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10. Risk Analysis

The purpose of the Risk Analysis module in HARP is to provide the tool for preparing Health Risk Assessments as specified in the Office of Environmental Health Hazard Assessment's document *Air Toxics Hot Spots Program Guidance Manual for Preparation of Health Risk Assessments* (OEHHA, 2003). This document is referred to throughout this manual as the "OEHHA Guidance Manual". Users of the HARP software are assumed to have a working understanding of the risk assessment methods and procedures outlined in the OEHHA Guidance Manual.

HARP can be used by Air Pollution Control and Air Quality Management Districts (Districts), facility operators, and other parties to manage and evaluate emissions inventory data and the potential health impacts associated these emissions. The use of HARP promotes statewide consistency, increases the efficiency of evaluating potential health impacts, and provides a cost-effective tool for developing facility health risk assessments.

Although designed to meet the programmatic requirements of the Hot Spots Program, the HARP software may be used for preparing risk assessments for other air related programs (e.g., air toxic control measure development, facility permitting applications). Therefore, each user of the HARP software should know the requirements of the regulation or program they are addressing before using the HARP software.

The HARP software may be used to assess the potential multipathway health impacts from a single facility or multiple facilities in (close) proximity to each other, where a single meteorological data set is appropriate for all the included facilities. However, other applications may be appropriate depending on the presence of adequate data and the user's expertise.

The Risk Analysis module allows the user to estimate the multipathway health impacts at multiple receptor locations from one or more pollutants released from one or more emission points. Carcinogenic and non-carcinogenic impacts may be evaluated. The user may conduct a point-estimate analysis or utilize the data distributions available to conduct a stochastic analysis. Users may also supply their own adequately supported point-estimates or data distributions by editing the network.

This chapter provides a description of the functions available in the risk assessment module of the HARP software. See Chapter 4 for a tutorial on HARP or Appendix A for a set of simple "how to" guides that are intended to assist users with some basic HARP applications.

The following topics are covered in the list of "how to" guides that are found in Appendix A.

- Emission inventory setup.
- Facility prioritization.
- Setting up an air dispersion run.
- Performing a risk assessment for one or more facilities with one or more release points.
- Performing a risk assessment by entering a ground level concentration (GLC).
- Mapping a facility.

10.1 HARP Risk Analysis Algorithms and Default Values

The risk analysis algorithms and default values used in HARP are based on the Office of Environmental Health Hazard Assessment's (OEHHA) Guidelines set forth in the *Technical Support Document for Exposure Assessment and Stochastic Analysis* (OEHHA, 2000). All equations, default parameter values, and variable distributions encoded into HARP are from the OEHHA Guidance Manual.

In addition to using the point-estimates of exposure and data distributions supplied in the OEHHA Guidance Manual, HARP users may input their own appropriately supported point-estimates or data distributions by editing the network. For more information on adding user-supplied data into the network to perform a Tier-2 or Tier-4 risk assessment, see Sections 10.7.6.2, 10.7.6.4, and 10.7.6.5.

10.1.1. Inhalation-Only or Multipathway Analysis

The OEHHA Guidance Manual provides guidance on when it is appropriate to conduct an inhalation-only or a multipathway analysis. A multipathway risk analysis includes the potential health impacts from other exposure pathways (e.g., soil or fish ingestion) in addition to the inhalation route. The multipathway analysis utilizes the algorithms in the OEHHA Guidance Manual to estimate how the chemicals are transported through the various physical pathways (for example food, drinking water, inhalation) to reach the human body. Within the human body, each chemical may have various adverse effects (e.g., cancer or non-cancer impacts) and they may impact various biological systems (for example lungs, cardiovascular, reproductive). These biological systems are referred to as toxicological endpoints. HARP combines both the Multipathway model and the toxicological endpoints into a single complex network. This Multipathway network takes into account the substances, exposure scenario, chemical concentrations, and run-control parameters each time the HARP program executes an analysis.

10.1.2 Point-Estimate vs. Stochastic Analysis

The stochastic analysis takes into account the variability of certain input parameters (for example breathing rate and food ingestion rates) among the human population. Stochastic analysis is accomplished by Monte Carlo simulation. HARP does this by randomly sampling the data distributions to obtain input parameters that are used in each trial or analysis. The program executes multiple trials, and the results of all of the trials are accumulated for post-processing. In the post-processing phase, the trial values are sorted and analyzed to create plots of the statistical distribution of the calculated potential cancer risk. These distributions can then be used to estimate the expected risk at a specific confidence level.

The point-estimate analysis uses a single value rather than a distribution of values in the dose equation for each exposure pathway. Both the point-estimate and stochastic analysis are performed by HARP. The choice of which type of analysis should be used for the HRA (point-estimate versus stochastic) will depend on the assessor's or programmatic needs for the risk assessment. For more guidance on which assessment is appropriate for you, see the

description for the tiered-approach to risk assessment in Section 8.2.5 of the OEHHA Guidance Manual.

10.1.3 Keeping a Record of Risk Assessment Results

The files listed below are the records that should be kept electronically for any HARP analysis. These files are needed to expedite re-creation of reported results. If additional information is needed to support inputs included in HARP, then they too should be kept as a record of support. Detailed information on reporting results for Hot Spot analyses can be found in the OEHHA Guidance Manual (Chapter 9) or you should contact your local District for information on presenting the results of a risk assessment. Critical files are marked with an asterisk.

- HARP Facility Database for included facilities (*filename.MDB*)*
- ISC workbook file with all ISC parameters (*filename.ISC*)*
- ISC input file generated by HARP when ISC is run (*filename.INP*)
- ISC output file generated by HARP when ISC in run (*filename.OUT*)
- List of error messages generated by ISC (*filename.ERR*)
- Plot file generated by ISC (*filename.PLT*)
- Representative meteorological data used for the facility air dispersion modeling (*filename.MET*)*
- Any digital elevation model files (if applicable) (*filename.DEM*)*
- Average and maximum χ/Q values for each source-receptor combination; generated by ISC (*filename.XOQ*)
- ISC binary output file; holds χ/Q for data for each hour (*filename.BIN*)
- Sources receptor file; contains list of sources and receptors for the ISC run; generated by HARP when you set up ISC (*filename.SRC*)
- Emission Rate files (if applicable) (*filename.EMS*)*
- Site-specific parameters used for all receptor risk modeling (*filename.SIT*)*
- (Screening) Adjustment Factor Files (if applicable) (*filename.ADJ*)*
- Point estimate risk values generated by HARP; this file is updated automatically each time you perform one of the point estimate risk analysis functions (*filename.RSK*)
- HARP Exception Report (*ExceptionReport.TXT*)*
- Risk Result Text files for Key Receptors (*filename.TXT*)
- Raw sample data (stochastic) (*filename.CSV*)*
- Stochastic Summary Report (*filename.TXT*)*

10.2 Organization of Risk Analysis Module

10.2.1 Window and Program Organization

There are two primary windows from which you perform risk analysis functions, the point-estimate risk window and the stochastic window. The point-estimate risk window is used for performing multipathway point-estimate risk analyses on one or more receptors. The Stochastic and Multipathway window is used to perform a stochastic analysis using one or more

data distributions of exposure and to view intermediate details of the multipathway analysis for a single receptor.

10.2.1.1 Main Risk Analysis Window

The main risk window is opened by selecting *Analysis/Risk Analysis* from the main HARP window. There are two choices in the menu depending on whether you used screening meteorology data or representative meteorology data in your dispersion analysis. The structure of the risk windows is discussed below. Data will only appear in the following windows once you have completed a dispersion analysis.

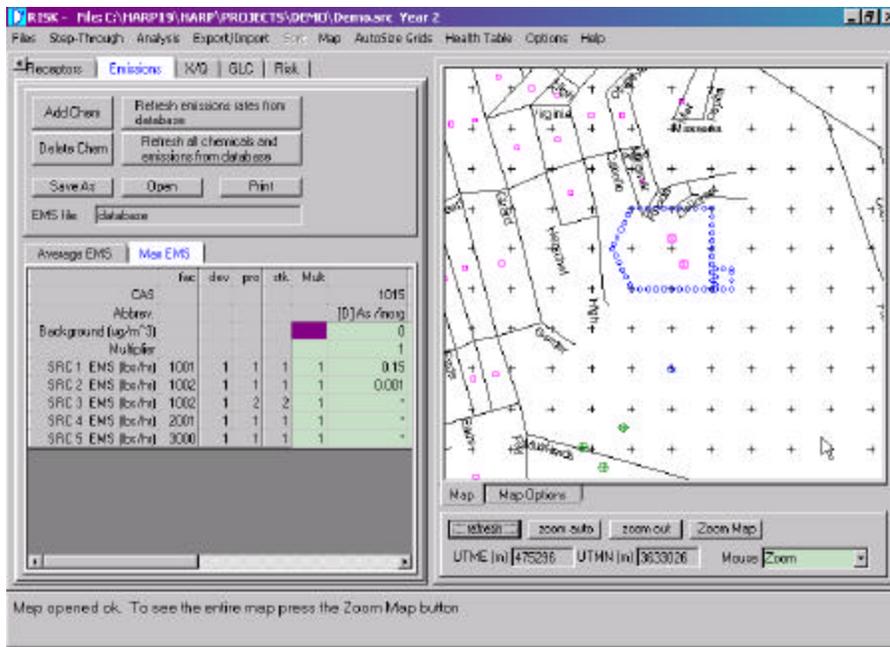
The input and output data that are used in the analysis are displayed in tabular form in the left-hand pane of the window. The right-hand pane of the window displays a map that allows you to visualize the results.

The data pane on the left of the window has several tabs that allow you to select which table you want to view. The tables contain details of sources and receptors used in the analysis, the emission rates, X/Q values (concentration estimated from the air dispersion model), ground level concentrations (GLCs), and risk estimates for each receptor.

The map pane shows a map with options to display streets, buildings, property boundaries, stacks (sources), receptors, elevations, and risk isopleths.

The map pane and the data pane will be synchronized via the mouse actions when the mouse action is set to *Pick Source* or *Pick Receptor* (bottom right of map pane). When you click on a cell on one of the tables in the data pane, the corresponding source or receptor is highlighted on the map pane. Conversely, when you click on a source or receptor on the map pane, the corresponding cell is highlighted on the data pane, provided you have.

If your computer has difficulty displaying map results for an entire receptor grid, you may have too many receptor points on your grid for your computer to display efficiently. If this situation exists, you may wish to go back to the air dispersion modeling setup and decrease the number of receptor points (Section 9.12.4) in your domain or change to a computer with more memory. If you would like to maintain a receptor grid that is closely spaced to obtain better resolution of the potential risk results, you may need to reduce the size of the entire grid to offset the increase in grid points and run additional analyses to cover the preferred domain.



MAIN RISK WINDOW

10.3 Data View Tabs: Viewing Input Data

When you open a source-receptor file (SRC file), HARP displays all of the source and receptor details under the various tabs on the left side of the risk window. There is not enough room on the risk window to display all of the tabs. Additional tabs can be viewed by pressing the small arrow at the left and right of each row of tabs.

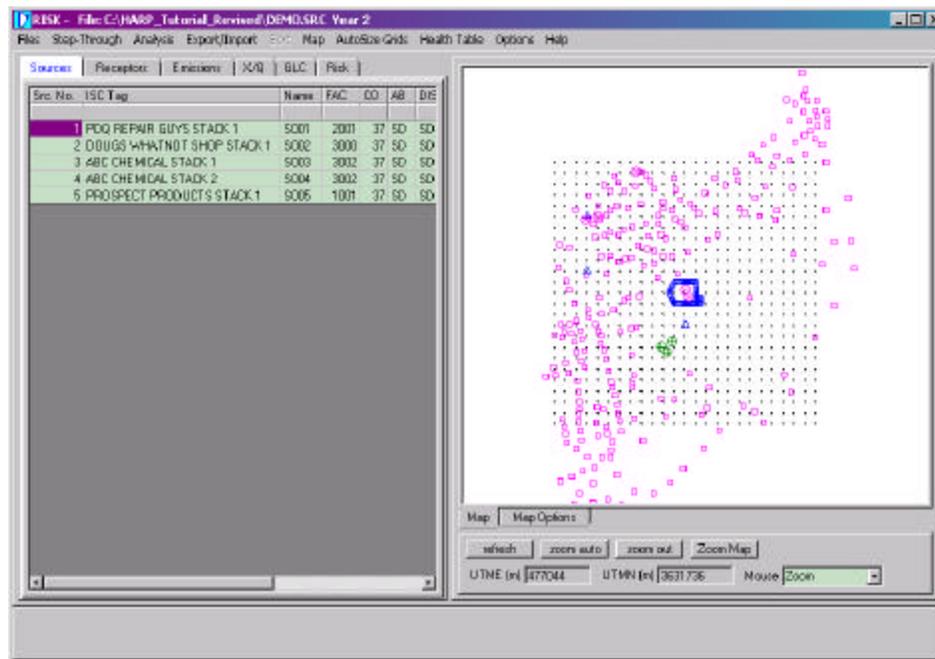


10.3.1 Source Details

The Sources tab on the risk window displays a list of all the sources that will be included in the risk analysis. This information is read by HARP from the SRC file. Note: To add or delete sources you must rerun the dispersion analysis.

Each source in the source details list corresponds to a single stack. If a facility has more than one stack then you will see multiple entries in the source details list for that facility. The columns labeled FAC, CO, AB, DIS, STACK are the facility, county, air basin, district and stack number for this stack. These correspond to the same fields in the HARP emissions inventory database and form the primary key in the stack table in that database. They are used by HARP to

look up emission rates for each chemical from each stack. The source details list also shows the UTM coordinates and elevation of each source.



SOURCE DETAILS

10.3.2 Receptor Details

The Receptors tab on the risk window displays a list of all the receptors that will be included in the risk analysis. This information is read by HARP from the SRC file. To add or delete receptors you must rerun the dispersion analysis.

The Receptors tab has several sub-tabs that each display receptor details for one of the receptor subgroups.

10.3.2.1 Grid Receptors

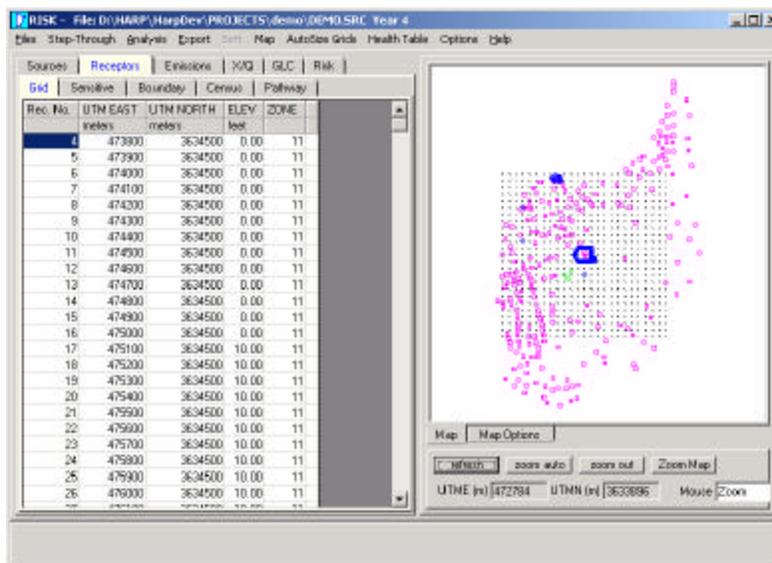
To view the details of the grid receptors, click the Grid tab under the Receptors tab on the risk window. Under the Grid tab you can view details of the grid receptors. The grid receptors are specified when you set up the dispersion analysis.

Grid receptors are a matrix of receptors organized on a rectangular grid over the area that you are analyzing. The grid receptor matrix covers grid points without regard for any identified facility boundaries (i.e., grid points are both inside and outside a facility). Contour lines can be applied to the risk values calculated on grid receptors to produce isopleths that can be viewed on the map (Section 10.6.11).

If your computer has difficulty displaying map results for an entire receptor grid, you may have too many receptor points on your grid for your computer to display efficiently. If this

situation exists, you may wish to go back to the air dispersion modeling setup and decrease the number of receptor points (Section 9.12.4) in your domain or change to a computer with more memory. If you would like to maintain a receptor grid that is closely spaced to obtain better resolution of the potential risk results, you may need to reduce the size of the entire grid to offset the increase in grid points and run additional analyses to cover the preferred domain.

The grid details tab shows the receptor number, the UTM coordinates and the elevations.



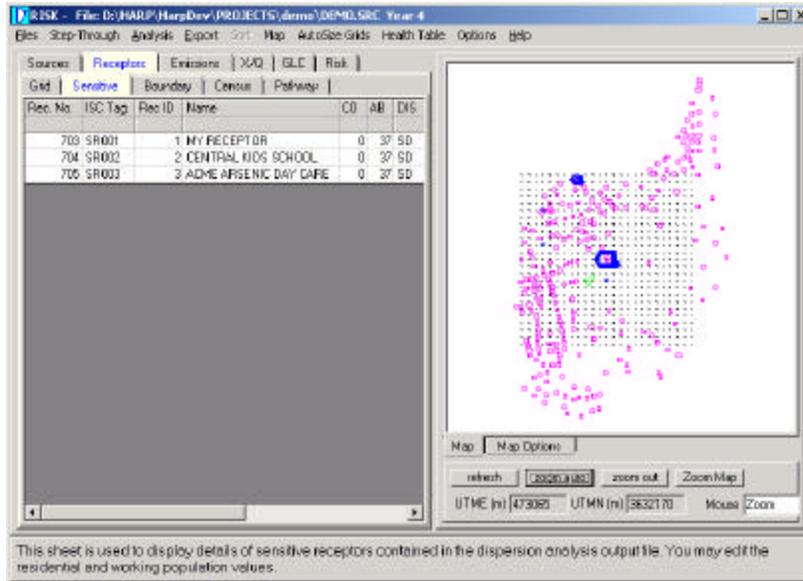
GRID RECEPTOR DETAILS

10.3.2.2 Sensitive Receptors

To view the details of the sensitive receptors, click the Sensitive tab under the Receptors tab on the risk window. The sensitive receptors are specified when you set up the dispersion analysis.

Sensitive receptors are special receptors that are of interest in your analysis. They are generally intended to be located at specific sensitive sites where certain populations may exist, such as a school or nursing home.

The sensitive receptor details show the county, air basin and district under the CO, AB, DIS columns. They correspond to the entries in the HARP emissions inventory database. The columns labeled WRK and RES are the working and residential populations at each receptor. (At present these quantities are not used in the analysis). The last three columns show the UTM coordinates and the elevation of each receptor.



POPULATION RECEPTOR DETAILS

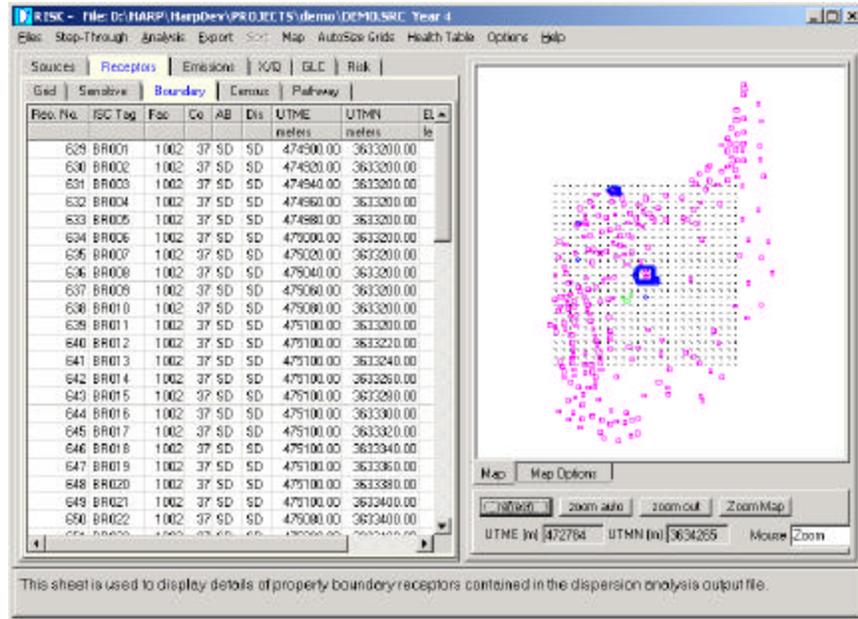
10.3.2.3 Boundary Receptors

To view the details of the boundary receptors, click the Boundary tab under the Receptors tab on the risk window.

The boundary receptors are specified when you set up the dispersion analysis. They are receptors that are placed at intervals along the property boundaries of a facility. They are typically included in the analysis because the Point of Maximum Impact (PMI) location frequently exists at a property boundary close to the stack where the concentration may be highest.

The boundary receptor details show the UTM coordinates and elevation of each receptor. The columns labeled FAC, CO, AB, DIS are the facility, county, air basin and district of the facility on whose property the receptor lies.

Note that the ground level concentration (GLC) at the boundary receptors may be estimated to be zero (0) due to the proximity of a large building. If this situation presents itself and you would like to obtain an estimated concentration or risk, you can turn off Building Downwash under Dispersion/Control (Section 9.12.2).

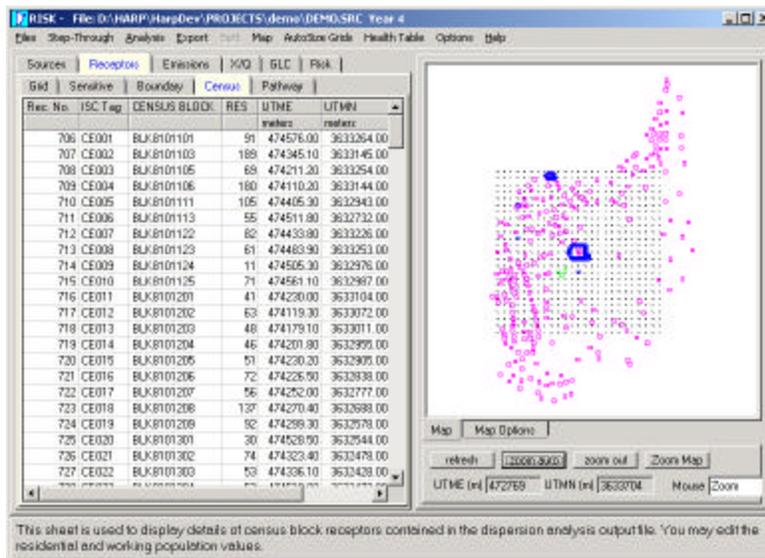


BOUNDARY RECEPTOR DETAILS

10.3.2.4 Census Receptors

To view the details of the census receptors, click the Census tab under the Receptors tab on the risk window.

The census receptors correspond to census blocks that were specified when you set up the dispersion analysis. The census details show the UTM coordinates and elevation of each census block receptor. The RES column shows the residential population of each block. The census receptors are used to calculate cancer burden or to obtain a population-based exposure estimate (see section 9.12.7).

