JavaHAWKS (JAVA HITRAN ATMOSPHERIC WORKSTATION) MANUAL

For MS Windows, UNIX, LINUX, and MAC Operating Systems

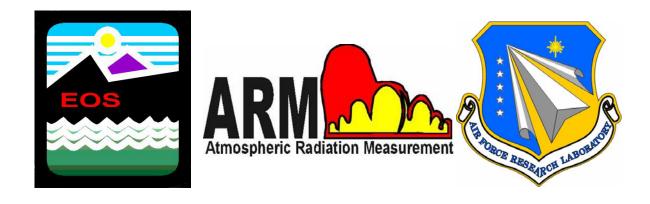


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This manual is designed to assist the user in easily adapting to the manipulation of the **HITRAN** (*High* Resolution *Tran*smission) molecular spectroscopic database and associated molecular databases by proper utilization of the JavaHAWKS software package.

1. Software Installation

The software has been written in the Java language so that we can maintain cross-platform performance, and at the same time maintain a single source code. In order to **install** and run the software, you must have a version of the Java runtime environment running on your computer. Java is common on most UNIX computers and many PC and MAC network systems. The installation program will search your computer for Java and will not complete the installation unless a suitable version of Java is installed on your computer. If this is the case, you are advised to consult your system administrator or other computer maintenance personnel about having Java installed on your computer. We cannot be responsible for assisting you in this task, since most systems administrators have specific requirements that must be met.

1.1. Installation Files

All installation files for different platforms are distributed via the HITRAN ftp-site (ftp://cfa-ftp.harvard.edu/pub/HITRAN/). These files are: (1) Win_Setup.exe; (2) Linux_Setup.bin; (3) Unix_Setup.bin; (4) MacOS_Setup.bin; (5) MacOSX_Setup.zip and (6) Software-Readme. The first five files are JavaHAWKS installers for different operating systems. The file "Installer of JavaHAWKS for Windows.exe" is for the PC, Linux_Setup is for Linux, Unix_Setup.bin is for any generic Unix system (e.g. Solaris, Linux, Unix, etc), MacOS_Setup.bin is for any Macintosh with operating system from 8.x to 9.x, and MacOSX_Setup.zip is for Macintosh with OS X operating system. Based on the platform one is using, a proper installer should be downloaded from the HITRAN ftp-site. Compared to previous installations of JavaHAWKS, these new installers will greatly simplify the procedures of installing JavaHAWKS on the user's computer, especially for Macintosh users. The Software-Readme file gives the user details about the installation of JavaHAWKS on different platforms and how the user launches the application, which is described below.

1.2. Installation Procedures

Please refer to the introductory paragraph in section 1 about having the Java runtime environment

installed on your computer before proceeding with the installation. It is the user's responsibility to decide which installation file he/she should download from the HITRAN ftp-site based on the platform he/she is using. Please refer to section 1.1 to decide which installer to download. Description of the installation procedures is given below for each of different platforms respectively.

PC Windows

1. Download the installation file "Installer of JavaHAWKS for Windows.exe" from the HITRAN FTP site.

- 2. Double click the downloaded file to launch the JavaHAWKS installation wizard.
- 3. Follow the installation procedures step-by-step until finally clicking the "Done" button.

Generic Unix/Linux

- 1. Download the installation file Unix_Setup.bin or Linux_Setup.bin from the HITRAN ftp-site to a temporary location.
- 2. Go to the temporary location from the shell.
- 3. Type in sh Unix_Setup.bin or sh Linux_Setup.bin from the command line and hit return. The JavaHAWKS installation wizard will appear.
- 4. Follow the installation procedures step-by-step until finally clicking the "Done" button.

Macintosh OS 8.0-9.x

- 1. Download the installation file MacOS_Setup.bin from the HITRAN ftp-site to a temporary location or to desktop.
- 2. Double click the downloaded file and a file called installer.bin will be created.
- 3. Double click the file installer.bin to launch the JavaHAWKS installation wizard.
- 4. Follow the installation procedures step-by-step until finally clicking the "Done" button.

Macintosh OS X

- 1. Download the installation file MacOSX_Setup.zip from the HITRAN ftp-site to a temporary location or to desktop.
- 2. Double click the downloaded file and a file called installer.bin will be created.
- 3. Double click the file installer.bin to launch the JavaHAWKS installation wizard.
- 4. Follow the installation procedures step-by-step until finally clicking the "Done" button.

1.3. Launching the JavaHAWKS application

Depending on the platform the user is employing, the way to launch the JavaHAWKS application may

be different. It also depends on how the user chooses to create the application icon during the installation. Following is a general description about how to launch the application for each different platform respectively.

PC Windows

The alternative ways to launch the JavaHAWKS application include the following.

- 1. If you choose to create an icon on the desktop during the installation, double clicking on the JavaHAWKS icon on the desktop will launch the application.
- 2. If you choose to create an icon in the **Start** menu during the installation, click the **Start** menu on the tool bar, and then from the **Program** list select JavaHAWKS to launch the application.
- 3. Locate the directory where JavaHAWKS is located from the command line. Type in JavaHAWKS.exe on the command line and hit return.

Generic Unix/Linux

- 1. First locate the directory where JavaHAWKS is located from the command line.
- 2. Type in JavaHAWKS on the command line and hit return.

Macintosh OS 8.0-9.x / OS X

- 1. If you choose to create an icon on the desktop during the installation, double clicking on the JavaHAWKS icon on the desktop will launch the application.
- 2. If you choose to create an icon in the **Start** menu during the installation, click the **Start** menu on the tool bar, and then from the Program list select JavaHAWKS to launch the application.

Paths

Put the path to the directory of JavaHAWKS instead of "~" in the Hawks.properties file for LINUX, UNIX, and Macintosh versions.

2. HITRAN and JavaHAWKS

The HITRAN Atmospheric Workstation is the latest version in a series of updates and enhancements to the international standard atmospheric molecular spectroscopic compilation. The database has a plethora of uses, the most prevalent one being as input to high-resolution transmission and radiance modeling codes of the atmosphere. Other examples of applications of HITRAN include laser propagation, hot gaseous source detection, pollution studies, background characterization, remote sensing of the atmosphere, climate assessment, greenhouse gas studies, ozone depletion, and laboratory spectroscopy.

HITRAN has traditionally supplied the necessary input for the molecular absorption part of the total attenuation in Lambert-Beer's law calculations. The other aspects of the attenuation are ascribed to aerosol extinction, continuum absorption, and scattering. The original public edition of the molecular spectroscopic database in a machine-readable form was in 1973 (the AFCRL Atmospheric Absorption Line Parameters Compilation¹). This first edition was comprised of the seven most infrared-active absorbers in the earth's atmosphere and only covered a spectral range of about 1 to 100 micrometers. In addition, the information for each available transition was essentially limited to the principal parameters: the line position (in vacuum wavenumbers, *i.e.* reciprocal centimeters, cm⁻¹), the intensity of the transition (in cm⁻¹/(molecule·cm⁻²) at 296K), the air-broadened halfwidth (cm⁻¹/atm), and the energy of the lower state of the transition (in cm⁻¹). Knowledge of the parameters at that time was limited, especially for the halfwidth which often simply was given a hard-sphere collision default value.

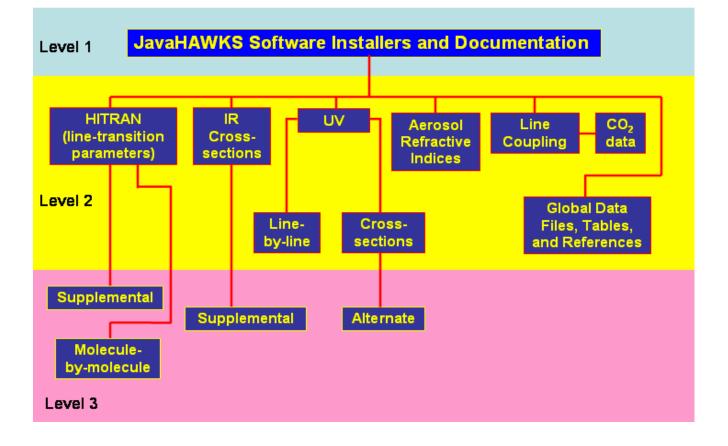
In the intervening decades, the molecular database has been substantially expanded, in terms of spectral coverage, molecular species, added parameters, increased number of molecular bands, and greatly improved accuracy. Details of the various editions and their enhancements are contained in Refs. 2-6. The archival documentation is also contained within the JavaHAWKS software.

The current edition contains 38 different species in the high-resolution portions (see Appendix B), with the inclusion of many of their significant isotopologues as well. The spectral range is from the radio through the ultraviolet (0 to about 60,000 cm⁻¹). From the initial inception of the database, the number of transitions has increased by an order of magnitude to about 1.25 million currently on the HITRAN line-by-line portion.

Another aspect of the development of the spectroscopic molecular database, or HITRAN as it is known, has been the improvement in user access. The initial versions were available on cards (a relic of the past, the cards held 80 characters of information and hence each 80-character HITRAN transition of the early editions was a single record) and on large magnetic tape. Tape became the principal means of distribution, but suffered from many inconveniences: slow sequential access, necessity of reading on mainframes, loss of integrity over time, damage, data corruption, etc. In 1992, HITRAN was made available on CD-ROM. This media enabled a great deal of data to be placed on a small, archival optical disk. More than 3000 copies of the 1992 and 1996 editions have been distributed on CD-ROM as the revolution in the use of personal computers and workstations with attached CD-ROM readers mushroomed in the early '90s. Commencing with the 2000 edition, which is HITRAN version 11.0,

HITRAN has been distributed via an ftp-site at the Harvard-Smithsonian Center for Astrophysics. Information for accessing the ftp-site is provided by completing the request form located in the HITRAN web-site, <u>http://cfa-www.Harvard.edu/HITRAN</u>.

