,bbSSell);
2726 fprintf(DBG,"\tbbSS.T[0].S[%d].f[%d]=%12.6e\n",\
         bbSSff,bbSSjii,bbSS.T[0].S[bbSSff].f[bbSSjii]);
2727
2728 fprintf(DBG, "\tbbSS.Rh[0].EJ[%d] = %12.6e\n", bbSSehh,
     bbSS.Rh[0].EJ[bbSSehh]);
2729 fprintf(DBG, "\tbbSS.R1[0].EJ[%d] = %12.6e\n", bbSSell,
     bbSS.R1[0].EJ[bbSSell]);
2730 fprintf(DBG,"\tbbSS.T[0].S[%d].ni[%d]=%12.6e\n",\
         bbSSff,bbSSjii,bbSS.T[0].S[bbSSff].ni[bbSSjii]);
2731
2732 fprintf(DBG,"\tbbSShipop=%12.6e, bbSStrprob=%12.6e, bbSSvh-
     pop=%12.6e ",\
2733
         bbSShipop, bbSStrprob, bbSSvhpop);
2734 fprintf(DBG,"bbSSfcf=%13.6e\n",bbSSfcf);
2735 fprintf(DBG, "\tbbSS.Rh[0].PJ[%d] = %12.6e\n", bbSSehh,
     bbSS.Rh[0].PJ[bbSSehh]);
2736 fprintf(DBG,"\tHL(%d,%.1f,%d,%d)=%12.6e\n",bbSSB,bbSSJ,\
2737
         bbSSL, bbSSdL, HL(bbSSB, bbSSJ, bbSSL, bbSSdL));
2738 fprintf(DBG, "\tbbSS.Rl[0].CJ[%d] = %12.6e\n", bbSSell,
     bbSS.R1[0].CJ[bbSSel1]);
2739 fprintf(DBG,"\tbbSS.T[0].S[%d].ni[%d]=%12.6e\n",\
2740
         bbSSff,bbSSjii,bbSS.T[0].S[bbSSff].ni[bbSSjii]);
2741 }
2742
             }
2743 if(bbSSdebugflag<DEBUG){
2744 if(bbSSflgb!=0) fprintf(DBG,"M M\n");
2745 else{
2746 fprintf(DBG,"%18.12e %18.12e \n",bbSS.T[0].S[bbSSff].f[bbSSjii],\
2747
       bbSS.T[0].S[bbSSff].ni[bbSSjii]);
2748
       }
2749 }
2750 if(bbSSflgb!=0) fprintf(BBSSFILE,"M M\n");
2751 else{
2752 fprintf(BBSSFILE,"%18.12e
     %18.12e\n",bbSS.T[0].S[bbSSff].f[bbSSjii],\
2753
       bbSS.T[0].S[bbSSff].ni[bbSSjii]);
2754
       }
2755
           } /* close if bbSSflga is zero. */
         } /* close upper-state J-of-K loop */
2756
       } /* close upper-state K loop */
2757
2758
       fclose(BBSSFILE);
2759
         } /* close if high-state v is natively populated */
2760
       if(bbSSfrchf==0){ /* if this v is cascade populated.*/
2761 sprintf(bbSSfile,"%s_molecules/%s/%s--%s_v%d--v%d_CAS.dat",
2762
       PREF,MOL[bbSS.m].Mol,bbSS.T[0].Nhi,bbSS.T[0].Nlo,bbSSe,bbSSf);
2763
         BBSSFILE=fopen(bbSSfile,"w");
2764
         if(BBSSFILE==NULL){
2765 printf("Error opening transition sub-file %s. Exit-
     ing.\n",bbSSfile);
2766
           exit(1);
2767
2768 fprintf(BBSSFILE,"# File created by %s.\n# File contains ",PRO-
     GRAM_NAME);
```

```
2769 fprintf(BBSSFILE,"P and R");
2770 fprintf(BBSSFILE," branches from the simulation titled %s\n",PREF);
2771 fprintf(BBSSFILE,"# THESE INTENSITIES ARE DUE TO CASCADE ONLY -- ");
2772 fprintf(BBSSFILE, "NO USER-DEFINED POPULATIONS\n");
2773 fprintf(BBSSFILE, "# Transition is Hund's Case (b) to Hund's Case
     (b).\n");
2774 fprintf(BBSSFILE,"# Molecule %s, \tHigh state: %s, v=%d\n",\
2775
         MOL[bbSS.m].Mol,bbSS.T[0].Nhi,bbSSe);
2776 fprintf(BBSSFILE,"#\t\tLow state: %s, v=%d\n# Columns are: ",\
         bbSS.T[0].Nlo,bbSSf);
2777
2778 fprintf(BBSSFILE, "K_hi K_lo J_hi P(J_hi+1)_v P_i R(J_hi-1)_v
     R_i n#(n");
2779
         bbSS.Rh=&bbSS.Sh[0].rc[bbSSfrch];
2780
         if((bbSS.hiK)<bbSS.Sh[0].rc[bbSSfrch].kc){
2781
           bbSSk=bbSS.hiK-1;
2782
           }
2783
         else bbSSk=bbSS.Sh[0].rc[bbSSfrch].kc-1;
2784
         if(bbSS.R1[0].Kdissoc<(bbSSk-1)){
2785 fprintf(PAR,"\nWARNING!! State %s of molecule %s has significant
     ",\
2786
         bbSS.T[0].Nhi,MOL[bbSS.m].Mol);
2787 fprintf(PAR, "CASCADE rotational population at level %d\n", bbSSk);
2788 fprintf(PAR,"\tBut lower state %s dissociates at level \%.1f\n",\
2789
         bbSS.T[0].Nlo,bbSS.Rl[0].Kdissoc);
2790 fprintf(PAR,"It is likely that the bound upper state is transiting
     to (an)");
2791 fprintf(PAR," unbound lower state(s).\n");
2792 fprintf(PAR,"Look for continuum emissions trailing off to the low-
     energy ");
2793 fprintf(PAR,"end of the v(hi)=%d to v(lo)=%d\nband in the real ",bb-
     SSe,bbSSf);
2794 fprintf(PAR,"spectrum (not the simulated one)\nCurrently, this pro-
     gram will");
2795 fprintf(PAR," not simulate bound-->unbound spectra.\n\n");
2796
           bbSSk=(int)(bbSS.R1[0].Kdissoc);
2797
           }
2798 if(bbSSdebugflag<DEBUG){
2799 fprintf(DBG,"bbSSfrch=%d, bbSSk=%d, ",bbSSfrch,bbSSk);
2800 fprintf(DBG, "bbSS.Sh[0].rc[%d].kc = %d\n", bbSSfrch,
     bbSS.Sh[0].rc[bbSSfrch].kc);
2801 fflush(DBG);
2802 }
      /* To make the output file easy to write, I'm cycling by high-state
        K first, then by high-state J. From that J/K(hi) pair, the pro-
        gram will look for a P transition and an R transition to K+1 then
        to K-1. If all the necessary states exist, it will check to see
        if there are any symmetry or nuclear spin effects to be concerned
        about. Taking these into account, it will calculate the transi-
        tion. */
      /* loop first by upper-state K-value */
2803 for(bbSSh=bbSSk;bbSSh>=0;bbSSh--){
2804
       bbSSjii=(bbSSh+1)*bbSS.nT-1; /* position in simset array */
2805
       bbSSeh=bbSSh*bbSS.nhJ; /* position in 2D for high EJ & PJ */
```

```
/* then loop by upper-state J for this K */
2806
       for(bbSSi=(bbSS.nhJ-1);bbSSi>=0;bbSSi--){
         bbSSJ=bbSSh+bbSSi-bbSSSh;
2807
2808
         bbSSehh=bbSSeh+bbSSi;
2809
         bbSSflga=0;
         if(bbSSh<bbSSHI[0].L) bbSSflga=1; /* if this K is less than
2810
        Lambda for the high state, don't proceed */
2811
         if(bbSSJ<0) bbSSflga=1; /* if J is less than zero, don't */
2812 if(bbSSdebugflag<DEBUG){
2813 fprintf(DBG,"bbSSh=%d, bbSSi=%d, bbSSSh=%.1f, bbSSHI[0].L=%d, bb-
     SSflga=%d\n",\
2814
         bbSSh,bbSSi,bbSSSh,bbSSHI[0].L,bbSSflga);
2815 fflush(DBG);
2816 }
2817
         if(bbSSflga==0){
2818
           bbSSflgb=0;
      /* Check Delta-J=+1 (P) and then Delta-J=-1 (R) for Delta-K=+1.
        First, check to see if the target K exists: */
2819
           if((bbSSh+1)<(bbSSL0[0].L)) bbSSflgb=1;</pre>
      /* Relative position in the low state E/P array */
2820
           bbSSel=(bbSSh+1)*bbSS.nlJ + bbSS.nlJ-bbSS.nhJ + \
              (int)(bbSSSh-bbSSS1) -1 + bbSSi;
2821
2822 if(bbSSdebugflag<DEBUG){</pre>
2823 fprintf(DBG,"\t(bbSSh+1)*bbSS.nlJ=%d, bbSS.nlJ-bbSS.nhJ=%d\n",\
2824
         (bbSSh+1)*bbSS.nlJ,bbSS.nlJ-bbSS.nhJ);
2825 fprintf(DBG,"\t(int)(bbSSSh-bbSSS1)=%d, bbSSi=%d, bbSSel=%d\n",\
         (int)(bbSSSh-bbSSS1),bbSSi,bbSSel);
2826
2827 fflush(DBG);
2828 }
2829
           if((bbSSel+1)>=(bbSS.Rl[0].kc*bbSS.nlJ)) bbSSflgb=1;
      /* Then check if the target value for J+1 is less than or greater
        than the allowed J's for K+1. */
           if((bbSSJ+1)>(bbSSh+1+bbSSS1)) bbSSflgb=1;
2830
2831
           if((bbSSJ+1)<(bbSSh+1-bbSSS1)) bbSSflgb=1;
      /* Still OK? Calculate transition */
2832
           if(bbSSflgb==0){
2833
             bbSSB=+1;
2834
             bbSSell=bbSSel+1;
2835
             bbSS.T[0].S[bbSSff].f[bbSSjii]=\
                bbSS.Rh[0].EJ[bbSSehh]-
2836
2837
               bbSS.R1[0].EJ[bbSSel1];
2838
             bbSScascadetemp=bbSStrprob*bbSSfcf*\
2839
               bbSS.Rh[0].CJ[bbSSehh]*\
2840
               HL(bbSSB,bbSSJ,bbSSL,bbSSdL);
2841 if(bbSSdebugflag<DEBUG){
2842 fprintf(DBG,"bbSS.T[0].S[%d].f[%d]=%13.5e ",bbSSff,bbSSjii,\
         bbSS.T[0].S[bbSSff].f[bbSSjii]);
2843
2844 fprintf(DBG, "bbSS.Rh[0].EJ[%d]=%13.5e ", bbSSehh,
     bbSS.Rh[0].EJ[bbSSehh]);
2845 fprintf(DBG, "bbSS.R1[0].EJ[%d]=%13.5e\n", bbSSell,
     bbSS.R1[0].EJ[bbSSel1]);
2846 fprintf(DBG,"bbSStrprob=%13.5e,
     bbSSfcf=%13.6e",bbSStrprob,bbSSfcf);
2847 fprintf(DBG,"bbSScascadetemp=%13.5e\n",bbSScascadetemp);
```

```
2848 fprintf(DBG, "bbSS.Rh[0].CJ[%d] = %13.5e, ", bbSSehh,
     bbSS.Rh[0].CJ[bbSSehh]);
bbSSdL, \
2850
         HL(bbSSB,bbSSJ,bbSSL,bbSSdL));
2851 fflush(DBG);
2852 }
2853
             bbSS.T[0].S[bbSSff].ci[bbSSjii]+=\
2854
               bbSScascadetemp;
2855
             bbSS.R1[0].CJ[bbSSell]+=bbSSfcfr*\
2856
               bbSScascadetemp;
2857 if(bbSSdebugflag<DEBUG){
2858 fprintf(DBG,"bbSS.T[0].S[%d].ci[%d]=%12.6e
     bbSS.R1[0].CJ[%d]=%12.6e\n",\
2859
       bbSSff,bbSSjii,bbSS.T[0].S[bbSSff].ci[bbSSjii],\
2860
       bbSSell,bbSS.R1[0].CJ[bbSSell]);
2861 }
2862
             bbSSjii--;
2863
             }
2864 if (bbSSdebugflag<DEBUG) {
2865 fprintf(DBG,"%d ",bbSSh);
2866 if(bbSSflgb!=0) fprintf(DBG," %d %.1f (1c) M M\n",(bbSSh+1),bbSSJ);
2867 else{
2868 fprintf(DBG,"%d %.1f %18.12e %18.12e (1c)\n",(bbSSh+1),\
       bbSSJ,bbSS.T[0].S[bbSSff].f[bbSSjii+1],
2869
2870
       bbSS.T[0].S[bbSSff].ci[bbSSjii+1]);
2871
       }
2872 }
2873 fprintf(BBSSFILE,"%d ",bbSSh);
2874 if(bbSSflgb!=0) fprintf(BBSSFILE, " %d %.1f M M ",(bbSSh+1),bbSSJ);
2875 else{
2876 fprintf(BBSSFILE, "%d %.1f %18.12e %18.12e ",(bbSSh+1),\
       bbSSJ,bbSS.T[0].S[bbSSff].f[bbSSjii+1],
2877
2878
       bbSS.T[0].S[bbSSff].ci[bbSSjii+1]);
2879
       }
     /* Now, Delta-J=-1 (R) for Delta-K=+1. */
2880
           bbSSflgb=0;
2881
           if((bbSSh+1)<(bbSSL0[0].L)) bbSSflgb=1;
2882
           if((bbSSJ-1)>(bbSSh+1+bbSSS1)) bbSSflgb=1;
2883
           if((bbSSJ-1)<(bbSSh+1-bbSSS1)) bbSSflgb=1;</pre>
2884
           if((bbSSJ-1)<0) bbSSflgb=1;</pre>
2885
           if((bbSSel-1)<0) bbSSflgb=1;</pre>
2886
           if(bbSSflgb==0){
2887
             bbSSB=-1;
2888
             bbSSell=bbSSel-1;
             bbSS.T[0].S[bbSSff].f[bbSSjii]=\
2889
               bbSS.Rh[0].EJ[bbSSehh]-
2890
2891
               bbSS.R1[0].EJ[bbSSel1];
2892
             bbSScascadetemp=bbSStrprob*bbSSfcf*\
2893
               bbSS.Rh[0].CJ[bbSSehh]*bbSSSATT*\
2894
               HL(bbSSB,bbSSJ,bbSSL,bbSSdL);
2895 if(bbSSdebugflag<DEBUG){
2896 fprintf(DBG,"bbSS.T[0].S[%d].f[%d]=%13.5e ",bbSSff,bbSSjii,\
         bbSS.T[0].S[bbSSff].f[bbSSjii]);
2897
```

```
2898 fprintf(DBG, "bbSS.Rh[0].EJ[%d] = %13.5e ", bbSSehh,
     bbSS.Rh[0].EJ[bbSSehh]);
2899 fprintf(DBG, "bbSS.R1[0].EJ[%d] = %13.5e\n", bbSSell,
     bbSS.R1[0].EJ[bbSSell]);
2900 fprintf(DBG,"bbSStrprob=%13.5e,
     bbSSfcf=%13.6e", bbSStrprob, bbSSfcf);
2901 fprintf(DBG,"bbSScascadetemp=%13.5e\n",bbSScascadetemp);
2902 fprintf(DBG, "bbSS.Rh[0].CJ[%d] = %13.5e, ", bbSSehh,
     bbSS.Rh[0].CJ[bbSSehh]);
2903 fprintf(DBG, "HL(%d,%.1f,%d,%d) = %13.5e\n", bbSSB, bbSSJ, bbSSL,
     bbSSdL, \
2904
         HL(bbSSB, bbSSJ, bbSSL, bbSSdL));
2905 fflush(DBG);
2906 }
2907
             bbSS.T[0].S[bbSSff].ci[bbSSjii]+=\
2908
               bbSScascadetemp;
2909
             bbSS.R1[0].CJ[bbSSell]+=bbSSfcfr*\
2910
               bbSScascadetemp;
2911 if(bbSSdebugflag<DEBUG){
2912 fprintf(DBG, "bbSS.T[0].S[%d].ci[%d] = %12.6e bbSS.R1[0].CJ[%d] =
     %12.6e\n",\
       bbSSff,bbSSjii,bbSS.T[0].S[bbSSff].ci[bbSSjii],\
2913
       bbSSell,bbSS.R1[0].CJ[bbSSell]);
2914
2915 }
2916
             bbSSjii--;
2917
2918 if(bbSSdebugflag<DEBUG){
2919 if(bbSSflgb!=0) fprintf(DBG,"M M\n");
2920 else{
2921 fprintf(DBG,"%18.12e %18.12e (1d)\n",
     bbSS.T[0].S[bbSSff].f[bbSSjii+1],
2922
       bbSS.T[0].S[bbSSff].ci[bbSSjii+1]);
2923
       }
2924 }
2925 if(bbSSflgb!=0) fprintf(BBSSFILE,"M M\n");
2926 else{
2927 fprintf(BBSSFILE, "%18.12e %18.12e\n",
     bbSS.T[0].S[bbSSff].f[bbSSjii+1],
2928
       bbSS.T[0].S[bbSSff].ci[bbSSjii+1]);
2929
       }
2930
           bbSSflgb=0;
      /* Check Delta-J=+1 (P) and then Delta-J=-1 (R) for Delta-K=-1.
        First, check to see if the target K exists: */
2931
           if((bbSSh-1)<(bbSSL0[0].L)) bbSSflgb=1;
      /* Relative position in the low state E/P array */
2932
           bbSSel=(bbSSh-1)*bbSS.nlJ + bbSS.nlJ-bbSS.nhJ + \
2933
             (int)(bbSSSh-bbSSS1) +1 + bbSSi;
2934 if(bbSSdebugflag<DEBUG){
2935 fprintf(DBG,"\t(bbSSh+1)*bbSS.nlJ=%d, bbSS.nlJ-bbSS.nhJ=%d\n",\
         (bbSSh+1)*bbSS.nlJ,bbSS.nlJ-bbSS.nhJ);
2936
2937 fprintf(DBG,"\t(int)(bbSSSh-bbSSS1)=%d, bbSSi=%d, bbSSel=%d\n",\
2938
         (int)(bbSSSh-bbSSS1),bbSSi,bbSSel);
2939 fflush(DBG);
2940 }
```

```
2941
           if((bbSSel+1)>=(bbSS.Rl[0].kc*bbSS.nlJ)) bbSSflgb=1;
      /* Then check if the target value for J+1 is less than or greater
        than the allowed J's for K-1. */
2942
           if((bbSSJ+1)>(bbSSh-1+bbSSS1)) bbSSflgb=1;
2943
           if((bbSSJ+1)<(bbSSh-1-bbSSS1)) bbSSflgb=1;</pre>
      /* Still OK? Calculate transition */
2944
           if(bbSSflgb==0){
2945
             bbSSB=+1;
2946
             bbSSell=bbSSel+1;
2947
             bbSS.T[0].S[bbSSff].f[bbSSjii]=\
               bbSS.Rh[0].EJ[bbSSehh]-\
2948
2949
               bbSS.R1[0].EJ[bbSSel1];
2950
             bbSScascadetemp=bbSStrprob*bbSSfcf*\
2951
               bbSS.Rh[0].CJ[bbSSehh]*bbSSSATT*\
2952
               HL(bbSSB,bbSSJ,bbSSL,bbSSdL);
2953 if(bbSSdebugflag<DEBUG){
2954 fprintf(DBG,"bbSS.T[0].S[%d].f[%d]=%13.5e ",bbSSff,bbSSjii,\
         bbSS.T[0].S[bbSSff].f[bbSSjii]);
2955
2956 fprintf(DBG, "bbSS.Rh[0].EJ[%d] = %13.5e ", bbSSehh,
     bbSS.Rh[0].EJ[bbSSehh]);
2957 fprintf(DBG, "bbSS.R1[0].EJ[%d] = %13.5e\n", bbSSell,
     bbSS.R1[0].EJ[bbSSel1]);
2958 fprintf(DBG, "bbSStrprob=%13.5e, bbSSfcf = %13.6e ", bbSStrprob,
     bbSSfcf);
2959 fprintf(DBG, "bbSScascadetemp = %13.5e\n", bbSScascadetemp);
2960 fprintf(DBG, "bbSS.Rh[0].CJ[1/kd] = %13.5e, ", bbSSehh,
     bbSS.Rh[0].CJ[bbSSehh]);
2961 fprintf(DBG, "HL(%d,%.1f,%d,%d)=%13.5e\n", bbSSB, bbSSJ, bbSSL,
     bbSSdL, \
2962
         HL(bbSSB,bbSSJ,bbSSL,bbSSdL));
2963 fflush(DBG);
2964 }
             bbSS.T[0].S[bbSSff].ci[bbSSjii]+=\
2965
2966
               bbSScascadetemp;
2967
             bbSS.R1[0].CJ[bbSSel1]+=bbSSfcfr*\
2968
               bbSScascadetemp;
2969 if(bbSSdebugflag<DEBUG){
2970 fprintf(DBG, "bbSS.T[0].S[%d].ci[%d] = %12.6e bbSS.R1[0].CJ[%d] =
     %12.6e\n",\
2971
       bbSSff,bbSSjii,bbSS.T[0].S[bbSSff].ci[bbSSjii],
2972
       bbSSell,bbSS.R1[0].CJ[bbSSell]);
2973 }
2974
             bbSSjii--;
             }
2975
2976 if(bbSSdebugflag<DEBUG){
2977 fprintf(DBG,"%d ",bbSSh);
2978 if(bbSSflgb!=0) fprintf(DBG," %d %.1f M M ",(bbSSh-1),bbSSJ);
2979 else{
2980 fprintf(DBG,"%d %.1f %18.12e %18.12e (1e)\n",(bbSSh-1),\
       bbSSJ,bbSS.T[0].S[bbSSff].f[bbSSjii+1],
2981
2982
       bbSS.T[0].S[bbSSff].ci[bbSSjii+1]);
2983
       }
2984 }
2985 fprintf(BBSSFILE,"%d ",bbSSh);
```

```
2986 if(bbSSflgb!=0) fprintf(BBSSFILE," %d %.1f M M ",(bbSSh-1),bbSSJ);
2987 else{
2988 fprintf(BBSSFILE,"%d %.1f %18.12e %18.12e ",(bbSSh-1),\
2989
       bbSSJ,bbSS.T[0].S[bbSSff].f[bbSSjii+1],\
2990
       bbSS.T[0].S[bbSSff].ci[bbSSjii+1]);
2991
       }
      /* Now, Delta-J=-1 (R) for Delta-K=-1. */
2992
           bbSSflgb=0;
2993
           if((bbSSh-1)<(bbSSL0[0].L)) bbSSflgb=1;</pre>
2994
           if((bbSSJ-1)>(bbSSh-1+bbSSS1)) bbSSflgb=1;
2995
           if((bbSSJ-1)<(bbSSh-1-bbSSS1)) bbSSflgb=1;
2996
           if((bbSSJ-1)<0) bbSSflgb=1;</pre>
2997
           if((bbSSel-1)<0) bbSSflgb=1;</pre>
2998
           if(bbSSflgb==0){
2999
             bbSSB=-1;
3000
             bbSSell=bbSSel-1;
3001
             bbSS.T[0].S[bbSSff].f[bbSSjii]=\
3002
               bbSS.Rh[0].EJ[bbSSehh]-
3003
               bbSS.R1[0].EJ[bbSSel1];
3004
             bbSScascadetemp=bbSStrprob*bbSSfcf*\
3005
               bbSS.Rh[0].CJ[bbSSehh]*\
3006
               HL(bbSSB,bbSSJ,bbSSL,bbSSdL);
3007 if(bbSSdebugflag<DEBUG){
3008 fprintf(DBG,"bbSS.T[0].S[%d].f[%d]=%13.5e ",bbSSff,bbSSjii,\
         bbSS.T[0].S[bbSSff].f[bbSSjii]);
3009
3010 fprintf(DBG, "bbSS.Rh[0].EJ[%d] = %13.5e ", bbSSehh,
     bbSS.Rh[0].EJ[bbSSehh]);
3011 fprintf(DBG, "bbSS.R1[0].EJ[%d] = %13.5e\n", bbSSell,
     bbSS.R1[0].EJ[bbSSel1]);
3012 fprintf(DBG,"bbSStrprob=%13.5e, bbSSfcf=%13.6e ",bbSStr-
     prob,bbSSfcf);
3013 fprintf(DBG,"bbSScascadetemp=%13.5e\n",bbSScascadetemp);
3014 fprintf(DBG, "bbSS.Rh[0].CJ[%d] = %13.5e, ", bbSSehh,
     bbSS.Rh[0].CJ[bbSSehh]);
3015 fprintf(DBG,"HL(%d,%.1f,%d,%d)=%13.5e\n", bbSSB, bbSSJ, bbSSL, bb-
     SSdL,\
3016
         HL(bbSSB,bbSSJ,bbSSL,bbSSdL));
3017 fflush(DBG);
3018 }
3019
             bbSS.T[0].S[bbSSff].ci[bbSSjii]+=\
3020
               bbSScascadetemp;
3021
             bbSS.R1[0].CJ[bbSSel1]+=bbSSfcfr*\
3022
               bbSScascadetemp;
3023 if(bbSSdebugflag<DEBUG){
3024 fprintf(DBG, "bbSS.T[0].S[%d].ci[%d] = %12.6e bbSS.R1[0].CJ[%d] =
     %12.6e\n",\
3025
       bbSSff,bbSSjii,bbSS.T[0].S[bbSSff].ci[bbSSjii],\
3026
       bbSSell,bbSS.R1[0].CJ[bbSSell]);
3027 }
3028
             }
3029 if(bbSSdebugflag<DEBUG){</pre>
3030 if(bbSSflgb!=0) fprintf(DBG,"M M\n");
3031 else{
```

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```

```
3032 fprintf(DBG, "%18.12e %18.12e (1f)\n",
     bbSS.T[0].S[bbSSff].f[bbSSjii],
       bbSS.T[0].S[bbSSff].ci[bbSSjii]);
3033
3034
       }
3035 }
3036 if(bbSSflgb!=0) fprintf(BBSSFILE,"M M\n");
3037 else{
3038 fprintf(BBSSFILE,"%18.12e
     18.12en", bbSS.T[0].S[bbSSff].f[bbSSjii], 
3039
       bbSS.T[0].S[bbSSff].ci[bbSSjii]);
3040
       }
3041
           } /* close if bbSSflga is zero. */
3042
         } /* close upper-state J-of-K loop */
       } /* close upper-state K loop */
3043
3044
       fclose(BBSSFILE);
3045
         } /* close if high-state v is cascade populated */
3046
       } /* close low-state v */
3047
       } /* close high-state v */
     /* check to see if this is all to do... */
3048 return;
3049 }
     3050
     /* This function calculates transitions between Hund's Cases (b)
       and (b) when both the upper and lower states are sigma states. */
3051 void bb_SigmaOther(BBTinfo bbSO){
     /* see parent function and header file for key to variable names */
     /* indexes and dummy variables: */
3052 int bbSOe=0,bbSOee=0,bbSOf=0,bbSOff=0;
3053 int bbSOh=0,bbSOk=0,bbSOfrnh=0,bbSOfrcl=0,bbSOfrch=0;
3054 int bbSOeh=0,bbSOehh=0,bbSOi=0,bbSOel=0,bbSOell=0,bbSOjii=0;
     /* variables for info about the two states */
3055 double
     bbS0J=0,bbS0Sh=0,bbS0Sl=0,bbS0trprob=0,bbS0vhpop=0,bbS0hipop=0;
     /* Intensity multiplier for satellite bands and FCF dummy vari-
       able*/
3056 double bbSOSATT=0,bbSOfcf=0,bbSOfcfr=0;
     /* variables for calculating Holn-London factors */
3057 int bbSOL=0, bbSOB=0, bbSOdL=0;
     /* variables for spin stats if the state is homonuclear */
3058 int bbSOg=0,bbSOisym=0,bbSOpsym=0;
3059 double bbSOIa=0, bbSOcascadetemp=0;
     /* a few flags for various purposes */
3060 int bbSOflga=0,bbSOflgb=0,bbSOfrnhf=0,bbSOfrchf=0;
     /* variables for creating and writing to output files */
3061 char bbSOfile[1000];
3062 FILE *BBSOFILE;
3063 Case_b_stateinfo *bbSOHI,*bbSOLO;
3064 if(bbSOdebugflag<DEBUG){
3065 fprintf(DBG,"bbSO.hvnlo=%d, bbSO.hvnnum=%d\n",\
3066
         bbSO.hvnlo,bbSO.hvnnum);
```

```
3067 fprintf(DBG,"bbSO.hvclo=%d, bbSO.hvcnum=%d\n",\
3068
         bbSO.hvclo,bbSO.hvcnum);
3069 fprintf(DBG,"bbSO.lvnlo=%d, bbSO.lvnnum=%d,\n",\
         bbSO.lvnlo,bbSO.lvnnum);
3070
3071 fprintf(DBG,"bbSO.lvclo=%d, bbSO.lvcnum=%d\n",\
3072
         bbSO.lvclo,bbSO.lvcnum);
3073 fprintf(DBG,"bbSO.hivlo=%d, bbSO.hivnum=%d,\n",\
3074
         bbSO.hivlo,bbSO.hivnum);
3075 fprintf(DBG,"bbSO.lovlo=%d, bbSO.lovnum=%d\n",\
3076
         bbSO.lovlo,bbSO.lovnum);
3077 fflush(DBG);
3078 }
3079 bbSOHI=bbSO.Ch;
3080 bbSOLO=bbSO.Cl;
3081 bbSOSh=bbSOHI[0].S;
3082 bbSOS1=bbSOL0[0].S;
3083 bbSOhipop=bbSO.Sh[0].pop;
3084 bbSOtrprob=bbSO.T[0].P[0];
3085 if(bbSOdebugflag<DEBUG){
3086 fprintf(DBG,"bbSOSh=%.1f, bbSOS1=%.1f, \n", bbSOSh, bbSOS1);
3087 fprintf(DBG,"bbSOhipop=%12.6e,
     bbSOtrprob=%12.6e\n",bbSOhipop,bbSOtrprob);
3088 fflush(DBG);
3089 }
3090 if(bbSOHI[0].L==0){
3091
       bbSOisym=bbSO.Sh[0].Isymm;
3092
       bbSOpsym=bbSO.Sh[0].pmsymm;
3093
       if(bbSOHI[0].g!=0){
         bbSOg=bbSOHI[0].g;
3094
         bbSOIa=bbSOHI[0].I/(bbSOHI[0].I+1);
3095
3096
         }
3097
       }
3098 if(bbSOL0[0].L==0){
3099
       bbSOisym=bbSO.S1[0].Isymm;
3100
       bbSOpsym=bbSO.S1[0].pmsymm;
3101
       if(bbSOLO[0].g!=0){
         bbSOg=bbSOLO[0].g;
3102
3103
         bbSOIa=bbSOLO[0].I/(bbSOLO[0].I+1);
3104
         }
3105
       }
3106 if((bbSOHI[0].L-bbSOL0[0].L)==+1) bbSOdL=+1;
3107 if((bbSOHI[0].L-bbSOLO[0].L)==-1) bbSOdL=-1;
3108 bbSOL=bbSOHI[0].L;
     /* start loop down through high vib levels */
3109 for(bbS0e=(bbS0.hivlo+bbS0.hivnum-1);bbS0e>=bbS0.hivlo;bbS0e--){
       bbSOee=(bbSOe-bbSO.hivlo)*bbSO.lovnum; /* simset posn. in 2D */
3110
3111
       bbSOfrnh=(bbSOe-bbSO.hvnlo); /* high state native vib position
        */
3112
       bbSOfrch=bbSOe; /* high state cascade vib position */
      /* these flags (bbSOfrnhf and bbSOfrchf) tell if this high vib state
        is populated natively, by cascade, or both. They will be used
        later */
```

```
414
if((bbSOe>=bbSO.hvnlo)&&(bbSOe<(bbSO.hvnlo+bbSO.hvnnum))){
    bbSOfrnhf=0;
    bbSOubper=bbSO.Wb[0] = [bbSOe bbSO burle];</pre>
```

```
3114
         bbSOfrnhf=0;
         bbSOvhpop=bbSO.Vh[0].p[bbSOe-bbSO.hvnlo];
3115
3116
3117
       else bbS0frnhf=-1;
       if((bbSOe>=bbSO.hvclo)&&(bbSOe<(bbSO.hvclo+bbSO.hvcnum))){
3118
3119
         bbSOfrchf=0;
3120
         }
3121
       else bbSOfrchf=-1;
3122 if(bbSOdebugflag<DEBUG){</pre>
3123 fprintf(DBG, "bbSOfrnhf=%d, bbSOvhpop=%12.6e, bbSOfrchf=%d, ",\
3124
         bbSOfrnhf,bbSOvhpop,bbSOfrchf);
3125 fprintf(DBG,"bbSOe=%d, bbSOee=%d\nbbSOfrnh=%d, bbSOfrch=%d,\n",\
3126
         bbSOe,bbSOee,bbSOfrnh,bbSOfrch);
3127 fprintf(DBG,"bbSO.Vh[0].p[%d-%d]=%12.6e\n",bbSOe,bbSO.hvnlo,\
          bbSO.Vh[0].p[bbSOe-bbSO.hvnlo]);
3128
3129 fflush(DBG);
3130 }
     /* start loop down through low vib levels */
3131 for(bbS0f=(bbS0.lovlo+bbS0.lovnum-1);bbS0f>=bbS0.lovlo;bbS0f--){
3132
       bbSOfcf=bbSO.T[0].v[bbSOe].fcfn[bbSOf];
3133
     if(bbS0fcf!=0){bbS0fcfr=bbS0.T[0].v[bbS0e].fcfc[bbS0f]/bbS0fcf;}
       bbSOff=bbSOee+bbSOf-bbSO.lovlo; /* position in last dimension */
3134
3135
       bbSOfrcl=bbSOf;
3136 if(bbSOdebugflag<DEBUG){</pre>
3137 fprintf(DBG,"bbS0f=%d, bbS0.lovlo=%d, bbS0.lovnum=%d, bb-
     SOfcf = 12.6e n'', 
         bbSOf,bbSO.lovlo,bbSO.lovnum,bbSOfcf);
3138
3139 fflush(DBG);
3140 }
3141 bbSOff=bbSOee+bbSOf-bbSO.lovlo; /* simset posn. in final dimension
        */
3142
       bbSO.T[0].S[bbSOff].n=bbSO.nT*bbSO.hiK;
3143
       bbSO.T[0].S[bbSOff].f=\
3144
         (double*)calloc(bbS0.T[0].S[bbS0ff].n,sizeof(double));
3145
       bbSO.T[0].S[bbSOff].ni=
3146
         (double*)calloc(bbS0.T[0].S[bbS0ff].n,sizeof(double));
3147
       bbSO.T[0].S[bbSOff].ci=\
3148
         (double*)calloc(bbS0.T[0].S[bbS0ff].n,sizeof(double));
3149 bbSO.Rl=&bbSO.S1[0].rc[bbSOfrc1];
3150 if(bbSOdebugflag<DEBUG){</pre>
3151 fprintf(DBG,"bbSOff=%d, bbSOfrcl=%d,
     bbSO.T[0].S[bbSOff].n=%d\n",\
3152
         bbSOff,bbSOfrcl,bbSO.T[0].S[bbSOff].n);
3153 fprintf(DBG,"bbS0.nT=%d, bbS0.hiK=%d\n",bbS0.nT,bbS0.hiK);
3154 fflush(DBG);
3155 }
     /* start with highest J value (same reason as before), and loop down
        looking for lower J's to which to transit. Assign intensities.
        If both states are Omega=0, then assign zero intensity to transi-
```

```
tions for J=0<->J=0. */
```

3113

- if(bbSOfrnhf==0){ /* if this v is natively populated.*/ 3156 3157 sprintf(bbSOfile,"%s_molecules/%s/%s--%s_v%d--v%d_NAT.dat",\ 3158 PREF,MOL[bbS0.m].Mol,bbS0.T[0].Nhi,bbS0.T[0].Nlo,bbS0e,bbS0f); 3159 BBSOFILE=fopen(bbSOfile,"w"); 3160 if(BBSOFILE==NULL){ 3161 printf("Error opening transition sub-file %s. Exiting.\n",bbSOfile); 3162 exit(1);} 3163 3164 fprintf(BBSOFILE, "# File created by %s.\n# File contains ", PRO-GRAM_NAME); 3165 fprintf(BBSOFILE, "P, Q and R"); 3166 fprintf(BBSOFILE," branches from the simulation titled $s\n", PREF$); 3167 fprintf(BBSOFILE,"# THESE INTENSITIES ARE DUE TO USER-SPECIFIED POPULATIONS"); 3168 fprintf(BBSOFILE, " ONLY -- NO CASCADE\n"); 3169 fprintf(BBSOFILE, "# Transition is Hund's Case (b) to Hund's Case (b).\n"); 3170 fprintf(BBSOFILE,"# Molecule %s, \tHigh state: %s, v=%d\n",\ 3171 MOL[bbS0.m].Mol,bbS0.T[0].Nhi,bbS0e); 3172 fprintf(BBSOFILE,"#\t\tLow state: %s, v=%d\n# Columns are: ",\ 3173 bbSO.T[0].Nlo,bbSOf); 3174 fprintf(BBSOFILE, "K_hi K_lo J_hi P(J_hi+1)_v P_i "); 3175 fprintf(BBSOFILE,"Q(J_hi+0)_v Q_i R(J_hi-1)_v R_i\n#\n"); 3176 bbSO.Rh=&bbSO.Sh[0].r[bbSOfrnh]; 3177 if((bbS0.hiK)<bbS0.Sh[0].r[bbS0frnh].k){</pre> 3178 bbSOk=bbSO.hiK-1; 3179 } else bbSOk=bbSO.Sh[0].r[bbSOfrnh].k-1; 3180 3181 if(bbSO.R1[0].Kdissoc<(bbSOk-1)){ 3182 fprintf(PAR,"\nWARNING!! State %s of molecule %s has significant ",\ bbSO.T[0].Nhi,MOL[bbSO.m].Mol); 3183 3184 fprintf(PAR, "rotational population at level %d\n", bbSOk); 3185 fprintf(PAR,"\tBut lower state %s dissociates at level %.1f\n",\ bbSO.T[0].Nlo,bbSO.Rl[0].Kdissoc); 3186 3187 fprintf(PAR,"It is likely that the bound upper state is transiting to (an)"); 3188 fprintf(PAR, " unbound lower state(s).\n"); 3189 fprintf(PAR,"Look for continuum emissions trailing off to the lowenergy "); 3190 fprintf(PAR,"end of the v(hi)=%d to v(lo)=%d\nband in the real ",bb-SOe,bbSOf); 3191 fprintf(PAR,"spectrum (not the simulated one)\nCurrently, this program will"); 3192 fprintf(PAR, " not simulate bound-->unbound spectra.\n\n"); 3193 bbSOk=(int)(bbSO.R1[0].Kdissoc); 3194 ł 3195 if(bbSOdebugflag<DEBUG){</pre> 3196 fprintf(DBG,"bbSOfrnh=%d, bbSOk=%d, ",bbSOfrnh,bbSOk);
- 3198 fflush(DBG);

```
/* To make the output file easy to write, I'm cycling by high-state
        K first, then by high-state J. From that J/K(hi) pair, the pro-
        gram will look for a P transition and an R transition to K+1 then
        to K-1. If all the necessary states exist, it will check to see
        if there are any symmetry or nuclear spin effects to be concerned
        about. Taking these into account, it will calculate the transi-
        tion. */
      /* loop first by upper-state K-value */
3200 for(bbSOh=bbSOk;bbSOh>=0;bbSOh--){
3201
       bbSOjii=(bbSOh+1)*bbSO.nT-1; /* position in simset array */
3202
       bbSOeh=bbSOh*bbSO.nhJ; /* position in 2D for high EJ & PJ */
      /* then loop by upper-state J for this K */
3203
       for(bbSOi=(bbSO.nhJ-1);bbSOi>=0;bbSOi--){
3204
         bbSOJ=bbSOh+bbSOi-bbSOSh;
3205
         bbSOehh=bbSOeh+bbSOi;
3206
         bbSOflga=0;
         if(bbSOh<bbSOHI[0].L) bbSOflga=1; /* if this K is less than
3207
        Lambda for the high state, don't proceed */
3208
         if(bbSOJ<0) bbSOflga=1; /* if J is less than zero, don't */
3209 if(bbSOdebugflag<DEBUG){
3210 fprintf(DBG,"bbSOh=%d, bbSOi=%d, bbSOSh=%.1f, bbSOHI[0].L=%d, bb-
     SOflga=%d\n",\
3211
         bbSOh, bbSOi, bbSOSh, bbSOHI[0].L, bbSOflga);
3212 fflush(DBG);
3213 }
3214
         if(bbSOflga==0){
      /* Check Delta-J=+1 (P), then Delta-J=0 (Q), and then Delta-J=-1
        (R) for Delta-K=+1. First, check to see if the target K exists:
        */
3215
           bbSOflgb=0;
3216
           if((bbSOh+1)<(bbSOLO[0].L)) bbSOflgb=1;</pre>
      /* Relative position in the low state E/P array */
3217
           bbSOel=(bbSOh+1)*bbSO.nlJ + bbSO.nlJ-bbSO.nhJ + \
3218
              (int)(bbSOSh-bbSOS1) -1 + bbSOi;
3219 if(bbSOdebugflag<DEBUG){</pre>
3220 fprintf(DBG,"\t(bbSOh+1)*bbSO.nlJ=%d, bbSO.nlJ-bbSO.nhJ=%d\n",\
3221
         (bbSOh+1)*bbSO.nlJ,bbSO.nlJ-bbSO.nhJ);
3222 fprintf(DBG,"\t(int)(bbSOSh-bbSOS1)=%d, bbSOi=%d, bbSOel=%d\n",\
         (int)(bbSOSh-bbSOS1),bbSOi,bbSOel);
3223
3224 fflush(DBG);
3225 }
3226
           if((bbSOel+1)>=(bbSO.R1[0].kc*bbSO.nlJ)) bbSOflgb=1;
      /* Then check if the target value for J+1 is less than or greater
        than the allowed J's for K+1. */
3227
           if((bbS0J+1)>(bbS0h+1+bbS0S1)) bbS0flgb=1;
3228
           if((bbSOJ+1)<(bbSOh+1-bbSOS1)) bbSOflgb=1;</pre>
      /* Still OK? Calculate transition */
3229
           if(bbSOflgb==0){
3230
              bbSOB=+1;
```

3199 }

3231

3232 3233

3234

bbSOell=bbSOel+1;

bbSO.T[0].S[bbSOff].f[bbS0jii]=\

bbSO.Rh[0].EJ[bbSOehh]-

bbSO.R1[0].EJ[bbSOel1];

```
bbSO.T[0].S[bbSOff].ni[bbS0jii]=\
3235
3236
               bbSOhipop*bbSOtrprob*bbSOvhpop*\
               bbSO.Rh[0].PJ[bbSOehh]*bbSOfcf*\
3237
3238
               HL(bbSOB,bbSOJ,bbSOL,bbSOdL);
3239 if(bbSOdebugflag<DEBUG){
3240 fprintf(DBG,"bbSO.Rh[0].EJ[%d]=%12.6e
     ",bbSOehh,bbSO.Rh[0].EJ[bbSOehh]);
3241 fprintf(DBG,"bbSO.R1[0].EJ[%d]=%12.6e
     ",bbSOell,bbSO.R1[0].EJ[bbSOell]);
3242 fprintf(DBG,"bbS0.T[0].S[%d].f[%d]=%12.6e ",bbS0ff,bbS0jii,\
         bbSO.T[0].S[bbSOff].f[bbS0jii]);
3243
3244 fprintf(DBG,"bbSOhipop%12.6e, bbSOtrprob%12.6e, bbSOvh-
     pop=%12.6e\n",\
         bbSOhipop,bbSOtrprob,bbSOvhpop);
3245
3246 fprintf(DBG,"bbSOfcf=%13.6e ",bbSOfcf);
3247 fprintf(DBG,"bbSO.Rh[0].PJ[%d]=%12.6e
     ",bbSOehh,bbSO.Rh[0].PJ[bbSOehh]);
3248 fprintf(DBG,"HL(%d,%.1f,%d,%d)=%12.6e
     ",bbSOB,bbSOJ,bbSOL,bbSOdL,\
3249
       HL(bbSOB,bbSOJ,bbSOL,bbSOdL));
3250 fprintf(DBG,"bbS0.T[0].S[%d].ni[%d]=%12.6e\n",bbS0ff,bbS0jii,\
       bbSO.T[0].S[bbSOff].ni[bbS0jii]);
3251
3252 }
      /* Check for nuclear effects and modify intensity if necessary. No
        need to do this if the high state is Sigma. */
3253
         if((bbSOg!=0)&&(bbSOLO[0].L==0)){ /* low state is Sigma */
3254
           if((((bbSOh+1)%2)==0)&&(bbSOisym==-1)){
3255
             bbSO.T[0].S[bbSOff].ni[bbS0jii]*=bbSOIa;
3256 if(bbSOdebugflag<DEBUG){
3257 fprintf(DBG,"Even low state is Ia intensity\n");
3258 fflush(DBG);
3259 }
3260
             }
3261
           if((((bbSOh+1)%2)==1)&&(bbSOisym==+1)){
3262
             bbSO.T[0].S[bbSOff].ni[bbS0jii]*=bbSOIa;
3263 if(bbSOdebugflag<DEBUG){
3264 fprintf(DBG, "Even low state is Ia intensity\n");
3265 fflush(DBG);
3266 }
3267
             }
           }
3268
     /* set low-state population for cascade */
3269
             bbSO.R1[0].CJ[bbSOell]+=bbSOfcfr*\
3270
               bbSO.T[0].S[bbSOff].ni[bbSOjii];
3271 if(bbSOdebugflag<DEBUG){
3272 fprintf(DBG,"bbSO.R1[0].CJ[%d]=%12.6e,
     bbSO.T[0].S[%d].ni[%d]=%12.6e\n",\
       bbSOell,bbSO.R1[0].CJ[bbSOell],bbSOff,\
3273
3274
       bbSOjii,bbSO.T[0].S[bbSOff].ni[bbSOjii]);
3275 }
3276
             bbSOjii--;
3277
3278 if(bbSOdebugflag<DEBUG){
3279 fprintf(DBG,"bbSO, K+1, J+1 native\n");
```

3280 fprintf(DBG,"%d ",bbSOh); 3281 if(bbS0flgb!=0) fprintf(BBS0FILE," %d %.1f M M ",(bbS0h+1),bbS0J); 3282 else{ 3283 fprintf(DBG,"%d %.1f %18.12e %18.12e ",(bbSOh+1),\ 3284 bbSOJ,bbSO.T[0].S[bbSOff].f[bbSOjii+1],\ 3285 bbSO.T[0].S[bbSOff].ni[bbS0jii+1]); 3286 } 3287 } 3288 fprintf(BBSOFILE,"%d ",bbSOh); 3289 if(bbSOflgb!=0) fprintf(BBSOFILE," %d %.1f M M ",(bbSOh+1),bbSOJ); 3290 else{ 3291 fprintf(BBSOFILE,"%d %.1f %18.12e %18.12e ",(bbSOh+1),\ bbSOJ,bbSO.T[0].S[bbSOff].f[bbSOjii+1], 3292 3293 bbSO.T[0].S[bbSOff].ni[bbSOjii+1]); 3294 } /* Now Delta-J=0 (Q) (for Delta-K=+1) */ 3295 bbSOflgb=0; 3296 if((bbSOh+1)<(bbSOLO[0].L)) bbSOflgb=1; /* Then check if the target value for J+1 is less than or greater than the allowed J's for K+1. */ 3297 if((bbS0J+0)>(bbS0h+1+bbS0S1)) bbS0flgb=1; 3298 if((bbS0J+0)<(bbS0h+1-bbS0S1)) bbS0flgb=1;</pre> 3299 if((bbSOJ+0)<0) bbSOflgb=1; /* Still OK? Calculate transition */ 3300 if(bbSOflgb==0){ 3301 bbSOB=+0;3302 bbSOell=bbSOel+0; 3303 bbSO.T[0].S[bbSOff].f[bbSOjii]=\ 3304 bbSO.Rh[0].EJ[bbSOehh]-3305 bbSO.R1[0].EJ[bbSOel1]; 3306 bbSO.T[0].S[bbSOff].ni[bbS0jii]=\ 3307 bbSOhipop*bbSOtrprob*bbSOvhpop*\ 3308 bbSO.Rh[0].PJ[bbSOehh]*bbSOSATT*\ 3309 HL(bbSOB,bbSOJ,bbSOL,bbSOdL)*bbSOfcf; 3310 if(bbSOdebugflag<DEBUG){ 3311 fprintf(DBG,"bbSO.Rh[0].EJ[%d]=%12.6e ",bbSOehh,bbSO.Rh[0].EJ[bbSOehh]); 3312 fprintf(DBG,"bbSO.R1[0].EJ[%d]=%12.6e ",bbSOell,bbSO.R1[0].EJ[bbSOell]); 3313 fprintf(DBG,"bbSO.T[0].S[%d].f[%d]=%12.6e ",bbSOff,bbSOjii,\ 3314 bbSO.T[0].S[bbSOff].f[bbS0jii]); 3315 fprintf(DBG,"bbSOhipop %12.6e, bbSOtrprob %12.6e, bbSOvhpop= %12.6e\n",\ 3316 bbSOhipop,bbSOtrprob,bbSOvhpop); 3317 fprintf(DBG,"bbSOfcf=%13.6e ",bbSOfcf); 3318 fprintf(DBG,"bbSO.Rh[0].PJ[%d]=%12.6e ",bbSOehh,bbSO.Rh[0].PJ[bbSOehh]); 3319 fprintf(DBG,"HL(%d,%.1f,%d,%d)=%12.6e ",bbSOB,bbSOJ,bbSOL,bbSOdL, \ HL(bbSOB,bbSOJ,bbSOL,bbSOdL)); 3320 3321 fprintf(DBG,"bbS0.T[0].S[%d].ni[%d]=%12.6e\n",bbS0ff,bbS0jii,\ bbSO.T[0].S[bbSOff].ni[bbS0jii]); 3322 3323 } /* Check for nuclear effects and modify intensity if necessary. */

```
if((bbS0g!=0)&&(bbS0L0[0].L==0)){ /* low state is Sigma */
3324
3325
           if((((bbSOh+1)%2)==0)&&(bbSOisym==-1)){
3326
             bbSO.T[0].S[bbSOff].ni[bbSOjii]*=bbSOIa;
3327
             }
3328
           if((((bbSOh+1)%2)==1)&&(bbSOisym==+1)){
3329
             bbSO.T[0].S[bbSOff].ni[bbS0jii]*=bbSOIa;
3330
             }
           }
3331
      /* set low-state population for cascade */
3332
             bbSO.R1[0].CJ[bbSOell]+=bbSOfcfr*\
3333
               bbSO.T[0].S[bbSOff].ni[bbS0jii];
3334 if(bbSOdebugflag<DEBUG){
3335 fprintf(DBG,"bbSO.R1[0].CJ[%d]=%12.6e,
     bbSO.T[0].S[%d].ni[%d]=%12.6e\n",\
3336
       bbSOell,bbSO.R1[0].CJ[bbSOell],bbSOff,\
3337
       bbS0jii,bbS0.T[0].S[bbS0ff].ni[bbS0jii]);
3338 }
3339
             bbSOjii--;
3340
3341 if(bbSOdebugflag<DEBUG){
3342 fprintf(DBG, "bbSO, K+1, J+0 native\n");
3343 fprintf(DBG,"%d ",bbSOh);
3344 if(bbS0flgb!=0) fprintf(DBG," %d %.1f M M ",(bbS0h+1),bbS0J);
3345 else{
3346 fprintf(DBG,"%d %.1f %18.12e %18.12e ",(bbSOh+1),\
       bbSOJ,bbSO.T[0].S[bbSOff].f[bbS0jii+1],\
3347
3348
       bbSO.T[0].S[bbSOff].ni[bbS0jii+1]);
3349
       }
3350 }
3351 if(bbSOflgb!=0) fprintf(BBSOFILE," M M ");
3352 else{
3353 fprintf(BBSOFILE," %18.12e %18.12e
     ",bbSO.T[0].S[bbSOff].f[bbSOjii+1],\
3354
       bbSO.T[0].S[bbSOff].ni[bbS0jii+1]);
3355
       }
      /* Now, Delta-J=-1 (R) for Delta-K=+1. */
3356
           bbSOflgb=0;
           if((bbSOh+1)<(bbSOLO[0].L)) bbSOflgb=1;</pre>
3357
3358
           if((bbSOJ-1)>(bbSOh+1+bbSOS1)) bbSOflgb=1;
3359
           if((bbSOJ-1)<(bbSOh+1-bbSOS1)) bbSOflgb=1;
3360
           if((bbS0J-1)<0) bbS0flgb=1;</pre>
3361
           if(bbSOflgb==0){
3362
             bbSOB=-1;
             bbSOell=bbSOel-1;
3363
             bbSO.T[0].S[bbSOff].f[bbSOjii]=\
3364
3365
                bbSO.Rh[0].EJ[bbSOehh]-
               bbSO.R1[0].EJ[bbSOel1];
3366
3367
             bbSO.T[0].S[bbSOff].ni[bbS0jii]=\
3368
               bbSOhipop*bbSOtrprob*bbSOvhpop*\
3369
               bbSO.Rh[0].PJ[bbSOehh]*bbSOSATT*\
3370
               HL(bbSOB,bbSOJ,bbSOL,bbSOdL)*bbSOfcf;
3371 if(bbSOdebugflag<DEBUG){
3372 fprintf(DBG,"bbSO.Rh[0].EJ[%d]=%12.6e
     ", bbSOehh, bbSO.Rh[0].EJ[bbSOehh]);
```

