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SNAP/RADTRAD 5: Description of Models and Methods

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I. ABSTRACT

This report documents the models and methods used in the Symbolic Nuclear Analysis Package/RADionuclide Transport, Removal and Dose Estimation code (SNAP/RADTRAD) plugin to the SNAP graphical user interface (GUI) and the RADionuclide Transport and Removal and Dose Estimation analytical code (RADTRAD-AC) developed for the U.S. Nuclear Regulatory Commission (NRC) Office of Nuclear Regulatory Research to estimate transport and removal of radionuclides and dose at selected receptors. SNAP/RADTRAD along with the RADTRAD-AC code is used to estimate the radionuclide release from the containment using either the NRC TID-14844 or NUREG-1465 source terms and assumptions, or a user-specified table. In addition, the code can account for a reduction in the quantity of radioactive material released due to containment sprays, natural deposition, filters, and other engineered safety features. The code uses a combination of tables and numerical models of source term reduction phenomena to determine the time-dependent dose at user-specified locations for a given accident scenario. The code system also provides the inventory, decay chain, and dose conversion factor tables needed for the dose calculation. SNAP/RADTRAD can be used to assess occupational radiation exposures, typically in the control room; to estimate site boundary doses; and to estimate dose attenuation due to modification of a facility or accident sequence.

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V. ACKNOWLEDGMENTS

Many people, both with the U.S. Nuclear Regulatory Commission as well as at contractor organizations have contributed to the development of SNAP/RADTRAD. The individual who has provided unflagging support for the development of SNAP/RADTRAD over the past several years is Mark Blumberg from the Office of Nuclear Reactor Regulation. Mark has been the Technical Monitor for the RADTRAD code's design, computational methods and testing since 1997. He has also provided much insight into dose analysis for licensing applications throughout the code's conversion to the JAVA computer programming language and the entire SNAP/RADTRAD development process. The agency would like to recognize Chester Gingrich from the Office of Nuclear Regulatory Research who was responsible for the initial conversion and code programming of RADTRAD into JAVA. Another individual who is acknowledged is Stephen LaVie from the Office of Nuclear Security and Incident Response whose development of the RNEditor code is a key element of the source term modeling approach used in SNAP/RADTRAD. Finally, the support of John Tomon of the Office of Research who is the current Contracting Officer's Representative and whose patience and guidance is greatly appreciated.

In the contractor organizations, the contributions of Ken Jones of Applied Programming Technology who, along with his programming staff, develop and maintain the SNAP code are greatly appreciated.

VI. ABBREVIATIONS

APT	Applied Programming Technology
AptPlot	Applied Programming Technology plotting package
APWR	advanced pressurized-water reactor
APWR-DBA	advanced pressurized-water reactor design basis accident
Bq	Becquerels
BWR	boiling-water reactor
BWR-DBA	boiling-water reactor design basis accident
BWR-GALE	boiling-water reactor gaseous and liquid effluent code
CEDE	committed effective dose equivalent
Ci	Curies
CRDA	control rod drop accident
DCF	dose conversion factor
DE	dose equivalent
DE I-131	dose equivalent iodine 131
DE Xe-133	dose equivalent xenon 133
DF	decontamination factor
DBA-TID	design-basis accident based on TID-14844
DBA-AST	design-basis accident using NUREG-1465 (Regulatory Guide 1.183) models
EAB	exclusion area boundary
FGR	Federal Guidance Report
FHA	fuel handling accident
GUI	graphical user interface
HEPA	high-efficiency particulate air
LOCA	loss-of-coolant accident
LPZ	low population zone
MSL	main steam line
MWth	megawatt thermal

NRC	U.S. Nuclear Regulatory Commission
ODE	ordinary differential equation
PWR	pressurized-water reactor
PWR-DBA	pressurized-water reactor design basis accident
PWR-GALE	pressurized -water reactor gaseous and liquid effluent code
RCS	reactor coolant system
RADTRAD	RADionuclide Transport, Removal, And Dose Estimation
RAMP	Radiation Protection Computer Code Analysis and Maintenance Program
REA	rod ejection accident
RG	Regulatory Guide
SI	International System of Units
SNAP	Symbolic Nuclear Analysis Package
Sv	Sieverts
TEDE	total effective dose equivalent
T/S	technical specification
XML	extensible markup language

1.0 INTRODUCTION

The purpose of the Symbolic Nuclear Analysis Package/RADionuclide Transport, Removal and Dose Estimation (SNAP/RADTRAD) code is to determine the dose from a release of radionuclides during a design basis accident to the exclusion area boundary (EAB), the low population zone (LPZ), and the control room and other locations of interest. As radioactive material is transported through the containment, the user can account for sprays and natural deposition to reduce the quantity of radioactive material. Material can flow between buildings, from buildings to the environment, or into control rooms through high-efficiency particulate air (HEPA) and charcoal filters, piping, or other connectors. Decay and in-growth of daughters can be calculated over time as the material is transported.

The focus of SNAP/RADTRAD is licensing analysis to show compliance with nuclear plant siting and control room dose limits for various loss-of-coolant accidents (LOCAs) and non-LOCA accidents. The RADTRAD code was originally developed by the Accident Analysis and Consequence Assessment Department at Sandia National Laboratories for the U.S. Nuclear Regulatory Commission (NRC) in 1997 as documented in NUREG/CR-6604, "RADTRAD: A Simplified Model for RADionuclide Transport and Removal and Dose Estimation," [1]. The code was revised to include a Visual Basic graphic user interface (GUI) for user convenience in 1999, which is described in NUREG/CR-6604, Supplement 1, "RADTRAD: A Simplified Model for RADionuclide Transport and Removal and Dose Estimation," [2]. Finally, NUREG/CR-6604, Supplement 2, "RADTRAD: A Simplified Model for RADionuclide Transport and Removal and Dose Estimation," [3] was published in 2002 discussing the testing of RADTRAD version 3.03.

The NRC decided to update RADTRAD by converting the code into JAVA and develop a RADTRAD plugin to interface with the SNAP graphical user interface (GUI). As part of this update to RADTRAD, the RADTRAD analytical code (RADTRAD-AC) was separated from SNAP and distributed as RADTRAD Version 4.0. The SNAP GUI with the RADTRAD plugin is used to develop models and prepare input which is then processed by the RADTRAD-AC (Version 4.0). The RADTRAD-AC then calculates the dose and generates the results. The combined package is referred to as SNAP/RADTRAD. Use of RADTRAD in the SNAP framework allows use of the SNAP features including the Model Editor for developing plant models. The Model Editor also provides tools for user input checking, for submitting and monitoring calculations, and for running multiple cases. The RADTRAD-AC generates data output files suitable for plotting with the Applied Programming Technology plotting package (AptPot).

As part of the development of the RADTRAD plugin for SNAP, the user documentation is being updated. This report provides the documentation for the use of and the calculation models in SNAP/RADTRAD.

2.0 MODEL DEVELOPMENT USING SNAP/RADTRAD

Running SNAP/RADTRAD will require some familiarity with the overall SNAP approach to developing and running models. In this section, the approach to using SNAP to develop, modify and execute RADTRAD problems will be discussed. However, SNAP includes many features which will not be discussed here. For the interested user, the Symbolic Nuclear Analysis Package User's Manual [4] provides more detailed information on the use of SNAP.

2.1 Overview of SNAP/RADTRAD

SNAP is a suite of computer applications used to develop, modify, and execute computer models principally for thermal hydraulic codes such as the TRAC/RELAP Advanced Computational Engine (TRACE) and Reactor Excursion and Leak Analysis Program (RELAP5). Of these tools, the *Configuration Tool*, *Model Editor* and the *Job Status* tools are most relevant to RADTRAD analysis. The *Configuration Tool* is used to configure global properties for running RADTRAD under SNAP. The *Model Editor* provides a GUI used to develop RADTRAD models. The *Job Status* tool is used to obtain the job status. Of these tools, the *Model Editor* is the tool used the most as it is the primary tool for developing SNAP/RADTRAD models.

Generally, the approach for developing a new SNAP/RADTRAD model is to define the compartments and connections in flow pathways that represent the plant and optionally the control room and/or the technical support center being analyzed. Note that flow pathways are used to connect components in SNAP/RADTRAD. During the specification of components and flow pathways, removal models should be considered and specified for each normal compartment as appropriate. For compartments, these removal models include filtration, sprays, or natural deposition. The user will need to specify each model required and specify the required data using the SNAP GUI as a guide.

Once the geometric, flow/leakage and removal information is specified for the compartments and flow pathways, a source term is then specified. A comprehensive list of nuclides based on International Commission on Radiological Protection (ICRP) Report 38 (ICRP-38) [5] has been included in SNAP/RADTRAD. The user will need to decide whether the analysis is either being done based on the occurrence of a LOCA by selecting either TID-14844, “Calculation of Distance Factors for Power and Test Reactor Sites,” [6] or NUREG-1465, “Accident Source Terms for Light-Water Nuclear Power Plants,” [7] and for a non-LOCA where both radionuclides from the fuel and the reactor coolant activity may be important contributors and make the appropriate selections for the plant being analyzed. A plant power level must be defined to obtain the correct source term. The physical form of iodine must also be defined as the rate of removal and filtration depends on the physical form of iodine.

Parameters related to the dose rate are specified, including *X*/Q data for each receptor location and dose conversion factors (DCFs). Default DCFs based on EPA-520/1-88-020, "Limiting Values of Radionuclide Intake and Air Concentration and Dose Conversion Factors for Inhalation, Submersion, and Ingestion," Federal Guidance Report No. 11 (FGR 11) [8] and EPA-402-R-93-081, "External Exposure to Radionuclides in Air, Water, and Soil," Federal Guidance Report No. 12 (FGR 12) [9] (see Section 3.6) are built into SNAP/RADTRAD. The EAB and the LPZ are defined by default in SNAP/RADTRAD. Other dose receptors can be added as needed. For each dose receptor that is located in the environment or draws from the environment such as a control room, time-dependent *X*/Q and breathing rate values must be specified. For the control room, occupancy factors must also be specified. Note that default values for breathing rates are provided which are suitable for most analyses.

SNAP/RADTRAD can be used to develop new models and modify existing models. The key aspect of model development is the use of compartments and connecting flow pathways to model a system. The approach used to prepare this section was to open the SNAP GUI and start exploring the features for RADTRAD model development. Therefore, the discussion in the following sections assumes that the user has SNAP available and open and that the user will follow along with the discussion by using the SNAP/RADTRAD Model Editor. There is no better way to learn how to use the SNAP GUI except to actually use it.

2.2 The Model Editor User Interface- Model Development

This subsection describes working within the SNAP/RADTRAD Model Editor to develop and modify models.

2.2.1 Overview of Existing Model Features

As noted earlier, the SNAP/RADTRAD Model Editor is the basic tool used to create, modify and run input models. To start the *Model Editor*, navigate to *Start->All Programs->SNAP->Model Editor*, and the *Model Editor* should start.

To illustrate many of the features in SNAP, the Test 23 sample problem will be used. This problem is found in the *Samples/Radtrad/Test23* subdirectory in the *snap* directory (see Section 1.3). It is recommended that a copy of the *Test23.med* file be placed in the user's working directory, which is the directory where the input and output files will be kept. It is also recommended that the user open *Test23* and follow along with the presentation in this section.

When the *Model Editor* is started, a splash screen appears for several seconds and then a *Welcome to Model Editor* screen appears as shown in Figure 2-1 with the Model Editor

window in the background. Note that if a previous *Model Editor* session has been exited without first closing the model in use then the *Restore Session* prompt screen will open, as also shown in Figure 2-1.

Several options are available on the *Welcome to Model Editor* screen, which are listed below:

- *Create A New Model*
- *Open a Model Document*
- *Import a New Model*
- *Start an Empty Session*
- *View Online Training Tutorials*
- *SNAP Version Updates*

Under each of these items a short description of each option is provided to explain what each option does.

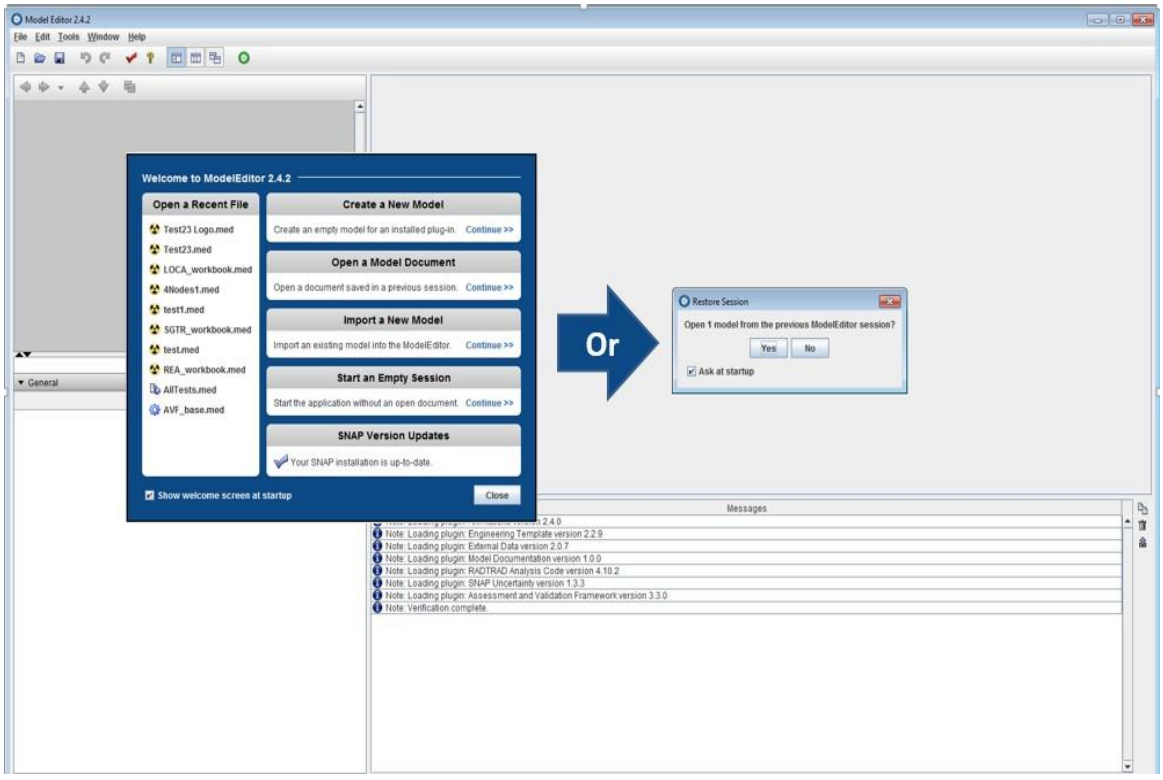


Figure 2-1 Opening the Model Editor

Once the SNAP Model Editor is open, the user can open sample Test23 by selecting the link under Open a Model Document as shown in Figure 2-1, navigate to the location of the *Test23* subdirectory under the samples directory found in the installation location of SNAP, and click on the file *Test23.med*. The Model Editor rendering of Test23 will open as shown in Figure 2-2. If not, click on the "default view" tab at the bottom of the page to see this view. Alternately, the user can open the *Test23.med* file in the working directory to start the SNAP Model Editor.

Finally, the model can also be opened by selecting *File->Open*, navigating to the input file (*.med* file) of interest, selecting that file and clicking on *open*, much like any Windows program. Notice that there are three separate input sections in the SNAP Model Editor window shown in Figure 2-2 which are: the *Navigator* window, the *Property* window and the *View / Dock* window where the model rendering appears. Also, notice that there are two tabs in the *View / Dock* window labeled *Default View* and *Test23 View*. In Figure 3-2 the *Default View* for Test23 is shown which gives the model rendering for Test23. The *Test23 View* provides the job stream view for Test23 and the tabs can be clicked-on to show either the modeling rendering or the job stream (similar to Microsoft Excel). Job streams will be discussed later in this section. There is also a *Message* window underneath the *View / Dock* window which lists messages from SNAP/RADTRAD.

Before editing, the user should note that each of the windows shown in Figure 2-2 can be resized either horizontally or vertically. Resizing is done by hovering the mouse cursor over the border between the windows until a double-headed arrow appears. Then the user clicks and drags the border to the desired location. The user will need to unlock the model by clicking on the *Lock* (🔒) icon shown in Figure 2-2. Notice that other icons adjacent to the *Lock* (🔒) icon will change to unlocked (🔓) on the toolbar.

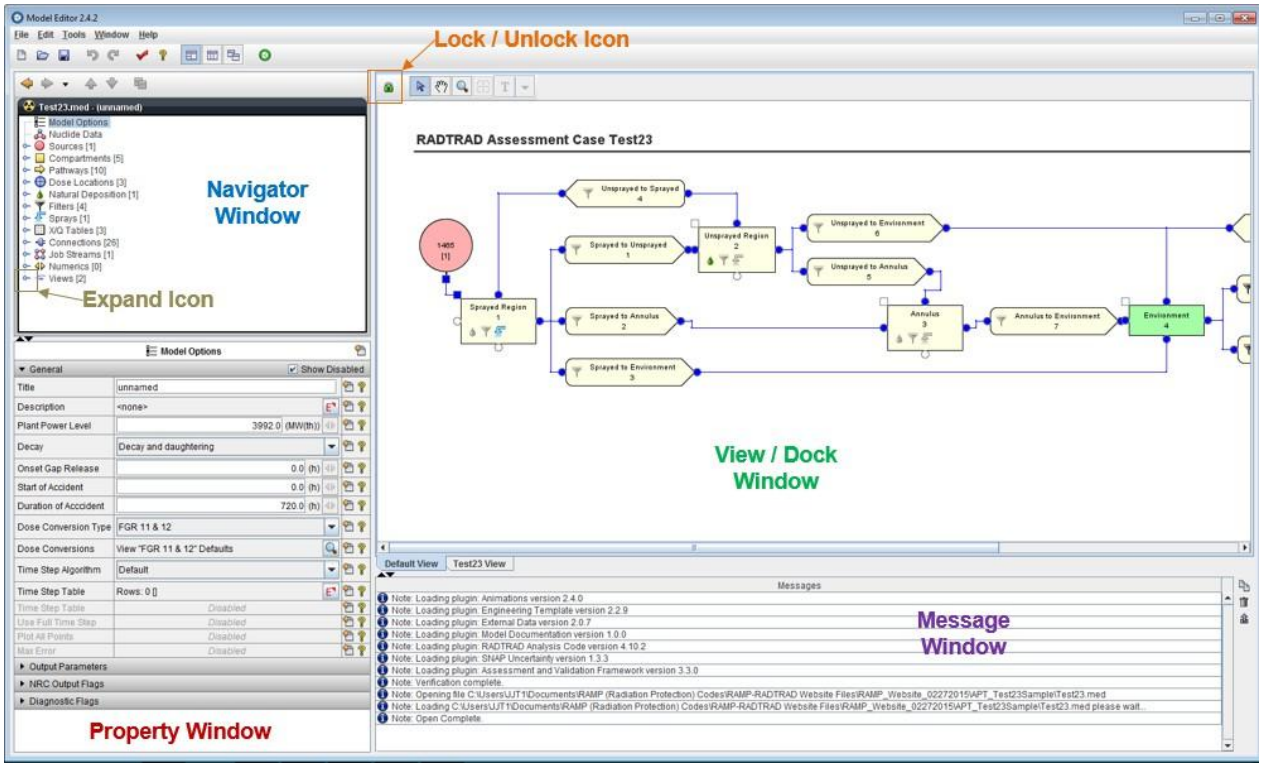


Figure 2-2 SNAP Model Editor Screen

One powerful feature in SNAP/RADTRAD is the ability to check the model for input errors. To illustrate the use of this feature, click on *Tools->Check Model* to perform a model check. Note that the message *Note: Model check complete. No errors found* in the *Message* window at the bottom of the screen.

The input groups are shown in the *Navigator* window. Clicking on the *Expand* ( ) icon will expand each group and node, showing the associated input data for that input group and node. Figure 2-3 presents an illustration of a node expansion which is obtained by clicking on the *Expand* ( ) icon next to *Compartments*, then clicking on *Compartment 1*. Note that Compartment 1 input appears in the *Property* window (lower left). The user should experiment with other input groups as the approach is the same. Input specification will be presented later in this section.

Note that the black bar where the input model name appears (*Test23.med*) contains some important features which are summarized in Section 2.4. One of these features is the ability to switch units from British to International System of Units (SI). Units switching is done by right-clicking on the black bar, selecting *Engineering Units->British* to change the units from SI to British.

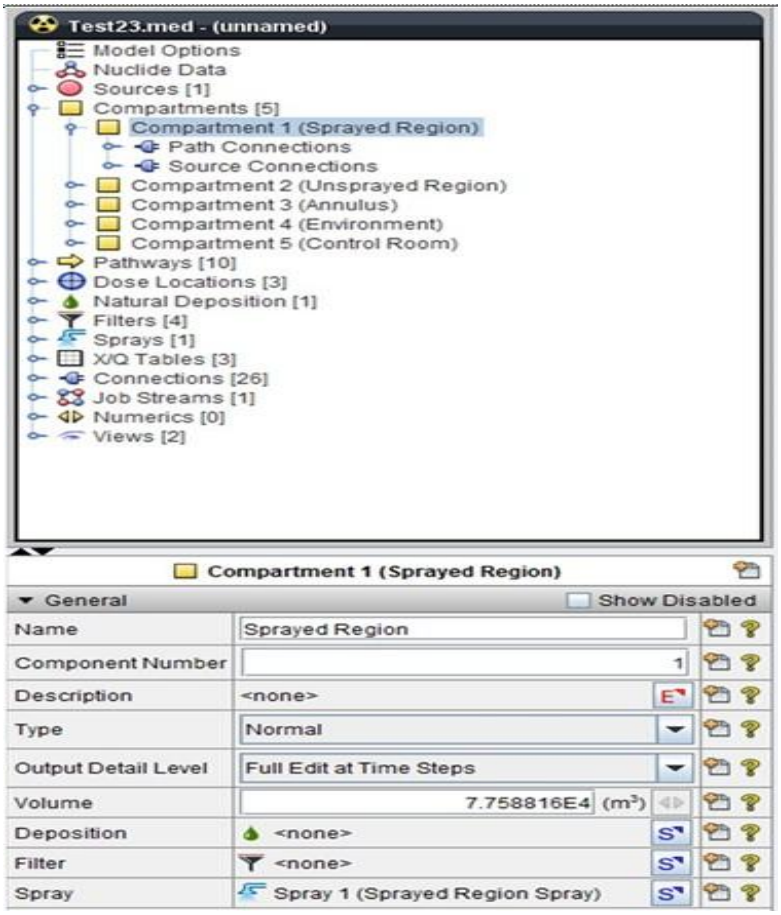


Figure 2-3 Illustration of the Expand Icon

Icons are used to represent the various components used in the *View / Dock* window that comprise a typical model. Figure 2-4 presents an illustration of the various icons used.

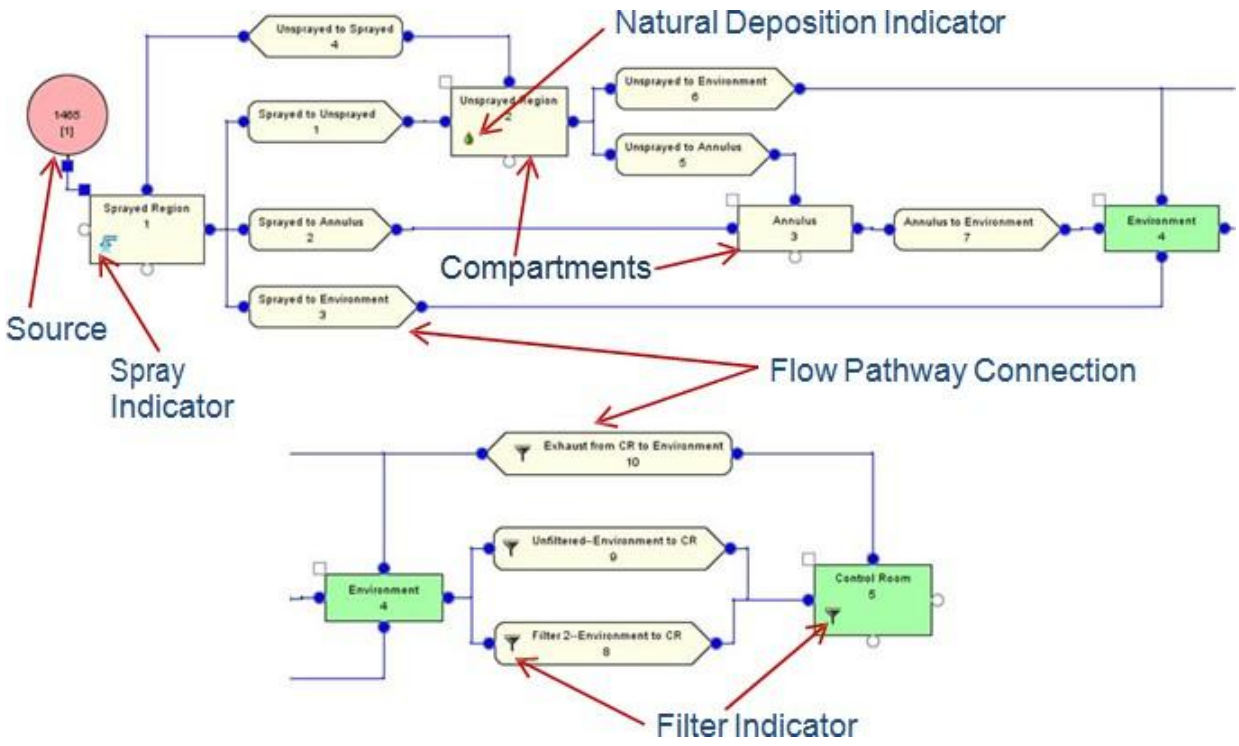


Figure 2-4 Illustration of the Various Icons used to Represent a SNAP/RADTRAD Model

1.1.1 Job Streams and Case Execution in SNAP/RADTRAD

Before continuing the discussion of existing model features and developing a new model, the Test23 case will be run to illustrate how cases are run.

Case execution is dependent on the job stream, which may be a source of confusion for new SNAP/RADTRAD users. Simply put, job streams are used to pass input and output data from one code to another for cases where multiple codes are used. SNAP is used to support a wide variety of analysis programs that pass data from one program to another. This feature is less of an issue with SNAP/RADTRAD because in most cases, output from SNAP/RADTRAD (RADTRAD-AC) is only passed to AptPlot for plotting. For the convenience of the user, a default job stream is predefined for all SNAP/RADTRAD cases.

Figure 2-5 presents a typical SNAP/RADTRAD job stream. The default job stream for SNAP/RADTRAD shows three steps: 1) input preparation shown in the *RADTRAD Model* (*Base_Model* node), 2) the analytical code execution in the *RADTRAD* (*RADTRAD* node) (middle box in Figure 2-5), and 3) the passing of plot data from SNAP/RADTRAD to AptPlot (*PlotStep* node). The input is passed from the Model Editor (*Base_Model* node) to the

RADTRAD-AC (*RADTRAD* node) and then the plot file data generated by the RADTRAD-AC is passed to the AptPlot (*PlotStep* node).

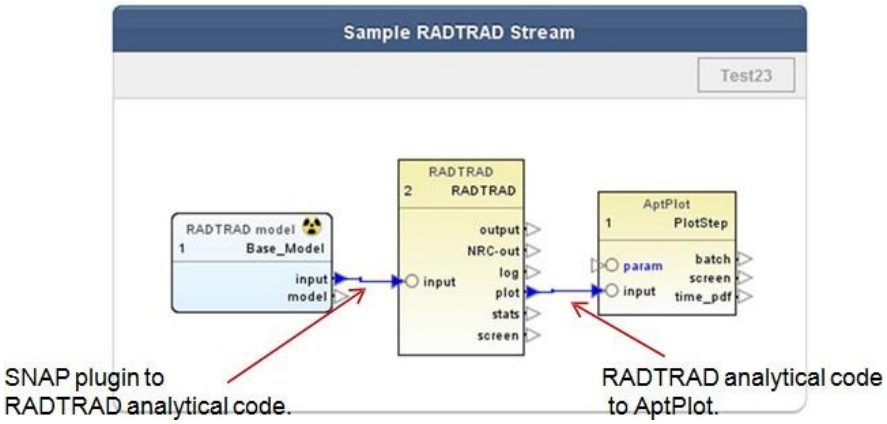


Figure 2-5 Typical Job Stream in SNAP/RADTRAD

As in the case of model input, job streams specification can also be checked. In the case of the Test23 problem, expand the *Job Stream* node in the *Navigator* window; select *Test23* and right-click, then select *Check Stream*. An error report window will appear in the *Message* window and in this case, no errors were found.

Part of the job stream input specification is to determine where the RADTRAD-AC output will be written. To display the location of the RADTRAD-AC output clicking on the *Expand* ( ) icon for the *Job Streams* node and select the *Test23* job stream to open the *Property* window as illustrated in Figure 2-6.

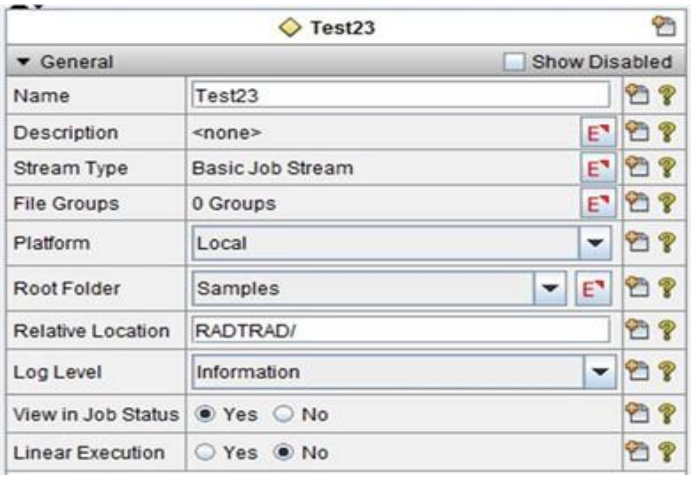


Figure 2-6 Job Stream Property Window

The two job stream properties which determine where the output is written are the *Root Folder* text box and the *Relative Location* text box. The SNAP/RADTRAD output is then the *Relative Folder* location appended to the *Root Folder* location. To review the root folder settings, click on the *Custom Editors* (E) icon and a window similar to that shown in Figure 2-7 appears. In this example, three root folders along with the path locations are shown.

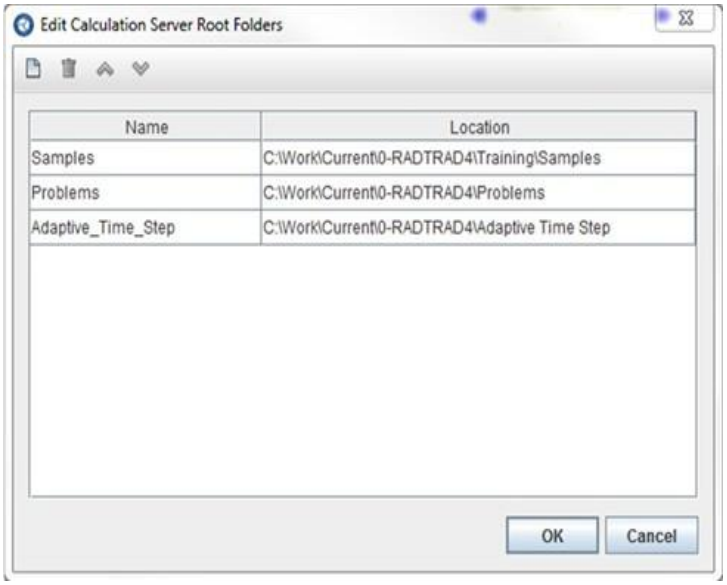


Figure 2-7 Typical Root Folder Settings in SNAP/RADTRAD

Assuming that the root folder is set to *Samples*, the path to the output will be *Samples\RADTRAD* or *C:\Work\Current\0-RADTRAD\Training\Samples\RADTRAD*. In a new installation, the root folder is not set. When the root folder is not set, the message *No Root Folders Available* appears in red as shown in Figure 2-8.

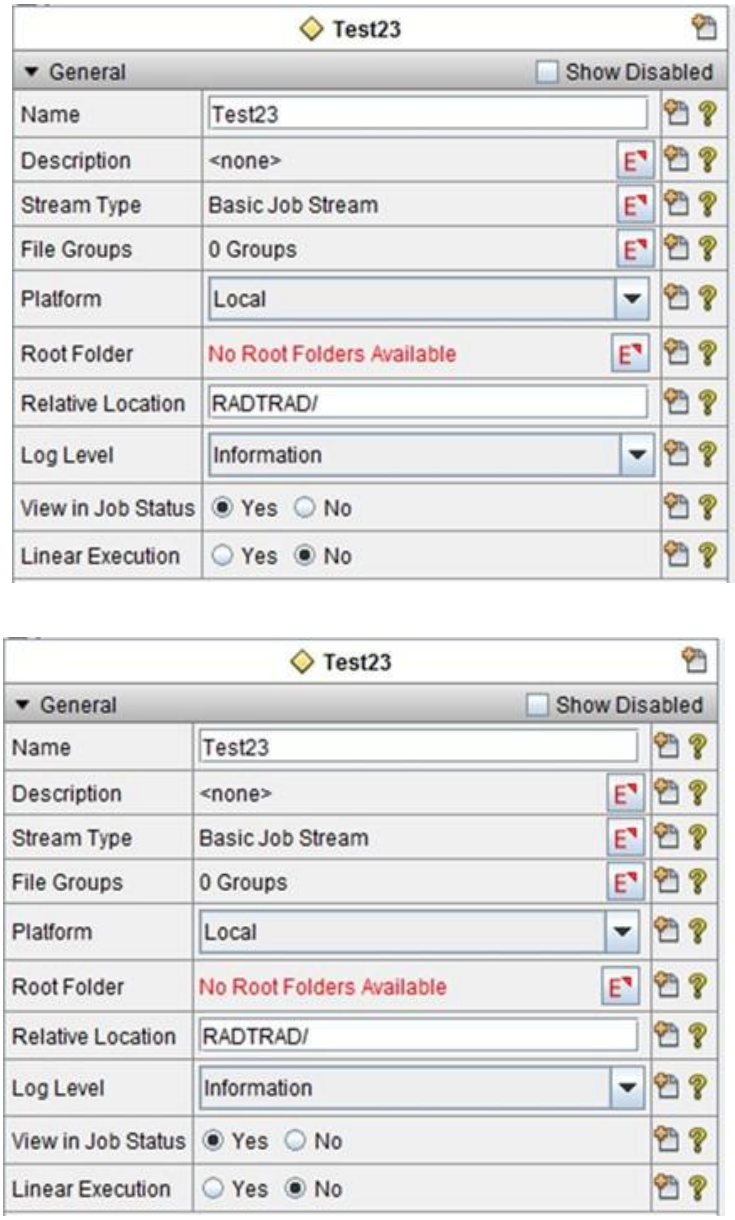


Figure 2-8 Job Stream Property Window with an Unset Root Folder

Setting the root folder requires selecting the *Custom Editors* ( ) icon under the *Root Folder* text box to open the *Edit Calculation Server Root Folders* window (Figure 2-7). Click on the *New* ( ) icon and navigate to the desired location in the *Select Folder Location* window. The root folder name will change to the last folder name in the directory path.

The relative location can be reset and should be reset to a name more mnemonic so that the SNAP/RADTRAD cases can be tracked. For example, to change the name, highlight the

Relative Location Name and type in a new name (*Sample_Test23*). Note that the file location is automatically appended.

Note that multiple root folders are allowed which is handy for organizing SNAP/RADTRAD case files. To add a root folder, click on the (E) icon *next to Root Folder in the Test23 job stream*. Click on the *New* ( ) icon (left on Toolbar) and navigate to where you want the root folder (ex. NPP Dose Analysis). The root folder path will be created. Also, a path of subdirectories can be specified in the *Relative Location* text box separated by a back slash (/). For example, the relative location can be set to *RADTRAD/LOCA,* so that the path to the output would be *Samples/RADTRAD/LOCA* assuming that the root folder is set to *Samples*.

A couple of points should be noted about root folders. First, the root folder directory needs to exist – otherwise you'll get a warning that the directory doesn't exist and the root folder will not be defined. Second, overlapping paths are not allowed and will generate an error.

Finally, one remaining item should be configured before proceeding to submit the job stream for execution. This remaining item is to the link the SNAP Model Editor to the RADTRAD-AC by navigating to *Tools->Configuration Tool* to open the *SNAP Configuration* window and then expanding the *Applications* node by clicking on the *Expand* ( ) icon. After the *Applications* node has been expanded, right click the *Applications* node to open the drop-down menu as shown in Figure 2-9. Select *New* on the drop-down menu to open the *Create Application* window. Enter *RADTRAD* in the *Application Name* text box and scroll down to select the *RADTRAD* application and click *OK* as shown in Figure 2-9.

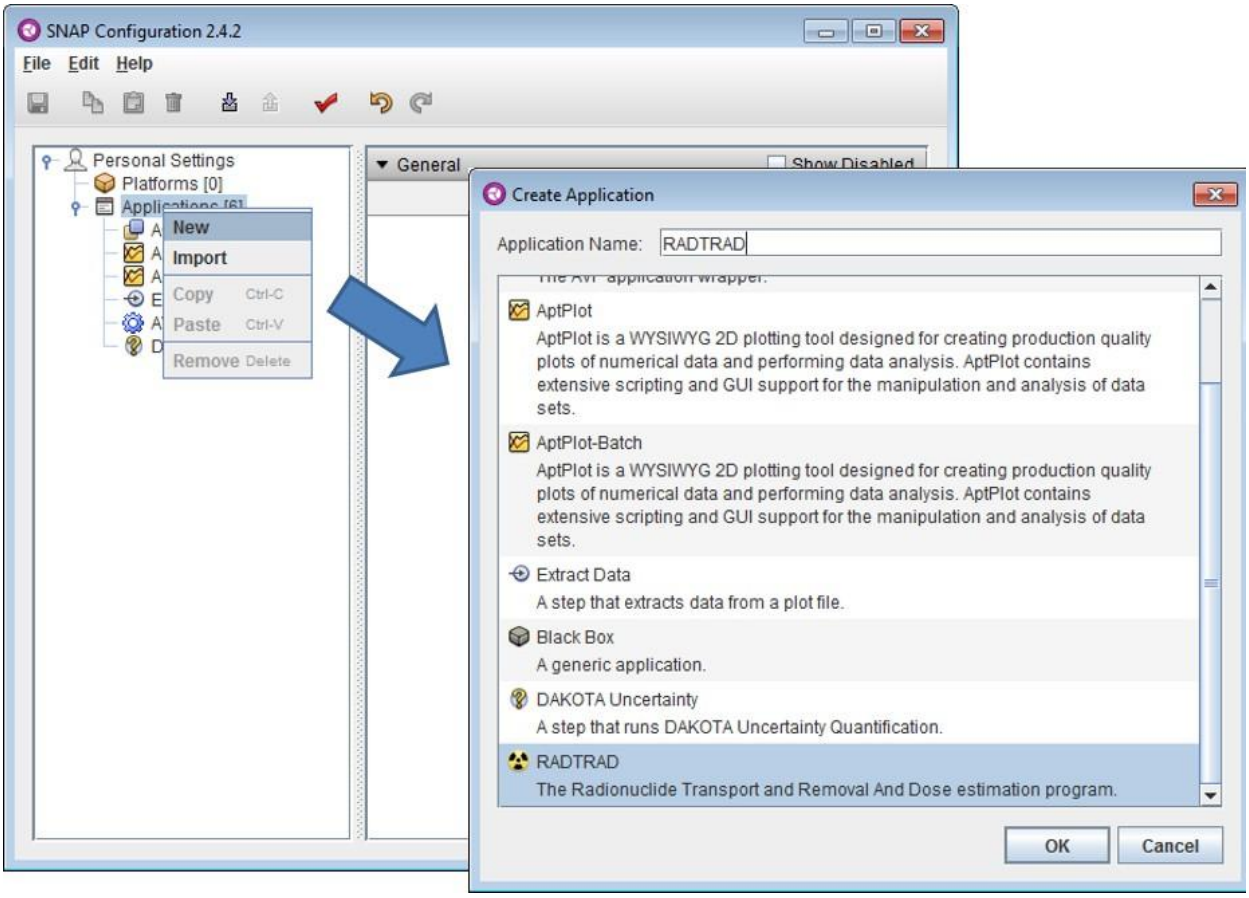


Figure 2-9 Linking the RADTRAD-AC Using the SNAP Configuration Tool

The *SNAP Configuration* window will then change to display the *RADTRAD* application with an error under the *Applications* node (Figure 2-10). On the right-hand side of the *SNAP Configuration* window under the *Application Location->Local Location* text box click the *Select* ( ) icon to open *Windows File* navigator. Navigate to *radtrad* subdirectory under the *snap* directory in the in the user's home directory as discussed in Section 2.3.3 and select the *radtrad.jar* file for the RADTRAD-AC (not the RADTRAD Plugin). (**Note**: The file directory path should look something like "C:\Users*{User Name}*\snap\radtrad\radtrad.jar" and **not** "C:\Users*{User Name}*\snap\Plugins\radtrad.jar.") Be sure to save these changes by selecting the *Save* ( ) icon and the *Close* button on the *Save Complete* window as shown in Figure 2-10. At this point, the user can run *Test23*.

