

SPK USER MANUAL

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SPK Help



Before You Start

This Help document is meant as a guide throughout the operation of the Model Design Agent (MDA). The MDA is an interface to the server-based SPK (System for Population Kinetics) computational engine for mixed effects models, and it allows the user to define, fit and simulate mixed effects nonlinear models, and view results. The MDA also produces a NONMEM(R)-compatible control file.

The following assumes that you have an account on MySPK and have downloaded the MDA on your computer. If you have not done so, please visit <http://spk.rfpk.washington.edu/info/> and click on the **MySPK** link. There you will also find instructions for installing the Java Runtime Environment necessary for running the MDA.

A printed version of the documentation is available by accessing the **User Manual** link on the MySPK webpage.

Bug reports are encouraged and very welcome. They should be filed through the SPK Bug Report page, <http://bugzilla.rfpk.washington.edu/>. The SPK Software Development Team uses the Bugzilla system. If you have problems filing a bug report, please use the contact information on the website. If you are a first time user, you may find it helpful to look at the **Getting Started** link on the MySPK webpage.

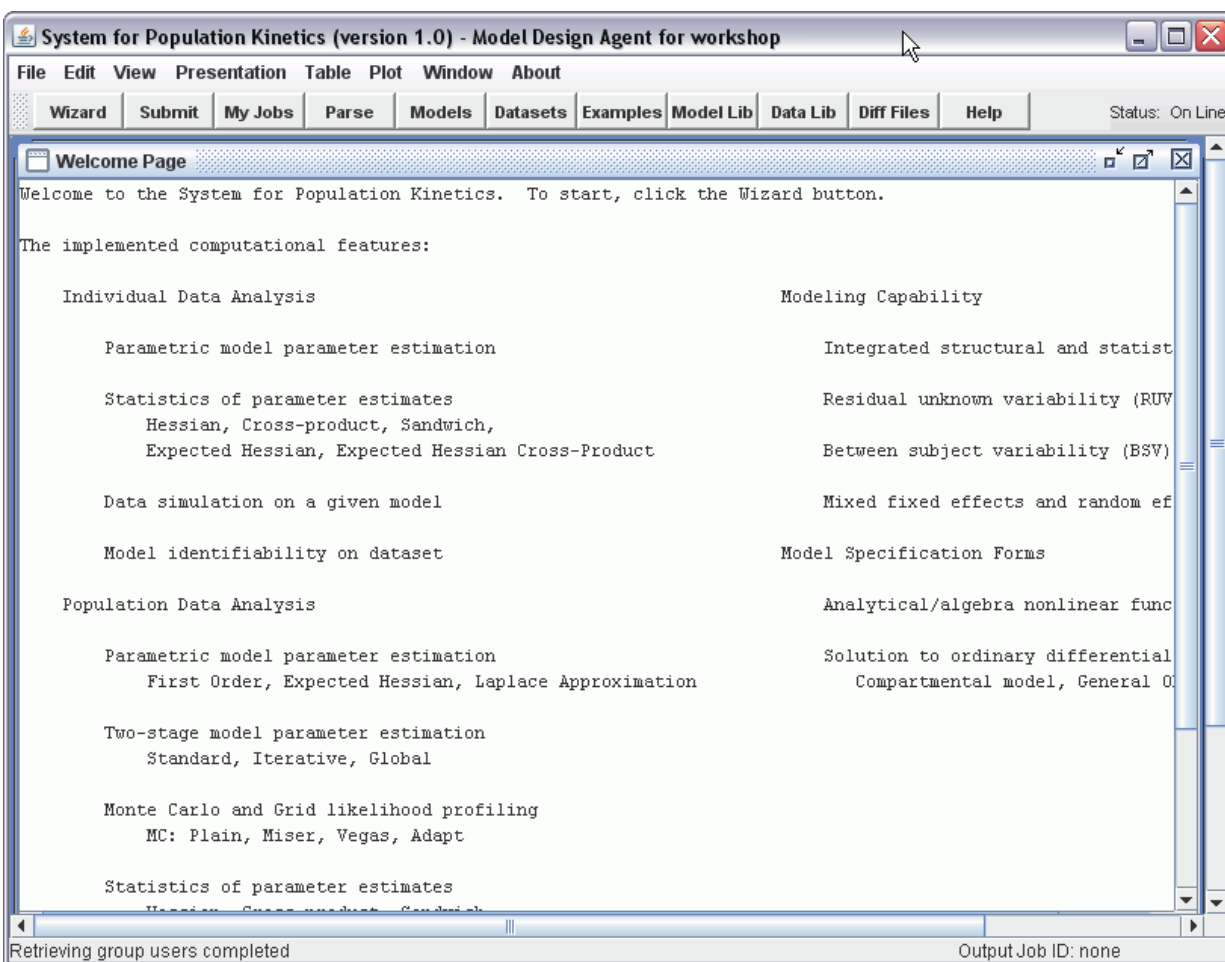
The development of the software described in this User Manual was partially supported by NIH/NIBIB grant P41 EB001975, "Resource Facility for Population Kinetics". If you use this software in a publication, please acknowledge this funding source using the wording above and please send a publication reprint or a PubMed citation to: RFPK Principal Investigator, Box 355061, University of Washington, Seattle, WA 98195-5061.

NONMEM(R) is a registered trademark of the Regents of the University of California. The software NONMEM(R) is distributed by GloboMax(R) LLC, Hanover, MD 21076 USA, <http://www.globomax.com/>. When NONMEM(R) is mentioned in this document, NONMEM Version V is intended.



Introduction

This is the first screen you will see once you have logged into MySPK and have downloaded the Model Design Agent (MDA)



If you see "Status: On Line" on the upper right corner of the MDA, you are connected to the Internet and you can use the MDA to view old jobs or submit new jobs to the SPK server. Buttons on the top have the following functions:

- **Wizard:** Starts an interactive tool that helps the user to interactively create a model file. The model file is compatible with a NONMEM(R) control file, and is saved as a SPK input file in XML. The tool can also take an existing model file or SPK input file, and helps the user

to modify it. If you are just getting started, this is the first button to click.

- **Submit:** Submits a job to the SPK server. Before clicking on this button, an SPK input file should be opened and displayed in the editor window. This button, when activated, brings up the **Job Submission Dialog**. In this dialog there are three tabbed panes for "Model", Dataset" and "Job", respectively. The "Model" and the "Dataset" panes allow the user to specify the names and descriptors of the model and the dataset used in the job. If one of the likelihood numerical integration methods is being used, these panes are ignored (since the parent job's model and dataset must be used in this case, and the system will do it automatically). The "Job" pane displays the analysis method for the job and allows the user to enter a short job abstract. Again, if a likelihood evaluation method (the radio button text is ended with "integration on likelihood") is selected, the job must have a parent and the parent job's input file must be loaded from the server before clicking the "Submit Job" button.
- **My Jobs:** Displays the user's job list in the SPK server. If a job is selected, the job information dialog box is displayed showing the model and dataset used by the job. The model, the dataset or the SPK job input/output can be returned and displayed in the MDA editor window, or the user may choose to automatically start the SPK input file preparation tool or the SPK output processing tool. The user can also find the job's history, the job's parent job and the job's identification number in the dialog.
- **Parse:** Processes the SPK output file shown in the editor window, parses the SPK output file in XML and allows the user to save data and tables that was returned from the server.
- **Models:** Displays the user's model list in the SPK server, gets and displays user selected model version in the editor window.
- **Datasets:** Displays the user's dataset list in the SPK server, gets and displays user selected dataset version in the editor window.
- **Examples:** Displays an example job list in the SPK server. If a job is selected, a dialog box is displayed showing the model and dataset used by the job. The model, the dataset or the SPK job input/output can be displayed in the MDA editor window, or the user may choose to start the SPK input file preparation tool or the SPK output

processing tool. The user can also find the job's history and the job's parent job in the dialog.