```
3373 fprintf(DBG,"bbSO.R1[0].EJ[%d]=%12.6e
     ",bbSOell,bbSO.R1[0].EJ[bbSOell]);
3374 fprintf(DBG,"bbSO.T[0].S[%d].f[%d]=%12.6e ",bbSOff,bbSOjii,\
         bbSO.T[0].S[bbSOff].f[bbS0jii]);
3375
3376 fprintf(DBG,"bbSOhipop%12.6e, bbSOtrprob%12.6e, bbSOvh-
     pop=%12.6e\n",\
3377
         bbSOhipop, bbSOtrprob, bbSOvhpop);
3378 fprintf(DBG,"bbSOfcf=%12.6e ",bbSOfcf);
3379 fprintf(DBG,"bbSO.Rh[0].PJ[%d]=%12.6e
     ",bbSOehh,bbSO.Rh[0].PJ[bbSOehh]);
3380 fprintf(DBG,"HL(%d,%.1f,%d,%d)=%12.6e
     ",bbSOB,bbSOJ,bbSOL,bbSOdL,\
3381
       HL(bbSOB,bbSOJ,bbSOL,bbSOdL));
3382 fprintf(DBG,"bbSO.T[0].S[%d].ni[%d]=%12.6e\n",bbSOff,bbSOjii,\
3383
       bbSO.T[0].S[bbSOff].ni[bbSOjii]);
3384 }
3385
         if((bbS0g!=0)&&(bbS0L0[0].L==0)){ /* low state is Sigma */
3386
           if((((bbSOh+1)%2)==0)&&(bbSOisym==-1)){
3387
             bbSO.T[0].S[bbSOff].ni[bbS0jii]*=bbS0Ia;
3388
             }
           if((((bbSOh+1)%2)==1)&&(bbSOisym==+1)){
3389
3390
             bbSO.T[0].S[bbSOff].ni[bbSOjii]*=bbSOIa;
3391
             }
           }
3392
3393
             bbSO.R1[0].CJ[bbSOell]+=bbSOfcfr*\
3394
               bbSO.T[0].S[bbSOff].ni[bbS0jii];
3395 if(bbSOdebugflag<DEBUG){
3396 fprintf(DBG,"bbSO.R1[0].CJ[%d]=%12.6e,
     bbSO.T[0].S[%d].ni[%d]=%12.6e\n",\
3397
       bbSOell,bbSO.R1[0].CJ[bbSOell],bbSOff,\
       bbSOjii,bbSO.T[0].S[bbSOff].ni[bbSOjii]);
3398
3399 }
3400
             bbSOjii--;
3401
             }
3402 if (bbSOdebugflag<DEBUG) {
3403 fprintf(DBG,"bbSO, K+1, J-1 native\n");
3404 if(bbSOflgb!=0) fprintf(DBG,"M M\n");
3405 else{
3406 fprintf(DBG,"%18.12e
     %18.12e\n",bbSO.T[0].S[bbSOff].f[bbSOjii+1],\
3407
       bbSO.T[0].S[bbSOff].ni[bbS0jii+1]);
3408
       }
3409 }
3410 if(bbSOflgb!=0) fprintf(BBSOFILE,"M M\n");
3411 else{
3412 fprintf(BBSOFILE,"%18.12e
     %18.12e\n",bbSO.T[0].S[bbSOff].f[bbS0jii+1],\
3413
       bbSO.T[0].S[bbSOff].ni[bbSOjii+1]);
3414
       }
      /* Check Delta-J=+1 (P), then Delta-J=0 (Q), and then Delta-J=-1
        (R) for Delta-K=+0. First, check to see if the target K exists:
        */
3415
           bbSOflgb=0;
```

if((bbSOh+0)<(bbSOLO[0].L)) bbSOflgb=1;</pre> 3416 /* Relative position in the low state E/P array */ 3417 bbSOel=(bbSOh+0)*bbSO.nlJ + bbSO.nlJ-bbSO.nhJ + \ 3418 (int)(bbSOSh-bbSOS1) +0 + bbSOi; 3419 if(bbSOdebugflag<DEBUG){ 3420 fprintf(DBG," $t(bbSOh+0)*bbSO.nlJ=%d, bbSO.nlJ-bbSO.nhJ=%d\n",$ 3421 (bbSOh+0)*bbSO.nlJ,bbSO.nlJ-bbSO.nhJ); 3422 fprintf(DBG,"\t(int)(bbSOSh-bbSOS1)=%d, bbSOi=%d, bbSOel=%d\n",\ 3423 (int)(bbSOSh-bbSOS1),bbSOi,bbSOel); 3424 fflush(DBG); 3425 } 3426 if((bbSOel+1)>=(bbSO.R1[0].kc*bbSO.nlJ)) bbSOflgb=1; /* Then check if the target value for J+1 is less than or greater than the allowed J's for K+0. */ 3427 if((bbSOJ+1)>(bbSOh+0+bbSOS1)) bbSOflgb=1; 3428 if((bbSOJ+1)<(bbSOh+0-bbSOS1)) bbSOflgb=1; /* Still OK? Calculate transition */ 3429 if(bbSOflgb==0){ 3430 bbSOB=+1;3431 bbSOell=bbSOel+1; 3432 bbSO.T[0].S[bbSOff].f[bbS0jii]=\ 3433 bbSO.Rh[0].EJ[bbSOehh]-3434 bbSO.R1[0].EJ[bbSOel1]; 3435 bbSO.T[0].S[bbSOff].ni[bbSOjii]=\ 3436 bbSOhipop*bbSOtrprob*bbSOvhpop*\ 3437 bbSO.Rh[0].PJ[bbSOehh]*bbSOSATT*\ 3438 HL(bbSOB,bbSOJ,bbSOL,bbSOdL)*bbSOfcf; 3439 if(bbSOdebugflag<DEBUG){ 3440 fprintf(DBG,"bbSO.Rh[0].EJ[%d]=%12.6e ",bbSOehh,bbSO.Rh[0].EJ[bbSOehh]); 3441 fprintf(DBG,"bbSO.R1[0].EJ[%d]=%12.6e ",bbSOell,bbSO.R1[0].EJ[bbSOell]); 3442 fprintf(DBG,"bbSO.T[0].S[%d].f[%d]=%12.6e ",bbSOff,bbSOjii,\ 3443 bbSO.T[0].S[bbSOff].f[bbS0jii]); 3444 fprintf(DBG,"bbSOhipop=%12.6e, bbSOtrprob=%12.6e, bbSOvhpop=%12.6e\n",\ 3445 bbSOhipop, bbSOtrprob, bbSOvhpop); 3446 fprintf(DBG,"bbSOfcf=%12.6e ",bbSOfcf); 3447 fprintf(DBG,"bbSO.Rh[0].PJ[%d]=%12.6e ",bbSOehh,bbSO.Rh[0].PJ[bbSOehh]); 3448 fprintf(DBG,"HL(%d,%.1f,%d,%d)=%12.6e ",bbSOB,bbSOJ,bbSOL,bbSOdL, \ 3449 HL(bbSOB,bbSOJ,bbSOL,bbSOdL)); 3450 fprintf(DBG,"bbSO.T[0].S[%d].ni[%d]=%12.6e\n",bbSOff,bbSOjii,\ 3451 bbSO.T[0].S[bbSOff].ni[bbSOjii]); 3452 } /* Check for nuclear effects and modify intensity if necessary. */ 3453 if((bbS0g!=0)&&(bbS0L0[0].L==0)){ /* low state is Sigma */ 3454 if((((bbSOh+0)%2)==0)&&(bbSOisym==-1)){ 3455 bbSO.T[0].S[bbSOff].ni[bbS0jii]*=bbSOIa; 3456 } if((((bbSOh+0)%2)==1)&&(bbSOisym==+1)){ 3457 3458 bbSO.T[0].S[bbSOff].ni[bbSOjii]*=bbSOIa; 3459 }
```
3460
           }
      /* set low-state population for cascade */
3461
             bbSO.R1[0].CJ[bbSOell]+=bbSOfcfr*\
3462
               bbSO.T[0].S[bbSOff].ni[bbS0jii];
3463 if(bbSOdebugflag<DEBUG){
3464 fprintf(DBG,"bbSO.R1[0].CJ[%d]=%12.6e,
     bbSO.T[0].S[%d].ni[%d]=%12.6e\n",\
3465
       bbSOell,bbSO.Rl[0].CJ[bbSOell],bbSOff,\
       bbSOjii,bbSO.T[0].S[bbSOff].ni[bbSOjii]);
3466
3467 }
3468
             bbSOjii--;
3469
             Ł
3470 if(bbSOdebugflag<DEBUG){
3471 fprintf(DBG,"bbSO, K+O, J+1 native\n");
3472 fprintf(DBG,"%d ",bbSOh);
3473 if(bbSOflgb!=0) fprintf(DBG," %d %.1f M M ",(bbSOh+0),bbSOJ);
3474 else{
3475 fprintf(DBG,"%d %.1f %18.12e %18.12e ",(bbSOh+0),\
3476
       bbSOJ,bbSO.T[0].S[bbSOff].f[bbSOjii+1],\
3477
       bbSO.T[0].S[bbSOff].ni[bbSOjii+1]);
3478
       }
3479 }
3480 fprintf(BBSOFILE,"%d ",bbSOh);
3481 if(bbSOflgb!=0) fprintf(BBSOFILE," %d %.1f M M ",(bbSOh+0),bbSOJ);
3482 else{
3483 fprintf(BBSOFILE,"%d %.1f %18.12e %18.12e ",(bbSOh+0),\
3484
       bbSOJ,bbSO.T[0].S[bbSOff].f[bbSOjii+1],
3485
       bbSO.T[0].S[bbSOff].ni[bbSOjii+1]);
3486
       }
      /* Now Delta-J=0 (Q) (for Delta-K=+0) */
3487
           bbSOflgb=0;
3488
           if((bbSOh+0)<(bbSOLO[0].L)) bbSOflgb=1;</pre>
      /* Then check if the target value for J+1 is less than or greater
        than the allowed J's for K+0. */
3489
           if((bbSOJ+0)>(bbSOh+0+bbSOS1)) bbSOflgb=1;
3490
           if((bbSOJ+0)<(bbSOh+0-bbSOS1)) bbSOflgb=1;
      /* Still OK? Calculate transition */
3491
           if(bbSOflgb==0){
3492
             bbSOB=0;
3493
             bbSOell=bbSOel+0;
3494
             bbSO.T[0].S[bbSOff].f[bbS0jii]=\
3495
               bbSO.Rh[0].EJ[bbSOehh]-
3496
               bbSO.R1[0].EJ[bbSOell];
3497
             bbSO.T[0].S[bbSOff].ni[bbS0jii]=\
3498
               bbSOhipop*bbSOtrprob*bbSOvhpop*\
3499
               bbSO.Rh[0].PJ[bbSOehh]*bbSOfcf*\
3500
               HL(bbSOB,bbSOJ,bbSOL,bbSOdL);
3501 if(bbSOdebugflag<DEBUG){
3502 fprintf(DBG,"bbSO.Rh[0].EJ[%d]=%12.6e
     ",bbSOehh,bbSO.Rh[0].EJ[bbSOehh]);
3503 fprintf(DBG,"bbS0.R1[0].EJ[%d]=%12.6e
     ",bbSOell,bbSO.R1[0].EJ[bbSOell]);
```

3504 fprintf(DBG,"bbSO.T[0].S[%d].f[%d]=%12.6e ",bbSOff,bbSOjii,\

```
bbSO.T[0].S[bbSOff].f[bbS0jii]);
3505
3506 fprintf(DBG,"bbSOhipop%12.6e, bbSOtrprob%12.6e, bbSOvh-
     pop=%12.6e\n",\
3507
         bbSOhipop,bbSOtrprob,bbSOvhpop);
3508 fprintf(DBG,"bbSOfcf=%12.6e ",bbSOfcf);
3509 fprintf(DBG,"bbSO.Rh[0].PJ[%d]=%12.6e
     ",bbSOehh,bbSO.Rh[0].PJ[bbSOehh]);
3510 fprintf(DBG,"HL(%d,%.1f,%d,%d)=%12.6e
     ",bbSOB,bbSOJ,bbSOL,bbSOdL,\
3511
       HL(bbSOB,bbSOJ,bbSOL,bbSOdL));
3512 fprintf(DBG,"bbS0.T[0].S[%d].ni[%d]=%12.6e\n",bbS0ff,bbS0jii,\
3513
       bbSO.T[0].S[bbSOff].ni[bbSOjii]);
3514 }
      /* Check for nuclear effects and modify intensity if necessary. */
3515
         if((bbSOg!=0)&&(bbSOLO[0].L==0)){ /* low state is Sigma */
3516
           if((((bbSOh+0)%2)==0)&&(bbSOisym==-1)){
3517
             bbSO.TLOJ.SLbbSOffJ.niLbbSOjiiJ*=bbSOIa;
3518
             }
3519
           if((((bbSOh+0)%2)==1)&&(bbSOisym==+1)){
3520
             bbSO.T[0].S[bbSOff].ni[bbSOjii]*=bbSOIa;
3521
             }
           }
3522
      /* set low-state population for cascade */
3523
             bbSO.R1[0].CJ[bbSOell]+=bbSOfcfr*\
3524
               bbSO.T[0].S[bbSOff].ni[bbSOjii];
3525 if(bbSOdebugflag<DEBUG){
3526 fprintf(DBG, "bbSO.R1[0].CJ[%d]=%12.6e,
     bbSO.T[0].S[%d].ni[%d]=%12.6e\n",\
3527
       bbSOell,bbSO.R1[0].CJ[bbSOell],bbSOff,\
3528
       bbSOjii,bbSO.T[0].S[bbSOff].ni[bbSOjii]);
3529 }
3530
             bbSOjii--;
3531
3532 if(bbSOdebugflag<DEBUG){
3533 fprintf(DBG,"bbSO, K+O, J+O native\n");
3534 fprintf(DBG,"%d ",bbSOh);
3535 if(bbSOflgb!=0) fprintf(DBG," M M ");
3536 else{
3537 fprintf(DBG," %18.12e %18.12e ",bbSO.T[0].S[bbSOff].f[bbS0jii+1],\
3538
       bbSO.T[0].S[bbSOff].ni[bbSOjii+1]);
3539
       }
3540 }
3541 if(bbSOflgb!=0) fprintf(BBSOFILE," M M ");
3542 else{
3543 fprintf(BBSOFILE,"%18.12e %18.12e
     ",bbSO.T[0].S[bbSOff].f[bbSOjii+1],
3544
       bbSO.T[0].S[bbSOff].ni[bbS0jii+1]);
3545
       }
      /* Now, Delta-J=-1 (R) for Delta-K=+0. */
3546
           bbSOflgb=0;
3547
           if((bbSOh+0)<(bbSOLO[0].L)) bbSOflgb=1;
3548
           if((bbSOJ-1)>(bbSOh+0+bbSOS1)) bbSOflgb=1;
3549
           if((bbSOJ-1)<(bbSOh+0-bbSOS1)) bbSOflgb=1;
3550
           if((bbS0J-1)<0) bbS0flgb=1;</pre>
```

```
3551
           if(bbSOflgb==0){
3552
             bbSOB=-1;
3553
             bbSOell=bbSOel-1;
             bbSO.T[0].S[bbSOff].f[bbSOjii]=\
3554
3555
               bbSO.Rh[0].EJ[bbSOehh]-
3556
               bbSO.R1[0].EJ[bbSOel1];
             bbSO.T[0].S[bbSOff].ni[bbS0jii]=\
3557
3558
               bbSOhipop*bbSOtrprob*bbSOvhpop*\
3559
               bbSO.Rh[0].PJ[bbSOehh]*bbSOSATT*\
3560
               HL(bbSOB,bbSOJ,bbSOL,bbSOdL)*bbSOfcf;
3561 if(bbSOdebugflag<DEBUG){
3562 fprintf(DBG,"bbSO.Rh[0].EJ[%d]=%12.6e
     ",bbSOehh,bbSO.Rh[0].EJ[bbSOehh]);
3563 fprintf(DBG,"bbSO.R1[0].EJ[%d]=%12.6e
     ",bbSOell,bbSO.R1[0].EJ[bbSOell]);
3564 fprintf(DBG,"bbSO.T[0].S[%d].f[%d]=%12.6e ",bbSOff,bbSOjii,\
         bbSO.T[0].S[bbSOff].f[bbSOjii]);
3565
3566 fprintf(DBG,"bbSOhipop=%12.6e, bbSOtrprob=%12.6e, bbSOvh-
     pop=%12.6e\n",\
3567
         bbSOhipop,bbSOtrprob,bbSOvhpop);
3568 fprintf(DBG,"bbSOfcf=%12.6e ",bbSOfcf);
3569 fprintf(DBG,"bbSO.Rh[0].PJ[%d]=%12.6e
     ",bbSOehh,bbSO.Rh[0].PJ[bbSOehh]);
3570 fprintf(DBG,"HL(%d,%.1f,%d,%d)=%12.6e
     ",bbSOB,bbSOJ,bbSOL,bbSOdL,\
3571
       HL(bbSOB,bbSOJ,bbSOL,bbSOdL));
3572 fprintf(DBG,"bbS0.T[0].S[%d].ni[%d]=%12.6e\n",bbS0ff,bbS0jii,\
3573
       bbSO.T[0].S[bbSOff].ni[bbSOjii]);
3574 }
3575
         if((bbS0g!=0)&&(bbS0L0[0].L==0)){ /* low state is Sigma */
           if((((bbSOh+0)%2)==0)&&(bbSOisym==-1)){
3576
3577
             bbSO.T[0].S[bbSOff].ni[bbS0jii]*=bbSOIa;
3578
             }
3579
           if((((bbSOh+0)%2)==1)&&(bbSOisym==+1)){
3580
             bbSO.T[0].S[bbSOff].ni[bbS0jii]*=bbSOIa;
3581
             }
           }
3582
3583
             bbSO.R1[0].CJ[bbSOel1]+=bbSOfcfr*\
3584
               bbSO.T[0].S[bbSOff].ni[bbSOjii];
3585 if(bbSOdebugflag<DEBUG){
3586 fprintf(DBG,"bbSO.R1[0].CJ[%d]=%12.6e,
     bbSO.T[0].S[%d].ni[%d]=%12.6e\n",\
3587
       bbSOell,bbSO.R1[0].CJ[bbSOell],bbSOff,\
3588
       bbSOjii,bbSO.T[0].S[bbSOff].ni[bbSOjii]);
3589 }
3590
             bbSOjii--;
             }
3591
3592 if(bbSOdebugflag<DEBUG){
3593 fprintf(DBG, "bbSO, K+O, J-1 native\n");
3594 if(bbSOflgb!=0) fprintf(DBG,"M M\n");
3595 else{
3596 fprintf(DBG,"%18.12e
     %18.12e\n",bbSO.T[0].S[bbSOff].f[bbS0jii+1],\
       bbSO.T[0].S[bbSOff].ni[bbS0jii+1]);
3597
```

3598 } 3599 } 3600 if(bbSOflgb!=0) fprintf(BBSOFILE,"M M\n"); 3601 else{ 3602 fprintf(BBSOFILE,"%18.12e %18.12e\n",bbSO.T[0].S[bbSOff].f[bbS0jii+1],\ 3603 bbSO.T[0].S[bbSOff].ni[bbSOjii+1]); 3604 } /* Check Delta-J=+1 (P), then Delta-J=0 and Delta-J=-1 (R) for Delta-K=-1. First, check to see if the target K exists: */ 3605 bbSOflgb=0; 3606 if((bbSOh-1)<(bbSOLO[0].L)) bbSOflgb=1; /* Relative position in the low state E/P array */ 3607 bbSOel=(bbSOh-1)*bbSO.nlJ + bbSO.nlJ-bbSO.nhJ + \ 3608 (int)(bbSOSh-bbSOS1) + 1 + bbSOi; 3609 if(bbSOdebugflag<DEBUG){ 3610 fprintf(DBG,"\t(bbS0h-1)*bbS0.nlJ=%d, bbS0.nlJ-bbS0.nhJ=%d\n",\ (bbSOh-1)*bbSO.nlJ,bbSO.nlJ-bbSO.nhJ); 3611 3612 fprintf(DBG,"\t(int)(bbSOSh-bbSOS1)=%d, bbSOi=%d, bbSOel=%d\n",\ 3613 (int)(bbSOSh-bbSOS1),bbSOi,bbSOel); 3614 fflush(DBG); 3615 } if((bbSOel+1)>=(bbSO.R1[0].kc*bbSO.nlJ)) bbSOflgb=1; 3616 /* Then check if the target value for J+1 is less than or greater than the allowed J's for K-1. */ if((bbSOJ+1)>(bbSOh-1+bbSOS1)) bbSOflgb=1; 3617 3618 if((bbSOJ+1)<(bbSOh-1-bbSOS1)) bbSOflgb=1; /* Still OK? Calculate transition */ 3619 if(bbSOflgb==0){ bbSOB=+1;3620 bbSOell=bbSOel+1; 3621 3622 bbSO.T[0].S[bbSOff].f[bbSOjii]=\ 3623 bbSO.Rh[0].EJ[bbSOehh]-3624 bbSO.R1[0].EJ[bbSOel1]; 3625 bbSO.T[0].S[bbSOff].ni[bbS0jii]=\ 3626 bbSOhipop*bbSOtrprob*bbSOvhpop*\ 3627 bbSO.Rh[0].PJ[bbSOehh]*bbSOSATT*\ 3628 HL(bbSOB,bbSOJ,bbSOL,bbSOdL)*bbSOfcf; 3629 if(bbSOdebugflag<DEBUG){ 3630 fprintf(DBG,"bbSO.Rh[0].EJ[%d]=%12.6e ",bbSOehh,bbSO.Rh[0].EJ[bbSOehh]); 3631 fprintf(DBG,"bbS0.R1[0].EJ[%d]=%12.6e ",bbSOell,bbSO.R1[0].EJ[bbSOell]); 3632 fprintf(DBG,"bbSO.T[0].S[%d].f[%d]=%12.6e ",bbSOff,bbSOjii,\ 3633 bbSO.T[0].S[bbSOff].f[bbSOjii]); 3634 fprintf(DBG,"bbSOhipop%12.6e, bbSOtrprob%12.6e, bbSOvhpop=%12.6e\n",\ 3635 bbSOhipop,bbSOtrprob,bbSOvhpop); 3636 fprintf(DBG,"bbSOfcf=%12.6e ",bbSOfcf); 3637 fprintf(DBG,"bbSO.Rh[0].PJ[%d]=%12.6e ",bbSOehh,bbSO.Rh[0].PJ[bbSOehh]); 3638 fprintf(DBG,"HL(%d,%.1f,%d,%d)=%12.6e ", bbSOB, bbSOJ, bbSOL, bbSOdL, \ 3639 HL(bbSOB,bbSOJ,bbSOL,bbSOdL));

```
3640 fprintf(DBG,"bbS0.T[0].S[%d].ni[%d]=%12.6e\n",bbS0ff,bbS0jii,\
3641
       bbSO.T[0].S[bbSOff].ni[bbSOjii]);
3642 }
      /* Check for nuclear effects and modify intensity if necessary. */
3643
         if((bbS0g!=0)&&(bbS0L0[0].L==0)){ /* low state is Sigma */
3644
           if((((bbSOh-1)%2)==0)&&(bbSOisym==-1)){
             bbSO.T[0].S[bbSOff].ni[bbS0jii]*=bbS0Ia;
3645
              }
3646
3647
           if((((bbSOh-1)%2)==1)&&(bbSOisym==+1)){
3648
             bbSO.T[0].S[bbSOff].ni[bbSOjii]*=bbSOIa;
              }
3649
           }
3650
3651
             bbSO.R1[0].CJ[bbSOell]+=bbSOfcfr*\
3652
               bbSO.T[0].S[bbSOff].ni[bbSOjii];
3653 if(bbSOdebugflag<DEBUG){
3654 fprintf(DBG,"bbSO.R1[0].CJ[%d]=%12.6e,
     bbSO.T[0].S[%d].ni[%d]=%12.6e\n",\
3655
       bbSOell,bbSO.Rl[0].CJ[bbSOell],bbSOff,\
3656
       bbS0jii,bbS0.T[0].S[bbS0ff].ni[bbS0jii]);
3657 }
3658
             bbSOjii--;
3659
              }
3660 if(bbSOdebugflag<DEBUG){
3661 fprintf(DBG,"bbSO, K-1, J+1 native\n");
3662 fprintf(DBG,"%d ",bbSOh);
3663 if(bbSOflgb!=0) fprintf(DBG," %d %.1f M M ",(bbSOh-1),bbSOJ);
3664 else{
3665 fprintf(DBG,"%d %.1f %18.12e %18.12e ",(bbSOh-1),\
3666
       bbSOJ,bbSO.T[0].S[bbSOff].f[bbSOjii+1],\
3667
       bbSO.T[0].S[bbSOff].ni[bbS0jii+1]);
3668
       }
3669 }
3670 fprintf(BBSOFILE, "%d ", bbSOh);
3671 if(bbS0flgb!=0) fprintf(BBS0FILE," %d %.1f M M ",(bbS0h-1),bbS0J);
3672 else{
3673 fprintf(BBSOFILE, "%d %.1f %18.12e %18.12e ",(bbSOh-1),\
3674
       bbSOJ,bbSO.T[0].S[bbSOff].f[bbSOjii+1],
3675
       bbSO.T[0].S[bbSOff].ni[bbSOjii+1]);
3676
       }
      /* Now, Delta-J=+0 (Q) for Delta-K=-1. */
3677
           bbSOflgb=0;
3678
           if((bbSOh-1)<(bbSOLO[0].L)) bbSOflgb=1;</pre>
      /* Then check if the target value for J+1 is less than or greater
        than the allowed J's for K-1. */
3679
           if((bbSOJ+0)>(bbSOh-1+bbSOS1)) bbSOflgb=1;
3680
           if((bbS0J+0)<(bbS0h-1-bbS0S1)) bbS0flgb=1;</pre>
      /* Still OK? Calculate transition */
3681
           if(bbSOflgb==0){
3682
             bbSOB=+0;
             bbSOell=bbSOel+0;
3683
             bbSO.T[0].S[bbSOff].f[bbS0jii]=\
3684
               bbSO.Rh[0].EJ[bbSOehh]-\
3685
3686
                bbSO.R1[0].EJ[bbSOel1];
             bbSO.T[0].S[bbSOff].ni[bbS0jii]=\
3687
```

```
3688
               bbSOhipop*bbSOtrprob*bbSOvhpop*\
3689
               bbSO.Rh[0].PJ[bbSOehh]*bbSOSATT*\
3690
               HL(bbSOB,bbSOJ,bbSOL,bbSOdL)*bbSOfcf;
3691 if(bbSOdebugflag<DEBUG){
3692 fprintf(DBG,"bbSO.Rh[0].EJ[%d]=%12.6e
     ",bbSOehh,bbSO.Rh[0].EJ[bbSOehh]);
3693 fprintf(DBG,"bbS0.Rl[0].EJ[%d]=%12.6e
     ",bbSOell,bbSO.R1[0].EJ[bbSOell]);
3694 fprintf(DBG,"bbS0.T[0].S[%d].f[%d]=%12.6e ",bbS0ff,bbS0jii,\
         bbSO.T[0].S[bbSOff].f[bbS0jii]);
3695
3696 fprintf(DBG,"bbSOhipop=%12.6e, bbSOtrprob=%12.6e, bbSOvh-
     pop=%12.6e\n",\
3697
         bbSOhipop,bbSOtrprob,bbSOvhpop);
3698 fprintf(DBG,"bbSOfcf=%12.6e ",bbSOfcf);
3699 fprintf(DBG,"bbSO.Rh[0].PJ[%d]=%12.6e
     ",bbSOehh,bbSO.Rh[0].PJ[bbSOehh]);
3700 fprintf(DBG,"HL(%d,%.1f,%d,%d)=%12.6e
     ", bbSOB, bbSOJ, bbSOL, bbSOdL, \backslash
3701
       HL(bbSOB,bbSOJ,bbSOL,bbSOdL));
3702 fprintf(DBG,"bbS0.T[0].S[%d].ni[%d]=%12.6e\n",bbS0ff,bbS0jii,\
       bbSO.T[0].S[bbSOff].ni[bbS0jii]);
3703
3704 }
      /* Check for nuclear effects and modify intensity if necessary. */
3705
         if((bbS0g!=0)&&(bbS0L0[0].L==0)){ /* low state is Sigma */
3706
           if((((bbSOh-1)%2)==0)&&(bbSOisym==-1)){
3707
             bbSO.T[0].S[bbSOff].ni[bbSOjii]*=bbSOIa;
3708
             }
           if((((bbSOh-1)%2)==1)&&(bbSOisym==+1)){
3709
3710
             bbSO.T[0].S[bbSOff].ni[bbSOjii]*=bbSOIa;
3711
             }
3712
           }
3713
             bbSO.R1[0].CJ[bbSOell]+=bbSOfcfr*\
               bbSO.T[0].S[bbSOff].ni[bbSOjii];
3714
3715 if(bbSOdebugflag<DEBUG){
3716 fprintf(DBG,"bbSO.R1[0].CJ[%d]=%12.6e,
     bbSO.T[0].S[%d].ni[%d]=%12.6e\n",\
3717
       bbSOell,bbSO.R1[0].CJ[bbSOell],bbSOff,\
3718
       bbSOjii,bbSO.T[0].S[bbSOff].ni[bbSOjii]);
3719 }
3720
             bbSOjii--;
3721
             }
3722 if(bbSOdebugflag<DEBUG){
3723 fprintf(DBG,"bbSO, K-1, J+0 native\n");
3724 fprintf(DBG,"%d ",bbSOh);
3725 if(bbS0flgb!=0) fprintf(DBG," %d %.1f M M ",(bbS0h-1),bbS0J);
3726 else{
3727 fprintf(DBG, "%d %.1f %18.12e %18.12e ", (bbSOh-1), \
3728
       bbSOJ,bbSO.T[0].S[bbSOff].f[bbSOjii+1],
3729
       bbSO.T[0].S[bbSOff].ni[bbS0jii+1]);
3730
       }
3731 }
3732 if(bbSOflgb!=0) fprintf(BBSOFILE,"M M ");
3733 else{
```

3734 fprintf(BBSOFILE," %18.12e %18.12e ,bbSO.T[0].S[bbSOff].f[bbS0jii+1],\ bbSO.T[0].S[bbSOff].ni[bbS0jii+1]); 3735 3736 } /* Now, Delta-J=-1 (R) for Delta-K=-1. */ 3737 bbSOflgb=0; 3738 if((bbSOh-1)<(bbSOLO[0].L)) bbSOflgb=1;</pre> 3739 if((bbSOJ-1)>(bbSOh-1+bbSOS1)) bbSOflgb=1; 3740 if((bbSOJ-1)<(bbSOh-1-bbSOS1)) bbSOflgb=1;</pre> 3741 if((bbSOJ-1)<0) bbSOflgb=1; 3742 if(bbSOflgb==0){ 3743 bbSOB=-1;3744 bbSOell=bbSOel-1; 3745 bbSO.T[0].S[bbSOff].f[bbSOjii]=\ 3746 bbSO.Rh[0].EJ[bbSOehh]-\ 3747 bbSO.R1[0].EJ[bbSOel1]; 3748 bbSO.T[0].S[bbSOff].ni[bbS0jii]=\ 3749 bbSOhipop*bbSOtrprob*bbSOvhpop*\ bbSO.Rh[0].PJ[bbSOehh]*bbSOfcf*\ 3750 3751 HL(bbSOB,bbSOJ,bbSOL,bbSOdL); 3752 if(bbSOdebugflag<DEBUG){ 3753 fprintf(DBG,"bbSO.Rh[0].EJ[%d]=%12.6e ",bbSOehh,bbSO.Rh[0].EJ[bbSOehh]); 3754 fprintf(DBG,"bbSO.R1[0].EJ[%d]=%12.6e ",bbSOell,bbSO.R1[0].EJ[bbSOell]); 3755 fprintf(DBG,"bbSO.T[0].S[%d].f[%d]=%12.6e ",bbSOff,bbSOjii,\ bbSO.T[0].S[bbSOff].f[bbS0jii]); 3756 3757 fprintf(DBG,"bbSOhipop=%12.6e, bbSOtrprob=%12.6e, bbSOvhpop=%12.6e\n",\ 3758 bbSOhipop,bbSOtrprob,bbSOvhpop); 3759 fprintf(DBG,"bbSOfcf=%12.6e ",bbSOfcf); 3760 fprintf(DBG,"bbSO.Rh[0].PJ[%d]=%12.6e ",bbSOehh,bbSO.Rh[0].PJ[bbSOehh]); 3761 fprintf(DBG,"HL(%d,%.1f,%d,%d)=%12.6e ",bbSOB,bbSOJ,bbSOL,bbSOdL, \ 3762 HL(bbSOB,bbSOJ,bbSOL,bbSOdL)); 3763 fprintf(DBG,"bbS0.T[0].S[%d].ni[%d]=%12.6e\n",bbS0ff,bbS0jii,\ 3764 bbSO.T[0].S[bbSOff].ni[bbSOjii]); 3765 } 3766 if((bbS0g!=0)&&(bbS0L0[0].L==0)){ /* low state is Sigma */ 3767 if((((bbSOh-1)%2)==0)&&(bbSOisym==-1)){ 3768 bbSO.T[0].S[bbSOff].ni[bbS0jii]*=bbSOIa; 3769 } if((((bbSOh-1)%2)==1)&&(bbSOisym==+1)){ 3770 3771 bbSO.T[0].S[bbSOff].ni[bbSOjii]*=bbSOIa; 3772 } } 3773 bbSO.R1[0].CJ[bbSOell]+=bbSOfcfr*\ 3774 3775 bbSO.T[0].S[bbSOff].ni[bbSOjii]; 3776 if(bbSOdebugflag<DEBUG){ 3777 fprintf(DBG,"bbSO.R1[0].CJ[%d]=%12.6e, bbSO.T[0].S[%d].ni[%d]=%12.6e\n",\ 3778 bbSOell,bbSO.R1[0].CJ[bbSOell],bbSOff,\ 3779 bbSOjii,bbSO.T[0].S[bbSOff].ni[bbSOjii]);

3780 } 3781 } 3782 if(bbSOdebugflag<DEBUG){ 3783 fprintf(DBG, "bbSO, K-1, J-1 native\n"); 3784 if(bbSOflgb!=0) fprintf(DBG,"M M\n"); 3785 else{ 3786 fprintf(DBG,"%18.12e %18.12e\n",bbSO.T[0].S[bbSOff].f[bbS0jii],\ bbSO.T[0].S[bbSOff].ni[bbS0jii]); 3787 3788 } 3789 } 3790 if(bbSOflgb!=0) fprintf(BBSOFILE,"M M\n"); 3791 else{ 3792 fprintf(BBSOFILE,"%18.12e %18.12e\n",bbSO.T[0].S[bbSOff].f[bbSOjii],\ 3793 bbSO.T[0].S[bbSOff].ni[bbS0jii]); 3794 } 3795 } /* close if bbSOflga is zero. */ 3796 } /* close upper-state J-of-K loop */ 3797 } /* close upper-state K loop */ 3798 fclose(BBSOFILE); 3799 } /* close if high-state v is natively populated */ 3800 if(bbSOfrchf==0){ /* if this v is cascade populated.*/ 3801 sprintf(bbSOfile,"%s_molecules/%s/%s--%s_v%d--v%d_CAS.dat", 3802 PREF,MOL[bbS0.m].Mol,bbS0.T[0].Nhi,bbS0.T[0].Nlo,bbS0e,bbS0f); 3803 BBSOFILE=fopen(bbSOfile,"w"); 3804 if(BBSOFILE==NULL){ 3805 printf("Error opening transition sub-file %s. Exiting.\n",bbSOfile); 3806 exit(1); 3807 } 3808 fprintf(BBSOFILE, "# File created by %s.\n# File contains ", PRO-GRAM_NAME); 3809 fprintf(BBSOFILE, "P and R"); 3810 fprintf(BBSOFILE," branches from the simulation titled %s\n",PREF); 3811 fprintf(BBSOFILE, "# THESE INTENSITIES ARE DUE TO CASCADE ONLY -- "); 3812 fprintf(BBSOFILE, "NO USER-DEFINED POPULATIONS\n"); 3813 fprintf(BBSOFILE,"# Transition is Hund's Case (b) to Hund's Case (b).\n"); 3814 fprintf(BBSOFILE,"# Molecule %s, \tHigh state: %s, v=%d\n",\ 3815 MOL[bbS0.m].Mol,bbS0.T[0].Nhi,bbS0e); 3816 fprintf(BBSOFILE,"#\t\tLow state: %s, v=%d\n# Columns are: ",\ bbSO.T[0].Nlo,bbSOf); 3817 3818 fprintf(BBSOFILE,"K_hi K_lo J_hi P(J_hi+1)_v P_i R(J_hi-1)_v $R_i n#(n");$ 3819 bbSO.Rh=&bbSO.Sh[0].rc[bbSOfrch]; 3820 if((bbSO.hiK)<bbSO.Sh[0].rc[bbSOfrch].kc){ 3821 bbSOk=bbSO.hiK-1; 3822 } else bbSOk=bbSO.Sh[0].rc[bbSOfrch].kc-1; 3823 3824 if(bbSO.R1[0].Kdissoc<(bbSOk-1)){ 3825 fprintf(PAR,"\nWARNING!! State %s of molecule %s has significant ",\

```
3826 bbSO.T[0].Nhi,MOL[bbSO.m].Mol);
```

3827 fprintf(PAR, "CASCADE rotational population at level %d\n", bbSOk);

```
3828 fprintf(PAR,"\tBut lower state %s dissociates at level %.1f\n",\
```

- 3829 bbSO.T[0].Nlo,bbSO.Rl[0].Kdissoc);
- 3830 fprintf(PAR,"It is likely that the bound upper state is transiting to (an)");
- 3831 fprintf(PAR," unbound lower state(s).\n");
- 3832 fprintf(PAR,"Look for continuum emissions trailing off to the lowenergy ");
- 3833 fprintf(PAR,"end of the v(hi)=%d to v(lo)=%d\nband in the real ",bb-SOe,bbSOf);
- 3834 fprintf(PAR,"spectrum (not the simulated one)\nCurrently, this program will");

```
3835 fprintf(PAR," not simulate bound-->unbound spectra.\n\n");
```

3836 bbSOk=(int)(bbSO.R1[0].Kdissoc);

```
3837
```

3838 if(bbSOdebugflag<DEBUG){</pre>

}

```
3839 fprintf(DBG,"bbSOfrch=%d, bbSOk=%d, ",bbSOfrch,bbSOk);
```

```
3840 fprintf(DBG, "bbSO.Sh[0].rc[%d].kc = %d\n", bbSOfrch,
```

```
bbSO.Sh[0].rc[bbSOfrch].kc);
```

- 3841 fflush(DBG);
- 3842 }

/* To make the output file easy to write, I'm cycling by high-state
K first, then by high-state J. From that J/K(hi) pair, the program will look for a P transition and an R transition to K+1 then
to K-1. If all the necessary states exist, it will check to see
if there are any symmetry or nuclear spin effects to be concerned
about. Taking these into account, it will calculate the transition. */

```
/* loop first by upper-state K-value */
```

```
3843 for(bbSOh=bbSOk;bbSOh>=0;bbSOh--){
```

```
3844 bbSOjii=(bbSOh+1)*bbSO.nT-1; /* position in simset array */
```

```
3845 bbSOeh=bbSOh*bbSO.nhJ; /* position in 2D for high EJ & PJ */
```

```
/* then loop by upper-state J for this K */
```

```
3846 for(bbSOi=(bbSO.nhJ-1);bbSOi>=0;bbSOi--){
```

- 3847 bbSOJ=bbSOh+bbSOi-bbSOSh;
- 3848 bbSOehh=bbSOeh+bbSOi;
- 3849 bbSOflga=0;

```
3850 if(bbSOh<bbSOHI[0].L) bbSOflga=1; /* if this K is less than
Lambda for the high state, don't proceed */
```

```
3851 if(bbS0J<0) bbS0flga=1; /* if J is less than zero, don't */</pre>
```

```
3852 if(bbSOdebugflag<DEBUG){
```

```
3853 fprintf(DBG,"bbSOh=%d, bbSOi=%d, bbSOSh=%.1f, bbSOHI[0].L=%d, bb-
SOflga=%d\n",\
```

```
3854 bbSOh,bbSOi,bbSOSh,bbSOHI[0].L,bbSOflga);
```

```
3855 fflush(DBG);
```

3856 }

```
3857 if(bbSOflga==0){
```

```
/* Check Delta-J=+1 (P), then Delta-J=0 (Q) and Delta-J=-1 (R) for
Delta-K=+1. First, check to see if the target K exists: */
3858 bbSOflgb=0;
```

```
3859 if((bbSOh+1)<(bbSOLO[0].L)) bbSOflgb=1;</pre>
```

```
/* Relative position in the low state E/P array */
```

```
3860 bbSOel=(bbSOh+1)*bbSO.nlJ + bbSO.nlJ-bbSO.nhJ + \
```

```
3861
             (int)(bbSOSh-bbSOS1) -1 + bbSOi;
3862 if(bbSOdebugflag<DEBUG){
3863 fprintf(DBG,"\t(bbS0h+1)*bbS0.nlJ=%d, bbS0.nlJ-bbS0.nhJ=%d\n",\
         (bbSOh+1)*bbSO.nlJ,bbSO.nlJ-bbSO.nhJ);
3864
3865 fprintf(DBG,"\t(int)(bbSOSh-bbSOS1)=%d, bbSOi=%d, bbSOel=%d\n",\
         (int)(bbSOSh-bbSOS1),bbSOi,bbSOel);
3866
3867 fflush(DBG);
3868 }
3869
           if((bbSOel+1)>=(bbSO.R1[0].kc*bbSO.nlJ)) bbSOflgb=1;
      /* Then check if the target value for J+1 is less than or greater
        than the allowed J's for K+1. */
           if((bbS0J+1)>(bbS0h+1+bbS0S1)) bbS0flgb=1;
3870
3871
           if((bbSOJ+1)<(bbSOh+1-bbSOS1)) bbSOflgb=1;
      /* Still OK? Calculate transition */
3872
           if(bbSOflgb==0){
3873
             bbSOB=+1;
             bbSOell=bbSOel+1;
3874
             bbSO.T[0].S[bbSOff].f[bbS0jii]=\
3875
3876
               bbSO.Rh[0].EJ[bbSOehh]-
3877
               bbSO.R1[0].EJ[bbSOel1];
3878
             bbSOcascadetemp=bbSOtrprob*bbSOfcf*\
3879
               bbSO.Rh[0].CJ[bbSOehh]*\
3880
               HL(bbSOB,bbSOJ,bbSOL,bbSOdL);
      /* Check for nuclear effects and modify intensity if necessary. */
3881
         if((bbS0g!=0)&&(bbS0L0[0].L==0)){ /* low state is Sigma */
3882
           if((((bbSOh+1)%2)==0)&&(bbSOisym==-1)){
3883
             bbSOcascadetemp*=bbSOIa;
3884
             }
3885
           if((((bbSOh+1)%2)==1)&&(bbSOisym==+1)){
3886
             bbSOcascadetemp*=bbSOIa;
3887
             }
           }
3888
3889
             bbSO.T[0].S[bbSOff].ci[bbS0jii]+=\
3890
               bbSOcascadetemp;
3891
             bbSO.R1[0].CJ[bbSOel1]+=bbSOfcfr*\
3892
               bbSOcascadetemp;
             bbSOjii--;
3893
3894
             ł
3895 if(bbSOdebugflag<DEBUG){
3896 fprintf(DBG,"%d ",bbSOh);
3897 if(bbSOflgb!=0) fprintf(DBG," %d %.1f (1c) M M\n",(bbSOh+1),bbSOJ);
3898 else{
3899 fprintf(DBG,"%d %.1f %18.12e %18.12e (1c)\n",(bbSOh+1),\
       bbSOJ,bbSO.T[0].S[bbSOff].f[bbSOjii+1],
3900
3901
       bbSO.T[0].S[bbSOff].ci[bbSOjii+1]);
3902
       }
3903 }
3904 fprintf(BBSOFILE,"%d ",bbSOh);
3905 if(bbS0flgb!=0) fprintf(BBS0FILE," %d %.1f M M ",(bbS0h+1),bbS0J);
3906 else{
3907 fprintf(BBSOFILE, "%d %.1f %18.12e %18.12e ",(bbSOh+1),\
3908
       bbSOJ,bbSO.T[0].S[bbSOff].f[bbSOjii+1],\
3909
       bbSO.T[0].S[bbSOff].ci[bbS0jii+1]);
3910
       }
```

```
/* Now, Delta-J=0 (Q), Delta-K=+1 */
3911
           bbSOflgb=0;
           if((bbSOh+1)<(bbSOLO[0].L)) bbSOflgb=1;</pre>
3912
     /* Then check if the target value for J+1 is less than or greater
        than the allowed J's for K+1. */
3913
           if((bbSOJ+0)>(bbSOh+1+bbSOS1)) bbSOflgb=1;
3914
           if((bbS0J+0)<(bbS0h+1-bbS0S1)) bbS0flgb=1;</pre>
3915
           if((bbSOJ+0)<0) bbSOflgb=1;
     /* Still OK? Calculate transition */
3916
           if(bbSOflgb==0){
3917
             bbSOB=+0;
3918
             bbSOell=bbSOel+0;
3919
             bbSO.T[0].S[bbSOff].f[bbSOjii]=\
3920
               bbSO.Rh[0].EJ[bbSOehh]-
3921
               bbSO.R1[0].EJ[bbSOel1];
3922
             bbSOcascadetemp=bbSOtrprob*bbSOfcf*\
3923
               bbSO.Rh[0].CJ[bbSOehh]*bbSOSATT*\
3924
               HL(bbSOB,bbSOJ,bbSOL,bbSOdL);
      /* Check for nuclear effects and modify intensity if necessary. */
3925
         if((bbSOg!=0)&&(bbSOLO[0].L==0)){ /* low state is Sigma */
3926
           if((((bbSOh+1)%2)==0)&&(bbSOisym==-1)){
3927
             bbSOcascadetemp*=bbSOIa;
3928
             }
3929
           if((((bbSOh+1)%2)==1)&&(bbSOisym==+1)){
3930
             bbSOcascadetemp*=bbSOIa;
             }
3931
           }
3932
3933
             bbSO.T[0].S[bbSOff].ci[bbSOjii]+=\
3934
                bbSOcascadetemp;
3935
             bbSO.R1[0].CJ[bbSOell]+=bbSOfcfr*\
3936
                bbSOcascadetemp;
3937
             bbSOjii--;
3938
             }
3939 if(bbSOdebugflag<DEBUG){
3940 if(bbSOflgb!=0) fprintf(DBG, " M M\n");
3941 else{
3942 fprintf(DBG,"%18.12e %18.12e
     (1c)\n",bbSO.T[0].S[bbSOff].f[bbSOjii+1], 
3943
       bbSO.T[0].S[bbSOff].ci[bbSOjii+1]);
3944
       }
3945 }
3946 if(bbSOflgb!=0) fprintf(BBSOFILE," M M ");
3947 else{
3948 fprintf(BBSOFILE," %18.12e %18.12e
     ",bbSO.T[0].S[bbSOff].f[bbSOjii+1],
3949
       bbSO.T[0].S[bbSOff].ci[bbSOjii+1]);
3950
       }
      /* Now, Delta-J=-1 (R) for Delta-K=+1. */
3951
           bbSOflgb=0;
3952
           if((bbSOh+1)<(bbSOLO[0].L)) bbSOflgb=1;
3953
           if((bbSOJ-1)>(bbSOh+1+bbSOS1)) bbSOflgb=1;
3954
           if((bbSOJ-1)<(bbSOh+1-bbSOS1)) bbSOflgb=1;
3955
           if((bbSOJ-1)<0) bbSOflgb=1;
3956
           if(bbSOflgb==0){
```

```
3957
             bbSOB=-1;
3958
             bbSOell=bbSOel-1;
3959
             bbSO.T[0].S[bbSOff].f[bbSOjii]=\
               bbSO.Rh[0].EJ[bbSOehh]-
3960
3961
               bbSO.R1[0].EJ[bbSOel1];
3962
             bbSOcascadetemp=bbSOtrprob*bbSOfcf*\
3963
               bbSO.Rh[0].CJ[bbSOehh]*bbSOSATT*\
3964
              HL(bbSOB,bbSOJ,bbSOL,bbSOdL);
         if((bbSOg!=0)&&(bbSOLO[0].L==0)){ /* low state is Sigma */
3965
3966
           if((((bbSOh+1)%2)==0)&&(bbSOisym==-1)){
3967
             bbSOcascadetemp*=bbSOIa;
3968
             }
3969
           if((((bbSOh+1)%2)==1)&&(bbSOisym==+1)){
3970
             bbSOcascadetemp*=bbSOIa;
3971
             }
           }
3972
3973
             bbSO.T[0].S[bbSOff].ci[bbSOjii]+=\
3974
               bbSOcascadetemp;
3975
             bbSO.R1[0].CJ[bbSOell]+=bbSOfcfr*\
3976
               bbSOcascadetemp;
3977
             bbSOjii--;
3978
             ł
3979 if(bbSOdebugflag<DEBUG){
3980 if(bbSOflgb!=0) fprintf(DBG,"M M\n");
3981 else{
3982 fprintf(DBG,"%18.12e %18.12e
     (1d)\n",bbSO.T[0].S[bbSOff].f[bbS0jii+1],\
3983
       bbSO.T[0].S[bbSOff].ci[bbSOjii+1]);
3984
       }
3985 }
3986 if(bbSOflgb!=0) fprintf(BBSOFILE,"M M\n");
3987 else{
3988 fprintf(BBSOFILE,"%18.12e
     %18.12e\n",bbSO.T[0].S[bbSOff].f[bbSOjii+1],\
3989
       bbSO.T[0].S[bbSOff].ci[bbS0jii+1]);
3990
       }
      /* Now, again for Delta-K=+0. Delta-J=+1 (P), then (Q) and (R) */
3991
           bbSOflgb=0;
3992
           if((bbSOh+0)<(bbSOLO[0].L)) bbSOflgb=1;
      /* Relative position in the low state E/P array */
3993
           bbSOel=(bbSOh+0)*bbSO.nlJ + bbSO.nlJ-bbSO.nhJ + \
3994
              (int)(bbSOSh-bbSOS1) + 0 + bbSOi;
3995 if(bbSOdebugflag<DEBUG){
3996 fprintf(DBG,"\t(bbS0h+0)*bbS0.nlJ=%d, bbS0.nlJ-bbS0.nhJ=%d\n",\
3997
         (bbSOh+0)*bbSO.nlJ,bbSO.nlJ-bbSO.nhJ);
3998 fprintf(DBG,"\t(int)(bbSOSh-bbSOS1)=%d, bbSOi=%d, bbSOel=%d\n",\
3999
         (int)(bbSOSh-bbSOS1),bbSOi,bbSOel);
4000 fflush(DBG);
4001 }
4002
           if((bbSOel+1)>=(bbSO.R1[0].kc*bbSO.nlJ)) bbSOflgb=1;
      /* Then check if the target value for J+1 is less than or greater
        than the allowed J's for K+0. */
4003
           if((bbSOJ+1)>(bbSOh+0+bbSOS1)) bbSOflgb=1;
```

if((bbSOJ+1)<(bbSOh+0-bbSOS1)) bbSOflgb=1; /* Still OK? Calculate transition */ if(bbSOflgb==0){ bbSOB=+1;bbSOell=bbSOel+1; bbSO.T[0].S[bbSOff].f[bbSOjii]=\ bbSO.Rh[0].EJ[bbSOehh]bbSO.R1[0].EJ[bbSOell]; bbSOcascadetemp=bbSOtrprob*bbSOfcf*\ bbSO.Rh[0].CJ[bbSOehh]*bbSOSATT*\ HL(bbSOB,bbSOJ,bbSOL,bbSOdL); /* Check for nuclear effects and modify intensity if necessary. */ if((bbSOg!=0)&&(bbSOLO[0].L==0)){ /* low state is Sigma */ if((((bbSOh+0)%2)==0)&&(bbSOisym==-1)){ bbSOcascadetemp*=bbSOIa; } if((((bbSOh+0)%2)==1)&&(bbSOisym==+1)){ bbSOcascadetemp*=bbSOIa; } } bbSO.T[0].S[bbSOff].ci[bbSOjii]+=\ bbSOcascadetemp; bbSO.R1[0].CJ[bbSOell]+=bbSOfcfr*\ bbSOcascadetemp; bbSOjii--; } 4028 if (bbSOdebugflag<DEBUG) { 4029 fprintf(DBG,"%d ",bbSOh); 4030 if(bbS0flgb!=0) fprintf(DBG," %d %.1f (1c) M M\n",(bbS0h+0),bbS0J); 4031 else{ 4032 fprintf(DBG,"%d %.1f %18.12e %18.12e (1c)\n",(bbSOh+0),\ bbSOJ,bbSO.T[0].S[bbSOff].f[bbSOjii+1], bbSO.T[0].S[bbSOff].ci[bbSOjii+1]); } 4037 fprintf(BBSOFILE,"%d ",bbSOh); 4038 if(bbSOflgb!=0) fprintf(BBSOFILE," %d %.1f M M ",(bbSOh+0),bbSOJ); 4039 else{ 4040 fprintf(BBSOFILE,"%d %.1f %18.12e %18.12e ",(bbSOh+0),\ bbSOJ,bbSO.T[0].S[bbSOff].f[bbSOjii+1],\ bbSO.T[0].S[bbSOff].ci[bbS0jii+1]); } /* Now, Delta-J=0 (Q), Delta-K=+0 */ bbSOflgb=0; if((bbSOh+0)<(bbSOLO[0].L)) bbSOflgb=1;</pre> /* Then check if the target value for J+1 is less than or greater than the allowed J's for K+0. */