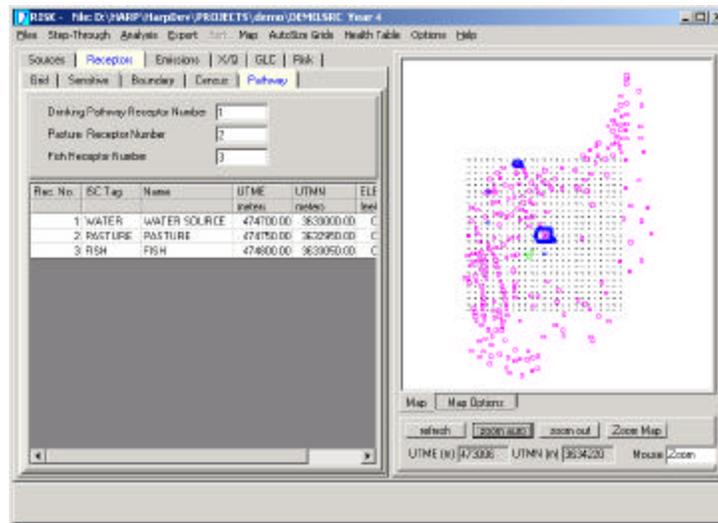


CENSUS RECEPTOR DETAILS

10.3.2.5 Pathway Receptors

To view the details of the pathway receptors, click the Pathway tab under the Receptors tab on the risk window.

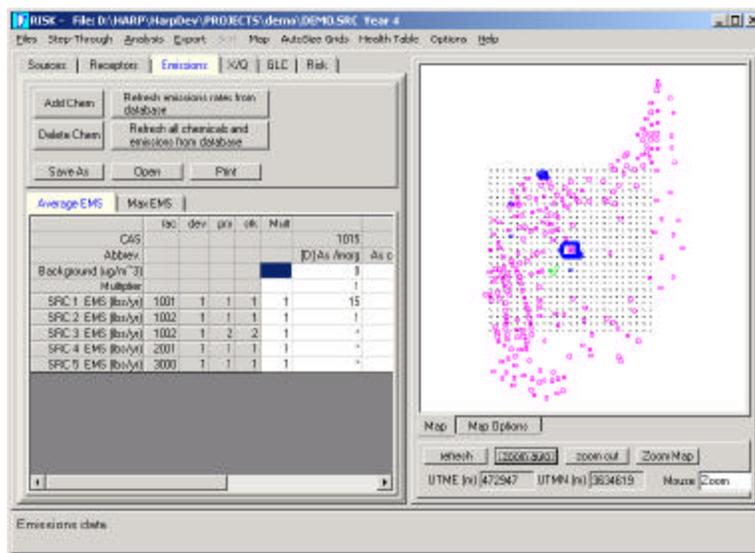
Pathway receptors are the three special receptors that are required for the multipathway risk analysis. They are always placed at the locations of the water, pasture, and fish. The pathway receptor details show the UTM coordinates and the elevation of each of these receptors.



PATHWAY RECEPTOR DETAILS

10.3.3 Emissions

To view the emissions data, click the emissions tab on the risk window. The window will appear similar to the following.



EMISSIONS DETAILS

Each row in the table corresponds to a single process. The columns labeled FAC, DEV, PRO, STK are the facility, device, process and stack. These keys are defined in the HARP emissions inventory database.

The stacks that are included in the analysis are specified when you set up the dispersion analysis. The processes that are connected to those stacks are determined automatically by HARP in order to fill out this table. It is necessary to breakdown the emission rates at the process level because it is the process rates that determine the emissions in the emissions inventory database.

The columns towards the right of the table correspond to different substances. The numbers in the cells under each chemical show the emission rate of that chemical from each of the processes. Cells containing an * (asterisk) indicates that the substance is not produced by that process.

The columns and rows labeled **Mult** are user-defined multipliers that you can change if you want to attenuate the emission rate of any chemical or process by some factor to see what the effect on risk would be. The default value for all the multipliers is 1. For example, if we add a 2, the risk would double. For further details refer to section 10.6.7.

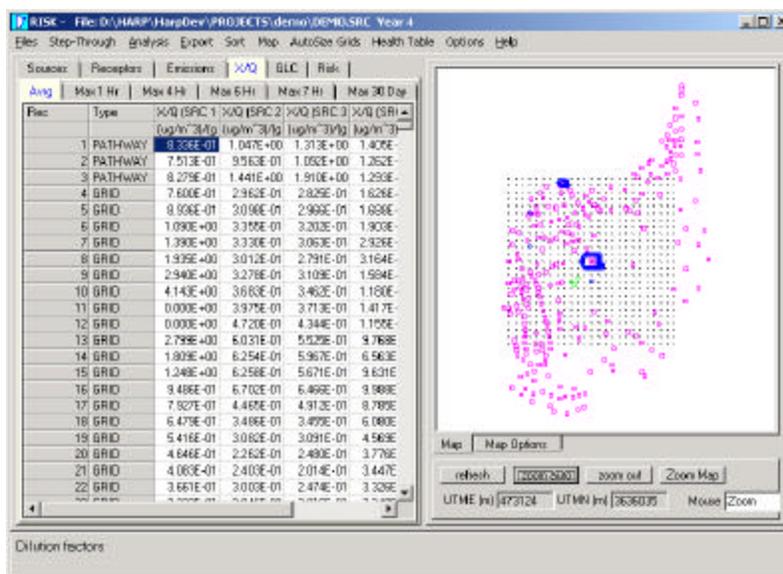
In the left column of this screen, there is a row that is titled “Background”. This row can be used to run a risk analysis across all receptors for a user-defined ground level concentration (GLC) in micrograms per cubic meter ($\mu\text{g}/\text{m}^3$) for one or more substances. For each substance that is included in the background assessment, insert the GLC value, insert a one (1) into the multiplier row, and blank out the source emissions row for each substance, then proceed to the “Risk Reports” window to define your risk analysis (Section 10.6). Additional information can be found in Appendix A.

10.3.3.1 X/Q

To view the X/Q data, click the X/Q tab on the risk window. There are several sub-tabs corresponding to different averaging periods that are required for the analysis.

The receptors are listed vertically along the left column and the sources are listed horizontally along the top row. The source numbers shown in this table correspond to the source numbers listed under the sources tab (see section 10.3.1). The receptor numbers correspond to the receptor numbers listed in each of the receptor detail tabs (see section 10.3.2).

For a modeling run that uses representative meteorological data, the Avrg tab shows the annual average X/Q values for every source-receptor combination. The Max 1-Hr tab shows the maximum value of the 1-hour average X/Q over the duration of the simulation. The remaining tabs show the maximum values of the running average X/Q taken over 4, 6, or 7-hours, and 30-days, respectively. For a modeling run that uses screening meteorological data, only the Max1-Hr tab will show X/Q values.



X/Q DETAILS

10.3.3.2 GLC

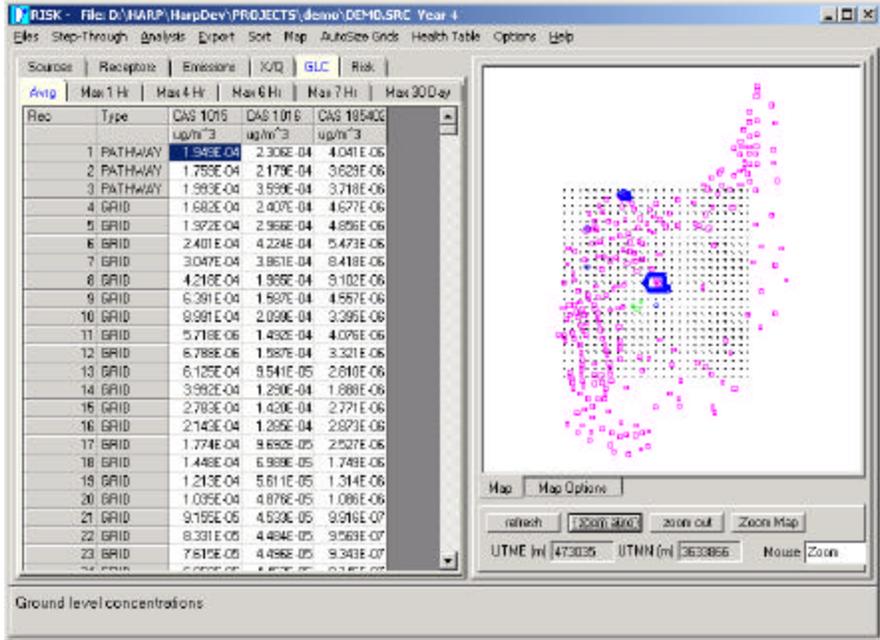
To view the GLC (ground level concentration) data, click the GLC tab on the risk window. There are several sub-tabs corresponding to different averaging periods that are required for the analysis. The receptors are listed vertically along the left column and the chemicals are listed horizontally along the top row.

The Avrg tab shows the average GLC values for every source-receptor combination. The Max 1-Hr tab shows the maximum value of the 1-hour average GLC over the duration of the simulation. The remaining tabs show the maximum values of the running average GLC taken over 4, 6, or 7-hours and 30-days, respectively.

GLC values shown in this table are calculated by HARP when you open the SRC file. They are calculated by multiplying the emission rate for each chemical (as shown in the emission details, see section 10.3.3) by the X/Q values for the corresponding stack and receptor (as shown in the X/Q details, see section 10.3.3.1), and summing over all processes that emit that chemical.

If you change the emission rates by editing the values under the emissions tab, you should update the GLC values by selecting *Analysis/Recalculate GLC* from the menu (see section 10.6.7 for details).

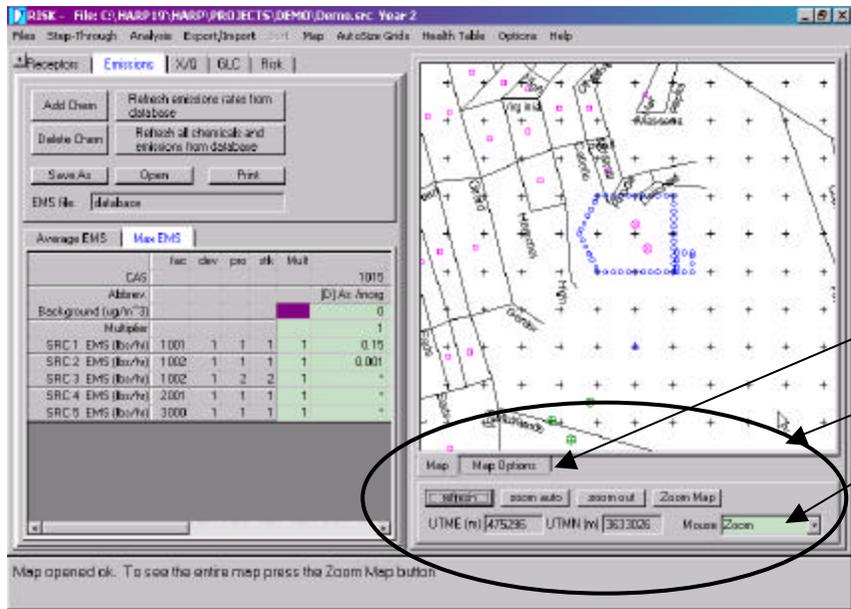
The units of GLC are micrograms per cubic meter.



GLC DETAILS

10.3.4 Navigating the Map on the Risk Window

The right side of the main risk window contains a map of the area included in the risk evaluation. The map pane has options to show maps with streets, buildings, property boundaries, stacks (sources), receptors, elevations, and risk isopleths. Labeling features are also provided. The Map Options button provides the ability to select which features will be displayed in this window or on a printed map.



MAIN RISK WINDOW

The map pane and the data pane are synchronized via the mouse actions (bottom right). When you click on a cell on one of the tables on the data pane, the corresponding source or receptor is highlighted on the map pane. Conversely, when you click on a source or receptor on the map pane, the corresponding cell is highlighted on the data pane, provided you have set the mouse action to Pick Source or Pick Receptor.

If your computer has difficulty displaying map results for an entire receptor grid, you may have too many receptor points on your grid for your computer to display efficiently. If this situation exists, you may wish to go back to the air dispersion modeling setup and decrease the number of receptor points (Section 9.12.4) in your domain or change to a computer with more memory. If you would like to maintain a receptor grid that is closely spaced to obtain better resolution of the potential risk results, you may need to reduce the size of the entire grid to offset the increase in grid points and run additional analyses to cover the preferred domain.

The maps include symbols that identify key features included in the modeling and risk analysis. These symbols are defined here.

- + Black cross hairs mark the location of grid receptors.
- Magenta squares mark the locations of census receptors.
- Ⓐ Green circles mark the locations of pathway receptors.
- ⓧ Sources (stacks) are shown on the map as magenta circles with X's in them.
- Blue circles near the center of the map identify the property boundary receptors. Note: if you select the button **Map Options** and check the boxes labeled **Properties and Bldgs** and click **Refresh**, then property and building boundaries are shown on the map as dotted lines.
- △ Blue circles mark the location of sensitive receptors.
- Solid black lines identify street locations with the names written adjacent to them.

10.3.4.1 Locating and Labeling Streets

Use the Map Options Button to show streets with or without their names. Font sizes and labeling frequency can also be tailored. Place a check mark or numeric value in the appropriate box to activate the desired feature. The refresh button should be used to update the map to include the features chosen in map options.

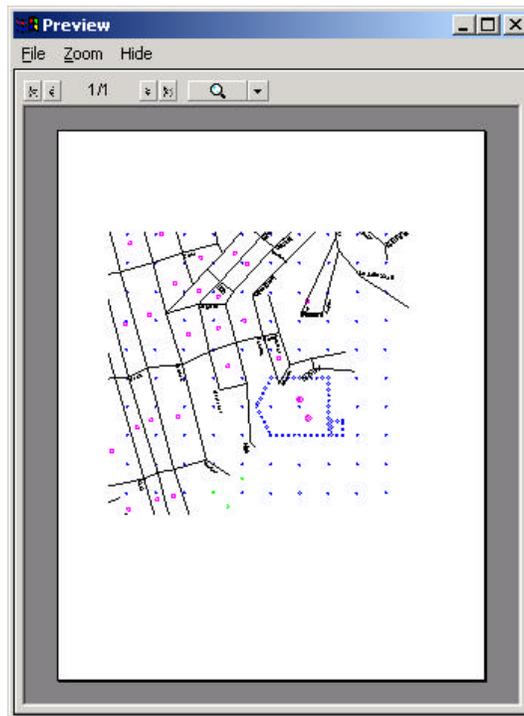
Note: A labeling frequency of one causes every intersection to be labeled with a street name. To reduce the labeling frequency to every other intersection, change the frequency to 2. For every third intersection, change it to 3, and so forth. The larger the number, the less frequent the names will be plotted.

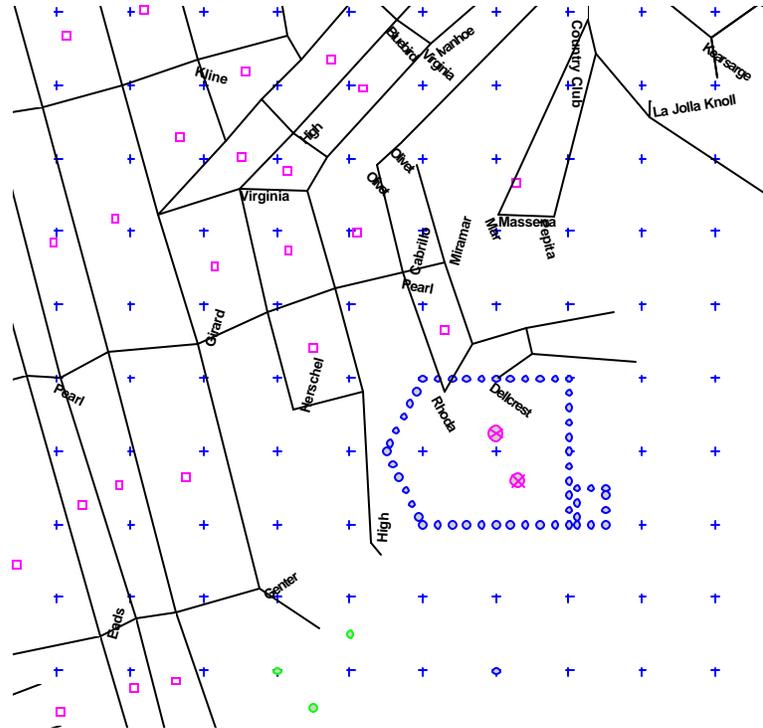
A street search feature is also included. Enter the name of the street that you want to locate in the search field. If you check **Whole word only**, then only streets that exactly match the word you enter will be highlighted. This is essential, for example, to find a street such as "L" street, where there would otherwise be too many matches for practical purposes.

Note: When the map is being redrawn, a **STOP** button will appear in the lower right corner. Press this button if you want to stop the drawing. See the tutorial in Chapter 4 for more information on mapping.

10.3.4.2 Printing and Exporting Maps

To print or export a map, adjust the drawing parameters as described in the previous section so that the map looks the way you want it to and select **Map/Print Preview**. The map will be displayed in a *Preview* window as shown below. From the *Preview* window you can select **File/Print** if you have a printer attached. The map will be printed exactly as it is shown. From the *Map Preview* window, select **File/Copy to Clipboard**. Open Microsoft Word or any other word processor and transfer the map to the appropriate location in the document. Select **Edit/Paste Special**, and then select **Enhanced Metafile** to paste the map into your document. Use the Word cropping tool to remove the white space from the edges of the map. Then format the picture, choosing a wrapping style that will fit within your text.





Sample Map Inserted into Word Documents

10.4 Files Used by the Risk Module

10.4.1 Project Directory

When running dispersion analysis or risk analysis most of the intermediate input and output files used by the program will reside in a single directory, which is called the project directory. This may be any directory of your choosing.

To specify the project directory, select **Project** from the HARP main menu. The following window will appear.



PROJECT WINDOW

Enter the name of the directory that you want to use as the project directory followed by the file name *project.ini* as shown above. You may use the browse button to open the Windows file dialog box and search for the directory.

NOTE: The directory that you specify must exist. If you want to create a new directory as your project directory, then you must use the Windows Explorer or other file manager to first create the directory.

After you have specified the directory, press the *OK* button.

10.4.2 Project File (File extension *.ini)

Project.ini is a file that HARP uses to store information about your project, such as the name of the database file that you want to use when working on this project. *Project.ini* is always located in the project directory.

NOTE: You do not have to create the file *project.ini* in advance. If the file does not exist, HARP will create it when you open a new project directory. The contents of *project.ini* are not important to most users, however it is an ASCII file that can be viewed or edited with any text editor.

10.4.3 Emissions Database File (File extension *.mdb)

The emissions database file (*HARP.mdb*) is a Microsoft Access file that contains primarily the emissions inventory data that you have entered into the system. The procedures for entering data are described in Chapter 5 and in the tutorial in Chapter 4.

When opening a new project, HARP will attempt to open the default database file, *HARP.MDB*, which is assumed to be located in the HARP directory. If it cannot open this file, HARP will warn you that you have not yet specified the name of an emissions database to be used for this project. You should then open a database file.

To open a database file select *Edit Data/Open Database* from the HARP main menu and use the browser to locate the database file that you want to use. The HARP installation program always installs a default database file called *HARP.MDB* in the HARP directory.

If you wish to create a different database file, then you should copy *HARP.MDB* to a different file name or different project directory, then open the new file as described in the previous paragraph. If you want to clear a new database file of previously entered data, select *Utilities/Multiyear* from the HARP main menu and use the delete feature.

10.4.4 ISC Input File (File extension *.inp)

The ISC input file is the file read by the ISC program and contains all information required by ISC for the dispersion analysis. The ISC input file is generated automatically by HARP when you run the dispersion analysis (see section 9.12).

The name of the ISC can be any valid file name with any extension. You specify the name when you set up the dispersion problem. NOTE: There can be no spaces in the file name. The format of the ISC input file is described separately in the ISC documentation.

10.4.5 Calculating X/Q

Before you can calculate risk you must know the ground level concentrations (GLCs) of each of the chemicals at the receptors of interest. This requires that you first run the dispersion analysis. The dispersion analysis generates X/Q values for every source-receptor combination that you specify. HARP then uses the X/Q values, combined with the emission inventory data from the database, to calculate GLC at every receptor.

CHI/Q or chi/q or X/Q is the concentration estimated from an air quality model based on an emission rate of one gram per second input to the model. Chi/q can be efficiently used to estimate the concentration of multiple inert pollutants simply by multiplying by the emission rate in grams per second. In this way, one model run may be conducted to evaluate the impact of several different inert pollutants.

The X/Q values are stored in two files: 1) the binary (.BIN) file contains hourly X/Q values that are used to calculate maximum hourly acute risk; 2) the X/Q summary file contains average and maximum X/Qs that are used to calculate cancer and chronic risk. These two files are generated automatically when you run the dispersion analysis, and they are opened when you open a source-receptor file by selecting *Files/Dispersion Analysis Results/Open Source-Receptor File* from the menu on the risk window.

10.4.5.1 Binary X/Q File (File extension *.bin)

The binary X/Q file is created each time you run ISC. This file contains the X/Q values for every source-receptor combination for every hour of the simulation. Consequently it can be a very large file. It is written in binary in order to reduce the size somewhat compared to ASCII.

This file always has the same root name as the ISC input file and an extension of .BIN. The binary X/Q file is used to compute maximum hourly acute risk (see section 10.6.10.2).

10.4.5.2 X/Q Summary File (File extension *.xoq)

The X/Q summary file contains average and maximum X/Q values for every source-receptor combination. It is created each time you run ISC. Because it does not contain hourly values it is much smaller than the binary X/Q file.

This file always has the same root name as the ISC input file and an extension of .XOQ.

The X/Q summary file contains annual average values that are used to compute cancer and chronic risk. It also contains maximum hourly values that are used for acute risk (see section 10.6.10). The X/Q summary file also contains maximum values of the short term running average concentrations for durations of 4, 6, 7 hours and 30 days. These intervals are preset because they correspond to the averaging times used to develop the acute health hazard indexes for certain chemicals. The maximum value used to compute acute risk for each chemical depends on the averaging time used to develop the acute Reference Exposure Level (REL) for that chemical.

10.4.6 Source-Receptor File (File extension *.src)

The source-receptor file (often called an SRC file) is a file that is created by HARP when you run the dispersion analysis. It contains a list of all of the sources (stacks) and receptors that were used in the ISC input, as well as details about those sources and receptors that are necessary to complete the risk analysis.

To perform a risk analysis, HARP uses the X/Q values (see section 10.4.5 for a definition of X/Q) provided by ISC (see sections 9.11 and 9.12 for instructions on setting up and running the dispersion analysis using ISC). The X/Q values are combined with the emission rates (usually taken directly from the emissions database) to determine ground level concentrations (GLCs) of each of the pollutants. A source-receptor file is required to perform a risk analysis because the normal ISC input and output files do not contain sufficient information to determine which sources in the dispersion results correspond to which stacks in the database. Without this information, HARP cannot determine emission rates. The ISC input and output files also lack descriptive information about the receptors. The SRC file contains information that allows HARP to distinguish between grid receptors, boundary receptors, census block receptors, and so forth.

Most users will never have to look at or understand the contents of an SRC file. However, you should know that: 1) it is an intermediate file that links the results of the dispersion analysis with the contents of the emissions database and subsequently with the risk analysis; 2) that you must have an SRC file in order to perform the risk analysis; and 3) that the SRC file is created automatically when you run the dispersion analysis.

When you first open the risk window, the next step is to open an SRC file. When you run a dispersion analysis for your project the SRC file will be saved in your project directory. To open an SRC file select *Files/Open Source-Receptor File (Dispersion analysis results)* from the menu on the risk window. Use the browser to select an existing SRC file.

Source-receptor files always have an extension of SRC. The full name of the file is determined by the name of the ISC input file that you specified when running the dispersion analysis. For example, if you specified that the ISC input file should be called DEMO.INP then the corresponding SRC file will be called DEMO.SRC. Thus all input and output files generated by a single run of the dispersion analysis will have the same root name but different extensions.