- **Model Lib:** Displays a list of the models available in the model library in the SPK server, retrieves and displays user selected model version in the editor window.
- **Data Lib:** Displays dataset list of the dataset library in the SPK server, gets and displays user selected dataset version in the editor window.
- **Diff Files:** Compares two text files. Any of the files may be either on the SPK server as model or data archives or on the user's computer.
- **Help:** Displays this document.



Prepare Input: Analysis Selection

Congratulations! You have just started the creation of a new model in the MDA. This is the screen you are seeing:

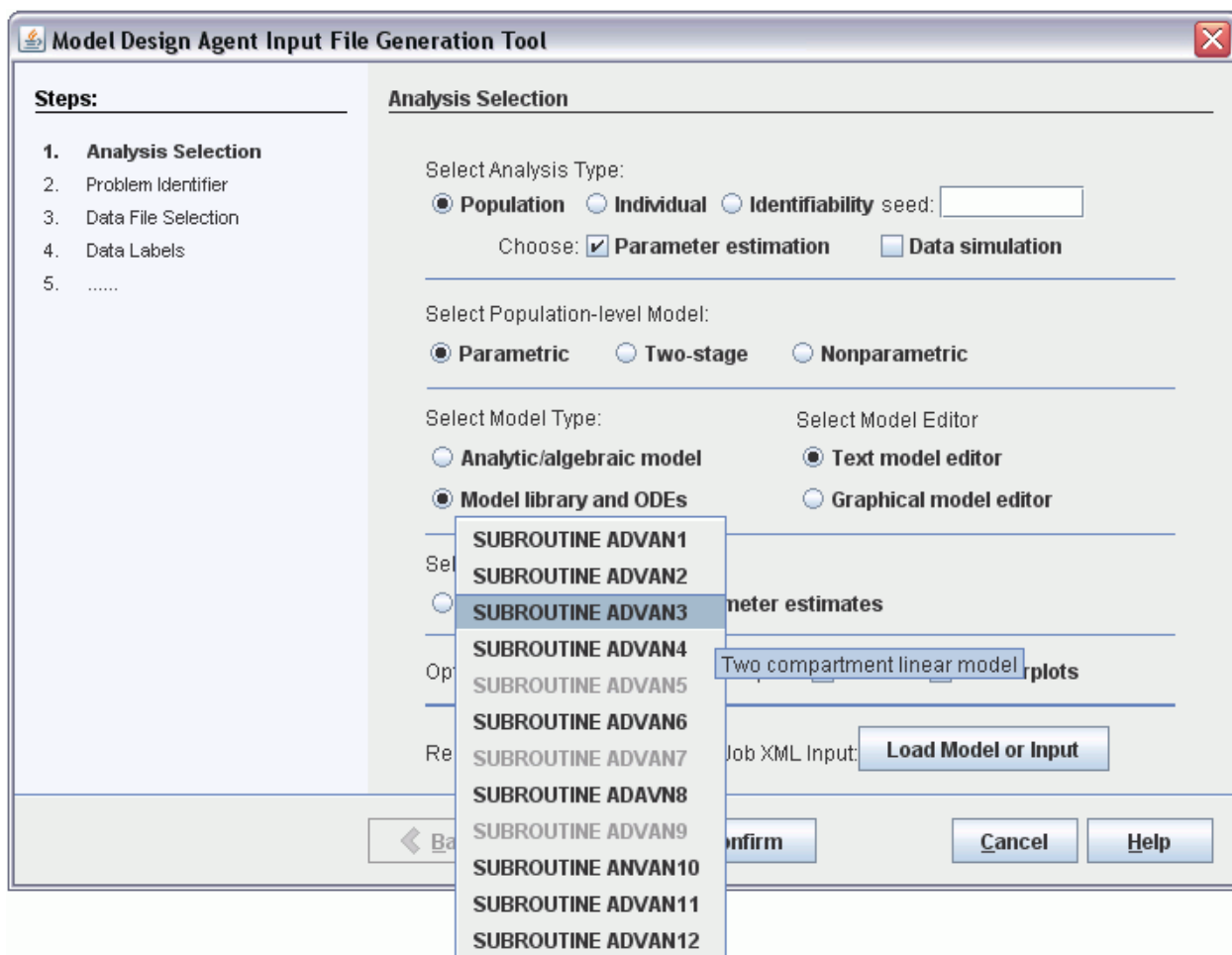
The screenshot shows a software window titled "Model Design Agent Input File Generation Tool". On the left is a "Steps:" sidebar with a list: 1. Analysis Selection (highlighted), 2. Problem Identifier, 3. Data File Selection, 4. Data Labels, 5. The main area is titled "Analysis Selection" and contains several sections of options:

- Select Analysis Type:** Radio buttons for **Population** (selected), **Individual**, and **Identifiability**. A "seed:" text box is next to **Identifiability**.
- Choose:** Checkboxes for **Parameter estimation** (checked) and **Data simulation**.
- Select Population-level Model:** Radio buttons for **Parametric** (selected), **Two-stage**, and **Nonparametric**.
- Select Model Type:** Radio buttons for **Analytic/algebraic model**, **Model library and ODEs**, **Text model editor**, and **Graphical model editor**.
- Select Statistics Option:** Radio button for **Compute statistics of parameter estimates**.
- Optional NONMEM Compatible Output:** Checkboxes for **Tables** and **Scatterplots**.
- At the bottom: "Reload Previous SPK Model or Job XML Input:" followed by a **Load Model or Input** button.

At the bottom of the window are five buttons: **Back**, **Next**, **Confirm**, **Cancel**, and **Help**.