```
4046
           if((bbS0J+0)>(bbS0h+0+bbS0S1)) bbS0flgb=1;
4047
           if((bbSOJ+0)<(bbSOh+0-bbSOS1)) bbSOf1gb=1;
     /* Still OK? Calculate transition */
4048
           if(bbSOflgb==0){
```

```
4049
              bbSOB=+0;
```

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4041 4042

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4045

4036 }

```
4050
             bbSOell=bbSOel+0;
```

```
bbSO.T[0].S[bbSOff].f[bbS0jii]=\
4051
```

4052 bbSO.Rh[0].EJ[bbSOehh]-\ 4053 bbSO.R1[0].EJ[bbSOel1]; 4054 bbSOcascadetemp=bbSOtrprob*bbSOfcf*\ 4055 bbSO.Rh[0].CJ[bbSOehh]*\ 4056 HL(bbSOB,bbSOJ,bbSOL,bbSOdL); /* Check for nuclear effects and modify intensity if necessary. */ 4057 if((bbSOg!=0)&&(bbSOLO[0].L==0)){ /* low state is Sigma */ 4058 if((((bbSOh+0)%2)==0)&&(bbSOisym==-1)){ 4059 bbSOcascadetemp*=bbSOIa; 4060 ł if((((bbSOh+0)%2)==1)&&(bbSOisym==+1)){ 4061 4062 bbSOcascadetemp*=bbSOIa; 4063 } 4064 } 4065 bbSO.T[0].S[bbSOff].ci[bbSOjii]+=\ 4066 bbSOcascadetemp; 4067 bbSO.R1[0].CJ[bbSOell]+=bbSOfcfr*\ 4068 bbSOcascadetemp; 4069 bbSOjii--; 4070 4071 if(bbSOdebugflag<DEBUG){ 4072 if(bbSOflgb!=0) fprintf(DBG," M M\n"); 4073 else{ 4074 fprintf(DBG,"%18.12e %18.12e (1c)\n",bbSO.T[0].S[bbSOff].f[bbS0jii+1],\ 4075 bbSO.T[0].S[bbSOff].ci[bbSOjii+1]); 4076 } 4077 } 4078 if(bbSOflgb!=0) fprintf(BBSOFILE," M M "); 4079 else{ 4080 fprintf(BBSOFILE," %18.12e %18.12e ",bbSO.T[0].S[bbSOff].f[bbSOjii+1], 4081 bbSO.T[0].S[bbSOff].ci[bbSOjii+1]); 4082 ł /* Now, Delta-J=-1 (R) for Delta-K=+0. */ 4083 bbSOflgb=0; if((bbSOh+0)<(bbSOLO[0].L)) bbSOflgb=1;</pre> 4084 4085 if((bbS0J-1)>(bbS0h+0+bbS0S1)) bbS0flgb=1; 4086 if((bbSOJ-1)<(bbSOh+0-bbSOS1)) bbSOflgb=1; 4087 if((bbSOJ-1)<0) bbSOflgb=1; 4088 if(bbSOflgb==0){ 4089 bbSOB=-1;bbSOell=bbSOel-1; 4090 bbSO.T[0].S[bbSOff].f[bbS0jii]=\ 4091 bbSO.Rh[0].EJ[bbSOehh]-4092 4093 bbSO.R1[0].EJ[bbSOel1]; 4094 bbSOcascadetemp=bbSOtrprob*bbSOfcf*\ 4095 bbSO.Rh[0].CJ[bbSOehh]*bbSOSATT*\ 4096 HL(bbSOB,bbSOJ,bbSOL,bbSOdL); if((bbSOg!=0)&&(bbSOLO[0].L==0)){ /* low state is Sigma */ 4097 4098 if((((bbSOh+0)%2)==0)&&(bbSOisym==-1)){ 4099 bbSOcascadetemp*=bbSOIa; 4100 } if((((bbSOh+0)%2)==1)&&(bbSOisym==+1)){ 4101

```
4102
             bbSOcascadetemp*=bbSOIa;
4103
              }
           }
4104
             bbSO.T[0].S[bbSOff].ci[bbSOjii]+=\
4105
4106
               bbSOcascadetemp;
4107
             bbSO.R1[0].CJ[bbSOell]+=bbSOfcfr*\
4108
                bbSOcascadetemp;
             bbSOjii--;
4109
4110
              }
4111 if (bbSOdebugflag<DEBUG) {
4112 if(bbSOflgb!=0) fprintf(DBG,"M M\n");
4113 else{
4114 fprintf(DBG,"%18.12e %18.12e
     (1d)\n",bbS0.T[0].S[bbS0ff].f[bbS0jii+1],\
4115
       bbSO.T[0].S[bbSOff].ci[bbSOjii+1]);
4116
       }
4117 }
4118 if(bbSOflgb!=0) fprintf(BBSOFILE,"M M\n");
4119 else{
4120 fprintf(BBSOFILE,"%18.12e
     %18.12e\n",bbSO.T[0].S[bbSOff].f[bbSOjii+1],\
4121
       bbSO.T[0].S[bbSOff].ci[bbSOjii+1]);
4122
       }
      /* Check Delta-J=+1 (P), then Delta-J=0 (Q) and Delta-J=-1 (R) for
        Delta-K=-1. First, check to see if the target K exists: */
4123
           bbSOflgb=0;
4124
           if((bbSOh-1)<(bbSOLO[0].L)) bbSOflgb=1;</pre>
      /* Relative position in the low state E/P array */
4125
           bbSOel=(bbSOh-1)*bbSO.nlJ + bbSO.nlJ-bbSO.nhJ + \
4126
              (int)(bbSOSh-bbSOS1) + 1 + bbSOi;
4127 if(bbSOdebugflag<DEBUG){
4128 fprintf(DBG,"\t(bbSOh-1)*bbSO.nlJ=%d, bbSO.nlJ-bbSO.nhJ=%d\n",\
         (bbSOh-1)*bbSO.nlJ,bbSO.nlJ-bbSO.nhJ);
4129
4130 fprintf(DBG,"\t(int)(bbSOSh-bbSOS1)=%d, bbSOi=%d, bbSOel=%d\n",\
4131
         (int)(bbSOSh-bbSOS1),bbSOi,bbSOel);
4132 fflush(DBG);
4133 }
4134
           if((bbSOel+1)>=(bbSO.R1[0].kc*bbSO.nlJ)) bbSOflgb=1;
      /* Then check if the target value for J+1 is less than or greater
        than the allowed J's for K+1. */
           if((bbS0J+1)>(bbS0h-1+bbS0S1)) bbS0flgb=1;
4135
4136
           if((bbS0J+1)<(bbS0h-1-bbS0S1)) bbS0flgb=1;</pre>
      /* Still OK? Calculate transition */
4137
           if(bbSOflgb==0){
4138
             bbSOB=+1;
4139
             bbSOell=bbSOel+1;
4140
             bbSO.T[0].S[bbSOff].f[bbSOjii]=\
4141
               bbSO.Rh[0].EJ[bbSOehh]-
4142
                bbSO.R1[0].EJ[bbSOel1];
4143
             bbSOcascadetemp=bbSOtrprob*bbSOfcf*\
4144
               bbSO.Rh[0].CJ[bbSOehh]*bbSOSATT*\
4145
               HL(bbSOB,bbSOJ,bbSOL,bbSOdL);
      /* Check for nuclear effects and modify intensity if necessary. */
```

```
4146
         if((bbS0g!=0)&&(bbS0L0[0].L==0)){ /* low state is Sigma */
4147
           if((((bbSOh-1)%2)==0)&&(bbSOisym==-1)){
4148
             bbSOcascadetemp*=bbSOIa;
             }
4149
4150
           if((((bbSOh-1)%2)==1)&&(bbSOisym==+1)){
4151
             bbSOcascadetemp*=bbSOIa;
4152
             }
           }
4153
4154
             bbSO.T[0].S[bbSOff].ci[bbSOjii]+=\
4155
                bbSOcascadetemp;
4156
             bbSO.R1[0].CJ[bbSOell]+=bbSOfcfr*\
4157
               bbSOcascadetemp;
4158
             bbSOjii--;
4159
             ł
4160 if (bbSOdebugflag<DEBUG) {
4161 fprintf(DBG,"%d ",bbSOh);
4162 if (bbSOflgb!=0) fprintf(DBG, " %d %.1f M M ", (bbSOh-1), bbSOJ);
4163 else{
4164 fprintf(DBG,"%d %.1f %18.12e %18.12e (1e)\n",(bbSOh-1),\
4165
       bbSOJ,bbSO.T[0].S[bbSOff].f[bbSOjii+1],\
4166
       bbSO.T[0].S[bbSOff].ci[bbSOjii+1]);
4167
       }
4168 }
4169 fprintf(BBSOFILE,"%d ",bbSOh);
4170 if(bbSOflgb!=0) fprintf(BBSOFILE, " %d %.1f M M ",(bbSOh-1),bbSOJ);
4171 else{
4172 fprintf(BBSOFILE, "%d %.1f %18.12e %18.12e ",(bbSOh-1),\
4173
       bbSOJ,bbSO.T[0].S[bbSOff].f[bbSOjii+1],
4174
       bbSO.T[0].S[bbSOff].ci[bbS0jii+1]);
4175
       }
      /* Now, Delta-J=+0 (Q), Delta-K=-1. */
4176
           bbSOflgb=0;
4177
           if((bbSOh-1)<(bbSOLO[0].L)) bbSOflgb=1;</pre>
      /* Then check if the target value for J+1 is less than or greater
        than the allowed J's for K+1. */
4178
           if((bbS0J+0)>(bbS0h-1+bbS0S1)) bbS0flgb=1;
4179
           if((bbSOJ+0)<(bbSOh-1-bbSOS1)) bbSOflgb=1;
      /* Still OK? Calculate transition */
4180
           if(bbSOflgb==0){
4181
             bbSOB=+0;
             bbSOell=bbSOel+0;
4182
4183
             bbSO.T[0].S[bbSOff].f[bbSOjii]=\
4184
                bbSO.Rh[0].EJ[bbSOehh]-
                bbSO.R1[0].EJ[bbSOel1];
4185
4186
             bbSOcascadetemp=bbSOtrprob*bbSOfcf*\
4187
               bbSO.Rh[0].CJ[bbSOehh]*bbSOSATT*\
               HL(bbSOB,bbSOJ,bbSOL,bbSOdL);
4188
      /* Check for nuclear effects and modify intensity if necessary. */
4189
         if((bbSOg!=0)&&(bbSOLO[0].L==0)){ /* low state is Sigma */
4190
           if((((bbSOh-1)%2)==0)&&(bbSOisym==-1)){
4191
             bbSOcascadetemp*=bbSOIa;
4192
4193
           if((((bbSOh-1)%2)==1)&&(bbSOisym==+1)){
4194
             bbSOcascadetemp*=bbSOIa;
```

} } bbSO.T[0].S[bbSOff].ci[bbSOjii]+=\ bbSOcascadetemp; bbSO.R1[0].CJ[bbSOell]+=bbSOfcfr*\ bbSOcascadetemp; bbSOjii--; } 4203 if(bbSOdebugflag<DEBUG){ 4204 if(bbSOflgb!=0) fprintf(DBG," M M "); 4206 fprintf(DBG,"%18.12e %18.12e n",bbSO.T[0].S[bbSOff].f[bbSOjii+1],bbSO.T[0].S[bbSOff].ci[bbS0jii+1]); 4210 if(bbSOflgb!=0) fprintf(BBSOFILE," M M "); 4212 fprintf(BBSOFILE,"%18.12e %18.12e ,bbSO.T[0].S[bbSOff].f[bbS0jii+1],\ bbSO.T[0].S[bbSOff].ci[bbSOjii+1]); /* Now, Delta-J=-1 (R) for Delta-K=-1. */ bbSOflgb=0; if((bbSOh-1)<(bbSOLO[0].L)) bbSOflgb=1;</pre> if((bbSOJ-1)>(bbSOh-1+bbSOS1)) bbSOflgb=1; if((bbS0J-1)<(bbS0h-1-bbS0S1)) bbS0flgb=1;</pre> if((bbSOJ-1)<0) bbSOflgb=1; if(bbSOflgb==0){ bbSOB=-1;bbSOell=bbSOel-1; bbSO.T[0].S[bbSOff].f[bbS0jii]=\ bbSO.Rh[0].EJ[bbSOehh]bbSO.R1[0].EJ[bbSOel1]; bbSOcascadetemp=bbSOtrprob*bbSOfcf*\ bbSO.Rh[0].CJ[bbSOehh]*\ HL(bbSOB,bbSOJ,bbSOL,bbSOdL); /* If the high state is Sigma, the nuclear spin-stats (if homonuclear) were taken care of in the rotational distribution function, so no need to bother with them here. */ if((bbSOg!=0)&&(bbSOLO[0].L==0)){ /* low state is Sigma */ if((((bbSOh-1)%2)==0)&&(bbSOisym==-1)){ bbSOcascadetemp*=bbSOIa; }

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4230

4242 if(bbSOdebugflag<DEBUG){

4209 }

4205 else{

4211 else{

}

}

```
4231
4232
           if((((bbSOh-1)%2)==1)&&(bbSOisym==+1)){
4233
4234
             bbSOcascadetemp*=bbSOIa;
4235
              }
           }
4236
4237
             bbSO.T[0].S[bbSOff].ci[bbSOjii]+=\
4238
                bbSOcascadetemp;
             bbSO.R1[0].CJ[bbSOell]+=bbSOfcfr*\
4239
4240
                bbSOcascadetemp;
4241
              }
```

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```

```
4243 if(bbSOflgb!=0) fprintf(DBG,"M M\n");
4244 else{
4245 fprintf(DBG,"%18.12e %18.12e
     (1f)\n",bbSO.T[0].S[bbSOff].f[bbS0jii],\
4246
       bbSO.T[0].S[bbSOff].ci[bbS0jii]);
4247
       }
4248 }
4249 if(bbSOflgb!=0) fprintf(BBSOFILE,"M M\n");
4250 else{
4251 fprintf(BBSOFILE,"%18.12e
     %18.12e\n",bbSO.T[0].S[bbSOff].f[bbSOjii],\
4252
       bbSO.T[0].S[bbSOff].ci[bbSOjii]);
4253
       }
4254
           } /* close if bbSOflga is zero. */
4255
         } /* close upper-state J-of-K loop */
4256
       } /* close upper-state K loop */
4257
       fclose(BBSOFILE);
4258
         } /* close if high-state v is cascade populated */
4259
       } /* close low-state v */
4260
       } /* close high-state v */
4261 return;
4262 }
     4263
     /* This function calculates transitions between Hund's Cases (b)
        and (b) when both the upper and lower states are sigma states. */
4264 void bb_Other(BBTinfo bbOO){
     /* see parent function and header file for key to variable names */
     /* indexes and dummy variables: */
4265 int bb00e=0,bb00ee=0,bb00f=0,bb00ff=0,bb00i=0,bb00jii=0;
4266 int bb00eh=0, bb00ehh=0, bb00el=0, bb00el1=0;
4267 int bb00h=0, bb00k=0, bb00frnh=0, bb00frcl=0, bb00frch=0;
      /* variables for info about the two states */
4268 double
     bbOOJ=0,bbOOSh=0,bbOOS1=0,bbOOtrprob=0,bbOOvhpop=0,bbOOhipop;
     /* Intensity multiplier for satellite bands, temporary variable and
        fcf var */
4269 double bb00SATT=0, bb00cascadetemp=0, bb00fcf=0, bb00fcfr=0;
     /* variables for calculating Holn-London factors */
4270 int bb00L=0, bb00B=0, bb00dL=0;
     /* a few flags for various purposes */
4271 int bb00flga=0,bb00flgb=0,bb00frnhf=0,bb00frchf=0,bb00LLflg=1;
     /* variables for creating and writing to output files */
4272 char bb00file[1000];
4273 FILE *BBOOFILE;
4274 Case_b_stateinfo *bb00HI,*bb00L0;
4275 if(bb00debugflag<DEBUG){
4276 fprintf(DBG,"bb00.hvnlo=%d, bb00.hvnnum=%d\n",\
         bb00.hvnlo,bb00.hvnnum);
4277
4278 fprintf(DBG,"bb00.hvclo=%d, bb00.hvcnum=%d\n",\
4279
         bb00.hvclo,bb00.hvcnum);
```

```
4280 fprintf(DBG,"bb00.lvnlo=%d, bb00.lvnnum=%d, \n", \
4281
         bb00.lvnlo,bb00.lvnnum);
4282 fprintf(DBG,"bb00.lvclo=%d, bb00.lvcnum=%d\n",\
4283
         bb00.lvclo,bb00.lvcnum);
4284 fprintf(DBG,"bb00.hivlo=%d, bb00.hivnum=%d,\n",\
         bb00.hivlo,bb00.hivnum);
4285
4286 fprintf(DBG,"bb00.lovlo=%d, bb00.lovnum=%d\n",\
4287
         bb00.lovlo,bb00.lovnum);
4288 fflush(DBG);
4289 }
4290 bb00HI=bb00.Ch;
4291 bb00L0=bb00.Cl;
4292 bb00Sh=bb00HI[0].S;
4293 bb00S1=bb00L0[0].S;
4294 bb00hipop=bb00.Sh[0].pop;
4295 bb00trprob=bb00.T[0].P[0];
4296 if(bb00HI[0].L==bb00L0[0].L){
4297
       bb00LLflg=0;
4298
       bb00dL=0;
4299
       }
4300 if((bb00HI[0].L-bb00L0[0].L)==+1) bb00dL=+1;
4301 if((bb00HI[0].L-bb00L0[0].L)==-1) bb00dL=-1;
4302 bb00L=bb00HI[0].L;
     /* start loop down through high vib levels */
4303 for(bb00e=(bb00.hivlo+bb00.hivnum-1);bb00e>=bb00.hivlo;bb00e--){
4304
       bb00ee=(bb00e-bb00.hivlo)*bb00.lovnum; /* simset posn. in 2D */
4305
       bb00frnh=(bb00e-bb00.hvnlo); /* high state native vib position
        */
4306
       bb00frch=bb00e; /* high state cascade vib position */
     /* these flags (bb00frnhf and bb00frchf) tell if this high vib state
        is populated natively, by cascade, or both. They will be used
        later */
4307
       if((bb00e>=bb00.hvnlo)&&(bb00e<(bb00.hvnlo+bb00.hvnnum))){
4308
         bb00frnhf=0;
4309
         bb00vhpop=bb00.Vh[0].p[bb00e-bb00.hvnlo];
         }
4310
4311
       else bb00frnhf=-1;
4312
       if((bb00e>=bb00.hvclo)&&(bb00e<(bb00.hvclo+bb00.hvcnum))){
4313
         bb00frchf=0;
4314
         }
       else bb00frchf=-1;
4315
4316 if (bbOOdebugflag<DEBUG) {
4317 fprintf(DBG,"bb00frnhf=%d, bb00vhpop=%f, bb00frchf=%d, ",\
         bb00frnhf,bb00vhpop,bb00frchf);
4318
4319 fprintf(DBG,"bb00e=%d, bb00ee=%d\nbb00frnh=%d, bb00frch=%d, ",\
4320
         bb00e,bb00ee,bb00frnh,bb00frch);
4321 fflush(DBG);
4322 }
     /* start loop down through low vib levels */
4323 for(bb00f=(bb00.lovlo+bb00.lovnum-1);bb00f>=bb00.lovlo;bb00f--){
4324
       bb00fcf=bb00.T[0].v[bb00e].fcfn[bb00f];
4325
     if(bb00fcf!=0){bb00fcfr=bb00.T[0].v[bb00e].fcfc[bb00f]/bb00fcf;}
```

```
4326
       bb00ff=bb00ee+bb00f-bb00.lovlo; /* position in last dimension */
4327
       bb00frcl=bb00f;
4328 if(bb00debugflag<DEBUG){
4329 fprintf(DBG,"bb00f=%d, bb00.lovlo=%d, bb00.lovnum=%d \n", \
4330
         bb00f,bb00.lovlo,bb00.lovnum);
4331 fflush(DBG);
4332 }
4333 bb00ff=bb00ee+bb00f-bb00.lovlo; /* simset posn. in final dimension
        */
4334
       bb00.T[0].S[bb00ff].n=bb00.nT*bb00.hiK;
4335
       bb00.T[0].S[bb00ff].f=\
4336
         (double*)calloc(bb00.T[0].S[bb00ff].n,sizeof(double));
4337
       bb00.T[0].S[bb00ff].ni=\
4338
         (double*)calloc(bb00.T[0].S[bb00ff].n,sizeof(double));
4339
       bb00.T[0].S[bb00ff].ci=\
4340
         (double*)calloc(bb00.T[0].S[bb00ff].n,sizeof(double));
4341 bb00.Rl=&bb00.Sl[0].rc[bb00frcl];
4342 if (bb00debugflag<DEBUG) {
4343 fprintf(DBG,"bb00ff=%d, bb00frcl=%d,
     bb00.T[0].S[bb00ff].n=%d\n",
4344
         bb00ff,bb00frcl,bb00.T[0].S[bb00ff].n);
4345 fflush(DBG);
4346 }
      /* start with highest J value (same reason as before), and loop down
        looking for lower J's to which to transit. assign intensities.
        If both states are Omega=0, then assign zero intensity to transi-
        tions for J=0<->J=0. */
4347
       if(bb00frnhf==0){ /* if this v is natively populated.*/
4348 sprintf(bb00file,"%s_molecules/%s/%s--%s_v%d--v%d_NAT.dat",\
4349
       PREF,MOL[bb00.m].Mol,bb00.T[0].Nhi,bb00.T[0].Nlo,bb00e,bb00f);
4350
         BBOOFILE=fopen(bbOOfile,"w");
4351
         if(BBOOFILE==NULL){
4352 printf("Error opening transition sub-file %s. Exit-
     ing.\n",bb00file);
4353
           exit(1);
4354
           }
4355 fprintf(BBOOFILE,"# File created by %s.\n# File contains ",PRO-
     GRAM_NAME);
4356 fprintf(BBOOFILE, "P, Q and R");
4357 fprintf(BB00FILE," branches from the simulation titled %s\n",PREF);
4358 fprintf(BB00FILE, "# THESE INTENSITIES ARE DUE TO USER-SPECIFIED
     POPULATIONS");
4359 fprintf(BBOOFILE," ONLY -- NO CASCADE\n");
4360 fprintf(BBOOFILE,"# Transition is Hund's Case (b) to Hund's Case
     (b).\n");
4361 fprintf(BB00FILE,"# Molecule %s, \tHigh state: %s, v=%d\n",\
         MOL[bb00.m].Mol,bb00.T[0].Nhi,bb00e);
4362
4363 fprintf(BB00FILE,"#\t\tLow state: %s, v=%d\n# Columns are: ",\
         bb00.T[0].Nlo,bb00f);
4364
4365 fprintf(BBOOFILE, "K_hi K_lo J_hi P(J_hi+1)_v P_i ");
4366 fprintf(BB00FILE,"Q(J_hi+0)_v Q_i R(J_hi-1)_v R_i\n#\n");
4367
         bb00.Rh=&bb00.Sh[0].r[bb00frnh];
4368
         if((bb00.hiK)<bb00.Sh[0].r[bb00frnh].k){
```

- 4369 bb00k=bb00.hiK-1;
- 4370 }
- 4371 else bb00k=bb00.Sh[0].r[bb00frnh].k-1;
- 4372 if(bb00.R1[0].Kdissoc<(bb00k-1)){
- 4373 fprintf(PAR,"\nWARNING!! State %s of molecule %s has significant ",\
- 4374 bb00.T[0].Nhi,MOL[bb00.m].Mol);
- 4375 fprintf(PAR, "rotational population at level %d\n", bbOOk);
- 4376 fprintf(PAR,"\tBut lower state %s dissociates at level %.1f\n",\
- 4377 bb00.T[0].Nlo,bb00.R1[0].Kdissoc);
- 4378 fprintf(PAR,"It is likely that the bound upper state is transiting to (an)");
- 4379 fprintf(PAR," unbound lower state(s).\n");
- 4380 fprintf(PAR,"Look for continuum emissions trailing off to the lowenergy ");
- 4381 fprintf(PAR,"end of the v(hi)=%d to v(lo)=%d\nband in the real ",bb00e,bb00f);
- 4382 fprintf(PAR,"spectrum (not the simulated one)\nCurrently, this program will");
- 4383 fprintf(PAR," not simulate bound-->unbound spectra.\n\n");
- 4384 bb00k=(int)(bb00.R1[0].Kdissoc);
- 4385
- 4386 if(bbOOdebugflag<DEBUG){

}

- 4387 fprintf(DBG,"bb00frnh=%d, bb00k=%d, ",bb00frnh,bb00k);
- 4388 fprintf(DBG, "bb00.Sh[0].r[%d].k = %d\n", bb00frnh,
- bb00.Sh[0].r[bb00frnh].k);
- 4389 fflush(DBG);
- 4390 }
 - /* To make the output file easy to write, I'm cycling by high-state
 K first, then by high-state J. From that J/K(hi) pair, the program will look for a P transition and an R transition to K+1 then
 to K-1. If all the necessary states exist, it will check to see
 if there are any symmetry or nuclear spin effects to be concerned
 about. Taking these into account, it will calculate the transition. */

/* loop first by upper-state K-value */

- 4391 for(bb00h=bb00k;bb00h>=0;bb00h--){
- 4392 bb00jii=(bb00h+1)*bb00.nT-1; /* position in simset array */
- 4393 bb00eh=bb00h*bb00.nhJ; /* position in 2D for high EJ & PJ */ /* then loop by upper-state J for this K */
- 4394 for(bb00i=(bb00.nhJ-1);bb00i>=0;bb00i--){
- 4395 bb00J=bb00h+bb00i-bb00Sh;
- 4396 bb00ehh=bb00eh+bb00i;
- 4397 bb00flga=0;
- 4398 if(bb00h<bb00HI[0].L) bb00flga=1; /* if this K is less than Lambda for the high state, don't proceed */
- 4399 if (bb00J<0) bb00flga=1; /* if J is less than zero, don't */
- 4400 if(bbOOdebugflag<DEBUG){
- 4401 fprintf(DBG,"bbOOh=%d, bbOOi=%d, bbOOSh=%.1f, bbOOHI[0].L=%d, bbOOflga=%d\n",\
- 4402 bb00h, bb00i, bb00Sh, bb00HI[0].L, bb00flga);
- 4403 fflush(DBG);
- 4404 }
- 4405 if(bb00flga==0){

```
/* Check Delta-J=+1 (P), then Delta-J=0 (Q), and then Delta-J=-1
        (R) for Delta-K=+1. First, check to see if the target K exists:
        */
4406
           bb00flgb=0;
4407
           if((bb00h+1)<(bb00L0[0].L)) bb00flgb=1;
      /* Relative position in the low state E/P array */
4408
           bb00el=(bb00h+1)*bb00.nlJ + bb00.nlJ-bb00.nhJ + \
4409
              (int)(bb00Sh-bb00S1) -1 + bb00i;
4410 if(bbOOdebugflag<DEBUG){
4411 fprintf(DBG,"\t(bb00h+1)*bb00.nlJ=%d, bb00.nlJ-bb00.nhJ=%d\n",\
4412
         (bb00h+1)*bb00.nlJ,bb00.nlJ-bb00.nhJ);
4413 fprintf(DBG,"\t(int)(bb00Sh-bb00S1)=%d, bb00i=%d, bb00el=%d\n",\
4414
         (int)(bb00Sh-bb00S1),bb00i,bb00e1);
4415 fflush(DBG);
4416 }
           if((bb00el+1)>=(bb00.R1[0].kc*bb00.nlJ)) bb00flgb=1;
4417
      /* Then check if the target value for J+1 is less than or greater
        than the allowed J's for K+1. */
4418
           if((bb00J+1)>(bb00h+1+bb00S1)) bb00flgb=1;
4419
           if((bb00J+1)<(bb00h+1-bb00S1)) bb00flgb=1;
      /* Still OK? Calculate transition */
4420
           if(bbO0flgb==0){
4421
             bb00B=+1;
4422
             bb00ell=bb00el+1;
             bb00.T[0].S[bb00ff].f[bb00jii]=\
4423
4424
               bb00.Rh[0].EJ[bb00ehh]-\
4425
               bb00.R1[0].EJ[bb00e11];
4426
             bb00.T[0].S[bb00ff].ni[bb00jii]=\
4427
               bb00hipop*bb00trprob*bb00vhpop*\
4428
               bb00.Rh[0].PJ[bb00ehh]*bb00fcf*
4429
               HL(bb00B,bb00J,bb00L,bb00dL);
      /* set low-state population for cascade */
4430
             bb00.R1[0].CJ[bb00e11]+=bb00fcfr*\
4431
               bb00.T[0].S[bb00ff].ni[bb00jii];
4432
             bbOOjii--;
4433
             }
4434 if (bb00debugflag<DEBUG) {
4435 fprintf(DBG,"%d ",bb00h);
4436 if(bb00flgb!=0) fprintf(DBG," %d %.1f M M ",(bb00h+1),bb00J);
4437 else{
4438 fprintf(DBG,"%d %.1f %18.12e %18.12e ",(bbOOh+1),\
       bb00J,bb00.T[0].S[bb00ff].f[bb00jii+1],\
4439
4440
       bb00.T[0].S[bb00ff].ni[bb00jii+1]);
4441
       }
4442 }
4443 fprintf(BBOOFILE,"%d ",bbOOh);
4444 if(bb00flgb!=0) fprintf(BB00FILE," %d %.1f M M ",(bb00h+1),bb00J);
4445 else{
4446 fprintf(BBOOFILE, "%d %.1f %18.12e %18.12e ", (bbOOh+1), \
4447
       bb00J,bb00.T[0].S[bb00ff].f[bb00jii+1],\
4448
       bb00.T[0].S[bb00ff].ni[bb00jii+1]); }
      /* Now Delta-J=0 (Q) (for Delta-K=+1) */
4449
           bb00flgb=0;
```

```
4450
           if((bb00h+1)<(bb00L0[0].L)) bb00flgb=1;
      /* Then check if the target value for J+1 is less than or greater
        than the allowed J's for K+1. */
4451
           if((bb00J+0)>(bb00h+1+bb00S1)) bb00flgb=1;
4452
           if((bb00J+0)<(bb00h+1-bb00S1)) bb00flgb=1;
      /* Still OK? Calculate transition */
4453
           if(bb00flgb==0){
             bb00B=0;
4454
4455
             bb00ell=bb00el+0;
4456
             bb00.T[0].S[bb00ff].f[bb00jii]=\
               bb00.Rh[0].EJ[bb00ehh]-\
4457
4458
               bb00.R1[0].EJ[bb00el1];
4459
             bb00.T[0].S[bb00ff].ni[bb00jii]=\
4460
               bb00hipop*bb00trprob*bb00vhpop*\
4461
               bb00.Rh[0].PJ[bb00ehh]*bb00SATT*\
4462
               HL(bb00B,bb00J,bb00L,bb00dL)*bb00fcf;
      /* set low-state population for cascade */
             bb00.R1[0].CJ[bb00ell]+=bb00fcfr*\
4463
4464
               bb00.T[0].S[bb00ff].ni[bb00jii];
4465
             bb00jii--;
4466
             }
4467 if(bb00debugflag<DEBUG){
4468 fprintf(DBG,"%d ",bbOOh);
4469 if(bb00flgb!=0) fprintf(DBG," %d %.1f M M ",(bb00h+1),bb00J);
4470 else{
4471 fprintf(DBG,"%d %.1f %18.12e %18.12e ",(bb00h+1),\
4472
       bb00J,bb00.T[0].S[bb00ff].f[bb00jii+1],\
4473
       bb00.T[0].S[bb00ff].ni[bb00jii+1]);
4474
       }
4475 }
4476 if(bb00flgb!=0) fprintf(BB00FILE," M M ");
4477 else{
4478 fprintf(BBOOFILE,"%18.12e %18.12e
     ",bb00.T[0].S[bb00ff].f[bb00jii+1],\
4479
       bb00.T[0].S[bb00ff].ni[bb00jii+1]);
4480
       ł
      /* Now, Delta-J=-1 (R) for Delta-K=+1. */
4481
           bb00flgb=0;
4482
           if((bb00h+1)<(bb00L0[0].L)) bb00flgb=1;
4483
           if((bb00J-1)>(bb00h+1+bb00S1)) bb00flgb=1;
4484
           if((bb00J-1)<(bb00h+1-bb00S1)) bb00flgb=1;
4485
           if((bb00J-1)<0) bb00flgb=1;
4486
           if(bb00flgb==0){
4487
             bb00B=-1;
4488
             bb00ell=bb00el-1;
4489
             bb00.T[0].S[bb00ff].f[bb00jii]=\
4490
               bb00.Rh[0].EJ[bb00ehh]-\
4491
               bb00.R1[0].EJ[bb00e11];
4492
             bb00.T[0].S[bb00ff].ni[bb00jii]=\
4493
               bb00hipop*bb00trprob*bb00vhpop*\
4494
               bb00.Rh[0].PJ[bb00ehh]*bb00SATT*\
4495
               HL(bb00B,bb00J,bb00L,bb00dL)*bb00fcf;
4496
             bb00.R1[0].CJ[bb00ell]+=bb00fcfr*\
4497
               bb00.T[0].S[bb00ff].ni[bb00jii];
```

4498 bb00jii--; 4499 } 4500 if(bb00debugflag<DEBUG){ 4501 if(bb00flgb!=0) fprintf(DBG,"M M\n"); 4502 else{ 4503 fprintf(DBG,"%18.12e %18.12e\n",bb00.T[0].S[bb00ff].f[bb00jii+1],\ 4504 bb00.T[0].S[bb00ff].ni[bb00jii+1]); 4505 } 4506 } 4507 if(bb00flgb!=0) fprintf(BB00FILE,"M M\n"); 4508 else{ 4509 fprintf(BBOOFILE,"%18.12e %18.12e\n",bb00.T[0].S[bb00ff].f[bb00jii+1],\ 4510 bb00.T[0].S[bb00ff].ni[bb00jii+1]); 4511 } /* Check Delta-J=+1 (P), then Delta-J=0 (Q), and then Delta-J=-1 (R) for Delta-K=+0. First, check to see if the target K exists: */ 4512 bb00flgb=0; 4513 if((bb00h+0)<(bb00L0[0].L)) bb00flgb=1; /* Relative position in the low state E/P array */ 4514 $bb00el=(bb00h+0)*bb00.nlJ + bb00.nlJ-bb00.nhJ + \$ 4515 (int)(bb00Sh-bb00S1) + 0 + bb00i;4516 if(bb00debugflag<DEBUG){ 4517 fprintf(DBG,"\t(bb00h+0)*bb00.nlJ=%d, bb00.nlJ-bb00.nhJ=%d\n",\ (bb00h+0)*bb00.nlJ,bb00.nlJ-bb00.nhJ); 4518 4519 fprintf(DBG,"\t(int)(bb00Sh-bb00S1)=%d, bb00i=%d, bb00e1=%d\n",\ 4520 (int)(bb00Sh-bb00S1),bb00i,bb00e1); 4521 fflush(DBG); 4522 } 4523 if((bb00el+1)>=(bb00.R1[0].kc*bb00.nlJ)) bb00flgb=1; /* Then check if the target value for J+1 is less than or greater than the allowed J's for K+0. */ 4524 if((bb00J+1)>(bb00h+0+bb00S1)) bb00flgb=1; 4525 if((bb00J+1)<(bb00h+0-bb00S1)) bb00flgb=1;</pre> /* Still OK? Calculate transition */ 4526 if(bb00flgb==0){ 4527 bb00B=+1; 4528 bb00ell=bb00el+1; bb00.T[0].S[bb00ff].f[bb00jii]=\ 4529 bb00.Rh[0].EJ[bb00ehh]-\ 4530 4531 bb00.R1[0].EJ[bb00e11]; 4532 bb00.T[0].S[bb00ff].ni[bb00jii]=\ 4533 bb00hipop*bb00trprob*bb00vhpop*\ 4534 bb00.Rh[0].PJ[bb00ehh]*bb00SATT*\ 4535 HL(bb00B,bb00J,bb00L,bb00dL)*bb00fcf; /* set low-state population for cascade */ bb00.R1[0].CJ[bb00ell]+=bb00fcfr*\ 4536 4537 bb00.T[0].S[bb00ff].ni[bb00jii]; 4538 bb00jii--; 4539 ł 4540 if(bb00debugflag<DEBUG){ 4541 fprintf(DBG,"%d ",bbOOh);

```
4542 if(bb00flgb!=0) fprintf(DBG," %d %.1f M M ",(bb00h+0),bb00J);
4543 else{
4544 fprintf(DBG,"%d %.1f %18.12e %18.12e ",(bb00h+0),\
       bb00J,bb00.T[0].S[bb00ff].f[bb00jii+1],\
4545
4546
       bb00.T[0].S[bb00ff].ni[bb00jii+1]);
4547
       }
4548 }
4549 fprintf(BBOOFILE,"%d ",bbOOh);
4550 if(bb00flgb!=0) fprintf(BB00FILE," %d %.1f M M ",(bb00h+0),bb00J);
4551 else{
4552 fprintf(BB00FILE, "%d %.1f %18.12e %18.12e ", (bb00h+0), \
4553
       bb00J,bb00.T[0].S[bb00ff].f[bb00jii+1],\
4554
       bb00.T[0].S[bb00ff].ni[bb00jii+1]);
4555
       }
      /* Now Delta-J=0 (Q) (for Delta-K=+0) */
4556
           bb00flgb=0;
4557
           if((bb00h+0)<(bb00L0[0].L)) bb00flgb=1;
      /* Then check if the target value for J+1 is less than or greater
        than the allowed J's for K+0. */
4558
           if((bb00J+0)>(bb00h+0+bb00S1)) bb00flgb=1;
4559
           if((bb00J+0)<(bb00h+0-bb00S1)) bb00flgb=1;
      /* Still OK? Calculate transition */
4560
           if(bb00flgb==0){
4561
             bb00B=0;
4562
             bb00ell=bb00el+0;
             bb00.T[0].S[bb00ff].f[bb00jii]=\
4563
4564
               bb00.Rh[0].EJ[bb00ehh]-\
4565
               bb00.R1[0].EJ[bb00e11];
4566
             bb00.T[0].S[bb00ff].ni[bb00jii]=\
4567
               bb00hipop*bb00trprob*bb00vhpop*\
               bb00.Rh[0].PJ[bb00ehh]*bb00fcf*\
4568
4569
               HL(bb00B,bb00J,bb00L,bb00dL);
      /* set low-state population for cascade */
4570
             bb00.R1[0].CJ[bb00ell]+=bb00fcfr*\
4571
               bb00.T[0].S[bb00ff].ni[bb00jii];
4572
             bb00jii--;
4573
             }
4574 if(bb00debugflag<DEBUG){
4575 fprintf(DBG,"%d ",bb00h);
4576 if(bb00flgb!=0) fprintf(DBG," M M ");
4577 else{
4578 fprintf(DBG," %18.12e %18.12e ",bb00.T[0].S[bb00ff].f[bb00jii+1],\
4579
       bb00.T[0].S[bb00ff].ni[bb00jii+1]);
4580
       }
4581 }
4582 if(bb00flgb!=0) fprintf(BB00FILE," M M ");
4583 else{
4584 fprintf(BBOOFILE,"%18.12e %18.12e
     ",bb00.T[0].S[bb00ff].f[bb00jii+1],\
4585
       bb00.T[0].S[bb00ff].ni[bb00jii+1]);
4586
       }
      /* Now, Delta-J=-1 (R) for Delta-K=+0. */
4587
           bb00flgb=0;
4588
           if((bb00h+0)<(bb00L0[0].L)) bb00flgb=1;
```

```
4590
           if((bb00J-1)<(bb00h+0-bb00S1)) bb00flgb=1;
4591
           if((bb00J-1)<0) bb00flgb=1;
4592
           if(bb00flgb==0){
4593
             bb00B=-1;
4594
             bb00ell=bb00el-1;
4595
             bb00.T[0].S[bb00ff].f[bb00jii]=\
               bb00.Rh[0].EJ[bb00ehh]-\
4596
               bb00.R1[0].EJ[bb00e11];
4597
4598
             bb00.T[0].S[bb00ff].ni[bb00jii]=\
4599
               bb00hipop*bb00trprob*bb00vhpop*\
4600
               bb00.Rh[0].PJ[bb00ehh]*bb00SATT*\
4601
               HL(bb00B,bb00J,bb00L,bb00dL)*bb00fcf;
4602
             bb00.R1[0].CJ[bb00ell]+=bb00fcfr*\
4603
               bb00.T[0].S[bb00ff].ni[bb00jii];
4604
             bb00jii--;
4605
             ł
4606 if (bbOOdebugflag<DEBUG) {
4607 if(bb00flgb!=0) fprintf(DBG,"M M\n");
4608 else{
4609 fprintf(DBG,"%18.12e
     %18.12e\n",bb00.T[0].S[bb00ff].f[bb00jii+1],\
4610
       bb00.T[0].S[bb00ff].ni[bb00jii+1]);
4611
       }
4612 }
4613 if(bb00flgb!=0) fprintf(BB00FILE,"M M\n");
4614 else{
4615 fprintf(BBOOFILE,"%18.12e
     %18.12e\n",bb00.T[0].S[bb00ff].f[bb00jii+1],\
4616
       bb00.T[0].S[bb00ff].ni[bb00jii+1]);
4617
       }
      /* Check Delta-J=+1 (P), then Delta-J=0 and Delta-J=-1 (R) for
        Delta-K=-1. First, check to see if the target K exists: */
4618
           bb00flgb=0;
4619
           if((bb00h-1)<(bb00L0[0].L)) bb00flgb=1;
      /* Relative position in the low state E/P array */
4620
           bb00el=(bb00h-1)*bb00.nlJ + bb00.nlJ-bb00.nhJ + \
              (int)(bb00Sh-bb00Sl) + 1 + bb00i;
4621
4622 if(bb00debugflag<DEBUG){
4623 fprintf(DBG,"\t(bb00h-1)*bb00.nlJ=%d, bb00.nlJ-bb00.nhJ=%d\n",\
         (bb00h-1)*bb00.nlJ,bb00.nlJ-bb00.nhJ);
4624
4625 fprintf(DBG,"\t(int)(bb00Sh-bb00S1)=%d, bb00i=%d, bb00e1=%d\n",\
4626
         (int)(bb00Sh-bb00S1),bb00i,bb00e1);
4627 fflush(DBG);
4628 }
4629
           if((bb00el+1)>=(bb00.R1[0].kc*bb00.nlJ)) bb00flgb=1;
      /* Then check if the target value for J+1 is less than or greater
        than the allowed J's for K-1. */
4630
           if((bb00J+1)>(bb00h-1+bb00S1)) bb00flgb=1;
4631
           if((bb00J+1)<(bb00h-1-bb00S1)) bb00flgb=1;
      /* Still OK? Calculate transition */
4632
           if(bb00flgb==0){
4633
             bb00B=+1;
4634
             bb00ell=bb00el+1;
```

if((bb00J-1)>(bb00h+0+bb00S1)) bb00flgb=1;

```
4635
             bb00.T[0].S[bb00ff].f[bb00jii]=\
4636
               bb00.Rh[0].EJ[bb00ehh]-\
4637
               bb00.R1[0].EJ[bb00e11];
4638
             bb00.T[0].S[bb00ff].ni[bb00jii]=\
4639
               bb00hipop*bb00trprob*bb00vhpop*\
               bb00.Rh[0].PJ[bb00ehh]*bb00SATT*\
4640
4641
               HL(bb00B,bb00J,bb00L,bb00dL)*bb00fcf;
             bb00.R1[0].CJ[bb00ell]+=bb00fcfr*\
4642
4643
               bb00.T[0].S[bb00ff].ni[bb00jii];
4644
             bb00jii--;
4645
             }
4646 if(bb00debugflag<DEBUG){
4647 fprintf(DBG,"%d ",bbOOh);
4648 if(bb00flgb!=0) fprintf(DBG," %d %.1f M M ",(bb00h-1),bb00J);
4649 else{
4650 fprintf(DBG, "%d %.1f %18.12e %18.12e ", (bbOOh-1), \
4651
       bb00J,bb00.T[0].S[bb00ff].f[bb00jii+1],
4652
       bb00.T[0].S[bb00ff].ni[bb00jii+1]);
4653
       }
4654 }
4655 fprintf(BBOOFILE,"%d ",bbOOh);
4656 if(bb00flgb!=0) fprintf(BB00FILE," %d %.1f M M ",(bb00h-1),bb00J);
4657 else{
4658 fprintf(BB00FILE, "%d %.1f %18.12e %18.12e ", (bb00h-1), \
4659
       bb00J,bb00.T[0].S[bb00ff].f[bb00jii+1],\
4660
       bb00.T[0].S[bb00ff].ni[bb00jii+1]);
4661
       }
      /* Now, Delta-J=+0 (Q) for Delta-K=-1. */
4662
           bb00flgb=0;
4663
           if((bb00h-1)<(bb00L0[0].L)) bb00flgb=1;
      /* Then check if the target value for J+1 is less than or greater
        than the allowed J's for K-1. */
           if((bb00J+0)>(bb00h-1+bb00S1)) bb00flgb=1;
4664
4665
           if((bb00J+0)<(bb00h-1-bb00S1)) bb00flgb=1;
      /* Still OK? Calculate transition */
4666
           if(bb00flgb==0){
4667
             bb00B=0;
4668
             bb00ell=bb00el+0;
4669
             bb00.T[0].S[bb00ff].f[bb00jii]=\
4670
               bb00.Rh[0].EJ[bb00ehh]-\
               bb00.R1[0].EJ[bb00e11];
4671
             bb00.T[0].S[bb00ff].ni[bb00jii]=\
4672
4673
               bb00hipop*bb00trprob*bb00vhpop*\
               bb00.Rh[0].PJ[bb00ehh]*bb00SATT*\
4674
               HL(bb00B,bb00J,bb00L,bb00dL)*bb00fcf;
4675
4676
             bb00.R1[0].CJ[bb00ell]+=bb00fcfr*\
4677
               bb00.T[0].S[bb00ff].ni[bb00jii];
4678
             bb00jii--;
4679
             ł
4680 if(bbOOdebugflag<DEBUG){
4681 fprintf(DBG,"%d ",bb00h);
4682 if(bb00flgb!=0) fprintf(DBG," %d %.1f M M ",(bb00h-1),bb00J);
4683 else{
4684 fprintf(DBG,"%d %.1f %18.12e %18.12e ",(bb00h-1),\
```

```
bb00J,bb00.T[0].S[bb00ff].f[bb00jii+1],\
4685
4686
       bb00.T[0].S[bb00ff].ni[bb00jii+1]);
4687
       }
4688 }
4689 if(bb00flgb!=0) fprintf(BB00FILE," M M ");
4690 else{
4691 fprintf(BBOOFILE, " %18.12e %18.12e
     ",bb00.T[0].S[bb00ff].f[bb00jii+1],\
4692
       bb00.T[0].S[bb00ff].ni[bb00jii+1]);
4693
       }
      /* Now, Delta-J=-1 (R) for Delta-K=-1. */
4694
           bb00flgb=0;
           if((bb00h-1)<(bb00L0[0].L)) bb00flgb=1;
4695
4696
           if((bb00J-1)>(bb00h-1+bb00S1)) bb00flgb=1;
4697
           if((bb00J-1)<(bb00h-1-bb00S1)) bb00flgb=1;
4698
           if((bb00J-1)<0) bb00flgb=1;
           if(bb00flgb==0){
4699
4700
             bb00B=-1;
4701
             bb00ell=bb00el-1;
             bb00.T[0].S[bb00ff].f[bb00jii]=\
4702
               bb00.Rh[0].EJ[bb00ehh]-\
4703
               bb00.R1[0].EJ[bb00e11];
4704
4705
             bb00.T[0].S[bb00ff].ni[bb00jii]=\
4706
               bb00hipop*bb00trprob*bb00vhpop*\
4707
               bb00.Rh[0].PJ[bb00ehh]*bb00fcf*\
              HL(bb00B,bb00J,bb00L,bb00dL);
4708
4709
             bb00.R1[0].CJ[bb00ell]+=bb00fcfr*\
4710
               bb00.T[0].S[bb00ff].ni[bb00jii];
             }
4711
4712 if(bb00debugflag<DEBUG){
4713 if(bbO0flgb!=0) fprintf(DBG,"M M\n");
4714 else{
4715 fprintf(DBG,"%18.12e %18.12e\n",bb00.T[0].S[bb00ff].f[bb00jii],\
4716
       bb00.T[0].S[bb00ff].ni[bb00jii]);
4717
       }
4718 }
4719 if(bb00flgb!=0) fprintf(BB00FILE,"M M\n");
4720 else{
4721 fprintf(BB00FILE,"%18.12e
     %18.12e\n",bb00.T[0].S[bb00ff].f[bb00jii],\
4722
       bb00.T[0].S[bb00ff].ni[bb00jii]);
4723
       }
4724
           } /* close if bb00flga is zero. */
4725
         } /* close upper-state J-of-K loop */
4726
       } /* close upper-state K loop */
4727
       fclose(BBOOFILE);
4728
         } /* close if high-state v is natively populated */
4729
       if(bb00frchf==0){ /* if this v is cascade populated.*/
4730 sprintf(bb00file,"%s_molecules/%s/%s--%s_v%d--v%d_CAS.dat",
4731
       PREF,MOL[bb00.m].Mol,bb00.T[0].Nhi,bb00.T[0].Nlo,bb00e,bb00f);
4732
         BBOOFILE=fopen(bbOOfile,"w");
4733
         if(BBOOFILE==NULL){
```

```
4734 printf("Error opening transition sub-file %s. Exit-
     ing.\n",bb00file);
4735
           exit(1);
4736
           }
4737 fprintf(BB00FILE,"# File created by %s.\n# File contains ",PRO-
     GRAM_NAME);
4738 fprintf(BBOOFILE, "P and R");
4739 fprintf(BB00FILE," branches from the simulation titled %s\n",PREF);
4740 fprintf(BBOOFILE, "# THESE INTENSITIES ARE DUE TO CASCADE ONLY -- ");
4741 fprintf(BBOOFILE, "NO USER-DEFINED POPULATIONS\n");
4742 fprintf(BBOOFILE, "# Transition is Hund's Case (b) to Hund's Case
     (b).\n");
4743 fprintf(BB00FILE,"# Molecule %s, \tHigh state: %s, v=%d\n",\
4744
         MOL[bb00.m].Mol,bb00.T[0].Nhi,bb00e);
4745 fprintf(BB00FILE,"#\t\tLow state: %s, v=%d\n# Columns are: ",\
4746
         bb00.T[0].Nlo,bb00f);
4747 fprintf(BBOOFILE, "K_hi K_lo J_hi P(J_hi+1)_v P_i R(J_hi-1)_v
     R_i n#(n");
4748
         bb00.Rh=&bb00.Sh[0].rc[bb00frch];
4749
         if((bb00.hiK)<bb00.Sh[0].rc[bb00frch].kc){
4750
           bb00k=bb00.hiK-1;
4751
           }
4752
         else bb00k=bb00.Sh[0].rc[bb00frch].kc-1;
4753
         if(bb00.R1[0].Kdissoc<(bb00k-1)){
4754 fprintf(PAR,"\nWARNING!! State %s of molecule %s has significant
     ",\
4755
         bb00.T[0].Nhi,MOL[bb00.m].Mol);
4756 fprintf(PAR, "CASCADE rotational population at level %d\n",bb00k);
4757 fprintf(PAR,"\tBut lower state %s dissociates at level %.1f\n",\
4758
         bb00.T[0].Nlo,bb00.Rl[0].Kdissoc);
4759 fprintf(PAR,"It is likely that the bound upper state is transiting
     to (an)");
4760 fprintf(PAR, " unbound lower state(s).\n");
4761 fprintf(PAR, "Look for continuum emissions trailing off to the low-
     energy ");
4762 fprintf(PAR, "end of the v(hi)=%d to v(lo)=%d\nband in the real
     ",bb00e,bb00f);
4763 fprintf(PAR, "spectrum (not the simulated one)\nCurrently, this pro-
     gram will");
4764 fprintf(PAR," not simulate bound-->unbound spectra.\n\n");
           bb00k=(int)(bb00.Rl[0].Kdissoc);
4765
4766
           }
4767 if (bb00debugflag<DEBUG) {
4768 fprintf(DBG,"bb00frch=%d, bb00k=%d, ",bb00frch,bb00k);
4769 fprintf(DBG, "bb00.Sh[0].rc[%d].kc = %d\n", bb00frch,
     bb00.Sh[0].rc[bb00frch].kc);
4770 fflush(DBG);
4771 }
      /* To make the output file easy to write, I'm cycling by high-state
        K first, then by high-state J. From that J/K(hi) pair, the pro-
        gram will look for a P transition and an R transition to K+1 then
        to K-1. If all the necessary states exist, it will check to see
        if there are any symmetry or nuclear spin effects to be concerned
```