10.4.7 Risk File (File extension *.rsk)

The risk file is an intermediate file that is created each time you calculate point-estimate risk for multiple receptors (see section 10.6). It contains the most recently calculated values of cancer, chronic and acute risk. These are the same values that appear on the Risk tab of the risk window. The risk file is always has the same root name as the ISC input file and an extension of .RSK.

The purpose of this file is to save risk values that you have calculated so that the next time you run the program you can resume where you left off, view the previous data on the map, and generate new contours.

Each time you open a source-receptor file (see section 10.4.6) HARP will ask if you would like to load the corresponding RSK file. You will be warned if the file does not exist.

10.4.8 Map and DEM Files (File extension *.map and *.dem)

There are two types of files used by the HARP mapping functions. The street map files have an extension of .MAP. The map files contain Tiger street map data from the U.S. Census Bureau that can be read and displayed in the risk window.

Elevation data can be obtained in the form of DEM (Digital Elevation Model) files from the United States Geological Survey (USGS). This data can be utilized by HARP to simplify the determination of elevations of sources and receptors so that you do not have to enter elevations manually. This data can be used to help to set up the ISC input for uneven terrain and to determine the elevation of any stack or receptor. The DEM files have an extension of .DEM.

These files are described in more detail in section 9.13, and the map features of HARP are described in the rest of section 10.3.4.

10.4.9 Stochastic Analysis Files

There are several files that are used only for stochastic analysis. These are described in section 10.4.

10.5 Loading Data into the Risk Window

Before you can run a risk analysis, you must have already entered your emission inventory data into the HARP database (CEIDARS-Lite) and run an air dispersion analysis. The dispersion analysis will generate the X/Q and SRC files which contain the information required by the risk module. A tutorial is contained in Chapter 4 and Appendix A includes a “how to” guide that will facilitate HARP’s risk analysis features.

10.5.1 Open the Risk Window

The main risk window can be opened by selecting *Analysis/Risk Analysis* from the main window. There are two choices in the menu depending on whether you intend to use screening meteorology data or representative meteorology data. Your choice will depend on what meteorology you used in the dispersion analysis. If you used representative meteorology, you must choose *Analysis/Risk Analysis (Representative Met Data)*.

10.5.2 Open a Source-Receptor File

When you run the dispersion analysis a source-receptor file is always generated (see section 10.4.6). You must have this source receptor file in order to proceed with the risk analysis.

The first step in the risk analysis is therefore to open the source receptor file. This is done by selecting ***Files/Open Source-Receptor File (Dispersion Results)*** from the menu of the risk window.

Several things happen when you open a source-receptor file. The source and receptor details are read from the SRC file and displayed on the various tabs in the data view window. The average and maximum X/Q values are read from the XOQ file and displayed under the X/Q tab. HARP then goes to the emissions inventory database and looks up the process and chemical emission rates for all processes that are connected to the stacks that were specified in the dispersion analysis. This information is then displayed under the Emissions tab. HARP then uses all of this information to calculate the average and maximum values of GLC, and displays this information under the GLC tab.

When you open an SRC file, HARP also automatically attempts to open the risk file having the same root name. The purpose of this file is to save risk values that you have calculated so that the next time you run the program you can resume where you left off, view the previous data on the map and generate new contours (see section 10.4.7). If it cannot find the risk file you will be warned. If it can find the risk file, then the cancer, chronic, and acute health risk values will be read from the file and displayed under the risk tab. The risk file only exists if you have previously performed one of the point-estimate analysis functions described in section 10.6.

10.5.3 Calculating GLC

In order to calculate risk you must know the ground level concentrations (GLC) at each of the receptors for each of the chemicals. GLCs are calculated by multiplying the emission rates by the X/Qs for each stack, receptor and chemical and summing for each receptor. This is normally done automatically by HARP when you open a source-receptor file.

GLCs can also be calculated manually by selecting ***Analysis/Recalculate GLC*** from the risk window menu. You would use this approach if you manually edit the emission rates rather than using the values that are automatically imported from the database.

10.5.3.1 Adding a Substance-Specific GLC as a Background Concentration

There may be a time when you would like to run a risk analysis with a GLC value for one or more substances from an outside air dispersion run. There are two paths described below that can be used to achieve this analysis.

The first method will allow you add a GLC for each substance across an entire receptor grid and run a multipathway point-estimate risk analysis. This method could be used for evaluating the contribution of background pollutants. Substance - specific GLC values can be added through the emissions information in the risk window as a background concentration. The GLC value that you enter will be applied to every receptor in the file as a background concentration.

From the main risk window, open any SRC file from your project or open the SRC file for the tutorial. This file will provide a surrogate receptor grid and SRC file. This file will serve as a template when inserting your background GLC value. Click on the *Emissions tab*. You will need to add and delete chemicals to match the analysis you want to run by using the buttons at the top of the emissions window. For each substance insert the GLC value as the background concentration, insert a one (1) into the multiplier row, and blank out the source emissions row for each substance. Then set-up and evaluate your point estimate risk analysis (Section 10.6). Additional information can be found in Appendix A.

The second method will allow you to analyze a single receptor only, but you can enter different GLC values for the target receptor and each of the three pathway receptors. This second method will allow you to run a multipathway point-estimate or stochastic analysis. To perform the second method, see section 10.7.2.2.1 or Appendix A.

Currently, HARP cannot directly accept the output from an air dispersion-modeling run that was performed outside of the HARP Software.

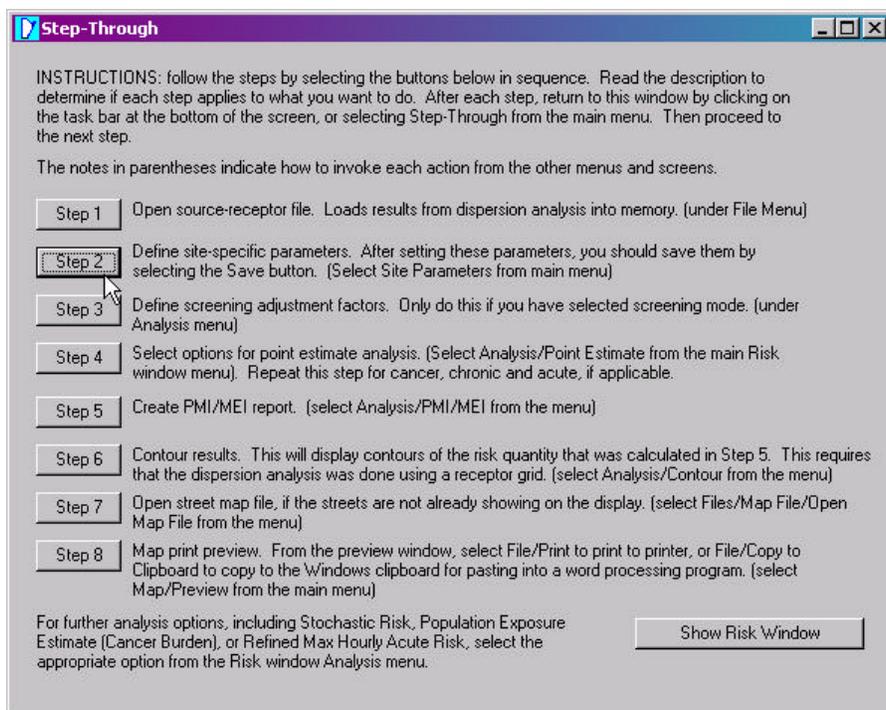
10.5.4 Displaying X/Q and GLC Details

When the number of receptors is very large (in the neighborhood of 5 or 10 thousand receptors or more) the display of the GLC and X/Q values takes a large amount of time. To speed up the loading of the SRC file and the subsequent calculations, HARP will automatically hide the X/Q and GLC values. When you want these values to be displayed, uncheck the menu item under *Options/Display GLC and X/Q Details*. When this item is checked, the GLC and X/Q values will be displayed immediately.

10.6 Setting-up a Point-estimate Risk Analysis

10.6.1 Simplified Risk Analysis/Step-Through

To simplify the risk analysis process for new users, all of the most common functions can be performed from a single window, call the Step-Through window. To display the Step-Through window, select *Step-Through* from the Risk window menu. The window is shown below.

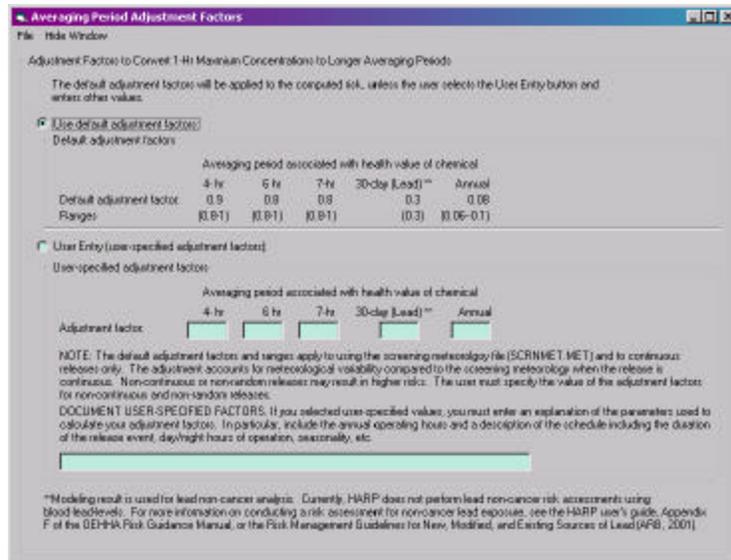


Click each of the buttons in sequence to perform each task. The explanation of what each button will do is shown on the window. The parenthetical portion of each button explanation indicates how you could perform the same function through the menus.

10.6.2 Screening Meteorology/Averaging Period Adjustment Factors

If you choose the screening meteorology option when you open the HARP Risk window, HARP will expect that the dispersion results that are being used for the risk analysis were done with screening meteorological data. If not, you will receive a warning message.

When you use screening meteorological data for the air dispersion analysis the result is a maximum one-hour X/Q value. U.S. EPA adjustment factors can be applied to estimate concentrations for longer averaging periods, such as the maximum annual average concentration. Appendix H in this manual and Appendix H in the OEHHHA Guideline Document contain further information on the use of adjustment factors. To adjust the air dispersion modeling results to longer averaging periods select ***Analysis/Define Averaging Period Adjustment Factors for Screening Meteorology*** from the menu of the Risk window. The following window will appear.



In this window you choose whether you will use the default adjustment factors or define your own. If you check the button labeled “*use default adjustment factors*”, HARP will assume that the source operates continuously and will use the adjustment factors shown, which are the values recommended by ARB and U.S. EPA for continuous sources.

If you check the button labeled “*User Entry*”, then you may provide your own adjustment factors. In this case, you must also justify the user-defined adjustment factor in the box at the bottom of the window. Note, the adjustment factors for longer averaging periods do not need to be prorated for the emissions schedule as explained in Appendix H in the OEHHA Guideline Document. The purpose of the emission operating schedule factor in Appendix H is to pro-rate the actual emission rate to an annualized emission rate for the facility. HARP distributes annual emissions (lbs/yr) to hourly emissions (g/s) based continuous emissions (8760 hrs/yr). Therefore the annual emissions are automatically pro-rated over a year in the event that actual emission schedules are less (e.g., 2000 hrs/yr). Immediately after exiting this window you must recalculate the GLCs or the GLCs will be updated when the risk is calculated. Do this by selecting *Analysis/Recalculate GLC* from the main risk menu.

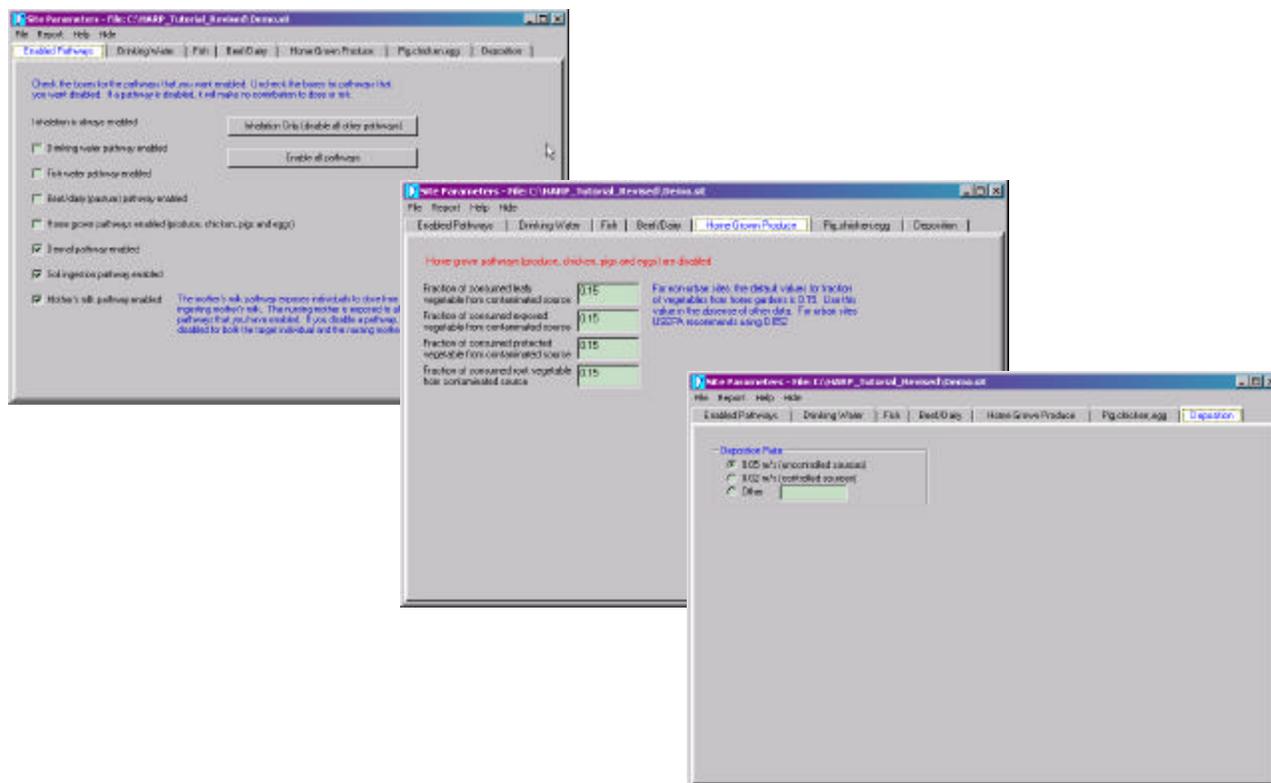
10.6.3 Site Parameters Window

The Site Parameters window allows an assessor to specify which exposure pathways will be included in the health risk assessment (HRA) analysis. These windows are used in all HRAs.

In the first window shown below (upper-left), an assessor will select the pathway(s) they will evaluate or enable in the HRA. Once the pathway(s) are enabled, the assessor will select the corresponding tab for each enabled pathway at the top of this screen. Selecting a tab in this first screen will open a second screen (center window) that contains site-specific questions that must be answered by the assessor for that exposure pathway. Questions included in these tabs inquire about site-specific physical characteristics of the exposed media and the frequency of exposure to that media or products consumed through that exposure pathway. Site-specific information is

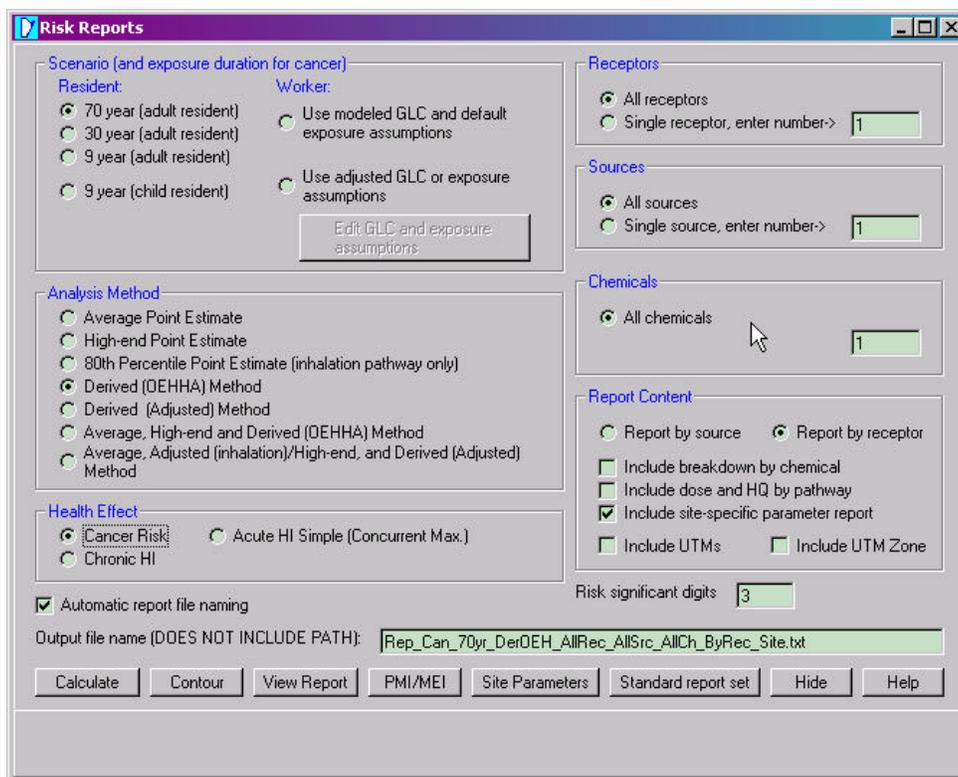
required for all exposure pathways except for the inhalation, dermal exposure, soil ingestion, and breast milk exposure pathways.

The deposition tab shown in the Site Parameters window should be selected for all assessments that include any non-inhalation exposure pathways (e.g., soil or fish ingestion pathways). This tab will ask you questions about the deposition rate of the particulate emissions from the emission source (lower-right). See the OEHHA Guidance Manual for more information about deposition rates.



10.6.4 Calculating Risk and Viewing a Reports

The Risk Reports window controls point-estimate risk reports. This window is displayed when you select *Analysis/Point-estimate (Includes Multipathway)* from the risk window. The Risk Reports window appears as shown below. This screen will allow a user to perform a Tier-1 risk assessment as described in the OEHHA Guidance Manual. In addition to using the point-estimates of exposure supplied in the OEHHA Guidance Manual, HARP users may input their own appropriately supported point-estimates or data distributions by editing the network. For more information on adding user-supplied data into the network to perform a Tier-2 or Tier-4 risk assessment, see sections 10.7.6.1, 10.7.6.4, and 10.7.6.5.



RISK REPORTS WINDOW

To create a report, select the report options as described in the following sections, then press the *Calculate* button. Users of the HARP software are assumed to have a working understanding of the risk assessment methods and procedures outlined in the OEHHA Guidance Manual.

When you generate a report, the report is written to a file, whose name you specify in the box labeled *Output File Name*. The file will always be located in the project directory.

The report may be viewed by pressing the button labeled *View Report*. Because the report is an ASCII file, it can also be opened or imported into any word processor.

10.6.5 Report Options

10.6.5.1 Scenarios

On the Risk Reports window, you may select one of two scenarios, either a residential (adult or child) receptor or a worker receptor. For a residential receptor you can select which exposure duration you wish to use in your analysis; 9, 30, or 70 years for an adult or 9 years for a child.

For the impacted worker, you can make selections based on how the modeling input characterized the timing of emissions from the source as compared the worker's schedule. In addition, there is a location input to identify variation in a worker's schedule (e.g., working

lifetime). Depending on your choice of how you wish to analyze the worker, you may be asked to supply information for the analysis (see screen below).

You will need to determine whether the air dispersion modeling run for the residential receptor is also appropriate for the worker's inhalation analysis. See Chapter 8 of OEHHA's Guidance Manual for more information on worker exposure. If the modeling run is appropriate for both receptors, you will select "Use Modeled GLC and Default Exposure Assumptions" and no further information will be required. If the modeled GLC for the residential receptor is not representative of the workers' inhalation exposure then you should either remodel the impacts (see chapter 9 on Dispersion Modeling) or adjust the GLC (upward) using a factor to approximate a more appropriate GLC. If you select the second button, "Adjust the GLC or the Exposure Assumptions", you will get a second screen. On that second screen, you can supply an adjustment factor used to approximate the GLC (applies to the inhalation pathway only) or change the standard exposure assumptions for the worker. If you provide a factor for to change the GLC or change an exposure assumption, you will be required to supply information explaining the basis for your change in the note window before you leave this screen. This information and your changes for the worker will appear in the output file (printed report).

Worker GLC Adjustment and Exposure

GLC adjustment factor: User-defined adjustment to the GLC based on facility emission schedule with respect to the worker schedule. This factor applies to the cancer and noncancer inhalation pathway only.

* Exposure frequency (EF): (Days/Year) For default use 245

* Exposure duration (ED): (Years) For default use 40

GLC adjustment factor note justify the GLC adjustment factor (e.g. worker schedule, facility schedule, etc.)

* Exposure Duration (ED) and Exposure Frequency (EF) are used for cancer assessments only.

10.6.5.2 Analysis Method

The Analysis Method toggles allow the use of various point-estimates of exposure and two methods for determining multipathway health impacts. The input parameters used here are presented in the OEHHA Guidance Manual and also reflect the *Air Resources Board's Recommended Interim Risk Management Policy for Inhalation-Based Residential Cancer Risk (October 2003)*. The analysis method does not apply to acute risk. The acute risk results will be the same regardless of which analysis method you choose.

HARP users may input their own appropriately supported point-estimates or data distributions by editing the network. For more information on adding user-supplied data into the network to perform a Tier-2 or Tier-4 risk assessment, see sections 10.7.6.1, 10.7.6.4, and 10.7.6.5.

10.6.5.3 Health Effect

You may choose one of three health effects: cancer, chronic or acute. The report will be generated only for the health effect that you choose.

Note: when you select either chronic or acute, both are actually calculated, but the printed report is output for only the one you select. Regardless of whether you pick chronic or acute, the results for both will be displayed under the risk tab and will become available for contouring.

10.6.5.4 Receptors

You have a choice of generating a report for all receptors or for only a single receptor. If you choose a single receptor then you must specify the receptor number. Receptor numbers are shown on each of the receptor detail lists under the receptor tabs on the risk window.

You would generally select a single receptor in combination with the *Report by Source* option in order to produce a detailed breakdown of the contribution of risk from multiple sources.

WARNING: If you select all receptors in combination with *Report by Source*, the report may be very long and will take some time to generate.

10.6.5.5 Sources

You have a choice of generating a report for all sources or for only a single source. If you choose a single source then you must specify the source number.

You would generally select single source in combination with the *Report by Receptor* option in order calculate risk from that source for all receptors in an area.

10.6.5.6 Chemicals

You have the choice of generating a report for all chemicals or for only a single chemical. If you choose a single chemical you must enter the chemical number.

Note that the chemical number is not the CAS number, but rather the index of the chemical as shown under the emissions tab.

10.6.5.7 Report Content

The options of *Report by Receptor* or *Report by Source* determine the format and content of the report.

If you select *Report by Receptor*, then the receptors are listed down the left column of the report, with pathways and endpoints across the top. The risk values are for a single source or all sources depending on what you selected under the source option.

If you select *Report by Source*, then the sources are listed down the left column of the report, with pathways and endpoints across the top. You would generally do this for only a single receptor. If you select *Report by Source* for all receptors, the report may be quite long.

There are quite a lot of combinations of the parameters described in this section, and consequently there are many different types of reports. The best way to familiarize yourself with the content of these reports is to experiment with different options.