There are several data processing options in the MDA:

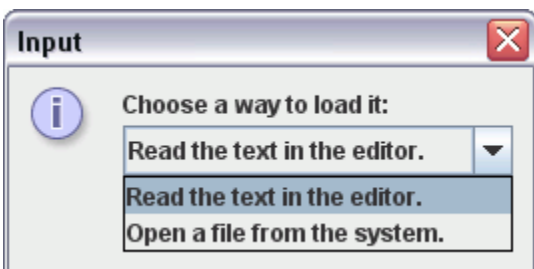
- The first option has to do with specifying whether you would like to analyze your data using **Population Analysis** (more than one subject), **Individual Analysis** (just one subject) or **Identifiability** (checking whether the model parameters can be uniquely identified by the given data). Briefly, individual analysis is applicable to an individual data set, while pooled (population) data should be analyzed using either a population analysis method or a two-stage method.
- The next step is to select the data analysis possibilities. One is **Parameter Estimation**, while the other is **Data Simulation**. At this stage the user can select both simultaneously or just one of them, depending on the intent. The parameter estimation features will quantify model parameters from available data; the simulation feature will create synthetic data from a model and its parameter values. Selecting both will first simulate data and then estimate parameters from the synthetic data.
- If a population analysis is selected, one of the analysis type radio buttons below must also be selected. The options are: **Parametric**, to use a likelihood approximation method such as the First Order, conditional on parametric population distributions such as Gaussian or log-normal; **Two-Stage**, to estimate the population parameters by sample averaging across individuals (recommended for rich data only); and lastly, **Nonparametric**, to estimate population probability distribution without assuming anything about their shape.
- The next option is the model type. You will have to specify whether you will be creating an **Analytic/Algebraic Model**, or whether you will be using the **Model Library and ODEs**. The Model Library includes the standard differential equation ADVAN and TRANS modeling frameworks used by NONMEM(R); the available ADVANs are visible in a drop-down menu, and their parameterizations are visible by pointing the mouse to the library model name. If you have selected **Model Library and ODEs**, you will also have the option to use a **Text Model Editor** (a textual wizard to write model equations and/or differential equations) and a **Graphical Model Editor** (where the model is built on the screen using point-and-click capabilities). This selection should be made at this time.



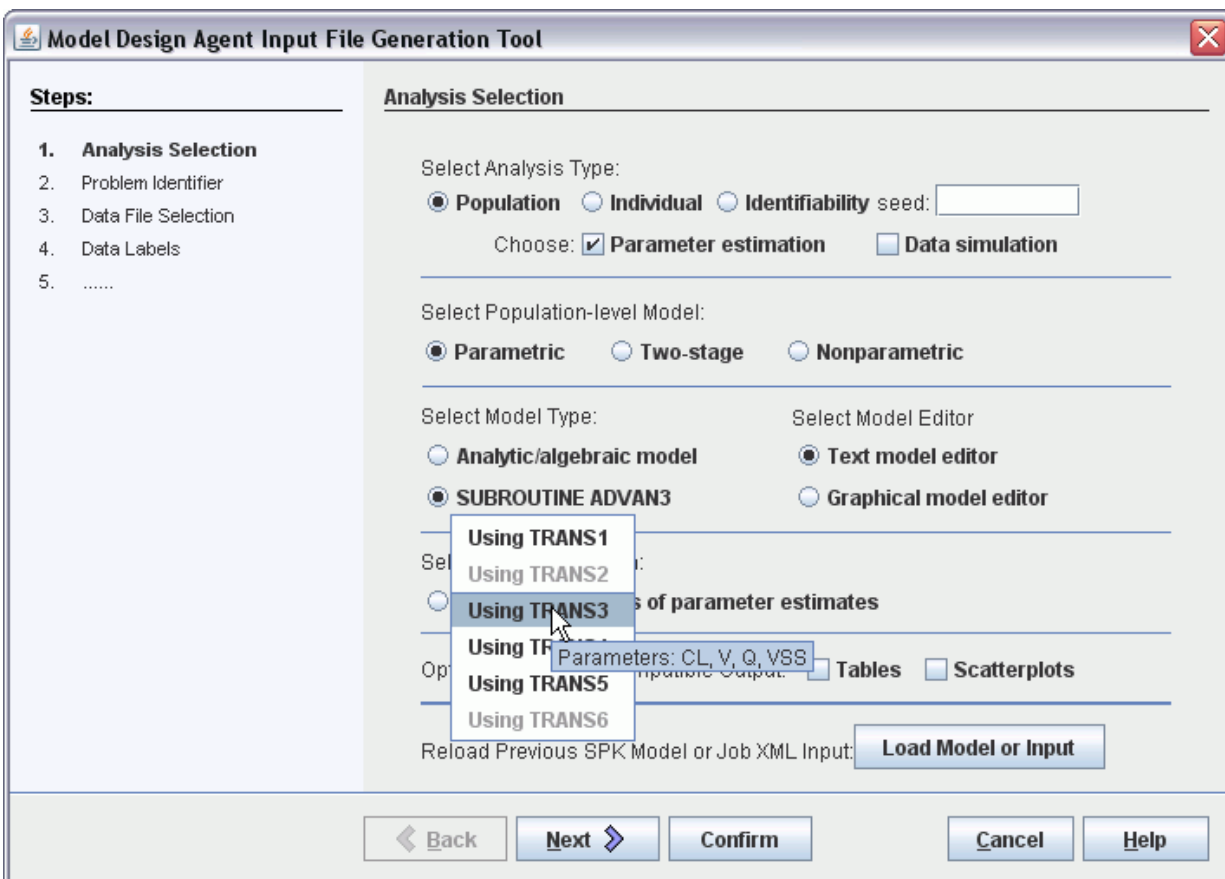
- Lastly, you will have to specify whether you desire statistics of the estimates by clicking next to **Compute Statistics of Parameter Estimates**. The calculation of statistical output requires computational resources, so it may lengthen the time it takes for your model to solve.
- Tables and plots are *automatically generated* by the MDA. However, if a NONMEM(R) compatible control file is desired, and depending on the desired output format, one or both of **Tables** or **Scatterplots** must be checked to obtain tabular and graphical output respectively. In other words, custom scatterplots and tables can always be created after the SPK model run is completed, so these buttons are only supplied for creating a NONMEM(R)-compatible input file.

The button labeled "**Load Model or Input**" allows you to reload a model you created with the MDA or a full SPK input file (which contains both model and data specifications). The model can be loaded from the MDA

Editor Window or from a file stored on your local file system. If you select this option, you will see a window that prompts you for a choice.



For example, the situation where we want to perform population analysis using the predefined ADVAN3 (two-compartment model with input in the first compartment) module and we are also requesting statistics on the estimates and both tabular and graphical outputs compatible with NONMEM(R) is shown in the screen shot below. Note that you will have to select a parameterization (TRANS) for ADVAN3



After you have performed the requested operations, the "Next" button will highlight and you can select it and continue. You can navigate back and forth in the MDA interface using the "Back" and "Next" buttons. The "Confirm" button displays the NONMEM(R) control file generated by the

MDA up to this step in the process. Clicking "Cancel" will abort the model definition, while selecting "Help" will bring you to the relevant Help topic.



Prepare Input: Problem Identifier

This area of the MDA allows you to define an identifier for the problem you are building. This is the screen you should see:

The identifier is up to 72 characters long and any alphanumeric character can be used. Special characters are also supported.

After you have performed the requested operations, the "Next" button will highlight and you can select it and continue. You can navigate back and forth in the MDA interface using the "Back" and "Next" buttons. The "Confirm" button displays the NONMEM(R) control file generated by the MDA up to this step in the process. Clicking "Cancel" will abort the model definition, while selecting "Help" will bring you to the relevant Help topic.



Prepare Input: Data File Selection

This area of the MDA is where data are selected for association with the model file. Data should be in tab, space or comma delimited column format with identifiers or other labels preceded by the character "C". There is no limit to the number of columns that can be in a single data file.