```
about. Taking these into account, it will calculate the transi-
        tion. */
      /* loop first by upper-state K-value */
4772 for(bb00h=(bb00k-1);bb00h>=0;bb00h--){
4773
       bb00jii=(bb00h+1)*bb00.nT-1; /* position in simset array */
4774
       bb00eh=bb00h*bb00.nhJ; /* position in 2D for high EJ & PJ */
      /* then loop by upper-state J for this K */
4775
       for(bb00i=(bb00.nhJ-1);bb00i>=0;bb00i--){
4776
         bb00J=bb00h+bb00i-bb00Sh;
4777
         bb00ehh=bb00eh+bb00i;
4778
         bb00flga=0;
4779
         if(bb00h<bb00HI[0].L) bb00flga=1; /* if this K is less than
        Lambda for the high state, don't proceed */
         if(bb00J<0) bb00flga=1; /* if J is less than zero, don't */
4780
4781 if(bb00debugflag<DEBUG){
4782 fprintf(DBG,"bb00h=%d, bb00i=%d, bb00Sh=%.1f, bb00HI[0].L=%d,
     bb00flga=%d\n",\
4783
         bb00h,bb00i,bb00Sh,bb00HI[0].L,bb00flga);
4784 fflush(DBG);
4785 }
4786
         if(bb00flga==0){
      /* Check Delta-J=+1 (P), then Delta-J=0 (Q) and Delta-J=-1 (R) for
        Delta-K=+1. First, check to see if the target K exists: */
4787
           bb00flgb=0;
4788
           if((bb00h+1)<(bb00L0[0].L)) bb00flgb=1;
      /* Relative position in the low state E/P array */
4789
           bb00el=(bb00h+1)*bb00.nlJ + bb00.nlJ-bb00.nhJ + \
4790
              (int)(bb00Sh-bb00S1) -1 + bb00i;
4791 if(bb00debugflag<DEBUG){
4792 fprintf(DBG,"\t(bb00h+1)*bb00.nlJ=%d, bb00.nlJ-bb00.nhJ=%d\n",\
4793
         (bb00h+1)*bb00.nlJ,bb00.nlJ-bb00.nhJ);
4794 fprintf(DBG,"\t(int)(bb00Sh-bb00S1)=%d, bb00i=%d, bb00e1=%d\n",\
4795
         (int)(bb00Sh-bb00S1),bb00i,bb00e1);
4796 fflush(DBG);
4797 }
4798
           if((bb00el+1)>=(bb00.R1[0].kc*bb00.nlJ)) bb00flgb=1;
      /* Then check if the target value for J+1 is less than or greater
        than the allowed J's for K+1. */
4799
           if((bb00J+1)>(bb00h+1+bb00S1)) bb00flgb=1;
4800
           if((bb00J+1)<(bb00h+1-bb00S1)) bb00flgb=1;
      /* Still OK? Calculate transition */
4801
           if(bb00flgb==0){
4802
             bb00B=+1;
4803
             bb00ell=bb00el+1;
             bb00.T[0].S[bb00ff].f[bb00jii]=\
4804
4805
               bb00.Rh[0].EJ[bb00ehh]-\
4806
               bb00.R1[0].EJ[bb00e11];
4807
             bb00cascadetemp=bb00trprob*bb00fcf*\
4808
               bb00.Rh[0].CJ[bb00ehh]*\
4809
               HL(bb00B,bb00J,bb00L,bb00dL);
             bb00.T[0].S[bb00ff].ci[bb00jii]+=\
4810
4811
               bb00cascadetemp;
4812
             bb00.R1[0].CJ[bb00ell]+=bb00fcfr*\
4813
               bb00cascadetemp;
```

4814 bb00jii--; 4815 } 4816 if(bb00debugflag<DEBUG){ 4817 fprintf(DBG,"%d ",bbOOh); 4818 if(bb00flgb!=0) fprintf(DBG," %d %.1f (1c) M M\n",(bb00h+1),bb00J); 4819 else{ 4820 fprintf(DBG,"%d %.1f %18.12e %18.12e (1c)\n",(bb00h+1),\ bb00J,bb00.T[0].S[bb00ff].f[bb00jii+1],\ 4821 4822 bb00.T[0].S[bb00ff].ci[bb00jii+1]); 4823 } 4824 } 4825 fprintf(BBOOFILE,"%d ",bbOOh); 4826 if(bb00flgb!=0) fprintf(BB00FILE," %d %.1f M M ",(bb00h+1),bb00J); 4827 else{ 4828 fprintf(BBOOFILE,"%d %.1f %18.12e %18.12e ",(bbOOh+1),\ bb00J,bb00.T[0].S[bb00ff].f[bb00jii+1],\ 4829 4830 bb00.T[0].S[bb00ff].ci[bb00jii+1]); 4831 } /* Now, Delta-J=O (Q), Delta-K=+1 */ 4832 bb00flgb=0; 4833 if((bb00h+1)<(bb00L0[0].L)) bb00flgb=1; /* Then check if the target value for J+1 is less than or greater than the allowed J's for K+1. */ 4834 if((bb00J+0)>(bb00h+1+bb00S1)) bb00flgb=1; 4835 if((bb00J+0)<(bb00h+1-bb00S1)) bb00flgb=1; /* Still OK? Calculate transition */ 4836 if(bbO0flgb==0){ 4837 bb00B=0; 4838 bb00ell=bb00el+0; 4839 bb00.T[0].S[bb00ff].f[bb00jii]=\ bb00.Rh[0].EJ[bb00ehh]-\ 4840 4841 bb00.R1[0].EJ[bb00e11]; 4842 bb00cascadetemp=bb00trprob*bb00fcf*\ 4843 bb00.Rh[0].CJ[bb00ehh]*bb00SATT*\ 4844 HL(bb00B,bb00J,bb00L,bb00dL); 4845 bb00.T[0].S[bb00ff].ci[bb00jii]+=\ 4846 bb00cascadetemp; 4847 bb00.R1[0].CJ[bb00ell]+=bb00fcfr*\ 4848 bb00cascadetemp; 4849 bb00jii--; 4850 4851 if(bb00debugflag<DEBUG){ 4852 if(bb00flgb!=0) fprintf(DBG," M M\n"); 4853 else{ 4854 fprintf(DBG,"%18.12e %18.12e (1c)\n",bb00.T[0].S[bb00ff].f[bb00jii+1],\ 4855 bb00.T[0].S[bb00ff].ci[bb00jii+1]); 4856 } 4857 } 4858 if(bb00flgb!=0) fprintf(BB00FILE," M M "); 4859 else{ 4860 fprintf(BBOOFILE," %18.12e %18.12e ",bb00.T[0].S[bb00ff].f[bb00jii+1],\

```
4861 bb00.T[0].S[bb00ff].ci[bb00jii+1]);
```

```
4862
       }
      /* Now, Delta-J=-1 (R) for Delta-K=+1. */
4863
           bb00flgb=0;
4864
           if((bb00h+1)<(bb00L0[0].L)) bb00flgb=1;
4865
           if((bb00J-1)>(bb00h+1+bb00S1)) bb00flgb=1;
4866
           if((bb00J-1)<(bb00h+1-bb00S1)) bb00flgb=1;
4867
           if((bb00J-1)<0) bb00flgb=1;
4868
           if(bb00flgb==0){
4869
             bb00B=-1;
4870
             bb00ell=bb00el-1;
4871
             bb00.T[0].S[bb00ff].f[bb00jii]=\
4872
               bb00.Rh[0].EJ[bb00ehh]-\
4873
               bb00.R1[0].EJ[bb00el1];
4874
             bb00cascadetemp=bb00trprob*bb00fcf*\
4875
               bb00.Rh[0].CJ[bb00ehh]*bb00SATT*\
              HL(bb00B,bb00J,bb00L,bb00dL);
4876
             bb00.T[0].S[bb00ff].ci[bb00jii]+=\
4877
4878
               bb00cascadetemp;
4879
             bb00.R1[0].CJ[bb00ell]+=bb00fcfr*\
4880
               bb00cascadetemp;
4881
             bb00jii--;
4882
4883 if(bb00debugflag<DEBUG){
4884 if(bbOOflgb!=0) fprintf(DBG,"M M\n");
4885 else{
4886 fprintf(DBG,"%18.12e %18.12e
     (1d)\n",bb00.T[0].S[bb00ff].f[bb00jii+1],\
4887
       bb00.T[0].S[bb00ff].ci[bb00jii+1]);
4888
       }
4889 }
4890 if(bb00flgb!=0) fprintf(BB00FILE,"M M\n");
4891 else{
4892 fprintf(BBOOFILE,"%18.12e
     %18.12e\n",bb00.T[0].S[bb00ff].f[bb00jii+1],\
4893
       bb00.T[0].S[bb00ff].ci[bb00jii+1]);
4894
       }
      /* Now, again for Delta-K=+0. Delta-J=+1 (P), then (Q) and (R) */
4895
           bb00flgb=0;
4896
           if((bb00h+0)<(bb00L0[0].L)) bb00flgb=1;
      /* Relative position in the low state E/P array */
4897
           bb00el=(bb00h+0)*bb00.nlJ + bb00.nlJ-bb00.nhJ + \
4898
              (int)(bb00Sh-bb00S1) + 0 + bb00i;
4899 if(bb00debugflag<DEBUG){
4900 fprintf(DBG,"\t(bb00h+0)*bb00.nlJ=%d, bb00.nlJ-bb00.nhJ=%d\n",\
4901
         (bb00h+0)*bb00.nlJ,bb00.nlJ-bb00.nhJ);
4902 fprintf(DBG,"\t(int)(bb00Sh-bb00S1)=%d, bb00i=%d, bb00e1=%d\n",\
         (int)(bb00Sh-bb00S1),bb00i,bb00e1);
4903
4904 fflush(DBG);
4905 }
4906
           if((bb00el+1)>=(bb00.R1[0].kc*bb00.nlJ)) bb00flgb=1;
      /* Then check if the target value for J+1 is less than or greater
```

```
than the allowed J's for K+O. */
```

```
4907 if((bb00J+1)>(bb00h+0+bb00S1)) bb00flgb=1;
```

```
4908 if((bb00J+1)<(bb00h+0-bb00S1)) bb00flgb=1;
```

```
/* Still OK? Calculate transition */
4909
           if(bbO0flgb==0){
4910
             bb00B=+1;
4911
             bb00ell=bb00el+1;
4912
             bb00.T[0].S[bb00ff].f[bb00jii]=\
                bb00.Rh[0].EJ[bb00ehh]-\
4913
4914
                bb00.R1[0].EJ[bb00e11];
4915
             bb00cascadetemp=bb00trprob*bb00fcf*\
4916
                bb00.Rh[0].CJ[bb00ehh]*bb00SATT*\
4917
               HL(bb00B,bb00J,bb00L,bb00dL);
4918
             bb00.T[0].S[bb00ff].ci[bb00jii]+=\
4919
                bb00cascadetemp;
             bb00.R1[0].CJ[bb00ell]+=bb00fcfr*\
4920
4921
                bb00cascadetemp;
4922
             bbOOjii--;
4923
             }
4924 if (bb00debugflag<DEBUG) {
4925 fprintf(DBG,"%d ",bb00h);
4926 if(bb00flgb!=0) fprintf(DBG," %d %.1f (1c) M M\n",(bb00h+0),bb00J);
4927 else{
4928 fprintf(DBG,"%d %.1f %18.12e %18.12e (1c)\n",(bb00h+0),\
4929
       bb00J,bb00.T[0].S[bb00ff].f[bb00jii+1],\
4930
       bb00.T[0].S[bb00ff].ci[bb00jii+1]);
4931
       }
4932 }
4933 fprintf(BBOOFILE,"%d ",bbOOh);
4934 if(bb00flgb!=0) fprintf(BB00FILE," %d %.1f M M ",(bb00h+0),bb00J);
4935 else{
4936 fprintf(BBOOFILE, "%d %.1f %18.12e %18.12e ",(bbOOh+0),\
4937
       bb00J,bb00.T[0].S[bb00ff].f[bb00jii+1],\
4938
       bb00.T[0].S[bb00ff].ci[bb00jii+1]);
4939
       }
      /* Now, Delta-J=0 (Q), Delta-K=+0 */
4940
           bb00flgb=0;
4941
           if((bb00h+0)<(bb00L0[0].L)) bb00flgb=1;
      /* Then check if the target value for J+1 is less than or greater
        than the allowed J's for K+0. */
4942
           if((bb00J+0)>(bb00h+0+bb00S1)) bb00flgb=1;
4943
           if((bb00J+0)<(bb00h+0-bb00S1)) bb00flgb=1;
      /* Still OK? Calculate transition */
4944
           if(bb00flgb==0){
4945
             bb00B=0;
4946
             bb00ell=bb00el+0;
             bb00.T[0].S[bb00ff].f[bb00jii]=\
4947
                bb00.Rh[0].EJ[bb00ehh]-\
4948
4949
                bb00.R1[0].EJ[bb00e11];
4950
             bb00cascadetemp=bb00trprob*bb00fcf*\
4951
                bb00.Rh[0].CJ[bb00ehh]*\
4952
               HL(bb00B,bb00J,bb00L,bb00dL);
4953
             bb00.T[0].S[bb00ff].ci[bb00jii]+=\
4954
                bb00cascadetemp;
4955
             bb00.R1[0].CJ[bb00ell]+=bb00fcfr*\
4956
                bb00cascadetemp;
4957
             bbOOjii--;
```

```
4960 if(bb00flgb!=0) fprintf(DBG," M M\n");
4961 else{
4962 fprintf(DBG,"%18.12e %18.12e
     (1c)\n",bb00.T[0].S[bb00ff].f[bb00jii+1],\
4963
       bb00.T[0].S[bb00ff].ci[bb00jii+1]);
4964
       }
4965 }
4966 if(bb00flgb!=0) fprintf(BB00FILE," M M ");
4967 else{
4968 fprintf(BBOOFILE," %18.12e %18.12e
     ",bb00.T[0].S[bb00ff].f[bb00jii+1],\
4969
       bb00.T[0].S[bb00ff].ci[bb00jii+1]);
4970
       }
      /* Now, Delta-J=-1 (R) for Delta-K=+0. */
4971
           bb00flgb=0;
4972
           if((bb00h+0)<(bb00L0[0].L)) bb00flgb=1;
4973
           if((bb00J-1)>(bb00h+0+bb00S1)) bb00flgb=1;
4974
           if((bb00J-1)<(bb00h+0-bb00S1)) bb00flgb=1;</pre>
4975
           if((bb00J-1)<0) bb00flgb=1;
4976
           if(bb00flgb==0){
             bb00B=-1;
4977
4978
             bb00ell=bb00el-1;
4979
             bb00.T[0].S[bb00ff].f[bb00jii]=\
4980
                bb00.Rh[0].EJ[bb00ehh]-\
4981
               bb00.R1[0].EJ[bb00e11];
4982
             bb00cascadetemp=bb00trprob*bb00fcf*\
4983
                bb00.Rh[0].CJ[bb00ehh]*bb00SATT*\
4984
              HL(bb00B,bb00J,bb00L,bb00dL);
4985
             bb00.T[0].S[bb00ff].ci[bb00jii]+=\
4986
                bb00cascadetemp;
4987
             bb00.R1[0].CJ[bb00ell]+=bb00fcfr*\
4988
               bb00cascadetemp;
4989
             bb00jii--;
             }
4990
4991 if(bbOOdebugflag<DEBUG){
4992 if(bbOOflgb!=0) fprintf(DBG,"M M\n");
4993 else{
4994 fprintf(DBG,"%18.12e %18.12e
     (1d)\n",bb00.T[0].S[bb00ff].f[bb00jii+1],\
4995
       bb00.T[0].S[bb00ff].ci[bb00jii+1]);
4996
       }
4997 }
4998 if(bb00flgb!=0) fprintf(BB00FILE,"M M\n");
4999 else{
5000 fprintf(BBOOFILE,"%18.12e
     %18.12e\n",bb00.T[0].S[bb00ff].f[bb00jii+1],\
5001
       bb00.T[0].S[bb00ff].ci[bb00jii+1]);
5002
       }
      /* Check Delta-J=+1 (P), then Delta-J=0 (Q) and Delta-J=-1 (R) for
        Delta-K=-1. First, check to see if the target K exists: */
5003
           bb00flgb=0;
5004
           if((bb00h-1)<(bb00L0[0].L)) bb00flgb=1;
```

4958

} 4959 if(bb00debugflag<DEBUG){

/* Relative position in the low state E/P array */ 5005 $bb00el=(bb00h-1)*bb00.nlJ + bb00.nlJ-bb00.nhJ + \$ 5006 (int)(bb00Sh-bb00S1) + 1 + bb00i;5007 if(bb00debugflag<DEBUG){ 5008 fprintf(DBG,"\t(bb00h-1)*bb00.nlJ=%d, bb00.nlJ-bb00.nhJ=%d\n",\ (bb00h-1)*bb00.nlJ,bb00.nlJ-bb00.nhJ); 5009 5010 fprintf(DBG,"\t(int)(bb00Sh-bb00S1)=%d, bb00i=%d, bb00e1=%d\n",\ 5011 (int)(bb00Sh-bb00S1),bb00i,bb00e1); 5012 fflush(DBG); 5013 } 5014 if((bb00el+1)>=(bb00.R1[0].kc*bb00.nlJ)) bb00flgb=1; /* Then check if the target value for J+1 is less than or greater than the allowed J's for K-1. */ if((bb00J+1)>(bb00h-1+bb00S1)) bb00flgb=1; 5015 5016 if((bb00J+1)<(bb00h-1-bb00S1)) bb00flgb=1; /* Still OK? Calculate transition */ 5017 if(bb00flgb==0){ 5018 bb00B=+1; 5019 bb00ell=bb00el+1; 5020 bb00.T[0].S[bb00ff].f[bb00jii]=\ 5021 bb00.Rh[0].EJ[bb00ehh]-\ 5022 bb00.R1[0].EJ[bb00el1]; bb00cascadetemp=bb00trprob*bb00fcf*\ 5023 5024 bb00.Rh[0].CJ[bb00ehh]*bb00SATT*\ 5025 HL(bb00B,bb00J,bb00L,bb00dL); bb00.T[0].S[bb00ff].ci[bb00jii]+=\ 5026 5027 bb00cascadetemp; bb00.R1[0].CJ[bb00ell]+=bb00fcfr*\ 5028 5029 bb00cascadetemp; 5030 bbOOjii--; 5031 ł 5032 if (bb00debugflag<DEBUG) { 5033 fprintf(DBG,"%d",bbOOh); 5034 if(bb00flgb!=0) fprintf(DBG," %d %.1f M M ",(bb00h-1),bb00J); 5035 else{ 5036 fprintf(DBG,"%d %.1f %18.12e %18.12e (1e)\n",(bbOOh-1),\ bb00J,bb00.T[0].S[bb00ff].f[bb00jii+1],\ 5037 5038 bb00.T[0].S[bb00ff].ci[bb00jii+1]); 5039 } 5040 } 5041 fprintf(BBOOFILE,"%d ",bbOOh); 5042 if(bb00flgb!=0) fprintf(BB00FILE," %d %.1f M M ",(bb00h-1),bb00J); 5043 else{ 5044 fprintf(BBOOFILE, "%d %.1f %18.12e %18.12e ", (bbOOh-1), \ 5045 bb00J,bb00.T[0].S[bb00ff].f[bb00jii+1],\ 5046 bb00.T[0].S[bb00ff].ci[bb00jii+1]); } 5047 /* Now, Delta-J=+0 (Q), Delta-K=-1. */ 5048 bb00flgb=0; 5049 if((bb00h-1)<(bb00L0[0].L)) bb00flgb=1; /* Then check if the target value for J+1 is less than or greater than the allowed J's for K-1. */ 5050 if((bb00J+0)>(bb00h-1+bb00S1)) bb00flgb=1; 5051 if((bb00J+0)<(bb00h-1-bb00S1)) bb00flgb=1;

```
/* Still OK? Calculate transition */
5052
           if(bbO0flgb==0){
5053
             bb00B=0;
5054
             bb00ell=bb00el+0;
5055
             bb00.T[0].S[bb00ff].f[bb00jii]=\
5056
               bb00.Rh[0].EJ[bb00ehh]-\
               bb00.R1[0].EJ[bb00el1];
5057
5058
             bb00cascadetemp=bb00trprob*bb00fcf*\
5059
               bb00.Rh[0].CJ[bb00ehh]*bb00SATT*\
5060
               HL(bb00B,bb00J,bb00L,bb00dL);
5061
             bb00.T[0].S[bb00ff].ci[bb00jii]+=\
5062
               bb00cascadetemp;
             bb00.R1[0].CJ[bb00ell]+=bb00fcfr*\
5063
               bb00cascadetemp;
5064
5065
             bbOOjii--;
5066
             }
5067 if(bbOOdebugflag<DEBUG){
5068 if(bbOOflgb!=0) fprintf(DBG," M M ");
5069 else{
5070 fprintf(DBG,"%18.12e %18.12e
     \n",bb00.T[0].S[bb00ff].f[bb00jii+1],\
5071
       bb00.T[0].S[bb00ff].ci[bb00jii+1]);
5072
       }
5073 }
5074 if(bb00flgb!=0) fprintf(BB00FILE," M M ");
5075 else{
5076 fprintf(BBOOFILE,"%18.12e %18.12e
     ",bb00.T[0].S[bb00ff].f[bb00jii+1],\
5077
       bb00.T[0].S[bb00ff].ci[bb00jii+1]);
5078
       }
      /* Now, Delta-J=-1 (R) for Delta-K=-1. */
5079
           bb00flgb=0;
5080
           if((bb00h-1)<(bb00L0[0].L)) bb00flgb=1;
5081
           if((bb00J-1)>(bb00h-1+bb00S1)) bb00flgb=1;
           if((bb00J-1)<(bb00h-1-bb00S1)) bb00flgb=1;
5082
5083
           if((bb00J-1)<0) bb00flgb=1;
5084
           if(bb00flgb==0){
5085
             bb00B=-1;
5086
             bb00ell=bb00el-1;
5087
             bb00.T[0].S[bb00ff].f[bb00jii]=\
5088
               bb00.Rh[0].EJ[bb00ehh]-\
5089
               bb00.R1[0].EJ[bb00e11];
5090
             bb00cascadetemp=bb00trprob*bb00fcf*\
               bb00.Rh[0].CJ[bb00ehh]*\
5091
5092
              HL(bb00B,bb00J,bb00L,bb00dL);
5093
             bb00.T[0].S[bb00ff].ci[bb00jii]+=\
5094
               bb00cascadetemp;
             bb00.R1[0].CJ[bb00ell]+=bb00fcfr*\
5095
5096
               bb00cascadetemp;
             }
5097
5098 if(bb00debugflag<DEBUG){
5099 if(bb00flgb!=0) fprintf(DBG,"M M\n");
5100 else{
```
```
5101 fprintf(DBG,"%18.12e %18.12e
     (1f)\n",bb00.T[0].S[bb00ff].f[bb00jii],\
5102
       bb00.T[0].S[bb00ff].ci[bb00jii]);
       }
5103
5104 }
5105 if(bb00flgb!=0) fprintf(BB00FILE,"M M\n");
5106 else{
5107 fprintf(BBOOFILE,"%18.12e
     %18.12e\n",bb00.T[0].S[bb00ff].f[bb00jii],\
5108
       bb00.T[0].S[bb00ff].ci[bb00jii]);
5109
       }
5110
           } /* close if bb00flga is zero. */
5111
         } /* close upper-state J-of-K loop */
5112
       } /* close upper-state K loop */
5113
       fclose(BBOOFILE);
5114
         } /* close if high-state v is cascade populated */
5115
       } /* close low-state v */
5116
       } /* close high-state v */
5117 return;
5118 }
     /* This function calculates energy levels only when needed for des-
        tination states in a transition. This function is called from a-
        a.c and a-b.c. For multiplet non-Sigma states, Hund's Case (a).
     The input variables are (1) the rotset where the energy levels
        should be stored, (2) the position in the case-a info array, (3)
        the value of Omega for this set of J's, (4) the vibrational quan-
        tum number, (5) the current highest value of J calculated, (6) the
       highest value needed */
5119 void
5120 case_a_cascade(rotset *cacR,int cacA,double cacO,int cacV,int
     cacJc,int cacJn){
5121 int cacb=0, cacL=0;
5122 double cacJ=0,cacDv=0,cacBe=0,cacAe=0,cacwe=0,cacwexe=0;
5123 double cacbeta=0, cacTe=0, cacDe=0, cacBv=0, cacTeVib=0;
5124 if (DEBUG>cacdebugflag) {
5125 fprintf(DBG,"\n\nTop of case_a_cascade\n\n");\
5126 fflush(DBG);
5127 }
5128 cacBe=CA[cacA].Be;
5129 cacAe=CA[cacA].ae;
5130 cacTe=CA[cacA].Te;
5131 cacwe=CA[cacA].we;
5132 cacwexe=CA[cacA].wexe;
5133 cacL=CA[cacA].L;
5134 cacbeta=CA[cacA].beta;
5135 if(DEBUG>cacdebugflag){
5136 fprintf(DBG,"Be=%f ae=%f Te=%f we=%f ",cacBe,cacAe,cacTe,cacwe);
5137 fprintf(DBG,"wexe=%f cacL=%d,
     cacbeta=%f\n",cacwexe,cacL,cacbeta);
5138 fflush(DBG);
```

```
5139 }
5140
     /* Calculate some stuff that will be useful later */
5141 cacDe=4*pow(cacBe,3)/(cacwe*cacwe); /* Centrifugal distortion */
5142 cacBv=cacBe-cacAe*(cacV+0.5);
5143 cacDv=cacDe+cacbeta*(cacV+0.5);
5144 cacTeVib=cacTe+(cacV+0.5)*cacwe-(cacV+0.5)*(cacV+0.5)*cacwexe;
5145 if (DEBUG>cacdebugflag) {
5146 fprintf(DBG,"cacO=%f cacDe=%f cacBv=%f cacDv=%f cacTeVib=%f\n",\
5147
         cacO, cacDe, cacBv, cacDv, cacTeVib);
5148 fflush(DBG);
5149 }
     /* There aren't any extra E's here. If someone ever wants to add in a
       splitting factor for the +/- wavefunctions, then double the space
       available (cacJn) and change the indexing and energy calculation
       in the loops below.*/
5150 cacR[0].J=(double*)realloc(cacR[0].J,(cacJn*sizeof(double)));
5151 cacR[0].EJ=(double*)realloc(cacR[0].EJ,(cacJn*sizeof(double)));
5152 cacR[0].CJ=(double*)realloc(cacR[0].CJ,(cacJn*sizeof(double)));
5153 for(cacb=cacJc;cacb<cacJn;cacb++){
5154
       cacJ=cacb+cac0;
5155
       cacR[0].J[cacb]=cacJ;
5156
       cacR[0].EJ[cacb]=cacTeVib+cacBv*(cacJ*(cacJ+1)-cacO*cacO)-\
5157
         cacDv*cacJ*cacJ*(cacJ+1)*(cacJ+1);
5158
       cacR[0].CJ[cacb]=0;
5159 if(DEBUG>cacdebugflag){
5160 fprintf(DBG,\
5161 "cacb=%d cacR[0].J[cacb]=%f cacR[0].EJ[cacb]=%f
     cacR[0].CJ[cacb]=%f\n'',\
         cacb,cacJ,cacR[0].EJ[cacb],cacR[0].CJ[cacb]);
5162
5163 fflush(DBG);
5164 }
5165
      }
5166 cacR[0].jc=cacJn;
5167 return;
5168 }
     /* This function calculates energy levels only when needed for des-
       tination states in a transition. This function is called from b-
       b.c.
     The input variables are (1) the rotset where the energy levels
       should be stored, (2) the position in the case-b info array, (3)
       the vibrational quantum number, (4) the current highest value of
       K calculated, (5) the highest value needed, (6) the multiplicity
        (J's per K) */
5169 void
5170 case_b_cascade(rotset *cbcR,int cbcA,int cbcV,int cbcKc,int
     cbcKn,int cbcM){
5171 int cbcb=0,cbcc=0,cbcL=0;
5172 double cbcK=0,cbcDv=0,cbcBe=0,cbcAe=0,cbcwe=0,cbcwexe=0;
5173 double cbcbeta=0,cbcTe=0,cbcDe=0,cbcBv=0,cbcTeVib=0;
```

```
5174 if(DEBUG>cbcdebugflag){
5175 fprintf(DBG,"\n\nTop of case_b_cascade\n\n");\
5176 fprintf(DBG,"cbcA=%d, cbcV=%d, cbcKc=%d, cbcKn=%d\n",\
         cbcA,cbcV,cbcKc,cbcKn);
5177
5178 fprintf(DBG,"cbcR[0].j=%d\n",cbcR[0].j);
5179 fflush(DBG);
5180 }
5181 cbcBe=CB[cbcA].Be;
5182 cbcAe=CB[cbcA].ae;
5183 cbcTe=CB[cbcA].Te;
5184 cbcwe=CB[cbcA].we;
5185 cbcwexe=CB[cbcA].wexe;
5186 cbcL=CB[cbcA].L;
5187 cbcbeta=CB[cbcA].beta;
5188 if(DEBUG>cbcdebugflag){
5189 fprintf(DBG,"Be=%f ae=%f Te=%f we=%f ",cbcBe,cbcAe,cbcTe,cbcwe);
5190 fprintf(DBG,"wexe=%f cbcL=%d,
     cbcbeta=%f\n",cbcwexe,cbcL,cbcbeta);
5191 fflush(DBG);
5192 }
5193
      /* Calculate some stuff that will be useful later */
5194 cbcDe=4*pow(cbcBe,3)/(cbcwe*cbcwe); /* Centrifugal distortion */
5195 cbcBv=cbcBe-cbcAe*(cbcV+0.5);
5196 cbcDv=cbcDe+cbcbeta*(cbcV+0.5);
5197 cbcTeVib=cbcTe+(cbcV+0.5)*cbcwe-(cbcV+0.5)*(cbcV+0.5)*cbcwexe;
5198 if (DEBUG>cbcdebugflag) {
5199 fprintf(DBG,"cbcDe=%f cbcBv=%f cbcDv=%f cbcTeVib=%f\n",\
         cbcDe,cbcBv,cbcDv,cbcTeVib);
5200
5201 fflush(DBG);
5202 }
      /* There aren't any extra E's here. If someone ever wants to add in a
        splitting factor for the +/- wavefunctions, then double the space
        available (cbcKn) and change the indexing and energy calculation
        in the loops below.*/
5203 \text{ cbcR}[0].J = (double*) \text{ realloc}(cbcR[0].J,
     (cbcM*cbcKn*sizeof(double)));
5204 cbcR[0].EJ = (double*) realloc(cbcR[0].EJ,
     (cbcM*cbcKn*sizeof(double)));
5205 cbcR[0].CJ = (double*) realloc(cbcR[0].CJ,
     (cbcM*cbcKn*sizeof(double)));
5206 for(cbcb=cbcKc;cbcb<cbcKn;cbcb++){
5207
       cbcK=cbcb;
       for(cbcc=0;cbcc<cbcM;cbcc++){</pre>
5208
5209
         cbcR[0].J[cbcb*cbcM+cbcc]=cbcK;
5210
         cbcR[0].EJ[cbcb*cbcM+cbcc]=cbcTeVib+cbcBv*(cbcK*(cbcK+1))-\
5211
           cbcDv*cbcK*cbcK*(cbcK+1)*(cbcK+1);
         cbcR[0].CJ[cbcb*cbcM+cbcc]=0;
5212
5213 if(DEBUG>cbcdebugflag){
5214 fprintf(DBG,\
5215 "cbcb=%d cbcR[0].J[cbcb]=%f cbcR[0].EJ[cbcb]=%f
     cbcR[0].CJ[cbcb]=%f\n'', \
5216
         cbcb,cbcK,cbcR[0].EJ[cbcb],cbcR[0].CJ[cbcb]);
```

```
5217 fflush(DBG);
5218 }
5219
        }
5220
      }
5221 cbcR[0].kc=cbcKn;
5222 return;
5223 }
     /* This function loops through all the line emissions (whether cal-
       culated in a transition function or read from a file) and adds
       their contributions to appropriate places in the simulation. The
       distinction between an instrument that scans or jumps from point
       to point is made here. */
5224 void do_simulation(){
     /* counting variables */
5225 int da=0,db=0,dc=0,dd=0,dn=0,dbin=0,dnn=0,dsw=0;
     /* flags */
5226 int ddoflag=0,ddoneflag=0;
     /* variables for assigning intensities */
5227 double
     dposn=0,dcslope=0,dnslope=0,ddumposn=0,ddumnint=0,ddumcint=0;
5228 double ddend=0,dwidth=0,dintmax=0;
     /* temporary simulations for writing separate atomic, molecular,
       etc, simulations to files */
5229 sim dmnsim, dmcsim, dasim, dosim, dtotsim;
     /* variables about files to create */
5230 char dnfile[2000],dcfile[2000];
5231 FILE *DNFILE, *DCFILE;
     /* Make the directory for storing simulation output */
5232 sprintf(dnfile,"mkdir %s_simulations",PREF);
5233 system(dnfile);
     /* get number of bins and allocate memory for simulations */
5234 dn=(int)(ceil((MAXV-MINV)/PSTEP));
5235 if(ddebugflag<DEBUG){
5236 fprintf(DBG, "Top of do_simulation. dn=%d\n", dn);
5237 fflush(DBG);
5238 }
5239 dtotsim.n=dmnsim.n=dmcsim.n=dasim.n=dosim.n=dn;
5240 dmnsim.x=(double*)calloc(dn,sizeof(double));
5241 dmnsim.y=(double*)calloc(dn,sizeof(double));
5242 dmcsim.x=(double*)calloc(dn,sizeof(double));
5243 dmcsim.y=(double*)calloc(dn,sizeof(double));
5244 dasim.x=(double*)calloc(dn,sizeof(double));
5245 dasim.y=(double*)calloc(dn,sizeof(double));
5246 dosim.x=(double*)calloc(dn,sizeof(double));
5247 dosim.y=(double*)calloc(dn,sizeof(double));
5248 dtotsim.x=(double*)calloc(dn,sizeof(double));
5249 dtotsim.y=(double*)calloc(dn,sizeof(double));
     5250 for(da=0;da<NUMMOL;da++){ /* Loop over all molecules */
      for(db=0;db<MOL[da].trans;db++){ /* then loop over transitions */</pre>
```

```
5252 if(ddebugflag<DEBUG){
5253 fprintf(DBG,"MOL[da].t[db].Nhi=%s, MOL[%d].t[%d].Nlo=%s",
5254
         MOL[da].t[db].Nhi,da,db,MOL[da].t[db].Nlo);
5255 fflush(DBG);
5256 }
5257
         for(dc=0;dc<MOL[da].t[db].nS;dc++){ /* loop through simsets */</pre>
5258 if(ddebugflag<DEBUG){
5259 fprintf(DBG, "da=%d, db=%d, dc=%d, MOL[da].t[db].fS[dc]=%d, ", \
5260
         da,db,dc,MOL[da].t[db].fS[dc]);
5261 fflush(DBG);
5262 }
      /* if inclusion flag says to include this simset */
5263
         if(MOL[da].t[db].fS[dc]==0){
      /* loop through transitions in simset */
5264 if(ddebugflag<DEBUG){
5265 fprintf(DBG, "MOL[%d].t[%d].S[%d].n=%d, ", \
         da,db,dc,MOL[da].t[db].S[dc].n);
5266
5267 fflush(DBG);
5268 }
5269
           for(dd=0;dd<MOL[da].t[db].S[dc].n;dd++){</pre>
     /* if the current frequency is not equal to zero */
5270
           if(MOL[da].t[db].S[dc].f[dd]!=0){
      /* see if line falls within requested simulation min/max */
5271 if(UNITTYPE==0) dposn=1e7/MOL[da].t[db].S[dc].f[dd];
5272 else dposn=MOL[da].t[db].S[dc].f[dd];
5273 ddoflag=0;
5274 if(dposn<(MINV-RESN)) ddoflag=1;
5275 if(dposn>(MAXV+RESN)) ddoflag=1;
5276 if(ddebugflag<DEBUG){
5277 fprintf(DBG,"UNITTYPE=%d, dposn=%12.6e,
     ddoflag=%d\n",UNITTYPE,dposn,ddoflag);
5278 fprintf(DBG,"MOL[%d].t[%d].S[%d].f[%d]=%12.6e\n",da,db,dc,dd,\
5279
         MOL[da].t[db].S[dc].f[dd]);
5280 fflush(DBG);
5281 }
5282 if(ddoflag==0){
      /* find bin where line originates, also get native and cascade
        slopes */
5283
       dbin=(int)(floor((dposn-MINV)/PSTEP));
       dcslope=MOL[da].pop*MOL[da].t[db].S[dc].ci[dd]/RESN;
5284
5285
       dnslope=MOL[da].pop*MOL[da].t[db].S[dc].ni[dd]/RESN;
5286 if(ddebugflag<DEBUG){
5287 fprintf(DBG,"RESN=%12.6e,
     MOL[%d].pop=%12.6e\n",RESN,da,MOL[da].pop);
5288 fprintf(DBG,"MOL[%d].t[%d].S[%d].ci[%d]=%12.6e\n",da,db,dc,dd,\
         MOL[da].t[db].S[dc].ci[dd]);
5289
5290 fprintf(DBG,"MOL[%d].t[%d].S[%d].ni[%d]=%12.6e\n",da,db,dc,dd,\
5291
         MOL[da].t[db].S[dc].ni[dd]);
5292 fprintf(DBG,"dposn=%12.6e, MINV=%12.6e,
     PSTEP=%12.6e\n",dposn,MINV,PSTEP);
5293 fflush(DBG);
5294 }
      /* increment through them and calculate the intensities for each
        bin -- integrate if SCAN and point if JUMP */
```

```
5295
       ddoneflag=1;
5296
       ddumposn=dposn;
5297
       ddumnint=MOL[da].pop*MOL[da].t[db].S[dc].ni[dd];
5298
       ddumcint=MOL[da].pop*MOL[da].t[db].S[dc].ci[dd];
5299
       dnn=0;
5300
       if(dbin<0) ddoneflag=0;</pre>
5301 if(ddebugflag<DEBUG){
5302 fprintf(DBG,"dbin=%d, dcslope=%12.6e, dnslope=%12.6e,
     ddumnint=%12.6e, ",\
5303
         dbin,dcslope,dnslope,ddumnint);
5304 fprintf(DBG, "ddumcint = %12.6e, ddoneflag = %d\n", ddumcint,
     ddoneflag);
5305 fflush(DBG);
5306 }
5307
       while(ddoneflag==1){ /* fill bins at/below dbin */
5308
         dsw=0;
5309
         ddend=MINV+(dbin-dnn)*PSTEP;
5310
         if(ddumposn==dposn) dsw+=1;
5311
         if(ddend<(dposn-RESN)) dsw+=2;
5312
         if(SCANTYPE==1) dsw+=4;
5313
         if((dbin-dnn)>(dn-1)) dsw=8;
5314 if(ddebugflag<DEBUG){
5315 fprintf(DBG,"AT/BELOW ddumposn=%12.6e, ddend=%12.6e,
     ",ddumposn,ddend);
5316 fprintf(DBG,"SCANTYPE=%d, dsw=%d, ",SCANTYPE,dsw);
5317 fflush(DBG);
5318 }
5319
         switch (dsw){
      /* the following for equipment that scans between "points" */
5320
           case 0:
5321
             dmnsim.y[dbin-dnn]+=\
                (ddumnint-0.5*dnslope*PSTEP)*PSTEP;
5322
5323
             dmcsim.y[dbin-dnn] += 
5324
                (ddumcint-0.5*dcslope*PSTEP)*PSTEP;
5325
             ddumnint-=dnslope*PSTEP;
5326
             ddumcint-=dcslope*PSTEP;
5327
             ddumposn-=PSTEP;
5328
             if(dnn==dbin) ddoneflag=0;
5329
             dnn++;
5330 if(ddebugflag<DEBUG){
5331 fprintf(DBG, "Case 0. dmnsim.y[%d]=%12.6e,
     dmcsim.y[%d]=%12.6e\n",\
5332
       (dbin-dnn+1),dmnsim.y[dbin-dnn+1],(dbin-dnn+1),dmcsim.y[dbin-
     dnn+1]);
5333 fprintf(DBG,"ddumnint=%12.6e, ddumcint=%12.6e, ddumposn=%12.6e,
     dnn=%d\n", \
5334
         ddumnint,ddumcint,ddumposn,dnn);
5335 fflush(DBG);
5336 }
5337
             break:
5338
           case 1:
5339
             dwidth=ddumposn-ddend;
5340
             dmnsim.y[dbin-dnn] += 
5341
                (ddumnint-0.5*dnslope*dwidth)*dwidth;
```

```
5342
             dmcsim.y[dbin-dnn] += 
5343
                (ddumcint-0.5*dcslope*dwidth)*dwidth;
5344
             ddumnint-=dnslope*dwidth;
5345
             ddumcint-=dcslope*dwidth;
5346
             ddumposn=ddend;
5347
             if(dnn==dbin) ddoneflag=0;
5348
             dnn++;
5349 if(ddebugflag<DEBUG){
5350 fprintf(DBG, "Case 1. dwidth=%12.6e, dmnsim.y[%d]=%12.6e,
     ",dwidth,\
5351
       (dbin-dnn+1),dmnsim.y[dbin-dnn+1]);
5352 fprintf(DBG,"dmcsim.y[%d]=%12.6e\n",(dbin-dnn+1),dmcsim.y[dbin-
     dnn+1]);
5353 fprintf(DBG,"ddumnint=%12.6e, ddumcint=%12.6e, ddumposn=%12.6e,
     dnn=%d\n",\
         ddumnint,ddumcint,ddumposn,dnn);
5354
5355 fflush(DBG);
5356 }
5357
             break;
5358
           case 2:
             if(dnslope!=0) dwidth=ddumnint/dnslope;
5359
5360
             else{
5361
               if(dcslope!=0) dwidth=ddumcint/dcslope;
5362
               else dwidth=0;
5363
               }
             dmnsim.y[dbin-dnn]+=ddumnint*0.5*dwidth;
5364
5365
             dmcsim.y[dbin-dnn]+=ddumcint*0.5*dwidth;
5366
             ddoneflag=0;
5367 if(ddebugflag<DEBUG){
5368 fprintf(DBG, "Case 2. dwidth=%12.6e, dmnsim.y[%d]=%12.6e,
     ",dwidth,\
       (dbin-dnn),dmnsim.y[dbin-dnn]);
5369
5370 fprintf(DBG,"dmcsim.y[%d]=%12.6e\n",(dbin-dnn),dmcsim.y[dbin-
     dnn]);
5371 fprintf(DBG,"ddumnint=%12.6e, ddumcint=%12.6e, ddumposn=%12.6e,
     dnn=%d\n",\
5372
         ddumnint,ddumcint,ddumposn,dnn);
5373 fflush(DBG);
5374 }
5375
             break;
5376
           case 3:
             dmnsim.y[dbin-dnn]+=ddumnint*0.5*PSTEP;
5377
5378
             dmcsim.y[dbin-dnn]+=ddumcint*0.5*PSTEP;
5379
             ddoneflag=0;
5380 if(ddebugflag<DEBUG){
5381 fprintf(DBG,"Case 3. dmnsim.y[%d]=%12.6e, ",(dbin-
     dnn),dmnsim.y[dbin-dnn]);
5382 fprintf(DBG,"dmcsim.y[%d]=%12.6e\n",(dbin-dnn),dmcsim.y[dbin-
     dnn]);
5383 fprintf(DBG,"ddumnint=%12.6e, ddumcint=%12.6e, ddumposn=%12.6e,
     dnn=%d\n",\
         ddumnint,ddumcint,ddumposn,dnn);
5384
5385 fflush(DBG);
5386 }
```

```
5387
             break;
      /* the following for equipment that jumps from point to point */
5388
           case 4:
5389
             ddumnint-=dnslope*PSTEP;
5390
             ddumcint-=dcslope*PSTEP;
5391
             dmnsim.y[dbin-dnn]+=ddumnint;
5392
             dmcsim.y[dbin-dnn]+=ddumcint;
5393
             ddumposn-=PSTEP;
5394
             if(dnn==dbin) ddoneflag=0;
5395
             dnn++;
5396 if(ddebugflag<DEBUG){
5397 fprintf(DBG, "Case 4. dmnsim.y[%d]=%12.6e,
     dmcsim.y[%d]=%12.6e\n",\
       (dbin-dnn+1),dmnsim.y[dbin-dnn+1],(dbin-dnn+1),dmcsim.y[dbin-
5398
     dnn+1]);
5399 fprintf(DBG,"ddumnint=%12.6e, ddumcint=%12.6e, ddumposn=%12.6e,
     dnn=%d n'', 
5400
         ddumnint,ddumcint,ddumposn,dnn);
5401 fflush(DBG);
5402 }
5403
             break;
5404
           case 5:
             dwidth=ddumposn-ddend;
5405
5406
             ddumnint-=dnslope*dwidth;
5407
             ddumcint-=dcslope*dwidth;
             dmnsim.y[dbin-dnn]+=ddumnint;
5408
5409
             dmcsim.y[dbin-dnn]+=ddumcint;
5410
             ddumposn=ddend;
             if(dnn==dbin) ddoneflag=0;
5411
5412
             dnn++;
5413 if(ddebugflag<DEBUG){
5414 fprintf(DBG,"Case 5. dwidth=%12.6e, dmnsim.y[%d]=%12.6e,
     ",dwidth,∖
5415
       (dbin-dnn+1),dmnsim.y[dbin-dnn+1]);
5416 fprintf(DBG,"dmcsim.y[%d]=%12.6e\n",(dbin-dnn+1),dmcsim.y[dbin-
     dnn+1]);
5417 fprintf(DBG,"ddumnint=%12.6e, ddumcint=%12.6e, ddumposn=%12.6e,
     dnn=%d\n",\
5418
         ddumnint,ddumcint,ddumposn,dnn);
5419 fflush(DBG);
5420 }
5421
             break;
5422
           case 6:
5423
             ddoneflag=0;
5424 if(ddebugflag<DEBUG){
5425 fprintf(DBG,"Case 6\n");
5426 fflush(DBG);
5427 }
5428
             break;
5429
           case 7:
5430
             dmnsim.y[dbin-dnn]+=ddumnint;
5431
             dmcsim.y[dbin-dnn]+=ddumcint;
5432
             ddoneflag=0;
5433 if(ddebugflag<DEBUG){
```

```
5434 fprintf(DBG, "Case 7. dmnsim.y[%d]=%12.6e, ", (dbin-
     dnn),dmnsim.y[dbin-dnn]);
5435 fprintf(DBG,"dmcsim.y[%d]=%12.6e\n",(dbin-dnn),dmcsim.y[dbin-
     dnn]);
5436 fprintf(DBG,"ddumnint=%12.6e, ddumcint=%12.6e, ddumposn=%12.6e,
     dnn=%d\n",\
         ddumnint,ddumcint,ddumposn,dnn);
5437
5438 fflush(DBG);
5439 }
5440
             break;
      /* the following for emissions that provide only "spillover" */
5441
           case 8:
5442
             if(ddumposn==dposn){
5443
                dwidth=ddumposn-ddend;
5444
                ddumnint-=dnslope*dwidth;
5445
               ddumcint-=dcslope*dwidth;
5446
                ddumposn=ddend;
5447
               if(dnn==dbin) ddoneflag=0;
5448
               dnn++;
5449
               }
5450
             else{
5451
                if(ddend<(dposn-RESN)){
5452
                  printf(\
5453
              "Fix switch case in do_sim at 1a.\n");
5454
                  exit(1);
                  }
5455
5456
               else{
5457
                  ddumnint-=dnslope*PSTEP;
5458
                  ddumcint-=dcslope*PSTEP;
5459
                  ddumposn-=PSTEP;
5460
                  if(dnn==dbin) ddoneflag=0;
5461
                  dnn++;
5462
                  }
5463
                }
5464 if (ddebugflag<DEBUG) {
5465 fprintf(DBG,"Case 8. dwidth=%12.6e, dbin=%d",dwidth,dbin);
5466 fprintf(DBG,"ddumnint=%12.6e, ddumcint=%12.6e, ddumposn=%12.6e,
     dnn=%d\n",\
5467
         ddumnint,ddumcint,ddumposn,dnn);
5468 fflush(DBG);
5469 }
5470
             break;
5471
           default:
5472
             printf("Go fix do_sim.\n");
5473
              exit(1);
5474
           } /* close switch-case */
         } /* close while for bins below the transition position */
5475
5476
       ddoneflag=1;
5477
       ddumposn=dposn;
5478
       ddumnint=MOL[da].pop*MOL[da].t[db].S[dc].ni[dd];
5479
       ddumcint=MOL[da].pop*MOL[da].t[db].S[dc].ci[dd];
5480
       dnn=0;
5481
       if(dbin>dn-1) ddoneflag=0;
5482 if(ddebugflag<DEBUG){
```

```
5483 fprintf(DBG,"dbin=%d, dcslope=%12.6e, dnslope=%12.6e,
     ddumnint=%12.6e, ",\
         dbin,dcslope,dnslope,ddumnint);
5484
5485 fprintf(DBG, "ddumcint = %12.6e, ddoneflag = %d\n", ddumcint,
     ddoneflag);
5486 fflush(DBG);
5487 }
       while(ddoneflag==1){ /* fill bins at/above dbin */
5488
5489
         dsw=0;
5490
         ddend=MINV+(dbin+dnn+1)*PSTEP;
5491
         if(dposn==ddumposn) dsw+=1;
5492
         if(ddend>(dposn+RESN)) dsw+=2;
5493
         if(SCANTYPE==1) dsw+=4;
5494
         if((dbin+dnn)<0) dsw=8;</pre>
5495 if(ddebugflag<DEBUG){
5496 fprintf(DBG,"AT/ABOVE ddumposn=%12.6e, ddend=%12.6e,
     ",ddumposn,ddend);
5497 fprintf(DBG, "SCANTYPE=%d, dsw=%d, ", SCANTYPE, dsw);
5498 fflush(DBG);
5499 }
5500
         switch (dsw){
      /* the following for equipment that scans between "points" */
5501
           case 0:
5502
             dmnsim.y[dbin+dnn]+=\
5503
                (ddumnint-0.5*dnslope*PSTEP)*PSTEP;
             dmcsim.y[dbin+dnn]+=
5504
5505
                (ddumcint-0.5*dcslope*PSTEP)*PSTEP;
5506
             ddumnint-=dnslope*PSTEP;
5507
             ddumcint-=dcslope*PSTEP;
5508
             ddumposn+=PSTEP;
5509
             dnn++;
             if((dnn+dbin)==dn) ddoneflag=0;
5510
5511 if(ddebugflag<DEBUG){
5512 fprintf(DBG,"Case 0. dmnsim.y[%d]=%12.6e,
     dmcsim.y[%d]=%12.6e\n",\
       (dbin+dnn-1),dmnsim.y[dbin+dnn-1],(dbin+dnn-
5513
     1),dmcsim.y[dbin+dnn-1]);
5514 fprintf(DBG,"ddumnint=%12.6e, ddumcint=%12.6e, ddumposn=%12.6e,
     dnn=%d n'', 
5515
         ddumnint,ddumcint,ddumposn,dnn);
5516 fflush(DBG);
5517 }
5518
             break;
5519
           case 1:
5520
             dwidth=ddend-ddumposn;
5521
             dmnsim.y[dbin+dnn]+=\
5522
                (ddumnint-0.5*dnslope*dwidth)*dwidth;
5523
             dmcsim.y[dbin+dnn]+=
5524
                (ddumcint-0.5*dcslope*dwidth)*dwidth;
5525
             ddumnint-=dnslope*dwidth;
5526
             ddumcint-=dcslope*dwidth;
5527
             ddumposn=ddend;
5528
             dnn++;
5529
             if((dnn+dbin)==dn) ddoneflag=0;
```