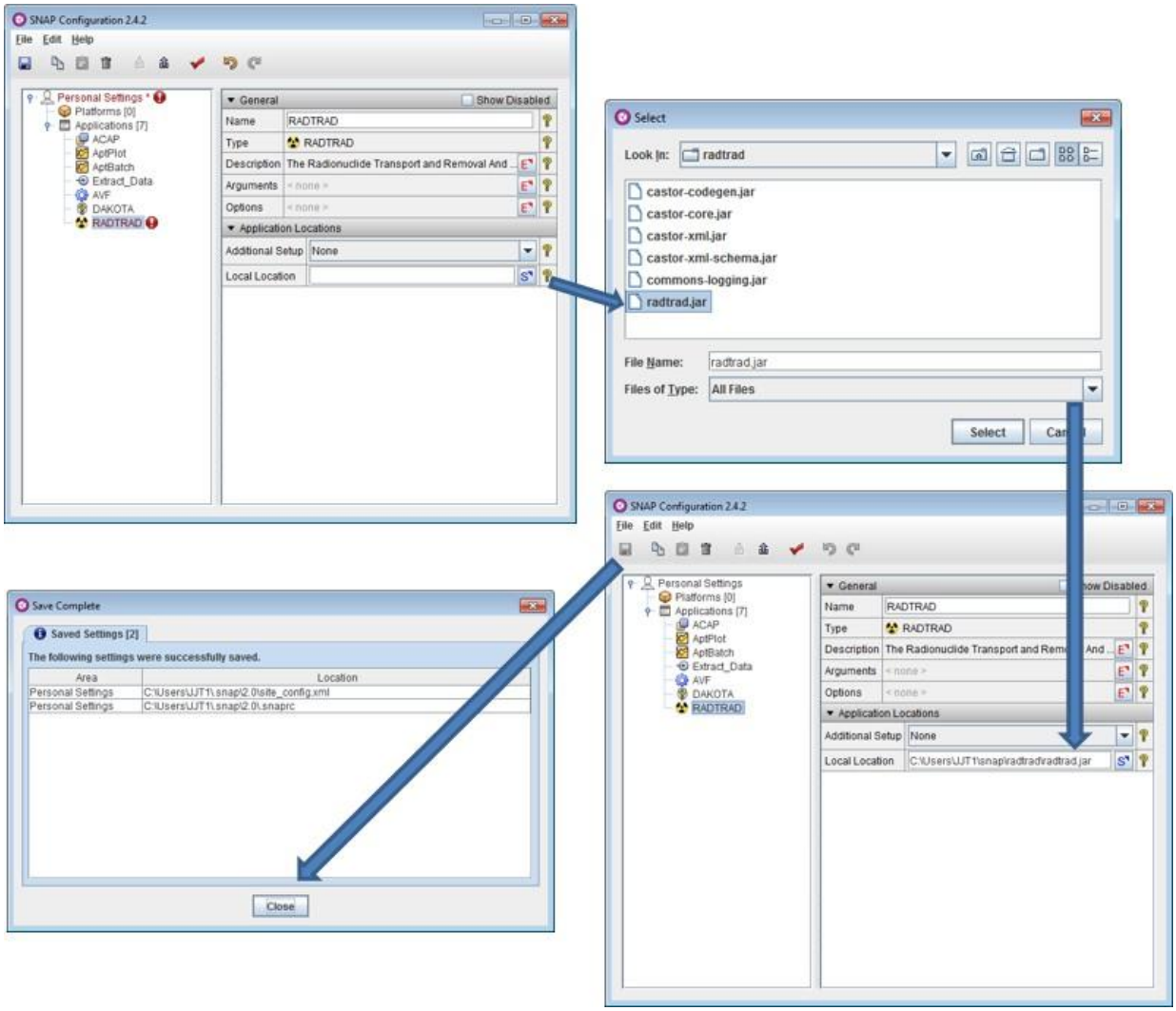


Figure 2-10 Saving the RADTRAD-AC using the SNAP Configuration Tool

To run the Test23 or any other case, click on *Tools->Submit Job*. A *Submit Job Stream* window will appear as shown in Figure 2-11. Click on *OK* and a confirmatory *Submit Stream* window will appear. Finally, click *OK* and the run will start. The *SNAP Job Status* window will appear which is also shown in Figure 2-11. The *SNAP Job Status* window, in Figure 2-11 displays a completed job stream run. If an error message shows up saying that there is an invalid job stream, delete the Test23 job stream and create a new Basic stream by right clicking on Job Streams and selecting new.

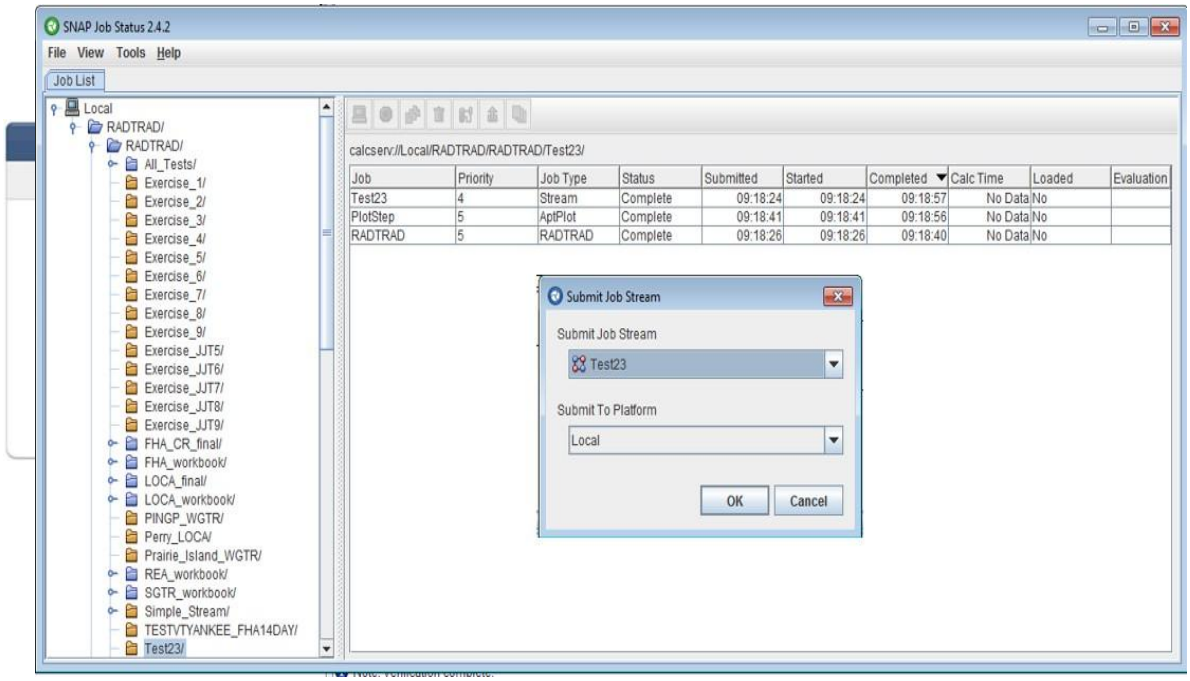


Figure 2-11 SNAP/RADTRAD Job Stream and Status Windows

The relationship between the SNAP/RADTRAD job stream and the actual case execution is shown in Figure 2-12. In the upper left-hand corner, the graphical job stream representation is shown. As noted earlier, this representation shows passing input from the Model Editor to the RADTRAD-AC and then to AptPlot. The job stream properties are shown in the *Navigator* window shown in the upper-right corner of Figure 2-12. The links between the various nodes are also shown. In the *SNAP Job Status* window, the status of each of the job stream steps is shown. Again, three steps are shown. The user interaction with the *SNAP Job Status* window will be discussed in Section 2.2.3.

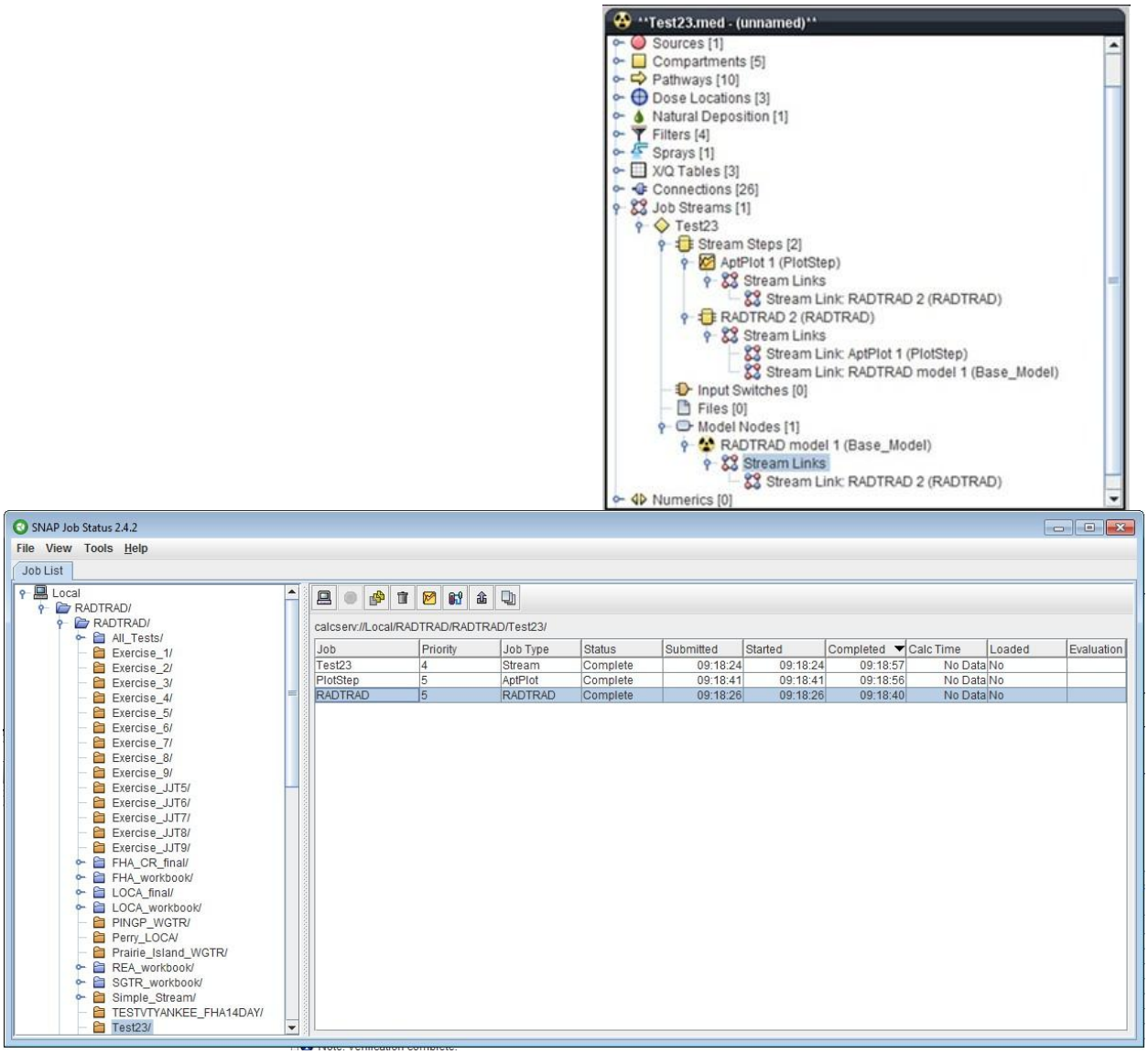


Figure 2-12 Relationship Between Job Stream Steps and Code Execution

Note that the *SNAP Job Status* window can be accessed from *Tools->Job Status* in the Model Editor for subsequent viewing. A summary of features relevant to SNAP/RADTAD available in the *SNAP Job Status* window are listed below:

- The *Job Console* ( ) icon – provides the time step history for the current job.
- The *Job Execution* ( ) icon – terminates the execution of the current job. This is only available when the job is running.

- The *Job Deletion* ( ) icon – removes the current job and files.
- The *AptPlot* ( ) icon – opens the selected job for plotting in AptPlot.
- The *File Viewer* ( ) icon – starts the output file viewer.

2.2.2 SNAP/RADTRAD Input and Output Files

There are several files produced that the user should be aware of in SNAP/RADTRAD. The main SNAP/RADTRAD interface file is the *casename.med* file where *casename* is the name of the case being analyzed. The *casename.med* file contains the data needed to render the model in the SNAP GUI, the default data used by the code and the user-specified input data. Section 2.4 discusses the actual input that can be specified for a SNAP/RADTRAD model.

When a SNAP/RADTRAD case is executed through the RADTRAD-AC, the data flow is not directly from the *casename.med* file. Rather, there are several data files that are produced by the SNAP/RADTRAD plugin that are read by the RADTRAD-AC. These files, which are in extensible markup language (XML) format, include DCFs (*.dfx*), nuclide data (*.nix*), plant information (*.psx*), release fraction (*.srx*), and nuclide inventory (*.icx*) files. Output files (*.out*, *.screen, .log,* and *.plot*) are produced by the RADTRAD-AC. Log files produced by SNAP/RADTRAD are job stream related files (*.streamlog* and *.tasklog*). Table 2-1 provides a brief description of these files.

When case execution is completed, the SNAP/RADTRAD output can be reviewed by clicking on the *File Viewer* ( ) icon. Note that there is a context in terms of the active job stream step and the output that is displayed. If the *casename* step is highlighted, then the job stream log will be available for viewing. If the *RADTRAD* step is highlighted as shown in the *SNAP Job Status* window in Figure 2-13, then the RADTRAD-AC output is available. If the *PlotStep* is highlighted, then the plot file data can be viewed using AptPlot. Figure 2-13 shows a screenshot of the drop-down menu cascade from the *File Viewer* ( ) icon for the *RADTRAD* job step from the *SNAP Job Status* window.

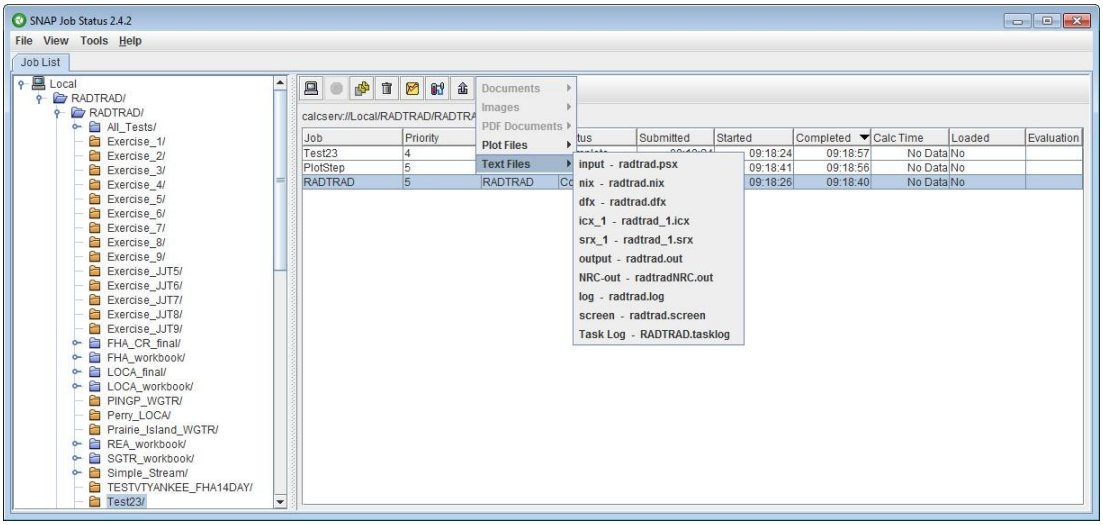


Figure 2-13 Drop-down Menus for SNAP/RADTRAD Output

Table 2-1 Files Available for Viewing Using the File Viewer in the Job Status Window

File Name	Description
Job Status Window *Casename* Files	
StreamLog - *Casename.streamlog* [a]	Output from job stream manager. Provides a high-level summary of the execution steps for the job stream. Typically not reviewed by the SNAP/RADTRAD user.
Job Status Window *RADTRAD* Files	
Plot Files->plot - *radtrad.plt* [c]	Data file for AptPlot from the RADTRAD-AC.
Text Files->input – *radtrad.psx* [b]	Plant data input file in XML format. Includes the plant-specific data specified by the user including model parameters, information for plant geometry for each compartment, information for each flow path, dose point information including X/Q and breathing rates, occupancy factors, and information for various radionuclide removal models (sprays, natural deposition, and filters).
Text Files->nix – *radtrad.nix* [b]	Nuclide data information from ICRP-38 in XML format. Includes the atomic mass, half-life (s), and branching ratios for radionuclide daughters.

Text Files->dfx – *radtrad.dfx* [b]	DCF file in XML format based on FGR 11 and 12 (see Section 4.6). Includes the organ-specific DCFs. Note that only the cloudshine (immersion), the inhaled chronic [total effective dose equivalent (TEDE)] and thyroid skin DCFs are used to determine dose. Organ-specific factors as well as those factors for groundshine, inhaled acute and ingestion are not used.
Text Files->*icx_1* – *radtrad_1.icx* [b] Text Files->*icx_2* – *radtrad_2.icx* [b] (etc.)	Initial radionuclide inventory file in XML format. Duration of source term release and release fractions.
Text Files->*srx_1* – *radtrad_1.srx* [b] Text Files->*srx_2* – *radtrad_2.srx* [b] (etc.)	Release fraction information file for each radionuclide group.
Text Files->*output* – *radtrad.out* [c]	Output file from the RADTRAD-AC in the original format.
Text Files->NRC-out – radtradNRC.out [c]	Output file from the RADTRAD-AC in the revised NRC format.
Text Files->log – radtrad.log [a]	Debug output. Includes warnings and errors useful to users and developers. .
Text Files->screen – radtrad.screen [c]	Problem time output to show progress of a given case.
Text Files->Task Log – RADTRAD_tasklog [a]	Output from SNAP job steam showing RADTRAD job step execution information (usually not referred to by the user).
Job Status Window *PlotStep* Files	
PDF Documents – time_pdf – time.pdf [c]	Time step results (usually not referred to by the user).
Text-Files->screen – aptplot.screen	Screen output from AptPlot (usually not referred to by the user).

Text-Files->Task Log – PlotStep.tasklog	Output from SNAP job steam showing AptPlot job step execution information (usually not referred to by the user).
a. SNAP/RADTRAD specific output. b. Input file to the RADTRAD-AC generated by SNAP/RADTRAD plugin. c. Output file from the RADTRAD-AC.	

The files produced by the RADTRAD-AC code which

are *radtrad.out*, *radtradNRC.out*, *radtrad.plt*, and *radtrad.screen* are the most relevant to the user. The *radtrad.out* file is basically the original (Version 3.03/3.10) output file. Major sections of this output file are:

- Input listing – provides a listing of the input in XML format that is used by the RADTRAD-AC.
- Input echo – provides an edited input summary of plant description (model), scenario (radionuclide source term/DCF) information, compartment/pathway data, X/Q, DCF and decay data, and other relevant input.
- Breakdown of dose results and nuclide inventory in various compartments at various time points generally selected by changes in events (i.e. time at which flow rate changes, and time at which X/Q changes). Activity balance information is also given.
- I-131 inventory in various compartments as a function of time.
- Cumulative dose results at various dose locations as a function of time.
- Worst two-hour doses at the EAB and the final doses and final doses for the LPZ and other dose locations.

The output contents can be controlled from *Model Options* node by expanding the *Output Parameters* tab in the *Property* window as shown in Figure 2-14. The main difference in the output is generally the editing of results for supplemental time steps when they are used and the model removal/decontamination factors. The *Output Parameters* flags are discussed in more detail in Table 2-5.

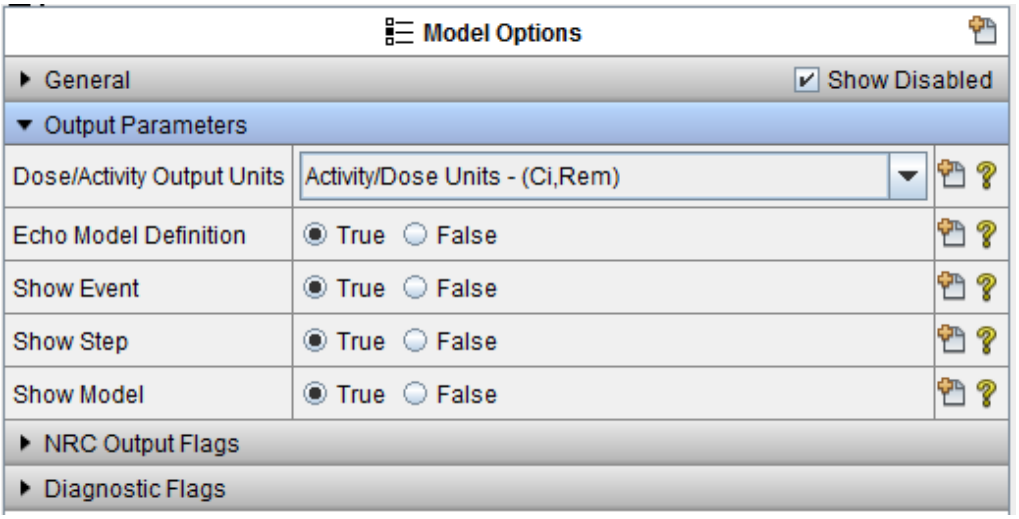


Figure 2-14 Expanded Output Parameters Tab in the Property Window

The *radtradNRC.out* output file provides a time-dependent summary of activity and dose calculations by nuclide. The contents of the *radtradNRC.out* file are controlled by expanding the *NRC Output Flags* tab under *Model Options* node in the *Property* window. See Figure 2-15 for the output parameters available. Major sections of this output are:

- Input echo – provides an edited input summary of plant description (model), scenario (radionuclide source term/DCF) information, compartment/pathway data, X/Q, DCF and decay data, and other relevant input.
- Output – activity distribution, cumulative and dose difference (delta-dose) for each dose component (inhalation, cloudshine, skin, thyroid, and TEDE).
- I-131 inventory in various compartments as a function of time.
- Cumulative dose results at various dose locations as a function of time.
- Worst two-hour doses at the EAB and the final doses and final doses for the LPZ and other dose locations.

The *NRC Output Flags* are discussed in more detail in Table 2-5. The *radtrad.screen* file lists the time step history for a given SNAP/RADTRAD case.

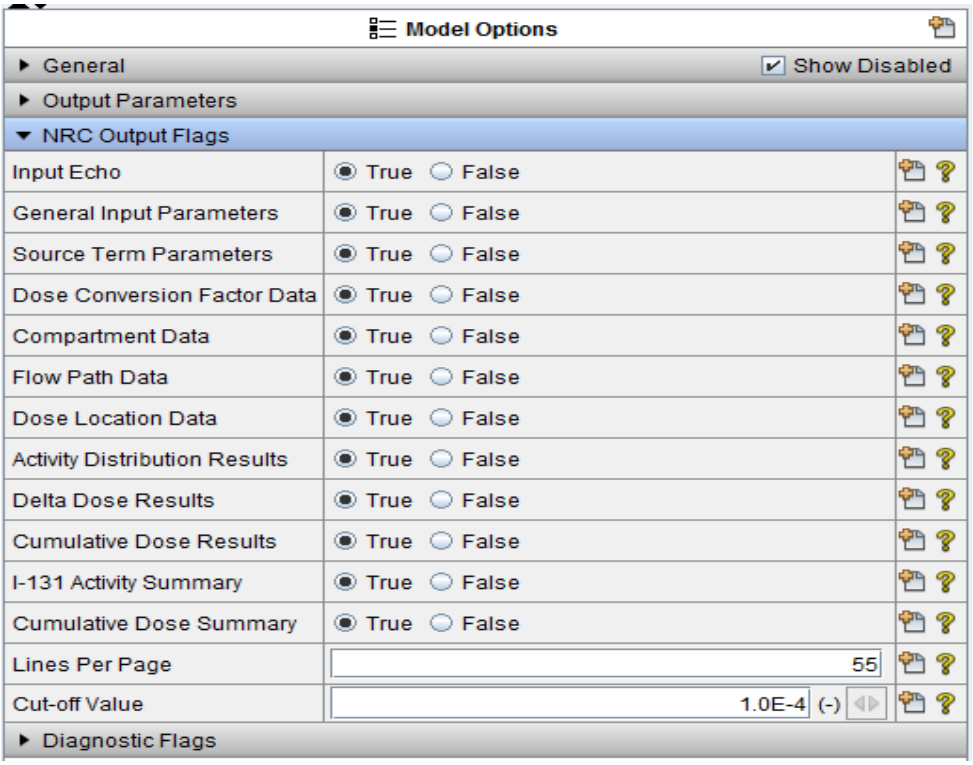


Figure 2-15 Expanded NRC Output Flags Tab in the Property Window

2.2.3 **AptPlot** Plotting Program

A feature of SNAP/RADTRAD is the ability to display plots of dose results. To display a plot, click on *Plot Files* and select *plot – radtrad.plt*. AptPlot will open. Alternately, click on the *AptPlot* ( ) icon in the *SNAP Job Status* window and AptPlot will open as illustrated in Figure 2-16.

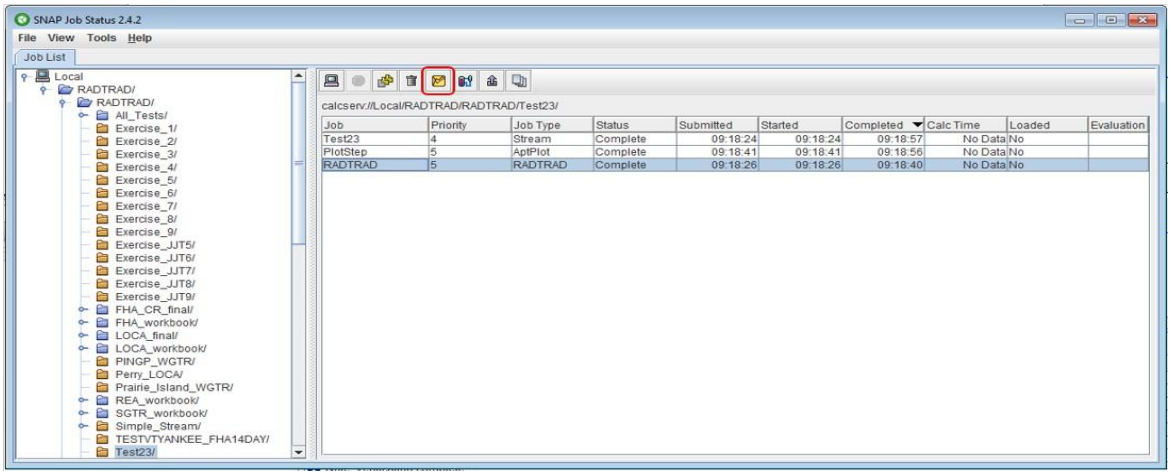


Figure 2-16 SNAP/RADTRAD Job Status Window with AptPlot Icon Highlighted

When AptPlot opens, the windows presented in Figure 2-17 will appear. Dose information by dose location (*ExclusionAreaBoundary*, *LowPopulationZone*, and *ControlRoom* spaces omitted) and dose category (*body*, *cloudshine*, *skin*, *tede*, and *thyroid*) for each nuclide separated by periods will be presented in the *Select EXTDATA Channels* window in Figure 2-18. In AptPlot, each data set is referred to as a data channel. Test Problem 23 is used to illustrate the features of AptPlot and it is suggested that the user open AptPlot for Test Problem 23 and follow the discussion below.

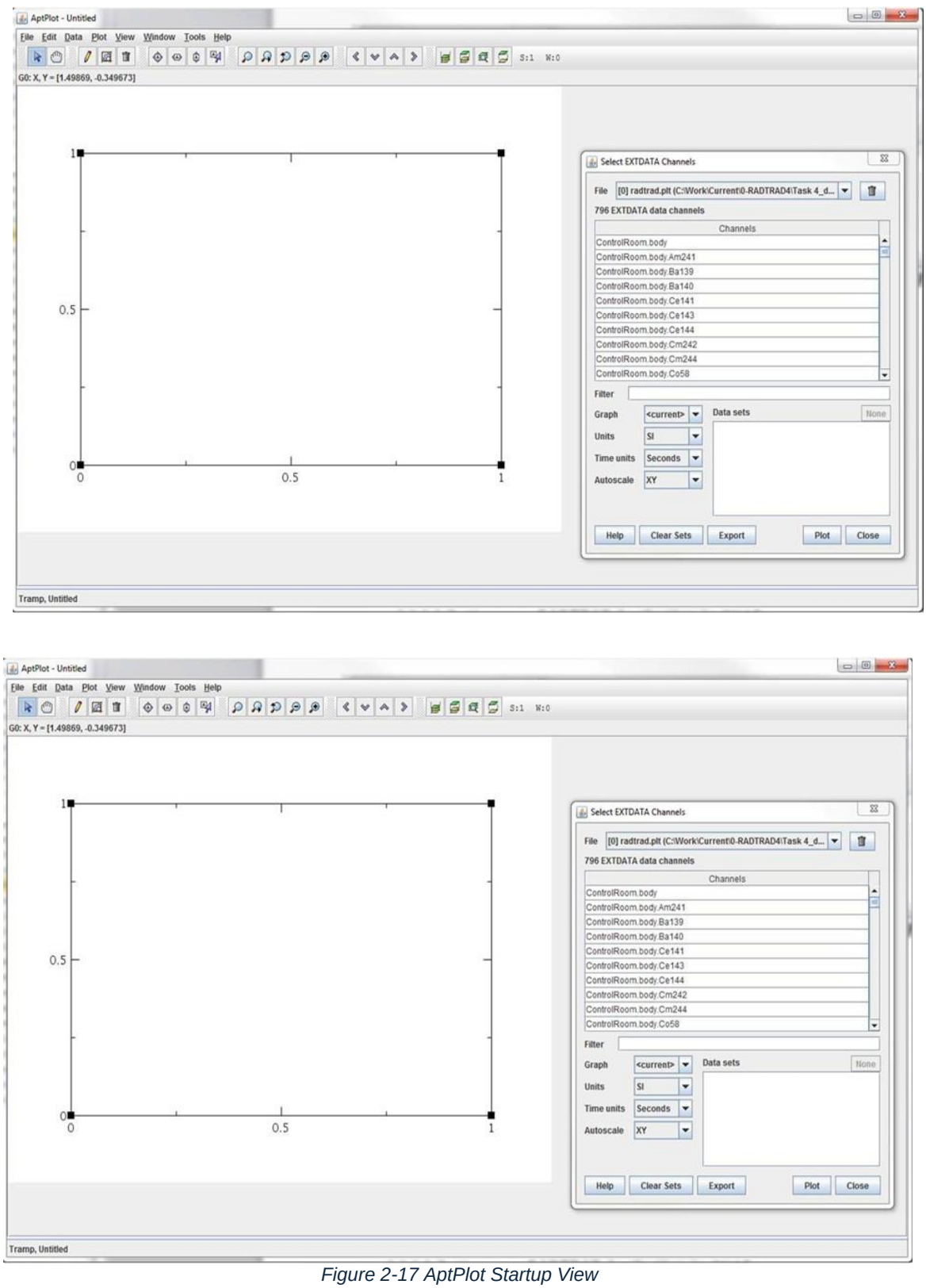
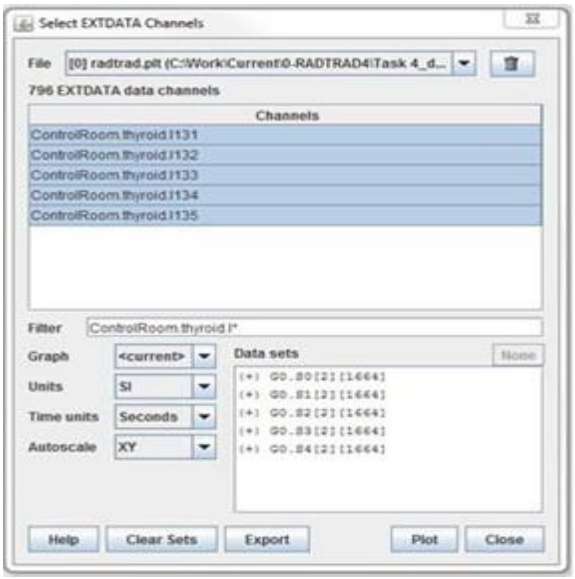


Figure 2-17 AptPlot Startup View

To make a plot, the user scrolls to the result of interest, highlights that result, clicks on the *Plot* button and the plot will appear. Note that the default time units are in seconds, but that can be changed to hours in the drop-down menu next to *Time Units* text box on the *Select EXTDATA Channels* window (Figure 2-18) prior to actually generating the plot.

AptPlot has many features for generating and formatting plots and the discussion presented here is not meant to be exhaustive. A comprehensive help manual can be obtained by selecting *Help->Help Topics* from the top menu. However, some of the more commonly used features are illustrated here.

As the user gains familiarity with the naming convention, the filter feature can be used to locate specific results of interest by entering the dose location, dose category, and nuclide of interest in the *Filter* text box (Figure 2-18). If the user wants to plot the TEDE dose results for the control room, enter the text string *ControlRoom.tede** in the *Filter* text box. Note that the total TEDE dose ends with *tede* (i.e. no nuclide is listed). Also note that the asterisks (wildcard) symbol is used to control the list of all items. Wildcards can be embedded in the string (i.e. *ControlRoom.*.I**) to list the control room dose categories for all iodine nuclides. It is very important to note that the case of a character counts in applying filters in AptPlot, otherwise the wildcard search feature will not work properly. The spelling of the dataset name in the data channel window provides a guide for spelling a channel name.



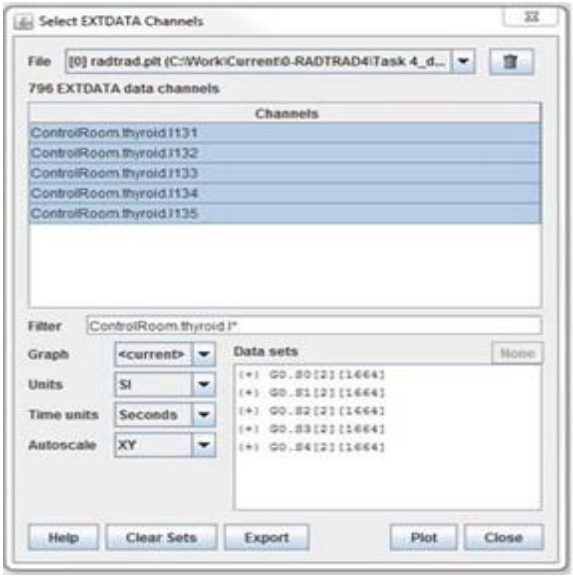


Figure 2-18 Select EXTDATA Channels Window for Multiple Plots

Multiple data results can be plotted by highlighting the data of interest and clicking the *Plot* button. As an example, suppose the user wants to plot the thyroid dose for I-131 through I-135 for Test Problem 23. The user would enter *ControlRoom.thyroid.I** in the *Filter* text box, then select the resulting data channels in the *Select EXTDATA Channels* window and click on the *Plot* button to make the plot. This string can be shortened to *C*R*th*I** as a further example of the application of wildcards. To select multiple data channels requires the use of shift-click or control-click feature as described below:

- *Shift-click* – used to select a range of datasets. In this case, click on *ControlRoom.thyroid.I131*. Then hold down the shift key and select *ControlRoom.thyroid.I135*.

- *Control-click* – used to select multiple datasets one at a time. Hold down the control key and click on each dataset, selecting that dataset. Each dataset is highlighted after selection.

With either approach, all of the dose datasets will be highlighted as shown in Figure 2-18. Once the datasets are highlighted, click on the *Plot* button and the plot will be generated. The resulting plot is shown on Figure 2-19.

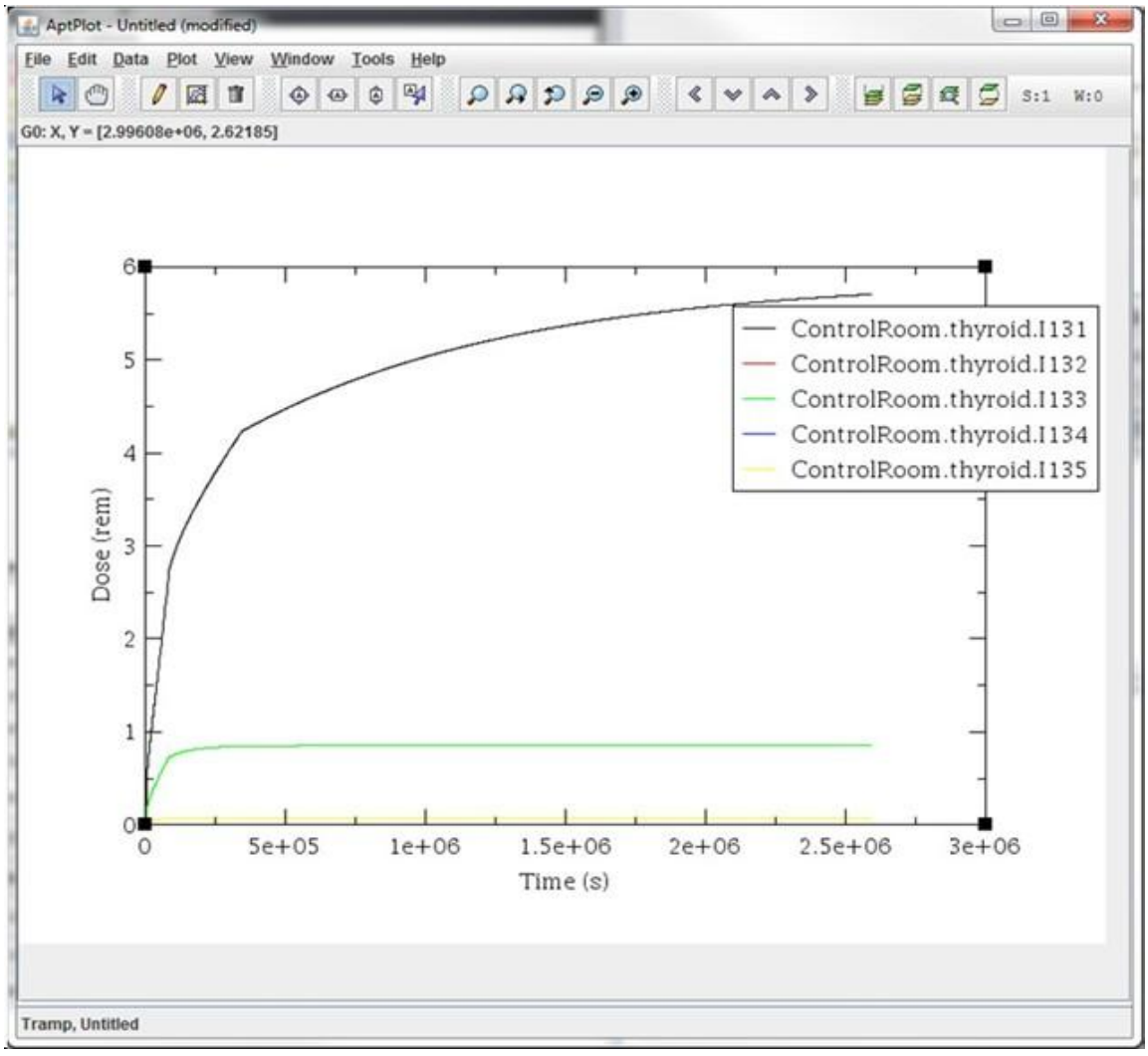


Figure 2-19 Control Room Dose Plots for Test23

Adjustments can be made to the plot by using the plot editing features in AptPlot. These features are accessed by selecting *Plot* in the top menu. A number of features are available, but generally *Plot->Graph appearance*, *Plot->Set appearance* and *Plot->Axis properties* provide the features needed to edit the plot. Screenshots of each of these windows are shown in Figures 2-20 through 2-22. Clicking on the tabs in each window shows various properties and features available to the user. A subset of these features is used to edit the plot.

Some typical AptPlot adjustments are illustrated below:

- Change the x-axis scale from seconds to hours: **–** Navigate to the *Select EXTDATA Channel* window shown in Figure 2-18 and click on *Clear Sets* in the lower left-hand portion of the screen. Then change the units in the *Time Units* drop-down menu from *Seconds* to *Hours*. Confirm that the dose components are highlighted as shown in Figure 2-18 using *shift-click* or *control-click*. Then, click on *Plot* and *Time (hours)* will appear on the x-axis.

- Reset y-axis to logarithmic scale: **–** Given that the I-131 dose is so dominant, it is hard to read the dose contributions from the other iodine nuclides. The y-axis scale can be changed to logarithmic by selecting *Plot->Axis properties* to open the *Axes* window (Figure 2-20). Change the axis setting in *Edit* text box from *X axis* to *Y axis* and click on the *Main* tab if it is not already selected in the *Axes* window (Figure 2-20). Then change the *Scale* text box from *Normal* to *Logarithmic* and click the *Apply* button to change the y-axis to logarithmic.

- Expand y-axis to cover dose range: **–** The dose range can be expanded by changing the Start and Stop values to 0.0001 and 10.0 in the *Axes* window. The Axes window is obtained by selecting *Plot->Axis properties* to open the *Axes* window (Figure 2-20). Click on the *Main* tab if it is not already selected. Change the edit box to *Y axis*. Then, enter *0.0001* in the *Start* text box and *10.0* in the *Stop* text box. Then click the *Apply* button to apply the change.

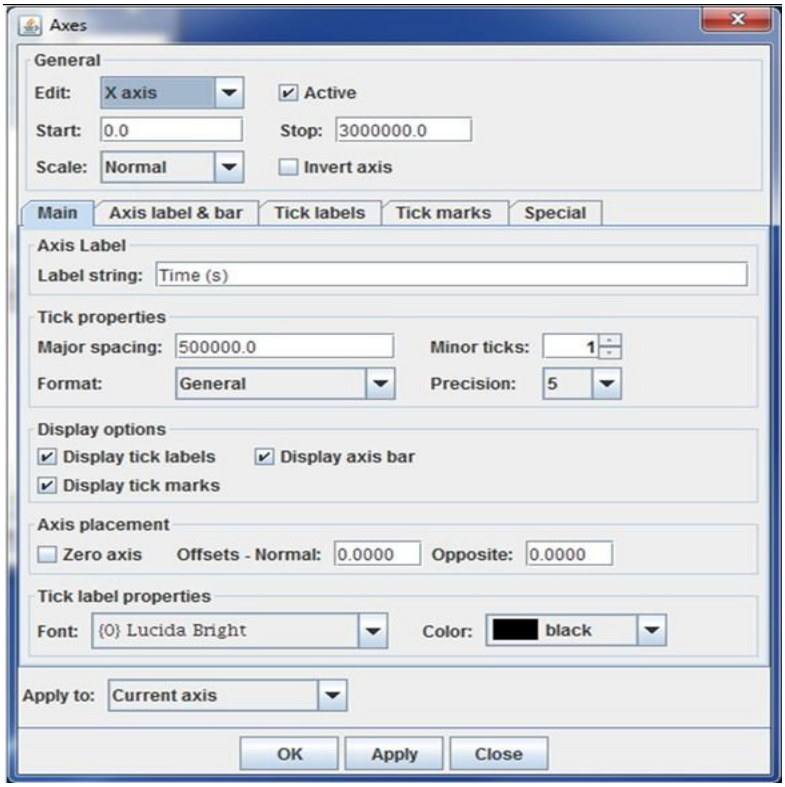


Figure 2-20 AptPlot Axes Window

- Use scientific notation for the y-axis: – The format for the y-axis labels is set by changing the *Edit* drop-down menu setting in the *General* section of Figure 2-20. Then, set the number format in the *Format* drop-down menu in the *Tick properties* section to *Scientific* from *General*. Also set the precision to *0* in the *Precisio*n drop- down menu and click the *Apply* button to reset the format.

- Line colors: – The line colors selected by AptPlot can be hard to see. Each line color can be individually adjusted by the user. To adjust a line color select Plot->Set appearance to open the Set appearance window (Figure 2-21). Highlight the dataset to be changed in the Data sets section near the top of the Set appearance window (Figure 2-21). Note that the name of the data contained in a given dataset is identified by the String text box in the Legend section in the lower part of the window. Also, note that the current color of a particular dataset is shown in the Color drop-down menu in the Line Properties section. Using that drop-down menu, select the desired color and click on the Apply button. Alternately, to change the color of all lines to black for example, highlight all datasets using shift-click or

control-click or alternately clicking on the All button. Then, select Black in the Color drop-down menu (if it is not already selected) and click on the Apply button.