There are four options available. If you have previously loaded an entire SPK input file (model and data), then the MDA has that data file in memory and can access it. You also have the option to load a new data file here. This is the screen shot you should be seeing:

The screenshot shows a window titled "Model Design Agent Input File Generation Tool" with a "Data File Selection" tab. On the left, a "Steps:" list shows: 1. Analysis Selection, 2. Problem Identifier, 3. **Data File Selection**, 4. Data Labels, and 5. The main area contains four radio button options:

- ☐ Use data file previously loaded from parent job. (Includes a "Data file name:" label and a "Save File" button)
- ☐ Load in dataset from My Datasets (Includes a "Save File" button)
- ☐ Load in dataset from Dataset Library (Includes a "Save File" button)
- ☒ Load in data file from local file system (Includes a label "Enter data file name (including full path) or browse.", a "Browse" button, and a "Read File" button)

Below the "Read File" button, red text reads: "Click 'Read File' button to load data file." At the bottom of the window are buttons for "Back", "Next", "Confirm", "Cancel", and "Help".

The dataset could be loaded from your database account, under My Datasets, it could be loaded from the Dataset Library or it could be loaded from the local file system. In this instance, if you select to browse, a dialog window will open and allow you to browse your local file system. The window may open in a different location on your hard disk. Select your data file name and click "Open". No special suffixes are necessary for the data file. Once your data file has been selected, you will need to

click the "Read File" button to proceed. The MDA will parse your data file and display a message with the number of columns it would find in your data file, for example: "There are 3 columns in your data file".

If you instead choose to select a dataset from your own datasets, a database browsing window will become available:

Dataset ID	Dataset Name	No. of Versions	Last Revised Time	Description
397	Phenobarbital Pop	1	PST 2006-08-24 11:57:00	Phenobarbital population dataset
396	Cadralazine Pop	1	PST 2006-08-23 18:14:15	Cadralazine population dataset
393	Theophylline Pop RSS	2	PST 2006-08-22 16:54:56	Theophylline dataset from Dataset Library with reduced samp...
392	Theophylline Pop	1	PST 2006-08-22 12:39:16	Theophylline population dataset from Dataset Library
390	Theophylline Sub01	1	PST 2006-08-21 13:13:14	Theophylline dataset Subject 01
387	Cpeptide Population	2	PST 2007-09-25 06:10:39	Cpeptide population data
385	Cpeptide Sub01	1	PST 2006-08-18 14:00:40	Cpeptide data for Subject 01
382	Cadralazine Px10	1	PST 2006-08-18 11:01:54	Cadralazine data for Patient 10
381	Cadralazine Px09	1	PST 2006-08-18 11:01:11	Cadralazine data for Patient 09
380	Cadralazine Px08	1	PST 2006-08-18 11:00:19	Cadralazine data for Patient 08
379	Cadralazine Px07	1	PST 2006-08-18 10:59:24	Cadralazine data for Patient 07
378	Cadralazine Px06	1	PST 2006-08-18 10:58:45	Cadralazine data for Patient 06

List ☒ Versions ☐ Jobs Group member: workshop Total found: 17 Previous Page Next Page

Clicking once on the dataset name will load the data into memory. In this particular instance, if we select the cadralazine dataset from Wakefield et al., 1996, you will be prompted for selecting a particular version:

Revision	Author	Revised Time	Log Message
1	Paolo_Vic...	PST 2006.08.23.18.14.15	Cadralazine population dataset without AMT

After you select it, the dataset name will appear in the Data File Selection Window, and you may click Next to proceed, as shown below:

The screenshot shows a software window titled "Model Design Agent Input File Generation Tool". On the left, a "Steps:" panel lists five steps: 1. Analysis Selection, 2. Problem Identifier, 3. **Data File Selection**, 4. Data Labels, and 5. Step 3 is highlighted. The main area is titled "Data File Selection" and contains four radio button options:

- ☐ Use data file previously loaded from parent job. Below this is a text field for "Data file name:" and a "Save File" button.
- ☒ Load in dataset from My Datasets. Below this is a text field containing "Cadralazine Pop" and a "Save File" button.
- ☐ Load in dataset from Dataset Library. Below this is an empty text field and a "Save File" button.
- ☐ Load in data file from local file system. Below this is a text field with the instruction "Enter data file name (including full path) or browse.", a "Browse" button, and a "Read File" button. A note below the text field says "Click 'Read File' button to load data file." and "There are 3 columns in the data file."

At the bottom of the window are five buttons: "Back" (with a left arrow), "Next" (with a right arrow), "Confirm", "Cancel", and "Help".

Selection of a dataset from the Dataset Library is done similarly.

After you have performed the requested operations, the "Next" button will highlight and you can select it and continue. You can navigate back and forth in the MDA interface using the "Back" and "Next" buttons. The "Confirm" button displays the NONMEM(R) control file generated by the MDA up to this step in the process. Clicking "Cancel" will abort the model definition, while selecting "Help" will bring you to the relevant Help topic.



Prepare Input: Data Labels

This is the section of the MDA where data labels are defined. This is the screen you should see:

Model Design Agent Input File Generation Tool

Steps:

1. Analysis Selection
2. Problem Identifier
3. Data File Selection
- 4. Data Labels**
5.

Data Labels

Click data column and choose data item name:

- ID (if used) item must be in first column
- DV (dependent variable) item is required
- Item name and alias must be uppercase and unique

☒ **Standard item**
DV
Alias

☐ **User-defined item**

☐ Centered

☐ **Drop data column**
Remove
Enter

Column 1	Column 2	Column 3
ID	TIME	DV
1	2	1.09
1	4	0.75
1	6	0.53
1	8	0.34
1	10	0.23

Edit Data

< Back
Next >
Confirm
Cancel
Help

A data label is an identifier for the corresponding data column. The particular dataset shown above has three columns. Data labels have been chosen with NONMEM(R) compatibility in mind, so there are a few reserved data labels that are identical to NONMEM convention. They are referred to as "Standard Items", and they are:

- **ID:** The patient ID is required to be in the first column, if the data are for multiple individuals.
- **DV:** The data value, i.e. the column that contains the data. There is only one column of data. This item is required for analysis.
- **MDV:** A flag that determines whether a data value is missing or not. MDV should be handled in your model, i.e. a different provision should be executed depending on the values that MDV assumes.
- **EVID:** This is the EVent IDentifier, which may for example be used to mark a certain event as a measurement, or an input, etc.
- **TIME:** Time is by default the independent variable. If you have a different independent variable, it should still be called TIME or it should be reassigned.

- **DATE DATE1 DATE2 DATE3:** This option allows you to express time in date format, where DATE1, DATE2 and DATE3 are day, month and calendar year.
- **AMT:** This is the amount administered in the dose. If the variable RATE (see below) is defined, duration of the infusion is given by AMT divided by RATE. If RATE is not given, then the dose is assumed to be an instantaneous bolus of amount AMT.
- **RATE:** This is the rate of infusion administration, defined as amount over time. The amount injected is given by AMT (see above).
- **CMT:** This is the compartment number of a compartment model.
- **SS, ADDL, II, ABS, LAG, UPPER, LOWER, L1, L2, PCMT, CALL, CONT** are currently disabled and their functionality will be added to the system at a later date.