```
5530 if(ddebugflag<DEBUG){
5531 fprintf(DBG,"Case 1. dwidth=%12.6e, dmnsim.y[%d]=%12.6e,
     ",dwidth,\
       (dbin+dnn-1),dmnsim.y[dbin+dnn-1]);
5532
5533 fprintf(DBG,"dmcsim.y[%d]=%12.6e\n",(dbin+dnn-
     1),dmcsim.y[dbin+dnn-1]);
5534 fprintf(DBG,"ddumnint=%12.6e, ddumcint=%12.6e, ddumposn=%12.6e,
     dnn=%d\n",\
5535
         ddumnint,ddumcint,ddumposn,dnn);
5536 fflush(DBG);
5537 }
5538
             break:
5539
           case 2:
5540
             if(dnslope!=0) dwidth=ddumnint/dnslope;
5541
             else{
5542
               if(dcslope!=0) dwidth=ddumcint/dcslope;
5543
               else dwidth=0;
5544
               }
5545
             dmnsim.y[dbin+dnn]+=ddumnint*0.5*dwidth;
5546
             dmcsim.y[dbin+dnn]+=ddumcint*0.5*dwidth;
5547
             ddoneflag=0;
5548 if(ddebugflag<DEBUG){
5549 fprintf(DBG,"Case 2. dwidth=%12.6e, dmnsim.y[%d] = %12.6e, ",
     dwidth,∖
5550
       (dbin+dnn),dmnsim.y[dbin+dnn]);
5551 fprintf(DBG, "dmcsim.y[%d] = %12.6e\n", (dbin+dnn), dmc-
     sim.y[dbin+dnn]);
5552 fprintf(DBG,"ddumnint=%12.6e, ddumcint=%12.6e, ddumposn=%12.6e,
     dnn=%d\n",\
5553
         ddumnint,ddumcint,ddumposn,dnn);
5554 fflush(DBG);
5555 }
5556
             break:
5557
           case 3:
5558
             dmnsim.y[dbin+dnn]+=ddumnint*0.5*PSTEP;
5559
             dmcsim.y[dbin+dnn]+=ddumcint*0.5*PSTEP;
5560
             ddoneflag=0;
5561 if(ddebugflag<DEBUG){
5562 fprintf(DBG,"Case 3. dmnsim.y[%d]=%12.6e, ", (dbin+dnn), dmn-
     sim.y[dbin+dnn]);
5563 fprintf(DBG,"dmcsim.y[%d] = %12.6e\n", (dbin+dnn), dmc-
     sim.y[dbin+dnn]);
5564 fprintf(DBG,"ddumnint=%12.6e, ddumcint=%12.6e, ddumposn=%12.6e,
     dnn=%d\n",\
5565
         ddumnint,ddumcint,ddumposn,dnn);
5566 fflush(DBG);
5567 }
5568
             break;
      /* the following for equipment that jumps from point to point */
5569
           case 4:
5570
             ddumnint-=dnslope*PSTEP;
             ddumcint-=dcslope*PSTEP;
5571
5572
             dmnsim.y[dbin+dnn]+=ddumnint;
5573
             dmcsim.y[dbin+dnn]+=ddumcint;
```

5574 ddumposn+=PSTEP; 5575 dnn++; 5576 if((dnn+dbin)==dn) ddoneflag=0; 5577 if(ddebugflag<DEBUG){ 5578 fprintf(DBG, "Case 4. dmnsim.y[%d]=%12.6e, dmcsim.y[%d] = %12.6e\n",\ (dbin+dnn-1), dmnsim.y[dbin+dnn-1], (dbin+dnn-1), 5579 dmcsim.y[dbin+dnn-1]); 5580 fprintf(DBG,"ddumnint=%12.6e, ddumcint=%12.6e, ddumposn=%12.6e, dnn=%d\n",\ 5581 ddumnint,ddumcint,ddumposn,dnn); 5582 fflush(DBG); 5583 } 5584 break; 5585 case 5: 5586 dwidth=ddend-ddumposn; ddumnint-=dnslope*dwidth; 5587 5588 ddumcint-=dcslope*dwidth; dmnsim.y[dbin+dnn]+=ddumnint; 5589 5590 dmcsim.y[dbin+dnn]+=ddumcint; 5591 ddumposn=ddend; 5592 dnn++; if((dnn+dbin)==dn) ddoneflag=0; 5593 5594 if(ddebugflag<DEBUG){ 5595 fprintf(DBG,"Case 5. dwidth=%12.6e, dmnsim.y[%d]=%12.6e, ",dwidth,\ 5596 (dbin+dnn-1),dmnsim.y[dbin+dnn-1]); 5597 fprintf(DBG,"dmcsim.y[%d]=%12.6e\n",(dbin+dnn-1),dmcsim.y[dbin+dnn-1]); 5598 fprintf(DBG,"ddumnint=%12.6e, ddumcint=%12.6e, ddumposn=%12.6e, dnn=%d\n",\ 5599 ddumnint,ddumcint,ddumposn,dnn); 5600 fflush(DBG); 5601 } 5602 break; 5603 case 6: 5604 ddoneflag=0; 5605 if(ddebugflag<DEBUG){ 5606 fprintf(DBG, "Case 6\n"); 5607 fflush(DBG); 5608 } 5609 break; 5610 case 7: dmnsim.y[dbin+dnn]+=ddumnint; 5611 dmcsim.y[dbin+dnn]+=ddumcint; 5612 5613 ddoneflag=0; 5614 if(ddebugflag<DEBUG){ 5615 fprintf(DBG,"Case 7. dmnsim.y[%d] = %12.6e, ", (dbin+dnn), dmnsim.y[dbin+dnn]); 5616 fprintf(DBG, "dmcsim.y[%d] = $12.6e^n$ ", (dbin+dnn), dmcsim.y[dbin+dnn]); 5617 fprintf(DBG,"ddumnint=%12.6e, ddumcint=%12.6e, ddumposn=%12.6e, dnn=%d\n",\ 5618 ddumnint,ddumcint,ddumposn,dnn);

```
5619 fflush(DBG);
5620 }
5621
             break;
      /* the following for emissions that provide only "spillover" */
5622
           case 8:
5623
              if(ddumposn==dposn){
5624
                dwidth=ddend-ddumposn;
5625
                ddumnint-=dnslope*dwidth;
5626
                ddumcint-=dcslope*dwidth;
5627
                ddumposn=ddend;
5628
                dnn++;
5629
                if((dnn+dbin)==dn) ddoneflag=0;
5630
                }
5631
             else{
5632
                if(ddend>(dposn+RESN)){
5633
                  printf(\
5634
              "Fix switch case in do_sim at 1b.\n");
5635
                  exit(1);
5636
                  }
                else{
5637
5638
                  ddumnint-=dnslope*PSTEP;
5639
                  ddumcint-=dcslope*PSTEP;
5640
                  ddumposn+=PSTEP;
5641
                  dnn++;
5642
                  if((dnn+dbin)==dn) ddoneflag=0;
5643
                  }
                }
5644
5645 if(ddebugflag<DEBUG){
5646 fprintf(DBG,"Case 8. dwidth=%12.6e, dbin=%d, ",dwidth,dbin);
5647 fprintf(DBG,"ddumnint=%12.6e, ddumcint=%12.6e, ddumposn=%12.6e,
     dnn=%d\n",\
5648
         ddumnint,ddumcint,ddumposn,dnn);
5649 fflush(DBG);
5650 }
5651
             break;
5652
           default:
5653
             printf("Go fix do_sim.\n");
5654
             exit(1);
5655
           } /* close switch-case */
5656
         } /* close fill bins above the transition position */
5657
       } /* close if frequency in range condition */
5658
              } /* close if non-zero frequency condition */
              } /* close simset-transitions loop */
5659
           } /* close if include condition */
5660
5661
           } /* close loop over simulations */
         } /* close loop over transitions */
5662
5663
       } /* close loop over molecules */
      /* start loop over previous simulation and write to file */
5664 sprintf(dnfile,"%s_simulations/Mol_native_pop",PREF);
5665 DNFILE=fopen(dnfile,"w");
5666 if(DNFILE==NULL){
5667
       printf("Error opening DNFILE for native pop. Exiting.\n");
5668
       exit(1);
```

```
5669
       }
5670 sprintf(dcfile,"%s_simulations/Mol_cascade_pop",PREF);
5671 DCFILE=fopen(dcfile,"w");
5672 if (DCFILE==NULL) {
5673
      printf("Error opening DCFILE for cascade pop. Exiting.\n");
5674
      exit(1);
5675
       }
5676 fprintf(DNFILE, "# File created by %s. \n", PROGRAM_NAME);
5677 fprintf(DNFILE,"# Contains simulated rovibronic emissions based on
     \n");
5678 fprintf(DNFILE,"# molecular populations specified by the user
     (only). n");
5679 fprintf(DNFILE,"# See file Mol_cascade_pop for emissions due to cas-
     cade.n";
5680 fprintf(DNFILE,"# See file %s_Sim_All for the whole simula-
     tion.\n#\n",PREF);
5681 fprintf(DCFILE,"# File created by %s. \n",PROGRAM_NAME);
5682 fprintf(DCFILE, "# Contains simulated rovibronic emissions based on
     \n");
5683 fprintf(DCFILE, "# cascade of molecular states (only).\n");
5684 fprintf(DCFILE,"# See file Mol_native_pop for emissions from molecu-
     lar.(n");
5685 fprintf(DCFILE, "# populations specified by the user.\n");
5686 fprintf(DCFILE, "# See file %s_Sim_All for the whole simula-
     tion.\n#\n",PREF);
5687 for(da=0;da<dn;da++){
5688
       dmnsim.x[da]=MINV+0.5*PSTEP+da*PSTEP;
5689
       dmcsim.x[da]=MINV+0.5*PSTEP+da*PSTEP;
5690
     fprintf(DNFILE,"%18.12e\t%18.12e\n",dmnsim.x[da],dmnsim.y[da]);
5691
     fprintf(DCFILE,"%18.12e\t%18.12e\n",dmcsim.x[da],dmcsim.y[da]);
5692
      }
5693 fclose(DNFILE);
5694 fclose(DCFILE);
     5695 for(da=0;da<NUMAT;da++){ /* loop over sets of atomic info */
5696 for(db=0;db<AT[da].n;db++){ /* loop through transitions in this set
       */
5697 if (AT[da].x[db]!=0) { /* if the current frequency is not equal to
       zero */
     /* see if line falls within requested simulation min/max */
5698 if(UNITTYPE==0) dposn=AT[da].x[db]/10;
5699 else dposn=1e8/AT[da].x[db];
5700 ddoflag=0;
5701 if(dposn<(MINV-RESN)) ddoflag=1;
5702 if(dposn>(MAXV+RESN)) ddoflag=1;
5703 if(ddoflag==0){
     /* find bin where line originates, also get native and cascade
       slopes */
       dbin=(int)(floor((dposn-MINV)/PSTEP));
5704
```

5705 dnslope=AT[da].p*AT[da].A[db]*AT[da].pop[db]/RESN;

```
/* increment through them and calculate the intensities for each
        bin -- integrate if SCAN and point if JUMP */
5706
       ddoneflag=1;
5707
       ddumposn=dposn;
5708
       ddumnint=AT[da].p*AT[da].A[db]*AT[da].pop[db];
5709
       dnn=0;
5710 if(ddebugflag<DEBUG){
5711 fprintf(DBG, "dbin=%d, dposn=%12.6e, dnslope=%12.6e,
     ddumnint=%12.6e\n",\
5712
         dbin,dposn,dnslope,ddumnint);
5713 fprintf(DBG,"AT[%d].p=%12.6e, AT[%d].A[%d]=%12.6e,
     AT[%d].pop[%d]=%12.6e\n",\
       da,AT[da].p,da,db,AT[da].A[db],da,db,AT[da].pop[db]);
5714
5715 fprintf(DBG,"RESN=%12.6e, MINV=%12.6e,
     PSTEP=%12.6e\n",RESN,MINV,PSTEP);
5716 fflush(DBG);
5717 }
5718
       if(dbin<0) ddoneflag=0;</pre>
       while(ddoneflag==1) { /* fill bins at/below dbin */
5719
5720
         dsw=0;
5721
         ddend=MINV+(dbin-dnn)*PSTEP;
5722
         if (dposn==ddumposn) dsw+=1;
5723
         if(ddend<(dposn-RESN)) dsw+=2;</pre>
5724
         if(SCANTYPE==1) dsw+=4;
         if((dbin-dnn)>(dn-1)) dsw=8;
5725
5726
         switch (dsw){
      /* the following for equipment that scans between "points" */
5727
           case 0:
5728
             dasim.y[dbin-dnn]+=\
5729
                (ddumnint-0.5*dnslope*PSTEP)*PSTEP;
5730
             ddumnint-=dnslope*PSTEP;
5731
             ddumposn-=PSTEP;
5732
             if(dnn==dbin) ddoneflag=0;
5733
             dnn++;
5734 if(ddebugflag<DEBUG){
5735 fprintf(DBG,"AT/BELOW Case 0. dasim.y[%d]=%12.6e, ",\
         (dbin-dnn+1),dasim.y[dbin-dnn+1]);
5736
5737 fprintf(DBG,"ddumnint=%12.6e, ddumposn=%12.6e, dnn=%d\n",\
         ddumnint, ddumposn, dnn);
5738
5739 fflush(DBG);
5740 }
5741
             break;
5742
           case 1:
5743
             dwidth=ddumposn-ddend;
5744
             dasim.y[dbin-dnn] += 
5745
                (ddumnint-0.5*dnslope*dwidth)*dwidth;
5746
             ddumnint-=dnslope*dwidth;
5747
             ddumposn=ddend;
5748
             if(dnn==dbin) ddoneflag=0;
5749
             dnn++;
5750 if(ddebugflag<DEBUG){
5751 fprintf(DBG,"AT/BELOW Case 1. dwidth=%12.6e, dasim.y[%d]=%12.6e,
     ",dwidth,\
       (dbin-dnn+1),dasim.y[dbin-dnn+1]);
5752
```

```
5753 fprintf(DBG,"ddumnint=%12.6e, ddumposn=%12.6e, dnn=%d\n",\
5754
         ddumnint,ddumposn,dnn);
5755 fflush(DBG);
5756 }
5757
             break;
5758
           case 2:
5759
             if(dnslope!=0) dwidth=ddumnint/dnslope;
5760
             else{
5761
               printf("dammit (below)\n");
5762
               exit(1);
5763
               }
5764
             dasim.y[dbin-dnn]+=ddumnint*0.5*dwidth;
5765
             ddoneflag=0;
5766 if(ddebugflag<DEBUG){
5767 fprintf(DBG,"AT/BELOW Case 2. dwidth=%12.6e, dasim.y[%d]=%12.6e,
     ",dwidth,\
5768
       (dbin-dnn), dasim.y[dbin-dnn]);
5769 fprintf(DBG,"ddumnint=%12.6e, ddumposn=%12.6e, dnn=%d\n",\
5770
         ddumnint,ddumposn,dnn);
5771 fflush(DBG);
5772 }
5773
             break;
5774
           case 3:
5775
             dasim.y[dbin-dnn]+=ddumnint*0.5*PSTEP;
5776
             ddoneflag=0;
5777 if(ddebugflag<DEBUG){
5778 fprintf(DBG,"AT/BELOW Case 3. dasim.y[%d]=%12.6e, ",\
         (dbin-dnn),dasim.y[dbin-dnn]);
5779
5780 fprintf(DBG,"ddumnint=%12.6e, ddumposn=%12.6e, dnn=%d\n",\
5781
         ddumnint,ddumposn,dnn);
5782 fflush(DBG);
5783 }
5784
             break:
      /* the following for equipment that jumps from point to point */
5785
           case 4:
5786
             ddumnint-=dnslope*PSTEP;
             dasim.y[dbin-dnn]+=ddumnint;
5787
             ddumposn-=PSTEP;
5788
5789
             if(dnn==dbin) ddoneflag=0;
5790
             dnn++;
5791 if(ddebugflag<DEBUG){
5792 fprintf(DBG,"AT/BELOW Case 4. dasim.y[%d]=%12.6e, ",\
5793
         (dbin-dnn+1),dmnsim.y[dbin-dnn+1]);
5794 fprintf(DBG,"ddumnint=%12.6e, ddumposn=%12.6e, dnn=%d\n",\
5795
         ddumnint,ddumposn,dnn);
5796 fflush(DBG);
5797 }
5798
             break;
5799
           case 5:
5800
             dwidth=ddumposn-ddend;
5801
             ddumnint-=dnslope*dwidth;
5802
             dasim.y[dbin-dnn]+=ddumnint;
5803
             ddumposn=ddend;
5804
             if(dnn==dbin) ddoneflag=0;
```

```
5805
             dnn++;
5806 if (ddebugflag<DEBUG) {
5807 fprintf(DBG,"AT/BELOW Case 5. dwidth=%12.6e, dasim.y[%d]=%12.6e,
     ",dwidth,∖
5808
       (dbin-dnn+1),dasim.y[dbin-dnn+1]);
5809 fprintf(DBG,"ddumnint=%12.6e, ddumposn=%12.6e, dnn=%d\n",\
5810
         ddumnint,ddumposn,dnn);
5811 fflush(DBG);
5812 }
5813
             break;
5814
           case 6:
5815
             ddoneflag=0;
5816 if(ddebugflag<DEBUG){
5817 fprintf(DBG,"AT/BELOW Case 6\n");
5818 fflush(DBG);
5819 }
5820
             break;
5821
           case 7:
5822
             dasim.y[dbin-dnn]+=ddumnint;
5823
             ddoneflag=0;
5824 if(ddebugflag<DEBUG){
5825 fprintf(DBG,"AT/BELOW Case 7. dasim.y[%d]=%12.6e, ",\
5826
         (dbin-dnn),dasim.y[dbin-dnn]);
5827 fprintf(DBG,"ddumnint=%12.6e, ddumposn=%12.6e, dnn=%d\n",\
5828
         ddumnint,ddumposn,dnn);
5829 fflush(DBG);
5830 }
5831
             break;
      /* the following for emissions that provide only "spillover" */
5832
           case 8:
5833
              if(ddumposn==dposn){
5834
                dwidth=ddumposn-ddend;
5835
                ddumnint-=dnslope*dwidth;
5836
                ddumcint-=dcslope*dwidth;
5837
                ddumposn=ddend;
5838
                if(dnn==dbin) ddoneflag=0;
5839
                dnn++;
5840
                }
5841
             else{
5842
                if(ddend<(dposn-RESN)){
5843
                  printf(\
5844
              "Fix switch case in do_sim at 1a.\n");
5845
                  exit(1);
                  }
5846
5847
                else{
5848
                  ddumnint-=dnslope*PSTEP;
                  ddumcint-=dcslope*PSTEP;
5849
5850
                  ddumposn-=PSTEP;
5851
                  if(dnn==dbin) ddoneflag=0;
5852
                  dnn++;
5853
                  }
                }
5854
5855 if(ddebugflag<DEBUG){
```

```
5856 fprintf(DBG,"AT/BELOW Case 8. dwidth=%12.6e, dbin=%d
     ",dwidth,dbin);
5857 fprintf(DBG,"ddumnint=%12.6e, ddumposn=%12.6e, dnn=%d\n",\
5858
         ddumnint,ddumposn,dnn);
5859 fflush(DBG);
5860 }
5861
             break;
5862
           default:
5863
             printf("Go fix do_sim.\n");
5864
             exit(1);
5865
           } /* close switch-case */
         } /* close while for bins below the transition position */
5866
5867
       ddoneflag=1;
5868
       ddumposn=dposn;
5869
       ddumnint=AT[da].p*AT[da].A[db]*AT[da].pop[db];
5870
       dnn=0;
5871
       if(dbin>dn-1) ddoneflag=0;
       while(ddoneflag==1){ /* fill bins at/above dbin */
5872
5873
         dsw=0;
5874
         ddend=MINV+(dbin+dnn+1)*PSTEP;
5875
         if(dposn==ddumposn) dsw+=1;
5876
         if(ddend>(dposn+RESN)) dsw+=2;
5877
         if(SCANTYPE==1) dsw+=4;
5878
         if((dbin+dnn)<0) dsw=8;</pre>
5879
         switch (dsw){
      /* the following for equipment that scans between "points" */
5880
           case 0:
5881
             dasim.y[dbin+dnn]+=\
5882
                (ddumnint-0.5*dnslope*PSTEP)*PSTEP;
5883
             ddumnint-=dnslope*PSTEP;
5884
             ddumposn+=PSTEP;
5885
             dnn++;
5886
             if((dnn+dbin)==dn) ddoneflag=0;
5887 if(ddebugflag<DEBUG){
5888 fprintf(DBG,"AT/ABOVE Case 0. dasim.y[%d]=%12.6e ",\
5889
         (dbin+dnn-1),dasim.y[dbin+dnn-1]);
5890 fprintf(DBG,"ddumnint=%12.6e, ddumposn=%12.6e, dnn=%d\n",\
5891
         ddumnint,ddumposn,dnn);
5892 fflush(DBG);
5893 }
5894
             break;
5895
           case 1:
5896
             dwidth=ddend-ddumposn;
5897
             dasim.y[dbin+dnn]+=
                (ddumnint-0.5*dnslope*dwidth)*dwidth;
5898
5899
             ddumnint-=dnslope*dwidth;
5900
             ddumposn=ddend;
5901
             dnn++;
5902
             if((dnn+dbin)==dn) ddoneflag=0;
5903 if(ddebugflag<DEBUG){
5904 fprintf(DBG,"AT/ABOVE Case 1. dwidth=%12.6e, dasim.y[%d]=%12.6e,
      ,dwidth,\
5905
       (dbin+dnn-1),dasim.y[dbin+dnn-1]);
5906 fprintf(DBG,"ddumnint=%12.6e, ddumposn=%12.6e, dnn=%d\n",\
```

```
5907
         ddumnint,ddumposn,dnn);
5908 fflush(DBG);
5909 }
5910
             break;
5911
           case 2:
5912
             if(dnslope!=0) dwidth=ddumnint/dnslope;
5913
             else{
5914
               printf("dammit...\n");
5915
               exit(1);
5916
               }
5917
             dasim.y[dbin+dnn]+=ddumnint*0.5*dwidth;
5918
             ddoneflag=0;
5919 if(ddebugflag<DEBUG){
5920 fprintf(DBG,"AT/ABOVE Case 2. dwidth=%12.6e, dasim.y[%d]=%12.6e,
     ",dwidth,\
       (dbin+dnn),dasim.y[dbin+dnn]);
5921
5922 fprintf(DBG,"ddumnint=%12.6e, dnslope=%12.6e, ddumposn=%12.6e,
     dnn=%d\n",\
5923
         ddumnint,dnslope,ddumposn,dnn);
5924 fflush(DBG);
5925 }
5926
             break;
5927
           case 3:
5928
             dasim.y[dbin+dnn]+=ddumnint*0.5*PSTEP;
5929
             ddoneflag=0;
5930 if(ddebugflag<DEBUG){
5931 fprintf(DBG, "AT/ABOVE Case 3. dasim.y[%d]=%12.6e, ",
         (dbin+dnn),dasim.y[dbin+dnn]);
5932
5933 fprintf(DBG,"ddumnint=%12.6e, ddumposn=%12.6e, dnn=%d\n",\
5934
         ddumnint,ddumposn,dnn);
5935 fflush(DBG);
5936 }
5937
             break:
      /* the following for equipment that jumps from point to point */
5938
           case 4:
5939
             ddumnint-=dnslope*PSTEP;
             dasim.y[dbin+dnn]+=ddumnint;
5940
5941
             ddumposn+=PSTEP;
5942
             dnn++:
             if((dnn+dbin)==dn) ddoneflag=0;
5943
5944 if(ddebugflag<DEBUG){
5945 fprintf(DBG,"AT/ABOVE Case 4. dasim.y[%d]=%12.6e ",\
5946
         (dbin+dnn-1),dasim.y[dbin+dnn-1]);
5947 fprintf(DBG,"ddumnint=%12.6e, ddumposn=%12.6e, dnn=%d\n",\
5948
         ddumnint,ddumposn,dnn);
5949 fflush(DBG);
5950 }
5951
             break;
5952
           case 5:
5953
             dwidth=ddend-ddumposn;
5954
             ddumnint-=dnslope*dwidth;
5955
             dasim.y[dbin+dnn]+=ddumnint;
5956
             ddumposn=ddend;
5957
             dnn++;
```

```
if((dnn+dbin)==dn) ddoneflag=0;
5958
5959 if(ddebugflag<DEBUG){
5960 fprintf(DBG,"AT/ABOVE Case 5. dwidth=%12.6e, dasim.y[%d]=%12.6e,
     ",dwidth,\
5961
       (dbin+dnn-1),dasim.y[dbin+dnn-1]);
5962 fprintf(DBG,"ddumnint=%12.6e, ddumposn=%12.6e, dnn=%d\n",\
         ddumnint,ddumposn,dnn);
5963
5964 fflush(DBG);
5965 }
5966
             break;
5967
           case 6:
5968
             ddoneflag=0;
5969 if(ddebugflag<DEBUG){
5970 fprintf(DBG,"AT/ABOVE Case 6\n");
5971 fflush(DBG);
5972 }
5973
             break:
5974
           case 7:
5975
             dasim.y[dbin+dnn]+=ddumnint;
5976
             ddoneflag=0;
5977 if(ddebugflag<DEBUG){
5978 fprintf(DBG,"AT/ABOVE Case 7. dasim.y[%d]=%12.6e, ",\
5979
         (dbin+dnn),dasim.y[dbin+dnn]);
5980 fprintf(DBG,"ddumnint=%12.6e, ddumposn=%12.6e, dnn=%d\n",\
5981
         ddumnint,ddumposn,dnn);
5982 fflush(DBG);
5983 }
5984
             break;
      /* the following for emissions that provide only "spillover" */
5985
           case 8:
              if(ddumposn==dposn){
5986
                dwidth=ddend-ddumposn;
5987
5988
                ddumnint-=dnslope*dwidth;
5989
               ddumposn=ddend;
5990
                dnn++;
5991
                if((dnn+dbin)==dn) ddoneflag=0;
                }
5992
5993
             else{
5994
                if(ddend>(dposn+RESN)){
5995
                  printf(\
5996
              "Fix switch case in do_sim at 1b.\n");
5997
                  exit(1);
5998
                  }
5999
                else{
6000
                  ddumnint-=dnslope*PSTEP;
6001
                  ddumposn+=PSTEP;
6002
                  dnn++;
6003
                  if((dnn+dbin)==dn) ddoneflag=0;
6004
                  }
                }
6005
6006 if (ddebugflag<DEBUG) {
6007 fprintf(DBG,"AT/ABOVE Case 8. dwidth=%12.6e dbin=%d",dwidth,dbin);
6008 fprintf(DBG,"ddumnint=%12.6e, ddumposn=%12.6e, dnn=%d\n",\
         ddumnint,ddumposn,dnn);
6009
```

```
6010 fflush(DBG);
6011 }
6012
             break;
6013
           default:
6014
             printf("Go fix do_sim.\n");
6015
             exit(1);
6016
           } /* close switch-case */
         } /* close fill bins above the transition position */
6017
6018
         } /* close if frequency in range condition */
6019
       } /* close if non-zero frequency condition */
6020
       } /* close atomic transitions loop */
       } /* close atomic sets loop */
6021
     /* start loop over previous simulation and write to file */
6022 sprintf(dnfile,"%s_simulations/Atomic_lines",PREF);
6023 DNFILE=fopen(dnfile,"w");
6024 if (DNFILE==NULL) {
6025
       printf("Error opening DNFILE for native pop. Exiting.\n");
6026
       exit(1);
6027
       }
6028 fprintf(DNFILE,"# File created by %s. \n", PROGRAM_NAME);
6029 fprintf(DNFILE,"# Contains simulated spectrum based on \n");
6030 fprintf(DNFILE,"# atomic information specified by the user
     (only). n");
6031 fprintf(DNFILE,"# See file Mol_cascade_pop for emissions due to cas-
     cade.\n");
6032 fprintf(DNFILE, "# See file Mol_native_pop for emissions from molecu-
     lar.(n");
6033 fprintf(DNFILE,"# populations specified by the user.\n");
6034 fprintf(DNFILE,"# See file %s_Sim_All for the whole simula-
     tion.\n#\n",PREF);
6035 for(da=0;da<dn;da++){
       dasim.x[da]=MINV+0.5*PSTEP+da*PSTEP;
6036
6037
       fprintf(DNFILE,"%18.12e\t%18.12e\n",dasim.x[da],dasim.y[da]);
6038
6039 fclose(DNFILE);
     /* add all simulations together -- find maximum intensity and ad-
        just */
6040 for(da=0;da<dn;da++){
6041
     dtotsim.y[da]=dmnsim.y[da]+dmcsim.y[da]+dasim.y[da]+dosim.y[da];
       if(dintmax<dtotsim.y[da]) dintmax=dtotsim.y[da];</pre>
6042
6043
       }
6044 for(da=0;da<dn;da++){
6045
       dtotsim.y[da] *=(MAXINT/dintmax);
6046
       }
     /* write total simulation to file */
     /* start loop over previous simulation and write to file */
6047 sprintf(dnfile,"%s_simulations/%s_Sim_All",PREF,PREF);
6048 DNFILE=fopen(dnfile,"w");
6049 if (DNFILE==NULL) {
6050
       printf("Error opening DNFILE for native pop. Exiting.\n");
6051
       exit(1);
6052
       }
6053 fprintf(DNFILE,"# File created by %s. \n",PROGRAM_NAME);
```

```
6054 fprintf(DNFILE,"# Contains total simulated spectrum based on \n");
6055 fprintf(DNFILE,"# all information specified by the user as well
     as\n");
6056 fprintf(DNFILE, "# diatomic emissions due to cascade (as possi-
     ble).\n");
6057 fprintf(DNFILE,"# See documentation for information about other
     files.\n");
6058 fprintf(DNFILE,"#\n");
6059 for(da=0;da<dn;da++){
6060
       dtotsim.x[da] =MINV+0.5*PSTEP+da*PSTEP;
       fprintf(DNFILE, "%18.12e\t %18.12e\n", dtotsim.x[da], dtot-
6061
    sim.y[da]);
6062
       }
6063 fclose(DNFILE);
6064 return;
6065 }
     /* This function determines the characteristics of the molecule as
       they relate to rotational levels and then calls another function
       to calculate energy levels and populations. */
6066 void manage_rotations(){
6067 int mra=0, mrb=0, mrstatetype=0;
6068 if (DEBUG>mrdebugflag) {
6069 fprintf(DBG,"\nTop of manage rotations\n\n");
6070 fflush(DBG);
6071 }
     /* loop over molecules */
6072 for(mra=0;mra<NUMMOL;mra++){
     /* loop over states */
6073
       for(mrb=0;mrb<MOL[mra].states;mrb++){</pre>
     /* determine type of state */
6074
         if(MOL[mra].s[mrb].Ca>-1){
6075
           if(CA[MOL[mra].s[mrb].Ca].L==0) mrstatetype=0;
           if(CA[MOL[mra].s[mrb].Ca].L>0) mrstatetype=2;
6076
           if(CA[MOL[mra].s[mrb].Ca].S==0) mrstatetype+=0;
6077
6078
           if(CA[MOL[mra].s[mrb].Ca].S>0) mrstatetype+=1;
6079
           }
6080
         if(MOL[mra].s[mrb].Cb>-1){
6081
           if(CB[MOL[mra].s[mrb].Cb].L==0) mrstatetype=0;
           if(CB[MOL[mra].s[mrb].Cb].L>0) mrstatetype=2;
6082
           if(CB[MOL[mra].s[mrb].Cb].S==0) mrstatetype+=0;
6083
6084
           if(CB[MOL[mra].s[mrb].Cb].S>0) mrstatetype+=1;
6085
           }
6086 if(DEBUG>mrdebugflag){
6087 fprintf(DBG,"mrstatetype is %d\n",mrstatetype);
6088 fflush(DBG);
6089 }
     /* call appropriate function */
         switch(mrstatetype){
6090
6091
           case 0:
6092 if(DEBUG>mrdebugflag){
```

```
6093 fprintf(DBG,"Singlet rotation function called (case 0).\n");
6094 fprintf(DBG,"Mol: %s; State:
     %s.\n",MOL[mra].Mol,MOL[mra].s[mrb].Name);
6095 fflush(DBG);
6096 }
6097
             singlet_JK(mra,mrb);
6098 if (DEBUG>mrdebugflag) {
6099 fprintf(DBG, "Returned from Singlet rotation function (case 0).\n");
6100 fflush(DBG);
6101 }
6102
             break;
6103
           case 1:
6104 if (DEBUG>mrdebugflag) {
6105 fprintf(DBG, "Multiplet L=0 rotation function called.\n");
6106 fprintf(DBG, "Mol: %s; State:
     %s.\n",MOL[mra].Mol,MOL[mra].s[mrb].Name);
6107 fflush(DBG);
6108 }
6109
             multiplet_zeroL_JK(mra,mrb);
6110
             break;
6111
           case 2:
6112 if (DEBUG>mrdebugflag) {
6113 fprintf(DBG,"Singlet rotation function called. (case 2)\n");
6114 fprintf(DBG, "Mol: MOL[%d].Mol %s, ",mra, MOL[mra].Mol);
6115 fprintf(DBG,"State: MOL[%d].s[%d].Name
     %s\n",mra,mrb,MOL[mra].s[mrb].Name);
6116 fflush(DBG);
6117 }
6118
             singlet_JK(mra,mrb);
6119 if (DEBUG>mrdebugflag) {
6120 fprintf(DBG,"Returned from Singlet rotation function (case 0).\n");
6121 fflush(DBG);
6122 }
6123
             break:
6124
           case 3:
6125 if(DEBUG>mrdebugflag){
6126 fprintf(DBG, "Multiplet L>0 rotation function called.\n");
6127 fprintf(DBG, "Mol: %s; State:
     %s.\n",MOL[mra].Mol,MOL[mra].s[mrb].Name);
6128 fflush(DBG);
6129 }
6130
             if(MOL[mra].s[mrb].Ca>-1){
6131 if(DEBUG>mrdebugflag){
6132 fprintf(DBG,"\tCase a \n");
6133 fflush(DBG);
6134 }
6135
               multiplet_nonzeroL_JK_a(mra,mrb);
6136
               }
             if(MOL[mra].s[mrb].Cb>-1){
6137
6138 if(DEBUG>mrdebugflag){
6139 fprintf(DBG,"\tCase b \n");
6140 fflush(DBG);
6141 }
6142
               multiplet_nonzeroL_JK_b(mra,mrb);
```

6143 } 6144 break; 6145 default: 6146 printf("Error in manage_rot switch case for mra=%d, mrb=%d. Exiting.\n",\ 6147 mra,mrb); 6148 exit(1);} /* close switch case */ 6149 6150 if(DEBUG>mrdebugflag){ 6151 fprintf(DBG,"\n switch-case just closed mra=%d, mrb=%d\n",mra,mrb); 6152 fflush(DBG); 6153 } } /* close loop over states */ 6154 6155 if(DEBUG>mrdebugflag){ 6156 fprintf(DBG,"\nstates loop closed mra=%d, mrb=%d\n",mra,mrb); 6157 fflush(DBG); 6158 } 6159 } /* close loop over molecules */ 6160 if (DEBUG>mrdebugflag) { 6161 fprintf(DBG,"\n about to return in manage_rotations\n"); 6162 fflush(DBG); 6163 } 6164 return; 6165 } /* This function calculates energy levels and rotational distributions (if needed) for all multiplet non-Sigma states (Hund's Case a) */ 6166 void multiplet_nonzeroL_JK_a(int mnaM, int mnaS){ 6167 int mnaa=0,mnab=0,mnaJck=1,mnaL=0,mnaV=0,mnaVnum=0,mnaOnum=0; 6168 int mnaCa=0,mnaJDnum=0,mnaD=1,mnaOOD=0,mnaOODend=0,mnaf=0; 6169 double mnaT=0,mnaDv=0,mnaBe=0,mnaAe=0,mnaJMAX=0,mnaJMAXc=0,mnaJMAXf=0; 6170 double mnaaA=0,mnaJcut=0,mnawe=0,mnawexe=0,mnaInt=0,mnaImax=0; 6171 double mnabeta=0,mnaFv=0,mnaTe=0,mnaDe=0,mnaBv=0,mnaTeVib=0; 6172 double mnaSpin=0,mnaJcurr=0,mnaOm=0,mnaBvDv=0; 6173 int mnaJnum=0,mnaJcountnum=0,mnaAlloc=0,mnaO=0,mnaO=0; 6174 char mnafnstr[1000]; 6175 FILE *MNAROT; 6176 if (DEBUG>mnadebugflag) { 6177 fprintf(DBG,"\n\nTop of multiplet_nonzeroL_JK_a. Molecule %s; State %s.\n\n",\ 6178 MOL[mnaM].Mol,MOL[mnaM].s[mnaS].Name); 6179 fflush(DBG); 6180 } /* Find lowest-level temperature designation */ 6181 if(MOL[mnaM].s[mnaS].T[0]!=0){ mnaT=MOL[mnaM].s[mnaS].T[0]; 6182 6183 if(DEBUG>mnadebugflag){

6184 fprintf(DBG, "Temperature defined at state level: %f",mnaT);

```
6185 fflush(DBG);
6186 }
       }
6187
6188 else{
6189
       if(MOL[mnaM].T!=0){
6190
         mnaT=MOL[mnaM].T;
6191 if (DEBUG>mnadebugflag) {
6192 fprintf(DBG,"Temperature defined at molecule level: %f",mnaT);
6193 fflush(DBG);
6194 }
6195
         }
6196
       else{
6197
         mnaT=TEMP;
6198 if(DEBUG>mnadebugflag){
6199 fprintf(DBG, "Temperature defined at global level: %f",mnaT);
6200 fflush(DBG);
6201 }
6202
         }
       }
6203
6204 if(mnaT==0){
6205
       fprintf(PAR, "WARNING!! temperature defined as zero for state ");
       fprintf(PAR, "%s of molecule %s.\n\n", \
6206
6207
         MOL[mnaM].s[mnaS].Name,MOL[mnaM].Mol);
6208
       }
      /* check for state identity sanity and complain if not same */
6209 if (MOL [mnaM].s[mnaS].Ca==-1){ /* if somehow this isn't Hund's Case
        a */
6210
       printf("Error in mutiplet_nonzeroL_JK_a. Any state this func-
     tion\n");
6211
       printf("calculates should be Hund's Case A.\nState ");
6212
       printf("%s of molecule %s doesn't think it's a Hund's Case a.\n",\
6213
         MOL[mnaM].s[mnaS].Name,MOL[mnaM].Mol);
6214
       printf("Fatal error. Exiting.\n");
6215
       exit(1);
6216
       }
6217
       mnaCa=MOL[mnaM].s[mnaS].Ca;
6218
       mnaBe=CA[mnaCa].Be;
6219
       mnaAe=CA[mnaCa].ae;
6220
       mnaTe=CA[mnaCa].Te;
6221
       mnawe=CA[mnaCa].we;
6222
       mnawexe=CA[mnaCa].wexe;
6223
       mnaL=CA[mnaCa].L;
6224
       mnaSpin=CA[mnaCa].S;
6225
       mnaOnum=CA[mnaCa].0;
       if(mnaOnum==0){mnaOnum=(int)(2*mnaSpin+1);}
6226
6227 if (DEBUG>mnadebugflag) {
6228 fprintf(DBG,"State is Case (a).\nBe=%f ae=%f ",mnaBe,mnaAe);
6229 fprintf(DBG,"Te=%f; we=%f; wexe=%f;\n",mnaTe,mnawe,mnawexe);
6230 fprintf(DBG,"mnaL=%d; mnaSpin=%f; mnaOnum=%d
     ",mnaL,mnaSpin,mnaOnum);
6231 fflush(DBG);
6232 }
6233
      /* Calculate some stuff that will be useful later */
```

```
483
```

```
distortion */
6235 if(DEBUG>mnadebugflag){
6236 fprintf(DBG,"mnaDe is %f;\n",mnaDe);
6237 fflush(DBG);
6238 }
6239 if(mnaL==0){ /* if this is a Sigma state, there's a problem */
6240 printf("How did multiplet_nonzeroL_JK_a get called if L==0? Exit-
     ing.\n");
6241
       exit(1);
6242
       }
     /* Print info to the parameter file */
6243 fprintf(PAR, "STATE %s is a ", MOL[mnaM].s[mnaS].Name);
6244 if(DEBUG>mnadebugflag){
6245 fprintf(DBG,"STATE %s is a ",MOL[mnaM].s[mnaS].Name);
6246 fflush(DBG);
6247 }
6248
      switch(mnaL){
6249
         case 1:
6250 if(DEBUG>mnadebugflag){
6251 fprintf(DBG,"Pi state -- Hund's Case (a)\n ");
6252 fflush(DBG);
6253 }
6254
           fprintf(PAR,"Pi state\n");
6255
           break;
6256
         case 2:
6257 if (DEBUG>mnadebugflag) {
6258 fprintf(DBG, "Delta state -- Hund's Case (a)\n ");
6259 fflush(DBG);
6260 }
6261
           fprintf(PAR,"Delta state\n");
6262
           break;
6263
         case 3:
6264 if (DEBUG>mnadebugflag) {
6265 fprintf(DBG,"Phi state -- Hund's Case (a)\n ");
6266 fflush(DBG);
6267 }
6268
           fprintf(PAR,"Phi state\n");
6269
           break;
6270
         default:
6271 fprintf(PAR,"state with Lambda>3 -- an exotic state\n");
6272 fprintf(PAR, "Interpret the results from this program with
     care.\n");
6273
           break;
6274
6275
     /* There may be multiple Omegas here */
6276 if (MOL [mnaM].s[mnaS].Dist!=-1){
     /* Estimate J max. This comes from taking the derivative of the pop-
       ulation distribution and setting it equal to zero. */
6277
       mnaBv=mnaBe-mnaAe/2;
6278
      mnaaA=mnaBv/(kB*mnaT);
6279
      mnaJMAX=1/sqrt(2*mnaaA) - 0.5;
6280
```

mnaJMAXc=ceil(mnaJMAX);

```
6281
       mnaJMAXf=floor(mnaJMAX);
6282
       mnaaA=mnaBv*mnaJMAXc*(mnaJMAXc+1)/(kB*mnaT);
6283
       mnaImax=(2*mnaJMAXc+1)*exp(-mnaaA);
6284
       mnaaA=mnaBv*mnaJMAXf*(mnaJMAXf+1)/(kB*mnaT);
6285
       mnaInt=(2*mnaJMAXf+1)*exp(-mnaaA);
6286 if(DEBUG>mnadebugflag){
6287 fprintf(DBG,"mnaBv=%f; mnaaA=%f; mnaJMAX=%f; mnaJMAXc=%f; mnaJ-
     MAXf=%f\n",\
6288
         mnaBv,mnaaA,mnaJMAX,mnaJMAXc,mnaJMAXf);
6289 fprintf(DBG, "mnaImax is %f; mnaInt is %f --- ", mnaImax, mnaInt);
6290 fflush(DBG);
6291 }
6292
       if((mnaImax)<(mnaInt)){mnaJMAX=mnaJMAXf;}</pre>
6293
       else{mnaJMAX=mnaJMAXc;}
6294 if(DEBUG>mnadebugflag){
6295 fprintf(DBG, "mnaJMAX is now %f\n ", mnaJMAX);
6296 fflush(DBG);
6297 }
     /* Find an upper limit for J/K corresponding to the user specifica-
        tion. To find out where this equation comes from, see the docu-
        mentation, particularly the documentation found in files or di-
        rectories with the word "trick" in the name. Note that this trick
        is only good down to a cutoff intensity of about 1/10,000 of the
        maximum value. */
6298
       mnaaA=mnaBv/(kB*mnaT);
       mnaJcut=sqrt((-2/mnaaA)/(JKm + JKb/(log(JKCUT)))) + 1/(2*mnaaA)
6299
     - 0.5;
6300
       mnaJcut=ceil(mnaJcut);
6301 if (DEBUG>mnadebugflag) {
6302 fprintf(DBG,"JKCUT is %f; mnaJcut is %f\n",JKCUT,mnaJcut);
6303 fflush(DBG);
6304 }
     /* check this number and chastise programmer if not good... Also, if
        not good, find a better number using a less elegant method. */
6305
       mnaaA=mnaBv*mnaJcut*(mnaJcut+1)/(kB*mnaT);
6306
       mnaInt=(2*mnaJcut+1)*exp(-mnaaA);
6307
       mnaaA=mnaBv*mnaJMAX*(mnaJMAX+1)/(kB*mnaT);
       mnaImax=(2*mnaJMAX+1)*exp(-mnaaA);
6308
6309 if (DEBUG>mnadebugflag) {
6310 fprintf(DBG,"mnaInt=%f; mnaImax=%f \n ",mnaInt,mnaImax);
6311 fflush(DBG);
6312 }
6313
       if((mnaInt/mnaImax)>JKCUT){
6314
         if(JKCUT>0){ /* put back to 0.0001 */
6315
           printf("Dammit... Go fix the J/K business... \n");
           printf("The calculated mnaJcut is %5.4f ",mnaJcut);
6316
6317
         mnaJck=1;
6318
6319
         while(mnaJck==1){
6320
           mnaJcut++:
6321
           mnaaA=mnaBv*mnaJcut*(mnaJcut+1)/(kB*mnaT);
6322
           mnaInt=(2*mnaJcut+1)*exp(-mnaaA);
6323
           if((mnaInt/mnaImax)<JKCUT){
6324
             mnaJck=0;
```

```
6325
             }
           } /*vvvvvvvv put back to 0.0001 vvvvvvv*/
6326
6327
         if(JKCUT>0) printf("The refined one is %5.4f \n",mnaJcut);
6328
         }
       }
6329
     /* Check for the distribution to be defined in a file. */
6330 if(MOL[mnaM].s[mnaS].Dist==-1){
6331
       mnaD=0;
6332
       mnaJDnum=(int)(CA[mnaCa].Jmax-CA[mnaCa].Jmin+1);
6333
       mnaJcut=(int)CA[mnaCa].Jmax;
6334 if(DEBUG>mnadebugflag){
6335 fprintf(DBG,"Distribution is by file.\n ");
6336 fflush(DBG);
6337 }
6338
       }
      /* Allocate memory for J/K array. Assign s/a and +/- flags. */
6339 mnaVnum=MOL[mnaM].s[mnaS].v[0].vnum; /* number of vib levels */
6340 mnaAlloc=mnaVnum*mnaOnum; /* allocate for vib levels and Omegas */
6341 MOL[mnaM].s[mnaS].nV=mnaVnum;
6342 MOL[mnaM].s[mnaS].nr=mnaAlloc;
6343 MOL[mnaM].s[mnaS].r=(rotset*)calloc(mnaAlloc, sizeof(rotset));
6344 MOL[mnaM].s[mnaS].rc=(rotset*)calloc((30*mnaOnum),
     sizeof(rotset));
6345 mnaJnum=mnaJcut+1; /* number of J's to consider */
6346 for(mna0=0;mna0<mna0num;mna0++){
6347
       for(mnaa=0;mnaa<mnaVnum;mnaa++){</pre>
         mnaO0=mnaO*mnaVnum+mnaa;
6348
6349
         MOL[mnaM].s[mnaS].r[mnaOO].j=mnaJnum;
6350
         MOL[mnaM].s[mnaS].r[mnaO0].J=\
6351
            (double*)calloc((mnaJnum),sizeof(double));
     /* There aren't any extra E's here. If someone ever wants to add in a
        splitting factor for the +/- wavefunctions, then double the space
        available (mnaJnum) and change the indexing and energy calcula-
        tion in the loops below.*/
6352
         MOL[mnaM].s[mnaS].r[mnaOO].EJ=
6353
            (double*)calloc((mnaJnum),sizeof(double));
         MOL[mnaM].s[mnaS].r[mnaO0].PJ=\
6354
6355
           (double*)calloc((mnaJnum),sizeof(double));
6356
         MOL[mnaM].s[mnaS].r[mnaO0].CJ=\
6357
           (double*)calloc((mnaJnum),sizeof(double));
6358
         }
       }
6359
     /* Loop through J/K values, calculating energies and populations
        (include nuclear effects if applicable). */
6360 for(mnaO=0;mnaO<mnaOnum;mnaO++){
6361
       if(CA[MOL[mnaM].s[mnaS].Ca].0==0){
6362
         mnaOm=mnaL-mnaSpin+mnaO;
6363
         }
6364
       else{
         mnaOm=CA[MOL[mnaM].s[mnaS].Ca].l0[mnaO];
6365
6366
         }
6367
       for(mnaa=0;mnaa<mnaVnum;mnaa++){</pre>
6368
         mna00=mna0*mnaVnum+mnaa;
6369
         mnaV=MOL[mnaM].s[mnaS].v[0].vlo+mnaa;
```

6370 mnaImax=0; 6371 mnaTeVib=mnaTe+(mnaV+0.5)*mnawe-(mnaV+0.5)*(mnaV+0.5)*mnawexe; 6372 if(DEBUG>mnadebugflag){ 6373 fprintf(DBG,"mnaVnum is %d; mnaTeVib=%f \n",mnaVnum,mnaTeVib); 6374 fflush(DBG); 6375 } 6376 mnaJcurr=mnaOm; 6377 if(mnawe!=0){ 6378 mnaBv=mnaBe-mnaAe*(mnaV+0.5); 6379 mnaDv=mnaDe+mnabeta*(mnaV+0.5); 6380 mnaBvDv=mnaBv/(2*mnaDv); MOL[mnaM].s[mnaS].r[mnaO0].Jdissoc=\ 6381 6382 floor((sqrt(1+4*mnaBvDv)-1)/2); } 6383 6384 else MOL[mnaM].s[mnaS].r[mnaOO].Jdissoc=RAND_MAX; 6385 if(MOL[mnaM].s[mnaS].r[mnaO0].Jdissoc>(mnaOm+mnaJnum)){ 6386 mnaJcountnum=mnaJnum; 6387 } 6388 else{ mnaJcountnum=(int)(MOL[mnaM].s[mnaS].r[mnaO0].Jdissoc-6389 mnaOm); 6390 fprintf(PAR,"\nWARNING!! MOLECULE DISSOCIATION (see below)\nAccording to"); 6391 fprintf(PAR,"the spectroscopic constants in the state file,\n state"); 6392 fprintf(PAR,"%s(%.1f) of Molecule %s in vibration level %d dissociates\n",\ 6393 MOL[mnaM].s[mnaS].Name,mnaOm,MOL[mnaM].Mol,mnaa); 6394 fprintf(PAR,"at rotational level J=%.1f,",MOL[mnaM].s[mnaS].r[mnaOO].Jdissoc); 6395 fprintf(PAR," which is significantly populated at temperature %.1f.\n",mnaT); 6396 fprintf(PAR,"Interpret results from this simulation carefullyn"); 6397 ł 6398 for(mnab=0;mnab<mnaJcountnum;mnab++){</pre> MOL[mnaM].s[mnaS].r[mna00].J[mnab]=mnaJcurr; 6399 6400 mnaFv=mnaBv*(mnaJcurr*(mnaJcurr+1) - mnaOm*mnaOm)-\ 6401 mnaDv*mnaJcurr*mnaJcurr*(mnaJcurr+1)*(mnaJcurr+1); MOL[mnaM].s[mnaS].r[mna00].EJ[mnab]=mnaFv; 6402 if(mnaD!=0){ 6403 6404 mnaInt=(2*mnaJcurr+1)*exp(-mnaFv/(kB*mnaT)); 6405 MOL[mnaM].s[mnaS].r[mnaOO].PJ[mnab]=mnaInt; } 6406 6407 if (DEBUG>mnadebugflag) { 6408 fprintf(DBG,"mnab is %d; mnaJcurr is %f; mnaFv=%f; mnaInt=%f\n",\ mnab,mnaJcurr,mnaFv,mnaInt); 6409 6410 fprintf(DBG,"MOL[%d].s[%d].r[%d].EJ[%d]=%f; MOL[%d].s[%d].r[%d].PJ[%d]=%f\n",\ 6411 mnaM,mnaS,mnaa,mnab,MOL[mnaM].s[mnaS].r[mna00].EJ[mnab],\ 6412 mnaM,mnaS,mnaa,mnab,MOL[mnaM].s[mnaS].r[mnaOO].PJ[mnab]); 6413 fflush(DBG); 6414 } 6415 mnaImax+=mnaInt;

```
6416 if (DEBUG>mnadebugflag) {
6417 fprintf(DBG,"\n mnaImax is %f\n\n",mnaImax);
6418 fflush(DBG);
6419 }
6420
         mnaJcurr++;
6421
         } /* close J number loop */
6422
       if(mnaD==0){ /* this means the dist is read from file */
6423
         mnaOOD=(mnaO*mnaVnum+mnaa)*mnaJDnum;
6424
         mnaOODend=(mnaO*mnaVnum+mnaa+1)*mnaJDnum;
6425
         mnaf=(int)(CA[mnaCa].Jmin-mnaOm);
6426
       for(mnab=mna00D;mnab<mna00Dend;mnab++){</pre>
6427
         MOL[mnaM].s[mnaS].r[mnaa].PJ[mnaf]=\
6428
           CA[mnaCa].Jpop[mnab];
6429
         mnaInt=MOL[mnaM].s[mnaS].r[mnaa].PJ[mnaf];
6430
         mnaImax+=mnaInt;
6431
         mnaf++;
6432
         }
         }
6433
6434
       mnaJcurr=mnaOm;
6435
       for(mnab=0;mnab<mnaJcountnum;mnab++){</pre>
6436
         MOL[mnaM].s[mnaS].r[mnaOO].EJ[mnab]+=mnaTeVib;
6437
         MOL[mnaM].s[mnaS].r[mna00].PJ[mnab]/=mnaImax;
6438 if(DEBUG>mnadebugflag){
6439 fprintf(DBG,"%d\t%f\t%f\t%f\n",mnab,mnaJcurr,\
6440
         MOL[mnaM].s[mnaS].r[mnaO0].EJ[mnab],\
         MOL[mnaM].s[mnaS].r[mnaOO].PJ[mnab]);
6441
6442 fflush(DBG);
6443 }
6444
         mnaJcurr++;
6445
         } /* close J number loop */
6446 if (DEBUG>mnadebugflag) {
6447 fprintf(DBG, "\n out of for loop \n");
6448 fflush(DBG);
6449 }
6450
         } /* close vibration number loop */
6451
       } /* close Omega number loop */
6452 sprintf(mnafnstr,"mkdir %s_molecules/%s",PREF,MOL[mnaM].Mol);
6453 system(mnafnstr);
6454 sprintf(mnafnstr, "%s_molecules/%s/%s_%s_rot.dat", PREF,
     MOL[mnaM].Mol,∖
         MOL[mnaM].Mol,MOL[mnaM].s[mnaS].Name);
6455
6456 MNAROT=fopen(mnafnstr,"w");
6457 if (MNAROT==NULL) {
       printf("Error opening output file (singlet_JK) %s. Exiting.\n",\
6458
6459
           mnafnstr);
6460
       exit(1);
       }
6461
6462 fprintf(MNAROT,"## File generated by program %s.\n",PROGRAM_NAME);
6463 fprintf(MNAROT, "## This file contains ");
6464 fprintf(MNAROT, "rotational state information about\n");
6465 fprintf(MNAROT,"## state %s of molecule %s.\n",\
         MOL[mnaM].s[mnaS].Name,MOL[mnaM].Mol);
6466
6467 fprintf(MNAROT,"##\tTo get the value of J add the Counter to the
     value\n");
```