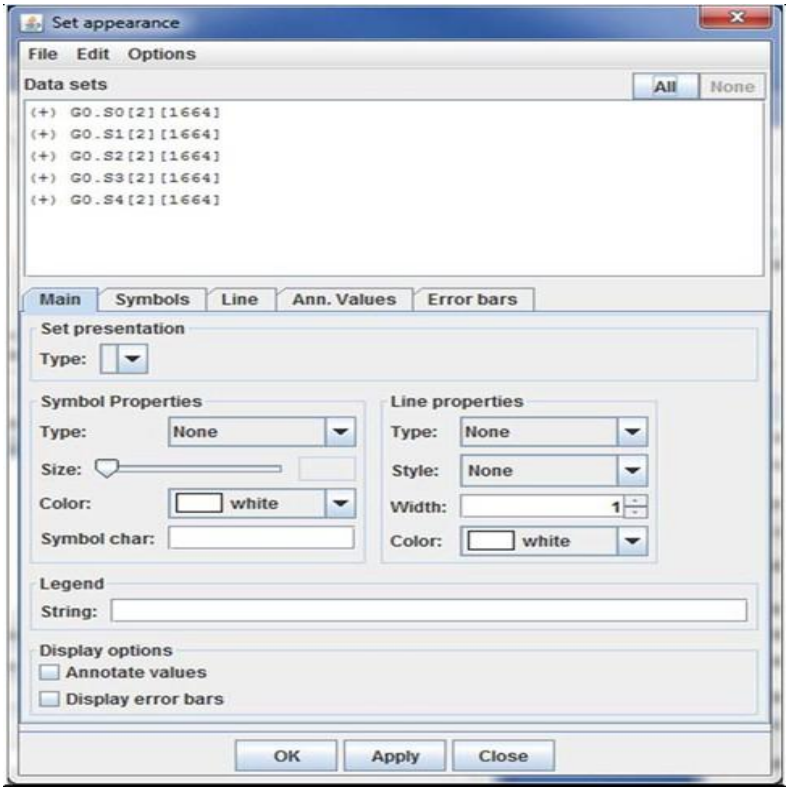


Figure 2-21 AptPlot Set Appearance Window

- Line symbols: – Symbols for the lines are set from the *Main* tab in the *Set appearance* window (Figure 2-21). To select a symbol for a particular data set, highlight the dataset in the *Data sets* section, then select a symbol type (circle, square, etc.) under the *Type* drop-down menu in the *Symbol Properties* section. Also, select the desired color in the *Color* drop-down menu and click the *Apply* button. A symbol will appear for each data point and since there are hundreds of data points, a symbol skip will have to be set. Select the *Symbols* tab in the *Set appearance* window and highlight the dataset to be changed. Then, set the *Symbol* skip to a value like *50* or *75* and click on the *Apply* button. This setting will display a symbol for every 50th or 75th point. Repeat these steps for each dataset.

- Line style: – Line styles (solid, dash, dot-dash, etc.) can be set by selecting the *Main* tab in the *Set appearance* window (Figure 2-21), highlighting the desired data set in the *Data sets* sections and selecting the desired style using the *Style* drop-down menu in the *Line Properties* section in a manner similar to setting line colors and line symbols. Each

line is set individually, and then click the *Apply* button as the settings for each dataset are completed.

- Titles and subtitles: – To add a title and subtitle to the plot select *Plot->Graph appearance* to open the *Graph appearance* window (Figure 2-22). In the *Main* tab section enter a title and subtitle as appropriate, then click on the *Apply* button. The title and subtitle will appear. Select the *Titles* tab and use the sliders to adjust the font size for the title and subtitle as desired. Note the font size can be incremented by clicking on the channel to the left or right of the slider icon.

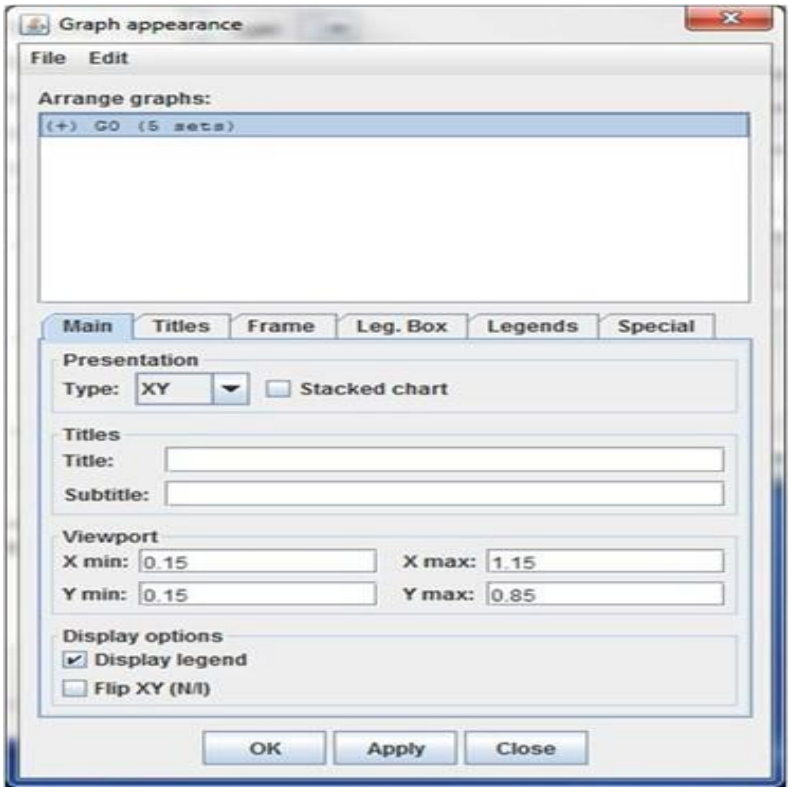
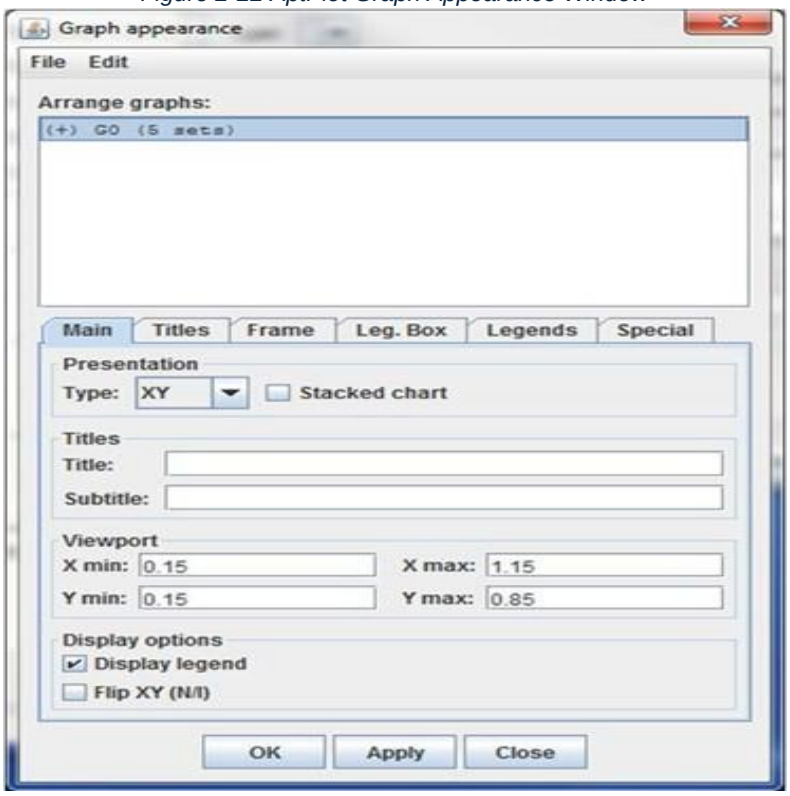

Graph appearance
File Edit
Arrange graphs:
(+) G0 (5 sets)
Main Titles Frame Leg. Box Legends Special
Presentation
Type: XY
Stacked chart
Titles
Title:
Subtitle:
Viewport
X min: 0.15
X max: 1.15
Y min: 0.15
Y max: 0.85
Display options
Display legend
Flip XY (N/I)
OK
Apply
Close

Figure 2-22 AptPlot Graph Appearance Window



Sometimes the legend box overwrites the dose results as in the plot shown in Figure 2-19. In order to correct this issue, the plot needs to be shrunk, which will require using several AptPlot features. These features are listed below:

- Edit the legend titles: – The title for each legend can be edited. This change is made by selecting *Plot->Set appearance* to open the *Set appearance* window (Figure 2-21) and highlighting the desired data set. Change the title in the *String* text box in the Legend section as appropriate. In this case, the iodine nuclide name is used. Click on the *Apply* button after each title modification is made.

- Change the font size for the legend: – First, the font size used in legend box will need to be reduced, which entails changing the legend title font and the symbol font. To change the font size of the legend title, select *Plot->Graph appearance* to open

  the *Graph appearance* window (Figure 2-22) and click on the *Legends* tab. Then, use the slider bar to adjust the font size to *75* for example and click on *Apply* button. The font size will change for all datasets. For the symbol size, navigate to the *Set appearance* window (Figure 2-21) and select all datasets. Then, change the *Size* setting in the *Symbol Properties* section to *75* using the slider.

- Change the size of the plot: – The plot overlays a white background which is basically set to allow a plot to be printed on 8.5 x 11 paper in landscape mode. So, it is desirable to maintain this setting although it can be changed by navigating to *View->Page* setup. However, the approach used here is to shrink the plot by adjusting the settings in the *Viewport* section in the *Graph appearance* window (Figure 2-22) by entering suitable values. In this case, the *X max* and *Y max* text box settings are changed to 1.0 and 0.8, respectively. These settings permit the legend box to be moved to the right-hand side of the plot, and then click on the *Apply* button. Then, to move the legend box, select the *Leg. Box* tab in the *Graph appearance* window (Figure 2-22) and adjust the box location in the *X* and *Y* text boxes in the *Location* section.

  Values of *1.05* and *0.60* will move the legend box to the right-hand side of the plot. Another approach is to change the *X max* text box setting to *1000* which will allow sufficient space for the legend box within the plot frame, although it will probably need to be moved for aesthetic reasons.

The plot is saved by selecting *File->Save and then* navigating to the desired directory location, entering a suitable name, then click on *OK*, similar to any Windows program. To access a previously saved AptPlot plot, select *File->Open*, and navigate to the directory location where the plot file is saved and select that file. Also, the format and title settings can be saved by selecting *Plot->Save defaults* and overwriting the *Defaults.agr* file. Note that *Plot->Reset defaults* will reset the defaults to the original settings. Figure 2-23 shows the resulting plot with the above modifications. Note that plots can be generated in a picture format such as *.png* or *.jpeg* by navigating to *File->Print setup*. At the top of the *Device setup* window, change the device to *.png* for example. In the *Output* section, check that the directory path and filename are suitable. Then, click on the *Print* button and the plot will be saved in *.png* format using the filename set for the plot file.

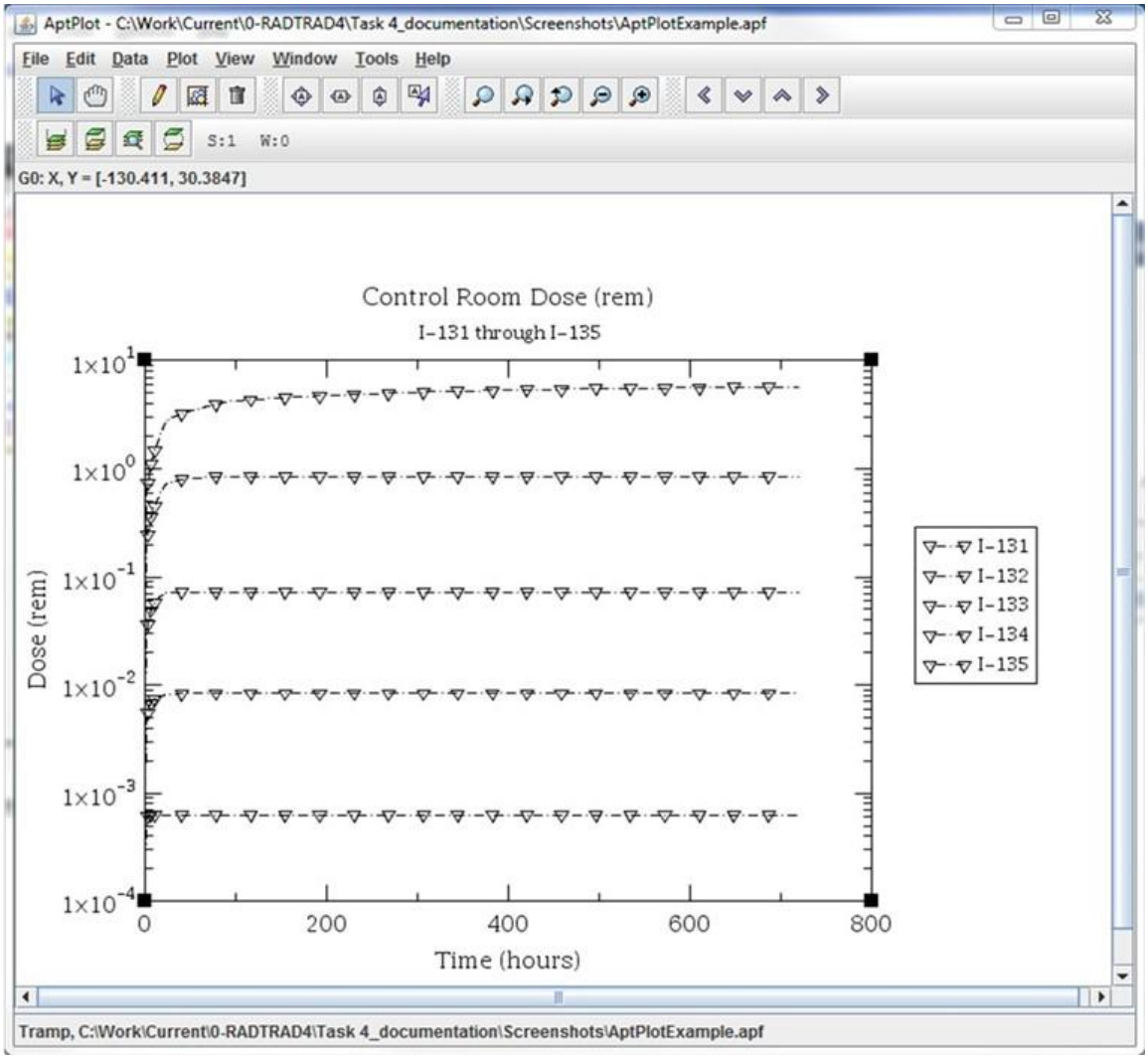


Figure 2-23 Reformatted Control Room Dose Plots for Test23

For those users who wish to use a spreadsheet for data analysis or for plotting, the dose data can be exported. The easiest way is to initiate a new plot session in a comma-delimited format that can be read by Microsoft Excel. This feature is accessed from the *Select EXTDATA Channels* window (Figure 2-18. As an example, set up and apply a filter for the I-131 to I-135 thyroid dose in the control room and select the resulting data channels as done previously.

Then, highlight the data channels and click on the *Export* button at the bottom of the window. A *Save* window will appear. Provide a filename, ending the filename with the *.csv* suffix and select comma separated values (CSV) as the file type (right hand side of the *Save* window). Then, click on *Save* to write the file. Microsoft Excel will read and organize the dose data by column for subsequent use.

2.3 SNAP/RADTRAD Model Development and Modification

Sections 2.1 and 2.2 introduced the SNAP/RADTRAD Model Editor user interface using Test Problem 23 as an example. In this section, the details of building a new model are presented. For this illustration, a model consisting of a simple containment compartment, leakage pathway, source and an environment compartment will be developed.

2.3.1 Model Editor Menus

The commands available in the Model Editor are typical of Windows programs. Across the top of the Model Editor, the *File*, *Edit*, *Tools*, *Window*, and *Help* commands are presented. Table 2-2 describes the commands associated with each of these menu items.

Table 2-2 Summary of Model Editor Menu Commands

Menu Command	Description
File Commands	
File->New	Creates a new model. A Select Model Type menu appears with available models listed. The SNAP/RADTRAD user picks *RADTRAD* and clicks on the *OK* button.
File->Open	Opens a previously developed model (*.med file*). The user navigates to the directory where the file is located and selects the file to be opened similar to any Windows program.
File->Open Recent	Allows the user to open a recently used SNAP/RADTRAD model (or AVF file). The user selects the file of interest and it will open in a new Model Editor session.
File->Save	Saves the current model with the same name as in any Windows program.
File->Save As	Saves the file under a new filename. The user navigates to the desired directory location and/or updates the filename and clicks the *Save* button as in any Windows program.
File->Close	Closes the current model. Provides a warning to the user in the case of any unsaved changes made to the model.
File->Close All	Closes multiple open models. Provides a warning to the user in the case of any unsaved changes made to the model.

File->Import	Imports a previously exported RADTRAD model from a set of ASCII or XML input files (see Section 3.2.3). Note that a *.psf* file is an ASCII file with the same input data as the XML formatted *.psx* files.
File->Export	Exports a set of SNAP/RADTRAD XML input files (*.psx*, *.nix*, *.srx*, *.icx*, and *.dfx*) to a directory selected by the user
File->Exit	Exits the Model Editor.
Edit Commands	
Edit->Undo	Reverses previous user inputs to a model similar to most Windows program.
Edit->Redo	Redoes a previous undo command similar to most Windows program.
Edit->Preferences	Allows the user to set various preferences related to fonts, colors, and other Model Editor features.
Edit->Plugin Manager	Opens a dialog listing all of the available SNAP plugins. Toggling the check-box next to each plugin allows for loading and unloading the plugin. This feature is not generally used for SNAP/RADTRAD because the RADTRAD-AC only uses the RADTRAD Plugin.
Tools Commands	
Tools->Check Model	Provides a check of the SNAP/RADTRAD input model. This feature is very useful for model development in SNAP/RADTRAD.
Tools->Submit Job	Submits a model through the job stream and starts the *SNAP Job Status Tool* (see Section 3.2.2).
Tools->Steam Tables	Not used in SNAP/RADTRAD.
Tools->Configuration Tool	Starts the SNAP/RADTRAD *Configuration Tool* used to configure global properties for running RADTRAD under SNAP
Tools->Job Status	Starts the SNAP/RADTRAD *SNAP Job Status* window (see Section 3.2.2).
Tools->Model Note Viewer	Displays model notes. The user can set up and edit notes as part of the model documentation.
Tools->Export to jEdit	Exports a model to the jEdit editing program. This feature requires the installation of jEdit.

Windows Commands	
Windows->Commands	*Scripting commands* window – not used in SNAP/RADTRAD.
Help Commands	
Help->Contents	Link to the SNAP Model Editor manual, which includes information about the RADTRAD Plugin.
Help->Check for Updates	Checks for updates at the APT, Inc. website. Note that computer security settings may inhibit this feature.
Help->Report an Issue	Allows the user to submit Issue Reports on SNAP/RADTRAD directly to APT, Inc. Note that issues related to the RADTRAD-AC should be reported via the SNAP/RADTRAD Forum webpage under the SNAP/RADTRAD Support link on the RAMP website.
Help->About	Provides information on the SNAP GUI and Plugin version, licensing agreements, and contact information. Note that plugin version numbers can be obtained by clicking on the *Plugins* button.

Figure 2-24 shows the icon arrangement and function of each icon in the Model Editor. Of particular interest is the ability to separate the *Navigator*, *Property*, and *View / Dock* windows into separate windows and to also arrange the windows vertically by clicking on the *Single/Multiple Windows Modes* icons shown in Figure 2-24. The remaining icons provide a shortcut to some of the menu commands listed in Table 2-2.

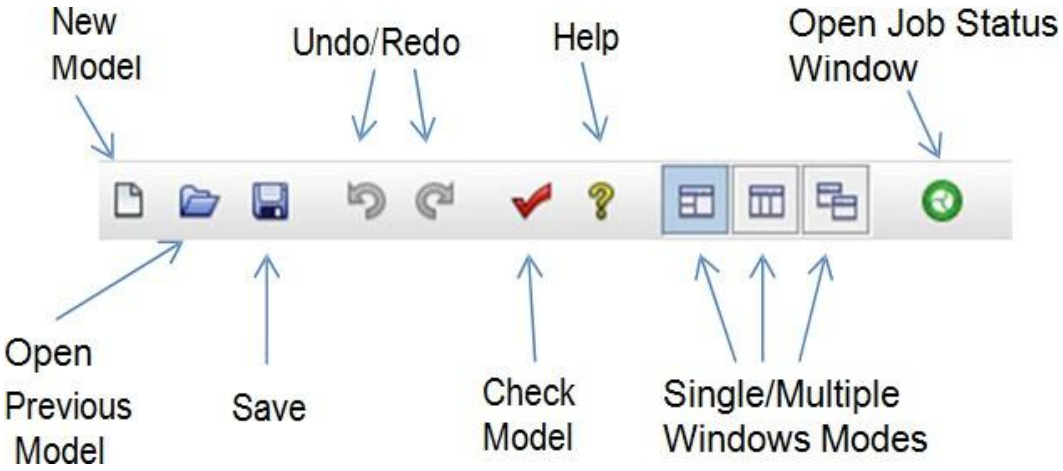


Figure 2-24 Model Editor Tool Bar Icon Description

Figure 2-25 shows the icon arrangement and the function for each icon in the *Navigator* window. Basically, these tools aid the user in navigating component nodes in the *Navigator* window and multiple models in the SNAP GUI.

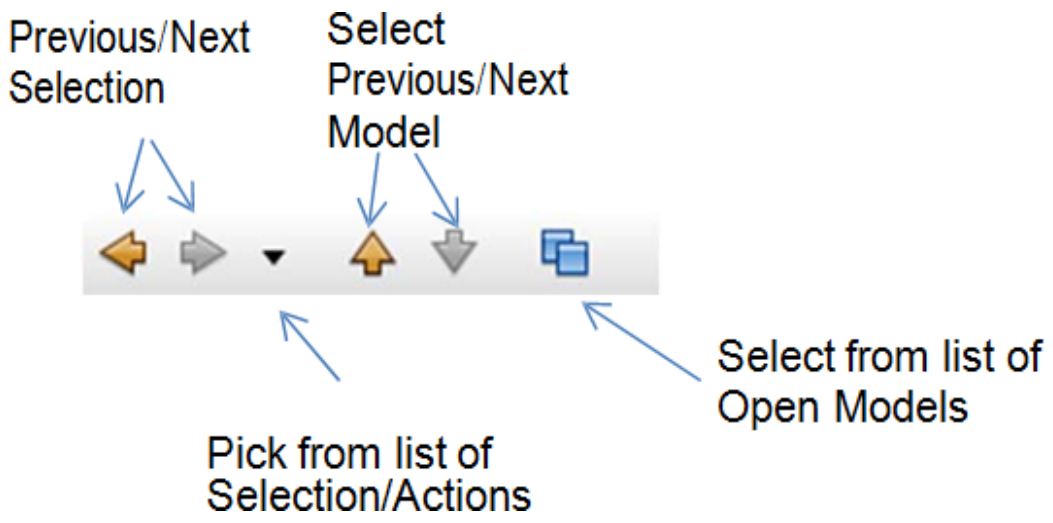


Figure 2-25 Navigator Window Tool Bar Icon Description

2.3.2 Building a SNAP/RADTRAD Model – Component Specification

The first step is to start the SNAP Model Editor and click on *Create a New Model* in the *Welcome* screen (Figure 2-1). Alternately, a new model in SNAP/RADTRAD can also be created by selecting the *File->New* command as noted in Table 2-2. Select *RADTRAD model* in the *Select Model Type* screen and notice that the Model Editor opens with no icons in the *View / Dock* window (similar to Figure 2-2). The basic model nodes are shown in the *Navigator* window. Expand the *Compartment [1]* node using the *Expand* ( ) icon in the *Navigator* window. Highlight (click on) the *Compartment 1 (Environment)* node, so that data fields for this compartment will appear in the *Property* window. Note that an environment compartment is defined by default.

The basic approach to building a SNAP/RADTRAD model is to set up an array of compartments, flow pathways and specify key parameters in the various components of the model. For sources, compartments, and pathways that ultimately appear in the *View / Dock* window, the basic pattern is to highlight (select) the component category (i.e. *Source*, *Compartments* and *Pathways*), right-click on the component category, and select *New* from the menu to add a numbered component to that component category. These steps result in a new model component being created.

A new compartment is added by right-clicking on the *Compartment* node in the *Navigator* window and selecting *New* from the drop-down menu that appears. A new compartment component *Compartment 2* is created. Components are not automatically added to the *View / Dock* window and must be added by the user. The new component (*Compartment 2*) is added to the *View / Dock* window by right-clicking on the *Compartment 2* and selecting *Add to View->Default View* from the drop-down menu. *Compartment 2* now appears in the *View / Dock* window.

The new component (*Compartment 2*) is unnamed. To add a name to the component, type a name (i.e. Containment) in the *Name* text box in the *Property* window. The name will simultaneously appear in both the *Navigator* and *View / Dock* windows [Compartment 2 (Containment)]. Alternately, newly defined components can also be dragged from the *Navigator* window to the *View / Dock* window by clicking on the component of interest and dragging it by holding the left mouse button down and moving the cursor to the *View / Dock* window.

The pre-defined *Environment* compartment is added to the *View / Dock* window in a manner similar to *Compartment 2 (Containment)* above. Right-click on *Compartment 1 (Environment)* and select *Add to View->Default View* or drag the component by clicking on the *Compartment 1 (Environment)* node and dragging it into the *View / Dock* window. The environment compartment will appear in the *View / Dock* window. Note that two dose locations (EAB and LPZ) are automatically specified with the environment compartment.

The next step is to define a flow pathway which is done by right-clicking on the pathway group node (*Pathways [0]*) and selecting *New* from the drop-down menu that appears. Add *Pathway 1* to the *View / Dock* window by right-clicking on *Pathway 1* and then selecting *Add to View->Default View* or drag the component by clicking on the *Pathway 1* node and dragging it into the *View / Dock* window. The flow pathway should be named by entering a suitable name in the *Name* text box in the *Property* window (i.e. *Leakage*).

Similarly, a source can be added by right-clicking on the *Sources* node in the *Navigator* window (*Sources [0*]) and selecting *New* from the drop-down menu that appears. After naming the component (i.e. *Fuel Release*), the component can be added to the *View / Dock* window in the same manner as used above for the compartments and flow pathways.

At this point, the user can see that a pattern is emerging. Each input group has an associated group node where components within that group can be defined and added to the *Navigator* window. Figure 2-26 displays the *Navigator* window for the components added in the previous steps above. The component nodes that can be added as part of a model are: *Sources*, *Compartments*, and *Pathways*. The nodes for *Dose Locations*, *Natural Deposition*, *Filters*, *Sprays*, and *X/Q Tables* are not drawn, but are defined in the same manner as compartments,

pathways, and sources by right-clicking on the component group node and selecting *New* from the drop-down menu that appears.

The user has developed a new model consisting of a source, a compartment representing the containment, a leakage pathway and an environmental compartment. Also, this new model was added to the *View / Dock* window by either dragging the new component nodes to the *View / Dock* window or right-clicking on the new component nodes, then selecting *Add to View->Default View*. Figure 2-27 shows the *View / Dock* window with the new model's components. Additionally, once the components are added to the *View / Dock* window, they can be moved around by the user for presentation clarity. Make sure the *Selection Tool* ( ) icon is activated before selecting a component icon to be moved in the *View / Dock* window. Features common to most Windows-based programs are available to aid the user in editing and arranging icons. The function of each icon can be determined by hovering the mouse pointer above the icon of interest. This action should cause a text pop-up to appear with a short statement of the function of that icon. The tools and features most commonly used in SNAP/RADTRAD are illustrated in Section 2.3.4.

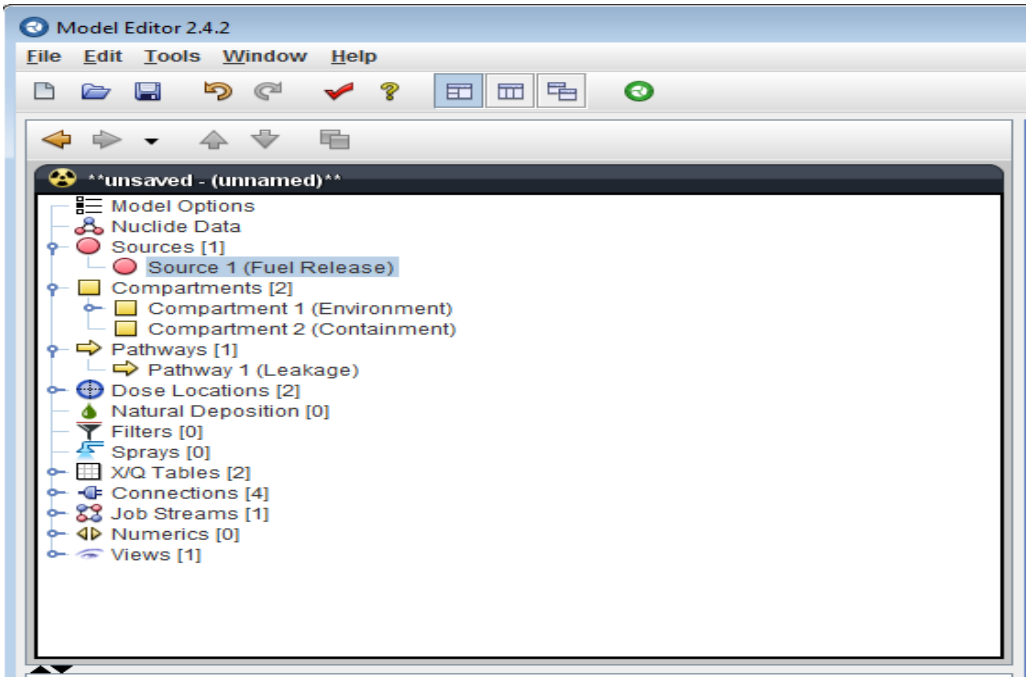


Figure 2-26 Navigator Window with Newly Added Model Components

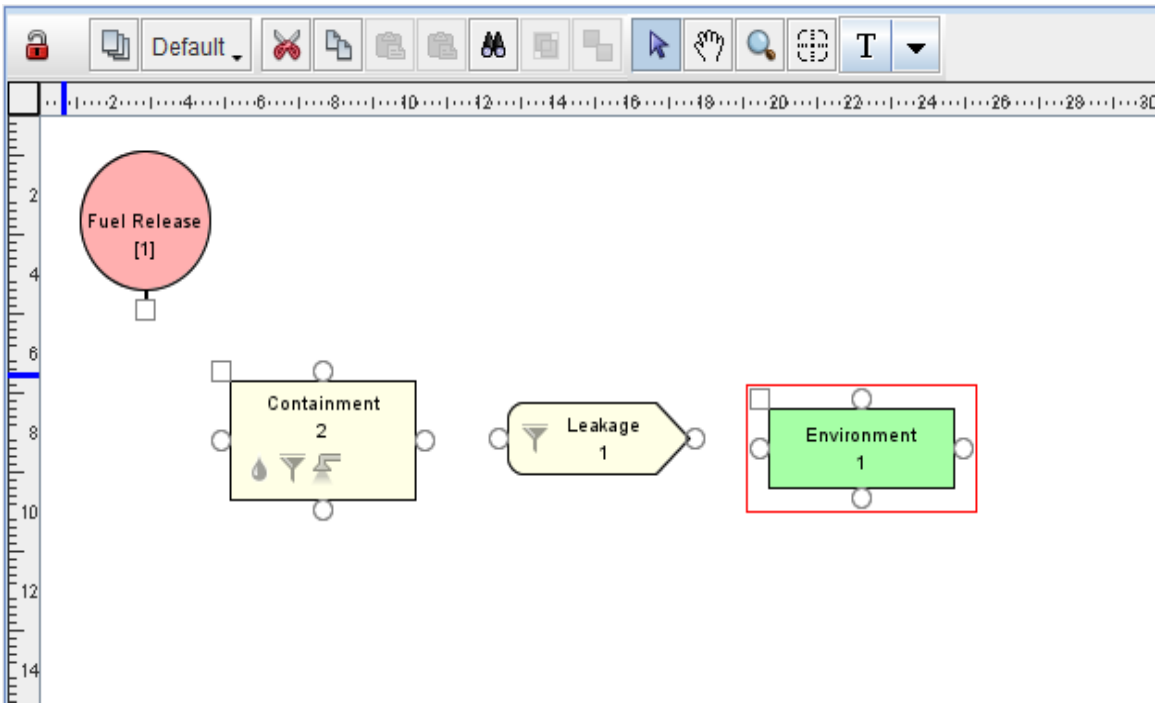
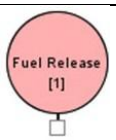
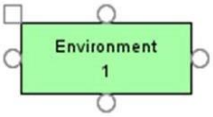


Figure 2-27 View / Dock Window for 4-Node Model (Unconnected)

Table 2-3 shows all of the icons which are available in the *View / Dock* window with a description of each icon. All of the icons for the compartments, sources and pathways have connection points for connecting flow pathways and source components to compartment components as illustrated in Figure 2-27. The number in the different icons in Figure 2-27 are the component numbers (i.e. the number of *Compartments*, *Pathways*, and *Sources*), which are generally consecutive in SNAP/RADTRAD models.

One feature that the user should be aware of is the orientation feature for flow pathway icons. In Figure 2-27, the orientation is pointing right; however, the orientation can be changed to pointing up, pointing down, or pointing left by right-clicking on the flow pathway icon and selecting *Drawn Orientation* from the drop-down menu that appears and then pick the desired orientation.

Table 2-3 Icons Used in the View / Dock Window

View / Dock Window Icons	Description
 Compartment Icon	Flow pathway connection point indicated by small circles on each edge. Small square at the upper-left corner is a source connection point.
 Source Icon	Small square at the lower edge is a source connection point to a compartment.
 Flow Pathway Icon	Flow pathway connection point indicated by small circles on each side.
 Environment Icon	Flow pathway connection point indicated by small circles on each edge. Small square at the upper-left corner is a source connection point.

	Icon denoting that natural deposition is active in a component (grayed-out indicates inactive).
	Icon denoting that a filter is defined in a component (grayed- out indicates no filter).
	Icon denoting that a spray is defined in a component (grayed-out indicates no spray).

The next step is to connect the components using the *Connection Tool* (⊞) icon shown in the *View / Dock* window tool bar (see Section 2.3.4). Connection points for the various icons are shown in Figure 2-27. These connection points are indicated by circles and squares on the periphery of the icons. The first step is to click on the *Connection Tool* (⊞) or (cross hairs) icon in the *View / Dock* window tool bar, which activates the connection tool. Then for compartment to flow pathway connections, click on the connection point (circle) on the edge of the compartment to be connected and drag holding the left mouse button down to the desired connection point (circle) on the flow pathway icon and release the button. The procedure is the same for the source to compartment connections except the connection points are denoted by squares. Note that square connection points can only be connect to other square connection points and likewise circle connection points to only other circle connection points. Figure 2-28 shows the model with the connections made.

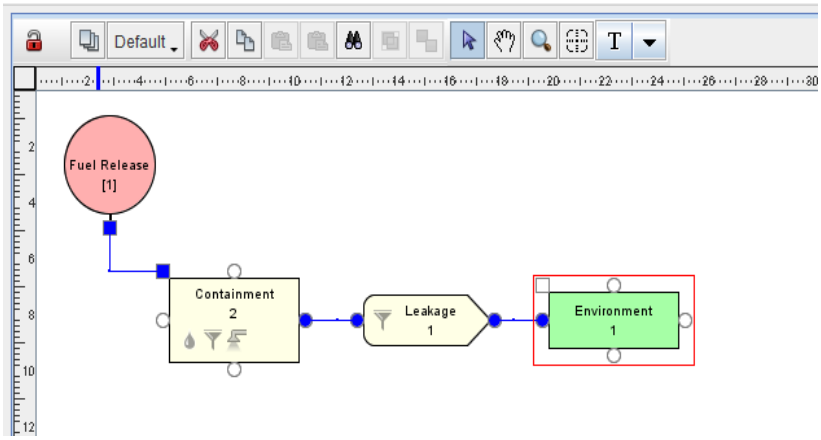


Figure 2-28 View / Dock Window for 4-Node Model (Connected)

Figure 2-29 shows the expanded node view of the *Navigator* window corresponding to all the components modeled in Figure 2-28. Basically, it is an expanded node view of the schematic representation shown in Figure 2-26. Users should get into the habit of naming the various

components of their models. This practice will help avoid errors, particularly as models get more complicated.

Figure 2-29 Navigator Window with all Nodes Expanded

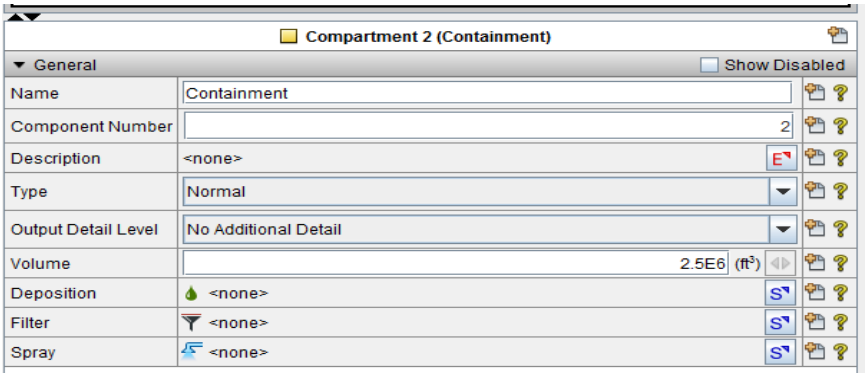
2.3.3 Building a SNAP/RADTRAD Model – Input Specification

Input specification is the next step in developing a SNAP/RADTRAD model. The Model Editor design basically guides the user through the various input parameters required. Clicking on any of the defined compartments presents a list of input data that needs to be specified in the *Property* window. Also, an important feature in SNAP/RADTRAD is the ability to check the model using the *Check Model* feature which is found by navigating to *Tools->Check Model*.

This illustration will start by completing the input for *Compartment 2 (Containment)* shown in Figure 2-28. The volume of this compartment will be set to 2.5E+06 ft^3. Note that the default units of the Model Editor are in SI. To switch units to British units, right-click on the black bar in the *Navigator* window, select *Engineering Units->Britis*h from the drop-down menu to change the units. Figure 2-30 shows the location of the black bar and the accompanying drop-down menu. Once the desired units are selected, click on the *Compartment 2 (Containment)* icon in the *View / Dock* window or in the *Navigator* window to open the *Compartment 2 (Containment)*

Property window. Enter *2.5E6* in the *Volum*e text box in the *Property* window. Also check that the *Compartment Type* text box is set to *Normal*. Other compartment types are discussed in Table 2-8. Figure 2-31 shows the *Property* window with the volume set to *2.5E6*. Note that deposition, filter, and sprays models are not used.

Figure 2-30 Navigator Window with the Balck Bar Menu for the Engineering Units Selection



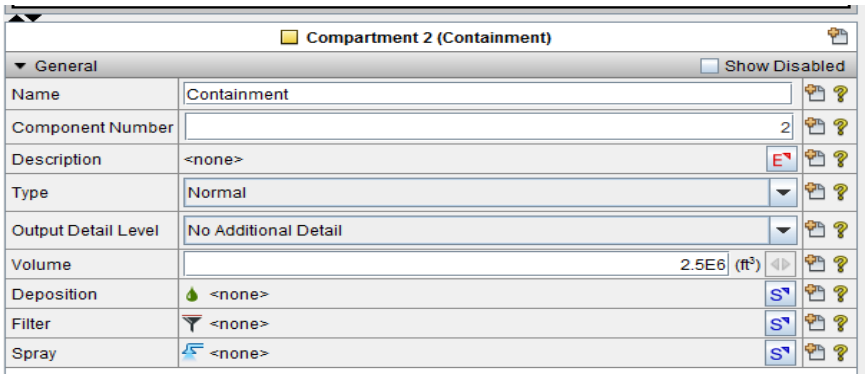


Figure 2-31 Property Window with Volume Entry for Compartment 2 (Containment)

Input for the flow pathway involves a data entry table to capture the time dependence of the assumed containment leakage rate of 0.1 percent per day (%/day). The first step is to change the *Pathway Type* text box in the *Property* window from *Piping* (default) to *Air leakage* (typically used for containments). Next, specify a leakage rate by clicking on the *Custom Editors* ( ) icon

adjacent to the *Leakage Rate* text box to open the *Editing Leakage Rate* window Figure 2-32. A data entry table window will open, which is one of the most common ways to specify input entries in SNAP/RADTRAD.

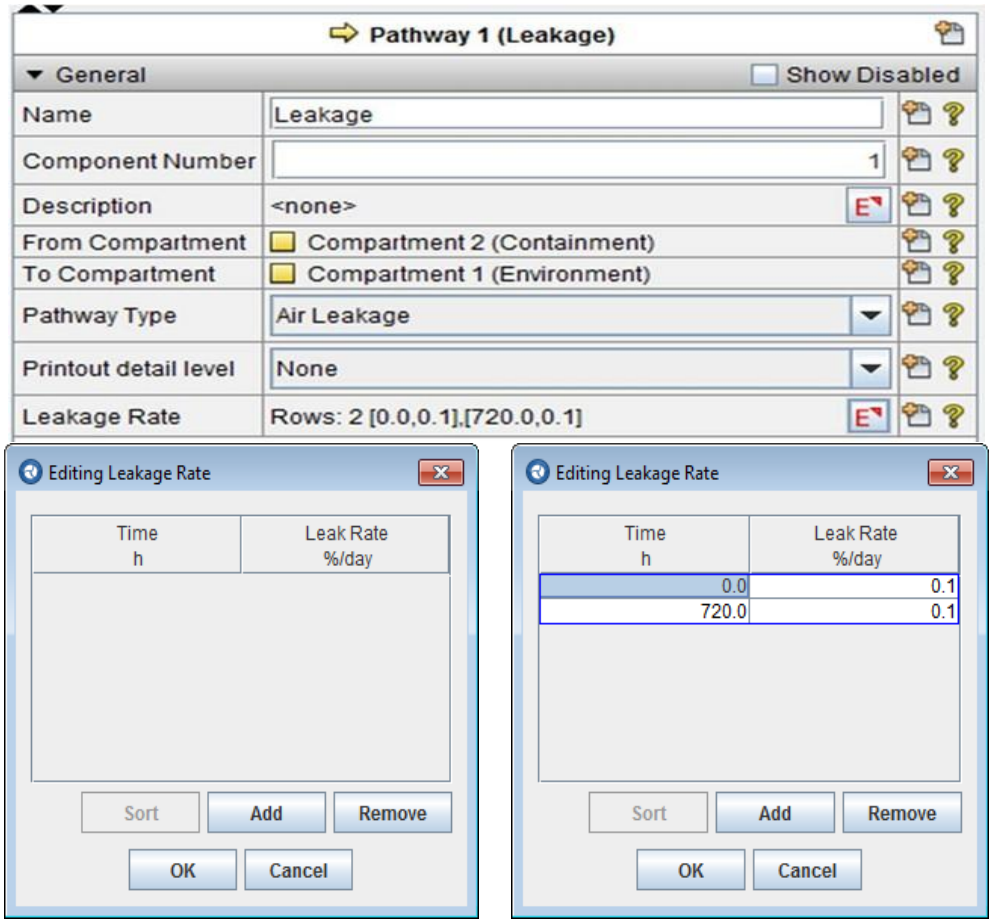


Figure 2-32 Pathway Input Windows for Sample Problem

The user can click on the *Add* button and add a leakage rate of 0.1 %/day for 0 to 720 hrs. Two rows will be needed in this instance. Users should be aware that there are several ways of entering the data using the *Custom Editors* ( ) icon and the edit table features in SNAP/RADTRAD. Some users prefer to set up the number of rows needed for all the data prior to entering the time and leakage rate data (e.g. select the *Add* button twice for this entry). While other users prefer to enter one row of data at a time before adding another row to the table.