Standard data items can be selected by using a pull-down menu:

Steps:

1. Analysis Selection
2. Problem Identifier
3. Data File Selection
- 4. Data Labels**
5.

Data Labels

Click data column and choose data item name:

- ID (if used) item must be in first column
- DV (dependent variable) item is required
- Item name and alias must be uppercase and unique

☒ **Standard item**

☐ **User-defined item**

☐ **Drop data column**

DV

MDV

EVID

TIME

DATE

DATE1

DATE2

DATE3

AMT

Alias

☐ Centered

Remove

Enter

Column 1	Column 2
ID	TIME
1	2
1	4
1	6
1	8
1	10

0.75

0.53

0.34

0.23

Edit Data

Back

Next

Confirm

Cancel

Help

By selecting the radio button next to "User-defined item", the user can define his/her own data identifier. Other options become available, as shown below.

Model Design Agent Input File Generation Tool

Steps:

1. Analysis Selection
2. Problem Identifier
3. Data File Selection
- 4. Data Labels**
5.

Data Labels

Click data column and choose data item name:

- ID (if used) item must be in first column
- DV (dependent variable) item is required
- Item name and alias must be uppercase and unique

☐ Standard item

☒ User-defined item

☐ Centered

☐ Drop data column

Column 1	Column 2	Column 3
ID	TIME	DV
1	2	1.09
1	4	0.75
1	6	0.53
1	8	0.34
1	10	0.23

The user can also elect to "Drop data column" by selecting the appropriate radio button. Whatever the action, after the selection the user has to click on the "Enter" button to associate the data label with the relevant column. In the instance below, we have selected TIME for column 2, and clicked on "Enter", and DV for column 3, and clicked on "Enter". Note that the column that is being modified will be highlighted in red. In this case, the data items were predefined.

Model Design Agent Input File Generation Tool

Steps:

1. Analysis Selection
2. Problem Identifier
3. Data File Selection
- 4. Data Labels**
5.

Data Labels

Click data column and choose data item name:

- ID (if used) item must be in first column
- DV (dependent variable) item is required
- Item name and alias must be uppercase and unique

☐ Standard item Alias


☐ User-defined item ☐ Centered

☒ Drop data column

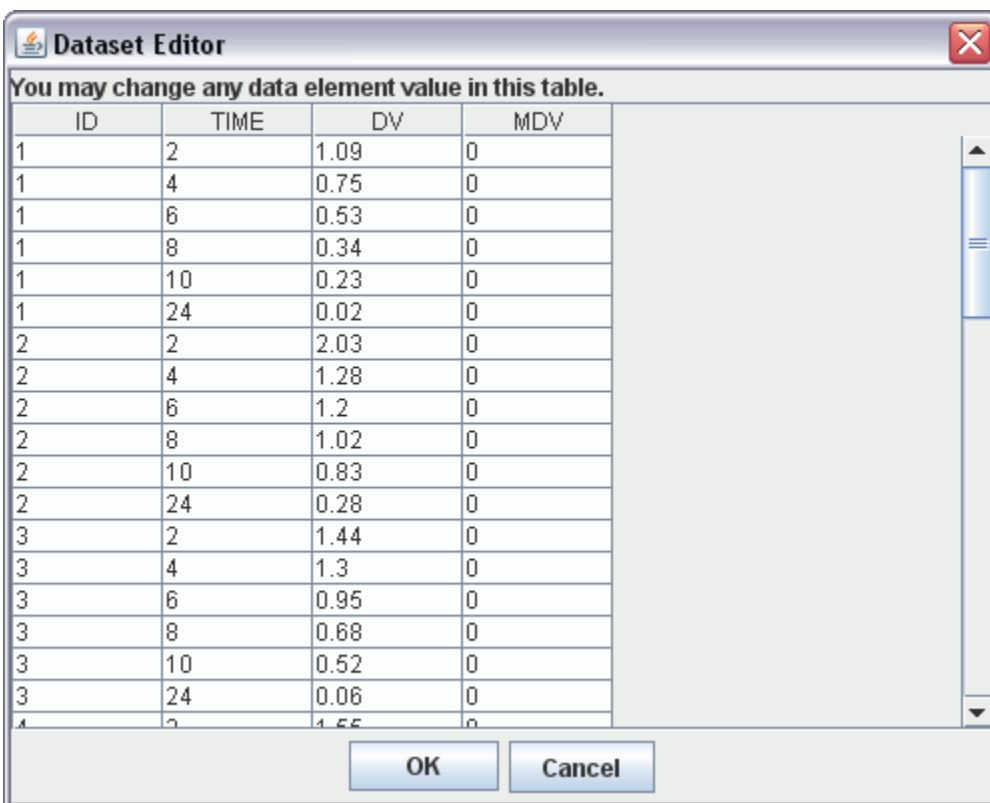
Column 1	Column 2	Column 3
ID	TIME	DV
1	2	1.09
1	4	0.75
1	6	0.53
1	8	0.34
1	10	0.23

Now, all the columns in the data file should be associated with identifiers, and you can proceed to the next step in building your model for the data. "Edit Data" will first prompt you whether you want to add a data column as MDV:

Question Dialog

 Do you want to add a data column as MDV?

This is a useful option when one or more data points should be neglected or otherwise unweighted in the analysis. After answering this, a Dataset Editor window will open where any element in the dataset can be changed (note that this will also require the generation of another version of the dataset).