```
6468 fprintf(MNAROT,"##\tof Omega for that set of columns,\n");
6469 fprintf(MNAROT,"## The columns are, in order:\n## Counter ");
6470 for(mnaO=0;mnaO<mnaOnum;mnaO++){
       if(CA[MOL[mnaM].s[mnaS].Ca].O==0){
6471
6472
         fprintf(MNAROT," OMEGA=%.1f<<",(mnaL-mnaSpin+mnaO));</pre>
6473
         }
6474
       else{
6475
         fprintf(MNAROT," OMEGA=%.1f<<",\</pre>
6476
             CA[MOL[mnaM].s[mnaS].Ca].10[mnaO]);
         }
6477
6478
       for(mnaa=0;mnaa<mnaVnum;mnaa++){</pre>
         mnaV=MOL[mnaM].s[mnaS].v[0].vlo+mnaa;
6479
6480
         fprintf(MNAROT, "F(v=%d) Pop(v=%d) ",mnaV,mnaV);
6481
6482
       fprintf(MNAROT,">> ");
       }
6483
6484 fprintf(MNAROT,"\n");
6485 mnaJcurr=mnaOm;
6486 for(mnab=0;mnab<mnaJcountnum;mnab++){
       fprintf(MNAROT,"%7d",mnab);
6487
6488
       for(mna0=0;mna0<mna0num;mna0++){</pre>
6489
         for(mnaa=0;mnaa<mnaVnum;mnaa++){</pre>
6490
           mna00=mna0*mnaVnum+mnaa;
6491
           fprintf(MNAROT,"\t%18.10e\t%18.10e",\
6492
             MOL[mnaM].s[mnaS].r[mnaOO].EJ[mnab], \
6493
             MOL[mnaM].s[mnaS].r[mna00].PJ[mnab]);
6494
           }
         }
6495
6496
       fprintf(MNAROT,"\n");
6497
       mnaJcurr++;
6498
       }
6499 fflush(MNAROT);
6500 fclose(MNAROT);
6501 if (DEBUG>mnadebugflag) {
6502 fprintf(DBG,"\n out of mnaa(Vnum) loop. mnaa=%d\n",mnaa);
6503 fflush(DBG);
6504 }
6505 return;
6506 }
     /* This function calculates energy levels and rotational distribu-
       tions (if needed) for all multiplet non-Sigma states (Hund's Case
       b) */
6507 void multiplet_nonzeroL_JK_b(int mnbM, int mnbS){
6508 int mnba=0,mnbb=0,mnbc=0,mnbKck=1,mnbL=0,mnbV=0,mnbVnum=0;
6509 int mnbCb=0,mnbJDnum=0,mnbJDmin=0,mnbD=1;
6510 double
    mnbT=0,mnbDv=0,mnbBe=0,mnbAe=0,mnbKMAX=0,mnbKMAXc=0,mnbKMAXf=0;
6511 double mnbaA=0,mnbKcut=0,mnbwe=0,mnbwexe=0,mnbInt=0,mnbImax=0;
6512 double mnbbeta=0,mnbFv=0,mnbTe=0,mnbDe=0,mnbBv=0,mnbTeVib=0;
6513 double mnbSpin=0,mnbJcurr=0,mnbBvDv=0,mnbKcountnum=0;
```

6514 int mnbKnum=0,mnbJnum=0,mnbcc=0;

```
6515 char mnbfnstr[1000];
6516 FILE *MNBROT;
6517 if (DEBUG>mnbdebugflag) {
6518 fprintf(DBG,"\n\nTop of multiplet_nonzeroL_JK_b. Molecule %s;            State
     %s.\n\n",\
6519
         MOL[mnbM].Mol,MOL[mnbM].s[mnbS].Name);
6520 fflush(DBG);
6521 }
      /* Find lowest-level temperature designation */
6522 if(MOL[mnbM].s[mnbS].T[0]!=0){
       mnbT=MOL[mnbM].s[mnbS].T[0];
6523
6524 if (DEBUG>mnbdebugflag) {
6525 fprintf(DBG, "Temperature defined at state level: %f", mnbT);
6526 fflush(DBG);
6527 }
6528
       }
6529 else{
6530
       if(MOL[mnbM].T!=0){
6531
         mnbT=MOL[mnbM].T;
6532 if(DEBUG>mnbdebugflag){
6533 fprintf(DBG,"Temperature defined at molecule level: %f",mnbT);
6534 fflush(DBG);
6535 }
6536
         }
6537
       else{
6538
         mnbT=TEMP;
6539 if(DEBUG>mnbdebugflag){
6540 fprintf(DBG,"Temperature defined at global level: %f",mnbT);
6541 fflush(DBG);
6542 }
6543
         }
       }
6544
6545 if(mnbT==0){
       fprintf(PAR, "WARNING!! temperature defined as zero for state ");
6546
       fprintf(PAR,"%s of molecule %s.\n\n",\
6547
6548
         MOL[mnbM].s[mnbS].Name,MOL[mnbM].Mol);
6549
       }
      /* check for state identity sanity and complain if not sane */
6550 if (MOL [mnbM].s[mnbS].Cb==-1) { /* if somehow this isn't Hund's Case
        b */
       printf("Error in mutiplet_nonzeroL_JK_b. Any state this func-
6551
     tion\n");
6552
       printf("calculates should be Hund's Case B.\nState ");
       printf("%s of molecule %s doesn't think it's a Hund's Case b.\n",\
6553
6554
         MOL[mnbM].s[mnbS].Name,MOL[mnbM].Mol);
6555
       printf("Fatal error. Exiting.\n");
6556
       exit(1);
6557
       }
6558
       mnbCb=MOL[mnbM].s[mnbS].Cb;
6559
       mnbBe=CB[mnbCb].Be;
6560
       mnbAe=CB[mnbCb].ae;
6561
       mnbTe=CB[mnbCb].Te;
```

```
6562
       mnbwe=CB[mnbCb].we;
6563
       mnbwexe=CB[mnbCb].wexe;
6564
       mnbL=CB[mnbCb].L;
6565
       mnbSpin=CB[mnbCb].S;
6566 if (DEBUG>mnbdebugflag) {
6567 fprintf(DBG,"State is Case (b).\nBe=%f ae=%f ",mnbBe,mnbAe);
6568 fprintf(DBG,"Te=%f; we=%f; wexe=%f; ",mnbTe,mnbwe,mnbwexe);
6569 fprintf(DBG, "mnbL=%d; mnbSpin=%f ",mnbL,mnbSpin);
6570 fflush(DBG);
6571 }
6572
     /* Calculate some stuff that will be useful later */
6573 if(mnbwe!=0) mnbDe=4*pow(mnbBe,3)/(mnbwe*mnbwe); /* Centrifugal
        distortion */
6574 if (DEBUG>mnbdebugflag) {
6575 fprintf(DBG,"mnbDe is %f;\n",mnbDe);
6576 fflush(DBG);
6577 }
6578 if (mnbL==0) { /* if this isn't a Sigma state, there's a problem */
6579 printf("How did multiplet_nonzeroL_JK_b get called if L==0? Exit-
     ing.(n");
6580
       exit(1);
6581
       }
     /* Print info to the parameter file */
6582 fprintf(PAR,"STATE %s is a ",MOL[mnbM].s[mnbS].Name);
6583 if(DEBUG>mnbdebugflag){
6584 fprintf(DBG,"STATE %s is a ",MOL[mnbM].s[mnbS].Name);
6585 fflush(DBG);
6586 }
6587
       switch(mnbL){
6588
         case 1:
6589 if(DEBUG>mnbdebugflag){
6590 fprintf(DBG, "Pi state -- Hund's Case (b)\n ");
6591 fflush(DBG);
6592 }
6593
           fprintf(PAR,"Pi state\n");
6594
           break:
6595
         case 2:
6596 if(DEBUG>mnbdebugflag){
6597 fprintf(DBG, "Delta state -- Hund's Case (b)\n ");
6598 fflush(DBG);
6599 }
6600
           fprintf(PAR,"Delta state\n");
6601
           break;
6602
         case 3:
6603 if (DEBUG>mnbdebugflag) {
6604 fprintf(DBG, "Phi state -- Hund's Case (b)\n ");
6605 fflush(DBG);
6606 }
6607
           fprintf(PAR,"Phi state\n");
6608
           break:
6609
         default:
6610 fprintf(PAR,"state with Lambda>3 -- an exotic state\n");
```

```
6611 fprintf(PAR,"Interpret the results from this program with
     care.\n");
6612
           break;
6613
         }
6614
6615 if(MOL[mnbM].s[mnbS].Dist!=-1){
     /* Estimate J/K max. This comes from taking the derivative of the
        population distribution and setting it equal to zero. */
6616
       mnbBv=mnbBe-mnbAe/2;
6617
       mnbaA=mnbBv/(kB*mnbT);
6618
       mnbKMAX=1/sqrt(2*mnbaA) - 0.5;
6619
       mnbKMAXc=ceil(mnbKMAX);
6620
       mnbKMAXf=floor(mnbKMAX);
6621
       mnbaA=mnbBv*mnbKMAXc*(mnbKMAXc+1)/(kB*mnbT);
6622
       mnbImax=(2*mnbKMAXc+1)*exp(-mnbaA);
6623
       mnbaA=mnbBv*mnbKMAXf*(mnbKMAXf+1)/(kB*mnbT);
6624
       mnbInt=(2*mnbKMAXf+1)*exp(-mnbaA);
6625 if(DEBUG>mnbdebugflag){
6626 fprintf(DBG,"mnbBv=%f; mnbaA=%f; mnbKMAX=%f; mnbKMAXc=%f; mnbJ-
     MAXf=%f\n",\
6627
         mnbBv,mnbaA,mnbKMAX,mnbKMAXc,mnbKMAXf);
6628 fprintf(DBG, "mnbImax is %f; mnbInt is %f --- ", mnbImax, mnbInt);
6629 fflush(DBG);
6630 }
6631
       if((mnbImax)<(mnbInt)){mnbKMAX=mnbKMAXf;}</pre>
6632
       else{mnbKMAX=mnbKMAXc;}
6633 if(DEBUG>mnbdebugflag){
6634 fprintf(DBG,"mnbKMAX is now %f\n ",mnbKMAX);
6635 fflush(DBG);
6636 }
     /* Find an upper limit for J/K corresponding to the user specifica-
        tion. To find out where this equation comes from, see the docu-
        mentation, particularly the documentation found in files or di-
        rectories with the word "trick" in the name. Note that this trick
        is only good down to a cutoff intensity of about 1/10,000 of the
        maximum value. */
6637
       mnbaA=mnbBv/(kB*mnbT);
       mnbKcut=sqrt((-2/mnbaA)/(JKm + JKb/(log(JKCUT)))) + 1/(2*mnbaA)
6638
     - 0.5;
6639
      mnbKcut=ceil(mnbKcut);
6640 if (DEBUG>mnbdebugflag) {
6641 fprintf(DBG,"JKCUT is %f; mnbKcut is %f\n",JKCUT,mnbKcut);
6642 fflush(DBG);
6643 }
      /* check this number and chastise programmer if not good... Also, if
        not good, find a better number using a less elegant method. */
6644
       mnbaA=mnbBv*mnbKcut*(mnbKcut+1)/(kB*mnbT);
6645
       mnbInt=(2*mnbKcut+1)*exp(-mnbaA);
6646
       mnbaA=mnbBv*mnbKMAX*(mnbKMAX+1)/(kB*mnbT);
6647
       mnbImax=(2*mnbKMAX+1)*exp(-mnbaA);
6648 if (DEBUG>mnbdebugflag) {
6649 fprintf(DBG,"mnbInt=%f; mnbImax=%f \n ",mnbInt,mnbImax);
6650 fflush(DBG);
6651 }
```

```
printf("Dammit... Go fix the J/K business... \n");
printf("The calculated mnbKcut is %5.4f ",mnbKcut);
```

6658 while(mnbKck==1){ 6659 mnbKcut++;

ł mnbKck=1:

```
6660
           mnbaA=mnbBv*mnbKcut*(mnbKcut+1)/(kB*mnbT);
```

if(JKCUT>0){ /* put back to 0.0001 */

mnbInt=(2*mnbKcut+1)*exp(-mnbaA); 6661 6662 if((mnbInt/mnbImax)<JKCUT){</pre>

if((mnbInt/mnbImax)>JKCUT){

- 6663 mnbKck=0;
- 6664 }
 - } /*vvvvvvvv put back to 0.0001 vvvvvvv*/
- if(JKCUT>0) printf("The refined one is %5.4f \n",mnbKcut); 6666
- 6667 } } 6668

6652

6653

6654

6655 6656

6657

- /* There are no Omegas here -- check for the distribution to be defined in a file. */
- 6669 if (MOL[mnbM].s[mnbS].Dist==-1){
- mnbD=0;6670
- mnbKcut=(int)CB[mnbCb].Kmax; 6671
- mnbJDmin=(int)CB[mnbCb].Kmin; 6672
- 6673 mnbJDnum=(int)CB[mnbCb].Jnum;
- 6674 if(DEBUG>mnbdebugflag){
- 6675 fprintf(DBG, "Distribution is by file.\n ");
- 6676 fflush(DBG);
- 6677 }
- 6678 }
 - /* Allocate memory for J/K array. Assign s/a and +/- flags. */
- 6679 mnbVnum=MOL[mnbM].s[mnbS].v[0].vnum; /* in other functions, where there might be multiple Omegas, this is vnum*numomega (so far as memory allocation goes) */
- 6680 MOL[mnbM].s[mnbS].nV=mnbVnum;
- 6681 MOL[mnbM].s[mnbS].nr=mnbVnum;
- 6682 MOL[mnbM].s[mnbS].r=(rotset*)calloc(mnbVnum,sizeof(rotset));
- 6683 MOL[mnbM].s[mnbS].rc=(rotset*)calloc(30,sizeof(rotset));
- 6684 mnbKnum=mnbKcut+1; /* number of K's to consider */
- 6685 mnbJnum=mnbKnum*((int)(2*(float)mnbSpin+1)); /* number of J's to consider -- this is the multiplcity times the number of K's considered */
- 6686 for(mnba=0;mnba<mnbVnum;mnba++){
- MOL[mnbM].s[mnbS].r[mnba].j=mnbJnum; 6687
- 6688 MOL[mnbM].s[mnbS].r[mnba].k=mnbKnum;
- 6689 MOL[mnbM].s[mnbS].r[mnba].J = (double*) calloc((mnbJnum), sizeof(double));
 - /* The extra E's are redundant here, but if someone ever wants to add in a splitting factor for the different J's relative to the nearest K, then the space is available */
- MOL[mnbM].s[mnbS].r[mnba].EJ = (double*) calloc((mnbJnum), 6690 sizeof(double));
- 6691 MOL[mnbM].s[mnbS].r[mnba].PJ = (double*) calloc((mnbJnum), sizeof(double));

```
MOL[mnbM].s[mnbS].r[mnba].CJ = (double*) calloc((mnbJnum),
6692
     sizeof(double));
6693
       }
      /* Loop through J/K values, calculating energies and populations
        (include nuclear effects if applicable). */
6694 for(mnba=0;mnba<mnbVnum;mnba++){
6695
       mnbV=MOL[mnbM].s[mnbS].v[0].vlo+mnba;
6696
       mnbImax=0;
6697
       mnbTeVib=mnbTe+(mnbV+0.5)*mnbwe-(mnbV+0.5)*(mnbV+0.5)*mnbwexe;
6698
       if(mnbwe!=0){
6699
         mnbBv=mnbBe-mnbAe*(mnbV+0.5);
         mnbDv=mnbDe+mnbbeta*(mnbV+0.5);
6700
6701
         mnbBvDv=mnbBv/(2*mnbDv);
6702
         MOL[mnbM].s[mnbS].r[mnba].Kdissoc=\
6703
           floor((sqrt(1+4*mnbBvDv)-1)/2);
6704
         }
6705
       else MOL[mnbM].s[mnbS].r[mnba].Kdissoc=RAND_MAX;
       if(MOL[mnbM].s[mnbS].r[mnba].Kdissoc>((double)mnbKnum)){
6706
6707
         mnbKcountnum=mnbKnum;
6708
         }
6709
       else{
         mnbKcountnum=(int)(MOL[mnbM].s[mnbS].r[mnba].Kdissoc);
6710
6711 fprintf(PAR,"\nWARNING!! MOLECULE DISSOCIATION (see be-
     low)\nAccording to");
6712 fprintf(PAR, "the spectroscopic constants in the state file, \n
     state");
6713 fprintf(PAR, "%s of Molecule %s in vibration level %d dissoci-
     ates\n",\
         MOL[mnbM].s[mnbS].Name,MOL[mnbM].Mol,mnba);
6714
6715 fprintf(PAR,"at rotational level
     K=%.1f,",MOL[mnbM].s[mnbS].r[mnba].Kdissoc);
6716 fprintf(PAR, "which is significantly populated at temperature
     %.1f.\n",mnbT);
6717 fprintf(PAR,"Interpret results from this simulation carefully\n");
6718
         ł
6719 if(DEBUG>mnbdebugflag){
6720 fprintf(DBG,"mnbVnum=%d; mnbTeVib=%f mnbBv=%12.6e,
     mnbDv=%12.6e\n",\
6721
         mnbVnum,mnbTeVib,mnbBv,mnbDv);
6722 fflush(DBG);
6723 }
6724
       for(mnbb=0;mnbb<mnbKcountnum;mnbb++){</pre>
         mnbFv=mnbBv*mnbb*(mnbb+1)-mnbDv*mnbb*mnbb*(mnbb+1)*(mnbb+1);
6725
6726
         for(mnbc=0;mnbc<((int)(2*mnbSpin+1));mnbc++){</pre>
6727
           mnbJcurr=(double)mnbb-mnbSpin+(double)mnbc;
6728
           mnbcc=mnbb*((int)(2*mnbSpin+1))+mnbc;
           if(mnbD!=0){
6729
6730
             mnbInt=(2*mnbJcurr+1)*exp(-mnbFv/(kB*mnbT));
6731
             MOL[mnbM].s[mnbS].r[mnba].PJ[mnbcc]=mnbInt;
6732
             }
6733
           MOL[mnbM].s[mnbS].r[mnba].EJ[mnbcc]=mnbFv;
           if((mnbb<mnbL)||(mnbJcurr<0)){</pre>
6734
6735
             MOL[mnbM].s[mnbS].r[mnba].EJ[mnbcc]=0;
6736
             MOL[mnbM].s[mnbS].r[mnba].PJ[mnbcc]=0;
```
6737 } 6738 if(DEBUG>mnbdebugflag){ 6739 fprintf(DBG,\ "mnbb is %d; mnbbeta=%12.6e, mnbJcurr is %f; mnbFv=%f; mn-6740 bInt=%f\n",\ 6741 mnbb,mnbbeta,mnbJcurr,mnbFv,mnbInt); 6742 fprintf(DBG,"MOL[%d].s[%d].r[%d].EJ[%d]=%f; MOL[%d].s[%d].r[%d].PJ[%d]=%f n'',6743 mnbM,mnbS,mnba,mnbcc,MOL[mnbM].s[mnbS].r[mnba].EJ[mnbcc],\ 6744 mnbM,mnbS,mnba,mnbcc,MOL[mnbM].s[mnbS].r[mnba].PJ[mnbcc]); 6745 fflush(DBG); 6746 } 6747 mnbImax+=mnbInt; 6748 if(DEBUG>mnbdebugflag){ 6749 fprintf(DBG,"\n mnbImax is %f\n\n",mnbImax); 6750 fflush(DBG); 6751 } 6752 } } 6753 6754 if(mnbD==0){ 6755 for(mnbb=(mnba*mnbJDnum);mnbb<((mnba+1)*mnbJDnum);mnbb++){</pre> /* the following is algebra for: K(2S+1) + J - [K-S] */ 6756 mnbcc=(int)(mnbSpin*(2*CB[mnbCb].K[mnbb]+1)+CB[mnbCb].J[mnbb]); 6757 MOL[mnbM].s[mnbS].r[mnba].PJ[mnbcc]=CB[mnbCb].Jpop[mnbb]; 6758 mnbInt=MOL[mnbM].s[mnbS].r[mnba].PJ[mnbcc]; 6759 mnbImax+=mnbInt; } 6760 } 6761 6762 for(mnbb=0;mnbb<mnbKcountnum;mnbb++){</pre> 6763 for(mnbc=0;mnbc<((int)(2*mnbSpin+1));mnbc++){</pre> mnbJcurr=(double)mnbb-mnbSpin+(double)mnbc; 6764 6765 mnbcc=mnbb*((int)(2*mnbSpin+1))+mnbc; 6766 MOL[mnbM].s[mnbS].r[mnba].EJ[mnbcc]+=mnbTeVib; MOL[mnbM].s[mnbS].r[mnba].PJ[mnbcc]/=mnbImax; 6767 6768 if((mnbb<mnbL)||(mnbJcurr<0)){</pre> 6769 MOL[mnbM].s[mnbS].r[mnba].EJ[mnbcc]=0; 6770 MOL[mnbM].s[mnbS].r[mnba].PJ[mnbcc]=0; 6771 } 6772 if (DEBUG>mnbdebugflag) { 6773 fprintf(DBG,"%d\t%f\t%d\t%f\t%f\n",mnbb,mnbJcurr,mnbcc,\ MOL[mnbM].s[mnbS].r[mnba].EJ[mnbcc], 6774 6775 MOL[mnbM].s[mnbS].r[mnba].PJ[mnbcc]); 6776 fflush(DBG); 6777 } 6778 } } 6779 6780 if (DEBUG>mnbdebugflag) { 6781 fprintf(DBG,"\n out of for loop \n"); 6782 fflush(DBG); 6783 } 6784 6785 sprintf(mnbfnstr,"mkdir %s_molecules/%s",PREF,MOL[mnbM].Mol); 6786 system(mnbfnstr);

```
6787 sprintf(mnbfnstr, "%s_molecules/%s/%s_%s_rot.dat", PREF,
     MOL[mnbM].Mol,\
         MOL[mnbM].Mol,MOL[mnbM].s[mnbS].Name);
6788
6789 MNBROT=fopen(mnbfnstr,"w");
6790 if (MNBROT==NULL) {
       printf("Error opening output file (singlet_JK) %s. Exiting.\n",\
6791
6792
           mnbfnstr);
6793
       exit(1);
6794
       }
6795 fprintf(MNBROT,"## File generated by program %s.\n",PROGRAM_NAME);
6796 fprintf(MNBROT, "## This file contains ");
6797 fprintf(MNBROT, "rotational state information about\n");
6798 fprintf(MNBROT,"## state %s of molecule %s.\n",\
6799
         MOL[mnbM].s[mnbS].Name,MOL[mnbM].Mol);
6800 fprintf(MNBROT,"## The columns are, in order:\n## K J");
6801 for(mnba=0;mnba<mnbVnum;mnba++){
6802
       mnbV=MOL[mnbM].s[mnbS].v[0].vlo+mnba;
       fprintf(MNBROT,"\tF(v=%d)\tPop(v=%d)",mnbV,mnbV);
6803
6804
       }
6805 fprintf(MNBROT,"\n");
6806 for(mnbb=0;mnbb<mnbKcountnum;mnbb++){
6807
       for(mnbc=0;mnbc<((int)(2*mnbSpin+1));mnbc++){</pre>
6808
         mnbJcurr=(double)mnbb-mnbSpin+(double)mnbc;
6809
         mnbcc=mnbb*((int)(2*mnbSpin+1))+mnbc;
         fprintf(MNBROT, "%d\t%f", mnbb, mnbJcurr);
6810
         for(mnba=0;mnba<mnbVnum;mnba++){</pre>
6811
6812
           fprintf(MNBROT,"\t%18.10e\t%18.10e",\
6813
             MOL[mnbM].s[mnbS].r[mnba].EJ[mnbcc],
6814
             MOL[mnbM].s[mnbS].r[mnba].PJ[mnbcc]);
6815
6816
         fprintf(MNBROT,"\n");
         }
6817
6818
       }
6819 fflush(MNBROT);
6820 fclose(MNBROT);
6821 if (DEBUG>mnbdebugflag) {
6822 fprintf(DBG,"\n out of mnba(Vnum) loop. mnba=%d\n",mnba);
6823 fflush(DBG);
6824 }
6825 return;
6826 }
     /****************** multiplet_zeroL_JK ***************/
     /* This function calculates energy levels and rotational distribu-
        tions (if needed) for all multiplet sigma states (always Hund's
        Case b) */
6827 void multiplet_zeroL_JK(int msM, int msS){
6828 int msa=0, msb=0, msc=0, msKck=1, msg=0, msL=0, msp=0, msV=0,
     msVnum=0, msItst=0;
6829 int msCb=0,msD=1,msKnum=0,msJnum=0,mscc=0,msJDmin=0,msJDnum=0;
6830 double msT=0, msDv=0, msBe=0, msAe=0, msKMAX=0, msKMAXc=0,
     msKMAXf=0, msaA=0, msKcut=0;
```

```
6831 double
     mswe=0,mswexe=0,msI=0,msInt=0,msImax=0,msbeta=0,msFv=0,msIs=0;
6832 double msIa=0, msTe=0, msDe=0, msBv=0, msTeVib=0, msSpin=0, msI-
     fac=0, msJcurr=0;
6833 double msBvDv=0;
6834 int msKcountnum=0;
6835 char msfnstr[1000];
6836 FILE *MSROT;
6837 if(DEBUG>msdebugflag){
6838 fprintf(DBG,"\n\nTop of multiplet_zeroL_JK. Molecule %s; State
     %s.\n\n",\
6839
         MOL[msM].Mol,MOL[msM].s[msS].Name);
6840 fflush(DBG);
6841 }
     /* Find lowest-level temperature designation */
6842 if(MOL[msM].s[msS].T[0]!=0){
       msT=MOL[msM].s[msS].T[0];
6843
6844 if(DEBUG>msdebugflag){
6845 fprintf(DBG,"Temperature defined at state level: %f",msT);
6846 fflush(DBG);
6847 }
       }
6848
6849 else{
6850
       if(MOL[msM].T!=0){
6851
         msT=MOL[msM].T;
6852 if (DEBUG>msdebugflag) {
6853 fprintf(DBG,"Temperature defined at molecule level: %f",msT);
6854 fflush(DBG);
6855 }
6856
         }
6857
       else{
6858
         msT=TEMP;
6859 if(DEBUG>msdebugflag){
6860 fprintf(DBG, "Temperature defined at global level: %f",msT);
6861 fflush(DBG);
6862 }
6863
         }
       }
6864
6865 if(msT==0){
6866
       fprintf(PAR, "WARNING!! temperature defined as zero for state ");
       fprintf(PAR,"%s of molecule %s.\n\n",\
6867
6868
         MOL[msM].s[msS].Name,MOL[msM].Mol);
6869
       }
     /* check for state identity sanity and complain if not sane */
6870 if (MOL[msM].s[msS].Cb==-1) { /* if somehow this isn't Hund's Case b
        */
       printf("Error in mutiplet_zeroL_JK. Any state this function\n");
6871
6872
       printf("calculates should be Hund's Case B.\nState ");
       printf("%s of molecule %s doesn't think it's a Hund's Case b.\n",\
6873
6874
         MOL[msM].s[msS].Name,MOL[msM].Mol);
6875
       printf("Fatal error. Exiting.\n");
```

```
6876 exit(1);
```

```
6877
       }
6878
       msCb=MOL[msM].s[msS].Cb;
6879
       msBe=CB[msCb].Be;
6880
       msAe=CB[msCb].ae;
6881
       msTe=CB[msCb].Te;
6882
       mswe=CB[msCb].we;
6883
       mswexe=CB[msCb].wexe;
6884
       msg=CB[msCb].g;
6885
       msI=CB[msCb].I;
6886
       msL=CB[msCb].L;
6887
       msp=CB[msCb].p;
6888
       msSpin=CB[msCb].S;
6889 if(DEBUG>msdebugflag){
6890 fprintf(DBG,"State is Case (b).\nBe=%f ae=%f ",msBe,msAe);
6891 fprintf(DBG,"Te=%f; we=%f; wexe=%f;
     \nmsg=%d",msTe,mswe,mswexe,msg);
6892 fprintf(DBG," msI=%f; msL=%d; msp=%d; msSpin=%f
     ",msI,msL,msp,msSpin);
6893 fflush(DBG);
6894 }
6895
      /* Calculate some stuff that will be useful later */
6896 if(mswe!=0) msDe=4*pow(msBe,3)/(mswe*mswe); /* Centrifugal dis-
        tortion */
6897 if (DEBUG>msdebugflag) {
6898 fprintf(DBG,"msDe is %f;\n",msDe);
6899 fflush(DBG);
6900 }
6901 if(msg!=0){
6902
       msIs=1;
       msIa=msI/(msI+1);
6903
6904 if (DEBUG>msdebugflag) {
6905 fprintf(DBG,"msIs=%f; msIa=%f; \n",msIs,msIa);
6906 fflush(DBG);
6907 }
6908
       }
6909 if(msL!=0){    /* if this isn't a Sigma state, there's a problem */
       printf("How did multiplet_zeroL_JK get called if L!=0? Exit-
6910
     ing.(n");
6911
       exit(1);
6912
       }
6913 fprintf(PAR,"STATE %s is a Sigma",MOL[msM].s[msS].Name);
6914 if (DEBUG>msdebugflag) {
6915 fprintf(DBG,"STATE %s is a Sigma",MOL[msM].s[msS].Name);
6916 fflush(DBG);
6917 }
6918 if (msg!=0) { /* if this is a homonuclear molecule */
6919
       if (msp==+1) { /* and this is a Sigma+ state */
         fprintf(PAR,"+ ");
6920
6921 if(DEBUG>msdebugflag){
6922 fprintf(DBG,"+");
6923 fflush(DBG);
6924 }
6925
         if (msg==+1) { /* and the state is gerade */
```

```
fprintf(PAR, "gerade state and even K's are (+), ");
6926
6927 if (DEBUG>msdebugflag) {
6928 fprintf(DBG, "gerade state and even K's are (+), ");
6929 fflush(DBG);
6930 }
6931
           MOL[msM].s[msS].pmsymm=+1;
6932
           if(fmod(msI,1.0)==0){
6933
             MOL[msM].s[msS].Isymm=+1;
6934
              fprintf(PAR,"s (boson) \n");
6935 if(DEBUG>msdebugflag){
6936 fprintf(DBG,"s (boson)\n");
6937 fflush(DBG);
6938 }
6939
                }
6940
           if(fmod(msI,1.0)==0.5){
6941
             MOL[msM].s[msS].Isymm=-1;
             fprintf(PAR,"a (fermion) \n");
6942
6943 if(DEBUG>msdebugflag){
6944 fprintf(DBG,"a (fermion)\n");
6945 fflush(DBG);
6946 }
6947
              }
           }
6948
6949
         else{ /* and the state is ungerade */
6950
         fprintf(PAR, "ungerade state and even K's are (+), ");
6951 if(DEBUG>msdebugflag){
6952 fprintf(DBG, "ungerade state and even K's are (+), ");
6953 fflush(DBG);
6954 }
6955
           MOL[msM].s[msS].pmsymm=+1;
           if(fmod(msI,1.0)==0){
6956
             MOL[msM].s[msS].Isymm=-1;
6957
             fprintf(PAR,"a (boson) \n");
6958
6959 if(DEBUG>msdebugflag){
6960 fprintf(DBG, "a (boson) \n");
6961 fflush(DBG);
6962 }
6963
6964
           if(fmod(msI,1.0)==0.5){
             MOL[msM].s[msS].Isymm=+1;
6965
             fprintf(PAR,"s (fermion) \n");
6966
6967 if (DEBUG>msdebugflag) {
6968 fprintf(DBG, "s (fermion)\n");
6969 fflush(DBG);
6970 }
6971
              }
           }
6972
         }
6973
6974
       else{ /* and this is a Sigma- state */
         fprintf(PAR, "- ");
6975
6976 if (DEBUG>msdebugflag) {
6977 fprintf(DBG,"-");
6978 fflush(DBG);
6979 }
```

```
if (msg==+1) { /* and the state is gerade */
6980
6981
         fprintf(PAR, "gerade state and even K's are (-), ");
6982 if (DEBUG>msdebugflag) {
6983 fprintf(DBG, "gerade state and even K's are (-), ");
6984 fflush(DBG);
6985 }
           MOL[msM].s[msS].pmsymm=-1;
6986
6987
           if(fmod(msI,1.0)==0){
6988
             MOL[msM].s[msS].Isymm=-1;
6989
              fprintf(PAR,"a (boson) \n");
6990 if (DEBUG>msdebugflag) {
6991 fprintf(DBG,"a (boson) \n");
6992 fflush(DBG);
6993 }
6994
              }
6995
           if(fmod(msI,1.0)==0.5){
6996
             MOL[msM].s[msS].Isymm=+1;
6997
             fprintf(PAR,"s (fermion) \n");
6998 if(DEBUG>msdebugflag){
6999 fprintf(DBG,"s (fermion)\n");
7000 fflush(DBG);
7001 }
7002
              }
           }
7003
7004
         else{ /* and the state is ungerade */
         fprintf(PAR, "ungerade state and even K's are (-), ");
7005
7006 if(DEBUG>msdebugflag){
7007 fprintf(DBG, "ungerade state and even K's are (-), ");
7008 fflush(DBG);
7009 }
7010
           MOL[msM].s[msS].pmsymm=-1;
7011
           if(fmod(msI,1.0)==0){
7012
             MOL[msM].s[msS].Isymm=+1;
7013
             fprintf(PAR,"s (boson) \n");
7014 if (DEBUG>msdebugflag) {
7015 fprintf(DBG,"s (boson)\n");
7016 fflush(DBG);
7017 }
7018
              }
7019
           if(fmod(msI,1.0)==0.5){
7020
             MOL[msM].s[msS].Isymm=-1;
7021
              fprintf(PAR,"a (fermion) \n");
7022 if(DEBUG>msdebugflag){
7023 fprintf(DBG,"a (fermion)\n");
7024 fflush(DBG);
7025 }
7026
              }
           }
7027
         }
7028
7029
       }
7030 else{ /* and this a heteronuclear molecule */
7031
       if(msp==+1){
7032
         fprintf(PAR, "+ state and even K's are (+) \n");
7033
         MOL[msM].s[msS].pmsymm=+1; /* and a Sigma+ state */
```

```
7034 if (DEBUG>msdebugflag) {
7035 fprintf(DBG,"+ state and even K's are (+)\n");
7036 fflush(DBG);
7037 }
7038
         }
7039
       else{
7040
         fprintf(PAR, "- state and even K's are (-)\n");
         MOL[msM].s[msS].pmsymm=-1; /* and a Sigma- state */
7041
7042 if (DEBUG>msdebugflag) {
7043 fprintf(DBG, "- state and even K's are (-)\n");
7044 fflush(DBG);
7045 }
7046
         }
       }
7047
7048 if (MOL[msM].s[msS].Dist!=-1) {
      /* Estimate J/K max. This comes from taking the derivative of the
        population distribution and setting it equal to zero. */
7049
       msBv=msBe-msAe/2;
7050
       msaA=msBv/(kB*msT);
7051
       msKMAX=1/sqrt(2*msaA) - 0.5;
7052
       msKMAXc=ceil(msKMAX);
7053
       msKMAXf=floor(msKMAX);
7054
       msaA=msBv*msKMAXc*(msKMAXc+1)/(kB*msT);
7055
       msImax=(2*msKMAXc+1)*exp(-msaA);
7056
       msaA=msBv*msKMAXf*(msKMAXf+1)/(kB*msT);
7057
       msInt=(2*msKMAXf+1)*exp(-msaA);
7058 if(DEBUG>msdebugflag){
7059 fprintf(DBG,"msBv=%f; msaA=%f; msKMAX=%f; msKMAXc=%f; msJ-
     MAXf=%f\n",\
7060
         msBv,msaA,msKMAX,msKMAXc,msKMAXf);
7061 fprintf(DBG,"msImax is %f; msInt is %f --- ",msImax,msInt);
7062 fflush(DBG);
7063 }
7064
       if((msImax)<(msInt)){msKMAX=msKMAXf;}</pre>
7065
       else{msKMAX=msKMAXc;}
7066 if(DEBUG>msdebugflag){
7067 fprintf(DBG, "msKMAX is now %f\n ", msKMAX);
7068 fflush(DBG);
7069 }
      /* Find an upper limit for J/K corresponding to the user specifica-
        tion. To find out where this equation comes from, see the docu-
        mentation, particularly the documentation found in files or di-
        rectories with the word "trick" in the name. Note that this trick
        is only good down to a cutoff intensity of about 1/10,000 of the
        maximum value. */
7070
       msaA=msBv/(kB*msT);
       msKcut=sqrt((-2/msaA)/(JKm + JKb/(log(JKCUT)))) + 1/(2*msaA) -
7071
     0.5;
7072
       msKcut=ceil(msKcut);
7073 if(DEBUG>msdebugflag){
7074 fprintf(DBG,"JKCUT is %f; msKcut is %f\n",JKCUT,msKcut);
7075 fflush(DBG);
7076 }
```

```
/* check this number and chastise programmer if not good... Also, if
        not good, find a better number using a less elegant method. */
7077
       msaA=msBv*msKcut*(msKcut+1)/(kB*msT);
7078
       msInt=(2*msKcut+1)*exp(-msaA);
7079
       msaA=msBv*msKMAX*(msKMAX+1)/(kB*msT);
7080
       msImax=(2*msKMAX+1)*exp(-msaA);
7081 if (DEBUG>msdebugflag) {
7082 fprintf(DBG,"msInt=%f; msImax=%f \n ",msInt,msImax);
7083 fflush(DBG);
7084 }
7085
       if((msInt/msImax)>JKCUT){
         if(JKCUT>0){ /* put back to 0.0001 */
7086
7087
           printf("Dammit... Go fix the J/K business... \n");
7088
           printf("The calculated msKcut is %5.4f ",msKcut);
7089
7090
         msKck=1;
7091
         while(msKck==1){
7092
           msKcut++;
7093
           msaA=msBv*msKcut*(msKcut+1)/(kB*msT);
7094
           msInt=(2*msKcut+1)*exp(-msaA);
7095
           if((msInt/msImax)<JKCUT){
7096
             msKck=0;
7097
             }
7098
           } /*vvvvvvvv put back to 0.0001 vvvvvvv*/
7099
         if(JKCUT>0) printf("The refined one is %5.4f \n",msKcut);
7100
         }
7101
       } /* close if distribution not in a file condition */
      /* There can't be more than one omega here -- check for the distribu-
        tion to be defined in a file. If it is, go back. */
7102 if (MOL[msM].s[msS].Dist==-1){
7103
       msD=0;
7104
       msKcut=(int)CB[msCb].Kmax;
7105
       msJDmin=(int)CB[msCb].Kmin;
7106
       msJDnum=(int)CB[msCb].Jnum;
7107 if(DEBUG>msdebugflag){
7108 fprintf(DBG, "Distribution is by file.\n ");
7109 fflush(DBG);
7110 }
7111
       }
      /* Allocate memory for J/K array. Assign s/a and +/- flags. */
7112 msVnum=MOL[msM].s[msS].v[0].vnum; /* in other functions, where
        there might be multiple Omegas, this is vnum*numomega (so far as
        memory allocation goes) */
7113 MOL[msM].s[msS].nV=msVnum;
7114 MOL[msM].s[msS].nr=msVnum;
7115 MOL[msM].s[msS].r=(rotset*)calloc(msVnum,sizeof(rotset));
7116 MOL[msM].s[msS].rc=(rotset*)calloc(30,sizeof(rotset));
7117 msKnum=msKcut+1; /* number of K's to consider */
7118 msJnum=msKnum*((int)(2*(float)msSpin+1)); /* number of J's to con-
        sider -- this is the multiplcity times the number of K's consid-
        ered */
7119 for(msa=0;msa<msVnum;msa++){
       MOL[msM].s[msS].r[msa].j=msJnum;
7120
```

7121 MOL[msM].s[msS].r[msa].k=msKnum;

```
7122
       MOL[msM].s[msS].r[msa].J = (double*) calloc((msJnum),
     sizeof(double));
     /* The extra E's are redundant here, but if someone ever wants to
        add in a splitting factor for the different J's relative to the
        nearest K, then the space is available */
7123
       MOL[msM].s[msS].r[msa].EJ = (double*) calloc((msJnum),
     sizeof(double));
       MOL[msM].s[msS].r[msa].PJ = (double*) calloc((msJnum),
7124
     sizeof(double));
       MOL[msM].s[msS].r[msa].CJ = (double*) calloc((msJnum),
7125
     sizeof(double));
7126
       }
      /* Loop through J/K values, calculating energies and populations
        (include nuclear effects if applicable). */
7127 for(msa=0;msa<msVnum;msa++){
7128
       msV=MOL[msM].s[msS].v[0].vlo+msa;
7129
       msImax=0:
7130
       msTeVib=msTe+(msV+0.5)*mswe-(msV+0.5)*(msV+0.5)*mswexe;
7131 if (DEBUG>msdebugflag) {
7132 fprintf(DBG,"msVnum is %d; msTeVib=%f \n",msVnum,msTeVib);
7133 fflush(DBG);
7134 }
7135
       if(mswe!=0){
7136
         msBv=msBe-msAe*(msV+0.5);
7137
         msDv=msDe+msbeta*(msV+0.5);
7138
         msBvDv=msBv/(2*msDv);
         MOL[msM].s[msS].r[msa].Kdissoc=floor((sqrt(1+4*msBvDv)-
7139
     1)/2);
7140
         }
7141
       else MOL[msM].s[msS].r[msa].Kdissoc=RAND_MAX;
7142 if(DEBUG>msdebugflag){
7143 fprintf(DBG,"msBv=%12.6e, msDv=%12.6e,
     msBvDv=%12.6e\n",msBv,msDv,msBvDv);
7144 fprintf(DBG,"msKcountnum=%d, msKnum=%d\n",msKcountnum,msKnum);
7145 fprintf(DBG, "MOL[%d].s[%d].r[%d].Kdissoc=%.1f\n",msM,msS,msa,\
7146
         MOL[msM].s[msS].r[msa].Kdissoc);
7147 fflush(DBG);
7148 }
7149
       if(MOL[msM].s[msS].r[msa].Kdissoc>((double)msKnum)){
7150
         msKcountnum=msKnum;
7151
         }
7152
       else{
         msKcountnum=(int)(MOL[msM].s[msS].r[msa].Kdissoc);
7153
7154 fprintf(PAR,"\nWARNING!! MOLECULE DISSOCIATION (see be-
     low)\nAccording to");
7155 fprintf(PAR,"the spectroscopic constants in the state file, \n
     state");
7156 fprintf(PAR, "%s of Molecule %s in vibration level %d dissoci-
     ates\n",\
         MOL[msM].s[msS].Name,MOL[msM].Mol,msa);
7157
7158 fprintf(PAR, "at rotational level
     K=%.1f,",MOL[msM].s[msS].r[msa].Kdissoc);
7159 fprintf(PAR," which is significantly populated at temperature
     \%.1f.\n",msT);
```

```
7160 fprintf(PAR,"Interpret results from this simulation carefullyn");
7161
         }
7162 if (DEBUG>msdebugflag) {
7163 fprintf(DBG,"msVnum=%d; msTeVib=%f msBv=%12.6e, msDv=%12.6e\n",\
         msVnum,msTeVib,msBv,msDv);
7164
7165 fprintf(DBG,"msKcountnum=%d, msKnum=%d\n",msKcountnum,msKnum);
7166 fprintf(DBG,"MOL[%d].s[%d].r[%d].Kdissoc=%.1f\n",msM,msS,msa,\
         MOL[msM].s[msS].r[msa].Kdissoc);
7167
7168 fflush(DBG);
7169 }
7170
       for(msb=0;msb<msKcountnum;msb++){</pre>
         msFv=msBv*msb*(msb+1)-msDv*msb*msb*(msb+1)*(msb+1);
7171
7172
         msIfac=1:
         if((msg!=0)&&(msD!=0)){
7173
           msItst=msb%2 + MOL[msM].s[msS].Isymm;
7174
7175 if (DEBUG>msdebugflag) {
7176 fprintf(DBG, "msg is %d\n", msg);
7177 fprintf(DBG,"msItst is %d\n",msItst);
7178 fflush(DBG);
7179 }
           switch(msItst){ /* see "switch_case.txt" in Tricks */
7180
7181
              case 0:
7182
                msIfac=msIs;
7183 if(DEBUG>msdebugflag){
7184 fprintf(DBG,"msIfac=%f",msIfac);
7185 fflush(DBG);
7186 }
7187
                break;
7188
             case 1:
7189
                msIfac=msIs;
7190 if (DEBUG>msdebugflag) {
7191 fprintf(DBG,"msIfac=%f",msIfac);
7192 fflush(DBG);
7193 }
7194
                break;
7195
             case -1:
7196
               msIfac=msIa;
7197 if (DEBUG>msdebugflag) {
7198 fprintf(DBG,"msIfac=%f",msIfac);
7199 fflush(DBG);
7200 }
7201
                break;
7202
             case 2:
7203
                msIfac=msIa;
7204 if (DEBUG>msdebugflag) {
7205 fprintf(DBG,"msIfac=%f",msIfac);
7206 fflush(DBG);
7207 }
7208
                break;
7209
             default:
7210 printf("problem with nuclear stats in singlet_JK. Exiting. \n");
7211
                exit(1);
7212
             }
7213
           }
```

```
7214
         for(msc=0;msc<((int)(2*msSpin+1));msc++){</pre>
7215
           msJcurr=(double)msb-msSpin+(double)msc;
7216
           mscc=msb*((int)(2*msSpin+1))+msc;
7217
           if(msD!=0){
7218
             msInt=msIfac*(2*msJcurr+1)*exp(-msFv/(kB*msT));
7219 if (DEBUG>msdebugflag) {
7220 fprintf(DBG,"msIfac=%.1f, msJcurr=%.1f, msFv=%.2f,
     (kB*msT)=\%.1f\n'',\
7221
         msIfac,msJcurr,msFv,kB*msT);
7222 fprintf(DBG,"msD!=0, msInt=%f\n",msInt);
7223 fflush(DBG);
7224 }
              }
7225
7226
           MOL[msM].s[msS].r[msa].EJ[mscc]=msFv;
7227
           if(msD!=0) MOL[msM].s[msS].r[msa].PJ[mscc]=msInt;
7228
           if(msJcurr<0){
7229
             MOL[msM].s[msS].r[msa].EJ[mscc]=0;
             MOL[msM].s[msS].r[msa].PJ[mscc]=0;
7230
7231
             }
7232 if(DEBUG>msdebugflag){
7233 fprintf(DBG,"msb is %d; msJcurr is %f; msFv=%f; msInt=%f\n",\
         msb,msJcurr,msFv,msInt);
7234
7235 fprintf(DBG,"MOL[%d].s[%d].r[%d].EJ[%d]=%f;
     MOL[%d].s[%d].r[%d].PJ[%d]=%f\n",\
7236
       msM, msS, msa, mscc, MOL[msM].s[msS].r[msa].EJ[mscc], msM, msS,
     msa, mscc,∖
       MOL[msM].s[msS].r[msa].PJ[mscc]);
7237
7238 fflush(DBG);
7239 }
7240
           msImax+=msInt;
7241 if(DEBUG>msdebugflag){
7242 fprintf(DBG,"\n msImax is %f\n\n",msImax);
7243 fflush(DBG);
7244 }
7245
           }
         }
7246
7247
       if(msD==0){
7248
       for(msb=(msa*msJDnum);msb<((msa+1)*msJDnum);msb++){</pre>
      /* the following is algebra for: K(2S+1) + J - [K-S] */
7249
         mscc=(int)(msSpin*(2*CB[msCb].K[msb]+1)+CB[msCb].J[msb]);
7250
         MOL[msM].s[msS].r[msa].PJ[mscc]=CB[msCb].Jpop[msb];
7251
         msInt=MOL[msM].s[msS].r[msa].PJ[mscc];
7252
         msImax+=msInt;
7253
         }
7254
7255
       for(msb=0;msb<msKcountnum;msb++){</pre>
7256
         for(msc=0;msc<((int)(2*msSpin+1));msc++){</pre>
7257
           msJcurr=(double)msb-msSpin+(double)msc;
7258
           mscc=msb*((int)(2*msSpin+1))+msc;
7259
           MOL[msM].s[msS].r[msa].EJ[mscc]+=msTeVib;
           MOL[msM].s[msS].r[msa].PJ[mscc]/=msImax;
7260
7261
           if(msJcurr<0){
7262
             MOL[msM].s[msS].r[msa].EJ[mscc]=0;
7263
             MOL[msM].s[msS].r[msa].PJ[mscc]=0;
```

```
505
```

```
7264
             }
7265 if (DEBUG>msdebugflag) {
7266 fprintf(DBG,"%d\t%f\t%d\t%f\t%f\n",msb,msJcurr,mscc,\
         MOL[msM].s[msS].r[msa].EJ[mscc],\
7267
7268
         MOL[msM].s[msS].r[msa].PJ[mscc]);
7269 fflush(DBG);
7270 }
7271
           }
7272
         }
7273 if(DEBUG>msdebugflag){
7274 fprintf(DBG,"\n out of for loop \n");
7275 fflush(DBG);
7276 }
7277
       }
7278 sprintf(msfnstr,"mkdir %s_molecules/%s",PREF,MOL[msM].Mol);
7279 system(msfnstr);
7280 sprintf(msfnstr, "%s_molecules/%s/%s_%s_rot.dat", PREF,
     MOL[msM].Mol,\
7281
         MOL[msM].Mol,MOL[msM].s[msS].Name);
7282 MSROT=fopen(msfnstr,"w");
7283 if(MSROT==NULL){
7284
       printf("Error opening output file (singlet_JK) %s. Exiting.\n",\
7285
           msfnstr);
7286
       exit(1);
7287
       }
7288 fprintf(MSROT,"## File generated by program %s.\n",PROGRAM_NAME);
7289 fprintf(MSROT,"## This file contains ");
7290 fprintf(MSROT, "rotational state information about\n");
7291 fprintf(MSROT,"## state %s of molecule %s.\n",\
7292
         MOL[msM].s[msS].Name,MOL[msM].Mol);
7293 fprintf(MSROT, "## The columns are, in order: \n## K J");
7294 for(msa=0;msa<msVnum;msa++){
7295
       msV=MOL[msM].s[msS].v[0].vlo+msa;
7296
       fprintf(MSROT,"\tF(v=%d)\tPop(v=%d)",msV,msV);
7297
       }
7298 fprintf(MSROT,"\n");
7299 for(msb=0;msb<msKcountnum;msb++){
       for(msc=0;msc<((int)(2*msSpin+1));msc++){</pre>
7300
7301
         msJcurr=(double)msb-msSpin+(double)msc;
7302
         mscc=msb*((int)(2*msSpin+1))+msc;
7303
         fprintf(MSROT,"%d\t%f",msb,msJcurr);
7304
         for(msa=0;msa<msVnum;msa++){</pre>
           fprintf(MSROT,"\t%18.10e\t%18.10e",\
7305
7306
             MOL[msM].s[msS].r[msa].EJ[mscc], \setminus
7307
             MOL[msM].s[msS].r[msa].PJ[mscc]);
7308
           }
7309
         fprintf(MSROT,"\n");
7310
       }
7311
7312 fflush(MSROT);
7313 fclose(MSROT);
7314 if(DEBUG>msdebugflag){
7315 fprintf(DBG,"\n out of msa(Vnum) loop. msa=%d\n",msa);
7316 fflush(DBG);
```