When using the second method, users should note that if a cell in an existing row is highlighted then the *Add* button will add the row before the existing row in the table. Likewise, if there is no cell highlighted in a row and the *Add* button is selected then the row will appear as the last entry row on the table. The user should also note that when new row is added the row will contain

"*Unknown*" in the data cells to be entered by the user. To enter data into the newly created cell the user should select the cell with the mouse and enter the data. The *Tab* button on the keyboard allows the user to move from cell to cell without selecting the cell with the mouse.

Data initially entered into a cell will appear in red until the user selects the *Enter* or the *Tab* key on the keyboard to move to the next cell in the row. Finally, the SNAP Model Editor also allows the user to sort data entered out of sequential order by selecting the *Sort* button on the bottom of the *Editing Leakage Rate* window (Figure 2-32). To delete a row, highlight the row to be deleted and click on the *Remove* button.

The next step is to specify the X/Q tables. The X/Q values used for this illustration are listed in Table 2-4 and the approach is basically the same as that used for the data table entry for the flow pathway. The first step is to click on the *Expand* ( ) icon next to the *X/Q Tables* node in the *Navigator* window, then click on *X/Q Table 1 (Exclusion Area Boundary)* node. In

the *Property* window for the *X/Q Table 1 (Exclusion Area Boundary)* click on the *Custom Editors* ( ) icon adjacent to the *X/Q Table* text box to open the *Editing X/Q Table* window Figure 2-33. As in the case of the *Editing Leakage Rate* window described above, the user can enter X/Q values from Table 2-4 in the *Editing X/Q Table* window. Using the *Add* and *Remove* buttons, the X/Q values for the EAB and LPZ can be completed by the user. With version 5.1.0 and later of RADTRAD, users can specify the timing option for the X/Q tables if Regulatory Guide Revision is set to Rev 1 in the model options. This can be done by clicking on the X/Q Table main section (not the individual table) and checking the box next to X/Q Time Option. A drop-down menu will become available and then the option for Time or Duration can be picked. The Time option remains as the figure shows below. The Duration option will instead set the duration of time that the specified X/Q value will be used but the duration will not be linked to a specific problem time. When this option is picked, RADTRAD-AC picks the problem time to use the X/Q values depending on when the worst two-hour dose occurs for each compartment. The highest or worst X/Q value in table will be used at the time of the worst two-hour dose. If the duration of the highest or worst X/Q value is longer than 2 hours, then the remaining time is split evenly before and after the worst two-hour period. The remaining X/Q values and durations are used in descending order of the value. If the total duration time listed in the X/Q tables do not sum up to the total problem time, then the smallest X/Q value is used for the remainder of the time. The output will show the times that the X/Q values are used when this option is chosen. Figure 2-33 also shows the completed *Editing X/Q Table* windows.

Table 2-4 Sample Problem X/Q Values

Time Interval (hrs)	X/Q Value by Location (sec/m^3)	
	EAB	LPZ
0 – 2	1.4E-04	4.5E-05
2 – 8		2.39E-05
8 – 24		1.29E-05
24 – 96		5.49E-06
96 – 720		1.61E-06

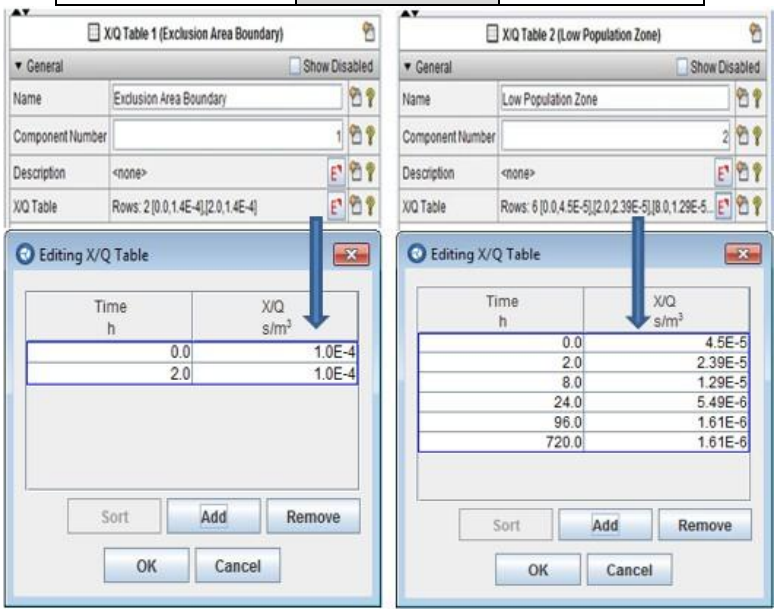


Figure 2-33 X/Q Input Tables for EAB (Left) and LPZ (Right)

The final item to be completed is the source term specification. The source term specification consists of two parts. The first part is to specify the radionuclide inventory in the fuel or reactor coolant and the second is the source or release fraction scenario specific to the accident type. Both combine to generate the radionuclide inventory to determine an overall source term. Additionally, there is also the setting for core power in the *Model Options* node that is used to determine the radionuclide inventory.

There are two sample default core inventory libraries (PWR and BWR) from Tables 1.4.3.2-2 and 1.4.3.2-3 of NUREG/CR-6604, which are not editable by the user.

- PWR – normalized Methods for Estimation of Leakages and Consequences of Releases (MELCOR) / Accident Consequence Code System (MACCS) sample 3412 megawatt thermal (MWth) PWR core inventory (60 nuclides).
- BWR – normalized MELCOR/MACCS sample 3578 MWth BWR core inventory (60 nuclides).

To view and access these sample default core inventory libraries in SNAP/RADTRAD, left click on *Nuclide Data* node in the *Navigator* window and locate the *Total Inventories* text box in the *Property* window. Select the *Custom Editors* ( ) icon adjacent to the *Total Inventories* text box to open the *Editing Total Inventories* Window Figure 2-34. The basic editing features for the *Edit Total Inventories* window is also shown in Figure 2-34. These features can be used to either edit an existing file or specify a new inventory file. For example, the PWR inventory file can be duplicated by selecting the PWR inventory and then clicking on the *Copy Existing File* icon which will make a duplicate and append a number to the file that can then be renamed by the user. Once a copy is made, the data becomes editable. Nuclides can be added, deleted, and rearranged using the *Nuclide Editing Tools* shown in Figure 2-34. In addition, nuclide files can be exported and imported. The user should note that values in the *Inventory (Ci)* column will appear as "*Unknown*" until the plant power lever is entered as described below.

For this illustration, the generic PWR inventory with a core power level of 3637 MWth and the alternative source term release fractions from Regulatory Guide 1.183 (RG 1.183), "Alternative Radiological Source Terms for Evaluating Design Basis Accidents at Nuclear Power Reactors"

[10] will be demonstrated. The source specification steps are as follows:

- Left-click on the *Model Options* node in the *Navigator* window, locate the *Plant Power Level* text box in the *Property* window and set the plant power level to *3637* MWth as shown in Figure 2-35.

- Expand the *Sources [1]* node and left-click on *Source 1 (Fuel Release)*, locate *Source Scenarios* text box in the *Property* window and left-click on the *Custom Editors* ( ) icon. In the *Edit Inventory Scenarios* window, add a new scenario by clicking on the *New* ( ) icon. When the *Select from Total Available Inventories* window opens select *PWR* and click the *OK* button to return to the *Edit Inventory Scenarios* window as shown in Figure 2-36.

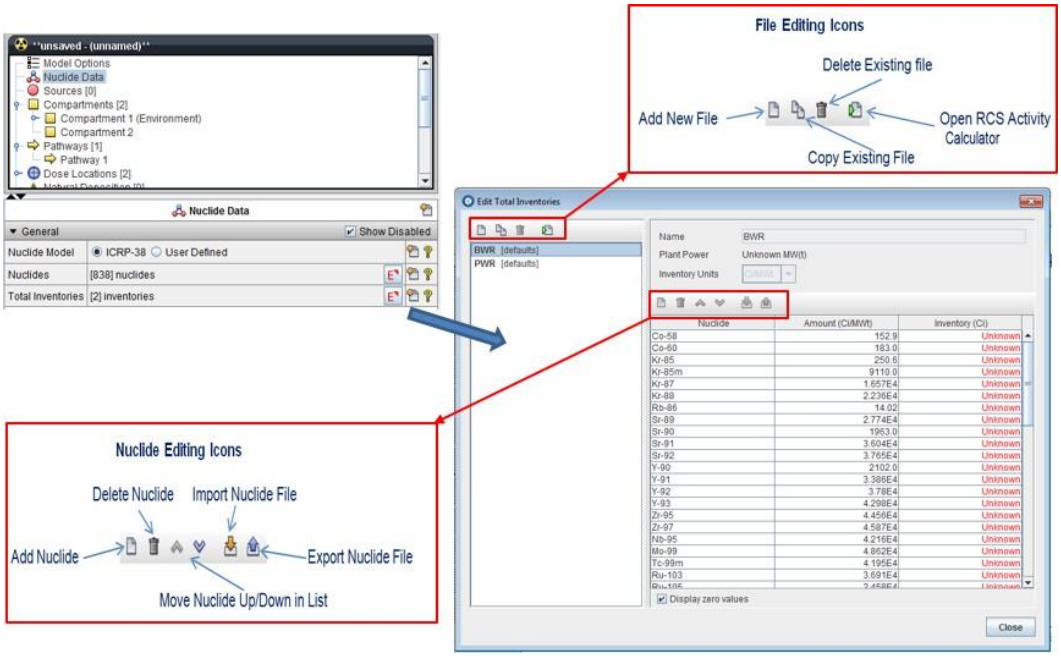


Figure 2-34 SNAP/RADTRAD Edit Total Inventories Window Editing Features

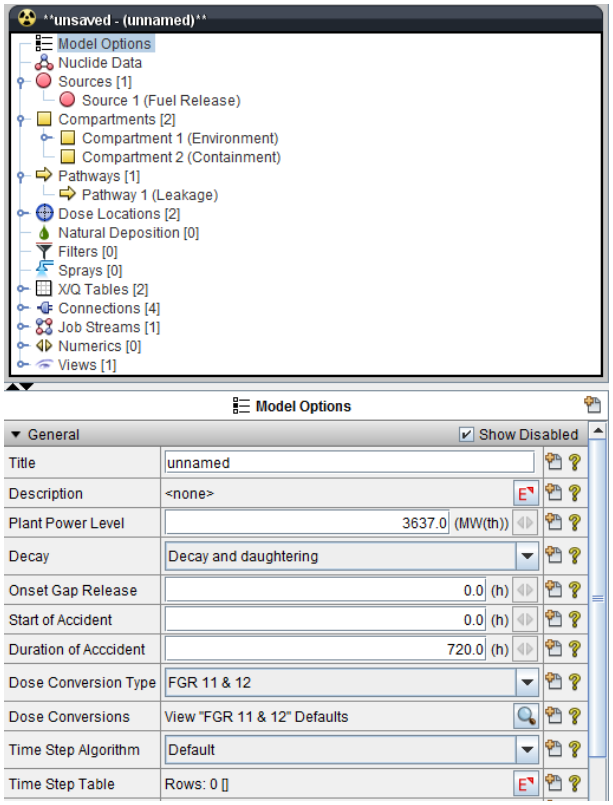


Figure 2-35 Setting the Power Plant Level

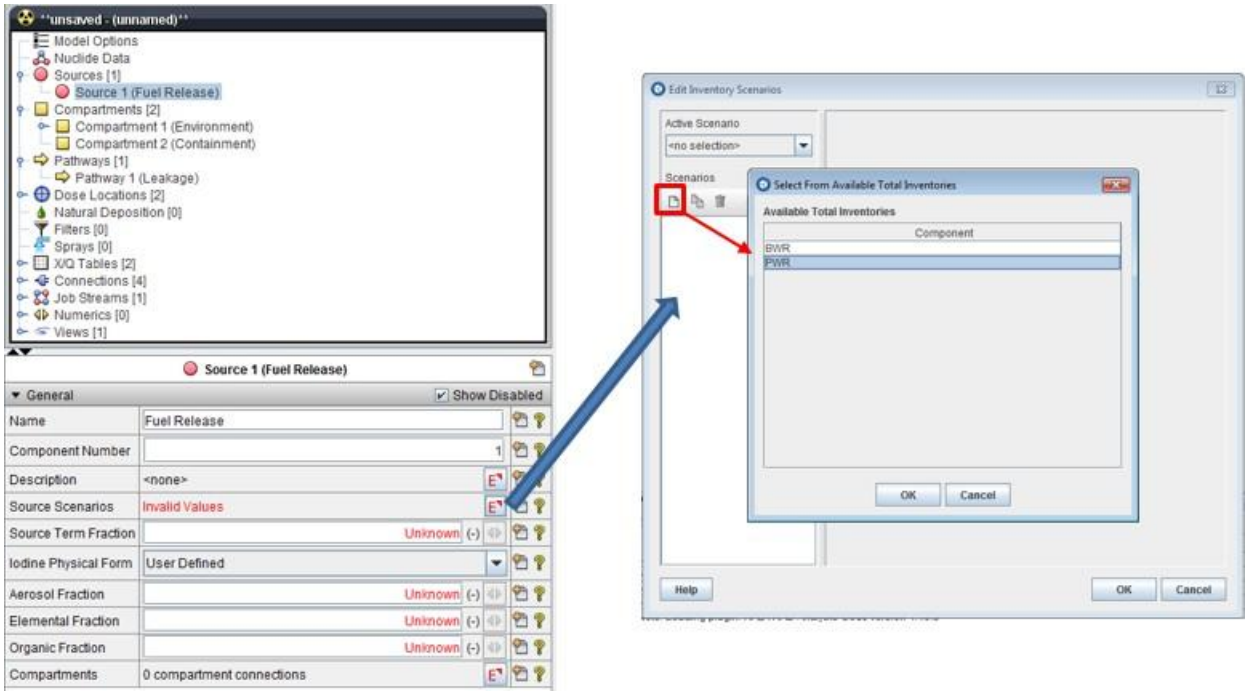


Figure 2-36 Selecting from Available SNAP/RADTRAD Inventories

- Enter the name *PWR Source* in the *Scenario Name* text box on the *Edit Inventory Scenarios* window. Notice that the *Active Scenario* name changes to *PWR Source*. Under the *Accident Parameters* tab, pick the *DBA AST* option under the *Accident Type* drop-down menu and select the *PWR* button under *Defaults Type* (see Figure 2-37).

- At this point, the user should review the data comprising the source term by clicking on each tab in the *Edit Total Inventories* window and noting the progression of the calculations leading to the total source term definition.

- Clicking on the *Adjusted Inventory* tab will list the core inventory based on the generic PWR file as shown in Figure 2-38. Note in Figure 2-38 that there are two columns. The column labeled *Amount* (*Ci)/MWth* lists the activity in curies (*Ci)/MWth* and the column labeled *Inventory* lists the total activity in *Ci*. Note that the inventory is calculated using the values in the *Amount* (*Ci)/MWth* column and the *Plant Power Level* set previously in the *Model Options* node.

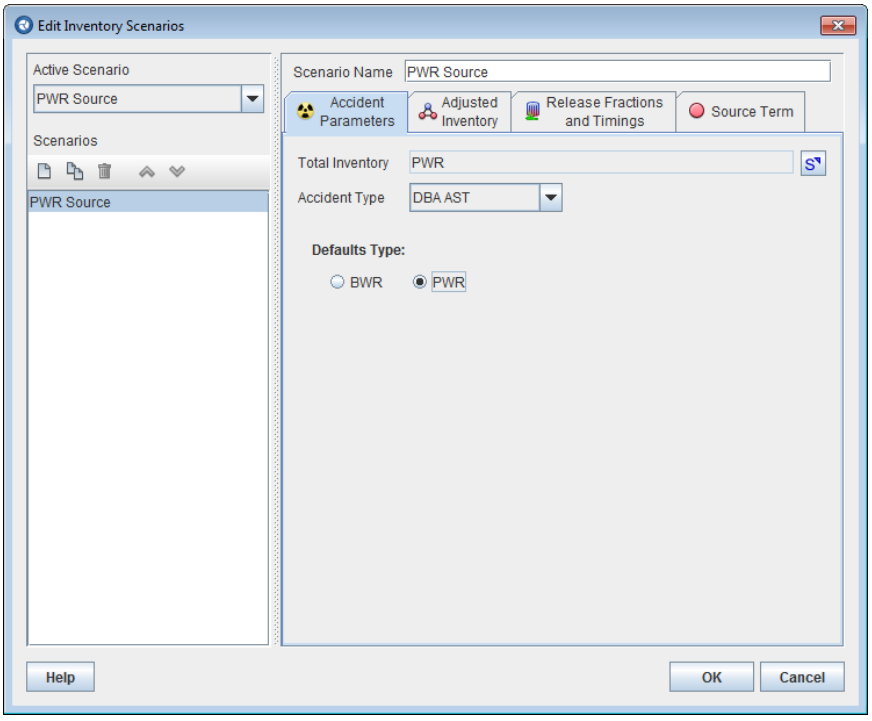


Figure 2-37 Edit Total Inventories Window Accident Parameters Tab

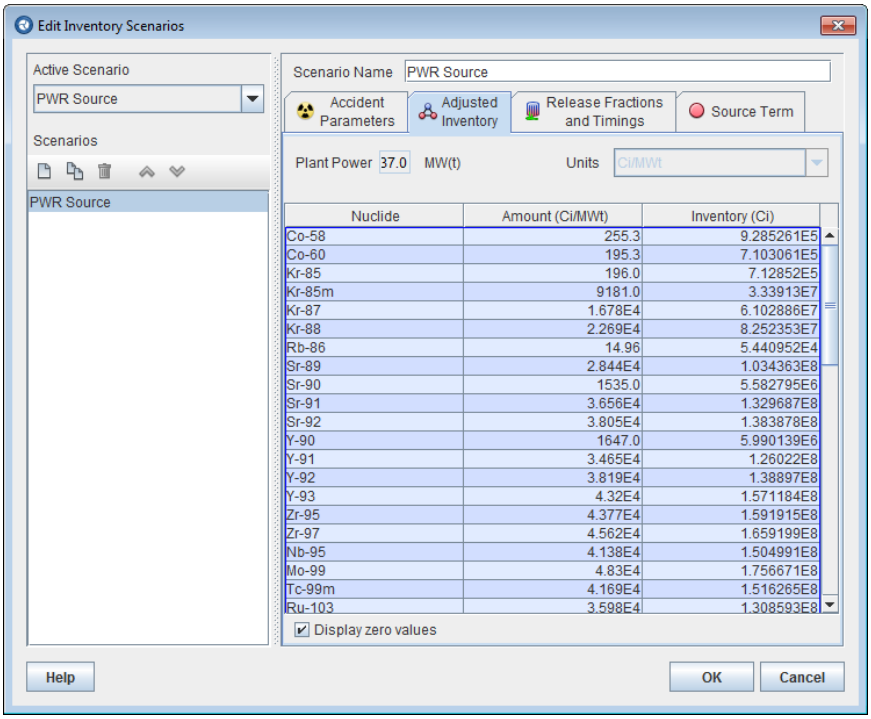


Figure 2-38 Edit Total Inventories Window Adjusted Inventory Tab

- Clicking on the *Release Fractions and Timings* tab displays the release fractions from Table 2 of RG 1.183 (see Section 3.3 for more details on this tab). The *Release Durations (hrs)* are also listed and are from Table 4 of RG 1.183 as shown on Figure 2-39.

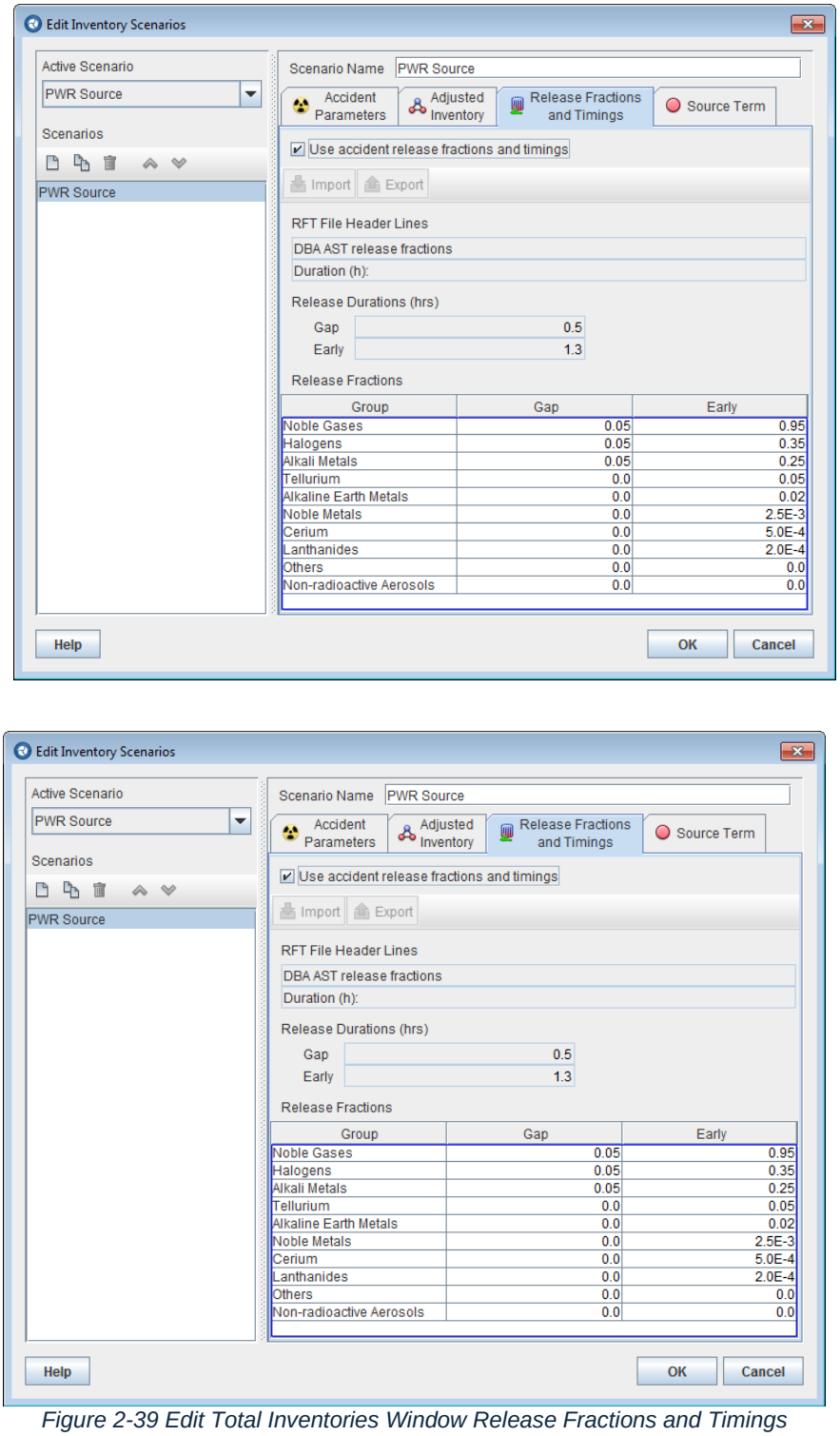


Figure 2-39 Edit Total Inventories Window Release Fractions and Timings

- Finally, clicking on the *Source Term* tab shows the calculated source term associated with the particular nuclide as shown in Figure 2-40. Further discussion of source term modeling in SNAP/RADTRAD is presented in Sections 2.4.2.

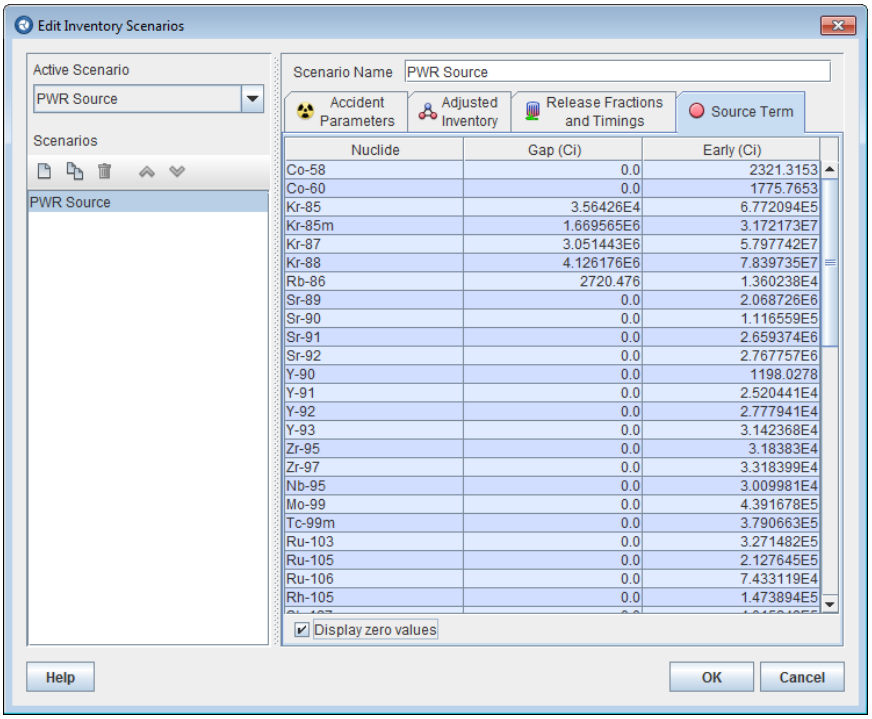


Figure 2-40 Edit Total Inventories Window Source Term Tab

The final step for the source term specification is to set the source term fraction and the iodine chemical forms to the RG 1.183 (NUREG-1465) values. The user sets the source term fraction by entering the value of *1* in the *Source Term Fractio*n text box of the *Property* window for *Source 1 (Fuel Release)* as shown in Figure 2-41. The iodine chemical form is set by using the drop-down menu associated with the *Iodine Physical Form* text box in the *Property* window for *Source 1 (Fuel Release)* as shown in Figure 2-41. The aerosol, elemental and organic iodine fractions are listed but are not editable (grayed-out).

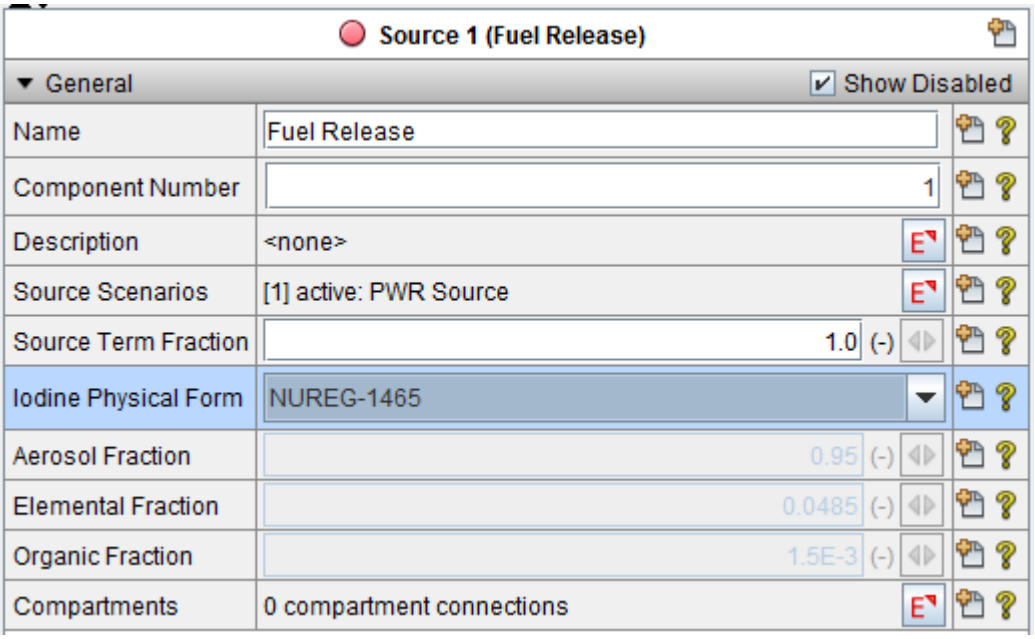


Figure 2-41 Property Window for Source Term Iodine Chemical Form Settings

The user can now run a model check by navigating to *Tools->Check Model* and looking for the notes in the *Message* window in the lower part of the Model Editor indicating that no errors were found as shown in Figure 2-42. There are three icons to the right of the message window used to copy or delete messages.

Figure 2-42 Model Editor Message Window with Icons

If an error is detected, an *Error Report* window appears listing the errors and warning messages as shown in the example *Error Report* window shown in Figure 2-43. The error messages,

which are generally self-explanatory, provide a guide to what needs to be fixed. Note that there are other classifications of messages (*Notes*, *Alerts*, *Warnings*, and *Errors*). Generally, SNAP displays messages in these different classifications automatically. The goal for model development is to have no errors or warnings generated by the SNAP Model Editor. Users should note that models may execute with warnings detected by the Model Editor, but they will not execute with errors. Once error checking is complete and no errors or warnings exist in the model, the user can run the case as described in Section 2.2.2 (*Tools->Submit Job*).

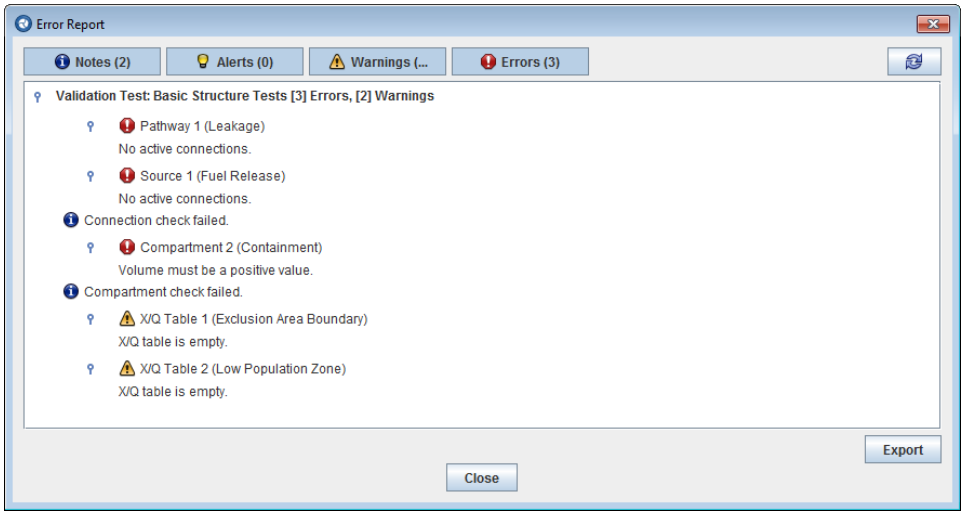


Figure 2-43 Example of a SNAP Model Editor Error Report Window

2.3.4 Building a SNAP/RADTRAD Model – Additional Features

There are a number of features and icons in the *View / Dock* window, as shown in Figure 2-44, that the SNAP/RADTRAD user should become familiar with for general model building. These features include the *Cut* (), *Copy* () and *Paste* () icons which are used by selecting the icon (*Compartment*, *Pathway*, etc.) in the *View / Dock* window to be cut or copied, then clicking on the *Cut* () or *Copy* () icon and pasting it in the *View / Dock* window.

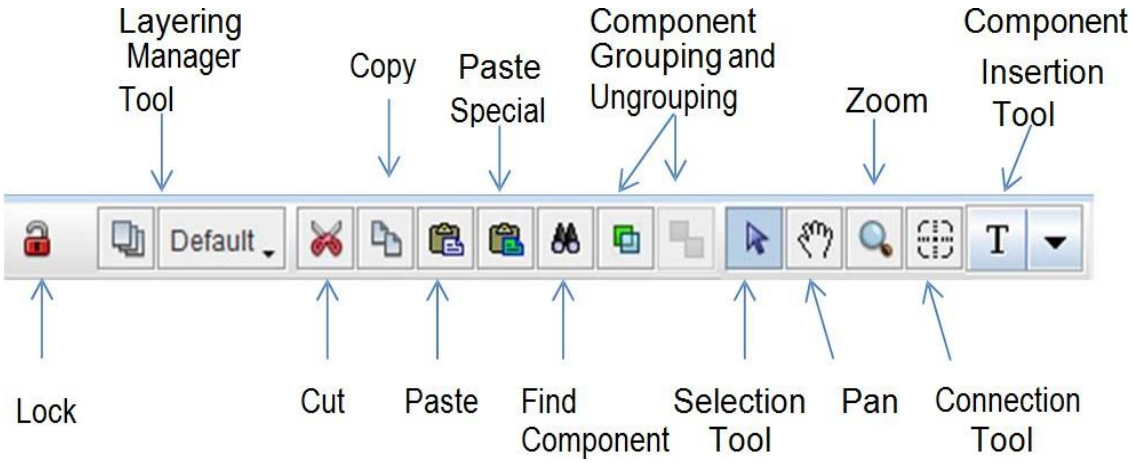
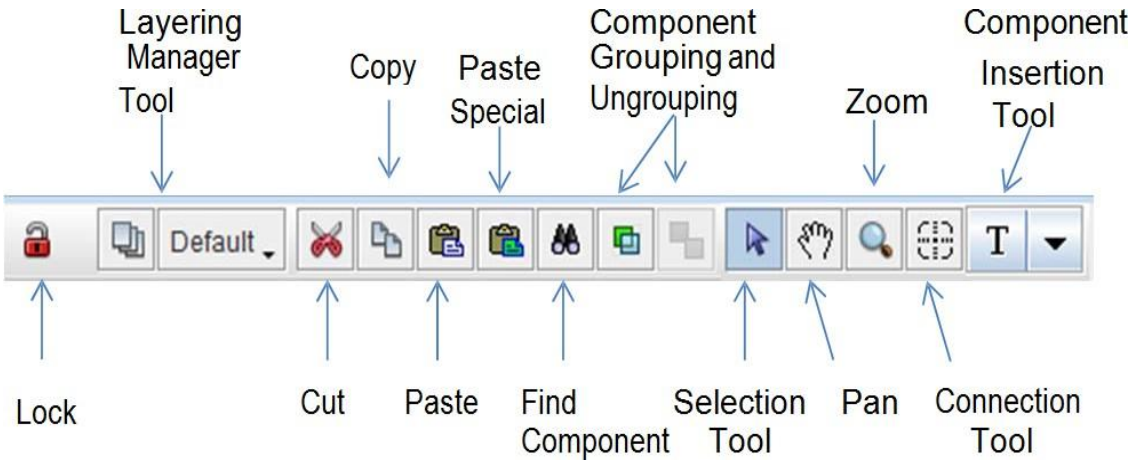


Figure 2-44 View / Dock Window Tool Bar Icons



The *Paste Special* ( ) icon allows the user to paste multiple copies or to control component renumbering. The features of the *Paste Special* ( ) icon are shown in Figure 2-45. The utility of this tool is to maintain unique component numbers in the copy and paste process. To duplicate a component using the *Copy* ( ) icon and *Paste Special* ( ) icon, confirm

the *Selection Tool* ( ) icon is activated (Figure 2-44) and then click on the component to be duplicated. Click on *Paste Special* ( ) icon and confirm that the numbering offset is selected, a value of 1 for the offset is fine. Then click on the *OK* button and the component will be duplicated.

duplicated. Click on *Paste Special* () icon and confirm that the numbering offset is selected, a value of 1 for the offset is fine. Then click on the *OK* button and the component will be duplicated.

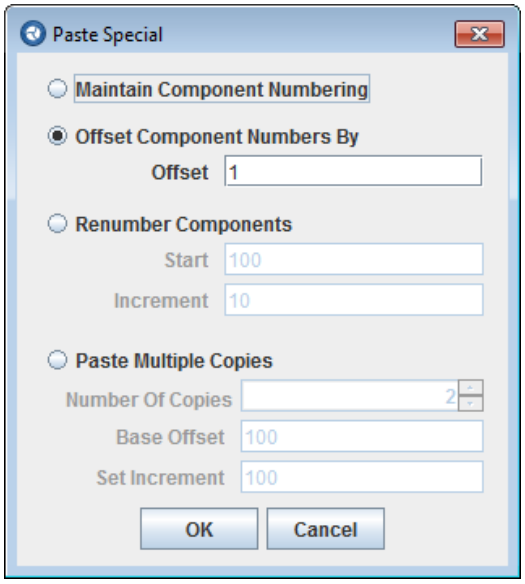


Figure 2-45 Features of the Paste Special Window

The *Selection Tool* ( ) icon, as the name implies, allows the selection of icons for copying. This tool needs to be activated as shown in Figure 2-44 to allow components to be selected or moved. A component is moved by clicking on the component and holding the left mouse button down while dragging the component to the desired location. The *Find Component* ( ) icon is used to find a component and it is usually used for large models with tens or hundreds of components and is typically not needed for SNAP/RADTRAD models.

Another very useful feature of SNAP/RADTRAD is the ability to group components (rubber band selection) and move them as a unit. The *Group* ( ) and *Ungroup* ( ) icons appear inactive (grayed out) until a group of components are defined. To define a component group, click the mouse button in an empty area of the *View / Dock* window, then drag the cursor around the group of components to be grouped (rubber banded) together. The *Group* ( ) icon, shown in Figure 2-44, will now become active. Click the *Group* ( ) icon to group the components together and note that the *Ungroup* ( ) icon the *View / Dock* window tool bar will become active. Clicking on the *Ungroup* ( ) icon ungroups the components in the previously defined group.

The *Zoom* ( ) icon is used to zoom in on sections of a model. Clicking on the *Zoom* ( ) icon and then clicking on the background of the *View / Dock* window will magnify the components. Additionally, some useful zoom and sizing features are available when the *Selection Tool* ( ) icon is activated by right-clicking on the *View / Dock* window background and clicking on Zoom in the drop-down menu. Alternately these features are available while the *Zoom* ( ) icon is

active by right-clicking on the *View / Dock* window background. Both methods open the *Zoom and Size* window shown in Figure 2-46

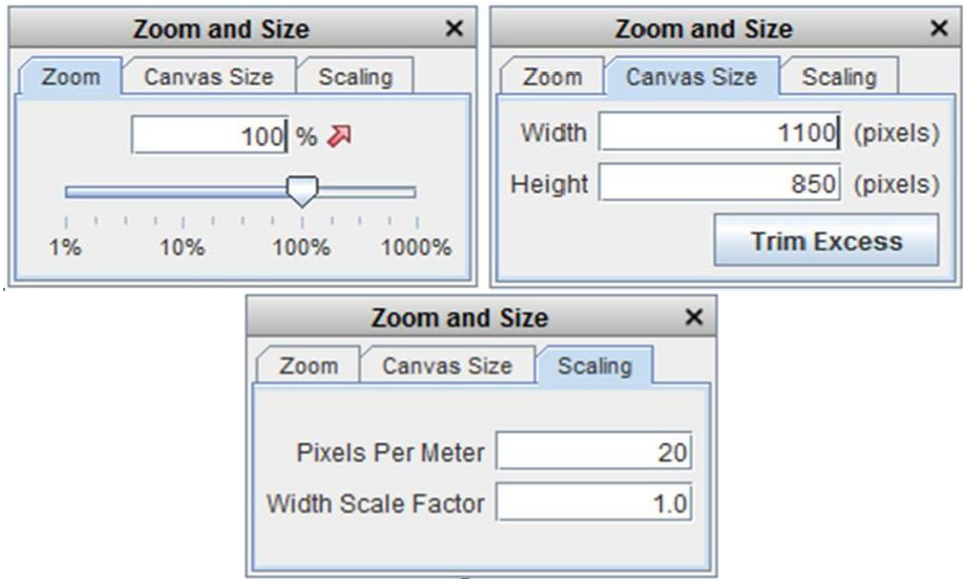


Figure 2-46 Zoom and Size Features

When the *Zoom* tab is activated, the zoom level can be set to any desired value by either using the slider or entering a number in the percent value in the text box. Note that clicking on the *red arrow* ( ) displays a drop-down list of preset values from which the user may make a suitable selection. When the *Canvas Size* tab is active, the width and height of the canvas can be set.

The canvas is the portion of the *View / Dock* window surrounded by a thin border on two sides (bottom and right sides) and the scaling ruler on the remaining two sides of a model as illustrated in Figure 2-47. All component icons are rendered on the canvas and for larger models, sometimes the canvas borders cannot be seen. The *Zoom* ( ) icon can be used to shrink the model and bring the borders into view. Also, if the canvas is larger than the model, clicking on the *Trim Excess* button will shrink the canvas area to fit the model.

In some SNAP models, the scale of icons is of interest to get a sense of perspective particularly for models where plant components are represented. Generally, SNAP/RADTRAD models are represented in a manner similar to a block diagram; however, a plant representation can be drawn using the *Component Insertion* ( ) icon on Figure 2-44.

SNAP/RADTRAD provides the feature of scaling meshes with some of the drawing features available using the *Component Insertion* ( ) icon. The *Component Insertion* ( ) icon allows the insertion of various components and basic drawing shapes into a model representation. Figure

2-48 displays the *Component Insertion* (T) icon menus illustrating the available features. These menus are accessed by clicking on the drop-down arrow.

The features that would be most used in developing a SNAP/RADTRAD model would be the *Compartments*, *Sources* and *Pathways* Insertions. These three features make it easy to build a model by navigating the menus to the component of interest, clicking on that component, then moving the cursor to the *View / Dock* window and clicking again. This approach provides an alternative and is quicker than the approach involving right-clicking on the desired nodes in the *Navigator* window described earlier.