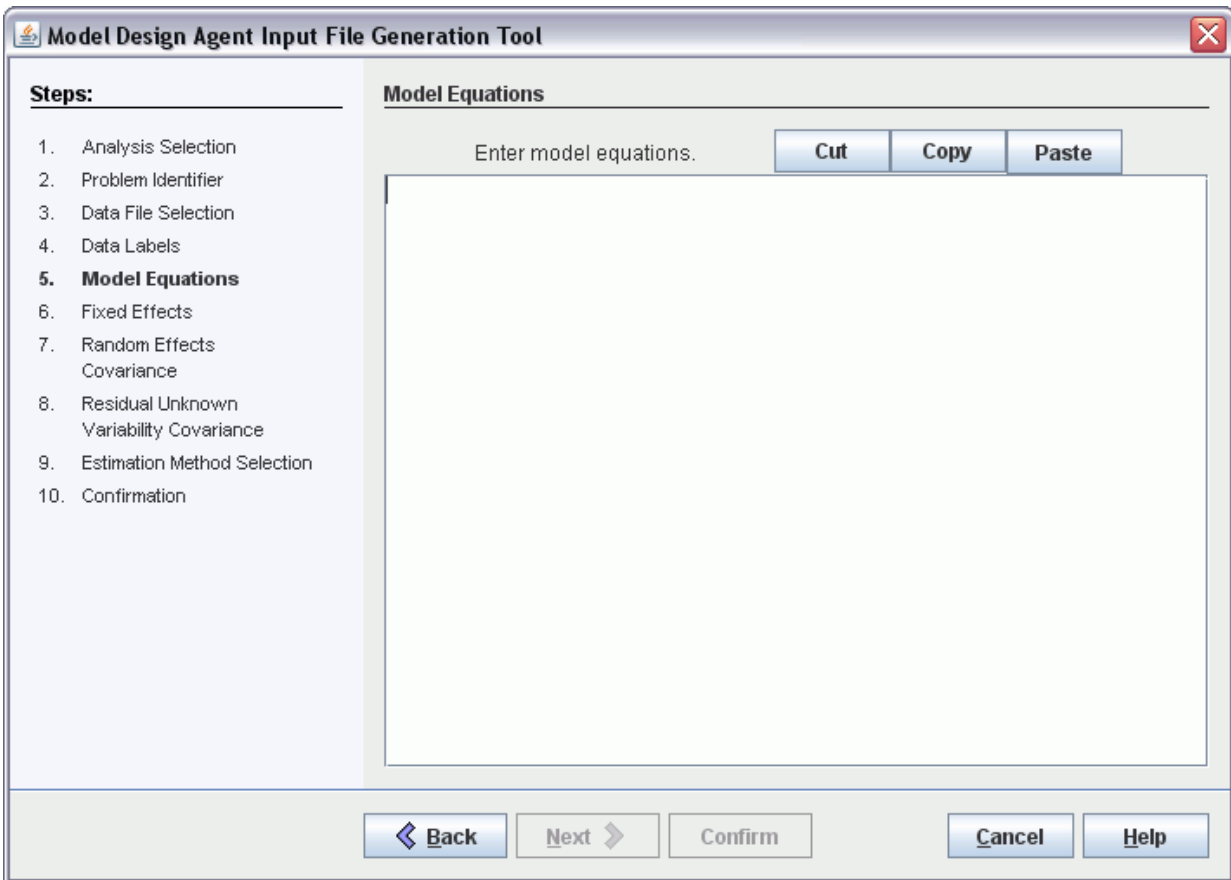


After you have performed the requested operations, the "Next" button will highlight and you can select it and continue. You can navigate back and forth in the MDA interface using the "Back" and "Next" buttons. The "Confirm" button displays the NONMEM(R) control file generated by the MDA up to this step in the process. Clicking "Cancel" will abort the model definition, while selecting "Help" will bring you to the relevant Help topic.



Prepare Input: Model Equations

This is where the mathematical-statistical model to be used for data analysis is defined, assuming the user has selected an algebraic model for the data analysis. The screen in question should be as follows:



The model equations associate the data column marked with a DV identifier with the output of a statistical model. Assuming the data come from a population, the statistical model explicitly represents both between-subject (BSV) and residual unknown (RUV) variation. On the other hand, individual analysis only models RUV. The model parameters are defined using NONMEM(R) compatible notation as follows:

- THETA(1), THETA(2), ... indicate the fixed effects of the mean, i.e. the model parameters that do not change between individuals. They are often the center of mass of the statistical distributions of the model parameters. They are deterministic;
- ETA(1), ETA(2), ... have two different meanings. For population analysis, they indicate the BSV random effects, i.e. random sources of variation at the between-subject level. They are random variables assumed to be Gaussian with mean zero and covariance of the random effects OMEGA. For individual analysis, they are used to model the RUV specific to the measurement.
- EPS(1), EPS(2), ... indicate the RUV random effects, i.e. random sources of variation at the between-subject level. They are random

variables assumed to be Gaussian with mean zero and covariance SIGMA. They are used in population analysis only;

- F is the model for the population data, i.e. the model variable which is being measured and associated with the DV time course.
- Y is the statistical model for the measurements in the DV data column; this is the variable that is directly associated with the data in the DV column. The association needs to be defined.

For example, a single exponential time course in an individual subject with Gaussian variation on the measurement would be modeled as:

$$\text{LAMBDA} = \text{THETA}(1)$$

$$F = \text{EXP}(\text{LAMBDA} * \text{TIME})$$

$$Y = F + \text{ETA}(1)$$

A single exponential time course with linear Gaussian variation on the exponent and Gaussian variation on the measurement would be modeled as:

$$\text{LAMBDA} = \text{THETA}(1) + \text{ETA}(1)$$

$$F = \text{EXP}(\text{LAMBDA} * \text{TIME})$$

$$Y = F + \text{EPS}(1)$$

Note that in the first example $\text{ETA}(1)$ models RUV, while in the second $\text{ETA}(1)$ models BSV and $\text{EPS}(1)$ is used for RUV. This is done to make SPK consistent with NONMEM(R) notation.

A single compartment pharmacokinetic model following a unitary pulse dose with Gaussian variation on the apparent volume of distribution, log-normal variation on the clearance and Gaussian variation on the measurement would be modeled as:

$$\text{CL} = \text{THETA}(1) * \text{EXP}(\text{ETA}(1))$$

$$V = \text{THETA}(2) + \text{ETA}(2)$$

$$F = \text{EXP}(-\text{CL}/V * \text{TIME})$$

$$Y = F + \text{EPS}(1)$$

The same model with proportional error on the measurement would read:

$$\text{CL} = \text{THETA}(1) * \text{EXP}(\text{ETA}(1))$$

$$V = \text{THETA}(2) + \text{ETA}(2)$$

$$F = \text{EXP}(-\text{CL}/V * \text{TIME})$$

$$Y = F * (1 + \text{EPS}(1))$$

In this instance, we chose to implement a single compartment model with clearance/volume parametrization, log-normally distributed parameters and a dose of 30 mg for all subjects:

$$D = 30$$

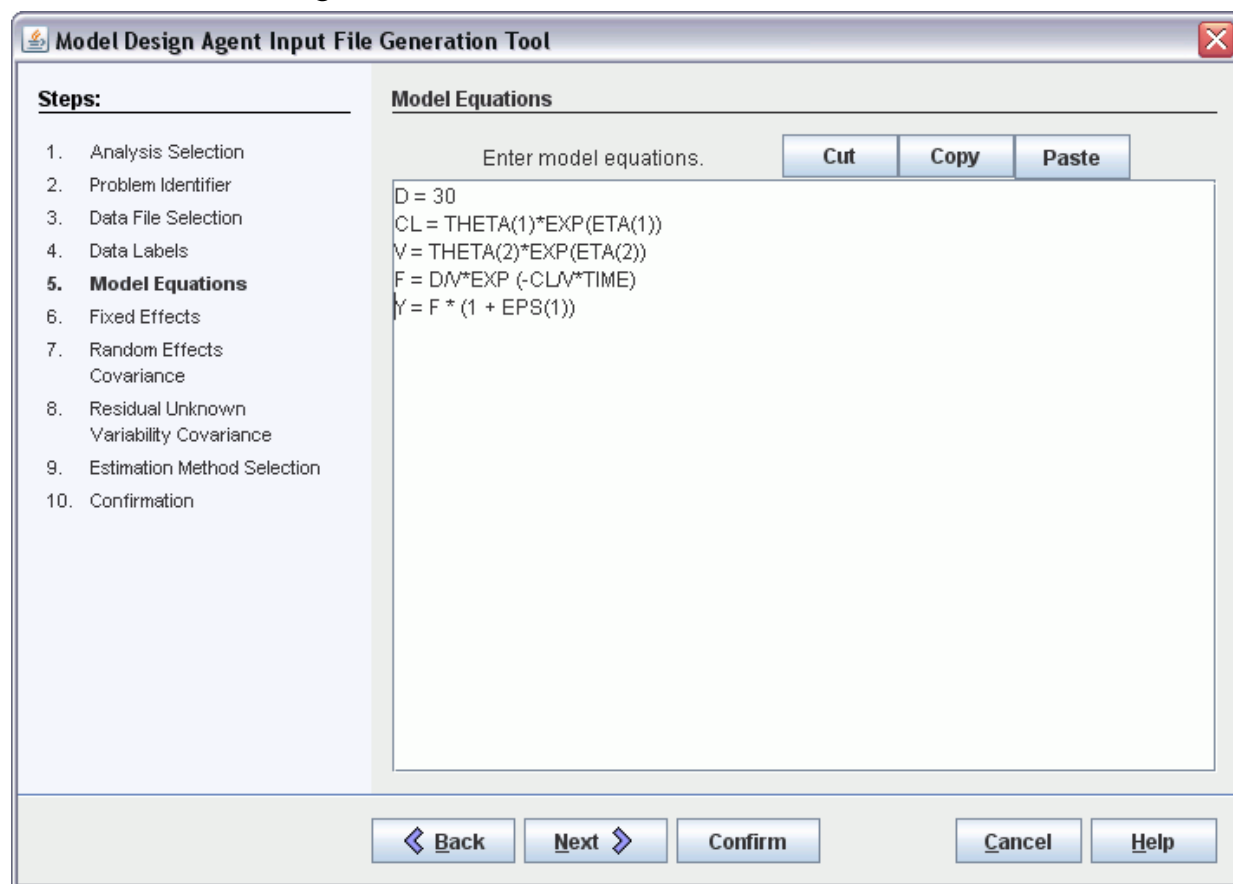
$$CL = \text{THETA}(1) * \text{EXP}(\text{ETA}(1))$$