```
7317 }
7318 return;
7319 }
     /* this function checks entries to see if there is a "MOL" entry
       where the program doesn't expect one. If it finds such an entry,
       it writes a message to stdout and to the parameter file and termi-
       nates the program. */
7320 char * new_mol_ck(char *curr_mol, char *curr_st){
7321 char nmol_ck[201];
7322 fscanf(INTR.F,"%s",nmol_ck);
7323 if(strcmp("MOL",nmol_ck)==0){
7324 printf("Unexpected MOL entry in state %s of molecule %s.\n",\
7325
      curr_st,curr_mol);
7326 printf("Please edit transition file and restart program. Exit-
     ing.\n");
7327 fprintf(PAR, "Unexpected MOL entry in state %s of molecule %s.\n", \
7328
      curr_st,curr_mol);
7329 fprintf(PAR, "Please edit transition file and restart program. Exit-
     ing.\n");
7330
      exit(1);
7331
      }
7332 return nmol_ck;
7333 }
     /* This function reads the FCF file. */
7334 void read_FCF_file(){
7335 int rpC=0, rpa=0, rpb=0, rpc=0, rpd=0, rpz=0, rpy=0, rpw=1, rpv=1,
     rpvs=0, rpck=0, rpcc=0;
7336 char rpsys[500], rpdum[500], rpfn[400], rpstrtoss[100];
7337 FILE *RPF;
7338 double rptoss=0,rpsumf=0,rpsumfvn=0,rpsumfvc=0,rpcma=0,rpcm=0;
7339 double rpTeH=0,rpTeL=0,rpweH=0,rpweL=0,rpwexeH=0,rpwexeL=0;
7340 sprintf(rpfn,".%s.temp1",PREF);
7341 sprintf(rpdum,".%s.temp2",PREF);
7342 for(rpa=0;rpa<NUMMOL;rpa++){
7343
       for(rpb=0;rpb<MOL[rpa].trans;rpb++){</pre>
     /* Get the state and determine the relevant spectroscopic con-
       stants. Also check for presence of multiple Omegas <<< This
       doesn't work at the moment. Below, only the first set of fcf's is
       assigned.*/
7344
       if(MOL[rpa].s[MOL[rpa].t[rpb].Hi].Ca!=-1){
7345
         rpC=MOL[rpa].s[MOL[rpa].t[rpb].Hi].Ca;
         rpw=CA[rpC].0;
7346
7347
        MOL[rpa].t[rpb].Ohi=rpw;
7348
         if(rpw<1){rpw=1;}</pre>
7349
        rpTeH=CA[rpC].Te;
```

```
7350
         rpweH=CA[rpC].we;
7351
         rpwexeH=CA[rpC].wexe;
7352
7353
       if(MOL[rpa].s[MOL[rpa].t[rpb].Hi].Cb!=-1){
7354
         rpC=MOL[rpa].s[MOL[rpa].t[rpb].Hi].Cb;
7355
         rpw=1;
7356
         rpTeH=CB[rpC].Te;
7357
         rpweH=CB[rpC].we;
7358
         rpwexeH=CB[rpC].wexe;
7359
      /* change this if support for Hund's Case C or D is added */
7360
       if((MOL[rpa].s[MOL[rpa].t[rpb].Hi].Ca==-1)&&
7361
         (MOL[rpa].s[MOL[rpa].t[rpb].Hi].Cb==-1)){
7362 printf("State %s of molecule
     ",MOL[rpa].s[MOL[rpa].t[rpb].Hi].Name);
7363 printf("%s is neither Hund's Case a nor b.
     Exiting.\n",MOL[rpa].Mol);
7364
         exit(1);
7365
       if(MOL[rpa].s[MOL[rpa].t[rpb].Lo].Ca!=-1){
7366
7367
         rpC=MOL[rpa].s[MOL[rpa].t[rpb].Lo].Ca;
7368
         rpv=CA[rpC].0;
7369
         MOL[rpa].t[rpb].Olo=rpv;
7370
         if(rpv<1){rpv=1;}</pre>
7371
         rpTeL=CA[rpC].Te;
         rpweL=CA[rpC].we;
7372
7373
         rpwexeL=CA[rpC].wexe;
7374
         }
7375
       if(MOL[rpa].s[MOL[rpa].t[rpb].Lo].Cb!=-1){
7376
         rpC=MOL[rpa].s[MOL[rpa].t[rpb].Lo].Cb;
7377
         rpw=1;
7378
         rpTeH=CB[rpC].Te;
7379
         rpweH=CB[rpC].we;
7380
         rpwexeH=CB[rpC].wexe;
7381
      /* change this if support for Hund's Case C or D is added */
7382
       if((MOL[rpa].s[MOL[rpa].t[rpb].Lo].Ca==-1)&&\
7383
         (MOL[rpa].s[MOL[rpa].t[rpb].Lo].Cb==-1)){
7384 printf("State %s of molecule
     ",MOL[rpa].s[MOL[rpa].t[rpb].Lo].Name);
7385 printf("%s is neither Hund's Case a nor b.
     Exiting.\n",MOL[rpa].Mol);
7386
         exit(1);
7387
         }
7388 MOL[rpa].t[rpb].v=(vfcf*)calloc(30*rpv*rpw,sizeof(vfcf));
7389 if(DEBUG>rpdebugflag){
7390 fprintf(DBG,"rpv=%d, rpw=%d\n",rpv,rpw);
7391 }
7392 for(rpz=0;rpz<rpw;rpz++){
7393
       for(rpy=0;rpy<rpv;rpy++){</pre>
7394
         for(rpc=0;rpc<30;rpc++){</pre>
7395
           rpcc=rpz*rpv*30+rpy*30+rpc; /* This is the 3D part of a 4D
        data set. This (3D) set is indexed so that the primary set is the
```

```
set of upper-level vibrational numbers. The next level is the
        number of lower-state Omegas. There are upper-state-Omega-number
        of sets of (30 upper vib levels)x(lower-state-Omega-number)
        pieces of data. later, each one of the lower vib levels gets its
        own set of 30 lower vib levels. */
      /* In output from Ervin's program, the second quantum number is that
        of the higher state. So, this grep is asking for all the entries
        that go to the high state rpc */
           sprintf(rpsys,"grep \"\\->%3d\" %s > %s",\
7396
7397
             rpc,MOL[rpa].t[rpb].f[rpz*rpv+rpy].f,rpfn);
7398 if(DEBUG>rpdebugflag){
       fprintf(DBG,"grep rpsys is %s\n",rpsys);
7399
7400 }
7401
           system(rpsys);
           sprintf(rpsys,"wc -l %s > %s",rpfn,rpdum);
7402
7403 if (DEBUG>rpdebugflag) {
7404
       fprintf(DBG,"wc rpsys is %s\n",rpsys);
7405 }
7406
           system(rpsys);
7407
           RPF=fopen(rpdum, "r");
7408
           if(RPF==NULL){
7409 printf("Error opening temporary file 2 in read FCF for rpa=%d,
     ",rpa);
7410 printf("rpb=%d, and rpc=%d; filename %s. Exiting.\n",\
         rpb,rpc,MOL[rpa].t[rpb].f[rpz*rpv+rpy].f);
7411
7412
             exit(1);
7413
             }
7414
           fscanf(RPF,"%d",&rpvs);
           fclose(RPF);
7415
7416
           RPF=fopen(rpfn,"r");
7417
           if(RPF==NULL){
7418 printf("Error opening temporary file 1 in read FCF for rpa=%d,
     ",rpa);
7419 printf("rpb=%d, and rpc=%d; filename %s. Exiting.\n",\
7420
         rpb,rpc,MOL[rpa].t[rpb].f[rpz*rpv+rpy].f);
7421
             exit(1);
             }
7422
7423 if(DEBUG>rpdebugflag){
       fprintf(DBG,"The following are the entries from the FCF
7424
     file.\n");
7425
       fprintf(DBG, "Entries that are saved to an array are in brack-
     ets[].\n");
       fprintf(DBG,"rpvs is %d\n",rpvs);
7426
7427 }
7428
       rpcma=rpTeH+rpweH*(rpc+0.5)-rpwexeH*(rpc+0.5)*(rpc+0.5)-rpTeL;
7429
           rpsumf=rpsumfvn=rpsumfvc=0;
7430
           for(rpd=0;rpd<rpvs;rpd++){</pre>
7431
         rpcm=rpcma-rpweL*(rpd+0.5)+rpwexeL*(rpd+0.5)*(rpd+0.5);
         fscanf(RPF, "%d", &MOL[rpa].t[rpb].v[rpc].vqn[rpd]);
7432
             fscanf(RPF,"%s",rpstrtoss); /* comma */
7433
7434
             fscanf(RPF,"%d",&rpck); /* vhi */
7435 if(DEBUG>rpdebugflag){
```

```
7436 fprintf(DBG,"[%d] %s %d
     ",MOL[rpa].t[rpb].v[rpc].vqn[rpd],rpstrtoss,rpck);
7437 }
7438
             if(rpck!=rpc){
7439 printf("rpc not equal to rpck(%d) for rpa=%d, rpb=%d, rpc=%d,
     rpd=%d\n",\
7440
                 rpck,rpa,rpb,rpc,rpd);
7441
             exit(1);
7442
             }
             fscanf(RPF,"%s ",rpstrtoss); /* comma */
7443
7444
             fscanf(RPF,"%lf",&rptoss); /* wavenumbers */
7445 if (DEBUG>rpdebugflag) {
7446 fprintf(DBG, "%s %f ", rpstrtoss, rptoss);
7447 fflush(DBG);
7448 }
7449
             fscanf(RPF,"%s ",rpstrtoss); /* comma */
7450
         fscanf(RPF,"%lf",&MOL[rpa].t[rpb].v[rpc].fcfn[rpd]);
7451
             if(rptoss<=0){ /* negative trans. frequency */
7452
               MOL[rpa].t[rpb].v[rpc].fcfn[rpd]=0;
7453
               }
7454
             MOL[rpa].t[rpb].v[rpc].fcfc[rpd]=\
7455
               MOL[rpa].t[rpb].v[rpc].fcfn[rpd];
7456
             rpsumf+=MOL[rpa].t[rpb].v[rpc].fcfc[rpd];
7457 if(DEBUG>rpdebugflag){
7458 fprintf(DBG,"%s
     [%f](n)\n",rpstrtoss,MOL[rpa].t[rpb].v[rpc].fcfn[rpd]);
7459 fprintf(DBG, "MOL[%d].t[%d].v[%d].fcfc[%d] = %f\n", rpa, rpb, rpc,
     rpd,\
7460
         MOL[rpa].t[rpb].v[rpc].fcfc[rpd]);
7461 fflush(DBG);
7462 }
7463
             MOL[rpa].t[rpb].v[rpc].fcfc[rpd]*=pow(rpcm,3);
7464
             MOL[rpa].t[rpb].v[rpc].fcfn[rpd]*=\
7465
               pow(rpcm,DETECTTYPE);
7466
             rpsumfvn+=MOL[rpa].t[rpb].v[rpc].fcfn[rpd];
7467
             rpsumfvc+=MOL[rpa].t[rpb].v[rpc].fcfc[rpd];
7468 if(DEBUG>rpdebugflag){
7469 fprintf(DBG, "rpsumf=%f [%f](n)\n", rpsumf,
     MOL[rpa].t[rpb].v[rpc].fcfn[rpd]);
7470 fprintf(DBG, "MOL[%d].t[%d].v[%d].fcfc[%d] = %f\n", rpa, rpb, rpc,
     rpd,\
7471
         MOL[rpa].t[rpb].v[rpc].fcfc[rpd]);
7472 fprintf(DBG,"rpsumfvn=%13.6e;
     rpsumfvc=%13.6e\n",rpsumfvn,rpsumfvc);
7473 fflush(DBG);
7474 }
7475
             fscanf(RPF,"%s ",rpstrtoss); /* comma */
             fscanf(RPF,"%lf",&rptoss);
7476
7477 if(DEBUG>rpdebugflag){
7478 fprintf(DBG, "%s %f ", rpstrtoss, rptoss);
7479 fflush(DBG);
7480 }
             fscanf(RPF,"%s ",rpstrtoss); /* comma */
7481
7482
             fscanf(RPF,"%lf",&rptoss); /* pec3 */
```

```
7483 if(DEBUG>rpdebugflag){
7484 fprintf(DBG,"%s %f\n",rpstrtoss,rptoss);
7485 fflush(DBG);
7486 }
7487
             } /* close read fcf & nm for loop */
      /* This piece of code scales FCF's for the frequency factor. This
        isn't the best way to do this for two reasons. One, this should be
        done at the rot-->rot transition level. Two, if the franck-condon
        factors don't all add to one, then this becomes an approximation
        to an approximation. */
7488
           if((rpsumf-1)>0.01){
7489 printf("rpsumf for state %s of
     molecule",MOL[rpa].s[MOL[rpa].t[rpb].Hi].Name);
7490 printf(" %s is %f (greater than one).
     Exiting.\n",MOL[rpa].Mol,rpsumf);
7491
             exit(1);
7492
             }
7493
           if((1-rpsumf)>0.01){
7494 fprintf(PAR, "WARNING!!: The sum of the Franck-Condon factors (rp-
     sumf) for");
7495 fprintf(PAR,"\n\tstate %s ",MOL[rpa].s[MOL[rpa].t[rpb].Hi].Name);
7496 fprintf(PAR, "of molecule %s is %f
     (v-hi=%d).\n",MOL[rpa].Mol,rpsumf,rpc);
7497
7498
           for(rpd=0;rpd<rpvs;rpd++){</pre>
           MOL[rpa].t[rpb].v[rpc].fcfc[rpd]*=rpsumf/rpsumfvc;
7499
7500
           MOL[rpa].t[rpb].v[rpc].fcfn[rpd]*=rpsumf/rpsumfvn;
7501 if(DEBUG>rpdebugflag){
7502 fprintf(DBG,"MOL[%d].t[%d].v[%d].fcfn[%d] = %f ; ", rpa, rpb, rpc,
     rpd,\
7503
         MOL[rpa].t[rpb].v[rpc].fcfn[rpd]);
7504 fprintf(DBG,"MOL[%d].t[%d].v[%d].fcfc[%d] = %f\n", rpa, rpb, rpc,
     rpd,\
7505
         MOL[rpa].t[rpb].v[rpc].fcfc[rpd]);
7506 fflush(DBG);
7507 }
7508
             } /* close scale fcf for frequency loop */
7509
           } /* close vib levels for loop */
7510
         } /* close rpy (num low Omegas) loop */
7511
       } /* close rpz (num high Omegas) loop */
7512
         } /* close transitions for loop */
7513
       } /* close NUMMOL for loop */
7514 sprintf(rpsys,"rm %s %s",rpfn,rpdum);
7515 system(rpsys);
7516 return;
7517 }
      /*************** read_atomic_file() ***************/
      /* This function reads atomic files. */
7518 void read_atomic_files(){
7519 int raa=0, rab=0, raz=0;
```

```
7520 char rtmp[500];
7521 FILE *ATF;
7522 if (DEBUG>radebugflag) {
7523 fprintf(DBG,"Top of read_atomic_files. NUMAT=%d.\n",NUMAT);
7524 fflush(DBG);
7525 }
7526 for(raa=0;raa<NUMAT;raa++){
       sprintf(rtmp,"wc -l %s > %s",AT[raa].f.f,TMPFILE);
7527
7528 if(DEBUG>radebugflag){
7529 fprintf(DBG, "System call string is %s.\n", rtmp);
7530 fflush(DBG);
7531 }
7532
       system(rtmp);
7533
       SYS=fopen(TMPFILE, "r");
7534
       if(SYS==NULL){
7535 printf("Error opening atomic temporary file #%d. Exiting.\n",raa);
7536
         exit(1);
7537
         }
7538
       fscanf(SYS,"%d",&raz);
7539 if(DEBUG>radebugflag){
7540 fprintf(DBG,"raz is %d.\n",raz);
7541 fflush(DBG);
7542 }
7543
       AT[raa].n=raz;
       fclose(SYS);
7544
7545
       AT[raa].x=(double*)calloc(raz,sizeof(double));
7546
       AT[raa].A=(double*)calloc(raz,sizeof(double));
7547
       AT[raa].pop=(double*)calloc(raz,sizeof(double));
       ATF=fopen(AT[raa].f.f,"r");
7548
7549
       if(ATF==NULL){
7550 printf("Error opening atomic info file #%d. Exiting.\n",raa);
7551
         exit(1);
7552
         }
7553
       for(rab=0;rab<raz;rab++){</pre>
         fscanf(ATF,"%lf %lf %lf",&AT[raa].x[rab],&AT[raa].A[rab],\
7554
7555
             &AT[raa].pop[rab]);
7556 if(DEBUG>radebugflag){
7557 fprintf(DBG,"xposition is %f, A is
     %f\n",AT[raa].x[rab],AT[raa].A[rab]);
7558 fflush(DBG);
7559 }
7560
         }
7561
       fclose(ATF);
7562
       }
7563 return;
7564 }
```

/* This function reads rotational distribution files.

A note on the J(K) array: positions in the array are given by:

rdc*rdJK*rdv + rdd*rdv + rde

where rdc is the current Omega number (not the value of this Omega); rdJK is the total number of lines in the J(K) distribution file as determined by "wc -l filename"; rdv is the number of vibration levels to be considered; rdd is the current J(K) number; rde is the current vibrational level number. */

```
7565 void read_rot_dist_files(){
```

```
7566 int rd-
```

```
numf=1,rda=0,rdb=0,rdc=0,rdd=0,rde=0,rdv=0,rdJK=0,rdsz=0,rdcs=0;
7567 int rdcc=0,rddd=0,rdee=0,rdnum=0;
```

7568 double rdJmax=0,rdJprev=0,rdJdum=0;

```
7569 char rdsys[500];
```

```
7570 sprintf(TMPFILE,".%s.temporary",PREF);
```

```
/* start loop over molecules and states. Reinitialize rdnumf */
```

```
7571 for(rda=0;rda<NUMMOL;rda++){
```

```
7572 if(DEBUG>rddebugflag){
```

```
7573 fprintf(DBG,"Top of rda loop for rda=%d. NUMMOL is %d\n",rda,NUMMOL);
```

```
7574 fflush(DBG);
```

```
7575 }
```

```
7576 for(rdb=0;rdb<MOL[rda].states;rdb++){</pre>
```

```
7577 if(DEBUG>rddebugflag){
```

```
7578 fprintf(DBG, "Top of rdb loop for rdb=%d\n", rdb);
```

```
7579 fflush(DBG);
```

```
7580 }
```

/* For each state, determine if there are files to read and, if so,
 is the state Case a or Case b, and the position in the Case array
 */

```
7581 if(MOL[rda].s[rdb].Dist==-1){
```

```
/* determine the number of vibrational levels to consider */
```

```
7582 rdv=MOL[rda].s[rdb].v[0].vnum;
7583 if(DEBUG>rddebugflag){
```

```
7584 fprintf(DBG,"State %s (molecule %s) has distribution file(s) ",\
7585 MOL[rda].s[rdb].Name,MOL[rda].Mol);
```

```
7586 fprintf(DBG,"and vnum is %d\n",MOL[rda].s[rdb].v[0].vnum);
```

```
7587 fflush(DBG);
7588 }
```

```
/* if Case a, figure out what rdnumf really is */
```

```
7589 if(MOL[rda].s[rdb].Ca>-1){
```

```
7590 rdcs=MOL[rda].s[rdb].Ca;
```

```
7591 rdnumf=CA[rdcs].0;
```

7592 rdJK=0;

```
7593 for(rdc=0;rdc<rdnumf;rdc++){
```

```
7594 sprintf(rdsys,"wc -1 %s > %s", 

MOI [mds] = [mdb] = f[mds] = f[mdb] = f[mdb
```

```
7595 MOL[rda].s[rdb].f[rdc].f,TMPFILE);
```

```
7596 system(rdsys);
```

```
7597 if(DEBUG>rddebugflag){
```

```
7598 fprintf(DBG,"System string is %s\n",rdsys);
```

```
7599 fflush(DBG);
```

```
7600 }
```

```
7601 SYS=fopen(TMPFILE,"r");
```

```
7602
           if(SYS==NULL){
7603 printf("Error opening temporary file for file %s. Exiting.\n",\
           MOL[rda].s[rdc].f[rdc].f);
7604
7605
             exit(1);
7606
             }
7607
           fscanf(SYS,"%d",&rdd);
7608
           if(rdd>rdJK) rdJK=rdd;
7609
           fclose(SYS);
7610
           }
7611
         rdsz=rdnumf*rdv*rdJK;
7612
         CA[rdcs].Jpop=(double*)calloc(rdsz,sizeof(double));
7613 if(DEBUG>rddebugflag){
7614 fprintf(DBG, "MOL[%d].Mol (%s) MOL[%d].s[%d].Name (%s)
     ",rda,MOL[rda].Mol,∖
         rda,rdb,MOL[rda].s[rdb].Name);
7615
7616 fprintf(DBG,"is defined as Case a.\nThere are %d lines in the
     file.\n",rdJK);
7617 fflush(DBG);
7618 }
7619
         }
7620
       else{
         if(MOL[rda].s[rdb].Cb==-1){
7621
7622 printf("Molecule Name %s State %s has no defined case. Exit-
     ing.\n",\
7623
           MOL[rda].Mol,MOL[rda].s[rdb].Name);
7624
           exit(1);
7625
           }
7626
         rdcs=MOL[rda].s[rdb].Cb;
7627
         rdnum=1;
7628
         sprintf(rdsys,"wc -1 %s > %s",\
7629
             MOL[rda].s[rdb].f[rdc].f,TMPFILE);
7630
         system(rdsys);
7631
         SYS=fopen(TMPFILE,"r");
7632
         if(SYS==NULL){
7633 printf("Error opening temporary file for file %s. Exiting.\n",\
7634
         MOL[rda].s[rdc].f[rdc].f);
7635
           exit(1);
7636
           }
7637
         fscanf(SYS,"%d",&rdJK);
7638
         fclose(SYS);
7639
         rdsz=rdv*rdJK;
7640
         CB[rdcs].Jnum=rdJK;
         CB[rdcs].Jpop=(double*)calloc(rdsz,sizeof(double));
7641
7642
         CB[rdcs].K=(double*)calloc(rdJK,sizeof(double));
7643
         CB[rdcs].J=(double*)calloc(rdJK,sizeof(double));
7644 if(DEBUG>rddebugflag){
7645 fprintf(DBG,"MOL[%d].Mol (%s) MOL[%d].s[%d].Name (%s)
     ",rda,MOL[rda].Mol,\
7646
         rda,rdb,MOL[rda].s[rdb].Name);
7647 fprintf(DBG,"is defined as Case b.\nThere are %d lines in the
     file.\n",rdJK);
7648 fflush(DBG);
7649 }
7650
         }
```

```
/* start loop over files [rdc] -- there will only be one file for
        Case b or for Case a where a list of Omegas aren't specified */
       for(rdc=0;rdc<rdnumf;rdc++){</pre>
7651
7652
         rdcc=rdc*rdJK*rdv;
7653
         rdJdum=rdJprev=rdJmax=0;
7654 if (DEBUG>rddebugflag) {
7655 fprintf(DBG,"rdcc is %d, rdc is %d\n",rdcc,rdc);
7656 fflush(DBG);
7657 }
7658
       MOL[rda].s[rdb].f[rdc].F=fopen(MOL[rda].s[rdb].f[rdc].f,"r");
         if(MOL[rda].s[rdb].f[rdc].F==NULL){
7659
7660 printf("Error opening distribution file %s. Exiting.\n",\
         MOL[rda].s[rdb].f[rdc].f);
7661
7662
           exit(1):
7663
           }
      /* start loop over lines in file [rdd] and read in J/K values */
7664
         for(rdd=0;rdd<rdJK;rdd++){</pre>
7665
           rddd=rdd*rdv;
7666
           fscanf(MOL[rda].s[rdb].f[rdc].F,"%lf",&rdJdum);
7667 if (DEBUG>rddebugflag) {
7668 fprintf(DBG,"rddd id %d, rdd is %d, rdJdum is
     %f\n",rddd,rdd,rdJdum);
7669 fflush(DBG);
7670 }
      /* check to make sure that the J(K) values in the file are sequential
        */
7671
           if(rdd==0){
7672
             rdJprev=rdJdum;
7673
              if(MOL[rda].s[rdb].Ca>-1){
               CA[rdcs].Jmin=rdJdum;
7674
7675 if(DEBUG>rddebugflag){
7676 fprintf(DBG, "CA[%d].Jmin is %f\n", rdcs, CA[rdcs].Jmin);
7677 fflush(DBG);
7678 }
7679
               }
7680
             else{
7681
               CB[rdcs].Kmin=rdJdum;
7682
               CB[rdcs].K[rdd]=rdJdum;
       fscanf(MOL[rda].s[rdb].f[rdc].F,"%lf",&CB[rdcs].J[rdd]);
7683
7684 if(DEBUG>rddebugflag){
7685 fprintf(DBG,"CB[%d].Kmin is %f\n",rdcs,CB[rdcs].Kmin);
7686 fprintf(DBG,"CB[%d].K[%d] is %f\n",rdcs,rdd,CB[rdcs].K[rdd]);
7687 fprintf(DBG,"CB[%d].J[%d] is %f\n",rdcs,rdd,CB[rdcs].J[rdd]);
7688 fflush(DBG);
7689 }
7690
                }
7691
             }
7692
           else{
7693
              if(rdJdum!=(rdJprev+1)){
7694 printf("Non-sequential J(or K) values found in file %s ",\
7695
         MOL[rda].s[rdb].f[rdc].f);
7696 printf("between lines numbered %d and %d.\n",rdd,(rdd-1));
7697 printf("The two J-values read are %f and %f.\n",rdJprev,rdJdum);
```

```
7698 printf("Exiting. Please edit distribution file and restart pro-
     gram.\n");
7699 fprintf(PAR, "Non-sequential J(or K) values found in file %s ",
         MOL[rda].s[rdb].f[rdc].f);
7700
7701 fprintf(PAR, "between lines numbered %d and %d.\n",rdd, (rdd-1));
7702 fprintf(PAR, "The two J-values read are %f and
     %f.\n",rdJprev,rdJdum);
7703 fprintf(PAR, "Exiting. Please edit distribution file and restart
     program.\n");
7704
             exit(1);
7705
               }
7706
              if(MOL[rda].s[rdb].Cb>-1){
7707
                CB[rdcs].K[rdd]=rdJdum;
       fscanf(MOL[rda].s[rdb].f[rdc].F,"%lf",&CB[rdcs].J[rdd]);
7708
7709 if (DEBUG>rddebugflag) {
7710 fprintf(DBG, "CB[%d].K[%d] is %f\n", rdcs, rdd, CB[rdcs].K[rdd]);
7711 fprintf(DBG,"CB[%d].J[%d] is %f\n",rdcs,rdd,CB[rdcs].J[rdd]);
7712 fflush(DBG);
7713 }
7714
                }
7715
             rdJprev=rdJdum;
      /* check for maximum J(K) value. */
7716
             if(rdJdum>rdJmax) rdJmax=rdJdum;
7717 if(DEBUG>rddebugflag){
7718 fprintf(DBG, "rdJmax is %f\n", rdJmax);
7719 fflush(DBG);
7720 }
7721
              }
     /* read in the populations for each vib level [rde] */
7722
           for(rde=0;rde<rdv;rde++){</pre>
7723
             rdee=rdcc+rddd+rde;
7724
             if(MOL[rda].s[rdb].Ca>-1){
7725
                fscanf(MOL[rda].s[rdb].f[rdc].F,\
7726
                  "%lf",&CA[rdcs].Jpop[rdee]);
7727 if (DEBUG>rddebugflag) {
7728 fprintf(DBG, "rdee is %d, rde is %d, ",rdee,rde);
7729 fprintf(DBG,"CA[%d].Jpop[%d] is
     %f\n",rdcs,rdee,CA[rdcs].Jpop[rdee]);
7730 fflush(DBG);
7731 }
7732
                }
7733
              if(MOL[rda].s[rdb].Cb>-1){
7734
                fscanf(MOL[rda].s[rdb].f[rdc].F,\
7735
                  "%lf",&CB[rdcs].Jpop[rdee]);
7736 if(DEBUG>rddebugflag){
7737 fprintf(DBG, "rdee is %d, rde is %d, ",rdee,rde);
7738 fprintf(DBG,"CB[%d].Jpop[%d] is
     %f\n",rdcs,rdee,CB[rdcs].Jpop[rdee]);
7739 fflush(DBG);
7740 }
7741
                }
7742
              } /* close read over v-levels */
7743
           } /* close loop over lines in file (J or K values) */
7744
         fclose(MOL[rda].s[rdb].f[rdc].F);
```

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```

```
7745
         if(MOL[rda].s[rdb].Ca>-1){
7746
           CA[rdcs].Jmax=rdJmax;
7747 if(DEBUG>rddebugflag){
7748 fprintf(DBG, "rdJmax is %f CA[%d].Jmax is
     %f\n",rdJmax,rdcs,CA[rdcs].Jmax);
7749 fflush(DBG);
7750 }
7751
         if(MOL[rda].s[rdb].Cb>-1){
7752
           CB[rdcs].Kmax=rdJmax;
7753 if(DEBUG>rddebugflag){
7754 fprintf(DBG,"rdJmax is %f CB[%d].Kmax is
     %f\n",rdJmax,rdcs,CB[rdcs].Kmax);
7755 fflush(DBG);
7756 }
7757
         } /* close loop over rdnumf (num Omegas if Case a, else 1) */
7758
7759 } /* close if Dist==-1 condition */
7760
         } /* close loop over number of states */
7761
       } /* close loop over number of molecules */
7762 return;
7763 }
      /********* read_state_and_transition_files() **********/
      /* This function reads the transition file and the state file. */
7764 void read_state_and_transition_files(){
7765 char tdum[2000],tdumm[8],tsys[2000],tstring[2000],thom[15]="N";
7766 int ta=0,tb=0,tc=0,td=0,te=0,tz=0,ty=0,tx=0,tw=0,tv=0,tu=0,tt=0;
7767 int tisomega=1,tnumomega=1,tf=0;
7768 char tmolck[201],tmoldum[201],tstdum[201],tsysdir[1000];
7769 double tmult=0,tomeglo=0,tomeghi=0,tmod0=1,tmodS=1,tvmaxpop=0;
7770 FILE *TSYSF;
7771 INTR.F=fopen(INTR.f,"r");
7772 if(INTR.F==NULL){
7773 printf("Error opening transition file. Exiting.\n");
7774 exit(1);
7775 }
7776 fscanf(INTR.F,"%lf",&TEMP);
7777 if(DEBUG>tdebugflag){
7778 fprintf(DBG,"%f\n",TEMP);
7779 fflush(DBG);
7780 }
7781 if(TEMP==0){ /* write warning to parameter file */
7782 fprintf(PAR, "WARNING!!! Temperature NOT defined globally.\n");
7783 fprintf(PAR,"If there is not a temperature designation for any mol-
     ecule or\n");
7784 fprintf(PAR,"state, that molecule or state will be at T=0
     (brrr...). (n\n");
7785
       }
7786 else{ /* write global temperature to parameter file */
7787 fprintf(PAR, "Temperature defined globally as %f.\n\n", TEMP);
7788
       }
```

```
7789
       fflush(PAR);
7790 fscanf(INTR.F,"%d",&NUMMOL);
7791 if (DEBUG>tdebugflag) {
7792 fprintf(DBG,"NUMMOL is %d\n",NUMMOL);
7793 fflush(DBG);
7794 }
      /****** BEGIN LOOP OVER MOLECULES **********/
7795 MOL=(Molecule *)calloc(NUMMOL, sizeof(Molecule));
7796 for(ta=0;ta<NUMMOL;ta++){
7797
       sprintf(tmoldum, "Molecule number %d",ta);
7798
       strcpy(tstdum,"No state specified yet");
7799
       fscanf(INTR.F,"%s",tmolck);
7800
       if(strcmp(tmolck, "MOL")!=0){
7801 printf("MOL entry not found at beginning of data for molecule");
7802 printf("number %d. Exiting. \nPlease edit transition file
     and",(ta+1));
7803 printf(" restart program.\n");
7804 fprintf(PAR, "MOL entry not found at beginning of data for mol-
     ecule");
7805 fprintf(PAR, "number %d. Exiting. \nPlease edit transition file
     and",(ta+1));
7806 fprintf(PAR, " restart program. \n");
7807
         exit(1);
7808
         }
7809
       strcpy(tmolck,new_mol_ck(tmoldum,tstdum));
       sscanf(tmolck,"%s",MOL[ta].Mol);
7810
7811
       strcpy(tmolck,new_mol_ck(MOL[ta].Mol,tstdum));
7812
       sscanf(tmolck,"%lf",&MOL[ta].pop);
7813
       strcpy(tmolck,new_mol_ck(MOL[ta].Mol,tstdum));
7814
       sscanf(tmolck,"%lf",&MOL[ta].T);
7815
       sprintf(tsysdir,"mkdir %s_molecules/%s",PREF,MOL[ta].Mol);
7816
       system(tsysdir);
7817 if(DEBUG>tdebugflag){
7818 fprintf(DBG, "The molecule is %s with pop %f and temp
     %f\n",MOL[ta].Mol,\
7819
         MOL[ta].pop,MOL[ta].T);
7820 fflush(DBG);
7821 }
7822
       if(MOL[ta].T==0){
7823 fprintf(PAR, "Temperature NOT specified for molecule
     %s.\n\n",MOL[ta].Mol);
7824
         }
7825
       else{
7826 fprintf(PAR, "Temperature specified as %f for molecule %s.\n\n", \
7827
         MOL[ta].T,MOL[ta].Mol);
7828
         }
7829
       fflush(PAR);
7830
       strcpy(tmolck,new_mol_ck(MOL[ta].Mol,tstdum));
       sscanf(tmolck,"%d",&MOL[ta].states);
7831
7832
       NUMST+=MOL[ta].states;
7833 if(DEBUG>tdebugflag){
7834 fprintf(DBG,"MOL[%d].states is %d\n",ta,MOL[ta].states);
```

```
7835 fflush(DBG);
7836 }
7837
       MOL[ta].s=(State *)calloc(MOL[ta].states, sizeof(State));
7838
       for(tb=0;tb<MOL[ta].states;tb++){</pre>
7839
         MOL[ta].s[tb].Ca=-1;
7840
         MOL[ta].s[tb].Cb=-1;
7841
         MOL[ta].s[tb].Cc=-1;
7842
         MOL[ta].s[tb].Cd=-1;
7843
         }
7844 if(DEBUG>tdebugflag){
7845 fprintf(DBG, "Mol. %s Rel. Pop. is %f at Temp. %f\tMOL[%d].states
     is %d\n",\
         MOL[ta].Mol,MOL[ta].pop,MOL[ta].T,ta,MOL[ta].states);
7846
7847 fflush(DBG);
7848 }
      /*** OPEN LOOP OVER STATES ***/
7849
       for(tb=0;tb<MOL[ta].states;tb++){</pre>
7850
         tisomega=1;
7851
         tnumomega=1;
7852
         sprintf(tstdum, "State number %d", (tb+1));
7853
         strcpy(tmolck,new_mol_ck(MOL[ta].Mol,tstdum));
7854
         sscanf(tmolck,"%s",MOL[ta].s[tb].Name);
         strcpy(tmolck,new_mol_ck(MOL[ta].Mol,MOL[ta].s[tb].Name));
7855
         sscanf(tmolck,"%lf",&MOL[ta].s[tb].pop);
7856
      /* read state info before getting to the Omega issue */
      /*sprintf(tsys,"grep
        \"%s %s[ |\t]\" %s > .%s.temporary",MOL[ta].Mol, <<- this is an
        alternate form of the next half-line. */
7857 sprintf(tsys,"grep \"%s %s[[:space:]]\" %s >
     .%s.temporary",MOL[ta].Mol,\
7858
       MOL[ta].s[tb].Name,INST.f,PREF);
         sprintf(tstring,".%s.temporary",PREF);
7859
7860
         system(tsys);
7861 if (DEBUG>tdebugflag) {
7862 fprintf(DBG,"tsys is %s; tstring is %s\n",tsys, tstring);
7863 fflush(DBG);
7864 }
         TSYSF=fopen(tstring,"r");
7865
7866
         if(TSYSF==NULL){
7867 printf("Error opening temporary file # %d for molecule %s in
     read_trans. \
7868 Exiting.\n",tb,MOL[ta].Mol);
7869
           exit(1);
7870
           }
7871
         fscanf(TSYSF, "%s",tdumm);
7872
         if(strcmp(tdumm,MOL[ta].Mol)!=0){
7873 printf("Error reading MOL in temporary file for tdumm=%s and
     MOL[%d].Mol=%s \
7874 and MOL[%d].s[%d].Name=%s.
     Exiting.\n",tdumm,ta,MOL[ta].Mol,ta,tb,\
         MOL[ta].s[tb].Name);
7875
7876
           exit(1);
7877
           }
```

```
7878
         fscanf(TSYSF,"%s",tdumm);
7879
         if(strcmp(tdumm,MOL[ta].s[tb].Name)!=0){
7880 printf("Error reading state in temporary file for tdumm=%s and
     MOL[%d].Mol=%s\
7881 and MOL[%d].s[%d].Name=%s.
     Exiting.\n",tdumm,ta,MOL[ta].Mol,ta,tb,\
7882
         MOL[ta].s[tb].Name);
7883
           exit(1);
7884
           }
7885
         fscanf(TSYSF,"%s",MOL[ta].s[tb].Case);
7886
         if(strcmp(MOL[ta].s[tb].Case,"a")==0){
7887
           tc=Case_a_num;
7888
           MOL[ta].s[tb].Ca=Case_a_num;
7889 if(DEBUG>tdebugflag){
7890 fprintf(DBG, "MOL[%d].s[%d].Ca is %d\n",ta,tb,MOL[ta].s[tb].Ca);
7891 fflush(DBG);
7892 }
7893
           CA=(Case_a_stateinfo*)realloc(CA, \
7894
                ((tc+1)*sizeof(Case_a_stateinfo)));
7895
           fscanf(TSYSF,"%d",&CA[tc].L);
7896 if (DEBUG>tdebugflag) {
7897 fprintf(DBG,"State %s of molecule %s has Lambda=%d and is n",
7898
         MOL[ta].s[tb].Name,MOL[ta].Mol,CA[tc].L);
7899 fprintf(DBG, "defined as Case a.\n");
7900 fflush(DBG);
7901 }
7902
           if(CA[tc].L==0){
7903 fprintf(PAR, "State %s of molecules %s
     ",MOL[ta].s[tb].Name,MOL[ta].Mol);
7904 fprintf(PAR,"has Lambda=0\n and is defined as Case a.\n");
7905 fprintf(PAR, "This program isn't set up to call Sigma states Case
     a.\n");
7906 fprintf(PAR, "Redefining this state as Case b.\n");
7907 fflush(PAR);
7908
             strcpy(MOL[ta].s[tb].Case,"b");
7909
             tc=Case_b_num;
             MOL[ta].s[tb].Cb=Case_b_num;
7910
7911
             MOL[ta].s[tb].Ca=-1;
7912
             CB=(Case_b_stateinfo*)realloc(CB, \
7913
                ((tc+1)*(sizeof(Case_b_stateinfo))));
7914
             CB[tc].L=0;
             fscanf(TSYSF,"%d",&CB[tc].p);
7915
             fscanf(TSYSF,"%lf",&tmult);
7916
7917
             CB[tc].S=(tmult-1)/2;
7918
             CB[tc].sflag=fmod(CB[tc].S,1);
7919
             fscanf(TSYSF,"%s",thom);
7920
             if(strcmp(thom,"Y")==0){
               fscanf(TSYSF,"%d",&CB[tc].g);
7921
7922
               fscanf(TSYSF,"%lf",&CB[tc].I);
7923
               }
             fscanf(TSYSF,"%lf",&CB[tc].Te);
7924
             fscanf(TSYSF,"%lf",&CB[tc].we);
7925
             fscanf(TSYSF,"%lf",&CB[tc].wexe);
7926
7927
             fscanf(TSYSF,"%lf",&CB[tc].Be);
```

```
7928
             fscanf(TSYSF,"%lf",&CB[tc].ae);
7929
             tnumomega=1; /* Case b, tnumomega = 1 */
7930
             Case_b_num++;
7931 if(DEBUG>tdebugflag){
7932 fprintf(DBG,"Redefined as Case (b): MOL[%d].s[%d].Cb is %d\n",\
7933
         ta,tb,MOL[ta].s[tb].Cb);
7934 fprintf(DBG,"tc: %d; Mult: %f; S: %f\n",tc,tmult,CB[tc].S);
7935 fprintf(DBG,"Homonuclear? %s; g: %d; I: %f;
     n'', thom, CB[tc].g, CB[tc].I);
7936 fprintf(DBG,"Te=%f; we=%f; wexe=%f; Be=%f;
     ae=%f\n",CB[tc].Te,CB[tc].we,\
7937
         CB[tc].wexe,CB[tc].Be,CB[tc].ae);
7938 fflush(DBG);
7939 }
7940 if(CB[tc].Be==0){
7941
       printf("It isn't possible to simulate a rotational spectrum
     if\n");
7942
       printf("the rotational constant (Be) is zero. Call me picky. :-
     )\n");
7943
       printf("The program will exit. Either edit the state file
     for\n");
7944
       printf("state %s of molecule %s or delete its transition(s).\n",\
7945
         MOL[ta].s[tb].Name,MOL[ta].Mol);
7946
       exit(1);
7947
       }
             }
7948
7949
           else{
             fscanf(TSYSF,"%lf",&tmult);
7950
7951
             CA[tc].S=(tmult-1)/2;
7952
             CA[tc].sflag=fmod(CA[tc].S,1);
7953
             fscanf(TSYSF,"%s",thom);
             if(strcmp(thom,"Y")==0){
7954
                fscanf(TSYSF,"%d",&CA[tc].g);
7955
7956
               fscanf(TSYSF,"%lf",&CA[tc].I);
7957
                }
7958
             fscanf(TSYSF,"%lf",&CA[tc].Te);
7959
             fscanf(TSYSF,"%lf",&CA[tc].we);
             fscanf(TSYSF,"%lf",&CA[tc].wexe);
7960
7961
             fscanf(TSYSF,"%lf",&CA[tc].Be);
7962
             fscanf(TSYSF,"%lf",&CA[tc].ae);
7963 if (DEBUG>tdebugflag) {
7964 fprintf(DBG,"tc: %d; Mult: %f; S: %f\n",tc,tmult,CA[tc].S);
7965 fprintf(DBG, "Homonuclear? %s; g: %d; I: %f;
     n'', thom, CA[tc].g, CA[tc].I);
7966 fprintf(DBG,"Te=%f; we=%f; wexe=%f; Be=%f;
     ae=%f\n",CA[tc].Te,CA[tc].we,\
7967
         CA[tc].wexe,CA[tc].Be,CA[tc].ae);
7968 fflush(DBG);
7969 }
7970
             tnumomega=tmult; /* Case a, tnumomega = the multiplicity
        unless the user specifies otherwise (see below) */
7971
             Case_a_num++;
7972 if(CA[tc].Be==0){
```

```
7973
       printf("It isn't possible to simulate a rotational spectrum
     if\n");
7974
       printf("the rotational constant (Be) is zero. Call me picky. :-
     )\n");
7975
       printf("The program will exit. Either edit the state file
     for\n");
7976
       printf("state %s of molecule %s or delete its transition(s).\n",\
         MOL[ta].s[tb].Name,MOL[ta].Mol);
7977
7978
       exit(1);
7979
       }
7980
              }
           }
7981
7982 if((strcmp(MOL[ta].s[tb].Case,"b")==0)&&(MOL[ta].s[tb].Cb==-1)){
           tc=Case_b_num;
7983
7984
           MOL[ta].s[tb].Cb=Case_b_num;
7985 CB = (Case_b_stateinfo*) realloc(CB,
     ((tc+1)*sizeof(Case_b_stateinfo)));
7986
           fscanf(TSYSF,"%d",&CB[tc].L);
           if(CB[tc].L==0){
7987
7988
             fscanf(TSYSF,"%d",&CB[tc].p);
7989
              }
7990 if (DEBUG>tdebugflag) {
7991 fprintf(DBG,"State %s of molecules %s has Lambda=%d and is n", \
7992
         MOL[ta].s[tb].Name,MOL[ta].Mol,CB[tc].L);
7993 fprintf(DBG, "defined as Case b.\n");
7994 fflush(DBG);
7995 }
7996
           fscanf(TSYSF,"%lf",&tmult);
7997
           tmodS=(float)fmod(tmult,1);
7998
           if(tmodS!=0){
7999 printf("Multiplicities must be integers. For state %s
     ",MOL[ta].s[tb].Name);
8000 printf("of molecule %s, ",MOL[ta].Mol);
8001 printf("the multiplicity is \%6.2f. Exiting.\n",tmult);
8002 printf("Please edit transtion file or state file and restart pro-
     gram.\n");
8003 fprintf(PAR, "Multiplicities must be integers. ");
8004 fprintf(PAR, "For state %s ", MOL[ta].s[tb].Name);
8005 fprintf(PAR, "of molecule %s, ", MOL[ta].Mol);
8006 fprintf(PAR, "the multiplicity is %6.2f. Exiting.\n",tmult);
8007 fprintf(PAR, "Please edit transtion file or state file and restart
     program.\n");
8008
             exit(1);
              }
8009
           CB[tc].S=(tmult-1)/2;
8010
8011
           CB[tc].sflag=fmod(CB[tc].S,1);
           fscanf(TSYSF,"%s",thom);
8012
           if(strcmp(thom,"Y")==0){
8013
             fscanf(TSYSF,"%d",&CB[tc].g);
8014
             fscanf(TSYSF,"%lf",&CB[tc].I);
8015
             }
8016
           fscanf(TSYSF,"%lf",&CB[tc].Te);
8017
           fscanf(TSYSF,"%lf",&CB[tc].we);
8018
8019
           fscanf(TSYSF,"%lf",&CB[tc].wexe);
```

```
8020
           fscanf(TSYSF,"%lf",&CB[tc].Be);
           fscanf(TSYSF,"%lf",&CB[tc].ae);
8021
8022 if (DEBUG>tdebugflag) {
8023 fprintf(DBG,"tc: %d; Mult: %f; S: %f\n",tc,tmult,CB[tc].S);
8024 fprintf(DBG, "Homonuclear? %s; g: %d; I: %f;
     n'', thom, CB[tc].g, CB[tc].I);
8025 fprintf(DBG,"Te=%f; we=%f; wexe=%f; Be=%f;
     ae=%f\n",CB[tc].Te,CB[tc].we,\
8026
         CB[tc].wexe,CB[tc].Be,CB[tc].ae);
8027 fflush(DBG);
8028 }
8029
           tnumomega=1; /* for Case b, tnumomega is always 1 */
8030
           Case_b_num++;
8031 if(CB[tc].Be==0){
       printf("It isn't possible to simulate a rotational spectrum
8032
     if\n");
8033
       printf("the rotational constant (Be) is zero. Call me picky. :-
     )\n");
8034
       printf("The program will exit. Either edit the state file
     for\n");
       printf("state %s of molecule %s or delete its transition(s).\n",\
8035
8036
         MOL[ta].s[tb].Name,MOL[ta].Mol);
8037
       exit(1);
8038
       }
8039
           }
8040
         fclose(TSYSF);
8041
         if((MOL[ta].s[tb].Cb==-1)&&(MOL[ta].s[tb].Ca==-1)){
8042 printf("Case neither a nor b in temporary file for
     MOL[ta].s[tb].Case=%s and \setminus
8043 MOL[%d].Mol=%s and MOL[%d].s[%d].Name=%s.
     Exiting.\n",MOL[ta].s[tb].Case,ta,
8044 MOL[ta].Mol,ta,tb,MOL[ta].s[tb].Name);
8045
           exit(1);
8046
           }
     /* Read in statement about Omega Specifications. Then, read in vi-
        brational level information and other info as appropriate */
8047
         strcpy(tmolck,new_mol_ck(MOL[ta].Mol,MOL[ta].s[tb].Name));
8048
         sscanf(tmolck,"%s",tdum);
8049
         if(strcmp(tdum,"Y")==0){
8050
           if(MOL[ta].s[tb].Ca==-1){
8051 printf("Omega restriction requested for a state that isn't Case
     a\n");
8052 printf("This program doesn't understand that. Exiting.n");
8053 printf("Please edit transtion (or state) file and restart pro-
     gram.n^{"};
8054 fprintf(PAR, "Omega restriction requested for a state that isn't
     Case a\n");
8055 fprintf(PAR, "This program doesn't understand that. Exiting.n");
8056 fprintf(PAR, "Please edit transtion (or state) file and restart pro-
     gram.\n\n");
8057 fflush(PAR);
8058
             exit(1);
8059
             }
```

```
8060
           tisomega=0;
8061
           tv=MOL[ta].s[tb].Ca;
8062
           strcpy(tmolck,new_mol_ck(MOL[ta].Mol,\
             MOL[ta].s[tb].Name));
8063
8064
           sscanf(tmolck,"%d",&tw);
8065
             CA[tv].O=tw;
8066
           if(tw<1){
8067
             tw=2*CA[tv].S+1;
8068
             tisomega=1;
8069 fprintf(PAR,"WARNING!!! Omega restriction requested, but with the
     default\n");
8070 fprintf(PAR,"!! number of omegas. The program will not read for a
     set of\n");
8071 fprintf(PAR,"!! user-specified omegas and populations. If the pro-
     gram\n");
8072 fprintf(PAR,"!! exits after complaining of a MOL entry in the wrong
     place, \n");
8073 fprintf(PAR,"!! this might be the reason why. \n\n");
8074
8075
           tnumomega=tw;
8076
           CA[tv].10=(double*)calloc(tw,sizeof(double));
8077
           CA[tv].pO=(double*)calloc(tw,sizeof(double));
8078
           tomeglo=fabs((double)CA[tv].L-CA[tv].S);
8079
           tomeghi=(double)CA[tv].L+CA[tv].S;
8080
           tmodS=(float)fmod(CA[tv].S,1);
8081
8082 MOL[ta].s[tb].nO=tnumomega;
8083 MOL[ta].s[tb].f=(fileset *)calloc(tnumomega,sizeof(fileset));
8084 MOL[ta].s[tb].T=(double *)calloc(tnumomega,sizeof(double));
8085 MOL[ta].s[tb].v=(vset *)calloc(tnumomega,sizeof(vset));
8086 if(DEBUG>tdebugflag){
8087 fprintf(DBG,"tnumomega is %d. Just allocated f, T,
     v.\n",tnumomega);
8088 fflush(DBG);
8089
       }
8090
       if(tisomega!=0){
8091
         tnumomega=1;
8092
8093
         for(te=0;te<tnumomega;te++){</pre>
8094
           if(tisomega==0){
8095
             strcpy(tmolck,new_mol_ck(MOL[ta].Mol,\
8096
               MOL[ta].s[tb].Name));
               sscanf(tmolck,"%lf",&CA[tv].10[te]);
8097
8098
               tmodO=(float)fmod(CA[tv].l0[te],1);
       if((CA[tv].10[te]<tomeglo)||(CA[tv].10[te]>tomeghi)){
8099
8100 printf("For state %s of molecule %s,
     ",MOL[ta].s[tb].Name,MOL[ta].Mol);
8101 printf("Omega values must lie between %f and
     %f.\n",tomeglo,tomeghi);
8102 printf("You requested an Omega of %f. Exiting.\n",CA[tv].10[te]);
8103 printf("Please edit the transition file (or the state file) and ");
8104 printf("restart the program.\n\n");
8105 fprintf(PAR, "For state %s of molecule %s,
     ",MOL[ta].s[tb].Name,MOL[ta].Mol);
```

```
8106 fprintf(PAR, "Omega values must lie between %f and
     %f.\n",tomeglo,tomeghi);
8107 fprintf(PAR, "You requested an Omega of %f.
     Exiting.\n",CA[tv].10[te]);
8108 fprintf(PAR, "Please edit the transition file (or the state file) and
     ");
8109 fprintf(PAR, "restart the program. \n\n");
8110
         exit(1);
8111
         }
8112
       if(tmodS!=tmodO){
8113 printf("For state %s of molecule %s,
     ",MOL[ta].s[tb].Name,MOL[ta].Mol);
8114 printf("Omega values for spins equal to %3.1f ",CA[tv].S);
8115 if(tmodS==0.5){printf("must be half-integral.\n");}
8116 if(tmodS==0){printf("must be integral.\n");}
8117 printf("You requested an Omega of %f. Exiting.\n",CA[tv].10[te]);
8118 printf("Please edit the transition file (or the state file) and ");
8119 printf("restart the program.\n\n");
8120 fprintf(PAR, "For state %s of molecule %s,
     ",MOL[ta].s[tb].Name,MOL[ta].Mol);
8121 fprintf(PAR,"Omega values for spins equal to %3.1f ",CA[tv].S);
8122 if(tmodS==0.5){fprintf(PAR,"must be half-integral.\n");}
8123 if(tmodS==0){fprintf(PAR,"must be integral.\n");}
8124 fprintf(PAR, "You requested an Omega of %f.
     Exiting.\n",CA[tv].10[te]);
8125 fprintf(PAR, "Please edit the transition file (or the state file) and
     ");
8126 fprintf(PAR, "restart the program. \n\n");
8127
         exit(1);
8128
         }
8129
              strcpy(tmolck,new_mol_ck(MOL[ta].Mol,\
8130
               MOL[ta].s[tb].Name));
             sscanf(tmolck,"%lf",&CA[tv].p0[te]);
8131
8132
              ł
8133 strcpy(tmolck,new_mol_ck(MOL[ta].Mol,MOL[ta].s[tb].Name));
         sscanf(tmolck,"%s",tdum);
8134
         tz=ty=tx=0;
8135
8136
         for(td=0;td<strlen(tdum);td++){</pre>
8137
           ty=isdigit((int)tdum[td]);
8138
           if((int)tdum[td]==46) tx++;
8139
           if((ty==0)&&((int)tdum[td]!=46)) tz=1;
8140
           }
8141
         if((tz==0)&&(tx<=1)){
           sscanf(tdum,"%lf",&MOL[ta].s[tb].T[te]);
8142
8143
           MOL[ta].s[tb].Dist=1;
8144 fprintf(PAR, "Temp for state %s of Molecule %s is
     %f\n",MOL[ta].s[tb].Name,\
         MOL[ta].Mol,MOL[ta].s[tb].T[te]);
8145
8146 fflush(PAR);
8147 if (DEBUG>tdebugflag) {
8148 fprintf(DBG,"Temp for state %s of Molecule %s is
     %f\n",MOL[ta].s[tb].Name,\
8149
         MOL[ta].Mol,MOL[ta].s[tb].T[te]);
```