10.6.5.8 Output File Name

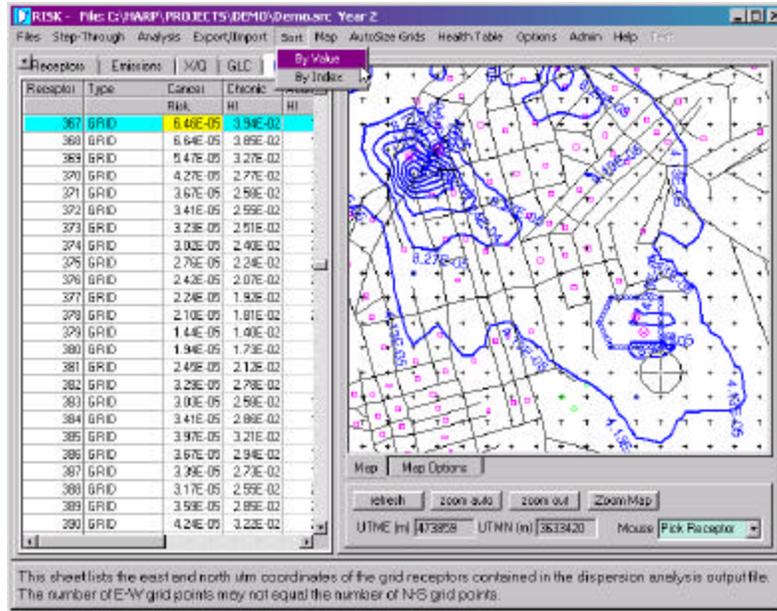
Whenever you generate a report, the report is output to an ASCII file that will be in your project directory. The reason for outputting to an ASCII file is to make it easy for you to incorporate these reports into a word processor. HARP will automatically name the file according to the buttons you choose when you set-up your risk scenario. You can turn off the automatic file-naming feature by clicking in the check box next to *Automatic File Naming*. You can change the name of the file if you wish by entering the name in the box labeled *Output File Name*.

10.6.5.9 Standard Report Set

If you need to send the results of your risk analysis to OEHHA for review, you will be asked to send a set of specific HARP files and risk reports. To make this easy on the risk assessor, HARP has a button labeled, *Standard Report Set* on the risk reports window. By pressing this button HARP will automatically generate the required reports and save them in your project directory. This set of reports can then be written to a CD with the other required files and mailed to OEHHA for their review. Because of the number of reports, this takes substantially longer to run than the individual cancer, chronic, and acute reports. A list of the files in the Standard Report Set can be found in Appendix G. For information on what OEHHA requires in a risk assessment that is to be submitted for their review, please see the OEHHA Guidance Manual.

10.6.6 Viewing and Sorting Tabular Risk Results

When you calculate your point-estimate risk scenario (by selecting *Calculate* button on the Risk Reports window) HARP generates an ASCII file containing the report, and also displays the results in a list under the Risk tab of the risk window. This is illustrated below.



RISK DETAILS TAB

The left two columns show the receptor numbers and receptor types. The three right-hand columns show the cancer risk (non-dimensional) and the chronic and acute health hazard indices.

Note: After calculating the cancer risk or the chronic noncancer health impacts, the situation may exist where the results show a potential health impact for some property boundary receptors, but those same receptor locations have a GLC of zero (0). This situation exists because an adjacent building (through the building downwash calculation) is precluding a GLC from being computed at the property boundary location. If you wish to disable downwash option, go to the *Control* window under Dispersion Modeling and turn it off, then rerun the dispersion modeling analysis (see Section 9.12.2.1).

With the downwash algorithm activated, the cancer risk or chronic noncancer impact that is shown at the property boundary receptor is from contributions through the water, pasture, or fish pathways. To zero out the risk at these locations, return to the Dispersion Modeling module, turn these pathway receptors off and rerun the dispersion-modeling run (see the Pathway Receptors Worksheet discussed in Section 9.12.8).

You can sort the rows in this table by clicking on one of the three columns and then selecting *Sort/By Value* from the menu. The rows will be reordered with the highest risk values at the top. To return to the normal display order, select *Sort/By Index* from the menu. The rows will be reordered by receptor number.

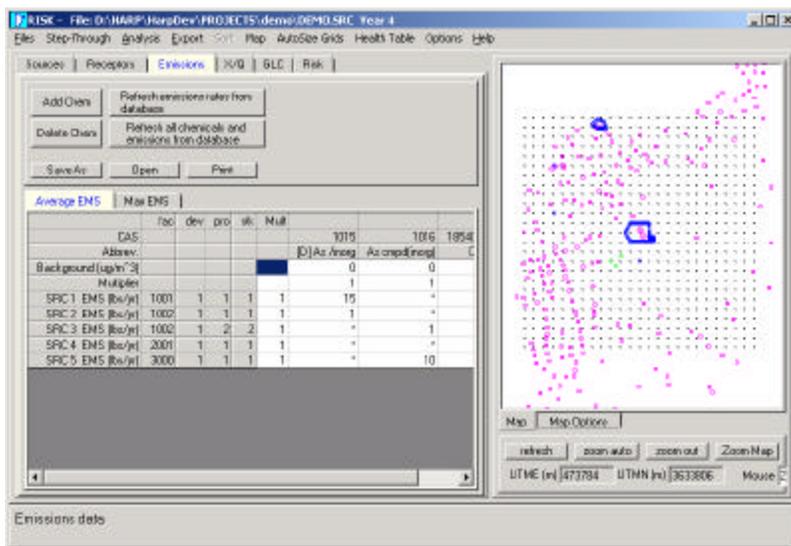
When you click on any row of this table, the corresponding receptor is highlighted with a circle and a cross hair, as illustrated above. Conversely, if you have the mouse mode set to *Pick Receptor*, and you click on a receptor on the map, the corresponding row in the receptor list will be highlighted.

10.6.7 Modifying Emissions (“What-if” analysis)

You may wish to perform the risk analysis using emission rate values that are different from the ones contained in the emission inventory database. HARP allows you to do this by editing the emission rates used in the risk analysis. This allows you to answer “what if” questions, such as what if the emission rate for a particular chemical or a particular process were increased or decreased. You may also examine how the risk would change if a chemical were deleted or a new chemical were added.

Cells containing an asterisk (*) indicate that there is no emission rate stored in the database for that chemical and process. You may replace the asterisk (*) with a value if you want to specify an emission rate.

The row in the table labeled *Background*, may be used to enter the background concentration (micrograms/m³) for each chemical. The background concentration is added to every receptor. See section 10.5.3.1 for more information.



EDITING EMISSION RATES

10.6.7.1 Adding and Deleting Chemicals

You may add a new chemical to the table by pressing the **Add Chem** button. You will be prompted with a list of available chemicals. This list reflects all substances that are included in the Emission Inventory Criteria and Guidelines (EICG) that have OEHHA health factors. When you select one of the chemicals it will be added to the table. In addition, HARP also contains all health factors listed in the OEHHA Guidance Manual (even if the substance is not listed in the EICG document). These substances can be added to a risk analysis by typing the substance name or CAS number directly into the Add Chemicals window. You must then fill in the emission rate values manually.

To delete a chemical from the table, click on the column containing the chemical you want to delete, then click the **Delete Chem** button.

10.6.7.2 Changing Emission Rates

When you first open a source-receptor file, HARP builds a table of emission rates by first reading the list of stacks from the SRC file, then looking in the emission inventory database to find the emission rates for all processes connected to those stacks. The results are displayed under the Emissions tab of the risk window.

You can modify the emission rates used in the risk analysis without returning to the emissions inventory database. This is done by selecting the Emissions tab on the risk window and editing the emission rates directly in the cells where they are shown. Changes that you make here will not be reflected in the database.

Note that under the Emission tab there are sub-tabs for average and maximum rates. You must edit the values under both of these tabs if you intend to do both cancer and noncancer analyses. The average emission rates are used for cancer and chronic risk analysis. The maximum emission rate is used for acute risk analysis.

After you have made changes to the emission rates, you must recalculate the GLCs by selecting **Analysis/Recalculate GLCs** from the menu. This recalculates the GLC values that will be used in the multipathway risk and displays the new values under the GLC tab.

10.6.7.3 Scaling Emission Rates

Under the Emissions tab on the risk window, the columns and rows labeled *Mult* are user-defined multipliers that you can change if you want to attenuate the emission rate of any chemical or process by some factor to see what the effect on risk would be. The default value for all the multipliers is 1. Each emission rate is multiplied by both the chemical scaling factor and the process scaling factor before it is used in the analysis. This can be used to artificially attenuate a particular process or chemical. This has the same effect as editing the individual emission rates in a row or column, but is simpler.

For example, if you want to find out how the risk would be affected by reducing a particular process rate by 50%, locate the row corresponding to that process and set the value of the scaling factor under the *Mult* column to 0.5. To determine how the risk would be affected by reducing the emissions of a particular chemical from all processes by 50%, locate the column for that chemical and set the chemical scaling factor in the *Mult* row to 0.5.

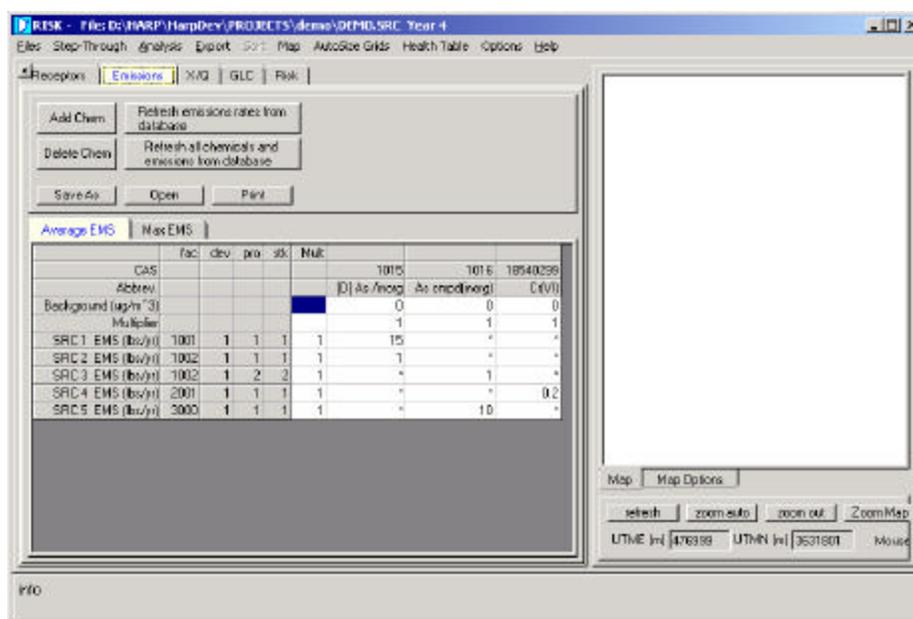
After you have made changes to the emission rates, you must recalculate the GLCs by selecting **Analysis/Recalculate GLCs** from the menu. This recalculates the GLC values that will be used in the multipathway risk and displays the new values under the GLC tab.

10.6.7.4 Restoring Emission Rates from Database

If you want to revert to the original emission rates as they are recorded in the database, select **Data/Fetch Emission Rates** from the menu. This will wipe out any changes that you have made and return the display to where you started.

10.6.7.5 Reading From or Saving the Emissions Table

Recall from the picture below that on the risk window the emissions of each chemical from each stack are shown under the emissions tab. These values are normally imported automatically from the emissions database. But they can also be edited manually, and chemicals may be added or deleted from this list. Whatever chemicals and emission rates are shown in this window is used in all subsequent risk analysis.



MAIN RISK WINDOW – EMISSIONS TAB

The emissions table can be saved to a file, or read from a file. The emissions table file has an .EMS extension. It is a comma-delimited file, whose format is described below.

The emissions table file contains a cell-by-cell dump of the contents of the emissions table exactly as it is shown in the window above.

The number 10 in the first cell indicates that the table has 10 rows. You may count the rows above to verify that this is the case. The number 9 in the second cell indicates that the table has 9 columns. Each of the remaining rows contains the contents of one of the cells in the 10 x 9 grid.

The number in the first column indicates which sheet the cell belongs to. A value of 1 means the cell is on the Average EMS tab. A value of 2 indicates that the cell is on the Max

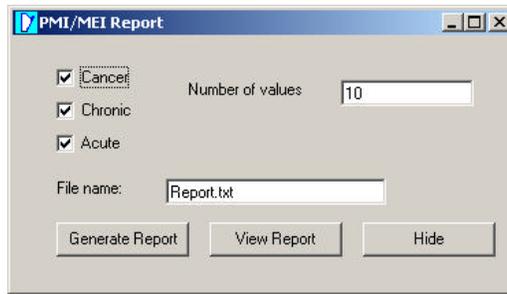
EMS tab above. The numbers in the second column are the row number, starting with zero for the first row. The numbers in the third column are the column number, starting with zero for the first column. The values in the fourth column below contain the contents of each of the cells.

The table below must match the structure of the table shown in the window above. In other words, there must be the same number of header rows and header columns as shown. The emissions data itself always starts in the sixth row and seventh column. You can verify that this is true by comparing the values below with the contents of the table above.

10			
9			
1	0	0	
1	0	1	fac
1	0	2	dev
1	0	3	pro
1	0	4	stk
1	0	5	Mult
1	0	6	
1	0	7	
1	0	8	
1	1	0	CAS
1	1	1	
1	1	2	
1	1	3	
1	1	4	
1	1	5	
1	1	6	1015
1	1	7	1016
1	1	8	18540299
1	2	0	Abbrev.
1	2	1	
1	2	2	
1	2	3	
1	2	4	
1	2	5	
1	2	6	[D] As /inorg
1	2	7	As cmpd(inorg)
1	2	8	Cr(VI)
1	3	0	Background (ug/m^3)
1	3	1	
1	3	2	
1	3	3	
1	3	4	
1	3	5	
1	3	6	0
1	3	7	0
1	3	8	0
1	4	0	Multiplier
1	4	1	
1	4	2	
1	4	3	
1	4	4	
1	4	5	
1	4	6	1
1	4	7	1
1	4	8	1
1	5	0	SRC 1 EMS (lbs/yr)
1	5	1	1001
1	5	2	1
1	5	3	1
1	5	4	1
1	5	5	1
1	5	6	15
1	5	7	*
1	5	8	*

10.6.8 PMI/MEI

To produce a report that shows the Point of Maximum Impact and Maximum Exposed Individual (PMI/MEI), select *Analysis/PMI/MEI* from the menu. The following PMI/MEI report options window will appear.



From this window you can produce a report that lists the highest risk receptors in descending order of risk. These receptor points may be both inside and outside of the facility property boundary. Depending on the purpose (programmatic requirements) of your analysis or the nature of activities within the facility (e.g., prisons, universities, or military bases), care should be taken to be sure that the appropriate location for the PMI is reported. See the OEHHA Guidance Manual for information on when on-sight receptors may be appropriate under the Hot Spots Program. Assessors should understand the location of the PMI before automatically reporting the highest receptor as the PMI location.

The number of receptors listed is determined by the value that you enter in the box labeled *Number of Values*. You can generate a report for one or more of the three health effects by checking cancer, chronic and acute. The report will be written to an ASCII file located in the project directory. The name of the file is whatever you enter in the box labeled *File Name*.

When you are done selecting the options, press the button labeled *Generate Report*. To view the most recent report that you generated, press the button labeled *View Report*. The report window will appear similar to the following:

REC	TYPE	CANCER	CHRONIC	ACUTE
209	BOUNDARY	5.41E-07	1.09E-02	7.62E-01
215	BOUNDARY	4.71E-07	8.21E-03	1.04E+00
210	BOUNDARY	4.57E-07	8.80E-03	8.45E-01
212	BOUNDARY	4.49E-07	8.11E-03	6.41E-01
211	BOUNDARY	4.38E-07	8.25E-03	8.19E-01
250	BOUNDARY	4.25E-07	8.50E-03	7.49E-01
216	BOUNDARY	4.24E-07	7.38E-03	7.68E-01
214	BOUNDARY	4.20E-07	7.34E-03	8.22E-01
213	BOUNDARY	4.10E-07	7.32E-03	6.65E-01
217	BOUNDARY	4.03E-07	6.70E-03	7.44E-01

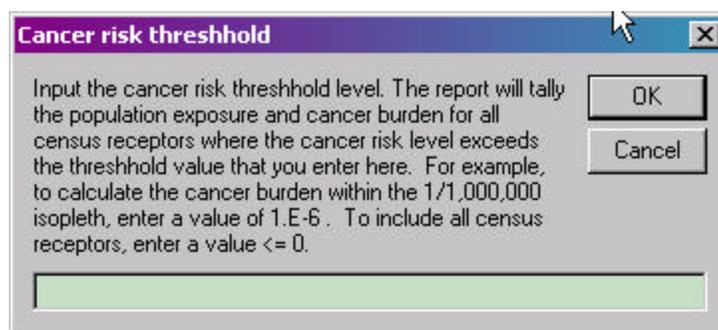
TYPICAL PMI/MEI REPORT FOR CANCER

This report is generated by checking the *Cancer* box in the report options window and setting the *number of values* to 10. The report lists 10 receptors with the highest cancer risk in order of risk. It also shows the corresponding chronic and acute risk for each of these receptors. If the cancer, chronic, and acute boxes were checked, a report for each health effect would be generated showing the list of receptors for each health effect.

10.6.9 Population Exposure Estimates

10.6.9.1 Cancer Population Exposure Estimates and Cancer Burden

To calculate cancer burden select *Analysis/Population Exposure/Cancer Population Exposure Estimate and Cancer Burden* from the menu. The following window will appear:



Input the cancer burden or risk thresholds as directed and press OK. The exposure assessment/cancer burden report will be written to a file and displayed in the Report window as shown below. The report consists of a list of all of the census block receptors whose cancer risk exceeds the threshold that you specify. The cancer burden for each of these receptors is calculated by multiplying the cancer risk by the residential population at each receptor. The total cancer burden is the sum of the cancer burden for each of the census receptors and is shown at the bottom of the report.

Preview

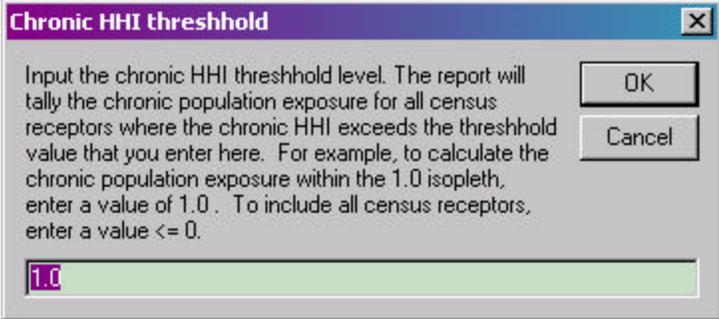
Print Zoom Previous page Nextpage FirstPage LastPage Exit

POPULATION EXPOSURE ESTIMATE REPORT - CHRONIC RISK
 File: C:\HARP\PROJECTS\DEMO\Cancer_Population_Exposure.txt

COUNT	REC	DESCRIPTION	CANCRD RISK	POP BURDEN	CANCRD BURDEN	CUM. POP	CUM. BURDEN	UTMR	UTPM	ZONE
1	829	BLR8202004	1.963E-04	0	0.000E+00	0	0.000E+00	474091	8634127	11
2	853	BLR8204002	1.252E-04	41	5.134E-03	41	5.134E-03	474035	8634191	11
3	798	BLR8201001	8.896E-05	16	4.989E-03	97	1.012E-02	474603	8624619	11
4	800	BLR8201007	7.906E-05	0	0.000E+00	97	1.012E-02	474464	8624476	11
5	691	BLR8202005	7.505E-05	69	4.725E-03	160	1.485E-02	474191	8624021	11
6	690	BLR8202005	6.195E-05	14	8.670E-04	174	1.570E-02	474093	8624010	11
7	797	BLR8201004	6.150E-05	16	9.853E-04	190	1.671E-02	474633	8624448	11
8	882	BLR8202007	5.929E-05	0	0.000E+00	190	1.671E-02	474238	8624048	11
9	851	BLR8204000	4.757E-05	828	1.560E-02	518	3.232E-02	478910	8624258	11
10	833	BLR8202008	4.513E-05	1	4.513E-05	519	3.235E-02	474307	8624027	11
11	828	BLR8202003	3.976E-05	86	3.419E-03	605	3.578E-02	474139	8624196	11
12	808	BLR8201010	3.633E-05	1	3.633E-05	606	3.582E-02	474510	8624308	11
13	806	BLR8201013	3.528E-05	33	1.164E-03	639	3.698E-02	474712	8624326	11
14	849	BLR8203005	3.507E-05	109	3.873E-03	748	4.080E-02	474116	8624250	11
15	839	BLR8202014	3.372E-05	67	2.259E-03	815	4.306E-02	474149	8623893	11
16	819	BLR8201026	3.357E-05	15	5.036E-04	830	4.357E-02	474487	8623926	11
17	825	BLR8202010	3.256E-05	7	2.249E-04	827	4.390E-02	474426	8623918	11
18	836	BLR8202011	3.398E-05	1	3.398E-05	838	4.393E-02	474370	8623907	11
19	827	BLR8202002	3.263E-05	0	0.000E+00	838	4.393E-02	474192	8624208	11
20	834	BLR8202009	3.258E-05	1	3.258E-05	839	4.397E-02	474353	8624073	11
21	837	BLR8202012	3.058E-05	0	0.000E+00	839	4.397E-02	474311	8623782	11
22	838	BLR8202013	3.058E-05	154	4.575E-03	993	4.854E-02	474234	8623896	11
23	848	BLR8203004	2.960E-05	9	2.664E-04	1002	4.881E-02	474307	8624502	11
24	824	BLR8201031	2.959E-05	24	7.102E-04	1026	4.922E-02	474535	8623748	11
25	850	BLR8203005	2.863E-05	149	4.094E-03	1169	5.362E-02	474036	8624387	11
26	821	BLR8201029	2.841E-05	86	1.023E-03	1205	5.454E-02	474569	8623898	11
27	807	BLR8201014	2.798E-05	31	8.489E-04	1236	5.549E-02	474797	8624252	11
28	795	BLR8201002	2.629E-05	43	1.131E-03	1279	5.622E-02	474879	8624352	11
29	823	BLR8201030	2.617E-05	130	2.879E-03	1389	5.950E-02	474635	8623770	11
30	826	BLR8202001	2.599E-05	0	0.000E+00	1389	5.950E-02	474238	8624250	11
31	841	BLR8202016	2.570E-05	140	3.598E-03	1529	6.309E-02	474198	8623666	11
32	822	BLR8201029	2.565E-05	12	3.079E-04	1541	6.340E-02	474635	8623880	11
33	805	BLR8201012	2.550E-05	0	0.000E+00	1541	6.340E-02	474719	8624263	11
34	820	BLR8201027	2.534E-05	13	3.294E-04	1554	6.373E-02	474577	8624015	11
35	796	BLR8201002	2.520E-05	22	8.097E-04	1596	6.454E-02	474820	8624441	11

10.6.9.2 Population Exposure Estimates for Chronic Population

To calculate a population exposure estimate for the chronic noncancer hazard index select *Analysis/Population Exposure/Chronic Population Exposure* from the menu. The following window will appear:



Input the chronic hazard index threshold as directed and press OK. The chronic noncancer exposure estimate report will be written to a file and displayed in the Report window as shown below. The report consists of a list of all census block receptors whose chronic hazard index exceeds the threshold that you specify.