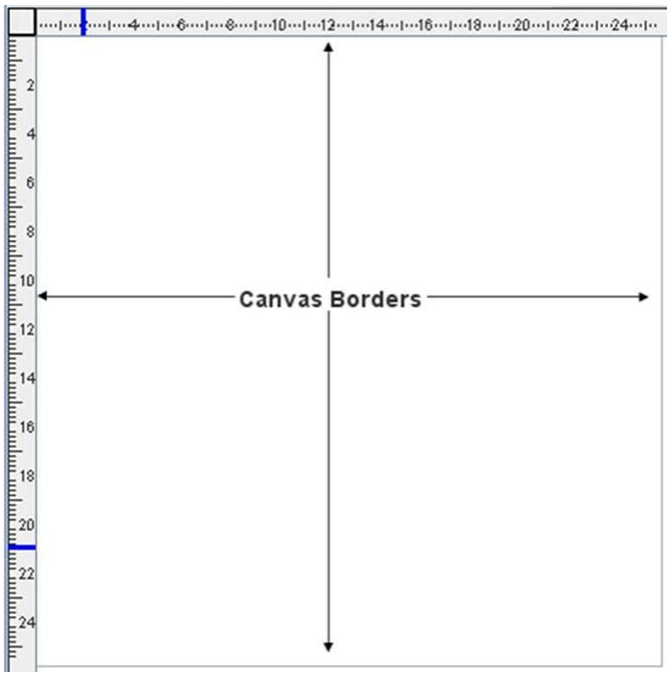


Figure 2-47 View / Dock Window Model Canvas

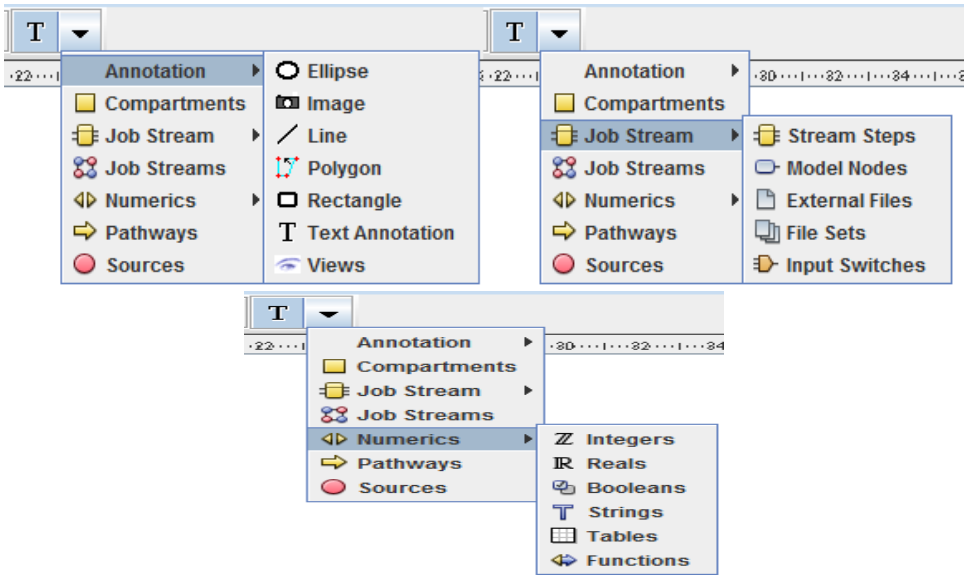


Figure 2-48 Component Insertion Icon Feature Menus

The other feature that is useful is the ability to annotate a model using the *Annotation* feature. This *Annotation* feature allows the user to draw basic shapes and to add descriptive text. The basic approach is to navigate to the annotation feature of interest, select that feature and then click on the *View / Dock* window which will draw the selected icon.

As an example, to draw an ellipse, navigate to *Annotation->Ellipse*, click on *Ellipse* in the menu, then move the cursor to the *View / Dock* window and click in that window to draw the selected shape. Right-clicking on the shape activates a menu that allows various drawing rendering features to be set. These features are typical of Windows-based drawing programs and are not discussed in detail.

The drawing features combined with scaling may be of interest to some users with an artistic tendency. When a new model is initiated, default values are set for the dimensions of the canvas which are a height of 850 pixels and a width of 1100 pixels. These values can be checked in the *Canvas Size* tab in the *Zoom and Size* window. Additionally, the user can enter custom values for the height and width by typing them and selecting the *Enter* key on the keyboard. The default scaling is 20 pixels per meter with a width scale factor of 1.0 which can be checked by clicking on the *Scaling* tab in the *Zoom and Size* window which is shown in Figure 2-46. Dividing the pixel values by the scaling factor yields a height of 42.5 meters and a width of 55 meters. Note that the ruler at the edge of the canvas shows these dimensions. Units are immaterial in this context as the dimensions can be expressed in yards, feet or any other unit. The scaling factor is the number of pixels per unit of length.

Once a suitable scaling is set, scaled drawings representing plant components can be made using the annotation features discussed above. A sample is shown in Figure 2-49 in which a cylinder is scaled to be 100 feet in diameter and 100 feet high.

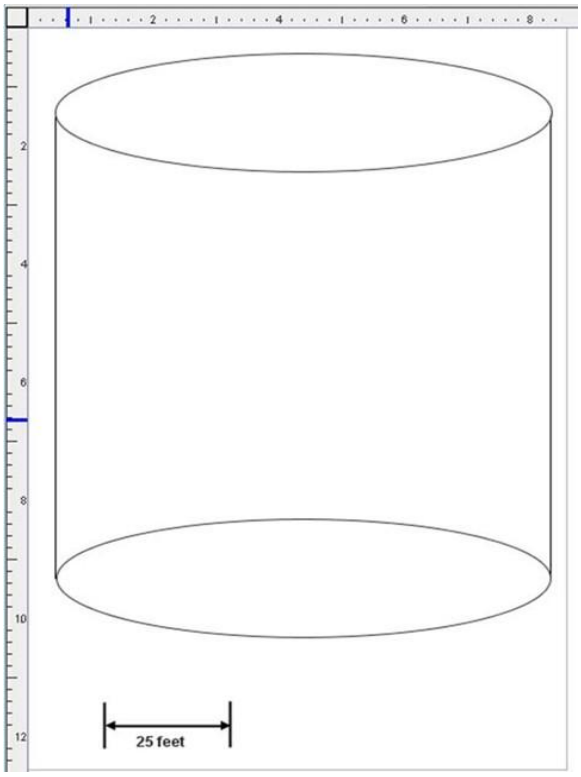


Figure 2-49 Cylinder Drawn using the Annotation Features of SNAP

It is noted that, in general, the icons used to represent various components in a SNAP/RADTRAD model are adequate for model presentation. These features are illustrated for those users who may want to explore and use these features for additional model annotation.

2.4 SNAP/RADTRAD Input Summary

Up to this point, the user has seen the various approaches to specifying input in SNAP/RADTRAD. The first step is to define a component (compartment, flow pathway, dose location, etc. using the right-click and left-click sequences shown earlier) and then specifying the actual input parameters using drop-down menus, text boxes, and input tables. However, up to this point, many of the available input parameters have not been discussed.

Tables 2-5 through 2-15 present a summary of all the inputs that can be specified in a SNAP/RADTRAD model. The organization of the tables follows the group node organization in

the *Navigator* window. Summary explanations of the input requirements are provided. In addition, screenshots are provided to help orient the user and to provide context with the input. Comments are also provided to aid the user in specifying input.

SNAP/RADTRAD input is largely self-explanatory given that the user has some dose analysis background. However, the user should be aware of the relationships among some of the group nodes from an input specification perspective. These relationships are as follows:

- general model options (Table 2-5);
- nuclide data and sources for specifying source terms (Tables 2-6 and 2-7);
- compartments, pathways, natural deposition, filters and sprays (Tables 2-8 through 2-12);
- dose locations (including breathing rates), and X/Q tables (Tables 2-13 and 2-14); and
- remaining inputs (Table 2-15).

The relationships will become obvious as the user works with the SNAP Model Editor. Sometimes the relationship is "one way." As an example, the user can tell which X/Q table is linked to a particular dose location by clicking on one of the *Dose Location* nodes. However, if the user clicks on a particular *X/Q Table* node, the associated dose location is not readily identified. Hence, it is important to name the various model components to keep track of associations.

2.4.1 Model Options

Model options are applied to the overall problem and the use of the default values should be acceptable for most problems, but should be checked by the user. Table 2-5 lists the available inputs for the *Model Options* node in SNAP/RADTRAD (Figure 2-50). Some general comments on model options are listed below:

- *Plant Power Level* needs to be specified as it is used to determine the overall inventory in the source term calculation.
- Either *Decay* or *Decay with daughter* production should be used for most problems.

- The *Onset of Gap Release* and the *Start of Accident*. Note that the values of the *Onset of Gap Release* and the *Start of the Accident* should remain at *0.0*. If values greater than *0.0* are used, the problem time is advanced by the specified time value. Therefore, specifying a value greater than 0.0 causes the lookup values for time-dependent data such as X/Q to be later than it should be. This issue will be addressed in future versions of the RADTRAD-AC.

- Options are provided to reduce the volume of output in the *Output Parameters* and *NRC Output Flags Property* window if the user desires to reduce the volume of output data.

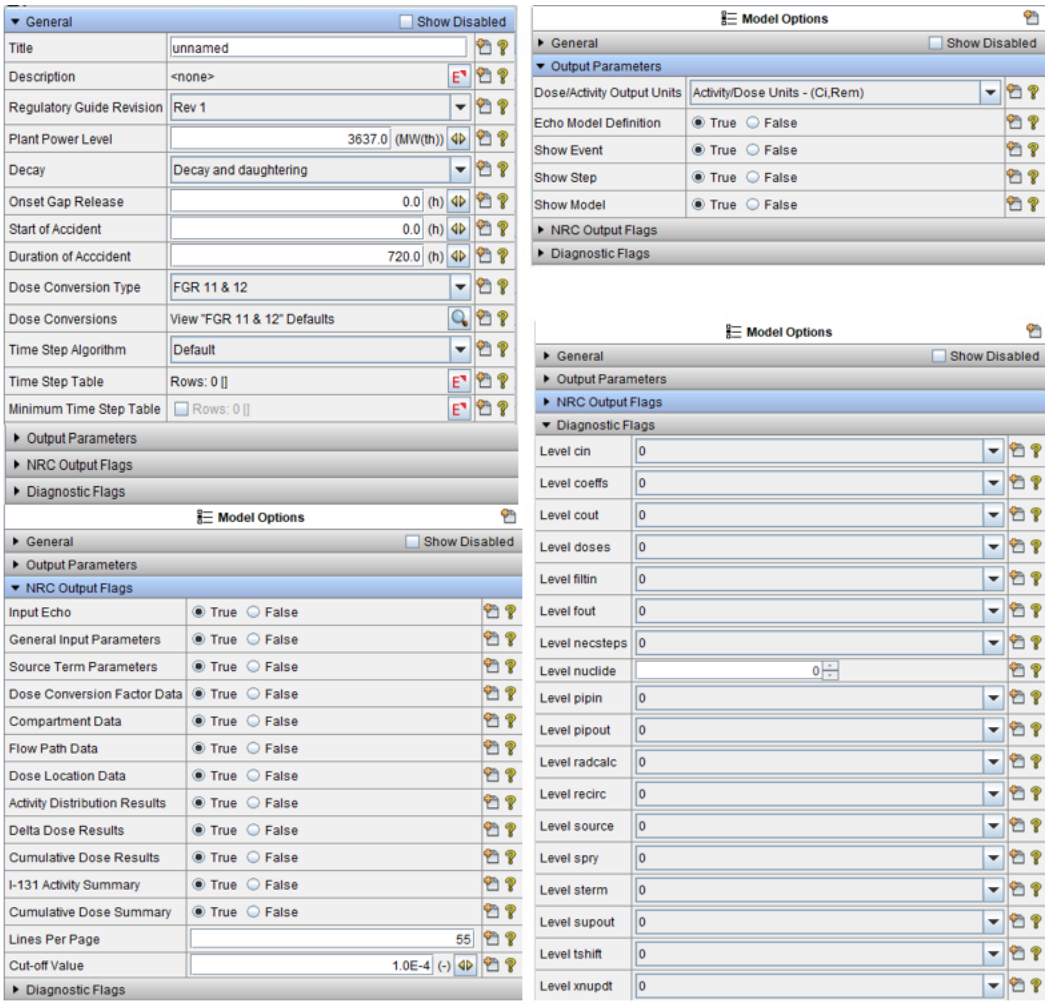


Figure 2-50 Property Window for the Model Options Node

Table 2-5 Summary of SNAP/RADTRAD Input - General Model Options

Input	Description
Model Options – General	
Title	Problem title (optional), specified by user. Typically, it is a good idea to name the problem particularly since multiple models can be accessed in a single SNAP Model Editor session.
Description	Problem description (optional), specified by user. It is a good idea to provide a short problem description for the record.
Regulatory Guide Revision	Input and functionality can differ between the versions of the regulatory guide 1.183. For backwards compatibility, the option to specify which revision is used was added.
Plant Power Level	Core power level in MWt (required).
Decay	Select one of the following options: • *Decay and daughtering* (default) • *No decay or daughtering* • *Decay, no daughtering*
Onset of Gap Release	Specify the time that the gap release from the fuel starts in hours (required). The default is 0.0 hours which is recommended for most SNAP/RADTRAD models.
Start of Accident	Specify the time that the accident starts in hours (required). This parameter is **only** significant if radionuclide decay is being calculated. The default is *0.0* hours which is recommended for most SNAP/RADTRAD models.
Duration of Accident	Specify the time the accident ends in hours (required). The default is *720* hours which is recommended for most SNAP/RADTRAD models.

Dose Conversion Type	Select one of the following options for DCFs: • *User defined* • *FGR 11 & 12* (default) Generally, the default *FGR 11&12* DCFs should be used.
Dose Conversions	Values for FGR 11 & 12 can be displayed. If user-defined is selected, then user can input DCFs.
Time Step Algorithm	Two algorithms are available for controlling the time step: • *Adaptive* • *Default* • *Default with Error Calculation* The *Default* time step algorithm is the original RADTRAD (version 3.10) algorithm implemented with the matrix exponential method [11] (see Section 3.1). The *Adaptive* and the *Default with Error Calculation* time step algorithms were introduced with the RADTRAD-AC (version 4.5) and are discussed in Section 3.2.
Time Step Table	Specified by user. This option allows the user to specify time steps for finer time step resolution for the default time step algorithm and also used to control the generation of output. If this option is not used, SNAP/RADTRAD generates time-dependent output at each time point where there is a change in the time-dependent input data such as X/Q, filtration efficiency, etc. The appropriate time step size is dependent on how quickly radioactivity is added or removed from the system being modelled. If the default time step algorithm is used the user should manually adjust the time step size to make sure the results are independent of the time step size. Finally, the user should note that entering values in this table will override the *Adaptive* time step algorithm if the minimum and maximum time step size are equal (see Section 3.2).
Minimum Time Step Table	The minimum time step table provides a way to limit RADTRAD when setting the time step sizes. In certain occasions, RADTRAD can make time step sizes small enough that can cause run times and output file to increase significantly. This time step table allows the user to have more control and avoid situations where a small time step is not desirable.

Use Full Time Step *(if Time Step Algorithm is Adaptive)*	When *Adaptive* time stepping is enabled, a full step solution is compared to a two half step solution to determine the error. The two half step solution is generally more accurate and is used by default. If *Use Full Time Step* is set to *True*, then the full step solution is used. Note that this option is valid if *Adaptive* time stepping is used or if *Default with Error Calculation* is turned on and the default value is set to *True*.
Plot All Points	When the *Adaptive* time stepping or *Default with Error Calculation* options are enabled, time steps will be repeated in order to calculate error. By default, repeated time steps are not plotted. If *Plot All Points* is enabled, set to *True*, then these points are written to the plot file.The default value is set to *False*.
Max Error *(if Time Step Algorithm is Adaptive)*	When *Adaptive* time stepping is enabled, this option indicates the error threshold used for *Adaptive* time stepping to determine when time step needs to be cut. This value is the fractional error and the default value is set to *1E-3*.
Model Options – Output Parameters	
The following output parameter flags only affect the *casename.out* output file.	
Dose/Activity Output Units	This flag option determines whether the RADTRAD output text files are generated in Curies and Rem based units [traditional RADTRAD units] or SI units (MBq, mSv). The default units are *Curies and Rem*.
Echo Model Definition	The flag options are either *True* or *False* and specified by the user. If set to *False*, the edited summary of the input is suppressed. The default value is set to *True*.
Show Event	This option determines whether the code should write output at each time interval. The flag options are either *True* or *False* and specified by the user. The default value is set to *True*.
Show Step	This option displays each time interval given by the time step control input on the output. The flag options are either *True* or *False* and specified by the user. The user should set this flag to *True* to get the output for all time steps. The default value is set to *True*.
Show Model	This displays the model output at each time interval in the output. The flag options are either *True* or *False* and specified by the user. The default value is set to *True*.
Model Options – NRC Output Flags	
The available flags that control the generation of output to the NRC-formatted output file.	

Note that the bulk of the output is generated for the Delta Dose and Cumulative Dose results.	
Input Echo	This option defines whether the input model will be echoed to the NRC output file. The flag options are either *True* or *False* and the default value is set to *True*.
General Input Parameters	This option defines whether general input parameters are written to the NRC output file. These parameters include the number of compartments, pathways, dose locations, and nuclides. The problem start and end time are also included in the parameters under this option. The flag options are either *True* or *False* and the default value is set to *True*.
Source Term Parameters	This option defines whether the source term parameters, as specified in the inputs, are written to the NRC output file. These parameters include the plant power level, inventory power, the consideration for radioactive decay and daughter production, start time of the release, and the delay time for the release if applicable. The iodine chemical fractions, nuclide group release fractions and timings, and nuclide inventory file are also included in the parameters under this option. The flag options are either *True* or *False* and the default value is set to *True*.
Dose Conversion Factor Data	This option defines whether the DCFs, as specified in the inputs, are written to the NRC output file. These include the nuclide DCFs and decay constants. The flag options are either *True* or *False* and the default value is set to *True*.
Compartment Data	This option defines whether compartment data parameters, as specified in the inputs, are written to the NRC output file. These parameters include the number of compartments and the specific data for each compartment such as the number, name, volume, type, dose location, radionuclide removal features (sprays, recirculation filters, and natural deposition), source input and output from the compartment, and flow path connections. The flag options are either *True* or *False* and the default value is set to *True*.
Flow Path Data	This option defines whether flow pathway data parameters, as specified in the inputs, are written to the NRC output file. These parameters include the number of pathways and the specific data for each pathway such as the number, name, to compartment, from compartment, nuclide transfer mechanism, and output mode. The flag options are either *True* or *False* and the default value is set to *True*.

Dose Location Data	This option defines whether dose location data parameters, as specified in the inputs, are written to the NRC output file. These parameters include the number of dose locations and the specific data for each dose location such as the name (EAB, LPZ, and control room), X/Q data, breathing rate data, and occupancy factor data. The flag options are either *True* or *False* and the default value is set to *True*.
Activity Distribution Results	This option defines whether activity distribution results at the end of each time step are written to the NRC output file. These results include the radionuclide, the group number, and the activity (Ci) in each compartment of the model at the end of the time step. The flag options are either *True* or *False* and the default value is set to *True*.
Delta Dose Results	This option defines whether delta dose results at the end of each time step are written to the NRC output file. These results include the change in doses (inhalation, cloudshine, skin, thyroid, and TEDE) for each radionuclide at the dose locations (EAB, LPZ, and control room) from the previous time step to end of the next time step. The flag options are either *True* or *False* and the default value is set to *True*.
Cumulative Dose Results	This option defines whether cumulative dose results at the end of each time step are written to the NRC output file. These results include the integrated doses (inhalation, cloudshine, skin, thyroid, and TEDE) for each radionuclide and dose location at the end of the time step. The flag options are either *True* or *False* and the default value is set to *True*.
I-131 Activity Summary	This option defines whether an I-131 activity summary table is written to the NRC output file. The results are a table of the I-131 activity (Ci) in each compartment at the end of each time step. The flag options are either *True* or *False* and the default value is set to *True*.
Cumulative Dose Summary	This option defines whether the cumulative dose summary table is written to the NRC output file. The results are a table of the cumulative thyroid, skin, TEDE and whole body doses at each dose location (EAB, LPZ, and control room) at the end of each time step. The flag options are either *True* or *False* and the default value is set to *True*.
Lines Per Page	This option specifies the maximum number of lines per page in the NRC output before inserting a page break. The user can adjust this value with the default value set at *55* lines per page.

Cut-off Value	This option specifies the cut-off value for table data. The nuclide summary tables written at each time step will use this value to determine which nuclides are written: at least one column for the nuclide must have a value greater than the cut-off, or it will not be written for that time step. The default value is set at *1.0E-04*.
Model Options – Diagnostic Flags	
Level – xxx	These flags are used for generating additional output for code debugging using write statements contained in the code subroutines. Increasing the flag value from zero to five will increase the information provided. Higher values indicate a greater amount of output, with a value of zero disabling the diagnostic. The default values for these *Diagnostic Flags* are set to zero. These flags are not generally used for SNAP/RADTRAD analyses. Some additional information regarding these flags can be found in Section 4.2.3 of NUREG/CR-6604.

2.4.1.1 *Dose Conversion Factors*

The DCFs are also managed under the *Model Options* node and relate concentration and dose to organs by nuclide. There are two modes of DCF management, *FGR 11&12* (default)

and *User Defined* DCFs. The user can select either of these two options by selecting the drop-down menu button next to the *Dose Conversion Type* text box as shown in Figure 2-51.

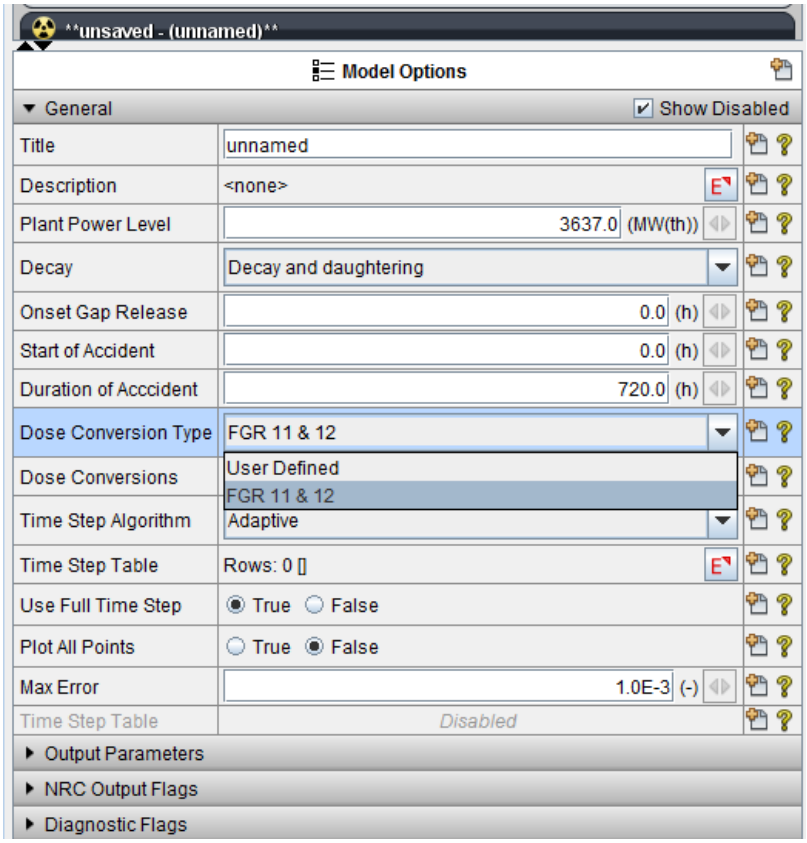


Figure 2-51 Setting Dose Conversion Factors in the Model Option Property Window

When set to *FGR 11&12* (default) option, the RADTRAD plugin automatically matches the nuclides in active scenario inventories (see Section 2.3.3) against an extensive database of DCF values taken from the reference data in FGR 11 and FGR 12. Additionally, the user can view these DCFs by selecting the *View* (🔍) icon next to the *Dose Conversion* text box to open the *Viewing "FGR11&12" Dose Conversion Defaults* window as shown in Figure 2-52. The user should note that icons on the tool bar in Figure 2-52 are "greyed" out indicating that these icons are not active with this option and that the user **cannot** change the FGR 11 and FGR 12 DCF values. Additionally, the user should note that the RADTRAD plugin flags an error when the source inventory contains nuclides that are not in the DCF file (nuclides in the DCF file that are not in a source inventory are not listed as an error). When exporting models, the RADTRAD plugin will only write the DCFs for nuclides found in the active source scenario inventory (in the order defined in the inventory). This helps to preserve the RADTRAD requirement of equivalent nuclides in the DCFs and the source inventory.

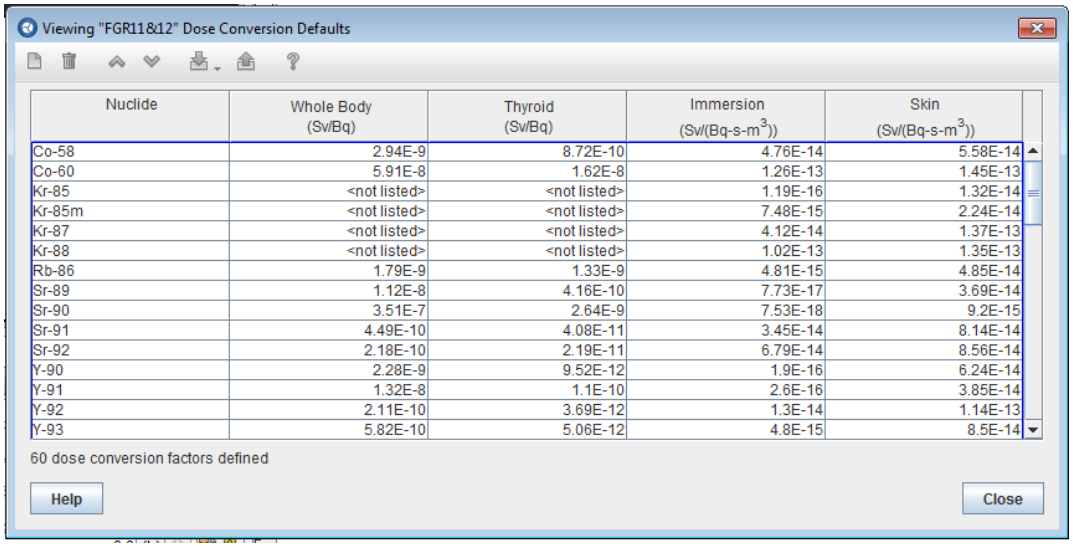


Figure 2-52 Viewing "FGR11&12" Dose Conversion Defaults Window

When the user selects the *User Defined* option, the icon next to the *Dose Conversion* text box changes from the *View* ( ) icon to the *Custom Editors* ( ) icon. The user can select the *Custom Editors* ( ) icon to open the *User-Defined Dose Conversion Factors* window as shown in Figure 2-53.

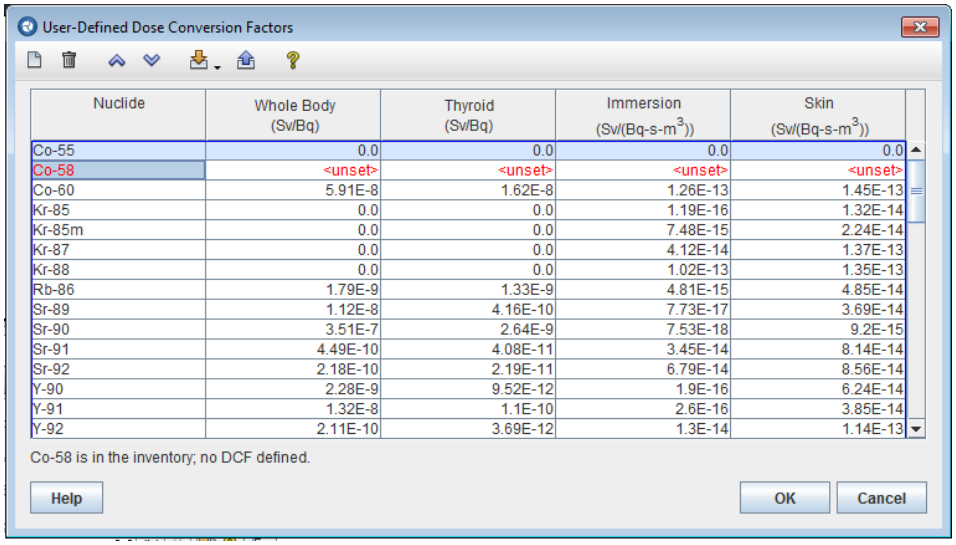


Figure 2-53 User-Defined Dose Conversion Factors Window

As noted in Figure 2-53, the icons on the tool bar are active with this option indicating that these icons can be used to change the DCF values. The names and functions of these icons on the tool bar are the same as those in Figure 2-34, with the exception of the *Import* ( ) icon.

The *Import* () icon on Figure 2-53 provides a drop-down menu option in which the user can select either the *FGR11&12* or *Import from file* option. The *Import from file* option will open a typical Windows file navigator window to allow the user to search for a specific file (the default file type option is **.dfx* and **.inp*). As shown in Figure 2-53 the DCFs are listed in a table format with one nuclide per row. Additionally, nuclides that are not present in a source inventory are highlighted with a blue background and nuclides listed in a source inventory that are not represented in the DCFs are displayed with DCF values listed as *<unset>*. For additional information on DCFs usage in the dose analysis see Section 3.6.

2.4.1.2 *Adaptive Time Step*

Generally, the *Default* time step algorithm is adequate for most RADTRAD calculations. If the user wants to determine if there are time step sensitivities, then two options are available:

1. *Default with Error Calculation*, and
2. *Adaptive* time step.

Error in the dose calculation can be determined by selecting the *Default with Error Calculation* option. The results can be viewed using the *AptPlot* program. Search for *error* or *error.scaled* to see the error results. To use the adaptive time step algorithm, select *Adaptive in the Time Step* option from the drop-down menu.

The *Adaptive* time step algorithm is new in SNAP/RADTRAD and it is considered to be experimental. Use of this algorithm adds a significant amount of running time to the problem. It is suggested that the user set up the problem using the *Default* time step algorithm option and check for any time step sensitivities using the *Default with Error Calculation* or *Adaptive* time step algorithm option. For additional information on the *Adaptive* time step algorithm see Section 3.2.

2.4.2 Nuclear Data and Source Scenarios

The source term specification was introduced in Section 2.3.3. However, a new feature that has been added to SNAP/RADTRAD is the ability to consider the reactor coolant system (RCS) activity for either a PWR or BWR. The user can access the *RCS Activity Calculator* window, Figure 2-54, by clicking on the *Nuclide* Data node in the Navigator window and then selecting the *Custom Editors* () icon for *Total Inventories* text box in the *Property* window to open the *Edit Total Inventories* window. Then select the *Open RCS Activity Calculator* () icon on the *Edit Total Inventories* window as shown in Figure 2-34. The user has the option to enter RCS activity or to allow SNAP/RADTRAD to calculate the RCS activity. Formulations for the calculation of RCS activity are presented in Section 3.4. Figure 2-54 displays the *RCS Activity Calculator* window where the user can select from either BWR or PWR.

The user will note that the *RCS Activity Calculator* window in Figure 2-54 is an input specification window where parameters need to be specified to determine the RCS activity. There are two options available to calculate RCS activity.

1. The user can input the RCS specific activity (*µCi/g*) in the *Activity* column (Figure 2-54) and then add the effect of iodine spiking by checking either the *Use pre-incident spike* or the *Use co-incident spike* box. If the user checks the *Use co-incident spike* box, then the *Calculate Appearance* button on Figure 2-54 will become active. Note that the co-incident spike model is not available for BWRs.

2. The user can also have SNAP/RADTRAD calculate the equilibrium Technical Specification (T/S) Limit RCS activity (without spiking) and add the effect of a pre-incident or co-incident spike to the total RCS activity.

In Figure 2-54, the user will note the *Activity* column is editable so that the user can input the known radionuclide specific activity, the RCS mass in kilograms and the RCS inventory will be calculated. Generally, the radionuclide specific activities based upon one percent fuel defects are presented in Chapter 11 of the Final Safety Evaluation Report for a given plant. Once the radionuclide specific activity is entered, the user has the option to calculate the iodine and xenon equilibrium activities from the specified equilibrium activity for the dose equivalent iodine 131 (DE I-131) or the dose equivalent xenon 133 (DE Xe-133) from the facility's technical specification (T/S) equilibrium specific activity. These calculations are done by checking or unchecking the appropriate boxes on the *RCS Activity Calculator* window. Note that the calculations are completed using the user-specified radionuclide specific activity (µCi/g).

Additionally, after selecting either the *BWR* or the *PWR* option on Figure 2-54, when the user selects the *Calculate Activity* button on Figure 2-54 either Figure 2-55 or 2-56 will open respectively. In either instance, the user inputs the required data and clicks the *OK* button to complete the calculation. Note that for the BWR, the user can apply the calculation to either steam or liquid (*Calculate activity in steam or liquid?*) by clicking on the radio button for either the *Steam activity* or *Liquid activity* option shown in Figure 2-56.

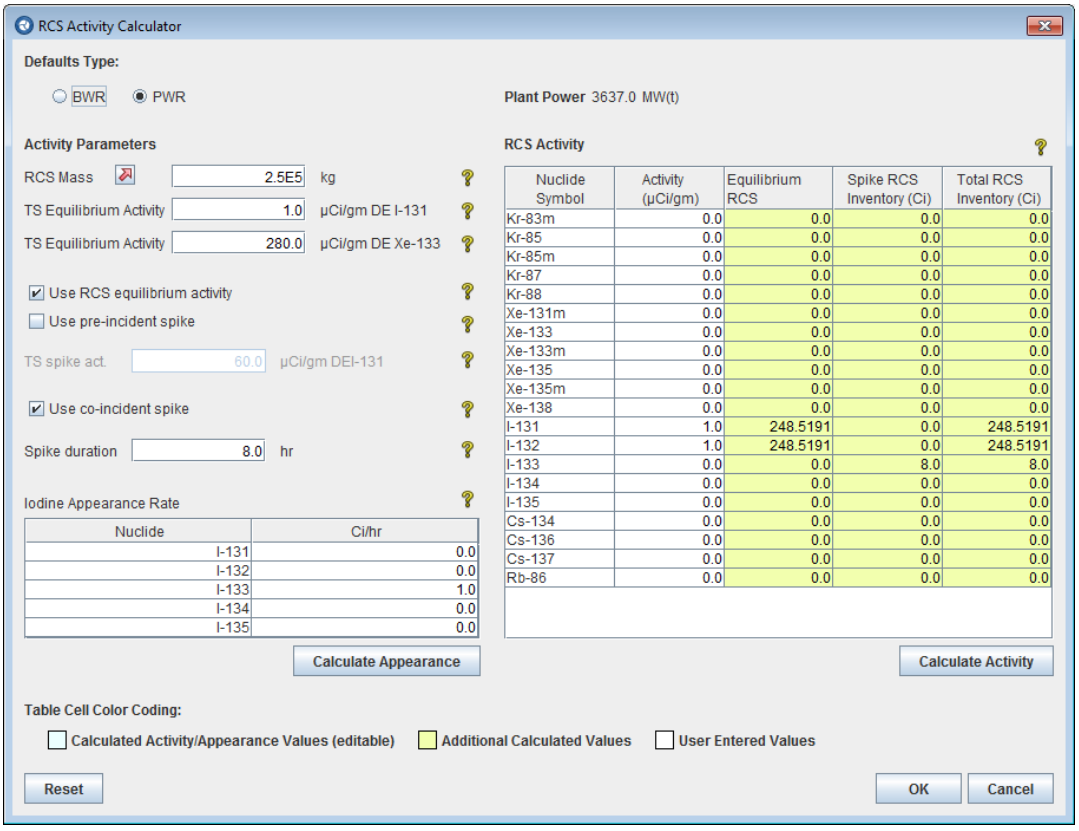


Figure 2-54 RCS Activity Calculator Window

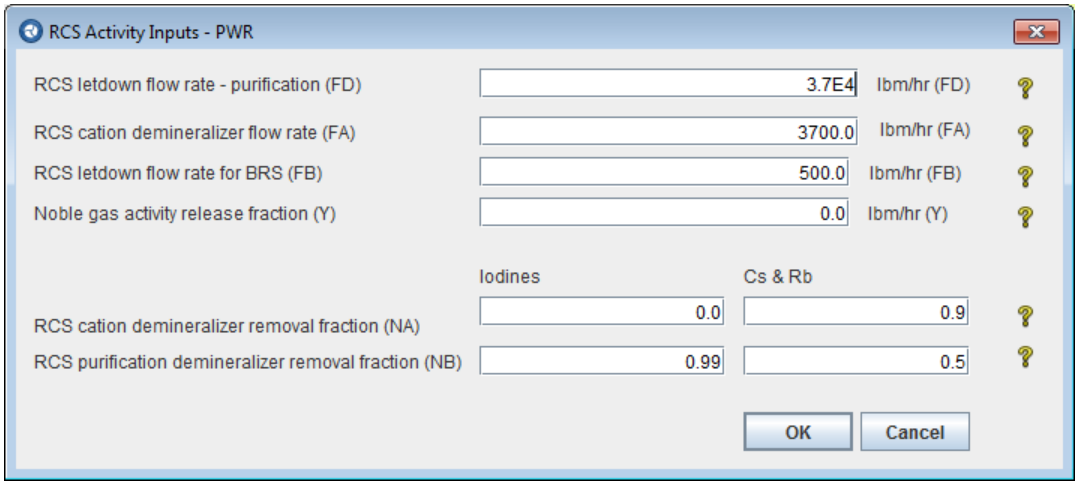


Figure 2-55 RCS Activity Inputs - PWR Window

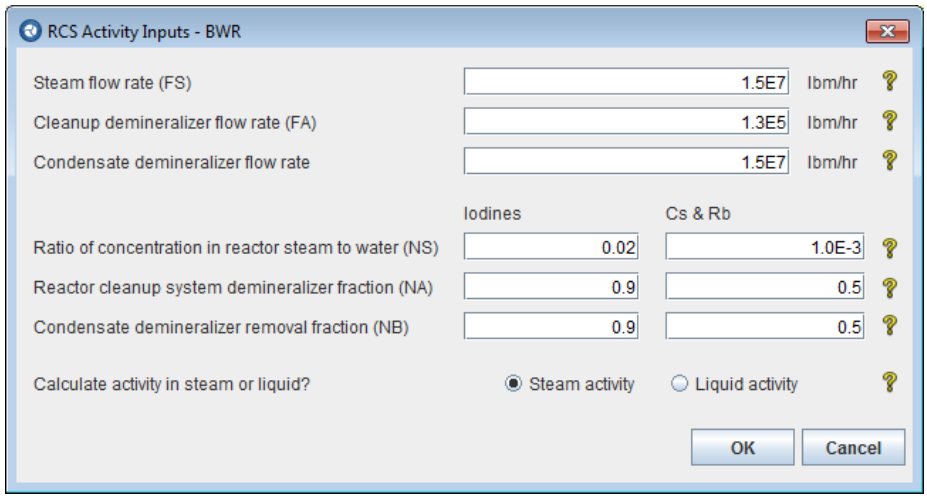


Figure 2-56 RCS Activity Inputs - BWR Window

To apply pre-incident or co-incident spiking to either user-supplied or code-calculated RCS radionuclide specific activities, the appropriate box is checked on the *RCS Activity Calculator* window (Figure 2-54) and the required input supplied. For the pre-incident spike, which is applicable to either PWRs or BWRs, the user checks the *Use pre-incident spike* box and supplies the T/S spike activity.

To use the co-incident spike, which is applicable only to PWRs, the user can select either user defined values by inputting the iodine appearance rate data into table in the *Iodine Appearance Rate* section of Figure 2-54 or choose to have the code calculate the iodine appearance rate by selecting the *Calculate Appearance* button. Note that the iodine appearance rate *Ci/hr* column is editable so that the user can enter appropriate values of the iodine appearance rate.

When the user clicks the *Calculate Appearance* button the *Calculate Iodine Appearance* window as shown in Figure 2-57 will open. The user will provide the required inputs and click the *OK* button which will update the iodine appearance rate values in the table in the *Iodine Appearance Rate* section of Figure 2-54.

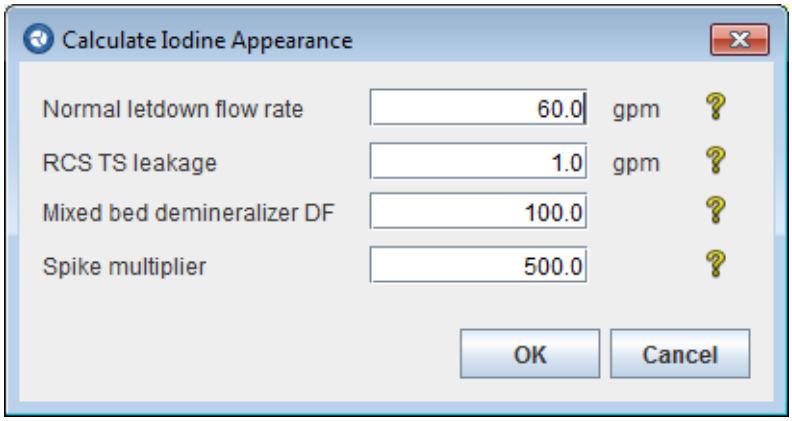


Figure 2-57 Calculate Iodine Activity Window

Once the RCS activity calculations are complete, the user clicks on the *OK* button on the *RCS Activity Calculator* window (Figure 2-54) and the total RCS activity is automatically transferred from the RCS activity calculator to the *Inventory (Ci)* column in the *Edit Total Inventories* window (Figure 2-34) and the specific inventory amount is back-calculated from the core power. Note that a new file is created each time the RCS activity calculator is invoked. These files are automatically named, but the user can rename them using the *Name* text box in the *Edit Total Inventories* window (Figure 2-34). Finally the models used to compute the RCS activity are discussed in Section 3.4 and an example showing the detailed use of the RCS Activity Calculator, in a SNAP/RADTRAD model, is demonstrated in the draft SNAP/RADTRAD Workbook (available at the RAMP website (https://www.usnrc-ramp.com).

Regardless of whether fuel or RCS activity is used, it is the total inventory that is the basis for the source term calculation accessed from the *Source Scenarios* text box, in the *Property* window, once a new source model is initiated. Recall from earlier discussions that part of the specification of a new source scenario is the appropriate nuclide inventory either from the reactor fuel, RCS or other source. Once that step is completed, an appropriate release model is specified from the available pre-defined release models listed under the *Accident Parameters* tab on the *Edit Inventory Scenario* window as shown in Figure 2-58. Alternately, the user has the option of setting release fractions and a release time under the *Release Fractions and Timings* tab. For releases of radionuclides from the reactor coolant, the release rate is usually controlled using the flow pathway leak or flow rate from the compartment where the reactor coolant is released. Accordingly, using a user-specified release fraction of 1.0 for noble gases, halogens, and alkali metals and a release duration of 1.0E-04 hours for the gap release as a surrogate should suffice. Note that the initial inventory prior to the application of release fractions appears under the *Adjusted Inventory* tab while the *Source Term* tab lists the actual releases to be used in the model after multiplication by the release fractions.