This edition continues the initiative started with the previous HITRAN 1996 by including additional databases of significance. HITRAN itself, the line-by-line portion of the compilation, is now part of a much larger ensemble of tools for modeling. First, the compilation includes HITRAN (significantly updated as always) and several other databases for the "matter" part of the modeling of the interaction of matter and radiation. In addition to HITRAN, the compilation has directories containing crosssection data of heavier species or molecules with very dense spectral features, UV cross-sections and line-by-line parameters, supplemental files (such as for parameters in HITRAN-like format, but consigned to a subordinate folder because they may be better represented for simulation studies in the cross-section files), aerosol indices of refraction, the accompanying HAWKS software and documentation, and algorithms and data for computing line-coupling effects on broadening. The following figure illustrates the file structure of the compilation.



Equally important is the vastly improved user interface on the current compilation, JavaHAWKS, that works on UNIX, MAC OS, and MS Windows environments. The features are described in the sections below, and it becomes apparent that the user now has many more functions to examine and process the data on the compilation (or associated external data) than were previously available.

3. Initiating the Operation of JavaHAWKS

Compared to the previous edition of the HITRAN database, the 2004 edition contains files for each individual molecule with the 160-character HITRAN molecular transition format. One major new characteristic of this version of JavaHAWKS is that it works for both the 100-character HITRAN molecular transition format and the upcoming 160-character HITRAN molecular transition format. The corresponding changes to the earlier version of JavaHAWKS, therefore, have been made so that it also works for the 160-character format HITRAN files as well as the 100-character formats HITRAN files. Both the 100-character and 160-character HITRAN molecular transition formats are described in detail and are shown in Appendix D.

Launch the JavaHAWKS application as described in section 1.2. The initial JavaHAWKS screen will then appear:



The following options are now available in the menu bar:



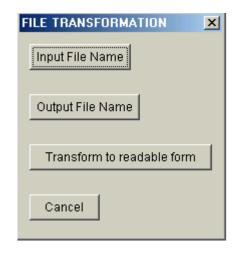
The choices produce pull-down screens or dialog boxes. Control is maintained by clicking the left mouse button.

3.1. File Option

By clicking on the FILE option, the user is given the option of performing two different tasks: **Change Format** and **Exit**. The choice, **Change Format**, is an option included for the convenience of allowing a more readable listing of the HITRAN parameters.

3.1.1. Change Format

For the input files with 100-character HITRAN format, the **Change Format** option performs the following two functions: first, it generates a HITRAN-like file with the molecule number in columns 1 and 2 replaced with the corresponding chemical symbol, e.g. 1 in column 2 is replaced by H20. Second, the vibration indices (v' and v") in columns 68 to 73 are replaced with the notation more familiar to spectroscopists, e.g. 5 1 is replaced by 001-000 for ozone. For the input files with 160character HITRAN format, **Change Format** works almost the same as working on the 100-character



HITRAN format except for a slight difference as described below. Since vibration levels in columns 68 to 97 in files with 160-character HITRAN format are already represented by the corresponding vibration notations, the **Change Format** option needs only to perform the replacement of the molecule number in columns 1 and 2 with the corresponding chemical symbol. Examples of HITRAN-like files generated using SELECT, as described in Section 3.2, are shown below along with the corresponding file generated by the **Change Format** option (the example is for ozone, molecule 3). The changes from one file to the other are highlighted in light blue.

100-Character Format HITRAN-like file:

5 .76 .000000 <mark>5 1</mark> 26 819	27 820	005 1 1 1	
5 .76 .000000 <mark>5 1</mark> 26 818	8 27 819	005 1 1 1	
.76 .000000 <mark>18 7</mark> 22 914	21 913	005 1 1 1	
.76 .000000 <mark>27 14</mark> 16 21	5 15 214	455 4 4 1	
0 .76 .000000 <mark>13 4</mark> 28 722	28 721	005 1 1 1	
001 000	26 818	27 819 005 1 1 1	
101 100	28 722	28 721 005 1 1 1	
.76 .000000 <mark>001-000</mark>	26 819 27 820	0 005 1 1 1	
.76 .000000 <mark>001-000</mark>	26 818 27 819	005111	
.76 .000000 <mark>111-110</mark>	22 914 21 913	3 005 1 1 1	
.76 .000000 <mark>003-002</mark>	16 215 15 214	4 455 4 4 1	
	5 .76 .000000 5 126 818 0 .76 .000000 18 722 914 0 .76 .000000 27 1416 215 0 .76 .000000 13 428 722 0 .76 .000000 13 428 722 0 .76 .00000 001-000 .76 .000000 001-000 .76 .000000 001-000 .76 .000000 111-110	5 .76 .000000 5 126 818 27 819 0 .76 .000000 18 722 914 21 913 0 .76 .000000 27 1416 215 15 214 0 .76 .000000 13 428 722 28 721 0 .76 .000000 13 428 722 28 721 001 000 26 818 27 819 111 110 22 914 20 914 003 002 16 215 16 215 .76 .000000 001-000 26 819 27 820 .76 .000000 001-000 26 819 27 820 .76 .000000 001-000 26 818 27 819 .76 .000000 111-110 22 914 21 913	5 .76 .000000 5 126 818 27 819 005 1 1 1 0 .76 .000000 18 722 914 21 913 005 1 1 1 0 .76 .000000 27 1416 215 15 214 455 4 4 1 0 .76 .000000 13 428 722 28 721 005 1 1 1 001 000 26 818 27 819 005 1 1 1 001 000 26 819 27 820 005 1 1 1 003 002 16 215 15 214 455 4 4 1 101 100 28 722 28 721 005 1 1 1 .76 .000000 001-000 26 819 27 820 005 1 1 .76 .000000

The option is simply run. "Input File Name" is the name of the HITRAN-like file you wish to transform into the new format. "Output File Name" is the name you select for the new file. The action is initiated by selecting "Transform to readable form", and the action is canceled by selection of the "Cancel" option.

3.1.2. Exit

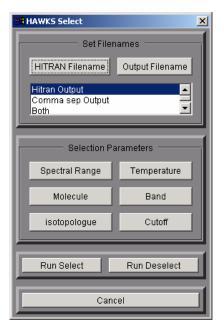
The Exit option enables an easy exit from the JavaHAWKS software.

1 1000.012900 6.440E-24 2.258E-03 .0707 .0919 1597.2180 .76 .000000 101-100

3.2. Select Option

The most important and detailed option screen is Select, which contains several choices described below.

Select is the principal operating program for a detailed manipulation of the HITRAN database, or any files in the HITRAN format. When SELECT is started, a set of default parameters, from your previous run, is retained.



28 722

28 721

005 1 1 1

3.2.1. HITRAN Filename

The first choice in the Select screen is HITRAN Filename. Clicking this button will bring up the select file input screen as shown on the right below. There are two choices for the user to bring up a HITRAN-like file. They are HITRAN File From Local Computer and HITRAN File From HITRAN Website. Corresponding to the first choice, there is a button "Select a local file" allowing you to open a

HITRAN-like file stored in your local computer by clicking it. Corresponding to the second choice is a pull down menu with all HITRAN files residing in the HITRAN web server listed. These files are either in the 100-character format or in the 160-character format. The user should keep in mind that the speed may be slow

Select HITRAN Format Input File	
HITRAN File From Local Computer	Select a local file
C [HITRAN File From HITRAN Website]	01_hit04.par 💌
Ок	Cancel

if he/she chooses to work with files on the HITRAN website. The speed depends on both the internet access speed and the size of the HITRAN file selected. If a file is selected locally, a dialog box as shown below appears and asks if you wish to open the previously used HITRAN-like file.

🏙 Do you want to use this HITRAN Database?		×
C:\HITRAN04-image\HITRAN2004\By-Molecule\01_hit(04.par	
	No	

If you answer "no," a second dialog box is displayed which contains standard features for changing drives, browsing paths, or choosing common file types.

3.2.2. Output Filename

The second choice in the <u>Select</u> screen is the <u>OUTPUT Filename</u>, which allows the user the option of storing the ASCII output file wherever it is desired. As with the "HITRAN File Name" option, the user is queried regarding the name to use for the new file, and is given the opportunity of changing drives, browsing paths, etc.

🌺 Do you want to save selection in this file?	×
C:\temp\f.out	
No Yes	

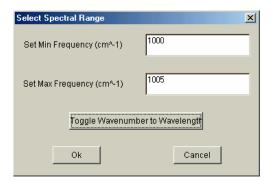
If you answer "No", it will ask you again to locate the place to store the new file. If you answer "yes" and the file the user selects already exists, the dialog below will ask you if you really want to overwrite the existing file.

Step following file already exists. Do you want to overwrite the file?	×
C:\temp\f.out	
	-
No Yes	

The Select function allows the user to generate a file in either the standard HITRAN format, or as a comma-separated values file (or both). The format of the latter file is based on the column definitions of the HITRAN database, and is of use to users who want to open the file with a program that delimits the file based on comma separators, e.g. Microsoft Excel®. An example of a comma-separated file, corresponding to the examples shown in Section 3.1.1 above, is given below:

3,2,1000.003800, 1.620E-23,	1.498E-02,.0706,.0908,	497.2245, .76	, .000000,	5,	1,26 819	,27 820	,005, 1 1 1
3,2,1000.003800, 1.620E-23,	1.498E-02,.0706,.0908,	497.2245, .76	, .000000,	5,	1,26 818	,27 819	,005, 1 1 1
3,1,1000.010100, 1.340E-24,	1.461E-02,.0709,.0912,	2246.4110, .76	, .000000,	18,	7,22 914	,21 913	,005, 1 1 1
3,1,1000.010700, 4.800E-24,	4.964E-02,.0748,.1026,	2168.1560, .76	, .000000,	27,	14,16 215	,15 214	,455, 4 4 1
3,1,1000.012900, 6.440E-24,	2.258E-03,.0707,.0919,	1597.2180, .76	, .000000,	13,	4,28 722	,28 721	,005, 1 1 1

3.2.3. Spectral Range



The third choice in this series is <u>Spectral Range</u>, which allows the user to identify the wavenumber (or wavelength) range of the data being gathered. One can choose the start and end of the selection in either wavenumber (cm⁻¹) or wavelength (μ m). This option is the essential choice (necessary and sufficient) in any SELECT procedure.