Preview

Print Zoom Previous page Next page First Page Last Page Exit

1.0

POPULATION EXPOSURE ESTIMATE REPORT - CHRONIC NONCANCER
 File: C:\HARP\PRODUCTS\HHSO\Chronic_Population_Exposure.txt

COUNT	REC	DESCRIPTION	CHRONIC HFI	POP	CON POP	UTMR	UTRN	ZONE
1	829	BLK8202004	5.348E-01	0	0	474081	3634127	11
2	853	BLK8204002	3.552E-01	41	41	474025	3634191	11
3	798	BLK8201005	2.502E-01	56	97	474608	3634519	11
4	800	BLK8201007	2.204E-01	0	97	474464	3634475	11
5	821	BLK8202006	2.062E-01	62	160	474161	3634021	11
6	797	BLK8201004	1.692E-01	16	176	474628	3634445	11
7	830	BLK8202005	1.690E-01	14	190	474098	3634010	11
8	822	BLK8202007	1.478E-01	0	190	474236	3634048	11
9	851	BLK8204000	1.258E-01	328	518	473910	3634258	11
10	828	BLK8202003	1.047E-01	86	604	474129	3634176	11
11	833	BLK8202008	1.042E-01	1	605	474307	3634027	11
12	803	BLK8201010	9.298E-02	1	606	474610	3634303	11
13	806	BLK8201013	9.192E-02	33	633	474712	3634326	11
14	839	BLK8202014	8.373E-02	67	706	474148	3633833	11
15	886	BLK8202011	8.467E-02	1	707	474370	3633807	11
16	835	BLK8202010	8.263E-02	7	714	474426	3633618	11
17	819	BLK8201026	8.007E-02	15	723	474487	3633526	11
18	849	BLK8203005	7.770E-02	108	838	474116	3634298	11
19	897	BLK8202012	7.732E-02	0	898	474311	3633792	11
20	898	BLK8202013	7.603E-02	154	992	474234	3633896	11
21	827	BLK8202002	7.502E-02	0	992	474192	3634209	11
22	848	BLK8203004	7.401E-02	9	1001	474307	3634592	11
23	824	BLK8201031	7.143E-02	4	1025	474635	3633748	11
24	807	BLK8201014	6.899E-02	31	1056	474797	3634252	11
25	824	BLK8202009	6.809E-02	1	1057	474343	3634073	11
26	850	BLK8203006	6.749E-02	143	1200	474056	3634907	11
27	821	BLK8201028	6.651E-02	36	1236	474649	3633896	11
28	796	BLK8201002	6.697E-02	43	1279	474679	3634322	11
29	806	BLK8201012	6.345E-02	0	1279	474719	3634263	11
30	796	BLK8201003	6.327E-02	32	1311	474830	3634441	11
31	840	BLK8202015	6.282E-02	151	1462	474018	3633852	11
32	841	BLK8202016	6.273E-02	140	1602	474198	3633666	11
33	823	BLK8201030	6.164E-02	110	1712	474635	3633770	11
34	801	BLK8201008	6.052E-02	0	1712	474661	3634425	11
35	822	BLK8201029	5.943E-02	12	1724	474635	3633880	11
36	846	BLK8203001	5.917E-02	40	1764	474266	3634669	11
37	820	BLK8201027	5.896E-02	19	1777	474577	3634016	11
38	886	BLK8207004	5.786E-02	113	1890	474649	3633637	11
39	808	BLK8201015	5.675E-02	22	1912	474825	3634175	11
40	847	BLK8203003	5.675E-02	42	1964	474236	3634491	11
41	802	BLK8202001	5.598E-02	9	1964	474236	3634491	11

10.6.9.3 Population Exposure Estimates for Acute (Estimated)

To calculate a population exposure estimate for the acute noncancer hazard index select *Analysis/Population Exposure/Acute Population Exposure (Estimated)* from the menu. The following window will appear:

Acute HHI threshold

Input the acute HHI threshold level. The report will tally the acute population exposure for all census receptors where the simple acute HHI exceeds the threshold value that you enter here. For example, to calculate the acute population exposure within the 1.0 isopleth, enter a value of 1.0. To include all census receptors, enter a value <= 0.

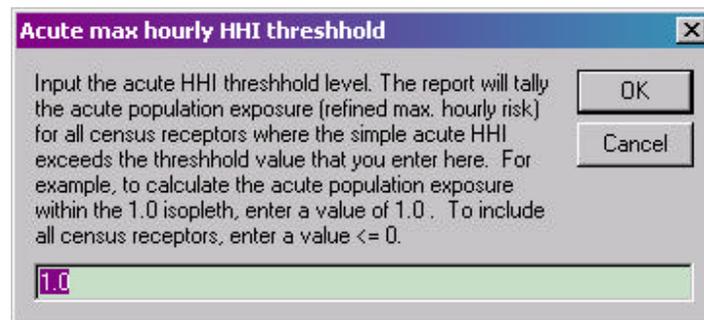
1.0

OK Cancel

Input the acute hazard index threshold as directed and press OK. The acute noncancer exposure estimate report will be written to a file and displayed in the Report window similar to the one shown (above) for the chronic noncancer hazard index. The report consists of a list of all census block receptors whose acute hazard index exceeds the threshold that you specify.

10.6.9.4 Population Exposure Estimates for Acute (Refined)

To calculate a population exposure estimate for the acute (refined) noncancer hazard index you must first have run the Refined Max Hourly Acute HHI analysis (see section 10.6.10.2). Once the Refined HHI analysis is complete, select *Analysis/Population Exposure/Acute Population Exposure (Refined)* from the menu. The following window will appear:



Input the acute hazard index threshold as directed and press OK. The acute noncancer exposure estimate report will be written to a file and displayed in the Report window similar to the one shown (above) for the chronic noncancer hazard index. The report consists of a list of all census block receptors whose acute hazard index exceeds the threshold that you specify.

10.6.10 Simple and Refined Acute Risk

10.6.10.1 Acute Risk (Simple)

HARP provides a very efficient way to estimate acute risk, which is referred to as simple acute risk. This method employs a timesaving approximation that is conservative in nature. Therefore, if you calculate the simple acute risk and find that the acute health hazard index (HHI) is less than 1, it may not be necessary to perform the more time consuming calculation of maximum hourly acute refined risk (see next section).

To calculate simple acute risk we assume that the X/Q at each receptor location and the emission rates from each source are at their maximum values at the same instant in time. This approximation allows us to simply use the maximum hourly X/Q for each source-receptor combination rather than considering the temporal variation of X/Q to calculate the GLCs. We then add the GLCs from all sources together at each receptor as if they had all occurred at the same time.

When you calculate acute risk from the risk reports window (see section 10.6.4), the simple acute risk approximation is made. If you find that the simple acute risk is high enough to warrant a more detailed analysis, you should calculate the refined maximum hourly acute health hazard index (HHI) (see section 10.6.10.2).

10.6.10.2 Refined Maximum Hourly Acute Risk

The maximum hourly acute risk refines the approximation used for the simple acute risk (see section 10.6.10.1). This is a more time consuming calculation, and is therefore usually done for a few receptors, typically the ones with the highest screening acute risk.

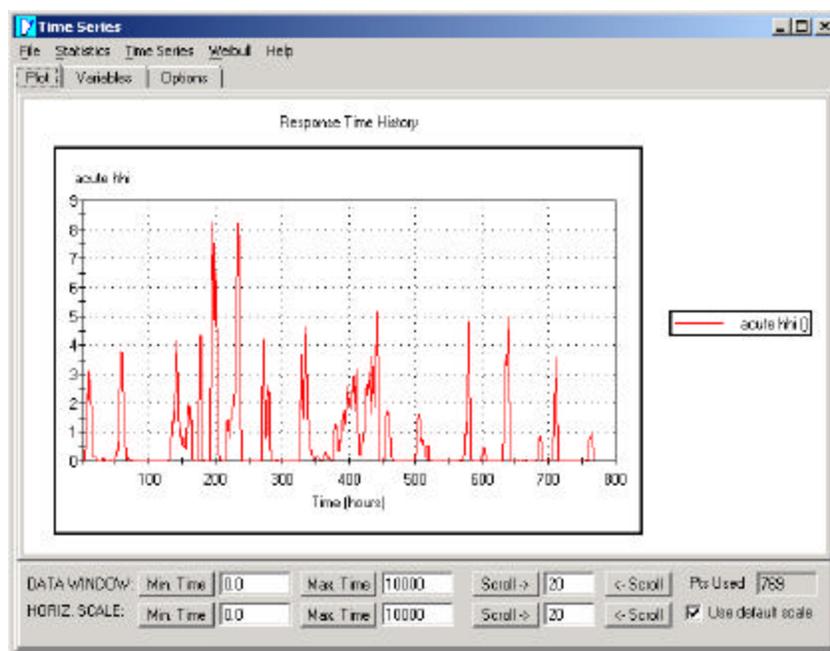
This calculation uses the hourly X/Q and the maximum emission rates from each source to calculate a GLC at each receptor location. Versus the simple approach, the refined approach allows us to consider the temporal variation of X/Q to calculate the GLCs. The GLCs from all sources are then added together to get the total GLC at that hour. From this the refined acute HHI is calculated. HARP then locates the maximum acute HHI over the time considered in the analysis.

This approach accounts for the fact that the X/Q from different sources will have a different time series and will not necessarily be at their maximums at the same time. This approach may produce a lower estimate of acute risk than the screening approximation. The refined method is still somewhat conservative because it uses the hourly maximum emission rate for every hour of the simulation rather than using time-distributed emission rates.

10.6.10.2.1 Refined Maximum Hourly Acute Risk for a Single Receptor

Before proceeding, be sure that you have opened an SRC file (see section 10.5.2).

To calculate maximum hourly acute risk for a single receptor, select *Analysis/Refined Max Hourly Acute HHI* from the menu. You will be prompted for the number of the receptor that you want to analyze. Enter the receptor number and press OK. After a few minutes the analysis will be completed and a window similar to the following will appear.



TIME SERIES OF ACUTE RISK

This window shows the time history of acute risk for the receptor you selected. From this plot you can see that the maximum value of acute risk HHI is 8.2, and that it occurs at 200 hours from the start of the simulation. Note that in the above example, the dispersion analysis was done for only 32 days for the purpose of demonstration. The length of the dispersion analysis determines the length of time for the maximum hourly acute risk analysis.

Under the *File* menu of this window there are options for printing this plot or copying it to the windows clipboard for insertion into a word processor. The *Statistics* menu item will create a simple table of statistics of the time series data. When you choose the *Statistics* option, you will be prompted for the file name. By default, it is called *stats.txt* and is located in your project directory.

Under the *Variables* tab, you can add (or delete) different variables to be plotted on the time series. Under the *Options* tab, you can change the location of the legend and choose whether or not symbols are drawn at each point on the plot or just lines without symbols. After making changes to the options or the variables to plot, click on ***Time Series*** to refresh the plot.

The *Min Time* and *Max Time* button at the bottom of the window, allow you to clip the graph to see just a small time range expanded. Set these values to some small range and refresh the plot by clicking the *Time Series* menu again.

To zoom into a specific area of the graph, hold down either the shift or control key while you drag the mouse around the area that you want to zoom into. To restore the graph to full view, press the lower case “r” key.

10.6.10.2.2 Refined Maximum Hourly Acute Risk for Multiple Receptors

HARP has the ability to perform the maximum hourly acute risk analysis for a set of receptors and collect the results into a summary report.

From the risk window menu select ***Analysis/Max Hourly Acute HHI/All Receptors Within An Isopleth***. You will be prompted with the following window.



When you enter a value into this window and press OK, HARP will perform the maximum hourly acute risk analysis for all receptors whose screening acute risk value exceeds the number you specify. In the above example, the user has requested the analysis to be performed for all receptors having an acute HHI exceeding 1, based on the screening acute analysis.

You must first perform the acute screening risk analysis before executing this function. After the analysis is completed the resulting report window will appear as shown below.

The screenshot shows a window titled 'Report' with a menu bar containing 'Print', 'Zoom', 'Previous page', 'Next page', 'First Page', 'Last Page', and 'Exit'. Below the menu bar is a search bar with '1/1' and a search icon. The main content area displays the following table:

RECEPTOR	MAX ACUTE RISK	HOUR	SCREENING RISK	RATIO
209	8.546E-01	330	1.261E+00	0.678
210	8.116E-01	711	1.267E+00	0.641
211	7.818E-01	65	1.121E+00	0.697
212	6.335E-01	757	1.070E+00	0.592
213	7.907E-01	516	1.145E+00	0.691
214	7.968E-01	469	1.192E+00	0.668
215	7.467E-01	214	1.304E+00	0.573
216	7.219E-01	466	1.337E+00	0.540
217	7.733E-01	466	1.116E+00	0.693
218	6.239E-01	700	1.004E+00	0.621
231	7.015E-01	492	1.063E+00	0.660
236	6.412E-01	75	1.290E+00	0.497
237	9.893E-01	744	1.503E+00	0.658
238	1.229E+00	301	1.646E+00	0.747
239	7.925E-01	101	1.222E+00	0.649
249	6.522E-01	639	1.266E+00	0.515
250	7.286E-01	639	1.095E+00	0.666
255	6.705E-01	466	1.048E+00	0.640
257	6.248E-01	466	1.037E+00	0.603
258	5.812E-01	443	1.064E+00	0.546

The report shows the maximum hourly acute risk for each of the receptors exceeding the screening threshold and the hour at which the maximum occurred. The last two columns show the acute screening risk for each receptor and the ratio between the maximum hourly acute risk (refined) and the screening risk. Note that this ratio is always less than 1, which simply reflects the conservative nature of the screening risk.

10.6.10.2.3 Refined Maximum Hourly Acute Risk for All Grid Receptors

HARP has the ability to perform the maximum hourly acute (refined) risk analysis for all receptors and collect the results into a summary report. From the risk window menu select *Analysis/Max Hourly Acute HHI/All Grid Receptors*. After the analysis is completed the resulting report window will appear as shown above for receptor within an isopleth. Depending on the complexity of the risk assessment (e.g., number or sources, receptors), this analysis may take some time to complete.

10.6.11 Creating Contours

HARP includes some mapping features that include placing contour lines (isopleths) over street maps. However, for detailed mapping problems, you may wish to export your data to a GIS mapping program (see Appendix M for export instructions).

From the *Risk* window, select *Analysis/Contour*. Note that *Contours* window will appear, similar to that shown below. The contour isopleths are generated using **ONLY GRID RECEPTORS**. The number of contours should be one number greater than the number of intervals that you want your data divided into (i.e., if 5 intervals of data is desired, enter 6 contours). If HARP will not calculate the contours, there may not be enough data. At least three

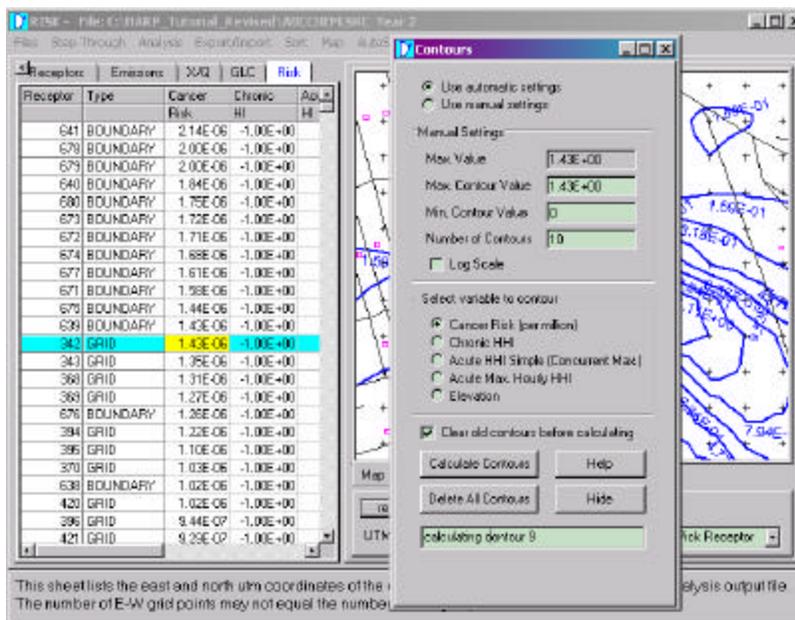
points of data (grid receptors) at that contour range are needed to make an isopleth. You should also look at your risk data to confirm that your maximum and minimum contour values are within the range of your data or you may need to rerun the dispersion analysis with smaller grid spacing.

To contour elevation from a loaded DEM file, select elevation. To contour risk, select either cancer, chronic or acute risk. Before generating risk contours you must first calculate the point-estimate risk for these health effects following the procedures in section 10.6.4.

HARP will plot the last risk that was calculated. So if you chose to run a risk analysis for “average, high-end, and derived”, the risk contours that will be plotted will be for “derived”. If you ran the OEHHA standard report set, HARP will plot the 70-year, cancer, derived (adjusted) scenario from Report #19. HARP plots contours in units of “per million.”

10.6.11.1 Contouring With Automatic Settings

From the **Risk** window, select **Analysis/Contour**. The **Contours** window will appear (shown below). Using the automatic settings will create contours that bound the risk data between the highest risk value and zero. Note that cancer risk contours are plotted in units of “per million”. The number of contours that you define will divide the risk results into evenly spaced intervals between these two points. After supplying the needed information click on “**Calculate Contours**” and the mapped results will appear on the Risk window. To refine the look of the mapped isopleths (e.g. label frequency, font size) use the features under “**Map Options**”. The time required to create the contours is proportional to the number of contours and the square of the number of grid points. A 20x20 grid will take 16 times longer to contour than a 10x10 grid because it has four times as many grid points.



CONTOURING WITH AUTOMATIC SETTINGS

10.6.11.2 Contouring With Manual Settings

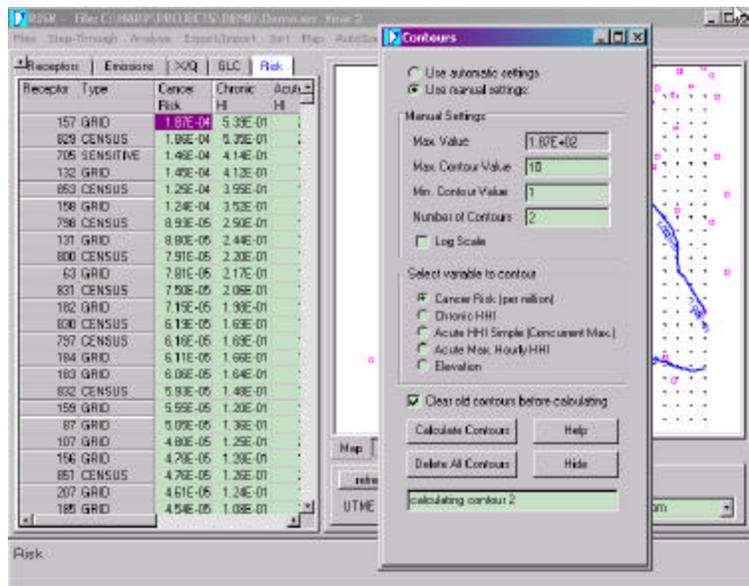
From the **Risk** window, select **Analysis/Contour**. The **Contours** window will appear (shown above). If you wish to manually identify the contours, check the box (at the top of the window) “*Use Manual Setting*”. By default, the box labeled “max value” will be populated with the highest cancer or noncancer health value for your analysis and the maximum contour level shown in the next box is set to the same value, while the minimum contour value is zero. Note that cancer risk contours are plotted in units of “per million”.

Reset the maximum and minimum contour levels to reflect the levels that you would like shown as your maximum and minimum contour lines. Identify the number of contour lines you want to display. The number of contours that you define will divide the risk results into evenly spaced intervals between the maximum and minimum values. In most cases, the number of contours should be one number greater than the number of intervals that you want your data divided into (i.e., if 5 intervals of data is desired, enter 6 contours).

Note: if you want to see just two isopleths at, for example, 1 and 10 chances per million, set 10 for the maximum and 1 for the minimum contour values, and place a 2 in the slot for the number of contours. This same result can be achieved by checking the “*Log Scale*” box. The log scale box will provide the results at intervals of Log10.

After supplying the needed information click on “*Calculate Contours*” and the mapped results will appear on the Risk window. To refine the look of the mapped isopleths (e.g. label frequency, font size) use the features under “*Map Options*”.

The time required to create the contours is proportional to the number of contours and the square of the number of grid points. A 20x20 grid will take 16 times longer to contour than a 10x10 grid because it has four times as many grid points.



CONTOURING WITH MANUAL SETTINGS

10.6.12 Printing Maps

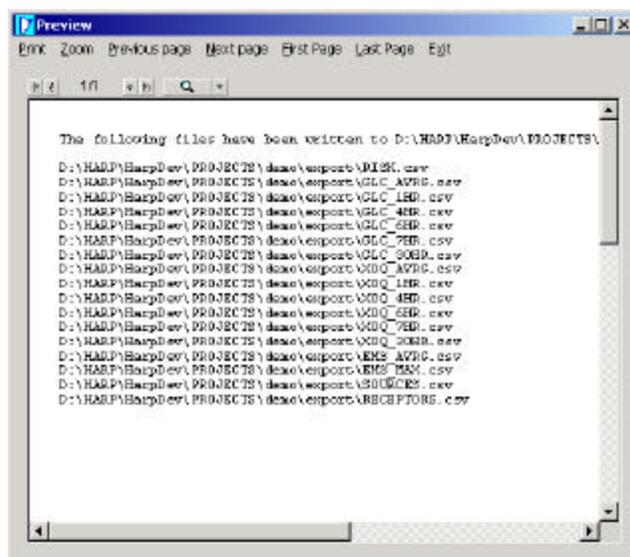
To print a map that is shown on the risk window, select **Map/Print Preview** from the menu. The print preview window will appear as shown below. To print the map directly to the printer, select **File/Print** from the menu.

To insert the map into a word processing document, first select **File/Copy to Clipboard** from the menu. Then open your document (using for example Microsoft Word) and press **Control-V** on our keyboard or select **Edit/Paste** from the word processor menu. Within the word processor program you can add text boxes and labels to indicate points of interest for the PMI, MEI, etc.



10.6.13 Exporting Data

All of the data that is shown on the risk window can be exported to comma-delimited files that can be easily loaded into Excel. To export the data, select **Export/Export All Details** from the menu of the Risk window. You will be prompted for the name of a directory where all of the exported files will be written. This would typically be the project directory, or a subdirectory under the project directory. After all of the data is exported, you will see report window showing the names and locations of the various files, as shown below. The format of each of these files is described in section 10.7.11.



10.6.14 Health Table

The health table is stored in the Microsoft Access database file HEALTH.MDB, which is installed in your HARP directory. The health table contains all of the chemical-specific data that is used in the risk analysis. This includes cancer potency values, chronic and acute noncancer reference exposure levels. For each chemical there are also a number of flags that indicate which pathways apply to each of the chemicals for cancer effects and which organ systems apply to each chemical for acute and chronic effects. This table is in a read-only format. To view the contents of the health table, click on **Health Table** from the main risk window.

10.7 Stochastic Analysis

10.7.1 Prerequisites

Before you can compute risk for a residential receptor, you must have entered your facility emissions data into the HARP database (CEIDARS-Lite) and have run the air dispersion analysis. Open the risk window by selecting **Analysis/Risk Analysis** (choose either the *Representative* or *Screening Met Data* option) from the HARP main menu. Then open the source-receptor file that was created from your air dispersion analysis (*.src) by clicking on **File/Open Source/Receptor File (Dispersion analysis results)** from the risk window (see section 10.5.2). This loads the X/Q values from the dispersion analysis into memory and automatically calculates the GLCs.