- For the *Use Total Inventory* option, user-defined release data are entered under the *Release Fractions and Timings* tab.

- For *DBA-TID* and *DBA-AST* options, the release fractions are listed under the *Release Fractions and Timings* tab. The basis for the values for these options is presented in Section 3.3.

- For the *Gap Release*, rod ejection accidents-control rod drop accidents (*REA-CRDA*), and fuel handling accidents (*FHA*) options, the default release fractions are set under the *Accident Parameters* tab as each accident is selected. The release fractions for the relevant nuclide groups are set to 1 under the *Release Fractions and Timings* tab.

Tables 2-6 and 2-7 list the available inputs for the *Nuclear Data* and *Source* nodes in SNAP/RADTRAD.

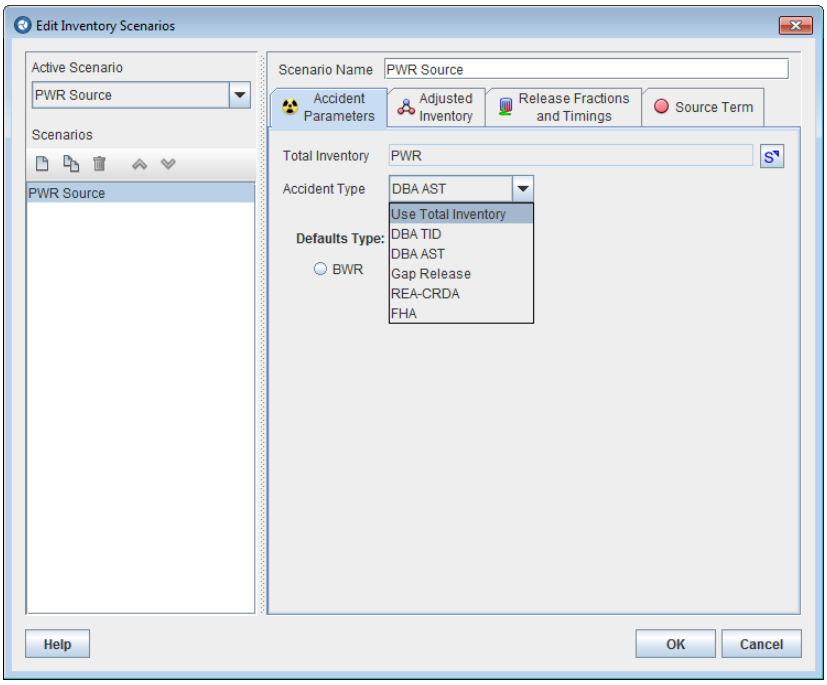


Figure 2-58 Available Pre-Defined SNAP/RADTRAD Release Models

Table 2-6 Summary of SNAP/RADTRAD Inputs - Nuclear Data

Input	Description
Nuclide Model	Select one of the following options: • *ICRP-38 definitions* (default) • *User Defined* It is recommended that the ICRP-38 data be used. **Note** that if the *User-Defined* option is selected and new nuclide definitions are specified and then the user switches to the *ICRP-38* option, the new nuclide definitions are deleted. References in the *Total Inventories* or the Sources to those nuclide definitions will be set to "<not defined>."
Nuclides	Specified by user when the *User Defined* option is chosen in the *Nuclide Model* input. Note that the nuclide definitions can be reviewed by selecting *Custom Editors* (E) icon. This will open the *Nuclide Definitions* window, which contains the *nuclide name*, *atomic mass,* and *half-life* on the left-hand side. When a user clicks on a nuclide on the left-hand side the daughter nuclides and its associated branching ratios will be displayed on the right-hand side of the window.

Total Inventories	Used to develop radionuclide inventories in the fuel or in the RCS. This input works in conjunction with the *Sources* node to develop a source term. The two sample default core inventories for a PWR and BWR from RADTRAD 3.03 are included in the SNAP Model Editor. Core inventories can also be specified by the user. Section 3.3.3 and Figures 3-34 through 3-40 provide more detailed instructions on how to use these inputs.

Table 2-7 Summary of SNAP/RADTRAD Inputs - Sources

Input	Description
Name	Specified by user for the source (optional).
Component Number	Multiple sources can be used in a model and the SNAP/RADTRAD Model Editor assigns the number. These numbers must begin with number 1 and increase sequentially for each additional source.
Description	Specified by user (optional).
Source Scenarios	Various source (release) scenarios are available to the users which are linked to the *Nuclide Data* definition. Source scenarios include LOCA DBAs and non-LOCA DBAs such as FHA, CRDA or REA, and Gap releases. Additionally, scenarios involving RCS activity, such as steam generator tube ruptures and main steam line breaks can also be defined. Section 3.4.2 and Figures 3-54 through 3-58 provide more detailed instructions on how to use this input to model these scenarios.
Source Term Fractions	User defined value which is the fraction of the inventory being released by the source. Multiple sources referencing the same inventory can divide the source term between them through this value.
Iodine Physical Form	Specified the fraction of iodine that is in elemental, organic or particulate chemical form. Predefined fractions are listed below and are user-selectable from the drop-down menu. • *TID-14844* – 0.05 aerosol (particulate), 0.91 (elemental), and 0.04 (organic) • *NUREG–1465* – 0.95 aerosol (particulate), 0.0485 (elemental), and 1.5E-3 (organic). • *User Defined* Note that if one of the predefined fraction options is selected, the above fractions appear in the *Aerosol Fraction*, *Elemental Fraction* or *Organic Fraction* text boxes. These fields are greyed-out and are not editable. Selecting the user-defined option from the iodine physical form drop-down menu allows the user to specify the aerosol, elemental, and organic fractions.

Compartments	Links the release scenario to a given compartment. Works in conjunction with the compartment specification.

2.4.3 Compartments, Pathways, Natural Deposition, Filters and Sprays

Section 2.3.2 presented the approach for defining compartments and pathways and connecting these two components. Once an initial model is developed, completing the model is a matter of input specification. Input specification is done by left clicking on the *Expand* ( ) icon (if it is not already expanded) of the associated component (*Compartments*, *Pathways*, *Natural Deposition, Filters* and *Sprays*) in the *Navigator* window, and completing the input specification fields of the *Property* window for that component. The input specification fields for the components in the *Property* window consist of input text boxes, drop-down menus or input tables that are accessed by the *Custom Editors* ( ) icon. Tables 2-8 through 2-12 list the available inputs for the *Compartments*, *Pathways*, *Natural Deposition*, *Filters* and *Sprays* in SNAP/RADTRAD.

Table 2-8 Summary of SNAP/RADTRAD Inputs - Compartments

Input	Description
Name	Specified by user (optional).
Component Number	Multiple compartments can be used in a model and the SNAP/RADTRAD Model Editor assigns the number. These numbers must begin with number 1 and increase sequentially for each additional component.
Description	Specified by user (optional).
Type	The user can select from the following options: • *Control Room Dose* – This option is used for a control room compartment which enables a dose location to be associated with the compartment. • *Environment* – This option couples radionuclide release points and dose locations through the specification of *X*/*Q*. • *Normal* – A general compartment type that can be interconnected to other compartments. Removal by sprays, natural deposition and filtration can be modeled in these compartments. • *Normal Dose* – This option is similar to the *Normal* compartment except that a dose location can be specified within the compartment. Note that an *Environment* compartment is defined by default in SNAP/RADTRAD. Additional compartments are specified by the user.

Output Level Detail	Sets the detail level used to output compartment data (nuclide activity and decontamination for the compartment) during model execution. The user can select from the following options: • *No additional detail* (default) • *Full edit at time steps* • *Full edit at end of problem only*. When set to *Full edit at time steps*, the editing of nuclide activity and decontamination for the compartment are printed to the output. These details may be printed at every time step or only once, at the end of the problem.
Volume	Specified by user (ft^3 or m^3 depending on user-specified units selection). Units switching is done by right-clicking on the black bar of the *Navigator* window and selecting Engineering Units and British or SI units.
Deposition	Works in conjunction with the *Natural Deposition* node summarized in Table 3-10. Used in *Normal* and *Normal Dose* compartments as appropriate.
Filter	Works in conjunction with the *Filter* node summarized in Table 3-11. Used in *Normal*, *Normal Dose* and *Control Room Dose* compartments as appropriate.
Spray	Works in conjunction with the *Spray* node summarized in Table 3-12. Used in *Normal* and *Normal Dose* compartments as appropriate.

Table 2-9 Summary of SNAP/RADTRAD Inputs - Pathways

Input	Description
Name	Specified by user (optional).
Component Number	Multiple pathways can be used in a model and the SNAP/RADTRAD Model Editor assigns the number. These numbers must begin with number 1 and increase sequentially for each additional component.
Description	Specified by user (optional).
From Compartment	Lists the upstream compartment in this pathway.
To Compartment	Lists the downstream compartment in this pathway.

Pathway Type	The method by which radionuclides are transported and deposited through the pathway. The user can select from the following options: • *Piping* (default) – transport in volumetric flow with a decontamination factor. • *Filtered pathway* – transport in volumetric flow through filters with a specified efficiency. • *Generic* – transport in volumetric flow with a decontamination factor (replaces legacy suppression pool mechanism). Allows for the user to independently specify the decontamination factors for aerosols (particulate), elemental iodine, organic iodine, and noble gases. • *Air leakage* – transport in volumetric percent (%/day). This is the typical path used for containment leakage. • *Generic w/non-Iodine aerosols* – transport is the same as the Generic option above without Iodine particulate. • *BWR Main Steam Lines* – Represents leakage from the outboard and inboard sections of BWR steam lines. This model is gathered from Regulatory Guide 1.183 Rev. 2 Appendix A.
Printout Level Detail	Determines what additional pathway details are written to the output file. The user can select from the following options: • *None* (default) – writes no extra details. • *Transport Each Time Step* – writes information about the transport for each group (noble gas, elemental, organic, and aerosol (particulate)) at each time step. • *Nuclide and Transport Each Time Step* – same as the option above, but includes information about each transported nuclide. • *Nuclide and Transport at End Only* – same as the option above, but only written out at the end of the calculation.

Aerosol Removal Model (if pathway type is Piping)	Specifies how aerosols (particulates) are deposited in the pipe. The user can select from the following options: • *No aerosol removal* (default) – aerosol removal is not modeled in the pipe. • *User Defined Decontamination Factors* – if the user selects this option the *Aerosol DF* text box appears below this option. Select the *Custom Editors* (E) icon for this text box to open the *Editing Aerosol DF* window. The user enters time-dependent decontamination factors and flow rates (ft^3/min or m^3/s) in the data entry table (see Section 3.3.3 for details regarding data entry using the *Custom Editors* (E) icon and the edit table features in SNAP/RADTRAD). • *Brockmann-Bixler Model* – If the user selects this option the following additional input text boxes appear below this option with user-specified values to be entered: ▪ *pipe volume* (ft^3 or m^3) ▪ *pipe surface area* (ft^2 or m^2) ▪ *pipe angle* (degrees) ▪ *pipe temperature* (°F or °C) ▪ *pipe pressure* (psi or kPa) ▪ *pipe aerosol settling velocity* (ft/min or m/s) ▪ *pipe aerosol flow rates* are entered by selecting the *Custom Editors* (E) icon to open the *Editing Pipe Aerosol Flow Rates* window. Enter the flow rates (ft/min or m/s) as a function of time in the data entry table. Note that addition guidance and information on these inputs is available by clicking on the *Help* (?) icon and Section 4.5.3.
Elemental Iodine Removal Model *(if pathway type is Piping)*	Determines how elemental iodine is deposited in the pipe. The user can select from the following options: • *None* (default) – elemental iodine removal is not modeled in the pipe. • *Enter DFs and Flow Rates* – if the user selects this option the removal rate is defined as a function of flow rate and DFs over time. When this option is selected the *Elemental Iodine DF* text box appears below this option. Select the *Custom Editors* (E) icon for this text box to open the *Editing Elemental Iodine DF* window. The user enters time-dependent DFs and flow rates (ft^3/min or m^3/s) in the data entry table. • *Enter Deposition Velocity* – If the user selects this option the *Elemental Iodine Deposition Velocity* text box appears below this option. The user enters iodine the deposition velocity (ft/min or m/s).

Organic Iodine Removal Model *(if pathway type is Piping)*	Determines how organic iodine is deposited in the pipe. The user can select from the following options: • None (default) – elemental iodine removal is not modeled in the pipe. • Enter DFs and Flow Rates – if the user selects this option, the removal rate is defined as a function of flow rate and DFs over time. When this option is selected, the Organic Iodine DF text box appears below this option. Select the Custom Editors ( ) icon for this text box to open the Editing Organic Iodine DF window. The user enters time-dependent DFs and flow rates (ft^3/min or m^3/s) in the data entry table. • Enter Deposition Velocity – if the user selects this option, the Organic Iodine Deposition Velocity text box appears below this option. The user inputs the iodine enter deposition velocity (ft/min or m/s). Note: The NRC does not credit organic deposition in design basis calculations.
Filter *(if pathway type is Filtered Pathway)*	Specified the air filter removing radionuclides from transport in the pathway. Use the Select ( ) icon to open the Select from Filters window to link to one of the available filter models or create a filter component.
Aerosol DF *(if pathway type is Generic or Generic w/non-Iodine Aerosols)*	Select the Custom Editors ( ) icon for this text box to open the Editing Organic Iodine DF window. Enter the time-dependent DFs and flow rates (ft^3/min or m^3/s) in the data entry table.
Elemental Iodine DF *(if pathway type is Generic or Generic w/non-Iodine Aerosols)*	Select the Custom Editors ( ) icon for this text box to open the Editing Elemental Iodine DF window. Enter the time-dependent DFs and flow rates (ft^3/min or m^3/s) in the data entry table.
Organic Iodine DF *(if pathway type is Generic or Generic w/non-Iodine Aerosols)*	Select the Custom Editors ( ) icon for this text box to open the Editing Organic Iodine DF window. Enter the time-dependent DFs and flow rates (ft^3/min or m^3/s) in the data entry table. Note: The NRC does not credit organic deposition in design basis calculations.
Nobel Gas Flow Rates *(if pathway type is Generic or Generic w/non-Iodine Aerosols)*	Select the Custom Editors ( ) icon for this text box to open the Editing Noble Gas Flow Rates window. Enter the time-dependent flow rates (ft^3/min or m^3/s) in the data entry table.

Leakage Rate *(if pathway type is Air Leakage)*	Select the Custom Editors ( ) icon for this text box to open the Editing Leakage Rate window. Enter the time-dependent flow rates (%/day) in the data entry table.
Aero Mass Median Diameter *(if pathway type is BWR Main Steam Lines)*	Aerodynamic mass median diameter (m) based on a distribution directly measured from experiments to evaluate the settling velocity where the specific aerosol parameter distributions of shape factor, density, and volume-equivalent diameter do not need to be defined.
Geometric Standard Deviation *(if pathway type is BWR Main Steam Lines)*	Geometric standard deviation used to create a normalized number distribution of particles of aerodynamic diameter
Geometric Mean *(if pathway type is BWR Main Steam Lines)*	An optional parameter that specifies a geometric mean when setting up the standard deviation.
Geometric Factor *(if pathway type is BWR Main Steam Lines)*	Factor used in specifying spacing intervals.
Viscosity *(if pathway type is BWR Main Steam Lines)*	Viscosity of the steam in the BWR Steam Lines (Pa-s).
Density *(if pathway type is BWR Main Steam Lines)*	Density of the steam in the BWR Steam Lines (kg/m^3).
MSL Inboard Area *(if pathway type is BWR Main Steam Lines)*	Settling surface area of the inboard pipe (m^2).
MSL Inboard Volume *(if pathway type is BWR Main Steam Lines)*	Inner volume of the inboard pipe (m^3).
MSL Inboard Flow Rate *(if pathway type is BWR Main Steam Lines)*	Flowrate through the inboard section of the BWR steam line (m^3/sec).

MSL Outboard Area *(if pathway type is BWR Main Steam Lines)*	Settling surface area of the outboard pipe (m^2).
MSL Outboard Volume *(if pathway type is BWR Main Steam Lines)*	Inner volume of the outboard pipe (m^3).
MSL Outboard Flow Rate *(if pathway type is BWR Main Steam Lines)*	Flowrate through the outboard section of the BWR steam line (m^3/sec).

Table 2-10 Summary of SNAP/RADTRDA Inputs - Natural Deposition

Input	Description
Name	Specified by user (optional).
Component Number	Multiple natural deposition models can be used in a model and the SNAP/RADTRAD Model Editor assigns the number. These numbers must begin with number 1 and increase sequentially for each additional component.
Description	Specified by user (optional).
Aerosol Deposition Model	Specifies the method by which the deposition removes radionuclides from the compartment. The user can select from the following options: • *None* (default) –no deposition is modelled. • *User Defined Coefficients* – deposition is determined from user-specified removal rate coefficients over time. • *Henry's Model Coefficients* – uses Henry's model for natural deposition. User specifies compartment height and particle density over time. See Section 4.5.2.1 for more model details and references. • *Powers' Deposition Model* – the Powers' model for natural deposition, calculated based on an uncertainty percentile associated with a reactor and accident type. This model is only for large buildings, and is not valid for deposition in passages such as pipes. See Section 4.5.2.2 for more model details and references.
Aerosol Removal Coefficients (if Aerosol Deposition Model is User Defined Coefficients)	Defines the aerosol (particulate) radionuclide removal as a function of time. Select the *Custom Editors* (E) icon for this text box to open the *Editing Aerosol Removal Coefficients* window. Enter the time-dependent removal coefficients (1/hour) in the data entry table.
Henry Deposition Table Data (if Aerosol Deposition Model is Henry's Model Coefficients)	The table is used by the code to determine the particle deposition rate from the compartment height and particle density over time. Select the *Custom Editors* (E) icon for this text box to open the *Editing Henry's Deposition Table Data* window. Enter the time-dependent height (ft or m) and particle density (lb/ft^3 or g/cm^3) in the data entry table.

Powers Accident Model Type (if Aerosol Deposition Model is Powers Deposition Model)	Sets the model of decontamination based on the type of reactor and accident. Select the accident type using the drop-down menu. • *PWR-DBA* • *BWR-DBA* • *APWR-DBA*
Power's Model Percentile (if Aerosol Deposition Model is Powers Deposition Model)	Sets the uncertainty percentile for the Powers model for natural deposition. Select the accident type using the drop-down menu. • *10%* • *50%* • *90%* Note: The 10% deposition model yields the most conservative aerosol removal coefficients.
Elemental Deposition Model Type	Determines the method by which the deposition removes elemental iodine from the compartment. The user can select from the following options: • *None* (default) –no decontamination is modelled. • *User Defined Coefficients* – decontamination is specified as a function of removal coefficients over time. When this option is selected the *Elemental Iodine Removal Coefficient* text box appears below this option.
Elemental Iodine Removal Coefficient (*if Elemental Deposition Model Type is User Defined Coefficients*)	Defines the elemental iodine radionuclide removal as a function of time. The removal coefficient is defined as the fraction of the total elemental iodine mass inserted into the containment removed per second. Select the *Custom Editors* () icon for this text box to open the *Editing Elemental Iodine Removal Coefficient* window. The user enters time-dependent elemental iodine removal coefficients (1/hour) in the data entry table.

Table 2-11 Summary of SNAP/RADTRAD Inputs - Filters

Input	Description
Name	Specified by user (optional).

Component Number	Multiple filters can be used in a model and the SNAP/RADTRAD Model Editor assigns the number. These numbers must begin with number 1 and increase sequentially for each additional component.
Description	Specified by user (optional).
Filter Table	The removal efficiency of filters and flow rate through the filters as a function of time. Select the *Custom Editors* () icon for this text box to open the *Editing Filter Table* window. Each row defines time dependent filter flows (ft^3/min or m^3/s) and efficiencies (%) for: • *aerosol (particulate)* • *elemental iodine* • *organic iodine filtration* There is no noble gas efficiency as it is assumed that the noble gases are not filtered. The efficiencies will change in a stepwise fashion at each specified time.

Table 2-12 Summary of SNAP/RADTRAD Inputs - Sprays

Input	Description
Name	Specified by user (optional).
Component Number	Multiple spray models can be used in a model and the SNAP/RADTRAD Model Editor assigns the number. These numbers must begin with number 1 and increase sequentially for each additional component.
Description	Specified by user (optional).

Aerosol Removal Model	Determines the method by which the spray removes aerosol (particulate) radionuclides from the compartment. The user can select from the following options: • *None* (default) – aerosols are not removed from the compartment. • *User Defined Coefficient Table* – allows the user to specify the aerosols removal rate coefficient over time. When this option is selected the *Aerosol Removal Coefficients*, *Aerosol DF Limit Enabled*, *Aerosol DF Limit*, *Aerosol Lambda/10 DF Limit Enabled*, and the *Aerosol Lambda/10 DF Limit* text boxes appear below this option. • *Powers' Model* – the aerosol removal rate is determined using by the Powers and Burson model, which takes into account sprayed and non-sprayed volume, deposition percentile, and spray flux ratio and height over time. When this option is selected the *Powers Model Spray Table*, *Powers Model Spray Ratio* and the *Powers Model Percentile* text boxes appear below this option. See Section 4.5.1 for more details.
Aerosol Removal Coefficients (if Aerosol Removal Model type is User Defined Coefficient Table)	Select the *Custom Editors* (E) icon for this text box to open the *Editing Aerosol Removal Coefficients* window. The user enters time-dependent aerosol removal coefficients (1/hour) in the data entry table.
Aerosol DF Limit Enabled *(if Aerosol Removal Model is User Defined Coefficient Table)*	The user selects from either *True* or *False*. If *True* is selected, the *Aerosol DF Limit* text box appears below this option.
Aerosol DF Limit *(if Aerosol Removal Model is User Defined Coefficient Table)*	The user enters a DF value to limit the amount of aerosol removal. Once this DF is reached in the compartment the aerosol lambda or removal coefficient is automatically set to zero. The DF value must be 1.0 or greater and the default value is *1.0E+06*.
Aerosol DF Limit, Aerosol Lambda/10 DF Limit Enabled *(if Aerosol Removal Model is User Defined Coefficient Table)*	The user selects from either *True* or *False*. If *True* is selected, the *Aerosol Lambda/10DF Limit* text box appears below this option.
Aerosol Lambda/10 DF Limit (if Aerosol Removal Model is the Powers Model)	The user enters a DF value to limit the amount of aerosol removal. Once this DF is reached in the compartment the aerosol lambda or removal coefficient is automatically set to $1/10^{th}$ its original value. The DF value must be 1.0 or greater and the default value is 50.

Powers Model Spray Table *(if Aerosol Removal Model is the Powers Model)*	Specified as a function of spray flux and the fall height of the spray droplets (typically the distance between the spray headers and the containment floor). Select the *Custom Editors* (E) icon for this text box to open the *Editing Powers Model Spray Table* window. Enter the time-dependent spray flux (cfm/ft^2 or (m^3/s)/m^2) and spray height (ft or m). Unit switching is done by right-clicking on the black bar of the *Navigator* window and selecting Engineering Units and choosing either British or SI units. The spray flux and height are discussed in NUREG/CR-5966, "A Simplified Model of Aerosol Removal by Containment Sprays" [12]. The Powers' model is valid in the spray flux ratio range 1.0E-05 to 2.5E-03 m^3/s-m^2 (0.002 and 0.5 cfm/ft^2) and a range of spray fall heights between 5 to 50 m (16.4 and 164 ft).
Powers Model Spray Ratio *(if Aerosol Removal Model is the Powers Model)*	The ratio of unsprayed to sprayed volume in the compartment. This is typically zero, as the unsprayed volume is often modeled as a separate compartment. Good mixing is assumed for any ratio above zero; if good mixing is not available, the sprayed and unsprayed compartments should be modeled separately.
Powers Model Percentile *(if Aerosol Removal Model is the Powers Model)*	The percentile model used in the calculation. Select the percent using the drop-down menu. • 10% • 50% • 90% Note: the 10% model yields the most conservative aerosol removal coefficients.
Elemental Iodine Removal Model	Determines the method by which the spray removes aerosol (particulate) radionuclides from the compartment. The user can select from the following options: • None (default) – elemental iodine is not removed from the compartment. • User Defined Coefficient Table – elemental iodine is removed using user-specific removal rate coefficients input by the user. When this option is selected, the Elemental Iodine Removal Coefficients, Elemental-I DF Limit Enables, and Elemental-I DF Limit text boxes appear below this option.

Elemental Iodine Removal Coefficients *(if Elemental Iodine Removal Model is set to the User Defined Coefficients)*	Defines the elemental iodine radionuclide removal coefficients used to determine the elemental iodine removal rate as a function of time. Select the Custom Editors () icon for this text box to open the Editing Elemental Iodine Removal Coefficients window. The user enters time-dependent elemental iodine removal coefficients (1/hr) in the data entry table.
Elemental-I DF Limit Enabled *(if Elemental Iodine Removal Model is set to the User Defined Coefficients)*	The user selects from either True or False. If True is selected, the Elemental-I DF Limit text box appears below this option.
Elemental-I DF Limit *(if Elemental Iodine Removal Model is set to the User Defined Coefficients)*	The user enters a DF value to limit the amount of elemental removal. Once this DF is reached in the compartment, the elemental lambda or removal coefficient is automatically set to zero. The DF value must be 1.0 or greater and the default value is 20.
Organic Iodine Removal Model	Determines the method by which the spray removes organic iodine from the compartment. The user can select from the following options: • None (default) – organic iodine is not removed from the compartment. • User Defined Coefficient Table – organic iodine is removed using user-specified removal rate coefficients as an organic removal coefficient over time. When this option is selected the Organic Iodine Removal Coefficients text box appears below this option.
Organic Iodine Removal Coefficients *(if Organic Iodine Removal Model is the User Defined Coefficients)*	Defines the organic iodine radionuclide removal as a function of time. Select the *Custom Editors* () icon for this text box to open the *Editing Organic Iodine Removal Coefficients* window. The user enters time-dependent elemental iodine removal coefficients (1/hour) in the data entry table. Note: The NRC does not credit organic deposition in design basis calculations.

2.4.4 Dose Locations, Breathing Rates, and X/Q Tables

Section 2.3.3 demonstrates the general approach for defining dose locations, breathing rates, and X/Q tables. Generally, the default breathing rates are used for most analyses and are entered under the *Dose Locations* node in the *Property* window. The values for X/Q are specified through the use of data entry tables as illustrated in Section 2.3.3 (Figure 2-33).

Tables 2-13 and 2-14 list the available inputs for the *Dose Locations* and *X/Q Tables* nodes in SNAP/RADTRAD.

Table 2-13 Summary of SNAP/RADTRAD Inputs - Dose Locations

<table>
<tr><th>Input</th><th colspan="3">Description</th></tr>
<tr><td>Name</td><td colspan="3">The EAB or LPZ dose location names are set by SNAP/RADTRAD. Other dose location names (i.e. control room) are created by the user.</td></tr>
<tr><td>Description</td><td colspan="3">The EAB or LPZ dose location descriptions are set by SNAP/RADTRAD. Other dose location descriptions (i.e. control room) must be created manually by the user.</td></tr>
<tr><td>Component Number</td><td colspan="3">Multiple dose locations can be used in a model and the SNAP/RADTRAD Model Editor assigns the number. These numbers must begin with number 1 and increase sequentially for each additional component.</td></tr>
<tr><td rowspan="4">Breathing Rates</td><td colspan="3">Defines the breathing rates at the dose locations as a function of time. Select the Custom Editors (E) icon for this text box to open the Editing Breathing Rates window. The user can then, if necessary, select the default breathing rates by left-clicking the Default button and choosing between either the EAB/LPZ or Control Room options. The default breathing rates for each are listed below:</td></tr>
<tr><td rowspan="3">EAB/LPZ</td><td>Time (h)</td><td>Breathing Rates (m^3/s)</td></tr>
<tr><td>0.0</td><td>3.5E-04</td></tr>
<tr><td>8.0</td><td>1.0E-04</td></tr>
</table>

		24.0	2.3E-04
	Control Room	Time (h)	Breathing Rates (m^3/s)
		0.0	3.5E-04
	Additionally, the user can enter time-dependent breathing rates (ft^3/min or m^3/s) in the data entry table.		
X/Q Table	Specifies the X/Q table to be used with this dose location. Use the Select (S) icon to open the Select from X/Q Tables window to link to one of the available X/Q Tables.		
Occupancy Factors	Specifies the occupancy factors table to be used with the control room (or the technical support center) dose locations. Use the Custom Editors (E) icon to open the Editing Occupancy Factors window. The user can then provide time dependent occupancy factors for the dose location. Occupancy factors may only be input for the control room compartment.		

Table 3-14 Summary of SNAP/RADTRAD Inputs - X/Q Tables

Input	Description
Name	X/Q values are specified for the EAB and LPZ dose locations by default in SNAP/RADTRAD. Users must specify X/Q data for the EAB and LPA. X/Q data for additional dose locations can be specified by the user (optional)
Component Number	The EAB is set to X/Q Table 1 and LPZ is set to X/Q Table 2 by default in SNAP/RADTRAD. User-specified X/Q tables are automatically numbered by SNAP/RADTRAD. The component number can be changed by the user, but it is suggested to keep X/Q (along with other components) in numerical order.
Description	Specified by the user to add a description of the component.
X/Q Table	Select the Custom Editors (E) icon for this text box to open the Editing X/Q Tables window. The user enters time-dependent or

	duration-dependent X/Q values (s/m^3) in the data entry table.
X/Q Time Option	When Regulator Guide Revision is set to Rev 1, the box to pick the timing option for the X/Q tables shows up in the uppermost X/Q Tables tab (shows up as X/Q Tables [<number of tables>]). When clicked, this box allows the user to pick between two options, Time and Duration. When Time is picked, the Time column in the X/Q tables will be set to a specific problem time. When Duration is picked, the Time column will change to Duration and the values will no longer be set to a certain problem time but will last the length of the duration specified. RADTRAD will use the highest value at the worst two-hour dose period for the dose location linked to the X/Q table. The duration will be split evenly before and after the worst two-hour dose time if the duration for the value is longer than two hours. The remaining values will be used in descending order from that time.

One note is the link between the dose location and X/Q table. Like most of the functions in the SNAP Model Editor there is a couple of different ways to create the link between the dose location and the X/Q Table. The easiest way to establish this link is by clicking on the main X/Q Tables [2] node in the Navigator window to view the Property window for this node. In the Property window, select the Custom Editors () icon to the right of the Onsite X/Q Tables text box to open the Onsite X/Q Table Map window (Figure 2-59). Alternatively, the user can also open the Onsite X/Q Table Map window by opening the Property window for the environment compartment and select the Custom Editors () icon to the right of the Onsite X/Q Tables text box.

The Onsite X/Q Table Map window will appear, and the user can link the X/Q table and dose location. In the Onsite X/Q Table Map window, the provided row headers list each of the pathways which are entering the environment. These are annotated further by the Release to Environment label to the left of the rows. Column headers in the Onsite X/Q Table Map window represent the pathways out of the environment. These are annotated by an Intake from Environment label placed above the table. Each column represents an exhaust while every row represents an inflow. To map an X/Q table, click within a cell to enable the Select icon. Click the Select icon to open the Select from X/Q Tables window; use this window to select the X/Q Table mapped to the inflow and exhaust. Users should note that SNAP/RADTRAD does not allow X/Q tables to be defined for exhaust from the control room to the environment. The remaining nodes under the Navigator window are listed and described in Table 2-15.

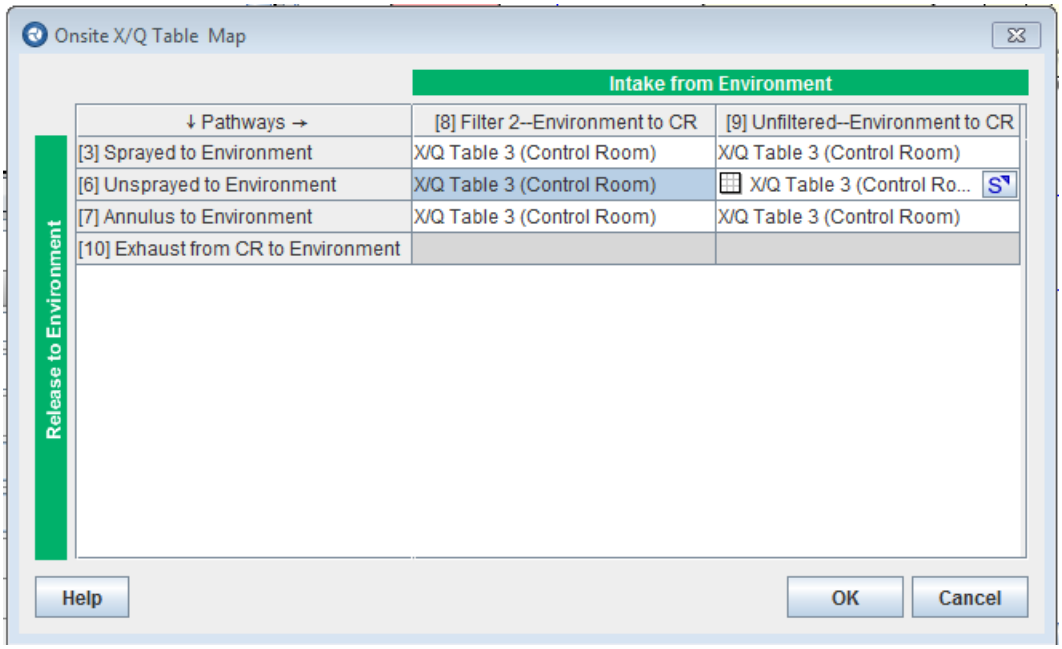


Figure 2-59 Onsite X/Q Table Map Window

Table 2-14 Summary of SNAP/RADTRAD Inputs - Remaining Inputs

Input	Description
Connections	
Connections among compartments (paths), dose locations, and source connections can be specified. Usually, drag and drop is used. Note that connections between compartments cannot be created by the *Navigator* window. A pathway needs to be defined and then the connection needs to be made using the *Connection Tool* ( ) icon in the *View / Dock* window (see Section 2.3.2).	
Job Streams	
Name	The name for this job stream. This will be used to generate the relative path for the tasks that make up this stream. The default value for the name is *Simple_Stream* and it is recommended that SNAP/RADTRAD users change this to a unique name that is identifiable to the model (see Section 2.2.2).
Description	Specified by user (optional).

Stream Type	Defines the type of calculation that may be implemented through this job stream. The user can select from the following options: • Basic Job Stream (default) – a simple job stream. • Numeric Combination – builds a set of input models by modifying one or more shared numeric variables. Each selecte4d shared numeric will either iterate through a list of predefined values or increment from a start value to an end value. • Tabular Parametric – the parametric case takes the form of a table of shared variable values. • Dakota Uncertainty – uncertainty support for the Dakota toolkit.
File Groups	Typically, the File Groups text box is not used in SNAP/RADTRAD. This option defines groups of input sources and forces files inside file sets to be associated one-to-one with other file sets or parametric model node outputs.
Platform	The platform that this stream will be submitted to by default. The default value for SNAP/RADTRAD is Local.
Root Folder	The calculation server folder where the job stream is executed (see Section 2.2.2). Select the Custom Editors () icon for this text box to open the Edit Calculation Server Root Folders window.
Relative Location	The relative location of this stream in relation to the selected staging location. The staging location is where intermediate files, such as the stream definition, will be stored while a job stream is running (see Section 2.4.2 of reference [4] for more details).
Log Level	Typically, the Log Level text box is not changed from the default value (Information) in SNAP/RADTRAD. Defines the current log level for messages produced by this stream.
View in Job Status	This property determines whether the SNAP Job Status window will be opened to view the status of this stream after submission. The default value for SNAP/RADTRAD is Yes.
Linear Execution	Job Streams using Linear Execution are executed one task at a time, prioritized by their Step Number. In a normal (non-linear) Job Stream, tasks will be executed as soon as their dependencies are available (i.e. up-stream tasks are complete) up to the maximum number allowed by the platform. This option should only be used in situations where the stream must

	execute one task at a time and each task must be completed before another can be executed. In most cases, including SNAP/RADTRAD, this value should be left at its default value (*No*).
Numerics	
The SNAP user-defined *Numerics* feature is designed to allow properties of a model to be modified and/or calculated outside the normal input for the model. A user may create real, integer, Boolean, string, and table variables, as well and functions. Typically, the *Numerics* node is **not used** in SNAP/RADTRAD. See Section 2.5 of reference [4] for more details about User-Defined Numerics in other SNAP applications.	
Views	
The user can specify multiple views so that various model icons can be seen. Usually, one view (*Default View*) is sufficient for SNAP/RADTRAD models. The *Property* window for the *Default View* node values can be modified by the user as needed, but typically the default values for the text boxes will be sufficient for most models. Section 2.3.4 describes some of the options associated with the *Default View* node *Property* window text boxes. The user can select the Help (?) icon for each *Default View* node *Property* window text box to obtain more information on each one.	

3.0 MODELS USED IN RADTRAD

The radiological consequences of an accident in a nuclear reactor depend upon the quantity of the radioactive material that escapes to the environment or enters into the control room.

SNAP/RADTRAD is designed to calculate doses at offsite locations, such as the EAB, LPZ and in the control room. Source term models from TID-14844 or from NUREG-1465 are incorporated into SNAP/RADTRAD to describe fission product release from the fuel to the containment. Models for natural deposition within a compartment and engineered removal mechanisms, such as sprays and filters are available in the code. Flow between compartments is modeled and HEPA and charcoal filters can be included in the flow paths for radionuclide removal due to filtration. Leakage to the environment can also be modeled and doses calculated to various points in the environment, such as the EAB and LPZ. After transporting the nuclides to different locations, SNAP/RADTRAD calculates the dose at user-specified locations. Note that much of the discussion in this section is based on the original RADTRAD documentation in NUREG/CR-6604 and its two supplements.

3.1 Governing Equations in RADTRAD

The basic RADTRAD-AC model is a multi-compartment model where each compartment represents a portion of the plant being analyzed. Generally, the containment volume(s), environment, and control room(s) are modeled as compartments. Figure 3-1 presents a diagram illustrating a typical SNAP/RADTRAD model. This figure shows a two-volume containment connected to the environment. A two-volume containment compartment may be used to represent the sprayed and unsprayed portions of the containment. A control room is shown which contains ventilation intakes from the environment through two filtered flow pathways, one recirculating and one that intakes directly from the environment. Recirculating filtered flow paths are typically used to reduce the airborne radionuclide concentration in the control room. An unfiltered intake to the control room from the environment representing in leakage is also represented. The control room ventilation discharges back to the environment. Dashed lines denote connections with transfer rates of zero and are shown for completeness (e.g. no backflow from the control room or environment to the containment).

The governing equations in the RADTRAD-AC are balanced first-order linear differential equations relating the release of radionuclides typically from the reactor core to a given compartment to the removal of radionuclides within a given compartment and the transfer of radionuclides among compartments. Within each compartment except the environment, the radionuclides that are airborne within that compartment are assumed to be uniformly distributed or mixed. The environment compartment is where the EAB and LPZ dose points are located. In many cases, the control room ventilation system draws suction from the environment. Note that coupling of transfer pathways from the containment to the EAB, LPZ and control room intakes is done using X/Q values. The X/Q values relate the amount of radionuclide released to the environment to the dispersed radionuclide concentration at a particular location in the environment. Since each X/Q value is associated with a release point and an intake location, the radionuclide inventory is not uniformly distributed in the environment compartment.

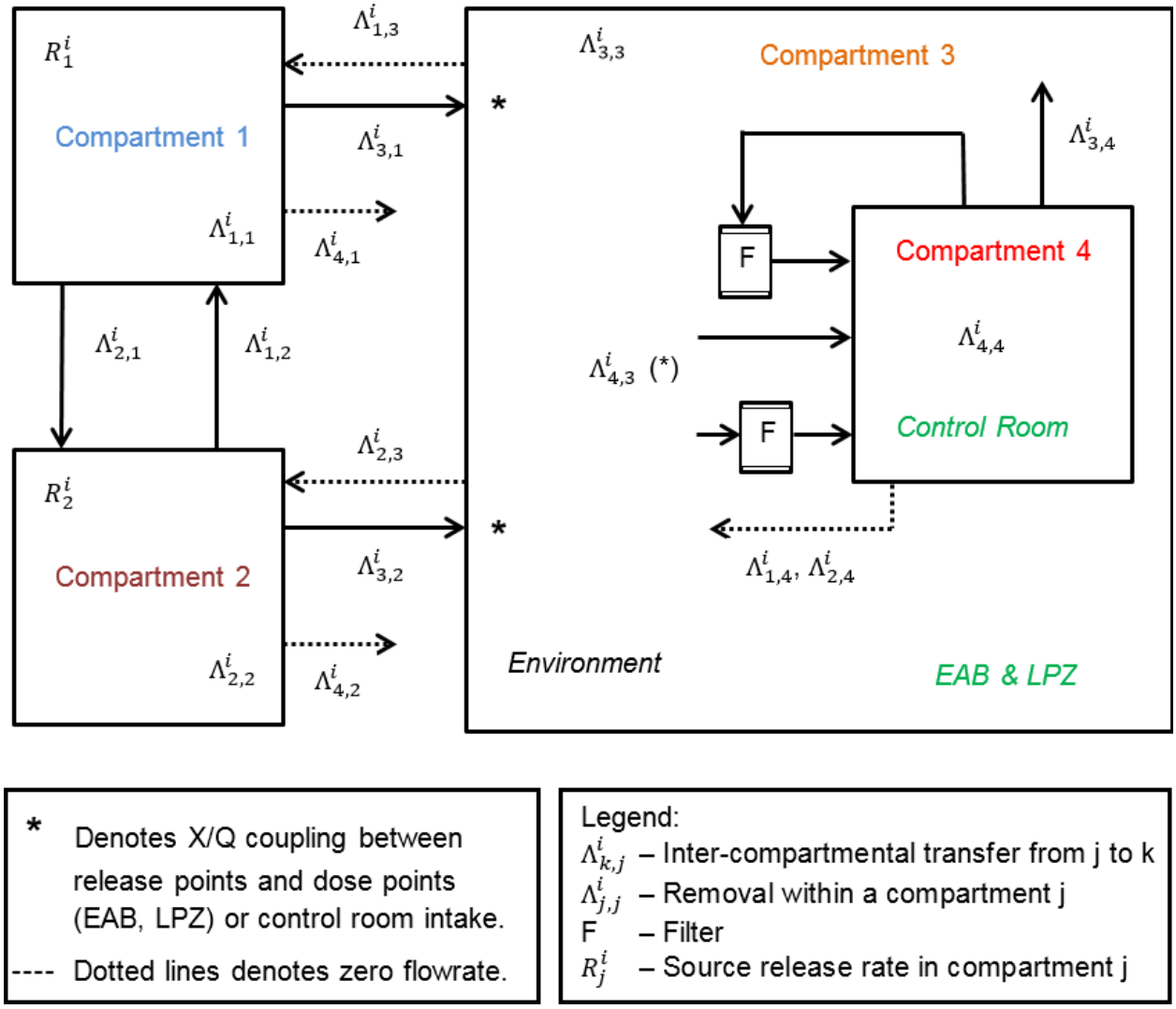


Figure 3-1 Schematic of a Typical SNAP/RADTRAD Dose Assessment Model

The equations used to calculate the quantity of radionuclide in each compartment can be presented concisely in terms of the $\Lambda_{k,j}^i$ coefficients. However, it is important to note that multiple factors contribute to each of these transfer and removal rate coefficients. After presenting the concise form of the transport equations, the specific terms included in the $\Lambda_{k,j}^i$ coefficients will be presented.