3.2.4. Molecule

The fourth optional choice in the <u>Select</u> screen is <u>Molecule</u>, which gives the user the option of including <u>All</u> the available molecules within the spectral range defined, the <u>First 7</u> molecules (coinciding to the original HITRAN), or <u>None</u>. <u>None</u> is provided as a convenient button to allow the user to subsequently select various specific assortments of molecules; hence this choice is probably the most frequently employed.

🎘 Select Mole	cule						
	First Seven	None					
⊠ н ₂ 0	⊠ co ₂	⊠ o ₃	⊠ N ₂ 0	🖾 co	⊠ сн ₄	⊠ o₂	NO NO
\boxtimes so ₂	NO2	🛛 NH3	И ниоз	🛛 он	HF	🛛 нсі	HBr
Ын	🖾 cio	🛛 ocs	⊠ н₂со	🛛 носі	⊠ N ₂	И НСИ	🛛 сн _з сі
⊠ н₂о₂	⊠ c ₂ H ₂	⊠ c ₂ H ₆	⊠ РН ₃	COF2	SF ₆	⊠ н ₂ s	🛛 нсоон
⊠ но ₂	⊠ 0	⊠ сюло2	NO+	HOBr	⊠ c ₂ H ₄	🛛 сн _з он	
Ok	Cancel						

3.2.5. Isotopologue

The fifth optional choice in the Select screen is <u>Isotopologue</u>, which gives the user the option of retaining all of the available isotopologues of a given selected molecule or selecting individual

🅾 Pick isot	opologues				· ·		
Select All		🗍 Select None			🔲 Selec	t Primary	
н ₂ о	co2	0 ₃	N ₂ O	со	сн4	0 ₂	NO
so2	NO2	NH ₃	HN03	он	HF	нсі	HBr
HI	CIO	OCS	H ₂ CO	HOCI	N ₂	HCN	сн _з сі
H ₂ 0 ₂	C2H2	C ₂ H ₆	PH3	COF ₂	SF ₆	H ₂ S	НСООН
HO2	0	CIONO ₂	NO+	HOBr	C2H4	сн _з он	
Ok		Cancel					

isotopologues to include in the output. Isotopologues are molecular entities that differ only in isotopic composition (for example ${}^{16}O{}^{12}C{}^{16}O$ and ${}^{16}O{}^{13}C{}^{16}O$) and isotopomers are molecular entities that have the same isotopic atoms, but arranged in different positions (for example ${}^{16}O{}^{16}O{}^{18}O$ and ${}^{16}O{}^{16}O$).

In the following example, the user has previously selected ozone as at least one of the molecules.

When the Isotopologue box is clicked on the ozone box, the screen at right appears (Select Isotopologues for O_3). In this example, one has chosen the odd assortment of the pair with ¹⁷O. Thus one can choose all of the isotopologues for a molecule (a typical choice, therefore the default) or specific sets of isotopologues, useful in some laboratory cell experiments. Of course, in the spectral range selected, there may not exist any data for some isotopologues.

Select isotopol	ogues for O3	×
isotopologues		Abundance
II All		J. Phys Chem. Ref. Data 13, 809-891 (1984)
None None		
	o ₃	.992901E+00
	¹⁶ 0 ¹⁶ 0 ¹⁸ 0	.398194E-02
	¹⁶ 0 ¹⁸ 0 ¹⁶ 0	.199097E-02
V .	¹⁶ 0 ¹⁶ 0 ¹⁷ 0	.740475E-03
V	¹⁶ 0 ¹⁷ 0 ¹⁶ 0	.370237E-03
Ok	Cancel	

The actual values of isotopic abundances used in HITRAN are given in the second column in the isotopologue selection box. These values enable the user to re-normalize the intensities, for example where the output is to correspond to a laboratory absorption experiment with enhanced isotopic mixtures.

3.2.6. Temperature

The sixth optional choice is <u>Temperature</u>, which lets the user set the desired temperature for the chosen set of lines. The present allowable range of temperatures is 70K to 3000K. The parameters in a

Select Temperature value	×
Set Temperature value	296.0
Ok	Cancel

HITRAN transition that depend on temperature, namely the intensity of the line and the halfwidths, are given at a standard reference of 296K. Being an atmospheric database, many transitions that are appropriate for high temperatures are liable to be missing, a fact that the user should

consider. This is particularly true in spectral regions where a molecule may have many "hot" bands originating from a low vibrational state. However, the temperature option is necessary for line files such as HITEMP, since the intensities in HITEMP line files are also given at the standard 296K and must be converted through the temperature option to the required temperature.

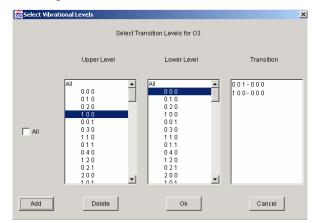
Another caveat is that the partition sums used in SELECT necessary to perform the temperature conversion may have errors at the higher temperatures, noticeable in the case of species with many very low vibrational states such as HNO₃. Nevertheless, we believe these errors are quite tolerable for most applications.

3.2.7. Band

The seventh optional choice in the <u>Select</u> screen is <u>Band</u>, which brings in the <u>VIB LEVEL</u> <u>SELECTION</u> screen, allowing the identification of vibrational levels for a specific molecule. This powerful feature allows the user to select individual vibrational bands from the input database file by highlighting a quantum level from the UPPER LEVEL box and one from the LOWER LEVEL box. The user then depresses the Add button to include his selection. This procedure can be repeated to obtain a series of bands. In addition, one can choose ALL as either the upper or lower level. In this

manner, it is possible to search the database for all transitions originating from one particular lower level to ALL possible upper levels. If a transition was highlighted by mistake, a button **Delete** is provided to delete the choice from the UPPER-LOWER box. In this case one highlights the transition not to be considered in the search and clicks on the delete button. When the selection of bands is complete, the user clicks on OK. The default for the Band option is ALL transitions.

Pick Vibrational	Levels						
H ₂ 0	co ₂	°3	N20	co	сн ₄	0 ₂	NO
so ₂	N02	NH ₃	HN03	ОН	HF	HCI	HBr
н	CIO	OCS	H ₂ CO	HOCI	N2	HCN	сн ₃ сі
H ₂ O ₂	с _z н ₂	с ₂ н ₈	РН3	COF2	SF ₈	H _Z S	нсоон
но2	0	CIONO2	N0+	HOBr	с ₂ н ₄	сн ₃ он	
Ok C	ancel						



NOTE: The use of the Band option should be considered very carefully. It should only be employed by those users thoroughly familiar with the manipulation of various vibrational transitions for specific molecules.

By clicking on a specific molecule (the example above is for O_3) the <u>Vibrational Selection for O_3 </u> screen appears. The user can now select upper level and lower level vibrational transitions for the given molecule. In the example above for O_3 , the transitions for v_1 and v_3 have been chosen. After highlighting the upper and lower levels, the user presses the **Add** button. If a level has been incorrectly added, it can be highlighted and removed by pressing the **Delete** button.

The current version of JavaHAWKS has added some new vibration levels for three classes of molecules compared to the old version. Class 3, which includes molecules NO, OH and ClO, has added new vibration levels from level 21 to 24; class 7, which includes molecule C_2H_2 , has added new vibration levels from level 11 to 28; new vibration levels from level 44 to 48 are added for class 10, which includes molecules CH₄, HNO₃, CH₃Cl, C₂H₆, SF₆, HCOOH, ClONO₂, and C₂H₄. Users who have used the last version of JavaHAWKS may also notice some changes in the vibration notations for class 7 (molecule C_2H_2).

3.2.8. Cutoff

The eighth optional choice in the **Select** screen is <u>Cutoff</u>, which gives the user the option of eliminating lines below a specified intensity. To implement, one types in the threshold intensity in exponent notation. JavaHAWKS will convert the exponent to a 3-digit value even if one number is typed in, *e.g.* 2.3E-9 becomes 2.3e-009. There are some transitions in HITRAN, and many in HITEMP, whose intensities (given at the standard 296K) are less than the single precision allowed by most compilers. In

Set Intensity Cutoff	×
Set Intensity Cutoff	2.3E-9
Ok	Cancel

that case <u>Cutoff</u> can be used to eliminate them from the selected output.

NOTE: This <u>Cutoff</u> option can be used to limit the dynamic range, but one generally does not know, a priori, what the

overall effect on simulations that use the output file will be. Therefore, this option, as with the choice of <u>Band</u>, is probably only useful to very experienced users of the database. Since the plotting package (see Section 3.6) allows control of the minimum plotted intensity, this cutoff option does not need to be used for that purpose.

3.2.9. RUN SELECT

The ninth choice in the **Select** option is <u>RUN SELECT</u>, which when activated, will produce an outline of the chosen case to run, as shown in the following example. This box is provided as a rough check for the user to verify his/her choices. If the output file already exists, a warning message will appear on this box.