To perform stochastic analysis, select **Analysis/Stochastic (Includes multipathway)** from the Risk window menu. The window that will appear is referred to as either the Stochastic/Multipathway or Network window, because it provides tools for viewing all details and intermediate calculations of the multipathway network. Because the stochastic analysis is closely tied to the network, these two general topics have been combined into a single window. See section 4.8 for a tutorial on stochastic analysis.

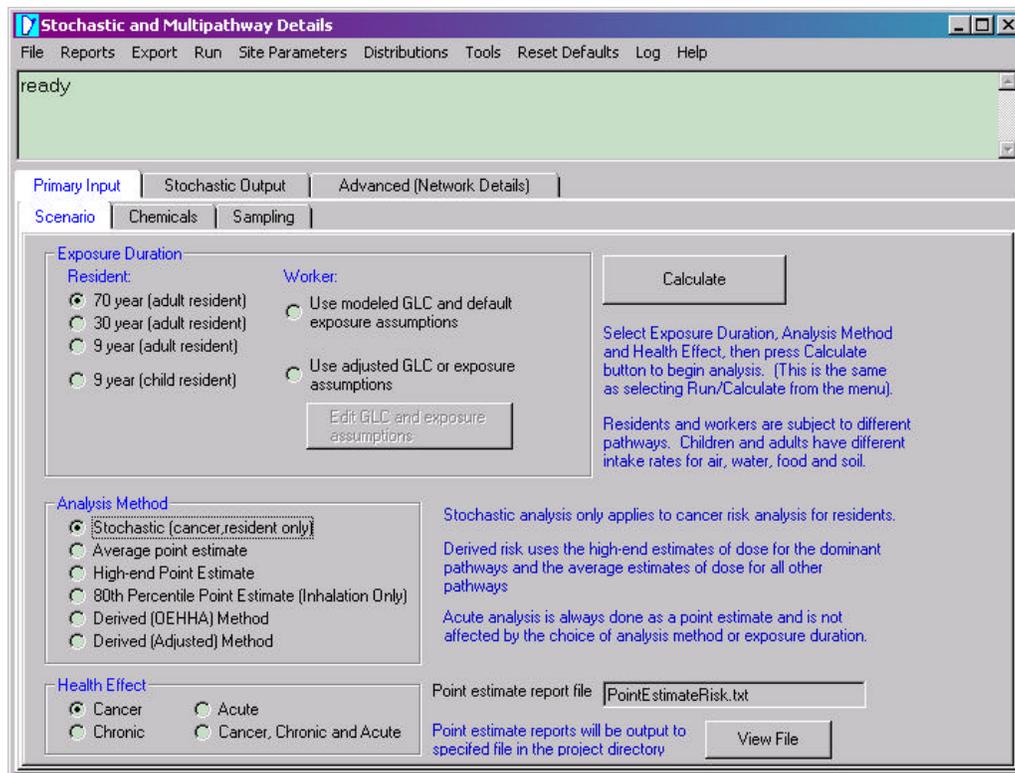
From the same window, it is also possible to perform point-estimate analysis for a single receptor and view every intermediate step in the analysis. At this point, it is assumed that the user is familiar with the setup of a point estimate analysis in HARP. If not, it may be best to perform the point-estimate analysis by following the follow the step-through guide under *Point-Estimate (includes Multipathway)* and see section 10.6 for more information.

10.7.1.2 Stochastic/Multipathway Window

The Stochastic/Multipathway window is opened by first opening the risk window and then selecting *Analysis/Stochastic (Includes multipathway)* from the menu.

The Stochastic/Multipathway window is organized under three tabs:

1. The *Primary Input* tab allows you to view and edit the primary input parameters used in the analysis. Some of these parameters apply only to stochastic analysis, and some of them apply to both stochastic and point-estimate analyses. For example, a stochastic analysis can only be applied to a residential receptor.
2. The *Stochastic Output* tab allows you to display and print several graphical and tabular reports generated from the stochastic analysis.
3. The *Advanced (Network Details)* tab allows you to view intermediate results at any point in the multipathway network. This tab exposes a lengthy and complex list showing every intermediate step in the calculations. It is considered to be for advanced users.



STOCHASTIC / MULITPATHWAY WINDOW

10.7.2 Primary Input

Before running a simulation, you should review and edit all of the parameters under the **Primary Input** tab of the Stochastic/Multipathway window. There are three sub-tabs which are described in the following sections: *Scenario*, *Chemical*, and *Sampling*.

10.7.2.1 Primary Input: Scenario

To edit the scenario parameters, first click the **Primary Input** tab on the Stochastic/Multipathway window. Then click the **Scenario** tab. The window will appear as shown above.

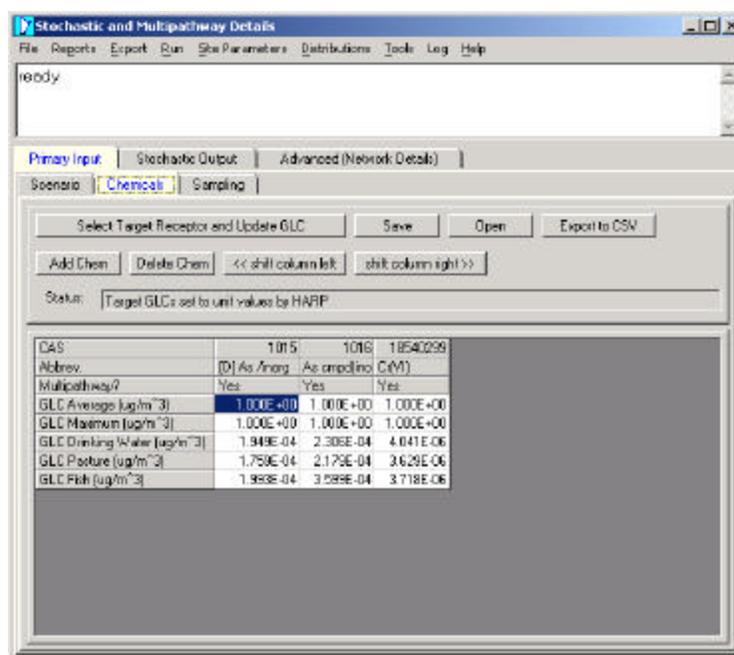
Select the exposure duration and receptor type for your analysis. Remember that a stochastic analysis can only be applied to a residential receptor.

Select the *Analysis Method*. If you select anything other than Stochastic, then only one sample trial will be executed and the result will be a point-estimate rather than a stochastic analysis. In that case the results will be read from the *Network Details* tab, and the results under the *Stochastic Output* tab will be meaningless. From this screen, analyses using point-estimates of exposure to estimate risk are normally only done by very experienced users for the purpose of examining intermediate values on the network.

Select the health effect of interest, either cancer or noncancer (acute or chronic); however, a stochastic analysis only applies to cancer. If you select noncancer, then the stochastic analysis button will be grayed out and inactive.

10.7.2.2 Primary Input: Chemicals

To edit the chemical GLC values, first click the **Primary Input** tab on the Stochastic window. Then click the **Chemicals** tab. The window will look similar to the following.



Then click the button labeled **Select Target Receptor and Update GLC**. You will be prompted for the receptor number that you wish to run the analysis for (receptor numbers can be found on the risk window). Enter the receptor number and press OK. The table will then be updated with current GLC values. The GLC values will be extracted from the risk window, so in order for this to work you must have previously opened a source-receptor file from the risk window.

The table shown under the **Chemicals** tab lists the GLCs for each of the chemicals at four receptors. The first receptor is the target receptor, (i.e. the receptor that is being analyzed). For the target receptor, both the average and maximum GLCs are shown. The average GLC is used for the cancer and chronic analysis, and the maximum GLC is used for the acute analysis. (Reminder: stochastic analyses only apply to cancer analysis).

The other three receptors shown above are the pathway receptors. These are receptors located at the drinking water source, the pasture location, and the location of locally caught fish. The locations of these receptors must be specified when you set up and run the dispersion analysis. These receptors are necessary to determine the concentration of chemicals in the animal products, drinking water, and locally caught fish.

The third row of this table shows whether each chemical is a multipathway chemical or not. For chemicals that are not multipathway, the GLCs for the three pathway receptors are not used and are therefore grayed out.

You may edit the GLC in this table directly in the cells where they are displayed. To restore the original values after you have edited them, click the button labeled **Select Target Receptor and Update GLC** and reenter the receptor number.

You may also add a chemical to the list by clicking the button labeled **Add Chem**. You will be prompted with a list of available chemicals. When you select a chemical from the list and press OK, the chemical will be added to the table of chemicals shown above.

To delete a chemical from the list, click on one of the cells in the column below that chemical, and then click the button labeled **Delete Chem**.

The **Export to CSV** button is used to export the table to a comma-delimited file (CSV file). This can then be imported into a spreadsheet or word processor for printing.

The right and left arrow buttons (>> and <<) are used to shift one of the chemicals to the right or left in the list. You must first click the column that you want to move, and then click the appropriate button. The reason you may want to do this is that the results of the multipathway analysis on the *Network Details* tab are shown for only the last chemical in the list. If you want to examine details for a particular chemical, move it to the last column.

10.7.2.2.1 Performing a Stochastic Risk Analysis for a Single Receptor Without A Dispersion Analysis

If you know the ground level concentrations at some location you can enter them directly on the Stochastic and Multipathway Details window and proceed with risk analysis without ever running the dispersion analysis. These are the steps:

Edit Chemical Ground Level Concentrations

On the *Stochastic and Multipathway Details* window, click the *Primary Input tab* and the *Chemicals tab*. Add or delete chemicals from the list, then edit the ground level concentrations for the appropriate locations. For more information see section 10.6.3.2.

Set Run Parameters

Input the site, scenario, and sampling parameters, identify the stochastic output results as described in the following sections.

Run Simulation

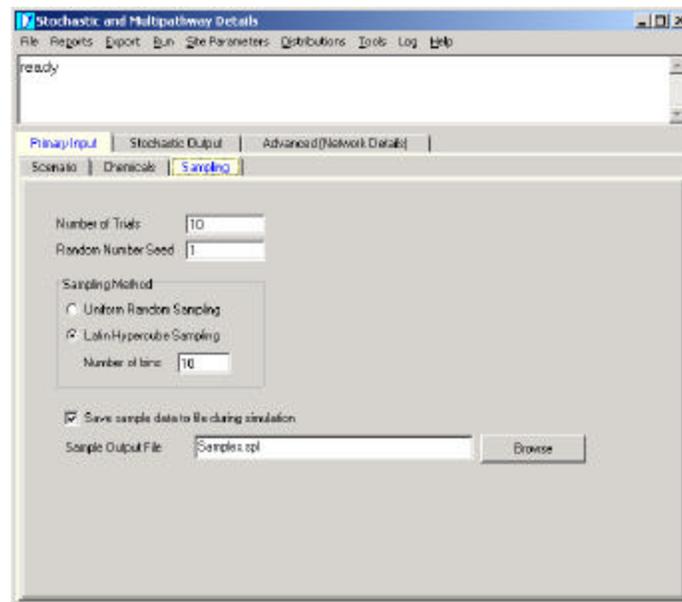
Select **Run/Continue Stochastic** from the menu. You may also interrupt the simulation by pressing the **Cancel Operation** button from the log window, then resume by selecting **Run/Continue Stochastic**. The **Continue Stochastic** option will run multiple trials continuously until the limit specified under the Sampling tab is reached. In comparison, if you choose **Run/Single Step Stochastic** HARP will execute one more trial in the Monte Carlo simulation. Run the simulation as described in the following section. Note that if you only want a point-estimate report, not a stochastic analysis, you can select one of the point-estimate options under the *Analysis Method* section under the Scenario tab.

10.7.2.2 Specify Site Parameters

If you have not done this previously, you will need to set-up your site parameters. From the top of the stochastic window, select the *Site Parameters* menu and fill in the appropriate exposure pathway information behind the tabs. (See section 10.6.3).

10.7.2.3 Primary Input: Sampling

To edit the sampling parameters, first click the *Primary Input* tab and then the *Sampling* tab on the Stochastic window. The window will then appear as shown below.



In the first box enter the number of trials that you want to execute in the Monte Carlo simulation. It is useful to enter a small number of trials to begin with (e.g., 1000), and examine the results to see that they make sense and that you have not made any input errors. When you are convinced that you have set-up everything correctly, you can then set the number of trials to a larger number (typically 5,000 to 10,000) to obtain accurate results.

After you have examined the results, and you feel that more trials are necessary, set the number of trials to indicate how many additional trials you want to run, and then select the random seed number.

The *random seed number* is used to initiate the randomization of trials during the stochastic simulation. The computer uses this seed number in a series of computations to generate an array of numbers for stochastic calculations. By default the number is set to one. If you do not change the random seed number, then each time you run the simulation, you will get exactly the same results. In other words, the random numbers will be the same sequence each time you run a simulation. If you want to run two different realizations of the same simulation, then change the random seed number between runs. If all other inputs are the same, then you will obtain results that are different, but in theory are statistically equivalent. The random

number seed can be any single precision floating point number. Negative and positive numbers are treated as the same (i.e. a negative sign is ignored).

Finally, select either uniform sampling or Latin hypercube sampling. Latin Hypercube sampling generally produces more accurate estimates of the extreme statistics. If you select Latin Hypercube sampling, then you must specify the number of bins from which to select the samples.

As the number of bins increase, the accuracy of the extreme statistics improves, which is to say that the chances of observing an extreme event among the trials is higher. In principle, using Latin Hypercube sampling improves the definition of the shape of the output distribution curves by forcing some samples to be taken near the tail ends of the distribution.

For example, if you are really interested in, say, the 99th percentile of risk, then you want to make sure that you get several trials where the variate values fall above the 99th percentile. If you are only doing 100 samples, the chances of this are small, so your results won't be very meaningful. In this case you might want to set the number of bins to 100 and take 1000 samples. The Latin Hypercube method will then guarantee that 10 of those samples fall above the 99th percentile for each of the variates. So, as a general rule you might say that the number of bins should be about 10-fold smaller than the number of samples. But it should also reflect the extreme-ness of the statistics that you are interested in. If you want to accurately resolve the 99.9th percentile (i.e. 1/1000 extrema), then you probably would want 1000 bins and several thousand samples.

Select ***Run/Continue Stochastic*** from the menu. You may also interrupt the simulation by pressing the ***Cancel Operation*** button from the log window, then resume by selecting ***Run/Continue Stochastic***. The ***Continue Stochastic*** option will run multiple trials continuously until the limit specified under the Sampling tab is reached. In comparison, if you choose ***Run/Single Step Stochastic*** HARP will execute one more trial in the Monte Carlo simulation.

10.7.3 Primary Input: Saving and Retrieving Raw Sample Data

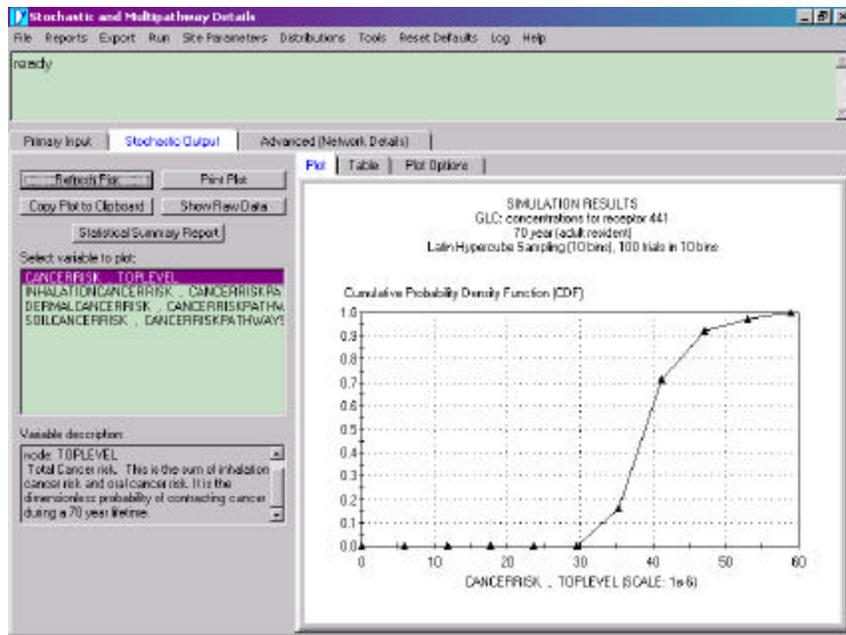
In the Sampling window shown above there is a check box labeled “*save sample data to file during simulation*”. If this box is checked, each of the samples will be saved to a file as the simulation proceeds. Later you can read the raw sample data back into the program without rerunning the simulation. This allows you to view the data from a previous simulation.

To load sample data from a file, select ***File/Open Stochastic Sample File*** from the menu.

10.7.4 Output Processing

10.7.4.1 Plot

To plot a distribution of an output variable, select the ***Output Stochastic*** tab on the Stochastic window. Then select the ***Plot*** tab. The window will appear similar to the following.



STOCHASTIC OUTPUT WINDOW

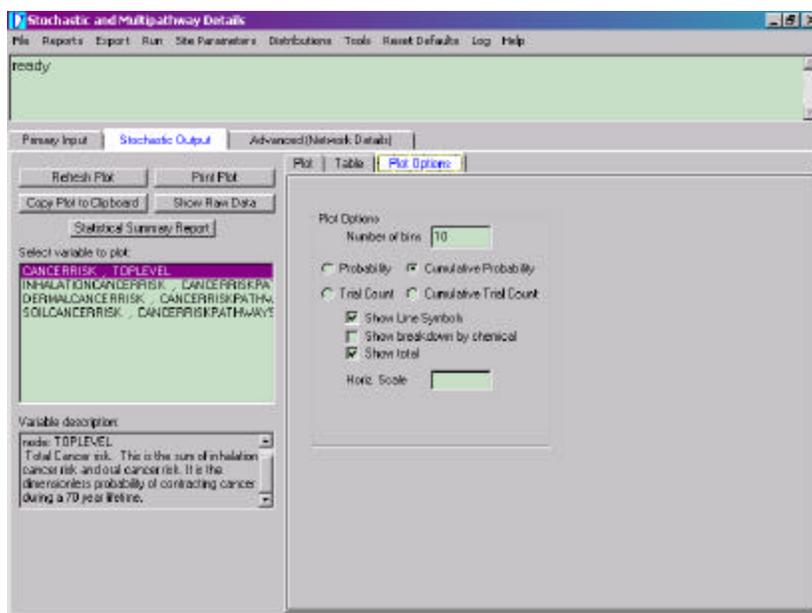
The left side of the window shows the variables that are available for plotting. The default variables that will be listed in this window are determined by the pathways that are selected in the *Site Parameters* window. “Top Level Cancer Risk” is always listed. This provides you with the total multipathway cancer risk. To change the list of variables available for plotting you must change the “save” option on the *Network Details* tab and rerun the simulation. Refer to section 10.7.6.1. To select a variable for plotting, highlight the name of the variable by clicking on it with the mouse. In the example above, the user has selected Cancer Risk as the variable to plot.

After selecting the variable, click the button labeled *Refresh Plot*. The right side of the window will then show a distribution plot for the selected variable. Various options are available for plotting, as described in the following section.

To print a plot, click the button labeled *Print Plot*. If you want to insert the plot into a word processing document, click the button labeled *Copy Plot to Clipboard*, then open your document (for example using Microsoft Word) and press Control-V or select *Edit/Paste* from the menu.

10.7.4.2 Plot Options

To change the plot options, click the *Plot Options* tab. The window will appear similar to the following. Select the option you want from the right hand pane and press the button labeled *Refresh Plot* to redraw the plot with the new options.



STOCHASTIC PLOT OPTIONS WINDOW

The distribution curves are generated by first sorting the raw sample data from the Monte-Carlo trials, then collecting the data into bins according to the values of the variable. The bins are bounded by equally spaced intervals of the variable values. For example, if the maximum risk from all the samples is 10^{-6} , and you specify 100 bins, then the first bin will contain the samples having risk values between 0 and 10^{-8} . The second bin will contain samples having risk values between 10^{-8} and 2.0×10^{-8} , and so on. The ordinates of the distribution curve are simply the count (or cumulative count) of the number of samples in each bin, divided by the total number of samples. This represents an estimate of the probability (or cumulative probability) that the risk will fall in that interval. Plotting the count for each of the bins against the risk value for each bin produces an estimate of the probability (or cumulative probability) of risk (or whatever variable is being plotted).

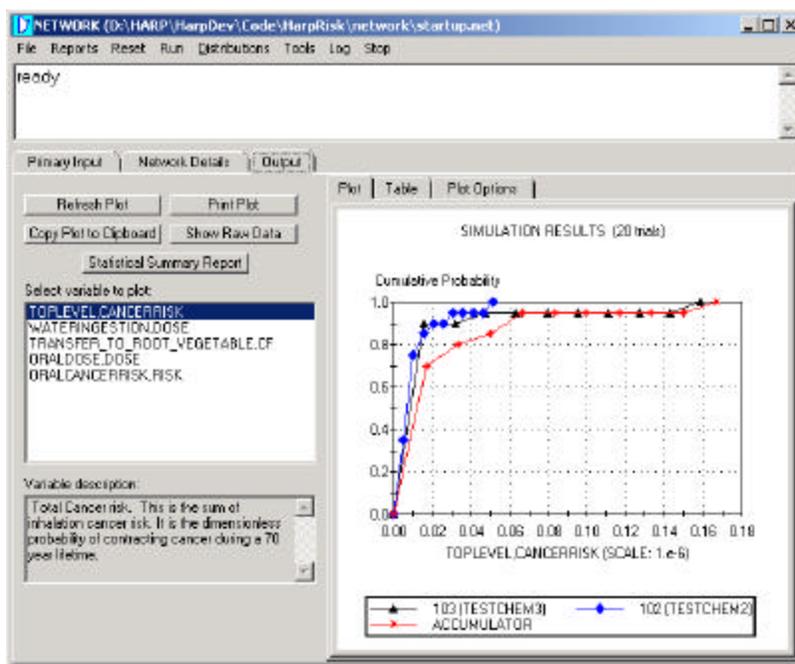
You can change the number of bins used in the analysis by entering a new value in the box labeled **Number of bins**. Reducing the number of bins has the effect of smoothing the curve.

You have four choices of what to plot. The most useful plot is cumulative probability, because it allows you to read the probability of exceeding any risk level directly from the graph. You may also choose to plot probability, rather than cumulative probability. This may be useful for comparing with standard statistical distribution curves that are presented in this way.

The trial count and cumulative trial count options generate plots where the vertical axis is the dimensional number of trials rather than the non-dimensional probability. This is generally used only for quality assurance testing and diagnostic purposes, but may be of interest to some users.

The check box labeled *Show Line Symbols* turns the symbols on or off. The symbols are useful to distinguish the curves when you have several chemicals and you have checked the box labeled *Show Breakdown By Chemical* (see below).

If you check the box labeled *Show Breakdown By Chemical*, then a separate curve will be shown for each chemical. In this case the plot will appear similar to the following.