In developing equations representing the system shown in Figure 3-1, the quantity within each compartment or transferred from compartment is expressed in terms of the number of atoms in a chemical element group presented in Section 3.3 (Table 3-2). The quantity can also be

expressed in terms of radionuclide inventory for each nuclide. In the equations below, the term species can refer to a radionuclide or chemical element.

Referring to Figure 3-1, the rate of change of the number of atoms in compartment 1 (upper left) is determined from Equation (3-1):

$$\frac{dN_1^i}{dt} = R_1^i - \Lambda_{1,1}^i N_1^i + \Lambda_{1,2}^i N_2^i + \Lambda_{1,3}^i N_3^i + \Lambda_{1,4}^i N_4^i \quad (3\text{-}1)$$

Where:

R_1^i = the source release rate of species i in compartment 1 in atoms/s

$\Lambda_{1,1}^i$ = the removal rate of species i within compartment 1 in 1/s

N_1^i = the inventory of species i in compartment 1 in atoms

$\Lambda_{1,2}^i$ = the transfer rate of species i from compartment 2 to compartment 1 in 1/s

N_2^i = the inventory of species i in compartment 2 in atoms

$\Lambda_{1,3}^i$ = the transfer rate of species i from compartment 3 to compartment 1 in 1/s

N_3^i = the inventory of species i in compartment 3 in atoms

$\Lambda_{1,4}^i$ = the transfer rate of species i from compartment 4 to compartment 1 in 1/s

N_4^i = the inventory of species i in compartment 4 in atoms

The rate of change of the number of atoms in compartment 2 is given by Equation (3-2):

$$\frac{dN_2^i}{dt} = R_2^i - \Lambda_{2,2}^i N_2^i + \Lambda_{2,1}^i N_1^i + \Lambda_{2,3}^i N_3^i + \Lambda_{2,4}^i N_4^i \quad (3\text{-}2)$$

Where:

R_2^i = the source release rate of species i in compartment 2 in atoms/s

$\Lambda_{2,2}^{i}$ = the removal rate of species i within compartment 2 in 1/s

$\Lambda_{2,1}^{i}$ = the transfer rate of species i from compartment 1 to compartment 2 in 1/s

$\Lambda_{2,3}^{i}$ = the transfer rate of species i from compartment 3 to compartment 2 in 1/s

$\Lambda_{2,4}^{i}$ = the transfer rate of species i from compartment 4 to compartment 2 in 1/s

The rate of change in the number of atoms in compartment 3 is given by Equation (3-3):

$$\frac{dN_3^i}{dt} = R_3^i - \Lambda_{3,3}^i N_3^i + \Lambda_{3,1}^i N_1^i + \Lambda_{3,2}^i N_2^i + \Lambda_{3,4}^i N_4^i$$

(3 - 3)

Where:

R_3^i = the source release rate of species i in compartment 3 in atoms/s

$\Lambda_{3,3}^i$ = the removal rate of species i within compartment 3 in 1/s

$\Lambda_{3,1}^i$ = the transfer rate of species i from compartment 1 to compartment 3 in 1/s

$\Lambda_{3,2}^i$ = the transfer rate of species i from compartment 2 to compartment 3 in 1/s

$\Lambda_{3,4}^i$ = the transfer rate of species i from compartment 4 to compartment 3 in 1/s

The rate of change of the number of atoms in compartment 4 is given by Equation (3-4):

$$\frac{dN_4^i}{dt} = R_4^i - \Lambda_{4,4}^i N_4^i + \Lambda_{4,1}^i N_1^i + \Lambda_{4,2}^i N_2^i + \Lambda_{4,3}^i N_3^i$$

(3 - 4)

Where:

R_4^i = the source release rate of species i in compartment 4 in atoms/s

$\Lambda_{4,4}^i$ = the removal rate of species i within compartment 4 in 1/s

$\Lambda_{4,1}^i$ = the transfer rate of species i from compartment 1 to compartment 4 in 1/s

$\Lambda_{4,2}^i$ = the transfer rate of species i from compartment 2 to compartment 4 in 1/s

$\Lambda_{4,3}^i$ = the transfer rate of species i from compartment 4 to compartment 4 in 1/s

More generally, the rate of change of the number of atoms in the k[th] compartment in a set of n interconnected compartments is given by Equation (3-5) below:

$$\frac{dN_k^i}{dt} = R_k^i - \sum_{j=1}^{n} \lambda_{j,j}^i N_k^i + \sum_{j=1,k\neq 1} \lambda_{k,j}^i N_j^i$$

(3 - 5)

In Equation (3-5), R^i_k is the source release rate of species i in compartment k in atoms/s. The first summation represents the removal of terms from compartment k due either to removal within the compartment or transfer to another compartment. The second summation represents transfer from compartment j to compartment k. The general matrix formulation of transport Equation (3-5) is represented in Equation (3-6).

$$\begin{pmatrix} \dot{N}_1^i \\ \dot{N}_2^i \\ \dot{N}_3^i \\ \vdots \\ \dot{N}_n^i \end{pmatrix} = \begin{pmatrix} R_1^i \\ R_2^i \\ R_3^i \\ \vdots \\ R_n^i \end{pmatrix} + \begin{pmatrix} -\Lambda_{1,1}^i & \Lambda_{1,2}^i & \Lambda_{1,3}^i & \dots & \Lambda_{1,n}^i \\ \Lambda_{2,1}^i & -\Lambda_{2,2}^i & \Lambda_{2,3}^i & \dots & \Lambda_{2,n}^i \\ \Lambda_{3,1}^i & \Lambda_{3,2}^i & \ddots & \dots & \Lambda_{3,n}^i \\ \vdots & \vdots & \vdots & \dots & \vdots \\ \Lambda_{n,1}^i & \Lambda_{n,2}^i & \Lambda_{n,3}^i & \dots & -\Lambda_{n,n}^i \end{pmatrix} \begin{pmatrix} N_1^i \\ N_2^i \\ N_3^i \\ \vdots \\ N_n^i \end{pmatrix}$$

(3 - 6)

Note that the time derivative is represented by $\dot{N}_j^i$. The Λ coefficient matrix is a transfer matrix where the diagonal terms are the removal coefficients applicable to a given compartment j (hence the – sign) and the off-diagonal terms are transfer coefficients relating the transfer of material from various compartments to compartment j.

Off-diagonal transfer terms are calculated as f/V where f is the flow rate out of a compartment (volume units/s) and V is the compartment volume, yielding units of 1/s. This ratio is multiplied by the radionuclide inventory in the upstream connecting compartment to provide a source to the connecting downstream compartment. Diagonal terms or removal terms are more complex because of the various removal processes that are modeled in the RADTRAD-AC. However, the idea is the same in that a removal coefficient expressed in units of 1/s is multiplied by the radionuclide inventory to yield a removal rate. The terms included in the diagonal removal coefficients and the off-diagonal transfer coefficients are shown below (Equation 3-7) with details on the calculation of removal coefficients provided in Section 3.5.

The terms included in the diagonal removal coefficients each have unit of 1/s and are:

$$\Lambda_{j,j}^{i} = \lambda_{j,spr}^{i} + \lambda_{j,dep}^{i} + \lambda_{j,filter}^{i} + \sum_{k=1,k\neq j}^{n} \lambda_{k,j}^{i}$$

(3 - 7)

Where:

$\lambda_{j,spr}^{i}$ = the spray removal coefficient in 1/s

$\lambda_{j,dep}^{i}$ = the natural deposition removal rate in 1/s

$\lambda_{j,filter}^{i}$ = the filtered removal rated within a compartment in 1/s

$\lambda_{k,j}^{i}$ = the removal rate from compartment j toward compartment k in 1/s

The removal rate $\lambda_{k,j}^{i}$ includes a few different types of transfer between compartments as shown in Equation (3-8).

$$\lambda_{k,j}^{i} = \lambda_{k,j,leak}^{i} + \lambda_{k,j,filter}^{i} + \frac{f_{k,j}}{V_j}$$

(3 - 8)

Where:

$\lambda_{k,j,leak}^{i}$ = the transfer via leakage paths in 1/s

$\lambda_{k,j,filter}^{i}$ = the natural deposition removal rate in 1/s

$f_{k,j}$ = the filtered removal rated within a compartment in 1/s

V_j = the removal rate from compartment j toward compartment k in 1/s

The removal terms from Equation (3-8) are related to the off-diagonal transfer terms in Equation (3-6). However not all of the nuclide leaving compartment *j* necessarily reaches compartment *k*. The filtered flow and the DF related flow terms require an additional coefficient that indicates the fraction of the nuclide that was removed in transit. The terms in the off-diagonal transfer coefficients are shown in Equation (3-9).

$$\Lambda_{j,k}^{i} = \lambda_{j,k,leak}^{i} + \left(1 - \frac{\eta_{j,k}^{i}}{100}\right)\lambda_{j,k,filter}^{i} + \left(\frac{1}{DF}\right)\frac{f_{j,k}^{i}}{V_k}$$

(3 - 9)

Where:

$\eta_{j,k}^{i}$ = the percent efficiency of the filter in the path from compartment k to j

DF = the nondimensional DF for path with flow from compartment k to j

Equation (3-6) is solved in the RADTRAD-AC using a matrix exponential method based on work done in references [11] and [13]. Matrix exponential methods are used to solve systems of linear differential equations of the form $\dot{N} = R + \Lambda N$ subject to an initial condition N_0. The units of the solution variable are expressed in atoms. This quantity can be converted to other units such as grams or Becquerels (Bq). Section 3.6 discusses how dose is calculated from the number of atoms.

Note that radionuclide decay is not explicitly included in Equation (3-6). Rather, decay is accounted for in the RADTRAD-AC by dividing the solution of the differential equations into two parts: (1) radioactive decay and daughter in-growth, and (2) radionuclide transport. Inclusion of radioactive decay and daughter in-growth modeling with Equation (3-4) significantly increases the size of the linear system as well as the computational load to solve the system. The separation of these calculations was used to overcome the limitations of personal computers available at the time the original version of the RADTRAD-AC was developed and has been retained to the present time.

Radioactive decay and daughter production occur within a compartment, so no intercompartmental transfer needs to be considered. The equations that are solved for these processes at each time step are shown in Equation (3-10).

$$\frac{dN_j^i}{dt} = \sum_{v=1}^{n-1} \lambda_v \beta_v^i N_j^c + \lambda_{decay}^i N_j^i$$

(3 - 10)

Where:

β_v^i = the fraction of nuclide v that decays to nuclide i (dimensionless)

λ_v = the decay rate associated with β_v^i in 1/s

N_j^v = the quantity of nuclide v in compartment j

λ_{decay}^i = the rate of decay of nuclide i in 1/s

The decay and transport calculations are performed alternately. That is, the code begins its integration over a time step by analyzing the effect of radioactive decay and daughter in-growth on the inventory of all compartments using Equation (3-10). After updating the inventory, the code calculates the effect of radionuclide transport between compartments during that same time step using Equation (3-6). This process of alternating between radioactive decay and daughter in-growth and radionuclide transport continues until the specified end time is reached. In calculations where radioactive decay is not modeled, the solution algorithm is simplified to the single step of calculating radionuclide transport.

During the course of its numerical integration, the code keeps track of the quantity of each nuclide at each location. Locations include not only compartment volumes, but surfaces and

filters as well. By tracking the radionuclides in this manner, conservation of mass can be verified.

The analytical solution of a matrix equation in the form $\dot{N} = AN + R$ is $N(t) = N(0)e^{At} - A^{-1}(e^{At} - 1)R$ from Equation 3.7 and 3.8 of reference [13], can be confirmed by substituting the solution into the matrix equation. Numerical solution of the transport equations is accomplished by constructing the solution as a Taylor series expansion of the analytical matric exponential solution in terms of t (specifically the e^{At} term which is the only time dependent term) and truncating the series when the estimated relative error is less than 1E-08. One advantage of this approach is its capacity to obtain good solutions over large time intervals. The key assumption is that there is no change in any phenomenon during a time step, i.e., that the coefficients in the ordinary differential equations (ODEs) are constant.

Without this assumption, the method would not apply. In order to accommodate this assumption, the code synchronizes time steps with the user-supplied phenomena in order to capture changes in the coefficients. Another advantage of this approach is that it is very fast and extremely robust. The algorithm is essentially identical to the one described in reference [13]. A useful discussion of matrix exponential methods and how they are solved is given in reference [14].

The assumption that all nuclides can be grouped according to their chemical and transport similarities is also applied in the solution. Thus, four transport groups were used: noble gases, elemental iodine, organic iodine, and aerosols. Note that the aerosol transport group includes all radionuclides assumed to be aerosol as listed in Section 3.3. These transport groups interact with their surroundings differently, but all components of any one group act the same. This implies that all xenon and krypton isotopes will transport identically and that cesium, barium, and all other aerosol isotopes will transport identically. The user specifies the fractions for the released iodine and thus partitions the iodine within the latter three groups.

3.2 Adaptive Time Step Algorithm

The RADTRAD-AC includes a default algorithm for selecting time step size that is fast and has proven to produce good results for typical models. However, the default time step algorithm does not perform error checking to verify that a solution has converged. The *Adaptive Time Step* option increases the computational cost significantly, but allows the RADTRAD-AC to estimate error and adjust the time step size keeping the error within a specified limit. For many models, the *Adaptive Time Step* option will not change results significantly because the default time step algorithm is adequate to achieve convergence.

As discussed above, a single system of coupled ODEs that simultaneously represents all of the phenomena considered by the RADTRAD-AC is defined. Computation time can be reduced by dividing the calculations into two parts: (1) transport and (2) radioactive decay. The fundamental premise behind this approach is that during a time step of small enough duration, ignoring the interdependence of the two components of the calculations results in negligible error. That is, numerically solving the transport equations defining transfer of material between compartments during a time step can be solved numerically, without taking account of the radioactive decay and in-growth occurring over that period, will have a negligible impact on the transport solution. Likewise, solving the radioactive decay and in-growth equations during a time step, without considering the simultaneous phenomenon of transport between compartments, will have a negligible impact on the decay and in- growth results. Reducing the time step size reduces the error that results from separately calculating transport and radioactive decay, and the RADTRAD-AC automatically reduces the default time step size when decay is active. If the user is concerned with this approach, adaptive time step control can be enabled to assure that the error introduced by this assumption is small.

The purpose of an adaptive time step algorithm is to actively choose the time step size in order to keep the solution error below a specified limit. The exact error is not known, so error must be estimated. The error estimate is then used to decide if the time step is too large (or too small) and adjust the time step size accordingly. The adaptive time step algorithm involves the following steps:

1. The error is estimated at each time step by calculating two solutions for the next time step, with one solution being more accurate. The magnitude of the difference between the solutions is used to estimate the error. The errors range from 0, if there is no error, to a maximum error of 1. The error is scaled in order to reduce the number of time steps taken in regions where the solution is not changing significantly. The scaled error is also limited to the range 0 to 1.

2. The scaled error is compared to the user specified maximum error and the following steps are taken depending on the magnitude of the error:

    a. If the error value is above the maximum error value (0.001 by default, but can be set by the user), then the time step size is cut in half and the calculation is repeated.

    b. If the error value is between the maximum error and 1/10 the maximum error, the time step size is kept.

c. If the error is below 1/10 the maximum error the time step size is doubled starting with the next time step.

This algorithm works without modifications as long as error decreases as the time step size decreases and the time step size stay above the minimum time step size. Modifications to this logic to address special cases are discussed later in this section.

The governing equations for the RADTRAD-AC are defined and solved in terms of the radionuclide inventory (atoms) in each compartment. The key results; however, are the dose to hypothetical individuals located at specified locations. The dose values were used in calculating an error estimate since they are the primary values of interest. Additionally, the dose values are included in the plot file which makes it easier to understand the adaptive time step controller behavior and diagnose problems.

The ODE solves for $N^i_j(t_m)$ which is the number or atoms of nuclide i in compartment at time t_m (the time at time step m). Based on the nuclide quantities, dose values are calculated at each dose location specified in the model. Two different dose pathways are modeled cloudshine and inhalation, to calculate dose to the skin, thyroid, and TEDE. These doses are referred to as 'dose categories' for the remainder of this section. The dose that is calculated can be represented as a function of time by a vector $D_k(t_m)$, where the k index represents the different dose categories. A separate error is calculated for each category, and the largest of these is recorded as the error.

To estimate the error at each time step m, two solutions are calculated for time $t_{m+1} = t_m + \Delta t$ starting from the base solution point N^i_j™, with associated dose represented as $D_{k,B}$ (dose for category k at the base point):

1. The first solution at time t_{m+1} is calculated by advancing the ODE solver by a full time step of size Δt. The associated dose is represented as $D_{k,S1}$ (solution 1 dose for category k).

2. The second solution for time t_{m+1} is calculated by advancing the ODE solver by two half time steps (i.e. time steps of size $\Delta t/2$). The associated dose is represented as $D_{k,S2}$ (solution 2 dose for category k).

In order to estimate the error, it is useful to define a measure of magnitude for the dose vector. The most obvious choice is the Euclidean length, which gives an overall measure of the magnitude of the dose vector. The magnitude (or norm) of the dose vector will be represented as $//D//$.

To estimate the local error for dose category kk, the magnitude of the difference between the two solutions $//D_{k,S2} - D_{k,S1}//$ is compared to the magnitude of the change in the solution over the time step. The magnitude of the change in the dose over the current time step for solution 1 and 2 is $//D_{k,S1} - D_{k,B}//$ and $//D_{k,S2} - D_{k,B}//$ respectively. To characterize the change in the magnitude, the two values are averaged ($(//D_{k,S1} - D_{k,B}// + //D_{k,S2} - D_{k,B}//)/2$. A slightly modified version of the following formula is used in Equation (3-11) to calculate a local error:

$$error = \frac{2\,\|D_{k,S2} - D_{k,S1}\|}{\|D_{k,S1} - D_{k,B}\| + \|D_{k,S2} - D_{k,B}\|}$$

(3 - 11)

If we consider that the points $D_{k,B}$, $D_{k,S1}$, and $D_{k,S2}$ form a triangle, and that the error above is the magnitude (or length) of one side of the triangle compared to the average magnitude of the two remaining sides, it can be shown that the range of values for the error is 0 to 2. A value of 0 occurs if the dose solutions $D_{k,S1}$ and $D_{k,S2}$ are identical, in which case the numerator is 0. The range 0 to 1 seems to be a more natural choice for specifying an allowable error fraction, so the error equation was modified slightly by dropping the factor of 2, resulting in Equation (3-12) for local error:

$$local\ error = \frac{\|D_{k,S2} - D_{k,S1}\|}{\|D_{k,S1} - D_{k,B}\| + \|D_{k,S2} - D_{k,B}\|}$$

(3 - 12)

To provide an example of how Equation (3-12) works, the error will be calculated for a set of two nuclides (I-131 and I-132). Table 3-1 represents the values for I-131 and I-132 at the base step and after solution 1 and solution 2 are calculated.

Table 3-1 Local Error Solutions for I-131 and I-132

Solution Step	I-131 Dose (rem)	I-132 Dose (rem)	Magnitude $(I\text{-}131^2 + I\text{-}132^2)^{0.5}$ (rem)
D_B (20 hrs)	0.75	0.00130	
D_{S1} (24 hrs)	0.92	0.00153	
D_{S2} (24 hrs)	0.90	0.00150	
$D_{S1} - D_B$	0.17	0.00023	0.17000016
$D_{S2} - D_B$	0.15	0.0002	0.15000013
$D_{S1} - D_{S2}$	0.02	0.00003	0.020000002

Note that the change in the dose value (0.17) over a solution step for I-131 ($D_{k,S1} - D_{k,B}$) is much larger than the change in the dose value of 0.00023 for I-132. This is reflected in the magnitude of the dose vector since the value is very close to the I-131 value of 0.17 rem. In the error calculation below the small tail value is dropped. In general, it is the dose channels with the largest change in dose over a time step that dominates the error calculation. Over this time step, the local error is calculated by Equation (3-13).

$$local\ error = \frac{0.02}{(0.17 + 0.15)} = 0.0625 \qquad (3\text{-}13)$$

The default threshold for error is 0.001, so the local error exceeds the default threshold by an order of magnitude.

In test simulations it was found that the RADTRAD-AC required very small time steps to limit error despite the fact that the rate of dose increase was very small over the first few seconds in these cases. In order to avoid taking an excessive number of time steps over a time period when the changes in dose were small, the error is scaled in proportion to how quickly the dose is increasing compared to a more global measure of the rate of change in dose.

An error scaling factor is calculated using the following steps:

1. The local rate of change for the dose is characterized by taking the change in dose (rem) over the time step (i.e. $\|D_{k,S2} - D_{k,B}\|$) and dividing this by the time step size Δt. This gives a local rate of change $d\|D\|/dt$.

2. Two more global rate of change values are then calculated:

    a. One global estimate of $d\|D\|/dt$ is calculated by taking a time step of the default time step size. The error may be large for this time step, but the rate of change in dose provides a general estimate of how rapidly the dose is expected to increase over time steps of the default size. The calculation is only performed over the first 1/10 of the simulation because early on, this is the best estimate that can be obtained of the rate of change in dose. Later in the simulation, the calculated dose provides a reasonable estimate.

    b. The value $d\|D\| = \|D_{k,S} - D_{k,B}\|$ is integrated (i.e. summed over the time steps) and divided by the total simulation time DT. This basically gives a rate at which dose would have to increase over the whole simulation to get the current dose magnitude.

3. The scaling factor is calculated by dividing the local rate of change by the maximum of the two global rate estimates from step 2. If the local dose is changing at a very slow rate compared to the global measure, then the error is of less concern since the error is small in comparison to time when dose is increasing rapidly. If the scaling factor exceeds 1, it is set to 1.

4. The scaled error is calculated by multiplying the error by the scaling factor. The scaled error can then be used to decide if the time step size needs to be cut, held constant, or increased.

In some cases, it may be desirable to directly control the time step size even if the adaptive time step algorithm is used. This can be done by opening the *Property* window for the *Model Options* node and then left-clicking on the *Custom Editors* () icon for the *Time Step Table* text box to open the *Editing Time Step Table* window as shown in Figure 3-2. The user can then use the *Add* button to add rows to the table and specify a time step table with the minimum and maximum time step size set to the same value as shown in Figure 3-3. This will override the adaptive time step algorithm.

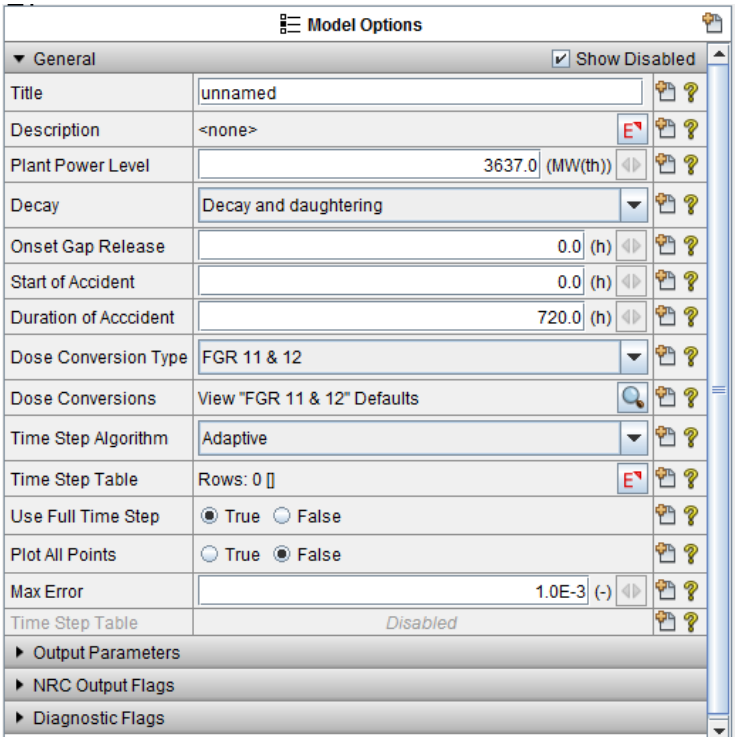


Figure 3-2 Property Window for the Model Option Node

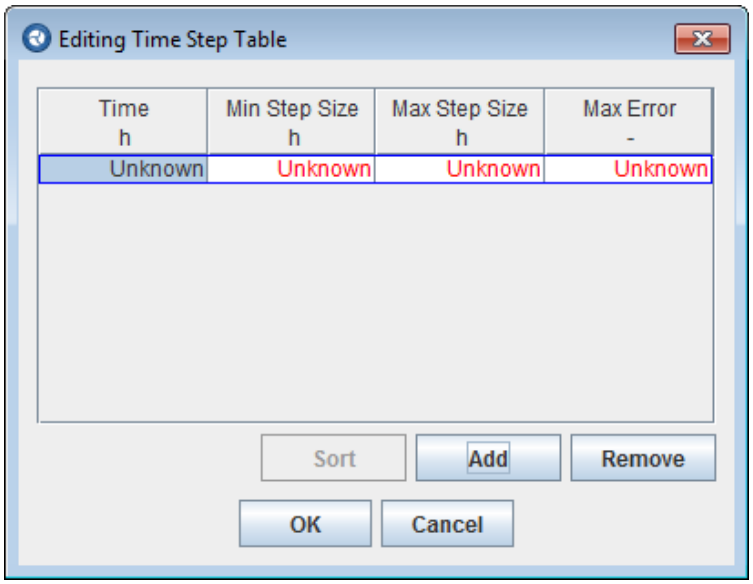


Figure 3-3 Editing Time Step Table Window

In test cases, it was found that the reported error was always large over the first few time steps. To stabilize the simulation, a few time steps are taken at the minimum time step size. The adaptive time step logic is interrupted occasionally over the first 1/10 of the simulation to take a step of the default size in order to calculate a scaling factor. In some cases the error may increase as the time step size is decreased due to round off error or due to instability of the numerical algorithm (which can happen if the time step size is too large). The adaptive time step algorithm tracks the error vs. time step size. If it detects a region where the error increases as the time step size decreases, the algorithm just uses a default time step for a few steps and returns control to the adaptive time step logic. In some cases the adaptive time step algorithm cuts the time step until the minimum time step size is reached. The adaptive time stepper will count how many steps it remains at the minimum time step size. If more than a few time steps are taken at the minimum time step, a time step of the default size is requested. This approach is used to keep the adaptive time algorithm from performing calculations for long periods at the minimum time step size.

3.3 Radionuclide Release Mechanisms

A large number of radionuclides in various chemical forms are generated in the fuel as the reactor operates. The nuclides which are generated are categorized into chemical groups in order to make the problem more tractable. Table 3-2 and Table 3-3 list the chemical grouping used in SNAP/RADTRAD. Note that the chemical grouping was revised from RADTRAD

version 3.03 because of the addition of the ICRP-38 nuclide set by combining strontium and barium into a single group and adding the other chemical elements as Group 9. Further changes were made in Revision 1 of Regulatory Guide 1.183 adding the Molybdenum group and slightly altering some of the other groups as shown in Table 3-3. The Revision one grouping is used when the model option for Regulatory Guide Revision is set to Rev 1. Since SNAP/RADTRAD treats all nuclides that are in Groups 3 and above as aerosols, there were no internal coding changes needed. A representative nuclide is used to identify each chemical group. The tenth group for non-radioactive aerosols is retained in SNAP/RADTRAD.

Table 3-2 Chemical Element Groups for SNAP/RADTRAD RG 1.183 Rev. 0

Group Number	Group Name	RG 1.183 Rev 0 Chemical Grouping	Additional Nuclides
1	Noble Gases	Kr, Xe	H *(H-3)*, Ne, Ar, Rn, N, O
2	Halogens	I	Br
3	Alkali Metals	Cs, Rb	
4	Tellurium Group	Te, Sb	Se
5	Barium, Strontium (Alkaline Earth Metals)	Sr, Ba	Sr, Ba
6	Noble Metals	Ru, Rh, Mo, Tc, Co	Pd
7	Cerium Group	Ce, Pu, Np	
8	Lanthanides	La, Zr, Nd, Nb, Pr, Y, Cm, Am	Eu, Pm, Sm
9	Others		Ac, Ag, Al, As, At, Au, Be, Bi, Bk, C, Ca, Cd, Cf, Cl, Cr, Cu, Dy, Er, Es, F, Fe, Fm, Fr, Ga, Gd, Ge, Hf, Hg, Ho, In, Ir, K, Lu, Md, Mg, Mn, Na, Ni, Os, P, Pa, Pb, Po, Pt, Ra, Re, S, Sc, Si, Sn, Ta, Tb, Th, Ti, Tl, Tm, U, V, W, Yb, Zn
10	Non-Radioactive Aerosols	No change	F, Cl [a]

a. F and Cl (halogens) are included in Group 10 since they likely do not behave like iodine.

Table 3-3 Chemical Element Grouping for SNAP/RADTRAD RG 18.183 Rev. 1

Group Number	Group Name	RG 1.183 Rev 1 Chemical Grouping	Additional Nuclides
1	Noble Gases	Kr, Xe	H *(H-3)*, Ne, Ar, Rn, N, O
2	Halogens	I	Br
3	Alkali Metals	Cs, Rb	
4	Tellurium Group	Te, Sb	Se
5	Barium, Strontium (Alkaline Earth Metals)	Sr, Ba	Sr, Ba
6	Noble Metals	Ru, Rh, Co	Pd
7	Cerium Group	Ce, Pu, Np	Zr
8	Lanthanides	La, Nd, Pr, Y, Cm, Am	Eu, Pm, Sm
9	Others		Ac, Ag, Al, As, At, Au, Be, Bi, Bk, C, Ca, Cd, Cf, Cl, Cr, Cu, Dy, Er, Es, F, Fe, Fm, Fr, Ga, Gd, Ge, Hf, Hg, Ho, In, Ir, K, Lu, Md, Mg, Mn, Na, Ni, Os, P, Pa, Pb, Po, Pt, Ra, Re, S, Sc, Si, Sn, Ta, Tb, Th, Ti, Tl, Tm, U, V, W, Yb, Zn
10	Non-Radioactive Aerosols	No change	F, Cl [a]
11	Molybdenum	Mo, Tc, Nb	

a. F and Cl (halogens) are included in Group 10 since they likely do not behave like iodine.

The iodine group is further subdivided into three physical forms, which are elemental, organic and aerosols. The fraction of each form depends on the source term model used. The radionuclide inventory for the fuel for all radionuclides of interest in dose analysis on a per MWth basis for PWR and BWR plants is included in SNAP/RADTRAD.

Two models available in SNAP/RADTRAD in which to model the release from the fuel are the TID-14844 model and the NUREG-1465 model. The TID-14844 model, which is generally applied to LOCA analysis, is based on the assumption that 100 percent of the noble gas radionuclides and 50 percent of the iodine radionuclides are available for release to the containment. The iodine release is reduced by a factor of 2 to account for deposition within the containment so that 25 percent of the iodine remains airborne in the containment based on the assumptions in Regulatory Guide 1.3 (RG 1.3), Revision 2, "Assumptions used for Evaluating the Potential Radiological Consequences of a Loss of Coolant Accidents for Boiling Water Reactors," [15] and Regulatory Guide 1.4 (RG 1.4), Revision 2, "Assumptions used for evaluating the Potential Radiological Consequences of a Loss of Coolant Accidents for Pressurized Water Reactors" [16]. No adjustment is made for the noble gases since radionuclides in this group are inert. The release is assumed to be instantaneous (a puff release) and is assumed to occur at the beginning of the accident (t=0). The fractions for the physical form of iodine used in the TID-14844 model are: elemental – 0.91, organic – 0.04, and aerosol – 0.05.

An alternative release model was developed in NUREG-1465 for LOCA analysis that considered the results of severe accident research conducted by the NRC. In this model, the release from the fuel is subdivided into the Gap release and the Early In-vessel release.

Radionuclides that have accumulated in the gap between the fuel pellet and the cladding that is released when cladding failure commences is the Gap release. The Early In-vessel release occurs as fuel rod temperatures increase driving the volatile nuclides, such as iodine from the fuel pellet into the vessel through the failed cladding. The release fractions for the Gap and Early In-vessel releases are summarized in the table below:

Table 3-4 Default DBA Release Rates

Group		Gap Release		Early In-Vessel Release	
		RG 1.183 Rev. 0	RG 1.183 Rev. 1	RG 1.183 Rev. 0	RG 1.183 Rev. 1
Nobel Gases	PWR	0.05	0.022	0.95	0.94
	BWR	0.05	0.008	0.95	0.96
Halogens	PWR	0.05	0.007	0.35	0.37
	BWR	0.05	0.003	0.25	0.54
Alkali Metals	PWR	0.05	0.005	0.25	0.23
	BWR	0.05	0.003	0.2	0.14
Tellurium	PWR	0	0.007	0.05	0.3
	BWR	0	0.003	0.05	0.39
Alkali Earth Metals	PWR	0	0.0014	0.02	0.004
	BWR	0	0	0.02	0.005
Noble Metals	PWR	0	0	0.0025	0.006
	BWR	0	0	0.0025	0.0027
Cerium	PWR	0	0	0.0005	1.5E-7
	BWR	0	0	0.0005	1.6E-7
Lanthanides	PWR	0	0	0.0002	1.5E-7
	BWR	0	0	0.0002	2.0E-7
Others	PWR	0	0	0	0
	BWR	0	0	0	0
Nonradioactive Aerosols	PWR	0	0	0	0
	BWR	0	0	0	0
Molybdenum	PWR	N/A	0	N/A	0.1
	BWR	N/A	0	N/A	0.03

The fractions for the physical form of iodine used in the NUREG-1465 model are: elemental – 0.0485, organic – 0.0015, and aerosol – 0.95.

Release phase duration is considered in NUREG-1465 in contrast to the instantaneous release model used in TID-14844. The release phase durations from Table 3-6 of NUREG-1465 are listed in Table 4-3. Additionally, the radionuclides for each phase are assumed to be uniformly released over the time period corresponding to that phase. These values do not differ between regulatory guidance revisions.

Table 3-5 Release Phase Durations for PWRs and BWRs

Release Phase	Duration (hours)	
	PWR	**BWR**
Gap	0.5	0.5
Early In-Vessel	1.3	1.5

Note that Gap release fraction models are available in SNAP/RADTRAD. The three models which are available are based on Table 3 of RG 1.183 Revision 0, Tables 3 and 4 of RG 1.183 Revision 1, and Regulatory Guide 1.25 (RG 1.25), “Assumptions Used for Evaluating the Potential Radiological Consequences of a Fuel Handling Accident in the Fuel Handling and Storage Facility for Boiling and Pressurized Water Reactors,” [17]. The Gap release fractions used are listed in Table 3-4. It should be noted that the release fractions for revision 1 are only used when the model option for Regulatory Guide Revision is set to Rev 1.

Table 3-6 Gap Fractions Used in SNAP/RADTRAD

Radionuclide		RG 1.25	RG 1.183 Rev. 0	RG 1.183 Rev. 1
I-131	PWR	0.12 [a]	0.08	0.07
	BWR	0.12 [a]	0.08	0.03
I-132	PWR	N/A	N/A	0.07
	BWR	N/A	N/A	0.03
Kr-85	PWR	0.3	0.1	0.40
	BWR	0.3	0.1	0.32
Other Noble Gases	PWR	0.1	0.05	0.06
	BWR	0.1	0.05	0.02
Other Iodines	PWR	0.1	0.05	0.04
	BWR	0.1	0.05	0.02
Alkali Metals	PWR	0.0	0.12	0.2
	BWR	0.0	0.12	0.16

a. The value in RG 1.25 is 0.1 and this value was increased by 20 percent to account for the use of extended burnup fuel, per NUREG/CR-5009, "Assessment of the Use of Extended Burnup Fuel in

Light Water Power Reactors," [18].

The FHA model for RG 1.183 Revision 0 also requires several other input parameters including the number of fuel rods or assemblies in the core, the number of fuel rods or assemblies damaged, the fraction of fuel rods or assemblies damaged, the radial peaking factor for the damaged assemblies, the pool iodine DF and the decay period. The pool iodine DF is set to a default value of 200 which is from Appendix B of RG 1.183 for water pool depths of 23 feet or greater. The decay time, essentially the time since plant shutdown is required in both options of the regulatory guide revision. Note that the decay calculation carried out by the SNAP/RADTRAD Model Editor input for the fuel handling accident does not include contributions from daughter products.

A new FHA model was added to Revision 1 of RG 1.183 that added in the re-evolution of elemental iodine. This model also requires the spent fuel pool volume, spent fuel pool surface area, the volumetric flow of the pool recirculation system, the recirculation system filter efficiency for iodine, the mass transfer coefficient, the acidity of the pool, and the inventory of nonradioactive iodine or I-127 (only seen in SNAP/RADTRAD when Rev 1 is set in the model options). Another addition to the Rev. 1 model is a box labeled pin pressure that will calculate the pool DF with regards to the fuel pin pressure. The equations below are equations B-1 through B-3 of RG 1.183 Revision 1.

$$DF_I = 81.046e^{0.305(t/d)}$$

(3 - 14)

Where:

$$t = 9.2261e^{-6E-4*x}$$

$$d = -0.0002x + 1.0009$$

And:

DF_I = elemental iodine DF
t = bubble rise time (s)
x = pin pressure (psig)
d = bubble diameter (cm)

It should be noted that this calculated pool DF is only applicable for pools with depths from 19-23 feet. The amount of iodine release that stayed in the pool is determined by the DF (either user-defined or calculated from the equations above) and is used to determine the total amount of iodine in the pool in moles from the following equation:

$$N_I = \sum \left(\frac{A_i(dis/s)}{\lambda_i(dis/atoms - s)} \right) / N_A$$

(3 - 15)

Where:

N_I = the total amount of iodine (moles)
A_i = activity for an individual isotope of iodine (Bq)

λ_i = decay constant for an individual isotope of iodine

Because SNAP does not allow you to enter stable isotopes into an inventory file, the equation above is only performed on radioactive isotopes of iodine that were provided in the inventory file. The following equation is used to account for the non-radioactive iodine (I-127):

$$N_{I-127} = \frac{m_{I-127}}{M_{I-127}}$$

(3 - 16)

Where:

$N_{I\text{-}127}$ = moles of iodine I-127
$m_{I\text{-}127}$ = user-provided amount of iodine I-127 (g)
$M_{I\text{-}127}$ = molar mass of I-127 (g/mol)

After the total amount of iodine in moles is gathered, the volatile fraction of iodine atoms in elemental form can be calculated.

$$X_e = \frac{B_m - \sqrt{B_m^2 - 16C_t^2}}{4C_t} \; [Equation\ B-11\ of\ RG\ 1.183\ Rev.1]$$

(3 - 17)

Where:

$$B_m = \frac{4C_t + 1}{R_i} \; [Equation\ B-10\ of\ RG\ 1.183\ Rev.1]$$

$$R_i = \frac{[I_2]}{[I-]^2} = \frac{C_h^2}{6.05x10^{-14} + 1.47x10^{-9}C_h} [Equation\ B-9\ of\ RG\ 1.183\ Rev.1]$$

$$C_h = [H^+] = 10^{-pH} [Equation\ B-8\ of\ RG\ 1.183\ Rev.1]$$

$$C_t = total\ I\ concentration(M)(moles\ I\ /L) = \frac{N_I + N_{I-127}}{1000 * V_{pool}}$$

$$[Equation\ B-7\ of\ RG\ 1.183\ Rev.1\ (with\ conversion\ from\ m^3\ to\ L)]$$

And:

V_{pool} = user-provided volume of the suppression pool (m^3)
pH = user-provided acidity of the suppression pool

With the fraction of iodine in elemental form (X_e), the evolution removal coefficient can be calculated using the following equation:

$$\lambda_e = \frac{K_L X_e S_{pool}}{V_{pool}} [Equation\ B - 12\ of\ RG\ 1.183\ Rev. 1]$$

(3 - 18)

Where:

K_L = mass transfer coefficient (default value of 3.66E-6 m/s)

S_{pool} = total pool surface area (m^2)

The user has an option to include a recirculation filter which is applied to the release fraction if the input value is greater than 0. The user can also include a compartment recirculation filter or a flow loop with a filter to model removal due to filtration.

The removal rate (λ_e) is then applied to each isotope of iodine (in atoms) in the pool to get an individual elemental release rate in atoms/s and is included in the dose calculations. The same is done for the total amount of iodine for the elemental group release rate. The release rate is calculated every time step and the change in time between time steps is used to calculate the change in iodine in the pool due to the release as well as applying removal due to decay (if decay is turned on).

3.4 Reactor Coolant System Activity Calculations

Models for specifying the release during a FHA, a REA, and CRDA have also been incorporated into SNAP/RADTRAD. The models generally follow those specified in RG 1.183. For the FHA, the user-selectable Gap release fractions are based on either RG 1.25 or RG 1.183 (both Rev. 0 and Rev. 1 are included) as listed in Table 3-4. In addition, relevant plant parameters (as described above) for modeling a FHA can be specified by the user. Similarly, for the REA-CRDA, a release model based on RG 1.183 is available in SNAP/RADTRAD (both Rev. 0 and Rev. 1). The release fractions used are the same as Table 3-4 except for Iodine and Noble Gases for RG 1.183 Rev. 0. RG 1.183 Rev. 0 has a footnote under the release fractions that states that Iodine and Noble Gases should have a 10% release, setting their fractions to 0.1. Also, the relevant plant parameters for cladding breach, fuel melt fraction and radial peaking factor can be set by the user in SNAP/RADTRAD. Additionally, when the model option for the Regulatory Guide Revision is set to Rev 1, the REA-CRDA accident type includes a box to include Transient Fission Gas Release. The transient fission gas release is additional fission release due to fuel fragmentation that is based on burnup and the average change in fuel rod

enthalpy. When the box is clicked, options to include the values for burnup and the change in enthalpy are included. SNAP/RADTRAD uses equations 1-4 in section 3.2 of RG 1.183 Rev. 1 to calculate the additional release values to be used. These values are then added on to the initial inventory for each nuclide. The transient fission gas release (T_{FGR}) value calculated by SNAP/RADTRAD is printed to the output when the Level Source diagnostic flag (in model options) is set to be greater than 0. These gap fractions are used in SNAP/RADTRAD to adjust the inventory. The adjusted inventory is then used as input (.icx file) to the RADTRAD-AC. So, the .icx input file will be the total inventory multiplied by the gap fractions listed in SNAP. The user should take this into consideration if any manual changes to the input file are made.