$$V = \text{THETA}(2) * \text{EXP}(\text{ETA}(2))$$

$$F = D/V * \text{EXP}(-CL/V * \text{TIME})$$

$$Y = F * (1 + \text{EPS}(1))$$

This is the resulting screen:



After you have performed the requested operations, the "Next" button will highlight and you can select it and continue. You can navigate back and forth in the MDA interface using the "Back" and "Next" buttons. The "Confirm" button displays the NONMEM(R) control file generated by the MDA up to this step in the process. Clicking "Cancel" will abort the model definition, while selecting "Help" will bring you to the relevant Help topic.



Compartment Model Design Tool

If you have selected **Graphical Model Editor** in the Analysis Selection window, you can now click on the Enter button to be able to define your model graphically.

Model Design Agent Input File Generation Tool

Steps:

1. Analysis Selection
2. Problem Identifier
3. Data File Selection
4. Data Labels
- 5. Model Library**
6. Fixed Effects
7. Random Effects Covariance
8. Residual Unknown Variability Covariance
9. Estimation Method Selection
10. Confirmation

Model Library

You have selected to use SUBROUTINE ADVAN6. You need to specify the number of significant digits in the computation for each compartment.

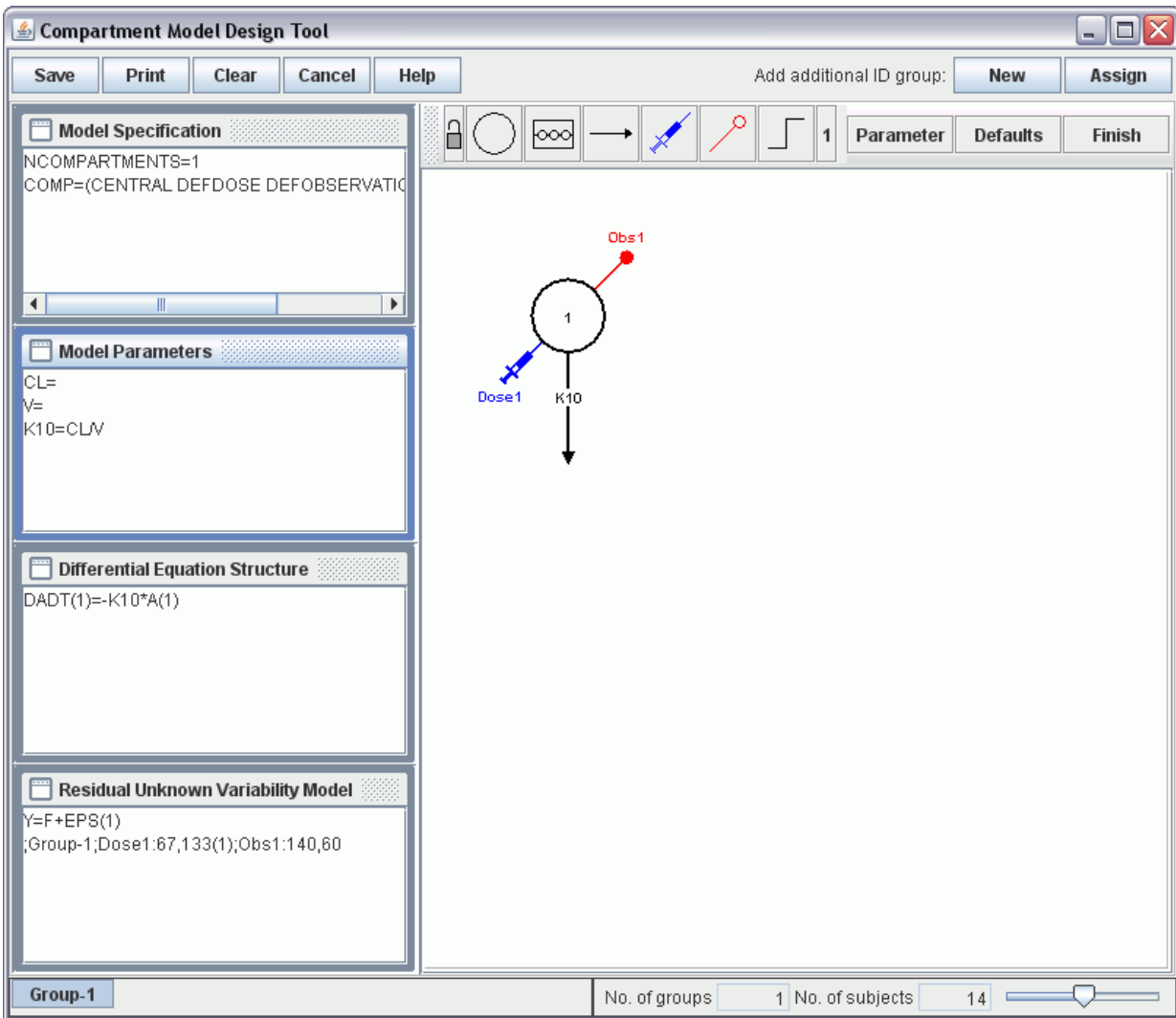
Significant digits

TRANS Subroutines

The options you have selected in NONMEM syntax

Click this button to enter Graphical Model Editor

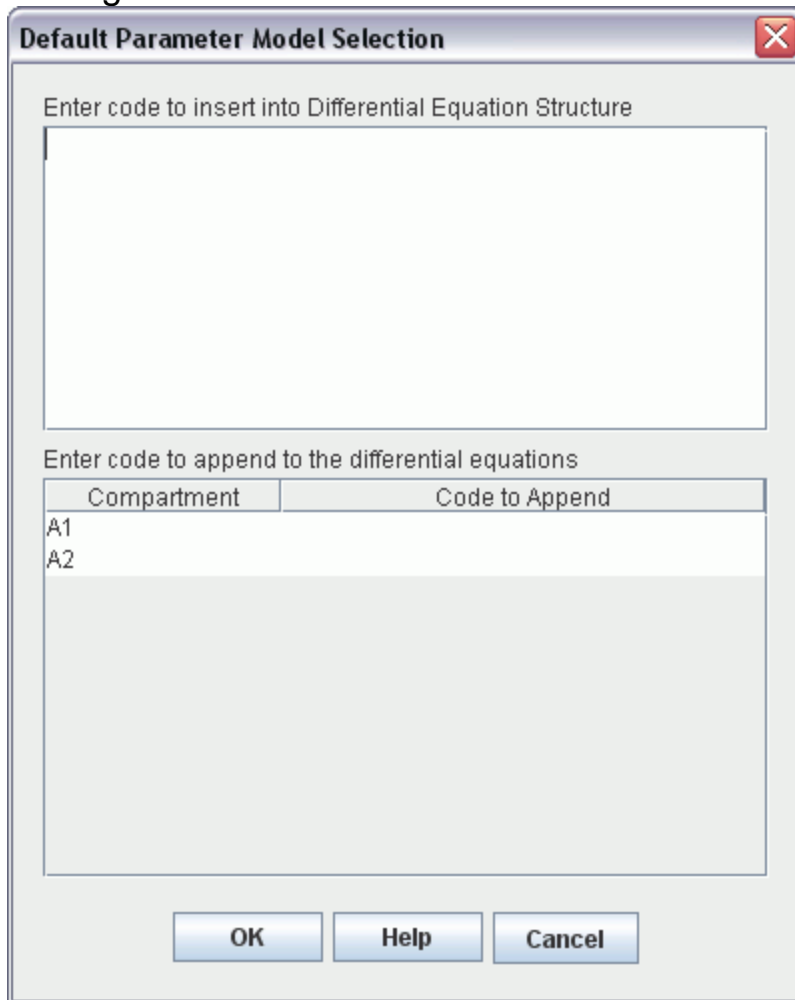
The Graphical Model Editor will be pre-filled with the model you have selected at the beginning. Various model features can be defined. In particular: the model can be saved (**Save**), its structure can be printed (**Print**), the canvas can be cleared for a new model (**Clear**), or control can be returned to the MDA (**Cancel**).