STOCHASTIC OUTPUT */WINDOW

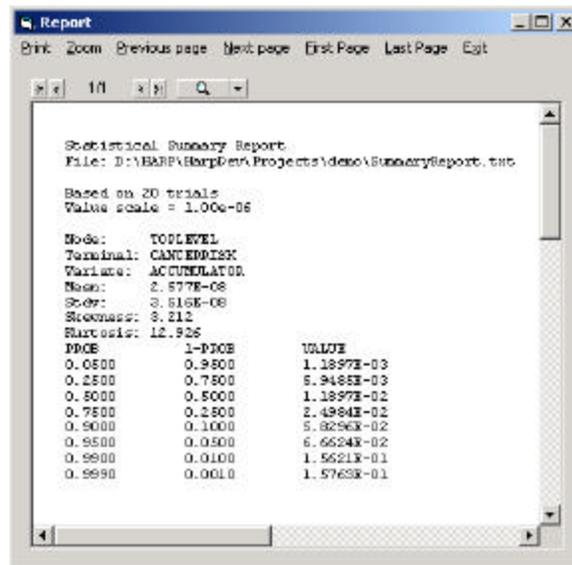
In this example the simulation was done for two chemicals. These are chemicals with CAS numbers 103 and 102 respectively. (These are fictitious chemicals included for testing purposes only.) The multipathway analysis calculates the contribution to cancer risk separately for each chemical and combines the results. In the process of doing this it collects sample data for each of the chemicals. By checking the box labeled *Show Breakdown By Chemical*, the distribution curves for all chemicals are shown on the graph. The total risk is always shown as the curve labeled ACCUMULATOR, since it is the accumulated risk from the different chemicals. You may turn the ACCUMULATOR curve on or off by checking or unchecking the box labeled *Show Total*.

The mathematical process of combining the results from multiple chemicals into a total risk value is a complicated matter. Because the risk contributions from each chemical are random and statistical in nature, and because the curves are generated by grouping samples into bins, the total risk as shown by the ACCUMULATOR curve cannot be directly derived from the curves of the individual chemicals. Instinctively, you would expect the risk values on the accumulator curve to be just the total of the risk values on the other curves. But this is seldom the case. This is further complicated by the issue of correlated vs. uncorrelated sampling, which is discussed in section 10.7.6.7.

Finally, you may set a scaling factor for the horizontal axis to improve the appearance of the plot. For cancer risk, where the values will typically be on the order of 10^{-6} , you would probably want to enter a value of 10^{-6} for the horizontal scale. To set the scale the horizontal axis to the actual values, set the value of horizontal scale to 1.0.

10.7.4.3 Statistical Summary Report

You can generate a statistical summary report by simply pressing the button labeled *Statistical Summary Report*. The report will be generated for whatever variable you currently have selected in the variable list (i.e. the same variable that you have plotted). The report will appear similar to the following window.



This report is always written to an ASCII file, whose name appears on the second line of the report as shown above. This file can be easily imported into any word processor.

As shown above, the statistical summary report shows the risk levels at preset probability levels. In the example above, the estimate of risk at a 99% probability level is $1.5621E-01$. This means that there is a 99 percent probability that the risk will be lower than this value, and a one percent probability that it will be higher. Note that the “Value Scale” is set to 1×10^{-6} , which means that the risk values shown on the right hand column have units of 1×10^{-6} . Therefore, the 99 percent probability cancer risk is actually **$1.5621E-07$ or 0.156** chances per million. The “Value Scale” is the same as the horizontal scale that you specify under the plot options (see section 10.7.4.2). For cancer risk, where the values will typically be on the order of 1×10^{-6} , you would probably want to enter a value of 1×10^{-6} for the horizontal scale. To set the scale the horizontal axis to the actual values, set the value of horizontal scale to 1.0.

The risk values are determined by linear interpolation between the points on the distribution curve that you have plotted. There is no attempt made to extrapolate the tail of the curve beyond the highest value sampled. The last point on the cumulative probability distribution curve has, by definition, a cumulative probability of 1.0, because all sampled points

have values lower than the maximum seen during the simulation. To ensure that you have accurately captured the shape of the tail of the curve (i.e. the low probability, high risk values) you should run a large number of trials. To add confidence to the risk estimates, you may want to perform a sensitivity study for your particular problem by running additional trials to observe whether the low-probability risk estimates change.

This report also lists the mean, standard deviation, skewness and kurtosis of the distribution curve.

10.7.4.4 Table

Whenever you generate a plot of a variable distribution, the numbers that are displayed on the plot are also echoed to a table. To see the table of plotted values, just click the **Refresh Plot** and then click the **Table** tab. To export the plot values select **File/Export/Distribution Data** from the menu on the Stochastic/Multipathway window. (See section 10.7.11 for more information on exporting results). The plot data are shown for only one variable at a time, namely the variable that you have plotted.

10.7.4.5 Raw Data

You may view the raw sample data collected during the simulation by clicking the button labeled **Show Raw Data**. The **Table** tab window will appear similar to the following.

	1001TESTCHEM3	1002TESTCHEM2	ACCUMULATOR
1	5.670179E-09	1.695400E-09	2.252619E-09
2	4.084553E-09	4.876880E-09	8.963445E-09
3	2.406803E-09	4.05046E-09	6.470231E-09
4	4.647886E-09	8.000259E-09	5.447919E-08
5	1.164406E-08	2.732517E-09	3.957303E-09
6	6.440606E-09	4.94795E-09	1.098996E-08
7	8.556845E-09	3.705073E-09	1.226538E-08
8	4.55703E-09	1.448581E-08	1.904234E-08
9	4.153637E-09	5.492407E-09	9.646046E-09
10	1.586571E-07	7.701607E-09	1.669593E-07
11	5.284499E-09	7.284437E-09	1.256933E-08
12	7.30758E-09	4.010572E-09	1.138919E-08
13	4.360814E-09	2.99619E-09	7.360433E-09
14	9.17793E-09	7.028685E-09	1.62095E-08
15	4.604656E-09	7.072464E-09	1.167712E-08
16	4.348303E-09	3.82076E-09	8.169064E-09
17	4.686196E-09	1.122433E-08	1.611252E-08
18	2.462017E-09	5.190682E-09	5.287133E-09
19	5.00779E-09	6.10568E-09	1.111346E-08
20	1.084549E-08	5.474835E-09	1.632043E-08

STOCHASTIC OUTPUT TABLE WINDOW

Each row of the table on the right hand pane represents one trial during the simulation. Each trial is listed (in gray) in the left column. The right-most column is the value of the selected variable (in this case Cancer Risk), and the other columns are the values of the same variable after each of the sub-trials corresponding to the individual chemicals. Because cancer risk is linear with respect to the contribution from the individual chemicals, the ACCUMULATOR column is just the sum of the other columns.

In the example above, only 20 trials were run. More typically, thousands of trials will be run, and the list will be quite long.

To export the raw sample data select **Export/Raw Sample Data** from the menu on the Stochastic window. (See section 10.7.11 for more information on exporting results). The raw sample data are shown for only one variable at a time, namely the variable that you have plotted

10.7.5 Running a Stochastic Simulation

Before running a simulation, you should have either selected a specific receptor location from a SRC file or have input the site specific GLC for the chemicals of interest. In addition, all site, scenario, and sampling parameters should have been identified (see section 10.7.2). To start a simulation, either select **Run/Calculate Stochastic** from the menu or press the **Calculate** button on the Primary Input/Scenario tab. You can observe the progress by noting the trial count that will appear in the top pane of the window.

To interrupt the simulation, press the **Cancel Operation** button on the log window. To resume the simulation after stopping, select **Run/Continue Stochastic** from the top menu. This will run multiple trials continuously until the limit specified under the *Sampling* tab is reached. Or select **Run/Single Step Stochastic** to execute one single trail in the Monte Carlo simulation.

You may plot results as the simulation is running without pressing the **Cancel Operation** button. Simply click the **Stochastic Output** tab, and then click the **Refresh Plot** button as the simulation is running. Refer to section 10.7.4.2 for a description of plot options. You may also create and display the statistical summary report without stopping the simulation by clicking the button labeled **Statistical Summary Report**. Both the plotted distribution and the statistical summary report will be based on the number of trials that were completed when the user created/updated the plot or report

When the plotted distribution and the values in the statistical summary report have stopped changing significantly, that is an indication that you may not need to run any more trials. Refer also to section 10.7.4.3.

10.7.6 Network Details

10.7.6.1 Network Details: Selecting Which Variables to Capture During a Stochastic Analysis

When you run a Monte-Carlo simulation, statistics are not gathered for all variables, because this would use a lot of memory for gathering information that is not usually of interest. The variable that is of most interest is, of course, the cancer risk. You may, however, be interested from time to time in statistics of some other variables, for example inhalation cancer risk, oral cancer risk, or cancer risk from a particular pathway. For the purposes of understanding the calculations, you might even want to examine the sample statistics of some lower-level variables, such as breathing rate or food ingestion rates.

You may direct HARP to capture trial statistics for any of the variables in the multipathway network. To do this first click the *Advanced (Network Details)* tab. The window will appear similar to what is shown below.

The screenshot shows the 'Stochastic and Multipathway Details' window with the 'Advanced (Network Details)' tab selected. The left pane displays a tree view of the network structure, with 'TOPLEVEL (subnet)' expanded. The right pane shows a table of parameters for the selected 'CANCERRISK' variable.

parameter name	type	source	chem result	trial result	units	locked	save	correlated
1 TOPLEVEL	SUBNET							
2 GLCTARGET	INPUT	EXTERNAL	1	n/a	up/m ³	n/a	no	n/a
3 GLCMAX	INPUT	EXTERNAL	1	n/a	up/m ³	n/a	no	n/a
4 GLCDRINKINGWATER	INPUT	EXTERNAL	1	n/a	up/m ³	n/a	no	n/a
5 GLCPASTURE	INPUT	EXTERNAL	1	n/a	up/m ³	n/a	no	n/a
6 GLCFISH	INPUT	EXTERNAL	1	n/a	up/m ³	n/a	no	n/a
7 DEPRATE	INPUT	EXTERNAL	2.0000E-02	n/a	m/s	n/a	no	n/a
9 EXPOSURE DURATION	CONTROL	EXTERNAL	70	n/a	years	n/a	no	n/a
9 ANALYSIS	CONTROL	EXTERNAL	CANCER	n/a	STRING	n/a	no	n/a
10 WORKERRESIDENT	CONTROL	EXTERNAL	RESIDENT	n/a	STRING	n/a	no	n/a
11 DISTRIBUTION	CONTROL	EXTERNAL	STOCHASTIC	n/a	STRING	n/a	no	n/a
12 ADJUSTED	CONTROL	EXTERNAL	NO	n/a	n/a	n/a	no	n/a
13 AGE GROUP	CONTROL	EXTERNAL	Adult	n/a	STRING	n/a	no	n/a
14 CAS	CONTROL	EXTERNAL	0.0000E+00	n/a	CAS	n/a	no	n/a
15 GLCADJUSTMENTFACTOR	CONTROL	EXTERNAL	1	n/a	n/a	n/a	no	n/a
16 CANCERRISK	OUTPUT	REF-(CANC)	value not set	accum not set	RISK (nd)	no	YES	n/a
17 CHRONICHI	OUTPUT	REF-(CHR)	value not set	value not set	HI (nd)	no	no	n/a
18 ACUTEHI	OUTPUT	REF-(ACUT)	value not set	value not set	HI (nd)	no	no	n/a
20 GLCINPUT	SUBNET							
22 GLCTARGET	SUM							
23 GLCINPUT	INPUT	REF-(TOPL)	value not set	n/a		no	no	n/a
24 MvAF	CONTROL	REF-(MOL)	value not set	n/a		no	no	n/a
25 GLC	OUTPUT	CALC	value not set	n/a		no	no	n/a
26								
27 GLCMAX	SUM							
28 GLCINPUT	INPUT	REF-(TOPL)	value not set	n/a		no	no	n/a
29 MvAF	CONTROL	REF-(MOL)	value not set	n/a		no	no	n/a
30 GLC	OUTPUT	CALC	value not set	n/a		no	no	n/a
31								

NETWORK DETAILS

If the left pane shows only one line called TOPLEVEL, just click the + sign next to the word TOPLEVEL to expand the network tree.

The right pane shows a list of all the variables and equations (called nodes in this manual). The column on the right labeled “save” is used to indicate which of the variables will be saved in the list of trials during the simulation. The word “YES” next to a variable indicates that trial samples will be saved and that the trial data for that variable will be available after the simulation for plotting or reporting. The word “no” next to a variable indicates that trial data will not be saved.

To save trial data for a variable, click on the corresponding row under the “save” column and type Yes or No. The next time you run a simulation, the variables that you have elected to save will appear in a list under the output tab, where you can select which ones you want to plot or analyze.

In the example above, note that there is a “YES” in the row corresponding to CancerRisk. This indicates that the trial samples of cancer risk will be saved for post-processing.

The pane at the top of the window contains an explanation of whatever is currently highlighted. To highlight a variable, simply click on the row containing the variable. You can use the arrow keys to scroll down the list of variables one row at a time and read the descriptions on the top pane. In many cases you will find a reference to the equation in the OEHHA Guidelines where each variable is used.

10.7.6.2 Network Details: Nodes and Terminals

The multipathway network is represented by a collection of nodes and terminals. A node is the abstract representation of a decision point, an equation to be calculated, or some other operation. The terminals are the input and output points of the node. A node takes the input and transforms it to the output. Terminals are always assigned values, which may be either numeric or string.

This technique for modeling the network allows the entire set of equations, all of the numeric parameters and the entire logic of the network as they are described in the OEHHA Guidance Manual, to be described as input to the HARP program rather than be encoded in the program itself. The input files are contained in the NETWORK subdirectory under the HARP main program directory. This rather large set of input files is read by HARP automatically when they are needed for the analysis. The principal advantage of this organization is that the network and the input parameters can be modified without changing or recompiling the program. This has been important in facilitating the quality assurance and validation of the network algorithms by ARB and OEHHA staff. HARP users will only modify these files if they are performing a Tier-2 or Tier-4 assessment. Any changes made in the network are included in the exception report and must be reported in the risk assessment (see the OEHHA Guidance Manual).

The entire network can be viewed by selecting the *Advanced (Network Details)* tab on the *Stochastic* window. The left side of the window shows the network hierarchy in an outline format. Branches of the outline can be expanded by clicking on the plus (+) signs and contracted by clicking on the minus (-) signs. Each branch of the outline represents a node. When you

click on a node in the outline, the right side of the window shows the values of all of the terminals attached to that node.

The network that is modeled by HARP is very complex, consisting of hundreds of nodes and few thousand terminals. It is not expected that most users will have the need or desire to understand it completely. However, if you understand the OEHHA Guidance Manual document, you understand the network.

10.7.6.3 Autosize Grids

The *Tools/Autosize* menu option causes all the column widths under the *Network Details* tab to be adjusted to the width required to see all of the contents in all of the cells.

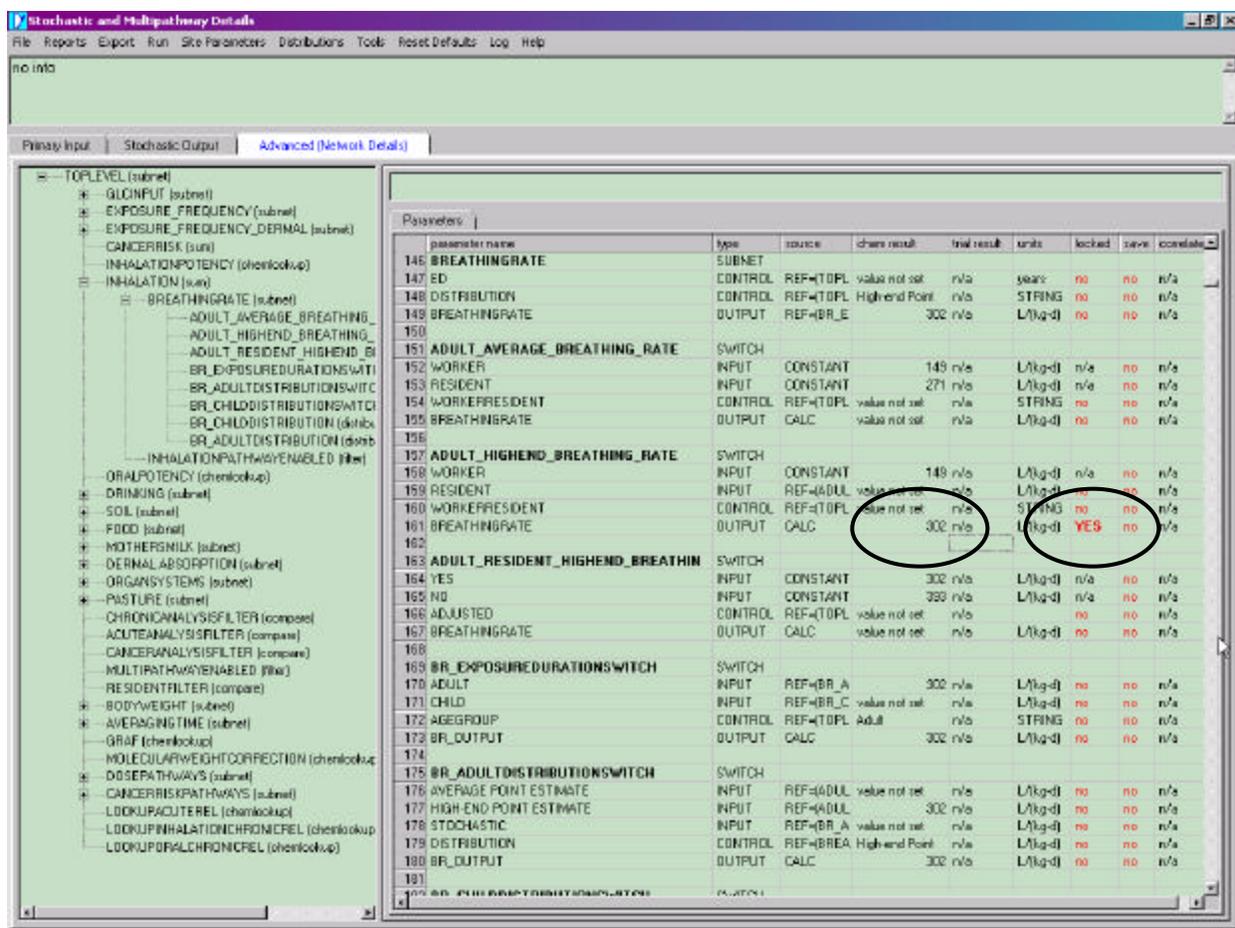
10.7.6.4 Network Details: Editing and Locking Variables for a Tier-2 or a Tier-4 Assessment

Through the *Advanced (Network Details)* tab, the value of any parameter, or variable, on the network can be edited by clicking on the cell to the right of that variable under the column labeled *Chem Result* and typing in a new value. “Value not set” means that the value will be calculated during the simulation if it is needed. Note that not all variables are computed during each simulation. Whether a particular variable is computed depends on what type of analysis you are doing. Variables that are not computed will still show a value of “Value not set” even after a simulation. For variables that are normally computed during the simulation, editing the value will have no effect unless the variable is also locked. To lock a variable, scroll to the right to the column labeled “*locked*” and change the value from no to YES.

If a variable is a constant, then it need not be locked, since constants do not change during a simulation. If a variable is a computed quantity, and you do not lock it, then its value will change during the simulation. In that case the program will overwrite any value that you enter.

The screen below illustrates how to modify the network for a single variable. In this example, the high-end point-estimate for the adult breathing rate (line 161) has been modified and the value in the column marked “locked” has been changed from no to YES. Changing the locked column assures that the value will remain locked during the simulation. Once all of the desired changes are made to the network, the user must recalculate the risk in the Risk Report window (see section 10.6.4). Note that after recalculating the risk, the breathing rate used in the calculation will show up on the network (line 149). The health impacts will be automatically updated in the Risk tab of the risk window (see section 10.6.6) or can be viewed by looking at the electronic or printed results.

Caution should be used if a user views the data in the network. Calculations in the network details are based on a ground level concentration of one microgram per cubic meter (1 $\mu\text{g}/\text{m}^3$). When HARP calculates the health effects for a risk scenario, the actual ground level concentrations are multiplied by the data in the network details.



For example, a receptor with a ground level concentration of $2 \mu\text{g}/\text{m}^3$ and a cancer risk of $6.0\text{E}-06$ (in the Risk tab of the Risk Report window) would show a cancer risk of $3.0\text{E}-06$ in the Advanced Network Details.

Also, HARP completes the calculations for each chemical separately. If you run a simulation that uses multiple chemicals, the numbers shown on the network represent the last chemical that was analyzed. You can change the order in which the chemicals are analyzed by selecting the Primary Input/Chemicals tabs and then clicking the “shift column” buttons. If you want to see details for a particular chemical, shift the column for that chemical all the way to the right so that it will be the last one analyzed. For the reasons presented here, it is best to view your results in the Risk tab of the Risk Report window, not in the network.

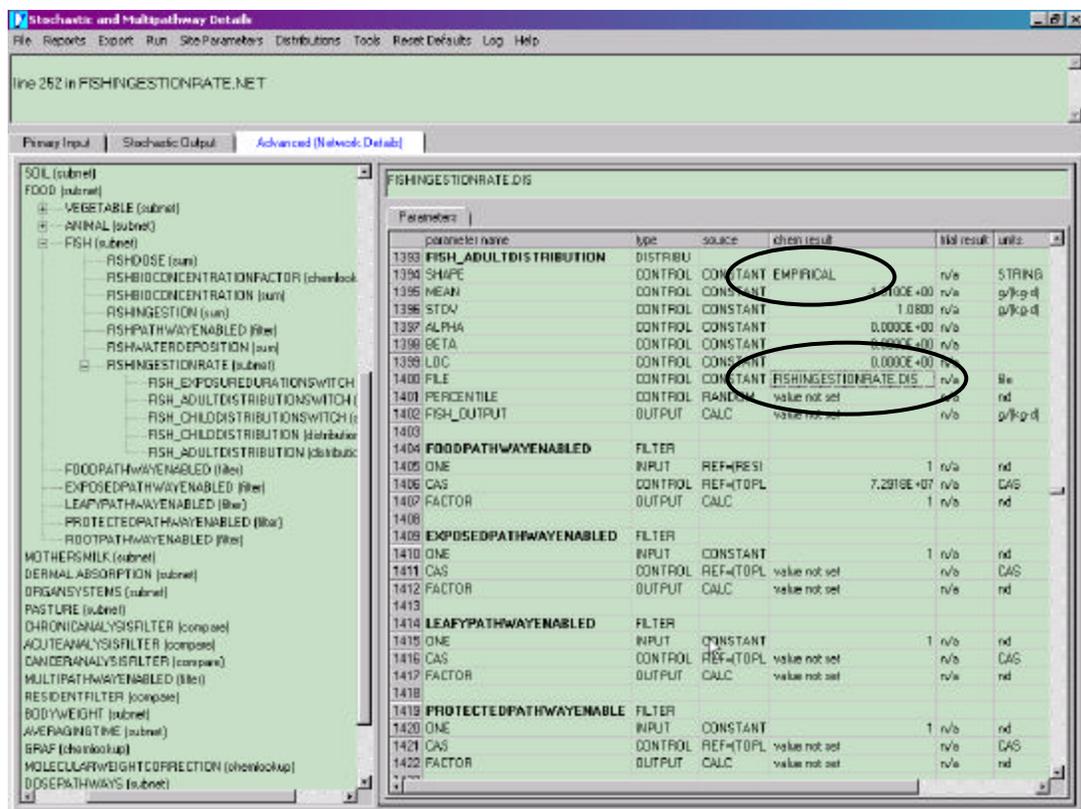
10.7.6.5 Network Details: Editing Distribution Shapes and Parameters for a Tier-4 Assessment

Through the *Advanced (Network Details)* tab, you can edit the parameters that describe a distribution type (called SHAPE, see line 1394) the same way you edit any single parameter. The parameters for a distribution define its shape (e.g. mean and standard deviation for a normal distribution). The distributions that may be used in HARP include (N)ORMAL,

(L)OGNORMAL, (W)EIBULL, (G)AMMA and (E)MPIRICAL. To edit the shape of a distribution, find the variable called SHAPE under a heading called DISTRIBUTION. Move across the row to the **Chem Result** column and type the first letter of the distribution name (N, L, W, G or E).