Like the automatic adjustment to the inventory in SNAP/RADTRAD, the ability to calculate the RCS activity, consider equilibrium activities based on DE I-131 and DE Xe-133 and iodine spiking has been incorporated into SNAP/RADTRAD. The RCS activity calculator, described in Section 2.4.2, determines the RCS concentrations using formulations based on the NUREG-0017, Revision 1, "Calculation of Releases of Radioactive Materials in Gaseous and Liquid Effluents from Pressurized Water Reactors (PWR- GALE Code)," [19], NUREG-0016, Revision 1, "Calculation of Releases of Radioactive Materials in Gaseous and Liquid Effluents from Boiling Water Reactors (BWR-GALE Code)," [20], and the ANSI/ANS-18.1-1999, "Radioactive Source Term for Normal Operation of Light Water Reactors," [21]. The formulations used are basically correlations correcting for plant-to-plant variations in power, system fluid and steam mass and flow rates and other plant-specific parameters applied to a reference PWR or BWR plant. The RCS activity calculations performed in SNAP/RADTRAD are similar to, but basically a subset of those performed by the PWR and BWR Gale codes.

Table 3-7 presents the formulae used by the SNAP/RADTRAD RCS activity calculator for the reference PWR plant to calculate coolant concentration adjustment factors for the radionuclide concentration in the RCS. Note that these formulations are applicable to plants with U-tube steam generators. The adjustment factors presented in Table 3-6 are multiplied by the reference PWR radionuclide concentrations given in Table 3-7 to obtain the RCS concentration (μCi/g).

Table 3-7 Formulations used to Determine RCS Water Radionuclide Concentrations in PWRs with U-tube Steam Generators

Element Class	**Adjustment Factor Formula** [a]
Noble Gases	$= \left(\frac{162 * P}{WP}\right)\left(\frac{0.0009 + \lambda}{R + \lambda}\right)$
Halogens	$= \left(\frac{162 * P}{WP}\right)\left(\frac{0.067 + \lambda}{R + \lambda}\right)$
Cs, Rb	$= \left(\frac{162 * P}{WP}\right)\left(\frac{0.037 + \lambda}{R + \lambda}\right)$

where

R = the removal rate - reactor coolant 1/hr
λ = the radionuclide decay constant in 1/hr
P = the core power in MWth
WP = the mass of reactor coolant system water lbm

Formulas for the removal rate (R) are presented below [b]

Noble Gases	$R = \frac{FB + (FD - FB) * Y}{WP}$
Halogens & Cs, Rb	$R = \frac{FD * NB + (1 - NB) * (FB + FA * NA)}{WP}$

where

FD = the removal rate in the reactor coolant in 1/hr
NB = the fraction of material removed in passing through the purification demineralizer
FB = the reactor coolant letdown flow in 1/hr
FA = the flow through the purification system cation demineralizer
NA = the fraction of material removed in passing through the cation demineralizer
Y = the ratio of the total amount of noble gases routed to gaseous radwaste from the purification system to the total amount routed from the primary coolant system (not including the boron recovery system)

a. The adjustment factor formula is from Table 2-7 of reference [19].

b. The formulas for the removal rates (*R*) are from Table 2-6 of reference [19] and Table 9 of reference [21]. The values for the constants are from a reference PWR described in Table 2-4 of reference [19] and Table 2 of reference [21]. The PWR-GALE code calculates the removal rates (*R*) for these nuclides for PWRs other than the reference PWR plant described in Table 2-4 of reference [19] and Table 2 of reference [21].

Table 3-8 RCS Radionuclide Concentrations for a Reference PWR Plant

Radionuclide	Concentration (µCi/g) [a]	Radionuclide	Concentration (µCi/g) [a]
Kr-83m [b]	0.0E+00	I-131	2.0E-03
Kr-85	4.3E-01	I-132	6.0E-02
Kr-85m	1.6E-02	I-133	2.6E-02
Kr-87	1.7E-02	I-134	1.0E-01
Kr-88	1.8E-02	I-135	5.5E-02
Xe-131m	7.3E-01	Cs-134	3.7E-05
Xe-133	2.9E-02	Cs-136	8.7E-04
Xe-133m	7.0E-02	Cs-137	5.3E-05
Xe-135	6.7E-02	Rb-86 [b]	0.0E+00
Xe-135m	1.3E-01		
Xe-138	6.1E-02		

a. The radionuclide concentrations are from Table 6 of reference [21].

b. The radionuclide concentration is not from Table 6 of reference [21].

Table 3-8 presents the formulae used by the SNAP/RADTRAD RCS activity calculator for the reference BWR plant to calculate coolant concentration adjustment factors for the radionuclide concentration in the RCS water and steam. The adjustment factors presented in Table 3-8 are multiplied by the reference BWR radionuclide concentrations given in Table 3-9 to obtain the RCS concentration (µCi/g) for either the RCS water or steam.

Table 3-9 Formulations used to Determine RCS Water Radionuclide Concentrations in BWRs

Element Class	Adjustment Factor Formula
Noble Gases [a]	1.0
Halogens	$= \left(\frac{112 * P}{WP}\right)\left(\frac{1.01 + \lambda}{R + \lambda}\right)$
Cs, Rb	$= \left(\frac{112 * P}{WP}\right)\left(\frac{0.19 + \lambda}{R + \lambda}\right)$

where

R = the removal rate - reactor coolant 1/hr
λ = the radionuclide decay constant in 1/hr
P = the core power in MWth
WP = the mass of RCS water lbm

Formulas for the removal rate (R) are presented below [b]

Noble Gases	1.0
Halogens & Cs, Rb	$R = \frac{FA * NA + NC * FS * NS * NB}{WP}$

where

FA = the water cleanup demineralizer flow rate in lb/hr
NA = the reactor water cleanup demineralizer DFs
NC = the ratio of condensate demineralizer flow rate to steam flow rate
FS = the steam flow rate in lb/hr
NS = the ratio of radionuclide concentration in reactor steam to the concentration in reactor water
NB = the condensate demineralizer DF

a. The adjustment factor formulas are from Table 2-5 of reference [20] and Table 10 of reference [21].

b. The formulas for the removal rates (R) are from Table 2-4 of reference [20] and Table 8 of reference [21]. The values for the constants are from a reference BWR described in Table 2-3 of reference [20] and Table 1 of reference [21]. The BWR-GALE code calculates the removal rates (R) for these nuclides for BWRs other than the reference BWR plant described in Table 2-3 of reference [20] and Table 1 of reference [21].

Table 3-10 RCS Radionuclide Concentrations for a Reference BWR Plant

Radionuclide	Liquid Concentration (μCi/g) [a]	Steam Concentration (μCi/g) [a]	Radionuclide	Liquid Concentration (μCi/g) [a]	Steam Concentration (μCi/g) [a]
Kr-83m	0.0E+00	5.9E-04	I-131	2.2E-03	4.4E-05
Kr-85	0.0E+00	4.0E-06	I-132	2.2E-02	4.4E-04
Kr-85m	0.0E+00	1.0E-03	I-133	1.5E-02	3.0E-04
Kr-87	0.0E+00	3.3E-03	I-134	4.3E-02	8.6E-04
Kr-88	0.0E+00	3.3E-03	I-135	2.2E-02	4.4E-04
Xe-131m	0.0E+00	3.3E-06	Cs-134	3.0E-05	3.0E-08
Xe-133	0.0E+00	1.4E-03	Cs-136	2.0E-05	2.0E-08
Xe-133m	0.0E+00	4.9E-05	Cs-137	8.0E-05	8.0E-08
Xe-135	0.0E+00	3.8E-03	Rb-86 [b]	0.0E+00	0.0E+00
Xe-135m	0.0E+00	4.4E-03			
Xe-138	0.0E+00	1.5E-02			

a. The radionuclide concentrations are from Table 5 of reference [21].

b. The radionuclide concentration is not from Table 5 of reference [21].

T/S equilibrium activity based on DE I-131 and DE Xe-133 are determined from the DCFs and the RCS concentration. Equations (4-14) and (4-15) show the formulation used

$$DE\ I131 = \frac{\sum_i C_i * DCF_i}{DCF_{I131}}$$

(3 - 19)

$$DEXe133 = \frac{\sum_i C_i * DCF_i}{DCF_{Xe133}}$$

(3 - 20)

Where:

DCF_i = the DCF for each iodine or xenon nuclide. [The thyroid DCF (Sieverts (Sv)/Bq) is used for iodine nuclides and the whole body DCF (Sv-m^3/Bq-s) is used for xenon nuclides.]

DCF_{I131} = the I-131 thyroid DCF (Sv/Bq)

DCF_{Xe133} = the Xe-133 whole body DCF (Sv-m^3/Bq-s)

C_i = the i-th radionuclide concentration in $\mu Ci/g$

The actual equilibrium factor is calculated from the user-specified value of DE I-131 (typically 1 µCi/g) divided by DE I-131. This factor is multiplied by the RCS activity to obtain the equilibrium activity based on DE I-131. The approach is the same for Xe-133 except that Xe-133 factors are applied. The calculation is performed separately for liquid and steam in BWRs.

The pre-incident spike activity is computed from the user-specified spike activity (typically 60 µCi/g) divided by DE I-131 and then multiplied by the RCS activity. The calculation is performed separately for liquid and steam in BWRs.

Co-incident spiking is somewhat more complicated as the iodine appearance rate must be determined. The appearance factor in units of Ci/h is computed.

$$AF = \left(MLD * \frac{1 - 1/DF}{WP}\right) * SpM * \left(\frac{3600}{1E6}\right) * WP * EFI \quad (3 - 21)$$

Where:

MLD = the normal letdown flow rate in gpm (converted to g/s in above equation)

DF = the mixed bed demineralizer DF

WP = the mass of RCS T/S leakage rate in gpm (converted to g/s in above equation)

SpM = the iodine spike multiplier

EFI = the equilibrium factor for iodine in $\mu Ci/g$

The total iodine appearance for co-incident spiking is computed by multiplying the appearance rate by the spike duration in hours to obtain the total iodine appearance. The iodine appearance is added to the equilibrium activity to obtain the total RCS activity for iodine. Note that co-incident spiking only applies to PWRs.

One item that should be noted is that there are several formulations for the calculation of the RCS inventory, including ANSI/ANS-18.1-1999, the PWR-GALE Code and the BWR-GALE Code. The current status of ANSI/ANS-18.1-1999 is that it has been administratively withdrawn because it was neither reaffirmed nor updated during a 10-year period. The American Nuclear Society has formed a Working Group in calendar year 2014 who are now updating ANSI/ANS-18.1-1999.

3.5 Removal Models

Models for radionuclide removal from the compartment atmosphere including sprays, natural deposition, leakage, and filters are included in SNAP/RADTRAD. The removal coefficients for the various removal mechanisms are equivalent. For example, filtration is expressed in terms of efficiencies, and natural deposition in terms of removal coefficients. These are related to each other as well as to DFs. The DF is defined as the ratio of the total material (aerosol or elemental iodine) subjected to a removal process to the total aerosol material that remains airborne. Equation (3-22) shows the relationship between the DF and the removal coefficient, λ.

$$\frac{dDF}{dt} = \lambda DF$$

(3 - 22)

The average DF is related to the mass fraction, m_f, remaining in the volume as shown in Equation (3-23).

$$m_f = \frac{M(t)}{M(0)} = \frac{1}{DF} = e^{-(\lambda t)}$$

(3 - 23)

Where:

$M(\mathrm{t})$ = the mass of aerosol as a function of time (t) in a compartment

$M(0)$ = the total mass subjected to removal in a compartment.

The DF is also related to the removal efficiency, η, as shown in Equation (3-24).

$$DF = \frac{1}{1 - \eta}$$

(3 - 24)

3.5.1 Spray Removal Model

The spray removal mechanism in SNAP/RADTRAD can be modeled using either the Powers' model, as described in NUREG/CR-5966, for aerosol removal or through the specification of user-defined removal coefficients. As the Powers' model is only applicable to aerosols, the SNAP/RADTRAD user will still need to specify removal coefficients for elemental and organic iodine.

The extent to which sprays will decontaminate an aerosol-laden atmosphere depends on the number of spray droplets falling through the atmosphere and the distance they fall. The water flux into the containment atmosphere is time dependent and the fall distance is dependent upon the containment design. The Powers' model is based on a correlation that determines the removal coefficient for an aerosol considering the spray water flux, Q ($m^3 \cdot H_2O/m^2 \cdot s$) and the fall height of the spray droplets $H(m)$ and considers uncertainty in the various parameters affecting spray removal. Since the model was developed from an uncertainty study, the user specifies a percentile. The "best estimate" value is associated with the 50th percentile, or median values; the lower bound is associated with the 10th percentile; and the reasonable upper bound, or largest DF, with the 90th percentile. The model was developed using values of 0.001, 0.1 and 0.25 cm^3 H_2O/cm^2 s for the spray water flux, Q, and fall heights of 500, 853, 1000, 1584, 2000, 3000, 4000, and 5000 cm. The aerosol removal coefficient is dependent on the fraction of the aerosol suspended in the atmosphere, m_f, which is defined as the aerosol mass in the atmosphere of a compartment at a given time, t, divided by the total aerosol mass released into the compartment atmosphere until this time. The model includes the effect of the unsprayed portions of the containment by incorporating the assumption that the circulation in the compartment is rapid compared with the removal rate. Equation (3-25) specifies the aerosol removal coefficient ($\lambda^i_{j,spr}$) at any time in units of 1/s.

$$\lambda^i_{j,spr} = \frac{1}{3600(1-\alpha)}(a - b log_{10}Q)\left[\left[1-\frac{m_f}{0.9}\right]^c + \left[\frac{m_f}{0.9}\right]^c\right] * [exp(A + BlnQ + CH + DQ^2H + EQH^2 + FQ + GQ^2H^2)]$$

(3 - 25)

The values for the constants A, B, C, D, E, F, G, a, b, and c in Table 4-10 are from Section 7 of NUREG/CR-5966. The parameter α is the ratio of the compartment volume not exposed to sprays to the compartment volume exposed to sprays (unsprayed volume/sprayed volume). If the assumption that the circulation is rapid compared with the removal rate is not valid, then the user can split the compartment into two separate compartments and model the flow from the unsprayed portions to the sprayed portions as a convective flow. In this case α would be zero for the compartment containing the sprays.

Table 3-11 Values for Coefficients used in the Powers' Spray Removal Model

Constant	Value		
	10th Percentile	**50th Percentile**	**90th Percentile**
A	5.5750	6.83707	7.10927
B	0.94362	1.0074	0.92549
C	0.0	-2.4045E-05	0.0
D	-6.9821E-03	-4.1731E-03	-8.0868E-04
E	-7.327E-07	9.006E-08	0.0
F	0.0	-1.2478	0.0
G	3.555E-06	0.0	0.0
a	0.1108	0.1815	0.3751
b	-0.00201	-0.01153	0.00648
c	0.8945	0.5843	0.2786

This expression was originally developed for a puff release of aerosols into a system. In those cases where there is a continuing release, the size distribution will continually be renewed by the injected particulate. The model has been extended for this case by setting coefficients A through G to zero. This makes the model assume that the size distribution has not changed in time and that most of the material suspended is fresh material provided by the source. The aerosols removed by the sprays are collected in the sump.

3.5.2 Natural Deposition Model

Natural deposition in SNAP/RADTRAD can be modeled using either Henry's correlation or Powers' model for aerosol removal due to natural deposition or through the specification of user-defined removal coefficients. As Henry's correlation and Powers' model are only

applicable to aerosols, the SNAP/RADTRAD user will still need to specify removal coefficients for elemental iodine.

3.5.2.1 *Henry's Correlation*

The correlation developed by Henry, described in reference [22], is based upon observation of experiments concerned with aerosol decontamination. The form of Equation (3-26) is based upon the consideration that sedimentation was the dominant phenomenon observed, and the coefficients were determined from experimental data from liquid metal reactor tests.

$$\lambda = C_1 \left(\frac{h_{ref}}{h}\right)\left(\frac{\rho_P}{\rho_{Pref}}\right)(\rho_A)^K \qquad (3 - 26)$$

where

h_{ref} = 5.0 m, as determined from the ABCOVE test AB5

h = the user-provided fall height in m

ρ_P = the user-provided particle density in kg/m^3

ρ_{Pref} = the theoretical sodium oxide particle density of 2270 kg/m, as determined from the ABCOVE test AB5

ρ_A = the aerosol mass in the volume.

The coefficients that best fit the data are:

Where:

$$\rho_A \geq 6.0E-05 \frac{kg}{m^3} \; then \; C_1 = 0.0220 \; and \; k = 0.60$$

$$\rho_A < 6.0E-05 \frac{kg}{m^3} \; then \; C_1 = 0.0016 \; and \; k = 0.33$$

Henry's correlation input can be modified to account for the influence of aerosol shape and moisture on the particle density by using Equation (3-27)

$$\rho_P = \alpha\rho_T + (1-\alpha)\rho_w$$

(3 - 27)

Where:

α = the ratio of the effective aerosol particle density to theoretical density

ρ_T = the theoretical density in kg/m^3

ρ_w = the density of water in kg/m^3.

In many cases the aerosol has only 20 percent of its theoretical density, so that in a high steam environment its effective density would be closer to that of water. This correlation is implemented in SNAP/RADTRAD.

3.5.2.2 *Powers' Model*

The Powers' model for aerosol removal due to natural deposition, in NUREG/CR-6604, is based on the observation of a self-preserving aerosol size distribution as a key component in

predicting aerosol behavior. Powers included the effects due to turbulence and to the multiple aerosol releases specified in NUREG-1465. The modified model was then compared with a series of CONTAIN computer code cases to verify the aging and aerosol size distributions due to the multiple sources. To account for the uncertainties, a large number of calculations were performed with the modified mechanistic model, with specific values for the type of reactor containment, reactor power, and the source term release phase, while varying the values of the uncertainty parameters. Typical uncertainty parameters were the containment pressure during the various release phases, the floor and wall surface areas, the zirconium inventory, the ratio of containment volume to thermal power, and the properties of the concrete. In all, over 20 parameters that were related to the phenomena were varied. Equation (3-28) shows the governing equation used in Powers' model

$$\frac{dDF_i(t)}{dt} = \lambda_{dep,I}(P_{th}, t)DF_i(t) \qquad (3\text{-}28)$$

where:

$\mathrm{DF_i(t)}$ = the DF for the i^{th} class of radioactive aerosol at time t where i indicates the phase at which the material was released into the containment: during the Gap or Early In-vessel phases

$\lambda_{dep,I}(P_{th}, t)$ = the decontamination coefficient at time t and power P_{th} for phase I

P_{th} = the thermal power of the reactor.

The decontamination coefficient should be weighted by each chemical group release rate as was done by Powers. However, SNAP/RADTRAD does not maintain the necessary weighting factors; hence a single chemical release rate based on iodine was used for the weighting coefficients.

The decontamination coefficient, λ, was solved over the various release time intervals and for the different types of reactors and various operating power levels using a Monte-Carlo uncertainty analysis. The results of these analyses are tabulated in Tables 3-12 and 3-13, for PWRs and BWRs, and are presented in terms of percentile DFs, $\lambda_{dep}(N\%, P_{th})$. Since the model was developed from an uncertainty study, the user specifies a percentile, $N\%$. The best estimate value is associated with the 50th percentile, or median values; the lower bound is associated with the 10th percentile; and the reasonable upper bound, or largest DF, with the 90th percentile.

Table 3-12 Correlations of Natural Deposition Decontamination Coefficients for PWRs DBAs

Release Phase	Time Interval (s)	Correlations (hr^{-1})
Gap	0 – 1800 (0 – 0.5 hr)	λ_{dep} (90) = 0.0365 + 3.580E-06 P(MWt) λ_{dep} (50) = 0.0268 + 3.475E-06 P(MWt) λ_{dep} (10) = 0.0182 + 3.260E-06 P(MWt)
Gap	1800 – 6480 (0.5 – 2.0 hr)	λ_{dep} (90) = 0.1036 [1 - exp (-2.239 P(MWt)/1000)] λ_{dep} (50) = 0.0820 [1 - exp (-1.159 P(MWt)/1000)] λ_{dep} (10) = 0.0645 [1 - exp (-0.938 P(MWt)/1000)]
Early In-Vessel	1800 – 6480 (0.5 – 1.8 hr)	λ_{dep} (90) = 0.0522 [1 - exp (-2.458 P(MWt)/1000)] λ_{dep} (50) = 0.0417 [1 - exp (-1.258 P(MWt)/1000)] λ_{dep} (10) = 0.0326 [1 - exp (-0.910 P(MWt)/1000)]
Gap + Early In-Vessel	6480 – 13,680 (1.8 – 3.8 hr)	λ_{dep} (90) = 0.421 [1 - exp (-2.530 P(MWt)/1000)] λ_{dep} (50) = 0.196 [1 - exp (-1.040 P(MWt)/1000)] λ_{dep} (10) = 0.094 [I - exp (-0.869 P(MWt)/1000)]
Gap + Early In-Vessel	13,680 – 49,680 (3.8 – 13.8 hr)	λ_{dep} (90) = 0.1920 - 1.35E-06 P(MWt) λ_{dep} (50) = 0.1382 + 6.85E-06 P(MWt) λ_{dep} (10) = 0.0811 + 10.15E-06 P(MWt)
Gap + Early In-Vessel	49,680 – 80,000 (13.8 – 22.22 hr)	λ_{dep} (90) = 0.1010 λ_{dep} (50) = 0.0912 λ_{dep} (10) = 0.0860 [1 - exp (-2.384 P(MWt)/1000)]

Table 3-13 Correlations of Natural Deposition Decontamination Coefficients for BWRs DBAs

Release Phase	Time Interval (s)	Correlations (hr^{-1})
Gap	0 – 1800 (0 – 0.5 hr)	λ_{dep} (90) = 2.903 [exp(-1060/P(MWt)] λ_{dep} (50) = 2.252 [exp(-1977/P(MWt)] λ_{dep} (10) = 1.285 [exp(-2199/P(MWt)]
Gap	1800 – 7200 (0.5 – 2.0 hr)	λ_{dep} (90) = 1.809 [exp(-777/P(MWt) λ_{dep} (50) = 1.722 [exp(-1777/P(MWt)] λ_{dep} (10) = 1.161 [exp(-2274/P(MWt)]
Early In-Vessel	1800 – 7200 (0.5 – 2.0 hr)	λ_{dep} (90) = 0.746 [exp(-626/P(MWt)] λ_{dep} (50) = 0.752 [exp(-1565/P(MWt)] λ_{dep} (10) = 0.520 [exp(-2173/P(MWt)]
Gap + Early In-Vessel	7200 – 18,000 (2.0 – 5.0 hr)	λ_{dep} (90) = 1.959 [exp(-548/P(MWt)] λ_{dep} (50) = 1.811 [exp(-1107/P(MWt)] λ_{dep} (10) = 1.551 [exp(-1507/P(MWt)]
Gap + Early In-Vessel	18,000 – 30,000 (5.0 – 8.33 hr)	λ_{dep} (90) = 1.533 [exp(-573/P(MWt)] λ_{dep} (50) = 1.317 [exp(-1225/P(MWt)] λ_{dep} (10) = 0.836 [exp(-1051/P(MWt)]
Gap + Early In-Vessel	30,000 – 43,200 (8.33 – 12.0 hr)	λ_{dep} (90) = 1.524 [exp(-647/P(MWt)] λ_{dep} (50) = 1.339 [exp(-1474/P(MWt)] λ_{dep} (10) = 0.780 [exp(-1316/P(MWt)]
Gap + Early In-Vessel	43,200 – 70,000 (12.0 – 19.4 hr)	λ_{dep} (90) = 1.564 [exp(-717/P(MWt)] λ_{dep} (50) = 1.373 [exp(-1634/P(MWt)] λ_{dep} (10) = 0.778 [exp(-1548/P(MWt)]
Gap + Early In-Vessel	70,000 – 86,400 (19.4 – 24.0 hr)	λ_{dep} (90) = 1.562 [exp(-719/P(MWt)] λ_{dep} (50) = 1.441 [exp(-1785/P(MWt)]

		λ_{dep} (10) = 0.780 [exp(-1686/P(MWt)]

Equations (3-29), (3-30) and (3-31) determine the current decontamination coefficient, λ_{net}, from the sum of the coefficients for each phase weighted by the iodine release rate, $S_{I2,I}$, for phase I.

$$\lambda_{net} = \frac{ln\{[DF(t+\Delta t)/DF(t)]\}}{\Delta t}$$

(3 - 29)

Where:

$$DF(t) = \frac{\sum_{I=1}^{4} S_{I2,I}}{\sum_{I=1}^{4} S_{I2,I}/DF_I}$$

(3 - 30)

$$DF_1 = \Pi_{I=1}^{4} exp[\lambda_{dep,I}(N\%, P_{th})t]$$

(3 - 31)

Table 3-14 also provides the decontamination coefficients for a DBA in an advanced pressurized-water reactor (APWR) design. These values are based upon work by Powers, which found that the CONTAIN-related calculation results were correlated with values in the table. These correlations do not vary with reactor thermal power; hence an approximation is used when the user selects a PWR design with a different power level.

Table 3-14 Correlations of Natural Deposition Decontamination Coefficients for APWR DBAs

Release Phase	Time Interval (s)	Correlations (hr^{-1})
Gap	0 – 1800 (0 – 0.5 hr)	λ_{dep} (90) = 0.466 λ_{dep} (50) = 0.233 λ_{dep} (10) = 0.029

Gap	1800 – 6480 (0.5 – 1.8 hr)	λ_{dep} (90) = 0.872 λ_{dep} (50) = 0.487 λ_{dep} (10) = 0.160
Early In-Vessel	1800 – 6480 (0.5 – 1.8 hr)	λ_{dep} (90) = 0.393 λ_{dep} (50) = 0.240 λ_{dep} (10) = 0.100
Gap + Early In-Vessel	6480 – 13,680 (1.8 – 3.8 hr)	λ_{dep} (90) = 1.210 λ_{dep} (50) = 0.980 λ_{dep} (10) = 0.731
Gap + Early In-Vessel	13,680 – 49,680 (3.8 – 13.8 hr)	λ_{dep} (90) = 0.594 λ_{dep} (50) = 0.397 λ_{dep} (10) = 0.245
Gap + Early In-Vessel	49,680 – 86,400 (13.8 – 24.0 hr)	λ_{dep} (90) = 0.598 λ_{dep} (50) = 0.327 λ_{dep} (10) = 0.107

The approximation used assumes that the significant difference between the PWR and the APWR design, in terms of natural deposition, is that the wall cooling enhances the phoretic deposition. Therefore, the difference in decontamination coefficient at 1800 MWt represents this phoretic deposition and is then scaled by the power ratio. Equation (3-32) represents the final approximation used

$$\lambda_{dep}(AP\_P_{th}) + [\lambda_{dep}(AP\_1800) - \lambda_{dep}(PWR\_1800)]\frac{P_{th}}{1800}$$

(3 - 32)

Where:

$\lambda_{dep}(AP\_P_{th})$ = the decontamination coefficient from the APWR at the power level indicated (P_{th} =1800 or design power)

$\lambda_{dep}(PWR\_P_{th})$ = the decontamination coefficient from the PWR DBA calculation for the power level indicated (P_{th} =1800 or design power).

3.5.3 Deposition in Piping Models

At the discretion of the user, piping can be modeled as a transfer pathway where deposition can occur. A model is available for the removal of fission products during transport through pipes.

Alternatively, the user may specify DFs and volumetric flow rates as a function of time. Noble gases are assumed not to interact with the piping and are transmitted without any depletion. The models chosen do not have documented limitations; however, the assumption is made that only primary deposition phenomena are being modeled. Scenarios in which supersaturated conditions occur, or in which very high or very low velocities are found, may give unrealistic results.

The models that are available in SNAP/RADTRAD for piping deposition include the Brockmann model for aerosol removal, the Bixler model for elemental iodine removal, and the Bixler model for organic iodine removal.

3.5.3.1 *Brockmann Model for Aerosol Removal*

The Brockmann model described in reference [23] is used to determine the amount of aerosol deposition that occurs in pipe bends and due to settling, turbulent inertia and diffusion. The mean particle diameter, d_p, used in the Brockmann model is assumed to be 1 μ with an average particle density, ρ_p, of 1000 kg/m^3. The temperature, pressure, open volume, and other parameters are provided by the user. Particles will settle due to gravitational force and deposit on the horizontally projecting lower surface of the flow path during transport. This turbulent flow deposition efficiency, η_g, is modeled in Equation (3-33).

$$\eta_g = 1 - exp(-U_g A_s/\pi Q)$$

(3 - 33)

$$U_g = \tau g$$

$$\tau = slip * d_p^2 \rho_p / 18\,\mu$$

$$slip = 1.0 + 2.0\frac{mfp}{dp}(1.257 + 0.4e^{-0.55dp/mfp})(dimentionless)$$

where:

U_g = the gravitational deposition velocity in m/s

τ = the particle relaxation time in s

Q = the user provided gas flow in m^3/s

A_s = the user provided total pipe surface area in m^2

μ = the viscosity of air, 1.93E-05 Pa-s

Mfp = the particle mean free path in cm

g = the gravitational acceleration in m/s^2

For instances of laminar flow, described in reference [24] the deposition efficiency is described by Equation (3-34).

$$\eta_g = 1 - \frac{2}{\pi}\left[2\epsilon\sqrt{1-\epsilon^{2/3}} - \epsilon^{1/3}\sqrt{1-\epsilon^{2/3}} + arcsin\sqrt{\epsilon^{1/3}}\right]$$

(3 - 34)

Where:

$$\epsilon = 0.75Z - 0.75\frac{LU_g}{UD}$$

And:

L = the horizontal pipe length ($A_s/\pi D$) in m
A_s = the user provided total pipe surface area in m^2
D = the pipe diameter ($4Vol/A_s$)
U_g = the gravitational deposition velocity in m/s
U = the linear velocity (Q/A_s) in m/s
Q = the user provided gas flow in m^3/s

The laminar and turbulent settling efficiencies are equivalent for Reynolds Number between 500 and 2300.

If the flow is turbulent, then turbulence in the central core can propel a particle into the laminar sublayer. If the particle inertia is high, then it will penetrate the sublayer and be collected on the wall. There have been experiments, reference [25], on inertial deposition velocity and Brockmann has modeled the turbulent deposition efficiency, η_{turb}, as shown in Equation (3-35).

$$\eta_{turb} = 1 - exp(U_t A_s/Q)$$

(3 - 35)

Where:

U_t = $0.01988\, U_{air}/Re^{1/8}$
Re = $\rho_{air} U_{air} d_H/\mu$

and

U_t = the turbulent inertial deposition velocity in m/s
U_{air} = the air velocity in m/s
d_H = the hydraulic diameter in m ($4\,Vol/A_s$)
ρ_{air} = the density of air in kg/m^3

When the flow in the pipe is slower as described in Equation (3-36), then the turbulent velocity is calculated using Equation (3-37).

$$\frac{\tau U_{air}}{d_H} Re^{3/4} < 326.3$$

(3 - 36)

$$U_t = 1.861E-07 \left[\frac{\tau U_{air}}{d_H}\right]^2 U_{air} Re^{11/8}$$

(3 - 37)

Small particles undergoing Brownian diffusion will diffuse from areas of high concentration to those of low concentration. Since the wall acts like a sink for these particles, there is net

diffusion from the bulk to the wall. This phenomenon has been analyzed in reference [26] and the diffusional deposition efficiency is modeled as shown in Equation (3-38).

$$\eta_{diff} = 1 - exp(-U_{diff} A_s / Q)$$

(3 - 38)

Where:

U_{diff} = the diffusion velocity in m/s

F_s = the user provided total pipe surface area in m^2

Q = the user provided gas flow in m^3/s.

In cases of laminar flow, this efficiency is modeled as shown in Equation (3-39).

$$\eta_{diff} = 2.56\zeta^{2/3} - 1.2\zeta - 0.177\zeta^{4/3}$$

(3 - 39)

Where:

ζ = the dimensionless diffusion parameter ($A_s D_{diff}/Q d_H$)

And:

A_s = the user provided total pipe surface area in m^2

D_{diff} = the particle diffusion coefficient in m^2/s

Q = the user provided gas flow in m^3/s

d_H = the hydraulic diameter in m [see Equation 3-35]

The particle diffusion coefficient is computed as shown in Equation (3-40) in units of cm^2/s units which is converted in the code to units of m^2/s.

$$D_{diff} = 1.38E - 16 T_g * \left[\frac{slip}{3\pi\mu dp}\right]$$

(3 - 40)

Where:

$slip = 1.0 + 2.0\frac{mfp}{dp}(1.257 + 0.4e^{-0.55dp/mfp})$ [See equation (3-33)]

And:

T_g	= the gas temperature in ºK
1.38E-16	= Boltzmann constand in g-cm^2/s^2-ºK
μ	= the viscosity of the gas in g/cm-s
dp	= the particle diameter in cm

When the flow is slow or the pipe length is large such that $\zeta > 0.02$, then the diffusional deposition efficiency is modeled as shown in Equation (3-41).

$$\eta_{diff} = 0.819exp(-3.657\zeta) + 0.097exp(-22.3\zeta) + 0.032exp(-57\zeta)$$

(3 - 41)

In cases of turbulent flow, the diffusional efficiency, from reference [27], is modeled as shown in Equation (3-42).

$$\eta_{diff} = 1 - exp\left[-\zeta^{2/3}0.0187Re^{13/24}\left(\frac{L}{d_H}\right)^{1/3}\right]$$

(3 - 42)

where

ζ	= the dimensionless diffusion parameter [see Equation (3-39)]
Re	= $\rho_{air}\, U_{air} d_H/\mu$ [see Equation (3-35)]
L	= the path length in m $(A_s/\pi d_H)$
A_s	= the user provided total pipe surface area in m^2
d_H	= the hydraulic diameter in m [see Equation (3-35)].

When the direction of gas flow is diverted in a bend, an aerosol particle may deviate from the gas flow due to its inertia and deposit on the wall. The efficiency of an aerosol particle in a bend is modeled as shown in Equation (3-43).

$$\eta_{bend} = \frac{\tau U_{air} \phi}{d_H}$$

(3 - 43)

where

τ = the particle relaxation time in s [see Equation (4-28)]

U_{air} = the air velocity in m/s

ϕ = the user-provided sum of the angles the flow has been diverted in radians

d_H = the hydraulic diameter in m [see Equation (4-30)].

When the flow is turbulent, the efficiency of an aerosol particle in a bend, from reference [28], is modeled as shown in Equation (3-44).

$$\eta_{\text{bend}} = 1.0 - \exp\frac{(-2.83\tau U_{\text{air}}\phi)}{d_H}$$

(3 - 44)

where

τ = the particle relaxation time in s [see Equation (3-33)]

U_{air} = the air velocity in m/s

d_H = the hydraulic diameter in m [see Equation (3-35)].

In cases of laminar flow, the efficiency of an aerosol particle in a bend is modeled as shown in Equation (3-45).

$$\eta_{bend} = \left(1.0 + \left(\frac{\tau U_{air}}{0.171 d_H}\right)^{P_1}\right)^{-P_2}$$

(3 - 45)

Where:

P_1 $= 0.452\left(\frac{\tau U_{air}}{0.171 d_H}\right) + 2.242$

P_2 $= \frac{2\phi}{\pi}$

Therefore, the total aerosol deposition efficiency is modeled as shown in equation (3-46).

$$\eta_T = 1.0 - (1.0\eta_g)(1.0 - \eta_{turb})(1.0 - \eta_{diff})(1.0 - \eta_{bend})$$

(3 - 46)

3.5.3.2 *Bixler Model for Elemental Iodine Removal*

The equation for the Bixler model for elemental iodine removal in pipes is given by Equation (3-47).

$$\eta_{ei} = 1 - exp\left(\frac{-A_s U_{ei}}{100Q}\right)$$

(3 - 47)

Where:

U_{ei} $= e^{2809/T-12.5}$

And:

T = the gas temperature in ºK

3.5.3.3 *Bixler Model for Organic Iodine Removal*

The equation for the Bixler model for organic iodine removal in pipes is given by Equation (3-48).

$$\eta_{oi} = 1 - exp\left(\frac{-A_s U_{oi}}{100Q}\right)$$

(3 - 48)

Where:

U_{oi} = $e^{2809/T-19.30}$

and

T = the gas temperature in °K.

Note: Organic iodine removal is not credited in design basis calculations.

3.5.4 BWR Main Steam Line

Regulatory Guide 1.183 Rev. 1 introduced a new model to removal rates of aerosol iodine in BWR Main Steam Lines (MSL). When the Rev 1 option is selected for the Regulatory Guide Revision option in model options, the pathway BWR Main Steam Line becomes available. The input options for this pathway are described in more detail in section 1.4.

The pathway calculates a removal rate for the outboard section and a removal rate for the inboard section of the MSL. The calculation uses the numerical integration method described in appendix A of Regulatory Guide 1.183 Rev. 1 which incorporates Equations A-1 through A-5. The amount of aerosol iodine being removed in the outboard section of the pipe is determined by the following equation:

$$N_{out} = \lambda_{out} N_{aero} \Delta t$$

(3 - 49)

Where:

λ_{out} = outboard removal rate (1/s)

N_{aero} = the amount of aerosol iodine in the outboard section of the MSL (atoms)

Δt = time step size (s)

The amount of aerosol iodine removed by the inboard section of the pipe is then shown by the following equation:

$$N_{in} = (N_{aero} - N_{out})\lambda_{in}\Delta t$$

(3 - 50)

Where:

λ_{in} = the inboard removal rate (1/s)

The RADTRAD-AC coefficient matrix combines equations (3-49) and (3-50) to get the removal rate from the to and from compartments attached to the MSL. It should be noted that the flow out of the compartment connect to the pathway is normalized by the user-specified outboard volume and not the attached compartment volume like the filtered pathways.

3.5.5 Filters

Heating, ventilation, and air conditioning (HVAC) system filter efficiency can be input by the user for the different nuclide groups as a function of time. The filter efficiency is specified as the fraction of material passing through the filter that is trapped on the filter media. This efficiency, expressed in terms of a decontamination coefficient as shown in Equation (3-51).

$$\lambda_{filter} = \left(\frac{\eta_{filter}}{100}\right)\lambda^{i}_{j,k,filter}$$

(3 - 5151)

Where:

$\lambda^{i}_{j,k,filter}$ = the volume-normalized flow rate from compartment through the filter in $1/s$

3.6 Dose Analysis

Doses in the environment, within a control room, or within a given volume due to inhalation and whole body immersion can be computed in SNAP/RADTRAD. The models used are presented

in the following sections and, as discussed in Section 2.4.1.1, the user can either choose the FGR 11 & 12 (default) or a user defined set of DCFs.

3.6.1 Offsite Dose Analysis

The dose to an individual at the EAB and the LPZ in the environment compartment is calculated in SNAP/RADTRAD. The dose due to cloudshine (immersion) for each nuclide, n, is calculated using Equation (3-52).

$$D_{c,n}^{env} = A_n \left(\frac{X}{Q}\right) DCF_{c,n}$$

(3 - 5252)

Where:

$D_{c,n}^{env}$ = the air immersion (cloudshine) dose due to nuclide n in the environment compartment in Sv

A_n = the integrated release of nuclide n in Bq

$\left(\frac{X}{Q}\right)$ = the user-provided atmospheric dilution factor in s/m^3

$DCF_{c,n}$ = the FGR 11 & 12 air immersion (cloudshine) DCF for nuclide n in Sv-m^3/Bq-s

The activity is related to the number of atoms of nuclide, n, as shown in Equation (3-53).

$$A_n = \lambda_n N_n$$

(3 -53 53)

Where:

λ_n = the radiological decay constant for nuclide n in 1/s.

The thyroid and committed effective dose equivalent (CEDE) doses due to inhalation from each nuclide, n, are calculated using Equation (3-54).

$$D_{i,n}^{env} = A_n \left(\frac{X}{Q}\right) BR * DCF_{c,n}$$

(3 - 5454)

Where:

$D_{i,n}^{env}$ = the inhalation dose commitment due to nuclide n in the environment compartment in Sv

A_n = the integrated release of nuclide n in Bq

$\left(\frac{X}{Q}\right)$ = the user-provided atmospheric dilution factor in s/m^3

BR = the user-provided breathing rate in m^3/s

$DCF_{c,n}$ = the FGR 11 & 12 inhalation DCF for nuclide n in Sv/Bq for the CEDE or thyroid

The TEDE is calculated as the sum of the CEDE and the immersion or cloudshine dose. Note that the conversion factor of 100 Rem = 1 Sv is applied to all the dose equations to obtain the dose in units of Rem. The total dose over the entire problem time is computed as the sum of the contributions over each time interval and each nuclide.

3.6.2 Control Room Dose Analysis

The dose to an individual in a control room is calculated from the time-integrated concentration of radionuclides in the control room compartment. The dose to the individual due to air immersion (cloudshine) in the control room is calculated using Equation (3-55).

$$D_{c,n}^{CR} = \left(\frac{DCF_{c,n}}{G_F}\right) OF \int C_n(t)dt$$

(3 - 5555)

Where:

$D_{c,n}^{CR}$ = air immersion dose (cloudshine) due to nuclide n in the control room compartment in Sv

$DCF_{c,n}$ = the FGR 11 & 12 air immersion (cloudshine) DCF for nuclide n in Sv-m^3/Bq-s

OF = the user-provided control room occupancy factor

$C_n(t)$ = the instantaneous concentration of radionuclide n in the control room in Bq/s

G_F = the Murphy-Campe geometric factor, given in reference [29], which relates the dose from an infinite cloud to the dose from a cloud of volume, V, in 1/m^3. This factor is defined in Equation (3-56).

$$G_F = \frac{351.6}{V^{0.338}}$$

(3 - 5656)

The thyroid and CEDE doses (inhalation dose) to an individual in the control room are calculated using Equation (3-57).

$$D_{i,n}^{CR} = \mathrm{BR} * OF * DCF_{i,n} \int C_n(t)dt$$

(3 - 5757)

Where:

$D_{i,n}^{CR}$ = the inhalation dose commitment due to nuclide n in the control room in Sv
$DCF_{i,n}$ = the FGR 11 & 12 inhalation DCF for nuclide n in Sv/Bq
OF = the user-provided control room occupancy factor
$C_n(t)$ = the instantaneous concentration of radionuclide n in the control room in Bq/s
BR = the user-provided breathing rate in m^3/s

The TEDE dose is calculated as the sum of the CEDE dose and the immersion or cloudshine dose. The total dose over the entire problem time is computed as the sum of the contributions over each time interval and each nuclide.

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