😤 Hawks Run Select Info
Input File C:\HITRAN04-image\HITRAN2004\By-Molecule\01_hit04.par
Output File C:\Temp\f.out
Min Wavenumber 0.001
Max Wavenumber 20000
Number of Selected Molecules All 39
Some isotopologues
All Bands
Cutoff Value 0
Temperature Value 296.0
Warning: Output file C:\Temp\f.out already exists.
Ok Cancel
i

R HAWKS- selecting records to D:\z.out	<u>- 🗆 ×</u>
Selecting	
Extracting data from D:\ontsoft\HITRAN2000(v11.0)\HITRAN\HITRAN2k.p to file D:\z.out)ar
49 %	
	ו נ
Exit	

By clicking on the OK button the Select program will begin its operation. As the program is searching the database to select the desired lines, a window is displayed with a "thermometer" which indicates the progress of the selection process.

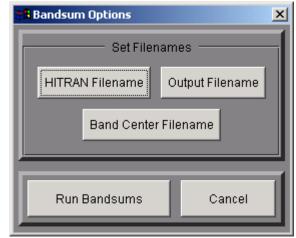
3.2.10. RUN DESELECT

The <u>RUN DESELECT</u> option is provided to the user to perform the inverse operation on the HITRAN database to Select. The concept here is to allow an editing feature for subtracting old or unwanted bands from a database and leaving the skeleton database to which one subsequently may add new or replacement data. One proceeds with the same selection criteria as one would in a normal Select procedure. The current version of this software extends the deselecting function to both isotopologues and bands, which was not the case in earlier versions of the software. In addition, in older versions of this software the choice of spectral interval was ignored: the initial database being "deselected" is taken in full. However, that **IS NOT THE CASE** with the current version. **Only lines between the initial and final wavenumber (wavelength) will be given in the resulting output file.** One should note that ample disk space needs to be considered in the general case of deselecting a few bands of a molecule from the HITRAN database. The resulting database that is written may very well be almost the same size as the original.

3.3. Band Stats Option

The **Band Stats** option runs the Bandsum program on a given file of data, or on the entire HITRAN database, for one or more molecules. The output gives: the number of lines for every band of each isotopologue; the minimum and maximum wavenumber, J values, line intensities, broadening

parameters, line shift; sum of the line intensities; and additional spectroscopic statistics of use for in-depth analysis. At the end of the output, a new section called Summary of Missing Bands is attached. Information contained in each line of this section includes the missing upper and lower vibrations for a specific molecule and isotopologue. This is a new feature to the previous version of JavaHAWKS. The program accessed by selecting the **Band Stats** option from the main menu will give the dialog box as shown here.



The HITRAN Filename and OUTPUT Filename options are used in the same way as described above in Sections 3.2.1, and 3.2.2 for the Select Option. Selecting the Band Center Data options brings up the dialog box that is used to select a file of band centers for each isotopologue of every molecule. Bandstats will work for both the 100- and 160-character line formats.

Do you want to use this bandcentral file?	×
C:\JHawks\Hawks\bandcent.dat	
No Yes	

The following bandcent input file example is for the new 160-character format:

1	161 '	0 0	1'	T	1	0	0 '	98.877	7
1	161 '	0 0	1'	I	0	2	0'	604.300	7
1	161 '	0 3	0'	1	0	2	0'	1515.163	7
1	161 '	0 2	0'	I	0	1	0'	1556.8804	
1	161 '	0 1	0'	I	0	0	0'	1594.7498	
1	161 '	1 0	0'	I	0	1	0'	2062.306	
1	161 '	0 0	1'	I	0	1	0'	2161.183	
1	161 '	0 3	0'	I	0	1	0'	3072.046	7
1	161 '	0 2	0'	1	0	0	0'	3151.6302	5
1	161 '	1 1	0'	1	0	1	0'	3640.245	7
1	161 '	1 0	0'	1	0	0	0'	3657.0532	21

Users will probably employ the default file either "Bandcent_Newformat.dat" or "Bandcent_Oldformat.dat" located in the HAWKS folder under JavaHAWKS. Advanced users may want to edit these files to tailor them to specific molecules being investigated.

The program is executed by selecting the **RUN BAND SUM** option. An ASCII table, with the filename selected with the **OUTPUT Filename** option, is created. A summary dialog box and a pair of "thermometer" boxes are displayed to indicate the status of the calculation.

Bandsum Run Info 🛛 🔀	Selecting
Input File D:\f.doc Output File D:\fBS2.doc Bandcenter File C:\JHawks\Hawks\bandcent.dat	Writing to D:VBS2.doc 54 %
Ok Cancel	Exit

The output statistics are as follows and are printed in one single line:

where V_0 is the bandcenter in cm⁻¹, Iso is the shorthand code for the isotopologue, V' is the upper-state

vibrational band quanta, V" is the lower-state vibrational band quanta, V_{min} is the minimum wavenumber found for the band (rounded down to the nearest integer wavenumber), V_{max} is the maximum wavenumber found for the band (rounded up to the nearest integer wavenumber), #lines is the number of transitions found for the band, ΣS is the sum of intensities in the band, S_{min} is the minimum intensity in the band, S_{max} is the maximum intensity in the band, J''_{max} is the maximum lowerstate rotational quantum value found. On the second line for the band, g_{min} is the minimum lower-state rotational quantum value found, E''_{min} is the minimum lower-state energy, E''_{max} is the maximum lower-state energy, g_{Smin} is the minimum value of self-broadened halfwidth, g_{smax} is the maximum value of self-broadened halfwidth, n_{min} is the minimum value of the temperature-dependence coefficient, n_{max} is the maximum value of the temperature-dependence coefficient, shiftmin is the maximum value of self-broadened halfwidth, is the minimum value of the pressure-shift, and shiftmax is the maximum value of the pressure-shift.

If you request a band in the bandcent.dat input file that is not found in the HITRAN-like file, the output will indicate zero lines, and pre-set extrema will be given for the ranges (50000 for the minima, and 0 for the maxima). On the other hand, if a band exists in the HITRAN file that was not requested in the bandcent.dat file, a summary is indicated at end of the output to inform you that you may want to add this band to your search.

3.4. Sort Option

3.4.1. Sort

The **Sort** option allows the user to sort by wavenumber of a HITRAN-like file (the field defined by positions 4 through 15), or to merge numerous individual HITRAN-like files into a single file.

Select file to	sort ?X
Look jn: 🔁) Tmp 💽 🗢 🖻 📸 🛛
1.0UT 2.0UT	
File <u>n</u> ame:	1.0UT <u>O</u> pen
Files of <u>t</u> ype:	All Files (*.*) Cancel

Select sort res	sult		<u>?</u> ×
Save jn: 🔂	Tmp	- 🗢 🔁	≠ 🎟 🕈
1.0UT			
🔟 2.0UT			
File <u>n</u> ame:	sortjout		<u>S</u> ave
Save as <u>t</u> ype:	All Files (*.*)	-	Cancel

17

When choosing the **Sort** option the user is asked to identify the physical location of the particular file to be sorted as displayed in the following dialog box on the left above.

Next the user is asked to identify the name and location for the sorted result as shown in the dialog box to the right above.

Before running Sort, users may select the sorting type by going into the <u>SORT TYPE</u> window from the Sort pull-down menu of the main window. There are two sort types provided: Sort by Wave Number and Sort by Quantum Number. When Sort by Wave Number is selected, the current version of JavaHAWKS queries the wavenumber first, and, if necessary, then queries in the order of molecule number, isotopologue number, intensity and so on, the other parameters in a transmission line. When Sort by Quantum Number is selected, unlike Sort by Wave Number, the current JavaHAWKS only queries three other parameters in addition to the quantum numbers. They are the molecule number, isotopologue number in the order that may be queried.

If the querying finds that two lines compared are identical, one line was discarded in the last version of JavaHAWKS. However, this is not the case of the current version of JavaHAWKS. In the current version, if two lines are identical, the second of the two lines encountered is not deleted but flagged with a "*" at its end. Users can conveniently use this feature to find out if there are any duplicated lines in a HITRAN-like file. Users may also need to remember that the sorted file with duplicated lines in it cannot be used as a normal HITRAN data file.

3.4.2. Merge

The second choice in the **Sort** pull-down screen is **Merge**. The **Merge** option allows the user to merge two or more separate HITRAN-like files into one file and gives the user the option of sending this merged file to whatever location is desired. The following screens will appear asking the user to identify files to be merged:

Select file to merge	Select merge result	<u>? x</u>	Select file to merge	<u>?</u> ×
Look in: 🔄 Tmp 💽 🖛 🗈 📸 🏢 -	Savejn: 🔄 Tmp	▼ ← 1 → 1	Look in: 🔁 Tmp	- 🖛 🗈 💣 🎟 -
■ 1.0UT	1.0UT		☐ 1.0UT ☐ 2.0UT	
100T 20UT sort.out	司 1.0UT 司 2.0UT 司 sort.out		2.DUT	
Eas sort. our	i sort. out		and solution	
l			1	
File name: 1.0UT	File name: merge.out	Save	File name: 2.0UT	<u>O</u> pen
Files of type: All Files (*.*) Cancel	Save as type: All Files (*.*)	▼ Cancel	Files of type: All Files (*.*)	▼ Cancel
	January Ja			

Click on the <u>CANCEL</u> button to end the selection of files being merged. A new dialog box will now appear (at the right above) directing the naming of the file containing the merged results.

NOTE: Merge will also sort the resulting file, if (and only if), the lines in the individual HITRAN files are already in order of increasing wavenumber. If there is an identical line existing in more than one file to be merged (that is there is an overlap between files), this line will be duplicated but flagged at its end with a "*" except the first one in the merging resulting file. Users may need to remember that the merged file with duplicated lines in it can not be used as a normal HITRAN data file.