```
8150 fflush(DBG);
```

```
8151 }
8152
           } /* close if tdum is a number (read temperature) */
         else{
8153
           sscanf(tdum,"%s",MOL[ta].s[tb].f[te].f);
8154
           MOL[ta].s[tb].Dist=-1;
8155
8156
           MOL[ta].s[tb].f[te].F=fopen(MOL[ta].s[tb].f[te].f,"r");
8157
           if(MOL[ta].s[tb].f[te].F==NULL){
8158 printf("Cannot open input file %s.
     Exiting.\n",MOL[ta].s[tb].f[te].f);
8159
             exit(1);
8160
             }
8161
           fclose(MOL[ta].s[tb].f[te].F);
8162 fprintf(PAR, "Distribution file for state %s of Molecule %s is
     %s\n",\
8163
         MOL[ta].s[tb].Name,MOL[ta].Mol,MOL[ta].s[tb].f[te].f);
8164 fflush(PAR);
8165 if (DEBUG>tdebugflag) {
8166 fprintf(DBG,"Dist (%d) file for state %s of Molecule %s is %s\n",\
8167
       MOL[ta].s[tb].Dist,MOL[ta].s[tb].Name,
8168
       MOL[ta].Mol,MOL[ta].s[tb].f[te].f);
8169 fflush(DBG);
8170 }
8171
           } /* close if tdum isn't a number (open file) */
8172 if(DEBUG>tdebugflag){
8173 fprintf(DBG, "%s\t %f\t %s\t (%d)\n", MOL[ta].s[tb].Name,
     MOL[ta].s[tb].pop, tdum, \
8174
         MOL[ta].s[tb].Dist);
8175 fflush(DBG);
8176 }
8177
         strcpy(tmolck,new_mol_ck(MOL[ta].Mol,MOL[ta].s[tb].Name));
         sscanf(tmolck,"%d",&MOL[ta].s[tb].v[te].vnum);
8178
8179 if(DEBUG>tdebugflag){
8180 fprintf(DBG,"vnum is %d\n",MOL[ta].s[tb].v[te].vnum);
8181 fflush(DBG);
8182 }
8183
         if(MOL[ta].s[tb].v[te].vnum>0){
8184
           strcpy(tmolck,new_mol_ck(MOL[ta].Mol,\
8185
                 MOL[ta].s[tb].Name));
8186
           sscanf(tmolck,"%d",&MOL[ta].s[tb].v[te].vlo);
8187 if(DEBUG>tdebugflag){
8188 fprintf(DBG,"vlo = %d ",MOL[ta].s[tb].v[te].vlo);
8189 fflush(DBG);
8190 }
8191 MOL[ta].s[tb].v[te].p=(double*)calloc(MOL[ta].s[tb].v[te].vnum,
8192
         sizeof(double));
8193 MOL[ta].s[tb].v[te].c = (int*) calloc(MOL[ta].s[tb].v[te].vnum,
     sizeof(int));
8194
           }
         tt=MOL[ta].s[tb].v[te].vlo;
8195
8196
         tvmaxpop=0;
8197
         for(td=0;td<MOL[ta].s[tb].v[te].vnum;td++){</pre>
8198
           strcpy(tmolck,new_mol_ck(MOL[ta].Mol,\
8199
                 MOL[ta].s[tb].Name));
8200
           sscanf(tmolck,"%lf",&MOL[ta].s[tb].v[te].p[td]);
```

```
8201
           tvmaxpop+=MOL[ta].s[tb].v[te].p[td];
8202 if (DEBUG>tdebugflag) {
8203 fprintf(DBG,"MOL[%d].s[%d].v[%d].p[%d]=%f\n",\
         ta,tb,te,td,MOL[ta].s[tb].v[te].p[td]);
8204
8205 fflush(DBG);
8206 }
8207
           }
      /* Make sure the vibrational populations sum to one in the simula-
        tion */
8208
         for(td=0;td<MOL[ta].s[tb].v[te].vnum;td++){</pre>
8209
           MOL[ta].s[tb].v[te].p[td]/=tvmaxpop;
8210
           ł
      /* Beginning of scan for file containing rotational distributions
        */
8211
         if(MOL[ta].s[tb].Dist==-1){
           if((MOL[ta].s[tb].Ca!=-1)&&(MOL[ta].s[tb].Cb!=-1)){
8212
8213 printf("MOL[%d].s[%d].Ca is %d\n",ta,tb,MOL[ta].s[tb].Ca);
8214 printf("MOL[%d].s[%d].Cb is %d\n",ta,tb,MOL[ta].s[tb].Cb);
8215
             printf("fix Ca/Cb assignment problem\n");
8216
             exit(1);
8217
              }
8218
           sprintf(tsys,"head -1 %s > .%s.temporary", \setminus
                MOL[ta].s[tb].f[te].f,PREF);
8219
8220
           system(tsys);
8221
           TSYSF=fopen(tstring,"r");
8222
           if(TSYSF==NULL){
8223
             printf("fix tstring 1\n");
8224
             exit(1);
8225
              }
8226
           fscanf(TSYSF,"%lf",&tmult);
8227
           if(MOL[ta].s[tb].Ca!=-1){
8228
             CA[tc].Jmin=tmult;
8229
              }
8230
           if(MOL[ta].s[tb].Cb!=-1){
8231
             CB[tc].Kmin=tmult;
8232
              }
           fclose(TSYSF);
8233
8234 if(DEBUG>tdebugflag){
8235 fprintf(DBG,"string for MOL[%d].s[%d].f[%d].f is %s\n",\
         ta,tb,te,MOL[ta].s[tb].f[te].f);
8236
8237 if(MOL[ta].s[tb].Ca!=-1){
8238 fprintf(DBG,"Jmin is %f, ",CA[tc].Jmin);
8239 }
8240 if (MOL[ta].s[tb].Cb!=-1){
8241 fprintf(DBG,"Kmin is %f, ",CB[tc].Kmin);
8242 }
8243 fflush(DBG);
8244 }
8245
           sprintf(tsys,"tail -1 %s > .%s.temporary", \
8246
                MOL[ta].s[tb].f[te].f,PREF);
8247
           system(tsys);
8248
           TSYSF=fopen(tstring,"r");
8249
           if(TSYSF==NULL){
8250
             printf("fix tstring 2\n");
```

```
8251
              exit(1);
8252
              }
           fscanf(TSYSF,"%lf",&tmult);
8253
8254
           if(MOL[ta].s[tb].Ca!=-1){
8255
             CA[tc].Jmax=tmult;
8256
              ł
8257
           if(MOL[ta].s[tb].Cb!=-1){
8258
              CB[tc].Kmax=tmult;
8259
              }
8260
           fclose(TSYSF);
8261 if (DEBUG>tdebugflag) {
8262 fprintf(DBG,"string for MOL[%d].s[%d].f[%d].f is %s\n",\
8263
         ta,tb,te,MOL[ta].s[tb].f[te].f);
8264 if(MOL[ta].s[tb].Ca!=-1){fprintf(DBG,"Jmax is %f, ",CA[tc].Jmax);
8265 if(MOL[ta].s[tb].Cb!=-1){fprintf(DBG,"Kmax is %f, ",CB[tc].Kmax);
8266 fflush(DBG);
8267 }
8268
           sprintf(tsys,"wc -l %s > .%s.temporary", \
8269
                MOL[ta].s[tb].f[te].f,PREF);
8270
           system(tsys);
8271
           TSYSF=fopen(tstring,"r");
           if(TSYSF==NULL){
8272
8273
             printf("fix tstring 3\n");
8274
             exit(1);
8275
             }
           fscanf(TSYSF,"%lf",&tmult);
8276
8277
           if(MOL[ta].s[tb].Ca!=-1){
              if(tmult!=(CA[tc].Jmax-CA[tc].Jmin+1)){
8278
8279
                printf("Jmax-Jmin range not wc -l\n");
8280
                printf("This might cause trouble\n");
8281
                ł
             }
8282
8283
           if(MOL[ta].s[tb].Cb!=-1){
8284
              if(tmult!=(CB[tc].Kmax-CB[tc].Kmin+1)){
                printf("Kmax-Kmin range not wc -l\n");
8285
8286
                printf("This might cause trouble\n");
8287
              }
8288
8289
           fclose(TSYSF);
8290 if (DEBUG>tdebugflag) {
8291 fprintf(DBG,"tmult is %f\n",tmult);
8292 fflush(DBG);
8293 }
8294
           } /* close read for rotation distribution file */
8295
           } /* close loop over number of specified omegas -- or over the
        one set of vibrational states */
8296
         } /* close states for loop */
      /* Preliminary stuff for loop over transitions for this molecule */
8297
       sprintf(tstdum,"(not a state, top of transition list)");
8298
       strcpy(tmolck,new_mol_ck(MOL[ta].Mol,tstdum));
8299
       sscanf(tmolck,"%d",&MOL[ta].trans);
```

```
8300 if (DEBUG>tdebugflag) {
8301 fprintf(DBG,"MOL[%d].trans is %d\n",ta,MOL[ta].trans);
8302 fflush(DBG);
8303 }
8304
       MOL[ta].t=(Trans*)calloc(MOL[ta].trans,sizeof(Trans));
      /* Start loop over transitions for this molecule */
       for(tb=0;tb<MOL[ta].trans;tb++){</pre>
8305
         sprintf(tstdum,"(not a state, transition number %d)",(tb+1));
8306
8307
         strcpy(tmolck,new_mol_ck(MOL[ta].Mol,tstdum));
8308
         sscanf(tmolck,"%s",tdum);
      /* Separate the two states in the transition */
8309
         tw=tv=0:
8310
         while(tw==0){
           MOL[ta].t[tb].Nhi[tv]=tdum[tv];
8311
8312
           if(tdum[tv]=='-'){
             MOL[ta].t[tb].Nhi[tv]='\0';
8313
8314
             tw=1:
             }
8315
8316
           tv++;
8317
           }
8318
         tu=tv;
8319
         tw=0;
8320
         while(tw==0){
8321
           MOL[ta].t[tb].Nlo[tv-tu]=tdum[tv];
8322
           if(tdum[tv]=='\0') tw=1;
8323
           tv++;
8324
           }
     /* Find the position in the state array for each state in the transi-
        tion */
8325
         tw=tv=tu=tt=0;
8326
         while((tw==0)&&(tv<MOL[ta].states)){</pre>
           if(strcmp(MOL[ta].s[tv].Name,MOL[ta].t[tb].Nhi)==0){
8327
8328
             MOL[ta].t[tb].Hi=tv;
8329
             MOL[ta].s[tv].no+=1;
8330 MOL[ta].s[tv].o = (int*) realloc(MOL[ta].s[tv].o,
     MOL[ta].s[tv].no*sizeof(int));
8331
             MOL[ta].s[tv].o[MOL[ta].s[tv].no-1]=tb;
8332
             tu=1;
8333 if(DEBUG>tdebugflag){
8334 fprintf(DBG, "MOL[%d].t[%d].Nhi %s matches
     ",ta,tb,MOL[ta].t[tb].Nhi);
8335 fprintf(DBG,"MOL[%d].s[%d].Name %s and
     ",ta,tv,MOL[ta].s[tv].Name);
8336 fprintf(DBG,"MOL[%d].t[%d].Hi is %d.\n",ta,tb,MOL[ta].t[tb].Hi);
8337 fprintf(DBG, "MOL[%d].s[%d].no is %d.\n",ta,tv,MOL[ta].s[tv].no);
8338 for(tf=0;tf<MOL[ta].s[tv].no;tf++){
8339 fprintf(DBG, "State %s is an origination state in
     ",MOL[ta].s[tv].Name);
8340 fprintf(DBG,"transition number %d.\n\n",tb);
       }
8341
8342 fflush(DBG);
8343 }
8344
              ł
8345
           if(strcmp(MOL[ta].s[tv].Name,MOL[ta].t[tb].Nlo)==0){
```

```
529
```

```
MOL[ta].t[tb].Lo=tv;
8346
8347
             MOL[ta].s[tv].nd+=1;
8348 MOL[ta].s[tv].d = (int*) realloc(MOL[ta].s[tv].d,
     MOL[ta].s[tv].nd*sizeof(int));
8349
             MOL[ta].s[tv].d[MOL[ta].s[tv].nd-1]=tb;
8350
             tt=1;
8351 if(DEBUG>tdebugflag){
8352 fprintf(DBG, "MOL[%d].t[%d].Nlo %s matches
     ",ta,tb,MOL[ta].t[tb].Nlo);
8353 fprintf(DBG, "MOL[%d].s[%d].Name %s and
     ",ta,tv,MOL[ta].s[tv].Name);
8354 fprintf(DBG,"MOL[%d].t[%d].Lo is %d.\n",ta,tb,MOL[ta].t[tb].Lo);
8355 fprintf(DBG, "MOL[%d].s[%d].nd is %d.\n",ta,tv,MOL[ta].s[tv].nd);
8356 for(tf=0;tf<MOL[ta].s[tv].nd;tf++){
8357 fprintf(DBG,"State %s is an destination state in
     ",MOL[ta].s[tv].Name);
8358 fprintf(DBG,"transition number %d.\n\n",tb);
8359
       }
8360 fflush(DBG);
8361 }
8362
             }
8363
           if((tu==1)&&(tt==1)){
8364
             tw=1;
8365
             }
8366
           tv++;
           }
8367
8368 if(DEBUG>tdebugflag){
8369 fprintf(DBG,"tdum is %s\n",tdum);
8370 fflush(DBG);
8371 }
8372
         if(tw==0){
8373 printf("Missing definition for at least one state in transition
     %s.",tdum);
8374 printf(" Exiting.\nPlease edit transition file and restart pro-
     gram\n");
8375 fprintf(PAR, "Missing definition for at least one state in transi-
     tion %s.",tdum);
8376 fprintf(PAR, "Exiting. \nPlease edit transition file and restart
     program.\n");
8377
           exit(1);
8378
           }
         if(MOL[ta].s[MOL[ta].t[tb].Hi].Ca!=-1){
8379
8380
           tw=CA[MOL[ta].s[MOL[ta].t[tb].Hi].Ca].0;
8381
           MOL[ta].t[tb].Ohi=tw;
           if(tw==0){tw=1;}
8382
8383
           }
8384
         else{
8385
           tw=1;
8386
           }
         if(MOL[ta].s[MOL[ta].t[tb].Lo].Ca!=-1){
8387
           tv=CA[MOL[ta].s[MOL[ta].t[tb].Lo].Ca].0;
8388
8389
           MOL[ta].t[tb].Olo=tv;
8390
           if(tv==0){tv=1;}
8391
           }
```
```
8392
         else{
8393
           tv=1;
8394
           }
8395
         MOL[ta].t[tb].f=(fileset*)calloc((tw*tv),sizeof(fileset));
8396
         MOL[ta].t[tb].P=(double*)calloc((tw*tv),sizeof(double));
8397
         MOL[ta].t[tb].cP=(int*)calloc((tw*tv),sizeof(int));
8398
         for(te=0;te<tw;te++){</pre>
8399
         for(td=0;td<tv;td++){</pre>
8400
           strcpy(tmolck,new_mol_ck(MOL[ta].Mol,tstdum));
8401
           sscanf(tmolck,"%lf",&MOL[ta].t[tb].P[te*tv+td]);
8402
           strcpy(tmolck,new_mol_ck(MOL[ta].Mol,tstdum));
           sscanf(tmolck,"%s",MOL[ta].t[tb].f[te*tv+td].f);
8403
8404 if (DEBUG>tdebugflag) {
8405 fprintf(DBG,"Prob is %f; file is %s\n",MOL[ta].t[tb].P[te*tv+td],\
8406
         MOL[ta].t[tb].f[te*tv+td].f);
8407 fflush(DBG);
8408 }
8409 if((MOL[ta].t[tb].P[te*tv+td]==0) &&
     (MOL[ta].t[tb].f[te*tv+td].f!="NULL")){
8410 fprintf(PAR, "WARNING!!! FCF-FILE specified for zero transition ");
8411 fprintf(PAR, "probability for transtion %s-%s \n\tand specified
     Omegas ",\
8412
         MOL[ta].t[tb].Nhi,MOL[ta].t[tb].Nlo);
8413 fprintf(PAR, "numbers %d (Hi) and %d (Lo). \n", (te+1), (td+1));
8414 fprintf(PAR,"\t(This is a non-fatal error, the program will con-
     tinue)\n");
8415
       }
8416 if((MOL[ta].t[tb].P[te*tv+td]!=0) &&
     (MOL[ta].t[tb].f[te*tv+td].f=="NULL")){
8417 printf("FCF-FILE specified as NULL for non-zero transition ");
8418 printf("probability\nfor transtion %s-%s and specified Omegas ",\
8419
         MOL[ta].t[tb].Nhi,MOL[ta].t[tb].Nlo);
8420 printf("numbers %d (Hi) and %d (Lo).\n",(te+1),(td+1));
8421 printf("Exiting. Please edit transition file and restart pro-
     gram.\n");
8422 fprintf(PAR, "FCF-FILE specified as NULL for non-zero transition ");
8423 fprintf(PAR,"probability\nfor transtion %s-%s and specified Omegas
     ",\
8424
         MOL[ta].t[tb].Nhi,MOL[ta].t[tb].Nlo);
8425 fprintf(PAR, "numbers %d (Hi) and %d (Lo).\n", (te+1), (td+1));
8426 fprintf(PAR, "Exiting. Please edit transition file and restart pro-
     gram.\n");
8427
       exit(1);
8428
       }
8429
         if(MOL[ta].t[tb].P[te*tv+td]!=0){
8430
           TSYSF=fopen(MOL[ta].t[tb].f[te*tv+td].f,"r");
8431 if(DEBUG>tdebugflag){
8432 fprintf(DBG,"FCF file for MOL[%d].t[%d].f[%d].f is %s.\n\n",\
         ta,tb,(te*tv+td),MOL[ta].t[tb].f[te*tv+td].f);
8433
8434 fflush(DBG);
8435
       }
8436
           if(TSYSF==NULL){
8437 printf("Error opening FCF file MOL[%d].t[%d].f[%d].f=%s. Exit-
     ing.\n\n",\
```

```
8438
         ta,tb,(te*tv+td),MOL[ta].t[tb].f[te*tv+td].f);
8439
             exit(1);
8440
             }
           fclose(TSYSF);
8441
8442
           } /* close if trans. prob. not zero file check */
8443
           } /* close td loop over omegas-in-transitions */
8444
           } /* close te loop over omegas-in-transitions */
8445
         } /* close transitions for loop */
8446
       } /* end NUMMOL loop */
8447 fclose(INTR.F);
8448 return;
8449 }
     /* This function calculates energy levels and rotational distribu-
        tions (if needed) for all singlet states (Hund's Cases a and b) */
8450 void singlet_JK(int sM, int sS){
8451 int sa=0,sb=0,sJck=1,sg=0,sL=0,sp=0,sV=0,sVnum=0,sItst=0;
8452 int sCa=0, sCb=0, sC=0, sD=1, sf=0;
8453 double
     sT=0,sDv=0,sBe=0,sAe=0,sJMAX=0,sJMAXc=0,sJMAXf=0,saA=0,sJcut=0;
8454 double
     swe=0,swexe=0,sI=0,sInt=0,sImax=0,s0mm=0,sbeta=0,sFv=0,sBvDv=0;
8455 double
     sIs=0,sIa=0,sTe=0,sDe=0,sBv=0,sTeVib=0,sJDmin=0,sJcountnum=0;
8456 double sbJ=0;
8457 char sfnstr[1000];
8458 FILE *SROT;
8459 if (DEBUG>sdebugflag) {
8460 fprintf(DBG,"\n\nTop of singlet_JK. Molecule %s; State %s.\n\n",\
8461
         MOL[sM].Mol,MOL[sM].s[sS].Name);
8462 fflush(DBG);
8463 }
     /* Find lowest-level temperature designation */
8464 if(MOL[sM].s[sS].T[0]!=0){
8465
       sT=MOL[sM].s[sS].T[0];
8466 if (DEBUG>sdebugflag) {
8467 fprintf(DBG, "Temperature defined at state level: %f", sT);
8468 fflush(DBG);
8469 }
8470
       }
8471 else{
8472
       if(MOL[sM].T!=0){
8473
         sT=MOL[sM].T;
8474 if (DEBUG>sdebugflag) {
8475 fprintf(DBG, "Temperature defined at molecule level: %f", sT);
8476 fflush(DBG);
8477 }
8478
         }
8479
       else{
8480
         sT=TEMP;
```

```
8481 if (DEBUG>sdebugflag) {
8482 fprintf(DBG, "Temperature defined at global level: %f",sT);
8483 fflush(DBG);
8484 }
8485
         }
       }
8486
8487 if(sT==0){
8488
       fprintf(PAR, "WARNING!! temperature defined as zero for state ");
       fprintf(PAR,"%s of molecule
8489
     %s.\n\n",MOL[sM].s[sS].Name,MOL[sM].Mol);
8490
       }
      /* get the necessary info -- the sOmm variable is there because for
        singlet states, the only difference in the energy functions I'm
        using here is that for Case a, Lambda occurs in Fv(J). So, I will
        always put Lambda in the energy term -- it just gets multiplied by
        zero if the case is b. */
8491 if (MOL[sM].s[sS].Ca>-1) { /* if this is Hund's Case a */
8492
       sC=0;
8493
       sCa=MOL[sM].s[sS].Ca;
8494
       sBe=CA[sCa].Be;
8495
       sAe=CA[sCa].ae;
8496
       sTe=CA[sCa].Te;
8497
       swe=CA[sCa].we;
8498
       swexe=CA[sCa].wexe;
8499
       sg=CA[sCa].g;
8500
       sI=CA[sCa].I;
8501
       sL=CA[sCa].L;
      /* This is the place to add in scan for the constant beta */
8502
       sOmm=1;
8503 if(DEBUG>sdebugflag){
8504 fprintf(DBG,"State is Case (a).\n");
8505 fprintf(DBG,"Be=%f; ae=%f; Te=%f; we=%f; wexe=%f;
     \n",sBe,sAe,sTe,swe,swexe);
8506 fprintf(DBG,"sg=%d; sI=%f; sL=%d; sOmm=%f ",sg,sI,sL,sOmm);
8507 fflush(DBG);
8508 }
8509
       }
8510 if (MOL[sM].s[sS].Cb>-1) { /* if this is Hund's Case b */
8511
       sC=1;
       sCb=MOL[sM].s[sS].Cb;
8512
       sBe=CB[sCb].Be;
8513
8514
       sAe=CB[sCb].ae;
8515
       sTe=CB[sCb].Te;
8516
       swe=CB[sCb].we;
8517
       swexe=CB[sCb].wexe;
8518
       sg=CB[sCb].g;
8519
       sI=CB[sCb].I;
8520
       sL=CB[sCb].L;
8521
       sp=CB[sCb].p;
8522
        /* add in scan for beta if that gets included */
8523
       sOmm=0;
8524 if (DEBUG>sdebugflag) {
8525 fprintf(DBG,"State is Case (b).\n");
```

```
8526 fprintf(DBG,"Be=%f; ae=%f; Te=%f; we=%f; wexe=%f;
     \n",sBe,sAe,sTe,swe,swexe);
8527 fprintf(DBG,"sg=%d; sI=%f; sL=%d; sp=%d; sOmm=%f
     ",sg,sI,sL,sp,sOmm);
8528 fflush(DBG);
8529 }
8530
      }
      /* Calculate some stuff that will be useful later */
8531 if(swe!=0) sDe=4*pow(sBe,3)/(swe*swe); /* Centrifugal distortion
        */
8532 if(DEBUG>sdebugflag){
8533 fprintf(DBG,"sDe is %f;\n",sDe);
8534 fflush(DBG);
8535 }
8536 if(sg!=0){
8537
       sIs=1; /* Equivalent to: sIs=(2*sI+1)*(sI+1); */
8538
       sIa=sI/(sI+1); /* Equiv. to: sIa=(2*sI+1)*sI; */
8539 if(DEBUG>sdebugflag){
8540 fprintf(DBG,"sIs=%f; sIa=%f; \n",sIs,sIa);
8541 fflush(DBG);
8542 }
8543
       }
8544 if(sL==0){ /* if this is a Sigma state */
       fprintf(PAR, "STATE %s is a Sigma", MOL[sM].s[sS].Name);
8545
8546 if(DEBUG>sdebugflag){
8547 fprintf(DBG,"STATE %s is a Sigma",MOL[sM].s[sS].Name);
8548 fflush(DBG);
8549 }
8550
       if (sg!=0) { /* and this is a homonuclear molecule */
8551
         if(sp==+1){ /* and this is a Sigma+ state */
8552
           fprintf(PAR,"+ ");
8553 if(DEBUG>sdebugflag){
8554 fprintf(DBG,"+ ");
8555 fflush(DBG);
8556 }
8557
           if (sg==+1) { /* and the state is gerade */
           fprintf(PAR, "gerade state and even K's are (+), ");
8558
8559 if(DEBUG>sdebugflag){
8560 fprintf(DBG, "gerade state and even K's are (+), ");
8561 fflush(DBG);
8562 }
8563
             MOL[sM].s[sS].pmsymm=+1;
8564
             if(fmod(sI,1.0)==0){
8565
               MOL[sM].s[sS].Isymm=+1;
               fprintf(PAR,"s (boson) \n");
8566
8567 if(DEBUG>sdebugflag){
8568 fprintf(DBG,"s (boson)\n");
8569 fflush(DBG);
8570 }
8571
                }
8572
             if(fmod(sI,1.0)==0.5){
8573
               MOL[sM].s[sS].Isymm=-1;
                fprintf(PAR,"a (fermion) \n");
8574
```

```
8575 if(DEBUG>sdebugflag){
8576 fprintf(DBG,"a (fermion)\n");
8577 fflush(DBG);
8578 }
8579
                }
              }
8580
8581
           else{ /* and the state is ungerade */
           fprintf(PAR, "ungerade state and even K's are (+), ");
8582
8583 if(DEBUG>sdebugflag){
8584 fprintf(DBG, "ungerade state and even K's are (+), ");
8585 fflush(DBG);
8586 }
8587
             MOL[sM].s[sS].pmsymm=+1;
              if(fmod(sI,1.0)==0){
8588
8589
                MOL[sM].s[sS].Isymm=-1;
                fprintf(PAR, "a (boson) \n");
8590
8591 if (DEBUG>sdebugflag) {
8592 fprintf(DBG,"a (boson) \n");
8593 fflush(DBG);
8594 }
8595
                }
8596
              if(fmod(sI,1.0)==0.5){
                MOL[sM].s[sS].Isymm=+1;
8597
                fprintf(PAR,"s (fermion) \n");
8598
8599 if(DEBUG>sdebugflag){
8600 fprintf(DBG,"s (fermion)\n");
8601 fflush(DBG);
8602 }
8603
                }
              }
8604
           }
8605
8606
         else{ /* and this is a Sigma- state */
           fprintf(PAR, "- ");
8607
8608 if (DEBUG>sdebugflag) {
8609 fprintf(DBG,"-");
8610 fflush(DBG);
8611 }
8612
           if (sg==+1) { /* and the state is gerade */
8613
           fprintf(PAR, "gerade state and even K's are (-), ");
8614 if(DEBUG>sdebugflag){
8615 fprintf(DBG, "gerade state and even K's are (-), ");
8616 fflush(DBG);
8617 }
8618
             MOL[sM].s[sS].pmsymm=-1;
              if(fmod(sI,1.0)==0){
8619
8620
                MOL[sM].s[sS].Isymm=-1;
                fprintf(PAR, "a (boson) \n");
8621
8622 if (DEBUG>sdebugflag) {
8623 fprintf(DBG, "a (boson) \n");
8624 fflush(DBG);
8625 }
8626
8627
              if(fmod(sI,1.0)==0.5){
8628
                MOL[sM].s[sS].Isymm=+1;
```

```
fprintf(PAR, "s (fermion) \n");
8629
8630 if(DEBUG>sdebugflag){
8631 fprintf(DBG,"s (fermion)\n");
8632 fflush(DBG);
8633 }
8634
                }
              }
8635
8636
           else{ /* and the state is ungerade */
8637
           fprintf(PAR, "ungerade state and even K's are (-), ");
8638 if(DEBUG>sdebugflag){
8639 fprintf(DBG, "ungerade state and even K's are (-), ");
8640 fflush(DBG);
8641 }
             MOL[sM].s[sS].pmsymm=-1;
8642
8643
              if(fmod(sI,1.0)==0){
8644
                MOL[sM].s[sS].Isymm=+1;
8645
                fprintf(PAR, "s (boson) \n");
8646 if (DEBUG>sdebugflag) {
8647 fprintf(DBG,"s (boson)\n");
8648 fflush(DBG);
8649 }
8650
                }
              if(fmod(sI,1.0)==0.5){
8651
8652
                MOL[sM].s[sS].Isymm=-1;
8653
                fprintf(PAR,"a (fermion) \n");
8654 if(DEBUG>sdebugflag){
8655 fprintf(DBG, "a (fermion)\n");
8656 fflush(DBG);
8657 }
8658
                }
             }
8659
           }
8660
         }
8661
8662
       else{ /* and this a heteronuclear molecule */
8663
         if(sp==+1){
8664
           fprintf(PAR,"+ state and even K's are (+)\n");
8665
           MOL[sM].s[sS].pmsymm=+1; /* and a Sigma+ state */
8666 if (DEBUG>sdebugflag) {
8667 fprintf(DBG,"+ state and even K's are (+)\n");
8668 fflush(DBG);
8669 }
8670
           }
8671
         else{
           fprintf(PAR, "- state and even K's are (-)\n");
8672
           MOL[sM].s[sS].pmsymm=-1; /* and a Sigma- state */
8673
8674 if(DEBUG>sdebugflag){
8675 fprintf(DBG, "- state and even K's are (-)\n");
8676 fflush(DBG);
8677 }
8678
           }
         }
8679
8680
       }
8681 else{ /* if not a Sigma state, print info to the parameter file */
       fprintf(PAR, "STATE %s is a ",MOL[sM].s[sS].Name);
8682
```

```
8683 if(DEBUG>sdebugflag){
8684 fprintf(DBG,"STATE %s is a ",MOL[sM].s[sS].Name);
8685 fflush(DBG);
8686 }
8687
       switch(sL){
8688
         case 1:
8689 if(DEBUG>sdebugflag){
8690 fprintf(DBG,"Pi state\n ");
8691 fflush(DBG);
8692 }
8693
           fprintf(PAR,"Pi state\n");
8694
           break;
8695
         case 2:
8696 if(DEBUG>sdebugflag){
8697 fprintf(DBG, "Delta state\n ");
8698 fflush(DBG);
8699 }
8700
           fprintf(PAR, "Delta state\n");
8701
           break;
8702
         case 3:
8703 if(DEBUG>sdebugflag){
8704 fprintf(DBG,"Phi state\n ");
8705 fflush(DBG);
8706 }
8707
           fprintf(PAR,"Phi state\n");
8708
           break;
8709
         default:
8710 fprintf(PAR, "state with Lambda>3 -- an exotic state\n");
8711 fprintf(PAR, "Interpret the results from this program with
     care.\n");
8712
           break;
         }
8713
8714
       }
8715 if(MOL[sM].s[sS].Dist!=-1){
      /* Estimate J/K max. This comes from taking the derivative of the
        population distribution and setting it equal to zero. */
8716
       sBv=sBe-sAe/2;
8717
       saA=sBv/(kB*sT);
       sJMAX=1/sqrt(2*saA) - 0.5;
8718
8719
       sJMAXc=ceil(sJMAX);
8720
       sJMAXf=floor(sJMAX);
     /* Note the Omega(=Lambda for singlet states) in the next calcula-
        tion. The prefactor, called sOmm, is set to zero for Case b states
        and to one for Case a states. So, the energy should be calculated
        properly for either state */
8721
       saA=(sBv*(sJMAXc*(sJMAXc+1)-sOmm*sL*sL))/(kB*sT);
8722
       sImax=(2*sJMAXc+1)*exp(-saA);
8723
       saA=(sBv*(sJMAXf*(sJMAXf+1)-sOmm*sL*sL))/(kB*sT);
       sInt=(2*sJMAXf+1)*exp(-saA);
8724
8725 if (DEBUG>sdebugflag) {
8726 fprintf(DBG,"sBv=%f; saA=%f; sJMAX=%f; sJMAXc=%f; aJMAXf=%f\n",\
8727
         sBv,saA,sJMAX,sJMAXc,sJMAXf);
8728 fprintf(DBG, "sImax is %f; sInt is %f --- ", sImax, sInt);
```

```
8729 fflush(DBG);
8730 }
       if((sImax)<(sInt)){sJMAX=sJMAXf;}</pre>
8731
8732
       else{sJMAX=sJMAXc;}
8733 if(DEBUG>sdebugflag){
8734 fprintf(DBG, "sJMAX is now %f\n ", sJMAX);
8735 fflush(DBG);
8736 }
      /* Find an upper limit for J/K corresponding to the user specifica-
        tion. To find out where this equation comes from, see the docu-
        mentation, particularly the documentation found in files or di-
        rectories with the word "trick" in the name. Note that this trick
        is only good down to a cutoff intensity of about 1/10,000 of the
        maximum value. */
8737
       saA=sBv/(kB*sT);
8738
       sJcut=sqrt((-2/saA)/(JKm + JKb/(log(JKCUT)))) + 1/(2*saA) - 0.5;
8739
       sJcut=ceil(sJcut);
8740 if (DEBUG>sdebugflag) {
8741 fprintf(DBG,"JKCUT is %f; sJcut is %f\n",JKCUT,sJcut);
8742 fflush(DBG);
8743 }
      /* check this number and chastise programmer if not good... Also, if
        not good, find a better number using a less elegant method. */
8744
       saA=(sBv*(sJcut*(sJcut+1)-sOmm*sL*sL))/(kB*sT);
8745
       sInt=(2*sJcut+1)*exp(-saA);
8746
       saA=(sBv*(sJMAX*(sJMAX+1)-sOmm*sL*sL))/(kB*sT);
8747
       sImax=(2*sJMAX+1)*exp(-saA);
8748 if (DEBUG>sdebugflag) {
8749 fprintf(DBG,"sInt=%f; sImax=%f \n ",sInt,sImax);
8750 fflush(DBG);
8751 }
8752
       if((sInt/sImax)>JKCUT){
8753
         if(JKCUT>0){ /* put back to 0.0001 */
8754
           printf("Dammit... Go fix the J/K business... \n");
8755
           printf("The calculated sJcut is %5.4f ",sJcut);
8756
8757
         sJck=1:
8758
         while(sJck==1){
8759
           sJcut++;
8760
           saA=(sBv*(sJcut*(sJcut+1)-sOmm*sL*sL))/(kB*sT);
8761
           sInt=(2*sJcut+1)*exp(-saA);
           if((sInt/sImax)<JKCUT){
8762
             sJck=0;
8763
8764
             }
8765
           } /*vvvvvvvv put back to 0.0001 vvvvvvv*/
8766
         if(JKCUT>0) printf("The refined one is %5.4f \n",sJcut);
8767
         }
       }
8768
      /* There can't be more than one omega here -- check for the distribu-
        tion to be defined in a file. */
8769 if (MOL[sM].s[sS].Dist==-1) {
8770
       sD=0:
```

537

```
8771
       if(sC==0){
         sJcut=CA[sCa].Jmax;
8772
8773
         sJDmin=CA[sCa].Jmin;
8774
         }
8775
       if(sC==1){
8776
         sJcut=CB[sCb].Kmax;
8777
         sJDmin=CB[sCb].Kmin;
8778
         }
8779 if(DEBUG>sdebugflag){
8780 fprintf(DBG, "Distribution is by file.\n ");
8781 fflush(DBG);
8782 }
8783
       }
      /* Allocate memory for J/K array. Assign s/a and +/- flags. */
8784 sVnum=MOL[sM].s[sS].v[0].vnum; /* in other functions, where there
        might be multiple Omegas, this is vnum*numomega (so far as memory
        allocation goes) */
8785 MOL[sM].s[sS].nV=sVnum;
8786 MOL[sM].s[sS].nr=sVnum;
8787 MOL[sM].s[sS].r=(rotset*)calloc(sVnum,sizeof(rotset));
8788 MOL[sM].s[sS].rc=(rotset*)calloc(30,sizeof(rotset));
8789 for(sa=0;sa<sVnum;sa++){
8790
       MOL[sM].s[sS].r[sa].k=sJcut+1;
8791
       MOL[sM].s[sS].r[sa].j=sJcut+1;
8792
     MOL[sM].s[sS].r[sa].J=(double*)calloc((sJcut+1),sizeof(double));
       MOL[sM].s[sS].r[sa].EJ = (double*) calloc((sJcut+1),
8793
     sizeof(double));
8794
       MOL[sM].s[sS].r[sa].PJ = (double*) calloc((sJcut+1),
     sizeof(double));
       MOL[sM].s[sS].r[sa].CJ = (double*) calloc((sJcut+1),
8795
     sizeof(double));
      /* I'm not allocating for K, even for Case b, because for singlet
        Case b states J=K */
8796
       }
      /* Loop through J/K values, calculating energies and populations
        (include nuclear effects if applicable). Only one energy calcu-
        lation is needed here since the energy equation I'm using here is
        the same for singlet states of Hund's Cases a and b.*/
8797 for(sa=0;sa<sVnum;sa++){
8798
       sV=MOL[sM].s[sS].v[0].vlo+sa;
8799
       sImax=0;
8800
       sTeVib=sTe+(sV+0.5)*swe-(sV+0.5)*(sV+0.5)*swexe;
8801
       if(swe!=0){
8802
         sBv=sBe-sAe*(sV+0.5);
8803
         sDv=sDe+sbeta*(sV+0.5);
8804
         sBvDv=sBv/(2*sDv);
         MOL[sM].s[sS].r[sa].Jdissoc=floor((sqrt(1+4*sBvDv)-1)/2);
8805
8806
         MOL[sM].s[sS].r[sa].Kdissoc=MOL[sM].s[sS].r[sa].Jdissoc;
8807
         }
8808
       else{
8809
         MOL[sM].s[sS].r[sa].Jdissoc=RAND_MAX;
8810
         MOL[sM].s[sS].r[sa].Kdissoc=RAND_MAX;
8811
         }
```

```
8812 if (DEBUG>sdebugflag) {
8813 fprintf(DBG,"sVnum is %d; sTeVib=%f \n",sVnum,sTeVib);
8814 fprintf(DBG,"sBv=%12.6e, sDv=%12.6e, sBvDv=%12.6e,
     ",sBv,sDv,sBvDv);
8815 fprintf(DBG,"MOL[%d].s[%d].r[%d].Kdissoc=%12.6e\n",sM,sS,sa,\
8816
         MOL[sM].s[sS].r[sa].Kdissoc);
8817 fflush(DBG);
8818 }
8819
       if(MOL[sM].s[sS].r[sa].Jdissoc>((double)sJcut)){
8820
         sJcountnum=sJcut+1;
8821
         }
8822
       else{
8823
         sJcountnum=(int)(MOL[sM].s[sS].r[sa].Jdissoc);
8824 fprintf(PAR,"\nWARNING!! MOLECULE DISSOCIATION (see be-
     low)\nAccording to");
8825 fprintf(PAR,"the spectroscopic constants in the state file,\n
     state");
8826 fprintf(PAR,"%s of Molecule %s in vibration level %d dissoci-
     ates\n",\
8827
         MOL[sM].s[sS].Name,MOL[sM].Mol,sa);
8828 fprintf(PAR,"at rotational level
     J=%.1f,",MOL[sM].s[sS].r[sa].Jdissoc);
8829 fprintf(PAR, " which is significantly populated at temperature
     %.1f.\n",sT);
8830 fprintf(PAR,"Interpret results from this simulation carefully\n");
8831
         ł
8832 if (DEBUG>sdebugflag) {
8833 fprintf(DBG,"sVnum=%d; sTeVib=%f sBv=%12.6e, sDv=%12.6e\n",\
8834
         sVnum,sTeVib,sBv,sDv);
8835 fflush(DBG);
8836 }
8837
       for(sb=0;sb<sJcountnum;sb++){</pre>
         sbJ=sb+sOmm*sL;
8838
8839
         MOL[sM].s[sS].r[sa].J[sb]=sbJ;
8840
     sFv=(sBv*(sbJ*(sbJ+1)-sOmm*sL*sL))-sDv*sbJ*(sbJ+1)*(sbJ+1);
8841
         MOL[sM].s[sS].r[sa].EJ[sb]=sFv;
8842
         if(sD!=0){
8843
           sInt=(2*sbJ+1)*exp(-sFv/(kB*sT));
8844 if(DEBUG>sdebugflag){
8845 fprintf(DBG,"sb is %d; sFv=%f; sInt=%f\n",sb,sFv,sInt);
8846 fflush(DBG);
8847 }
             }
8848
8849
         if((sg!=0)&&(sD!=0)){
      /* Note the following bit of trickery. It works even if the state in
        question has Lambda>0 and doesn't need to have alternating spin-
        stats. The reason for this is that the value of Isymm is zero for
        those states. If Isymm is -1, even K's are a. If Isymm is +1, even
        K's are s. So, there are six possibilities:
      sb%2--> 0 (K is even) 1 (K is odd)
      \Isymm/
```

```
-1 -1 (a) 0 (s)
      +1 +1 (s) 2 (a)
      00 (s-equiv.) 1 (s-equiv)
      The factor for the a state is relative to the weight of the s state
        (weight with s = 1). So, only when the result of the calculation
        is -1 or 2 does sIa need to be multiplied. (but I'm lazy so the
        switch still has all the cases in it...) */
8850
           sItst=sb%2 + MOL[sM].s[sS].Isymm;
8851 if(DEBUG>sdebugflag){
8852 fprintf(DBG, "sg is 0\n");
8853 fflush(DBG);
8854 }
8855
           switch(sItst){
8856
              case 0:
8857
                sInt*=sIs;
8858 if(DEBUG>sdebugflag){
8859 fprintf(DBG,"sInt=%f",sInt);
8860 fflush(DBG);
8861 }
8862
                break;
8863
              case 1:
8864
                sInt*=sIs;
8865 if(DEBUG>sdebugflag){
8866 fprintf(DBG,"sInt=%f",sInt);
8867 fflush(DBG);
8868 }
8869
                break;
8870
              case -1:
8871
                sInt*=sIa;
8872 if(DEBUG>sdebugflag){
8873 fprintf(DBG,"sInt=%f",sInt);
8874 fflush(DBG);
8875 }
8876
                break;
8877
              case 2:
8878
                sInt*=sIa;
8879 if (DEBUG>sdebugflag) {
8880 fprintf(DBG,"sInt=%f",sInt);
8881 fflush(DBG);
8882 }
8883
                break;
8884
              default:
8885 printf("problem with nuclear stats in singlet_JK. Exiting. n");
8886
                exit(1);
8887
              }
           }
8888
         if((sD==0)&&(sb>=sJDmin)){
8889
           if(sC==0){
8890
              sf=(CA[sCa].Jmax-CA[sCa].Jmin+1)*sa+sb-sJDmin;
8891
              MOL[sM].s[sS].r[sa].PJ[sb]=\
8892
8893
                CA[sCa].Jpop[sf];
```

```
8894
             }
8895
           if(sC==1){
8896
              sf=(CB[sCb].Jnum)*sa+sb-sJDmin;
8897
             MOL[sM].s[sS].r[sa].PJ[sb]=\
8898
               CB[sCb].Jpop[sf];
             }
8899
8900
           sInt=MOL[sM].s[sS].r[sa].PJ[sb];
8901 if (DEBUG>sdebugflag) {
8902 fprintf(DBG,"sb is %d; sFv=%f; sInt=%f\n",sb,sFv,sInt);
8903 fflush(DBG);
8904 }
8905
           }
8906
         if(sD!=0) MOL[sM].s[sS].r[sa].PJ[sb]=sInt;
8907
         sImax+=sInt;
8908 if (DEBUG>sdebugflag) {
8909 fprintf(DBG,"\n sImax is %f\n\n",sImax);
8910 fflush(DBG);
8911 }
8912
         }
8913
       for(sb=0;sb<sJcountnum;sb++){</pre>
8914
         MOL[sM].s[sS].r[sa].EJ[sb]+=sTeVib;
         MOL[sM].s[sS].r[sa].PJ[sb]/=sImax;
8915
8916 if (DEBUG>sdebugflag) {
8917 fprintf(DBG,"%d\t%f\t%f\n",sb,MOL[sM].s[sS].r[sa].EJ[sb],\
8918
         MOL[sM].s[sS].r[sa].PJ[sb]);
8919 fflush(DBG);
8920 }
8921
         }
8922 if (DEBUG>sdebugflag) {
8923 fprintf(DBG,"\n out of for loop \n");
8924 fflush(DBG);
8925 }
8926
       }
8927 sprintf(sfnstr,"mkdir %s_molecules/%s",PREF,MOL[sM].Mol);
8928 system(sfnstr);
8929 sprintf(sfnstr,"%s_molecules/%s/%s_%s_rot.dat",PREF,MOL[sM].Mol,\
8930
         MOL[sM].Mol,MOL[sM].s[sS].Name);
8931 SROT=fopen(sfnstr,"w");
8932 if (SROT==NULL) {
       printf("Error opening output file (singlet_JK) %s. Exiting.\n",\
8933
8934
           sfnstr);
8935
       exit(1);
8936
       }
8937 fprintf(SROT, "## File generated by program %s.\n", PROGRAM_NAME);
8938 fprintf(SROT,"## This file contains ");
8939 fprintf(SROT, "rotational state information about\n");
8940 fprintf(SROT, "## state %s of molecule
     %s.\n",MOL[sM].s[sS].Name,MOL[sM].Mol);
8941 fprintf(SROT,"## The columns are, in order:\n## J");
8942 for(sa=0;sa<sVnum;sa++){
8943
       sV=MOL[sM].s[sS].v[0].vlo+sa;
8944
       fprintf(SROT,"\tF(v=%d)\tPop(v=%d)",sV,sV);
8945
       }
8946 fprintf(SROT,"\n");
```

```
8947 for(sb=0;sb<sJcountnum;sb++){
8948
       fprintf(SROT,"%d",sb);
8949
       for(sa=0;sa<sVnum;sa++){</pre>
         fprintf(SROT,"\t%18.10e\t%18.10e",\
8950
8951
           MOL[sM].s[sS].r[sa].EJ[sb], \setminus
8952
           MOL[sM].s[sS].r[sa].PJ[sb]);
         }
8953
8954
       fprintf(SROT,"\n");
8955
       }
8956 fflush(SROT);
8957 fclose(SROT);
8958 if(DEBUG>sdebugflag){
8959 fprintf(DBG,"\n out of sa(Vnum) loop. sa=%d\n",sa);
8960 fflush(DBG);
8961 }
8962 return;
8963 }
     /* This function can be used to read in any file whose contents con-
        sist solely of two columns of numbers. */
8964 void read_XY_file(XYlist *XY){
8965 int XYa=0;
8966 char XYsys[500];
8967 FILE *XYF;
8968 sprintf(XYsys, "wc -1 %s > %s", XY[0].f.f, TMPFILE);
8969 system(XYsys);
8970 if(DEBUG>XYdebugflag){
8971 fprintf(DBG, "XYsys is %s.\n", XYsys);
8972 fflush(DBG);
8973 }
8974 SYS=fopen(TMPFILE, "r");
8975 if(SYS==NULL){
8976 printf("Error opening system temporary file. Exiting.\n");
8977 exit(1);
8978 }
8979 fscanf(SYS,"%d",&XY[0].n);
8980 fclose(SYS);
8981 if(DEBUG>XYdebugflag){
8982 fprintf(DBG, "Here 1\n");
8983 fflush(DBG);
8984 }
8985 XY[0].x=(double*)calloc(XY[0].n,sizeof(double));
8986 if(DEBUG>XYdebugflag){
8987 fprintf(DBG, "Here 2\n");
8988 fflush(DBG);
8989 }
8990 XY[0].y=(double*)calloc(XY[0].n,sizeof(double));
8991 if(DEBUG>XYdebugflag){
8992 fprintf(DBG, "Here 3\n");
```

```
8993 fflush(DBG);
8994 }
8995 XYF=fopen(XY[0].f.f,"r");
8996 if(XYF==NULL){
8997 printf("Error opening XY input file %s. Exiting.\n",XY[0].f.f);
8998 exit(1);
8999 }
9000 if(DEBUG>XYdebugflag){
9001 fprintf(DBG, "Here 4\n");
9002 fflush(DBG);
9003 }
9004 for(XYa=0;XYa<XY[0].n;XYa++){
       fscanf(XYF,"%lf",&XY[0].x[XYa]);
9005
9006 if(DEBUG>XYdebugflag){
9007 fprintf(DBG,"X is %f ",XY[0].x[XYa]);
9008 fflush(DBG);
9009 }
9010
       fscanf(XYF,"%lf",&XY[0].y[XYa]);
9011 if(DEBUG>XYdebugflag){
9012 fprintf(DBG,"Y is %f\n",XY[0].y[XYa]);
9013 fflush(DBG);
9014 }
9015
       }
9016 fclose(XYF);
9017 return;
9018 }
```

APPENDIX D

MASS SPECTRA

These are the mass spectra, where available, taken prior to each run.



Figure 4-1.10 a: Pre-run mass spectra for CH_5^+ (upper) and $(CH_3)_2OH^+$ (lower).



Figure 4-1.10 a: Pre-run mass spectra for CO^+ (upper) and HCO^+ (lower).



Figure 4-1.10 a: Pre-run mass spectra for CS_2^+ (upper) and H_3^+ (lower).





mass spec He, Ar, NH3, H2.

Figure 4-1.10 a: Pre-run mass spectra for H_3S^+ (upper) and NH_3^+ (lower).



Figure 4-1.10 a: Pre-run mass spectra for N_2OH^+ (upper) and O_2H^+ (lower).



Figure 4-1.10 a: Pre-run mass spectra for OCS^+ (upper) and $HOCS^+$ (lower).



QHe=16.0;pHe=1.817;H20105.7,93.9;pAr=*1mT

Figure 4-1.10 a: Pre-run mass spectra for N_2 and H_2O contamination in XeH⁺ run (upper) and XeH⁺ (lower).

APPENDIX E

OPTICAL SYSTEM TRANSMISSION EFFICIENCY FORMULAE

System Efficiency Correction Curves for the

UV–VIS and VUV Spectrometry Systems

UV-VIS:

Experimental Conditions for Discussion in Section	ı 4-3.2
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nm Range	Correction Formula
200-280	$0.023255 - 0.02634921(nm/100) - 0.000962396(nm/100)^2$
	$+0.004420605(nm/100)^3 + 0.001546166(nm/100)^4$
	$-0.00009261899(nm/100)^5 - 0.0001919025(nm/100)^6$
280-400	$-0.4958784 + 0.3426415(nm/100) - 0.03660233(nm/100)^2$
	$+0.008210709(nm/100)^3 - 0.009085676(nm/100)^4$
	$-0.0008663098(nm/100)^{5} + 0.00122605(nm/100)^{6}$
	$-0.0001590731(nm/100)^7$
400-500	$-0.190926 + -0.148401(nm/100) + 0.07299296(nm/100)^{2}$
	$+0.007812568(nm/100)^{3}-0.003174406(nm/100)^{4}$
	$-0.0004277098(nm/100)^{5} + 0.00009378758(nm/100)^{6}$
500-600	$0.1477934 - 0.02398665(nm/100) - 0.003425963(nm/100)^2$
	$+0.0006856264(nm/100)^3 - 0.000064683813(nm/100)^4$
	$+0.00001120682(nm/100)^5 - 0.0000005838109(nm/100)^6$
600-700	$0.1244297 - 0.4202022(nm/1000) + 0.4710591(nm/1000)^2$
	$-0.1728368(nm/1000)^3$
700-800	$0.007713982 + 0.00113327(nm/100) - 0.0002124426(nm/100)^2$
	$-0.000009682039(nm/100)^3 - 0.000005127594(nm/100)^4$
	$0.0000008066386(nm/100)^5 - 0.00000001307592(nm/100)^6$
VUV^* :	
nm Range	Correction Formula
140-200	$0.5507449 - 1.502763(nm/100) + 1.462712(nm/100)^2$
	$-0.6013169(nm/100)^3 + 0.09019877(nm/100)^4$

200-300	$-0.3136474 + 0.2604572(nm/100) + 0.03235921(nm/100)^{2}$
	$-0.06216563(nm/100)^3 + 0.01186695(nm/100)^4$