In addition to the pre-programmed distributions (Normal, LogNormal, Weibull, Gamma) you may provide your own (E)mpirical distribution in the form of an external data file that HARP uses as a lookup table. In order to use an externally defined distribution, see the example screen below and follow these steps:

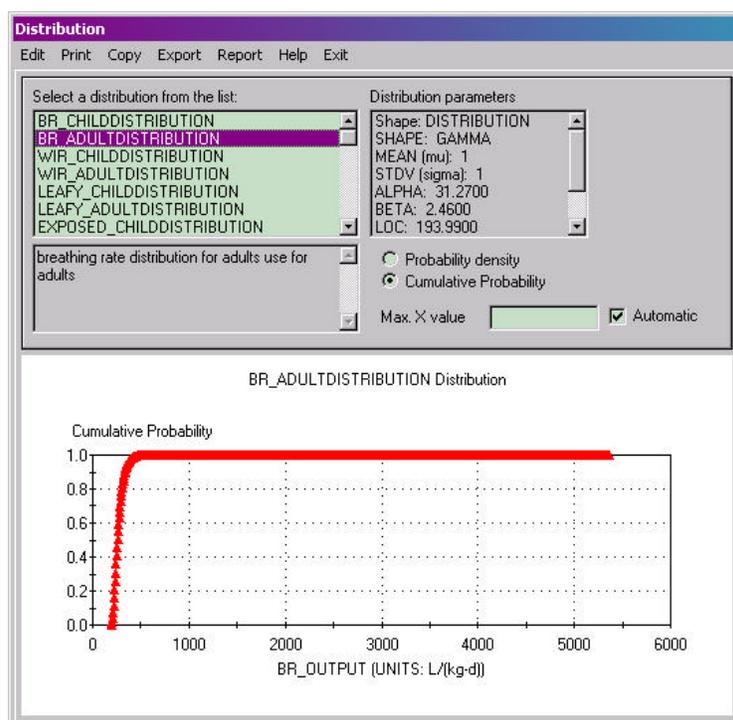
1. Locate the distribution of interest under the Advanced (Network Details) tab. In this example, we are looking at the fish ingestion distribution (line 1393).
2. Change the distribution type to Empirical by clicking on the value of the SHAPE parameter and typing the letter E (line 1394).
3. Click on the row labeled "File" (line 1400) and enter the name of the file that contains the empirical distribution data. This file must be located in the \network directory below the main HARP directory, and it must have a .DIS file extension
4. Note that no values for the distribution parameters are needed for an empirical distribution (e.g., standard deviation (stdv), mean, location (loc), alpha, or beta).
5. Create the distribution file using a text editor. The format of the file is described in section 10.8.1.



10.7.6.6 Network Details: Viewing the Input Distributions

There are about 37 variables defined in the OEHHA Guidance Manual as being stochastic in nature (as opposed to having point-estimate values). The distribution shapes and distribution parameters are pre-defined in the network according to the values recommended by OEHHA. The shapes and parameters can be edited by the user (see section 10.7.6.5) and can also be saved to a parameter file and later retrieved.

To view the currently defined distributions select *Distributions* from the menu on the Stochastic/Multipathway window. This will expose the distribution window, similar to what is shown below. This window is used only for examining the input distributions, not for editing them.



DISTRIBUTION WINDOW

The scrolling list on the left side of the window shows a list of all of the variables for which input distributions have been specified. When you click on any variable in this list, the distribution parameters are shown in the upper right pane and a plot of the distribution curve is shown in the lower pane. The plot may be shown as either a probability distribution function or cumulative probability distribution function by clicking the corresponding button on the middle-right-side of the window.

If you would like to change the scale of the x-axis for the distribution, uncheck the automatic box and enter a new maximum value for the x-axis in the *Max X value* slot. After entering the value, press the “*Refresh Plot*” button, and the plot of the distribution will be updated with the new maximum value in the x-axis.

10.7.6.7 Network Details: Correlated vs. Uncorrelated Sampling

By default, the sampling of random variables is correlated between one chemical and the next. This means that when a variate (for example breathing rate) takes on a high value for one chemical, it must take on a high value for all chemicals. Random variables always have a YES or NO in the correlated column.

Only a few of the parameters (37 at last count) have this option enabled. For the rest of the variables, the “correlated” column shows n/a and is locked. The variables for which this parameter applies are the random numbers associated with each of the random variates defined in the OEHHA Guidance Manual. To see a list of the random variables and their distributions refer to section 10.7.6.6.

You may elect to change the sampling procedure for one or more random variables by changing it from correlated to uncorrelated. This is done by first clicking the *Network Details* tab on the Stochastic/Multipathway window. Then scroll to the right most column of the Network Details pane and change the value under the “correlated” column from “YES” to “No”.

When you stipulate that the sampling of a variable is uncorrelated, HARP will use a different random variable value for each of the chemicals within a single trial for that variable. For example, if breathing rate were processed using uncorrelated sampling, this would imply, that the breathing rate for different chemicals could be different during a single trial. If the sampling is uncorrelated, then the breathing rate for one chemical may be (and probably will be) different from for the other chemicals (i.e. the breathing rate is uncorrelated from one chemical to the next).

10.7.7 Network Tools

10.7.7.1 Network Tools: Print Network Outline to File

From the Stochastic window, select *Tools/Network Documentation/Outline to File (txt format)*. This will generate an ASCII file containing a detailed outline of the entire multipathway network. This is for documentation purposes. The file that is produced can be viewed with a text editor or loaded into any work processor.

10.7.7.2 Network Tools: Print Network Description to File

From the Stochastic/Multipathway window, select *Tools/Network Documentation/Network Description (txt format)*. This will generate an ASCII file containing a detailed list of all of the nodes in the multipathway network. Each node will include a verbal description and a list of all of the terminals connected to that node. This is for documentation purposes. The file that is produced can be viewed with a text editor or loaded into any work processor.

10.7.8 Exception Report

The exception report is a report that shows if the user has set any of the variables in the network to non-default settings. Because there are so many variables in the network, it may be difficult to remember which, if any, you have changed. The exception report will tell you which ones you have changed.

To generate an exception report, click on **Report/Exception Report (txt file)** from the Stochastic/Multipathway window. You should print and save the exception report as a general practice if you make any changes to the network parameters. This will provide evidence and documentation to future reviewers as to exactly what input you may have modified.

10.7.9 Log Window

The log window appears automatically in many circumstances to show progress during certain operations and to show any errors or warnings that may have occurred. To expose the log window at any time, select **Log** from the menu of the Stochastic/Multipathway window.

10.7.10 Exporting Data

10.7.10.1 Exporting Raw Sample Data

After running a simulation, you may export the raw sample data by selecting **Export/Raw Sample Data (CSV format)** from the menu on the Stochastic/Multipathway window. The raw sample data will be exported only for one variable at a time, namely the variable that you have selected to plot (see section 10.7.4.2).

The raw sample data will be exported in a comma-delimited (CSV) format, which can be easily imported into Excel for plotting, sorting, or further analysis. The format of this file is described in section 10.7.11.

10.7.10.2 Exporting Distribution Data

After running a simulation and generating a plot (see section 10.7.4.1), you may export the distribution data by selecting **Export/Distribution Data** from the menu on the Stochastic/Multipathway window. The values that were used to generate the plot will be exported only for one variable at a time, namely the variable that you have selected to plot (see section 10.7.4.2). The exported data will be the same as what is shown under the *Table* tab immediately after generating a plot.

The number of data points exported depends on the number of bins selected to generate the plot (see section 10.7.4.2).

The distribution data will be exported in a comma-delimited (CSV) format, which can be easily imported into Excel for plotting, sorting, or further analysis.

The format of each of this file is described in section 10.7.11.

10.7.10.3 Network Details

When you select *Export/Network Details* from the menu of the Stochastic/Multipathway window, HARP will write the entire contents of the *Network Details* display tab to a file.

This feature is probably only useful to a limited number of sophisticated users for diagnostic purposes. The output is lengthy.

The Network Details tab displays the state of the network at the end of the last chemical for the last trial. Therefore, it is not very enlightening if you have just run a multi-chemical stochastic analysis. It is primarily useful for diagnosing the results for a point-estimate.

10.7.11 File Formats

This section describes the formats of the files exported from the point-estimate and stochastic risk analyses. These files can be imported into other programs for further analysis. All of these files are in ASCII comma-delimited format, which means they can easily be imported and viewed using Excel. To open one of these files with Excel, use the *File/Open* menu of Excel, or drag the file from the Windows Explorer into the Excel window.

10.7.11.1 File Formats: Point-estimate Risk Analysis Export

There are six X/Q files exported from the Risk window. They are:

XOQ_AVRG.CSV
XOQ_1HR.CSV
XOQ_4HR.CSV
XOQ_6HR.CSV
XOQ_7HR.CSV
XOQ_30DAY.CSV

Each of these files have the same format, which is shown below. The first row contains the name of the file. The second row contains the column headers. The SRC numbers in the column headers identify which emission source (stack) the data corresponds to. The third row contains the units. Each of the subsequent rows contains the data for each of the columns. The first column is the receptor number. The second column is the receptor type. The remaining columns, up to the last three, contain the X/Q values for each source receptor combination. The last three columns contain the UTM coordinates and the UTM zone.

The table shown below was created by simply opening the XOQ_AVRG.CSV file with Excel and printing the contents.

File: D:\HARP\HarpDev\PROJECTS\demo\export\XOQ_AVRG.csv									
Rec	Type	X/Q (SRC 1) (ug/m ³)/(g/s)	X/Q (SRC 2) (ug/m ³)/(g/s)	X/Q (SRC 3) (ug/m ³)/(g/s)	X/Q (SRC 4) (ug/m ³)/(g/s)	X/Q (SRC 5) (ug/m ³)/(g/s)	UTME	UTMN	ZONE
1	PATHWAY	8.34E-01	1.04E+00	1.29E+00	1.41E+00	1.47E+00	474700	3633000	11
2	PATHWAY	7.51E-01	9.50E-01	1.12E+00	1.26E+00	1.41E+00	474750	3632950	11
3	PATHWAY	8.28E-01	1.43E+00	1.90E+00	1.29E+00	2.31E+00	474800	3633050	11
4	GRID	7.60E-01	2.98E-01	2.84E-01	1.63E+00	1.65E+00	473800	3634500	11
5	GRID	8.94E-01	3.10E-01	2.96E-01	1.69E+00	2.03E+00	473900	3634500	11
6	GRID	1.09E+00	3.35E-01	3.20E-01	1.90E+00	2.90E+00	474000	3634500	11
7	GRID	1.39E+00	3.33E-01	3.06E-01	2.93E+00	2.65E+00	474100	3634500	11
8	GRID	1.94E+00	3.00E-01	2.78E-01	3.16E+00	1.35E+00	474200	3634500	11
9	GRID	2.94E+00	3.27E-01	3.10E-01	1.58E+00	1.07E+00	474300	3634500	11
10	GRID	4.14E+00	3.68E-01	3.46E-01	1.18E+00	1.43E+00	474400	3634500	11
11	GRID	0.00E+00	3.97E-01	3.71E-01	1.42E+00	1.00E+00	474500	3634500	11
12	GRID	0.00E+00	4.72E-01	4.34E-01	1.16E+00	1.06E+00	474600	3634500	11
13	GRID	2.80E+00	6.03E-01	5.53E-01	9.77E-01	6.08E-01	474700	3634500	11
14	GRID	1.81E+00	6.25E-01	5.97E-01	6.56E-01	8.37E-01	474800	3634500	11
15	GRID	1.25E+00	6.26E-01	5.67E-01	9.63E-01	9.31E-01	474900	3634500	11
16	GRID	9.49E-01	6.70E-01	6.47E-01	9.99E-01	8.29E-01	475000	3634500	11

There are six GLC files exported from the Risk window. They are:

GLC_AVRG.CSV
 GLC_1HR.CSV
 GLC_4HR.CSV
 GLC_6HR.CSV
 GLC_7HR.CSV
 GLC_30DAY.CSV

Each of these files has the same format, which is shown below. The first row contains the name of the file. The second row contains the column headers. The CAS numbers in the column headers identify which chemical the data corresponds to. The third row contains the units. Each of the subsequent rows contains the data for each of the columns. The first column is the receptor number. The second column is the receptor type. The remaining columns, up to the last three, contain the GLC values for each chemical at each receptor. The last three columns contain the UTM coordinates and the UTM zone.

File: D:\HARP\HarpDev\PROJECTS\demo\export\GLC_AVRG.csv							
Rec	Type	CAS 1015	CAS 1016	CAS 18540299	UTME	UTMN	ZONE
		ug/m ³	ug/m ³	ug/m ³			
1	PATHWAY	1.95E-04	2.30E-04	4.04E-06	474700	3633000	11
2	PATHWAY	1.76E-04	2.18E-04	3.63E-06	474750	3632950	11
3	PATHWAY	1.99E-04	3.60E-04	3.72E-06	474800	3633050	11
4	GRID	1.68E-04	2.41E-04	4.68E-06	473800	3634500	11
5	GRID	1.97E-04	2.97E-04	4.86E-06	473900	3634500	11
6	GRID	2.40E-04	4.22E-04	5.47E-06	474000	3634500	11
7	GRID	3.05E-04	3.86E-04	8.42E-06	474100	3634500	11
8	GRID	4.22E-04	1.99E-04	9.10E-06	474200	3634500	11
9	GRID	6.39E-04	1.59E-04	4.56E-06	474300	3634500	11
10	GRID	8.99E-04	2.10E-04	3.40E-06	474400	3634500	11
11	GRID	5.72E-06	1.49E-04	4.08E-06	474500	3634500	11
12	GRID	6.79E-06	1.59E-04	3.32E-06	474600	3634500	11
13	GRID	6.13E-04	9.54E-05	2.81E-06	474700	3634500	11
14	GRID	3.99E-04	1.29E-04	1.89E-06	474800	3634500	11
15	GRID	2.78E-04	1.42E-04	2.77E-06	474900	3634500	11
16	GRID	2.14E-04	1.29E-04	2.87E-06	475000	3634500	11

The list of sources is exported to the file SOURCES.CSV. It has the format shown below. As usual, the first line is the name of the file. The second and third lines are labels and units, respectively. Each row corresponds to a release point (stack). The columns labeled FAC, CO, AB, DIS and STACK form a unique key that is used by HARP to reference back to the emissions database for each stack.

File: C:\HARP\PROJECTS\DEMO\SOURCES.csv											
Src. No.	ISC Tag	Name	FAC	CO	AB	DIS	STACK	UTME	UTMN	ELEV	ZONE
								meters	meters	feet	
1	PROSPECT PRODUCTS STACK 1	S001	1001	37	SD	SD	1	474470.45	3634603.3	75	11
2	PDQ REPAIR GUYS STACK 1	S002	2001	37	SD	SD	1	474120.45	3634197.3	1.5	11
3	DOUGS WHATNOT SHOP STACK 1	S003	3000	37	SD	SD	1	474005.45	3634167.3	10	11
4	ABC CHEMICAL STACK 1	S004	3002	37	SD	SD	1	474920.45	3633522.3	264	11
5	ABC CHEMICAL STACK 2	S005	3002	37	SD	SD	2	474950.45	3633457.3	264	11

The file RECEPTORS.CSV contains a list of all the receptors exported by HARP. The format is as shown below. The first column is the receptor number and the second column is the receptor type. POPRES and POPWORK are the residential and working populations respectively. If the receptor is a census block receptor, the POPRES comes from the census database. POPWORK only applies to sensitive receptors.

INDEX	TYPE	POPRES	POPWORK	UTME	UTMN	ZONE
1	PATHWAY	0	0	474700	3633000	11
2	PATHWAY	0	0	474750	3632950	11
3	PATHWAY	0	0	474800	3633050	11
4	GRID	0	0	473800	3634500	11
5	GRID	0	0	473900	3634500	11
6	GRID	0	0	474000	3634500	11
7	GRID	0	0	474100	3634500	11
8	GRID	0	0	474200	3634500	11
9	GRID	0	0	474300	3634500	11
10	GRID	0	0	474400	3634500	11
11	GRID	0	0	474500	3634500	11
12	GRID	0	0	474600	3634500	11
13	GRID	0	0	474700	3634500	11
14	GRID	0	0	474800	3634500	11

The file RISK.CSV contains the risk values computed for all receptors. Cancer, Chronic and Acute Simple are the risk values normally computed from the Risk Reports window. The column labeled Acute Max Hourly is the refined acute risk, which is often not computed, since it is time consuming. A value of -1.0 in any column indicates that the value has not been computed.

File: D:\HARP\HarpDev\PROJECTS\demo\export\RISK.csv								
Receptor	Type	Cancer	Chronic	Acute Simple	Acute Max Hourly	UTME	UTMN	ZONE
		Risk	HI	HI	HI			
4	GRID	6.74E-06	2.47E-02	3.04E+00	-1.00E+00	473800	3634500	11
5	GRID	7.46E-06	2.86E-02	3.12E+00	-1.00E+00	473900	3634500	11
6	GRID	8.94E-06	3.63E-02	3.10E+00	-1.00E+00	474000	3634500	11
7	GRID	9.57E-06	3.76E-02	2.93E+00	-1.00E+00	474100	3634500	11
8	GRID	9.08E-06	3.43E-02	4.10E+00	-1.00E+00	474200	3634500	11
9	GRID	9.93E-06	4.24E-02	4.94E+00	-1.00E+00	474300	3634500	11
10	GRID	1.23E-05	5.66E-02	5.33E+00	-1.00E+00	474400	3634500	11
11	GRID	4.57E-06	1.31E-02	3.94E-02	-1.00E+00	474500	3634500	11
12	GRID	4.55E-06	1.36E-02	5.17E-02	-1.00E+00	474600	3634500	11
13	GRID	8.95E-06	3.83E-02	3.79E+00	-1.00E+00	474700	3634500	11
14	GRID	7.35E-06	3.02E-02	2.57E+00	-1.00E+00	474800	3634500	11
15	GRID	6.58E-06	2.52E-02	2.17E+00	-1.00E+00	474900	3634500	11
16	GRID	5.95E-06	2.17E-02	1.78E+00	-1.00E+00	475000	3634500	11

The emission rates that appear under the emissions tab of the risk window are exported to two files, EMS_AVRG and EMS_MAX, which contain the average and maximum emission rates respectively. The format of each of these files is shown below. It is simply an exact copy of what is seen on the risk window, in a comma-delimited format.

File: D:\HARP\HarpDev\PROJECTS\demo\export\EMS_AVRG.csv								
	fac	dev	pro	stk	Mult			
CAS						1015	1016	18540299
Abbrev.						[D] As /inorg	As cmpd(inorg)	Cr(VI)
Background (ug/m^3)						0	0	0
Multiplier						1	1	1
SRC 1 EM	1001	1	1	1	1	15 *		*
SRC 2 EM	1002	1	1	1	1	1 *		*
SRC 3 EM	1002	1	2	2	1 *		1 *	
SRC 4 EM	2001	1	1	1	1 *	*		0.2
SRC 5 EM	3000	1	1	1	1 *		10 *	

10.7.11.2 File Formats: Stochastic Risk Analysis Export

From the Stochastic/Multipathway window, if you select Export/Raw Sample Data from the menu, HARP will export the raw sample data from the Monte Carlo simulation to the file RawSampleData.csv, in the format shown below.

The first row is the name of the file, and the second row is just a label. The third and fourth rows contain the node and terminal of the variable whose data is listed. In this example, the cancer risk variable has been exported. Each column contains the risk data for one of the chemicals alone. The last column is the total cumulative risk data for all chemicals. The sequential numbers in the first column are the trial numbers. If this data were sorted by the ACCUMULATOR column, then collected into discrete bins, and the results plotted, we would have the distribution curve that appears on the HARP plot window.

File: D:\HARP\HarpDev\PROJECTS\demo\export\RawSampleData.csv				
Raw Sample Data				
TOPLEVEL				
CANCERRISK				
	1015 ([D] As /inorg)	1016 (As cmpd(inor	18540299 (Cr(VI))	ACCUMULATOR
1	4.98E-03	4.99E-03	0.1108809	0.120852
2	1.10E-02	1.10E-02	0.128206	0.1502579
3	6.29E-03	6.29E-03	0.1604588	0.1730468
4	6.44E-03	6.44E-03	0.1342763	0.1471512
5	2.33E-02	2.33E-02	0.1460266	0.1926576
6	6.72E-03	6.72E-03	0.102552	0.1159912
7	6.40E-03	6.40E-03	0.1471196	0.1599123
8	5.23E-03	5.23E-03	0.114715	0.1251819
9	4.22E-03	4.22E-03	0.1212692	0.1297136
10	7.06E-03	7.06E-03	0.1703304	0.1844475
11	1.56E-02	1.56E-02	0.1278404	0.159084
12	6.95E-03	6.96E-03	0.1363375	0.1502468
13	4.91E-03	4.91E-03	0.1144479	0.1242586
14	5.41E-03	5.41E-03	0.103138	0.1139598
15	8.41E-03	8.41E-03	0.1504905	0.1673077
16	7.35E-03	7.36E-03	0.1521957	0.1669055
17	4.80E-03	4.80E-03	0.1126247	0.1222298
18	5.55E-03	5.55E-03	0.1831509	0.1942482
19	1.02E-02	1.03E-02	0.1304031	0.1509027

The file Distribution.csv contains the points that are plotted on the distribution curve that HARP displays under the *Stochastic Output* tab. The format is shown below. The number of points, and their magnitudes, are affected by the plot parameters. You can use this file to create your own annotated plots using Excel, where the plot data matches what is shown on the HARP plot window. In this file the second column is the value of the variate being plotted, and the third column shows the cumulative probability. It is cumulative in this case, because that is was selected under the plot options before the data was exported.

File: D:\HARP\HarpDev\PROJECTS\demo\export\Distribution.csv				
Sampled Distribution Data				
TOPLEVEL				
CANCERRISK				
	ACCUMULATOR			
	0	0		
	2.46E-02	0		
	0.049199566	0		
	7.38E-02	0		
	9.84E-02	0		
	0.122998916	0.14		
	0.147598699	0.48		
	0.172198482	0.83		
	0.196798265	0.94		
	0.221398048	0.98		
	0.245997831	1		

10.8 Empirical Distribution File

Section 10.7.7.5 describes how to modify the distribution parameters for one of the stochastic variables. One option is to specify the distribution parameters as an empirical lookup table. This section describes the format of the file, which you can create with a text editor or any other means at your disposal.

The box below shows a sample distribution file. All distribution files follow this exact same format. The file is ASCII, and the name of the file should have a .DIS extension.

1. First line is a descriptive header that can be anything you choose.
2. Second line must contain the word **EMPIRICAL**, exactly as shown.
3. Third line is an integer number that tells how many pairs of values follow. In this example, there are 15 pairs of numbers that describe the empirical distribution curve.
4. The remaining lines are (x, y) point pairs that describe the distribution. The x values are the dimensional value of the parameter, for example fish ingestion rate. The dimensions depend on which parameter this represents (consult the OEHHA Guidance Manual for details on each parameter). The y values are the cumulative probability that the actual value in any sample will be less than or equal to the corresponding x-value. In the example shown here, for instance, there is a 90 percent probability that the fish ingestion rate will be less than or equal to 1.02. If you prefer, you can insert all the data for distribution, rather than just inserting the selected points along the distribution.