3.5. Internet Option

The **Internet** option has been added to the main menu bar in the latest version of JavaHAWKS. This option allows users to interact with the outside world through the Internet by providing access to the HITRAN database and other data sources. There are five choices under the Internet option. They are <u>HITRAN Website</u>, <u>HITRAN FTP Site</u>, <u>JPL Submillimeter Data</u>, <u>Cologne Spectroscopy Data</u>, and <u>CfA UV Xsection Data</u>.

3.5.1 HITRAN Website

When the <u>HITRAN Website</u> is selected under the **Internet** Option, JavaHAWKS will start the internet connection and bring users directly to the updates webpage of the HITRAN website (http://www.hitran.com/hitran/updates.html). From this page, you can get the most recent JavaHAWKS software as well as the most recent HITRAN updates.



3.5.2 HITRAN FTP Site

When the <u>HITRAN FTP Site</u> is selected under the **Internet** option, JavaHAWKS will start the internet connection and bring users to the location to download archival HITRAN files in the HITRAN FTP site.

3.5.3 JPL Submillimeter Data

The third choice under the **Internet** option is <u>JPL Submillimeter Data</u>. This choice will lead you to access to JPL (Jet Propulsion Laboratory)

Downloading Data From JPL	And Converted Into Hitran File 🛛 🔀
Data Source: Jet Propu	Ilsion Laboratory (JPL)
Select Frequency Unit	Wave Number(cm^-1)
	O Wavelength (um)
Set Min Frequency	0.1
Set Max Frequency	1.0
Select a Molecule	16001 O-atom
Output File Name	Browse Internet
Ok	Cancel

submillimeter catalog,⁷ download a JPL catalog file from the database and then convert the downloaded data into a HITRAN format file. Selection of this item will bring in a screen called <u>Downloading Data</u> <u>From JPL and Converting Into HITRAN File</u>, which lets you set up the downloading parameters. The parameters include wavenumber units (in wavenumber or in wavelength), minimum wavenumber, maximum wavenumber and the molecule you are interested in. The <u>Output File Name</u> button will ask you to specify a location to save the converted data. Pressing the <u>Browse Internet</u> button will initialize the data downloading over the internet and then the conversion to a HITRAN format file. This reformatting includes converting the line intensities to the HITRAN units and standard of 296K, changing the vibrational notation, and converting the JPL error bars to the HITRAN system. Since the JPL catalog does not contain information about collision-broadening, these parameters are left blank in the conversion to the HITRAN-like file. A file with the data in its original format will also be saved under the current JavaHAWKS working directory.

Users should keep in mind that downloading data over the internet might fail if there is an internet connection problem or if the host of the data source has shut down its server. JavaHAWKS provides a window message for you, letting you know if it has successfully downloaded the

😹 JavaHAWKS Message Box
Download data from JPL successfully.
Total lines selected: 360
Data is converted into HITRAN 160-character format,
And is saved into the file C:\JHawks\f.out.

data. If it is successful, a window message comes up telling you how many lines you have downloaded and where you have saved the converted file. Otherwise, a message of internet connection failure shows up. Depending on the user's internet connection speed, the download process may be slow.

3.5.4 Cologne Spectroscopy Data

🛞 Downloading Data From Cologne Site And Converted Into HITRAN File 🛛 🗶		
Data Source: Cologne Database for Molecular Spectroscopy (CDMS)		
Select Frequency Unit	(● (Wave Number(cm<1))	
	C Wavelength (um)	
Set Min Frequency	1.0E-5	
Set Max Frequency	100.0	
Select a Molecule	027501 HCN v=0 💌	
Output File Name	Browse Internet	
Ok	Cancel	

The fourth choice under the **Internet** option is <u>Cologne Spectroscopy</u> <u>Data</u>. This choice will give you access to the CDMS (Cologne Database for Molecular Spectroscopy⁸) files, download a CDMS file from the database and then convert the downloaded data into a HITRAN format file. Selection of this item will bring in a screen called <u>Downloading Data From Cologne Site And Converting Into</u> <u>HITRAN File</u>, which lets you set up the downloading parameters. The procedures to download and convert the CDMS data are same as those to download and convert the JPL data described in section 3.5.3.

3.5.5 CfA UV Xsection Data

Select A M	olecule		×
Click on a molecule to get data from:			
H ₂ 0	2	0 ₃	CO
0 ₂	so2	NO2	N2
C ₂ H ₂	N ₂ O		
Ok	Cancel		

The fifth choice under the **Internet** option is <u>CfA UV</u> <u>Xsection Data</u>. This choice allows you to download UV cross-section data from the molecular database at the Harvard-Smithsonian Center for Astrophysics (CfA) and to convert the data to a file with the HITRAN cross-section file format. Selecting this choice will bring up a screen listing those molecules with available UV cross-section data files.

More than one UV cross-section data file exists for each molecule in the molecular database at the CfA. Clicking on the molecule that you are interested in will bring up the next screen, which allows you to select one of the UV cross section data files. Specify the location you want to save the converted cross section file in HITRAN format. Clicking the <u>Browse And Convert</u> button will complete the process of data downloading and converting. The CfA absorption cross-section data are listed linearly in wavelength; the conversion to HITRAN format has created a grid linear in wavenumber. Again, downloading data over the internet may fail if there is an internet connection problem or if the host of the data source has shut down its server. A message box will come up, indicating success or failure of the download.

🌺 Convert Cfa Xsection File Into	Hitran Format Xsection File 🗙	👷 JavaHAWKS Message Box	×
******Nitrogen Dic	xide (NO2)******	Have successfully transferred Cfa xsection file so241k213.	(SC
Select a File To Convert From:	no2r35s.pub 🔽	into HITRAN xsection file C:\JHawks\f.xsc.	
Output File Name	Browse Internet And Convert		
Ok	Cancel		

3.6. Reference Option

The next pull-down screen is <u>Reference</u>. It contains three separate options: <u>Molecule</u>, <u>Wavenumber</u>, and <u>X</u>section, for obtaining information on references utilized in creating the database. If you are using **JavaHAWKS** for the first time, these three options will be "grayed" out. The reference files are in the Adobe portable document format (pdf). Java is unable to search for the appropriate reader; you must point the **JavaHAWKS** software to the correct location of either the Adobe reader or Adobe Acrobat. You do this by selecting the "Acrobat Reader" in the dialog box shown below. You may wish to

Select Acrob	at Reader	<u>?×</u>
Look in: 🔂	Acrobat	▼ 🖶 📸 🕶
ActiveX Browser Capture Frame Import Optional	PalmPilot Photoshop plug_ins Scan Users Acrobat.exe	
File <u>n</u> ame:	Acrobat.exe	<u>O</u> pen
Files of type:	All Files (*.*)	Cancel

consult your system administrator if you cannot find the reader, or are uncertain of how to proceed. Copies of the reader can be obtained from Adobe by using the link contained in the HITRAN web-site under the documentation sub-page.

After the reader has been selected, the "Molecule",

"Wavelength", and "Xsection" options will be active.

3.6.1. Molecule

The first option, <u>M</u>olecule, allows the user to address the molecular reference table utilized by the HITRAN database for identifying the series of references for the line position, line intensity, and air-broadened halfwidth. Selection of this option will open the Adobe reader with the corresponding molecule pdf file. From links in this reference table, you can obtain the abstracts relating to the HITRAN parameters (such as line positions, line intensity and air-broadened halfwidth) of a line stored in HITRAN database.

3.6.2. Wavenumber

This feature is yet to be implemented in the JavaHAWKS software. It will be added in a future version.

3.6.3. Xsection

The third option in the <u>R</u>eference pull down screen is <u>X</u>section. Selection of this option will open the Adobe reader with the corresponding cross-section references.

3.7. Plot Option

The sixth optional screen is <u>Plot</u>. The JavaHAWKS <u>Plot</u> screen has two selections: "Plot Line by Line", which allows the user to plot the "Intensity", "Transition Probability Squared" in the 100-character format ("Einstein-A coefficient" in the 160-character format), or "Lower State Energy" from HITRAN-like files as a function of wavenumber; and "Plot Xsection", which allows the user to plot the cross-section data as a function of wavenumber. Selecting "Plot Line by Line" will display the screen shown here. This screen is divided into sections. The upper section, Select Parameters, is used to open

Select new plot	X			
Select Para	meters			
Select File to Plot	Difference Plot			
X-Axis	Y-Axis			
Select Plot				
Intensity	Intensity - Entire Range			
Transition Probability Squared	Lower State Energy			
Cancel				

the file to be plotted, set the X- and Y-axes, and make difference plots. Difference plots are discussed below in Section 3.7.1. The second section of the pull-down window, Select Plot, determines what will be plotted, for example the intensity of the lines (the most common usage) or the lower state energy. Both the X-axis and Y-axis have autoscaling, so that the user can immediately create a plot by selecting one of the options in the second section.

When the button Select File to Plot is clicked, the screen on

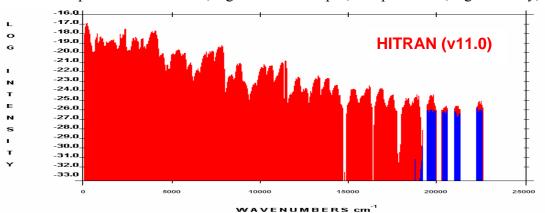
the left will appear, asking you if you want to plot a file stored in your local computer or a HITRAN file from the HITRAN web server. The user should keep in mind that plotting a file residing on the

Select HITRAN Format Plot File	×
HITRAN Format File From Local Computer	Select a local file
C [HITRAN Format File From HITRAN Website]	01_hit02.par 💌
Ok	Cancel

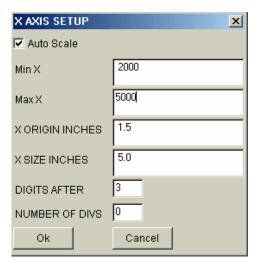
HITRAN web server may take some time. This is especially true if the user use a modem to access the internet. The resulting plot will be a stick plot. In general, when there is a high density of lines in the spectral interval, the plot displayed on the screen will have **blue** and **red**

lines. This is to indicate the maximum and minimum value in each channel. Typical computer monitors have less than 2000 horizontal and vertical pixels. However, the data may have many thousands of data points. Consequently, the data have been placed in bins corresponding to the number of display channels. The red and blue lines are used to indicate the maximum and minimum value in each display channel. One can easily expand the X-axis to see individual lines.

The first step is to select the file, e.g. HITRAN2K.par, and parameter, e.g. intensity, to plot.



The X- and Y-axes can be manually adjusted using the appropriate dialog box.



The user is provided different methods of defining the X axis for the given plot. If <u>Auto Scale</u> is chosen, the program will control the setting of the maximum and minimum for the X axis. When turning off the <u>Auto Scale</u> option, one is required to enter real numbers

Y AXIS SETUP	X
🔽 Auto Scale	
AXIS TYPE	Log 💌
AXIS STYLE	Bar 🔺 Line 💌
Min Y	0.0
Мах Ү	1.80e-23
Y ORIGIN INCHES	1.5
Y SIZE INCHES	4.0
DIGITS AFTER	0
NUMBER OF DIVISIONS	0
Ok	Cancel

in the Min X and Max X boxes. The <u>X ORIGIN</u> allows one to set the distance from the left of the screen to the X axis. <u>X SIZE</u> allows

modification of the size of the X axis. These latter two options are very useful for those who have large display screens. <u>DIGITS AFTER</u> is the number of digits after the decimal point for the axis values, and <u>NUMBER OF DIVS</u> is the number of divisions (marked off by tick marks) over the entire axis.

For the Y axis, the user is provided similar methods of defining the axis for the given plot, with two additions, "Axis Type", and "Axis Style". Axis Type allows the user to plot the Y-values in either a linear or log scale. For log plots, one enters the value in exponential format, for example 1.5e-23 (**remember to turn off Auto Scale first**). For "Axis Style" the user can select either a Bar plot (a histogram plot equal to the parameter being plotted at the corresponding wavenumber) or a Line plot (a "connect the dots" plot).

Proceeding clockwise, the first optional form of plotting the results is by <u>Intensity</u> vs wavenumber. The second optional form of plotting is by <u>Transitional Probability-Squared</u> or <u>Einstein-A coefficient</u> (depending upon whether the HITRAN file being plotted is 100-character format or the new 160-character format) vs wavenumber. The third optional form of plotting is the <u>Lower State Energy</u>. The final form of plotting is the <u>Intensity-Entire Range</u> of the applicable wavenumber. This latter choice over-rules the X-axis wavenumber selection and plots over the entire range of data in the opened file.

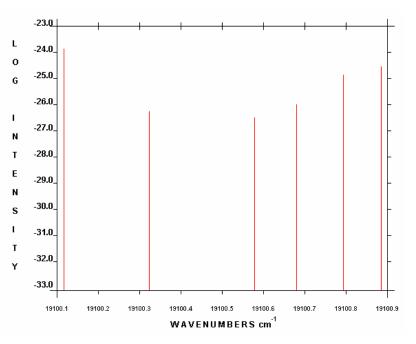
A typical plot (intensity vs wavenumber) of a HITRAN file is shown above.

3.7.1 Difference Plot

This option lets the user take the difference of two spectral plots. This can be a useful tool to determine small shifts in wavenumber (or line strength) between two files. The following screen is displayed when the **Difference Plot** option is selected:



After selecting the first file, the user is prompted to select the second file (the second file is subtracted from the first). We will use f1.out and f2.out as an example to show how Dif file works. A stick plot of f1.out is shown below:

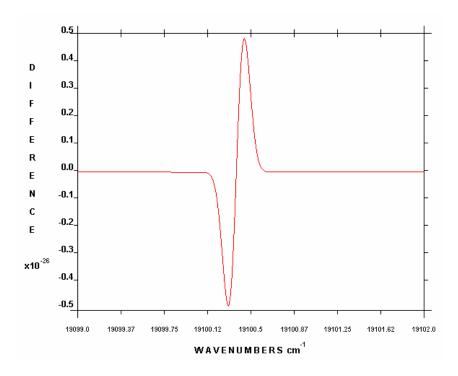


The second file (f2.out) is identical to the first except that the line at 19100.3239 cm⁻¹ has been shifted to 19100.43239 cm⁻¹. After the two files have been selected, the user is prompted to input a normalized

Enter Normalized Scaling Width	×
Normalized Scaling Width (0 ~ 1)	0.05
Ok	Cancel

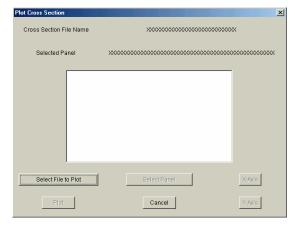
scaling width, which is a value between 0 and 1 (see the figure on left). We have arbitrarily chosen a Doppler line shape to broaden the lines for subtraction. This is not an attempt to simulate a spectroscopic feature, but simply a means chosen to

enable reasonable subtraction of lines. We used 0.5 in the current example with the resulting difference plot shown below.



3.7.2. Plotting Cross-Section Data

The HITRAN cross-sections files can be displayed on the screen and printed as a hard copy by using the "Plot Xsect" option from the "Plot" menu. HITRAN cross-section files have the extension *.xsc; however any file of the same format can be displayed using this option. The cross-section files are



organized into a series of temperature/pressure sets (or panels), which are described in Ref.5. The user is presented a series of dialog boxes after selecting the "Plot Xsect" option to select the desired file and panel. The first dialog box is shown on the left, with the choice to select a file to plot. The user should depress the "Select File to Plot" option to select a cross section file to plot. Like the "Plot Line by Line" option, the user has the choice to plot either a

file stored in the local computer or a file residing on the HITRAN web server, as shown on the left below. If the user chooses to plot a local file, a file dialog box will appear as shown on the right below.

ד 📸 🔁 🗈

<u>O</u>pen

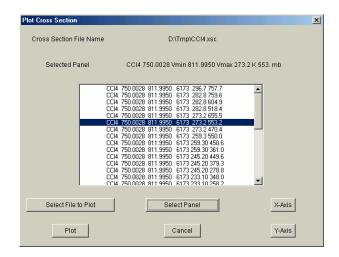
Cancel

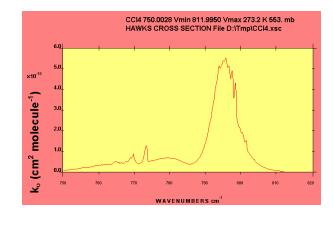
? X

Select Cross Section Plot File	×	Select File to Plot
Cocal Cross Section File	Select a local file	Look in: 🔁 Tmp
C Cross Section File From HITRAN Website	C2F6.xsc	
Ok	Cancel	
		File <u>n</u> ame: CCI4.xsc
		Files of type: All Files (*.*)

Next the user should select the temperature/pressure,

i.e. panel, of interest by highlighting the panel in the display window (shown in the left figure below), and depressing the "Select Panel" option. Finally, depress the "Plot" option to display the figure, shown below to the right.





The user can access editing features, identical to those of the line-by-line display, by selecting the "Plot" option in the upper left hand corner of the screen.

3.7.3. Edit Plot and Print Plot

Edit HAWKS Intensity file D:\Tmp\3.out			
Select Parameters			
X-Axis Y-Axis			
Select Plot			
Ok			
Cancel			

After a plot is displayed on the screen, a "Plot" option is available in the upper left hand corner of the screen. This allows the user to: "Redraw" the plot, "Print" the plot, "Edit" the plot, and "Exit" or return to the main screen.

The **Edit Plot** option allows the user to change the plot parameters. Selecting this option brings up the previously shown

X axis and Y axis dialog boxes. The X axis and Y axis choices have the same functions as described above.

A hard copy of the plot displayed on the screen can be made by using the "Print" options.

3.8. Help Option

The eighth optional pull down screen is **Help**. This option gives the user informative help on all of the molecules stored in the database as well as pertinent information on the structure and uses of the HITRAN database. A complete informative package of information on all of the molecules and isotopologues is provided within the **Help** pull-down menu. You can find historical documentation about the HITRAN database, from earliest HITRAN documentation (1973) to the most recent documentation. This informative package consists of pdf files and users can open them with Acrobat Reader to find relevant information.

3.8.1. About

Another choice in the **HELP** section is <u>About</u>, which is a standard statement describing the construction of the **JavaHAWKS** program for the HITRAN database.

4. Acknowledgments

The contributors to the spectroscopy of this effort are too numerous to cite here. We urge users of **JavaHAWKS** to consult the references contained on all transitions updated since 1986, and we apologize for any omissions or oversights that may have been made.

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APPENDIX A. Directories and Files in HITRAN (v11.0)

HITRAN (v12.0) contains the directories and files listed below with their sizes.

Directory of \Hitran04\		nad190.niedziela	85,506
HITRAN-Readme.pdf	22,517	Norman etal.dat	279,165
HAWKSmanual.pdf	~1,132,830	norman-indices.dat	308,232
Win Setup.exe	29,501,946	PalmerandWilliams.dat	32,966
Linux setup.bin	29,301,940	QuerryandTyler.dat	278,447
		Remsberg.dat	27,464
Jnix_Setup.bin	20,448,010	Richwine etal.dat	20,544
MacOS_Setup.bin	20,487,680	Shettle.dat	39,702
MacOSX_Setup.zip	20,037,001	SteeleandHamill.dat	1,800
Aerosols	<dir></dir>	SutherlandandKhanna.dat	8,113
Global_Data	<dir></dir>		
HTRAN2004	<dir></dir>	Timmermans.dat	12,154
R-XSect	<dir></dir>	Tisdale_etal.dat	321,060
line-Coupling	<dir></dir>	Toon_etal.dat	29,984
JV	<dir></dir>	Warren.dat	34,262
Directory of \Hitran04\Aero	osols\	Directory of \hitran04\Glob	al_Data
Aerosol-Readme.pdf	19,761	ref-table2004.pdf	367,716
DowningandWilliams.dat	16,412	molparam.txt	6,544
2so4T183.biermann	413,406	parsum.dat	8,359,118
		bandcent.dat	157,021
2so4T200.niedziela	161,550	TIPS 2003.zip	118,711
2so4T188.biermann	515,023	1110_2005.2ip	110,/11
2so4T210.niedziela	195,737	Directory of \hitran04\HITI	RAN2004\
2so4T193.biermann	616,640	-	
2so4T220.niedziela	298,298	By-Molecule	<dir></dir>
2so4T203.biermann	718,257	SuppleImental	<dir></dir>
2so4T230.niedziela	127,363	HITRAN04.par	280,983,978
2so4T213.biermann	819,874		
2so4T240.niedziela	264,111	Directory of \hitran04\HITI	RAN2004\By-Molecule\
2so4T215.biermann	616,640	By-Molecule-Readme.pdf	65,626
2so4T260.niedziela	298,298	01 hit04 par	10,237,752
2so4T223.biermann	616,640	02 hit04 par	10,191,906
2so4T280.niedziela	264,111	03 hit04 par	50,459,922
2so4T233.biermann	1,023,108	04 hit04 par	7,749,270
2so4T300.niedziela	195,737	05 hit04 par	
			725,274
2so4T253.biermann	1,023,108	06_hit04 par	40,733,280
2so4T263.biermann	515,023	07_hit04 par	1,041,336
2so4T273.biermann	1,327,959	08_hit04 par	16,569,360
2so4T293.biermann	1,531,193	09_hit04 par	6,294,186
no3T213.biermann	515,021	10_hit04 par	16,884,126
no3T223.biermann	616,638	11_hit04 par	4,711,608
no3T233.biermann	718,255	12_hit04 par	43,928,892
no3T253.biermann	718,255	13 hit04 par	6,864,426
no3T263.biermann	515,021	14 hit04 par	17,334
no3T273.biermann	1,023,106	15 hit04 par	99,306
no3T293.biermann	1,023,106	16 hit04 par	209,466
ce130.clapp	139,956	17 hit04 par	130,572
ce140.clapp	139,998	18 hit04 par	1,171,260
ce150.clapp	139,998	19 hit04 par	3,227,040
ce160.clapp			
	139,914	20_hit04 par	437,724
ce170.clapp	139,830	21_hit04 par	2,636,712
ce180.clapp	139,662	22_hit04.par	19,440
ce190.clapp	139,914	23_hit04.par	688,986
ce200.clapp	139,914	24_hit04.par	5,041,278
		25 hit04.par	1(22(522
ce210.clapp	139,914		16,326,522
ce210.clapp	30,046	25_11104.par 26_hit04.par	16,326,522 569,754
ce200.chapp ce210.clapp Kou_etal.dat nad160.niedziela			

29_hit04.par	11,437,362
31_hit04.par	3,367,656
32_hit04.par	4,018,896
33_hit04.par	6,286,248
34_hit04.par	324
36_hit04.par	195,372
37_hit04.par	705,996
38_hit04.par	2,102,436
39_hit04.par	3,223,638

Directory of \hitran04\HITRAN2004\Supplemental\

30_hit04.par	3,709,962
35_hit04.par	5,216,238

Directory of \hitran04\IR-XSect\

2	
IRCrossSection-Readme.pdf	59,383
C2F6 IR00.xsc	15,598,934
CCl4 IR00.xsc	2,018,175
CFC-11 IR00.xsc	16,717,448
CFC-113 IR00.xsc	55,692
CFC-114 IR00.xsc	1,496,952
CFC-115 IR00.xsc	777,852
CFC-12 IR00.xsc	21,401,118
CFC-13_IR01.xsc	745,414
CFC-14 IR01.xsc	3,898,920
ClONO2_IR04.xsc	23,732,873
HCFC-123_IR00.xsc	1,868,640
HCFC-124_IR00.xsc	669,629
HCFC-141b_IR00.xsc	1,920,354
HCFC-142b_IR00.xsc	1,984,920
HCFC-21_IR00.xsc	51,306
HCFC-22_IR01.xsc	13,926,811
HCFC-225ca_IR00.xsc	2,060,502
HCFC-225cb_IR00.xsc	2,346,000
HFC-125_IR00.xsc	592,824
HFC-134_IR00.xsc	6,703,434
HFC-134a_IR00.xsc	19,833,114
HFC-143a_IR00.xsc	4,572,846
HFC-152a_IR00.xsc	1,707,582
HFC-32_IR00.xsc	3,813,440
HNO4_IR04.xsc	204,879
N2O5_IR04.xsc	889,440
SF5cf3_IR04.xsc	1,347,810
SF6_IR00.xsc	1,328,960
Supplemental	<dir></dir>
Directory of \hitran04\IR-XSe	ect\Supplement

Directory of **\hitran04\IR-XSect\Supplemental** CFC-11-92 IR00 xsc 319 464

CFC-11-92_IK00.XSC	519,404
CFC-12-92 IR00.xsc	690,336
ClONO2-96_IR00.xsc	73,950

Directory of \hitran04\Line-Coupling\CO2\

Data_Q	<dir></dir>
Soft_Q	<dir></dir>
Test Q	<dir></dir>
LineCoupling-Readme.txt	43,511

Directory of \hitran04\UV	
Line-by-line	<dir></dir>
Cross-sections	<dir></dir>
Directory of \hitran04\UV\Li	ine-by-line

07_UV04.par 1,785,240 13_UV04.par 174,798

Directory of \hitran04\UV\Cross-sections

BrO_UV04.xsc	110,224
H2CO-UV04.xsc	925,836
N2O-UV00.xsc	143,230
NO2-UV00.xsc	571,264
NO3_UV04.xsc	176,266
O2-O2_UV04.xsc	154,960
O3-UV04.xsc	356,676
OClO_UV04.xsc	1,387,768
SO2-UV00.xsc	2,377,764

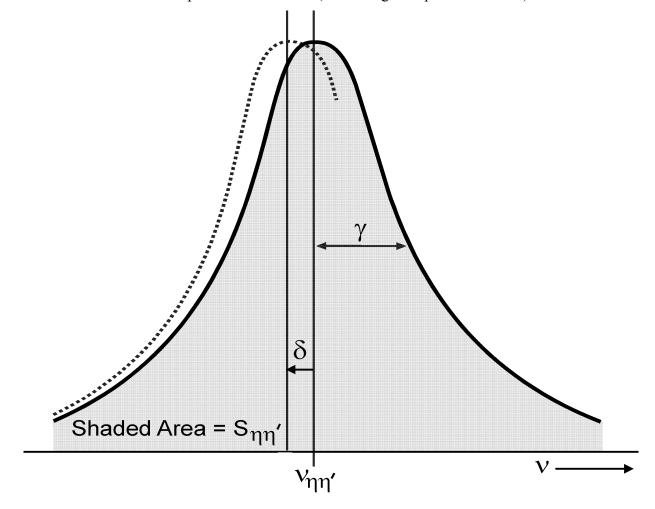
HITRAN Molecule Number	Molecule Chemical Symbol	Number of trans- itions	HITRAN Molecule Number	Molecule Chemical Symbol	Number of trans- itions
1	H ₂ O	63197	21	HOCI	16276
2	CO ₂	62913	22	N_2	120
3	O ₃	311481	23	HCN	4253
4	N ₂ O	47835	24	CH ₃ Cl	31119
5	СО	4477	25	H_2O_2	100781
6	CH ₄	251440	26	C_2H_2	3517
7	O ₂	6428	27	C ₂ H ₆	4749
8	NO	102280	28	PH ₃	11790
9	SO ₂	38853	29	COF ₂	70601
10	NO ₂	104223	30	SF ₆	22901
11	NH ₃	29084	31	H ₂ S	20788
12	HNO ₃	271166	32	НСООН	24808
13	ОН	42373	33	HO ₂	38804
14	HF	107	34	0	2
15	HCl	613	35	CIONO ₂	32199
16	HBr	1293	36	NO ⁺	1206
17	HI	806	37	HOBr	4358
18	ClO	7230	38	C_2H_4	12978
19	OCS	19920	39	CH ₃ OH	19899
20	H ₂ CO	2702			

APPENDIX B. HITRAN (v12.0) Molecules with Associated Indices

This table gives the HITRAN numbering scheme for the molecular species on various line-byline portions of **JavaHAWKS**. Shaded areas are for molecules relegated to the "supplemental" folder.

APPENDIX C. Schematic of Fundamental Spectroscopic Parameters of a Line Transition in HITRAN.

The dotted line refers to a perturbed transition (with a negative pressure-shift δ).



APPENDIX D. Formats for Line-by-line Parameters and Cross-section Headers

M I _V I2 I F12.6		S E10.3	R E10.3	γ _{air} F5 4	γ _{self} F5 4	E" F10.4	n F4.2	δ F8 6	iv'	iv" 13	q' <mark>A9</mark>	q"	ier iref 3I1 <mark>3</mark> I2
					1 3.4	110	1 7.4	1 0.0		10			
	10	20	30	4	• 0	50		60		70	8	0	90

"1986-2001" line parameter format:

"2002+" line parameter format:

MI	ν		S	A	4	γ_{air}	γ_{self}	Е"	n	δ	v'		v"	Q'	Q"		ierr	iref	*	ġ	g ["]
12	1 F12.6		E10.3	E1	10.3	F5.4	F5.4	F10.4	F4.2	F8.6	A15		A15	A15	A15		611	612	A1	F7.1	F7.1
				•																	
		10	20		30		40	50		60	70	80	90	100	110	120	130	140		150	160

Note: v' and v" are ASCII representations of upper and lower global quanta; * is flag for line coupling; g' and g" are upper and lower statistical weights.

"2000" Cross-section Header format: Press Max Res. Common Name Not Br Re Chemical symbol Temp Wavenumber No. [Torr] X-section Max Pts. **[K]** Min No used 15 10 10 20 7 10 6 10 20 30 **40** 50 **60** 70 80 90

Note: Chemical Symbol is right adjusted; Res. is resolution in cm^{-1} for FTS measurements, and in milli-Angstroms for grating measurements in the UV (xxxmÅ), and **Br** indicates any broadening gas, such as air.

Example of 100-character HITRAN line-transition format.

Mol/Iso	ν _{ij}	S_{ij}	R _{ij}	γ _{air}	γ_{self}	<i>E</i> ''	n _{air}	δ _{air}	iv'	iv"	q'	q''	ierr	iref
21	800.451076	3.197E-26	6.579E-05	.0676	.0818	2481.5624	.78	.000000	14	6		P 37	465	221
291	800.454690	9.724E-22	1.896E-02	.0845	.1750	369.6303	.94	.000000	9	1	341619	331519	000	4 4 1
291	800.454690	3.242E-22	2.107E-03	.0845	.1750	369.6303	.94	.000000	9	1	341519	331419	000	4 4 1
121	800.455380	1.037E-22	1.657E-03	.1100	.0000	530.3300	.75	.000000	32	14	46 640	45 540	000	4 4 1
121	800.455380	1.037E-22	1.657E-03	.1100	.0000	530.3300	.75	.000000	32	14	46 740	45 640	000	4 4 1
101	800.456743	1.680E-23	1.659E-04	.0670	.0000	851.0494	.50	.000000	2	1	45 244 0-	44 143 0-	301	661
101	800.457045	1.710E-23	1.689E-04	.0670	.0000	851.0469	.50	.000000	2	1	45 244 1-	44 143 1-	301	661
101	800.457310	1.740E-23	1.718E-04	.0670	.0000	851.0442	.50	.000000	2	1	45 244 2-	44 143 2-	301	661
121	800.457760	4.726E-23	4.614E-03	.1100	.0000	920.0900	.75	.000000	32	14	502922	492822	000	4 4 1
121	800.457760	4.726E-23	4.614E-03	.1100	.0000	920.0900	.75	.000000	32	14	502922	492722	000	4 4 1
24	800.465942	9.792E-27	6.063E-04	.0754	.1043	1341.2052	.69	.000000	8	3		R 13	425	221
121	800.466160	1.061E-22	2.720E-03	.1100	.0000	632.1200	.75	.000000	32	14	471236	461136	000	4 4 1
121	800.466160	1.061E-22	2.720E-03	.1100	.0000	632.1200	.75	.000000	32	14	471136	461036	000	4 4 1
35	800.472900	3.878E-26	6.919E-04	.0686	.0871	629.0354	.76	.000000	2	1	1814 4	1713 5	455	551
101	800.473083	1.270E-23	1.254E-04	.0670	.0000	851.0095	.50	.000000	2	1	45 244 0+	44 143 0+	301	661
101	800.474860	1.210E-23	1.195E-04	.0670	.0000	851.0064	.50	.000000	2	1	45 244-1+	44 143-1+	301	661
31	800.475500	1.680E-24	3.617E-05	.0653	.0890	1092.4340	.76	.000000	2	1	51 547	50 248	002	1 1 2
291	800.476220	9.597E-22	6.010E-03	.0845	.1750	361.9747	.94	.000000	9	1	341420	331320	000	4 4 1
291	800.476220	3.199E-22	6.010E-03	.0845	.1750	361.9747	.94	.000000	9	1	341520	331420	000	4 4 1
101	800.476937	1.160E-23	1.145E-04	.0670	.0000	851.0037	.50	.000000	2	1	45 244-2+	44 143-2+	301	661
101	800.484334	1.740E-23	2.153E-05	.0670	.0000	106.0760	.50	.000000	2	1	8 4 4-1+	9 3 7-1+	301	661

FORT	FORTRAN Format (I2,I1,F12.6,1P2E10.3,0P2F5.4,F10.4,F4.2,F8.6,2I3,2A9,3I1,3I2) corresponding to:										
Mol	I2	Molecule number	<i>E''</i>	F10.4	Lower state energy in cm ⁻¹						
Iso	I1	Isotopologue number (1= most abundant, 2= second most abundant, etc.)	n _{air}	F4.2	Coefficient of temperature dependence of air-broadened halfwidth						
v _{ij}	F12.6	Wavenumber in cm ⁻¹	δ_{air}	F8.6	Air-broadened pressure shift of line transition in cm ⁻¹ /atm @ 296K						
S _{ij}	E10.3	Intensity in $\text{cm}^{-1}/(\text{molecule x cm}^{-2})$ @ 296K	iv', iv"	2I3	Upper-state global quanta index, lower-state global quanta indices						
R _{ij}	E10.3	Weighted transition moment-squared in Debyes	q', q"	2A9	Upper-state local quanta, lower-state local quanta						
Yair	F5.4	Air-broadened halfwidth (HWHM) in cm ⁻¹ /atm @ 296K	ierr	3I1	Uncertainty indices for wavenumber, intensity, and air-broadened halfwidth						
Yself	F5.4	Self-broadened halfwidth (HWHM) in cm ⁻¹ /atm @ 296K	iref	312	Indices for table of references corresponding to wavenumber, intensity, and halfwidth						

Example of 100-character HITRAN line-transition format.

Example of 160-character HITRAN line-transition format.

FORTRAN Format (I2,I1,F12.6,1P2E10.3,0P2F5.4,F10.4,F4.2,F8.6,2A15,2A15,6I1,6I2,A1,2F7.1) corresponding to:										
I2	Molecule number	δ_{air}	F8.6	Air-broadened pressure shift of line transition in cm ⁻¹ /atm @ 296K						
I1	Isotopologue number (1= most abundant, 2= second most abundant, etc.)	v', v"	2A15	Upper-state global quanta, lower-state global quanta						
F12.6	Wavenumber in cm ⁻¹	q', q"	2A15	Upper-state local quanta, lower-state local quanta						
E10.3	Intensity in cm ⁻¹ /(molecule x cm ⁻²) @ 296K	ierr	611	Uncertainty indices for wavenumber, intensity, air- and self- broadened halfwidths, temperature-dependence, and pressure shift						
E10.3	Einstein-A coefficient	iref	612	Indices for table of references corresponding to wavenumber, intensity, air- and self-broadened halfwidths, temeperature- dependence, and pressure shift						
F5.4	Air-broadened halfwidth (HWHM) in cm ⁻¹ /atm @ 296K	Flag	A1	Flag (*) for lines supplied with line-coupling algorithm						
F5.4	Self-broadened halfwidth (HWHM) in cm ⁻¹ /atm @ 296K	g '	F7.1	Upper-state statistical weight						
F10.4	Lower state energy in cm ⁻¹	<i>g</i> ″	F7.1	Lower-state statistical weight						
F4.2	Coefficient of temperature dependence of air-broadened halfwidth									
	12 11 F12.6 E10.3 E10.3 F5.4 F5.4 F10.4	12 Molecule number 11 Isotopologue number (1= most abundant, 2= second most abundant, etc.) F12.6 Wavenumber in cm ⁻¹ E10.3 Intensity in cm ⁻¹ /(molecule x cm ⁻²) @ 296K E10.3 Einstein-A coefficient F5.4 Air-broadened halfwidth (HWHM) in cm ⁻¹ /atm @ 296K F5.4 Self-broadened halfwidth (HWHM) in cm ⁻¹ /atm @ 296K F10.4 Lower state energy in cm ⁻¹	12Molecule number δ_{air} 11Isotopologue number (1= most abundant, 2= second most abundant, etc.) v', v'' F12.6Wavenumber in cm ⁻¹ q', q'' E10.3Intensity in cm ⁻¹ /(molecule x cm ⁻²) @ 296KierrE10.3Einstein-A coefficientirefF5.4Air-broadened halfwidth (HWHM) in cm ⁻¹ /atm @ 296KFlagF5.4Self-broadened halfwidth (HWHM) in cm ⁻¹ /atm @ 296Kg'F10.4Lower state energy in cm ⁻¹ g''	12Molecule number δ_{air} F8.611Isotopologue number (1= most abundant, 2= second most abundant, etc.) $\mathbf{v'}, \mathbf{v''}$ 2A15F12.6Wavenumber in cm ⁻¹ $\mathbf{q'}, \mathbf{q''}$ 2A15E10.3Intensity in cm ⁻¹ /(molecule x cm ⁻²) @ 296Kierr611E10.3Einstein-A coefficientiref612F5.4Air-broadened halfwidth (HWHM) in cm ⁻¹ /atm @ 296KFlagA1F5.4Self-broadened halfwidth (HWHM) in cm ⁻¹ /atm @ 296Kg'F7.1F10.4Lower state energy in cm ⁻¹ $\mathbf{q''}$ F7.1						

FORTRAN Format (12.11.F12.6.1P2E10.3.0P2F5.4.F10.4.F4.2.F8.6.2A15.2A15.6I1.6I2.A1.2F7.1) corresponding to