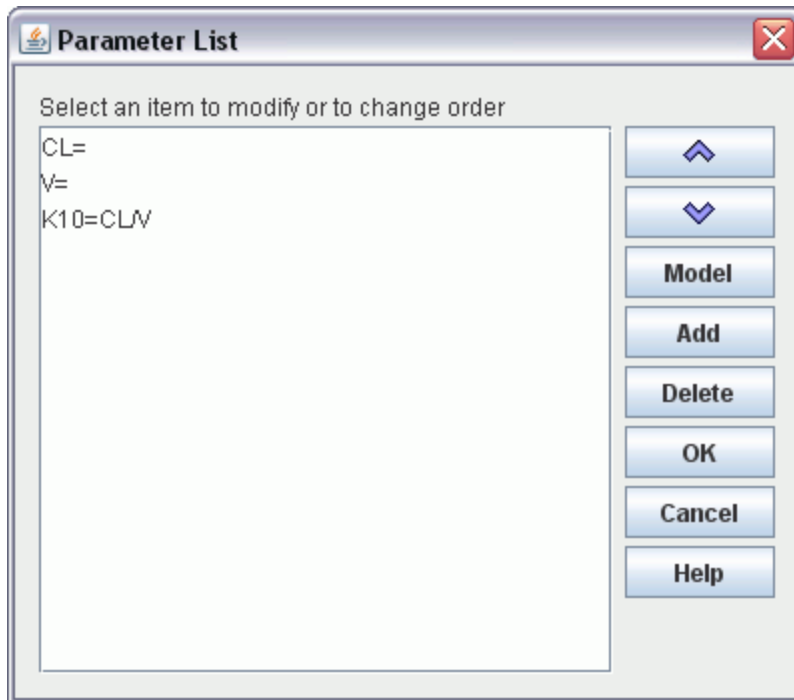
The four windows on the left (**Model Specification**, **Model Parameters**, **Differential Equation Structure** and **Residual Unknown Variability Model**) cannot be changed, rather they visualize model features that were defined elsewhere in the system. The sequence of buttons on the top row allows the user to:

- *Lock*: place in the model several compartments, or transfer rates, without having to select a compartment or transfer rate every time;
- *Compartment*: clicking on the compartment icon and then on the canvas places a compartment on the canvas;
- *Delay*: clicking on the delay icon and then on the canvas places a delay unit on the canvas;
- *Transfer Rate*: clicking on the transfer rate icon and then on the origin and destination compartment defines a transfer rate between those two compartments;

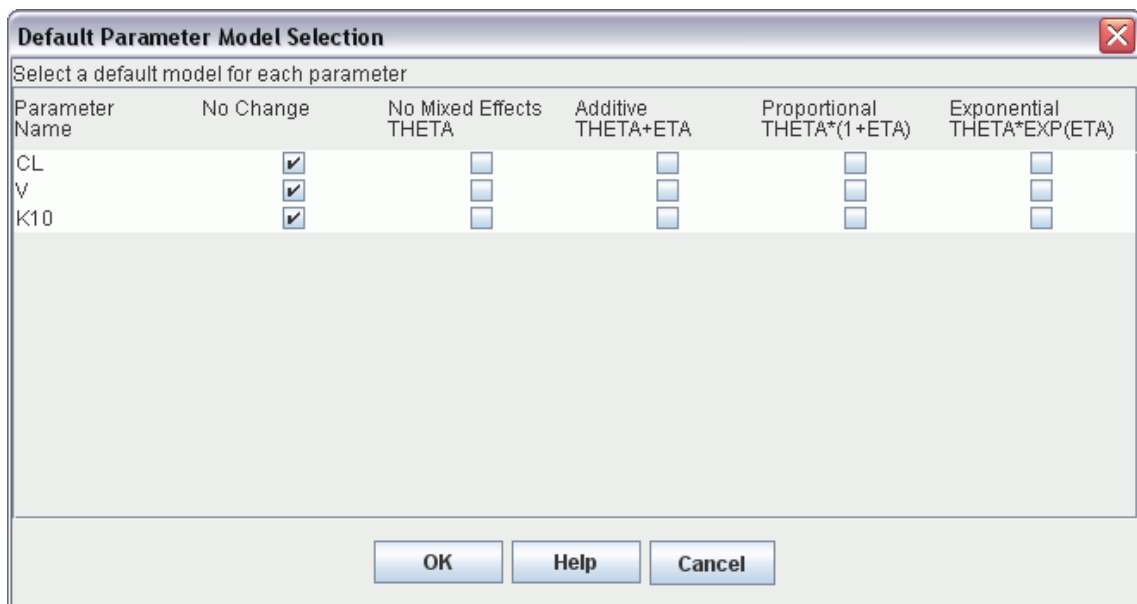
- *Input*: clicking on the input syringe icon and then on the input compartment and on the canvas defines an input function in the input compartment;
- *Measurement*: clicking on the measurement icon and then on the output compartment and on the canvas defines a measurement in the output compartment;
- *Change Condition*: clicking on the change condition button allows the user to access the change condition definition window, to change elements in the model.



- *Toggle*: clicking on the toggle button (marked with a [1]) allows the user to toggle between compartment number and name in the model canvas.
- *Parameter*: clicking on the parameter button displays the model parameters in a separate window:



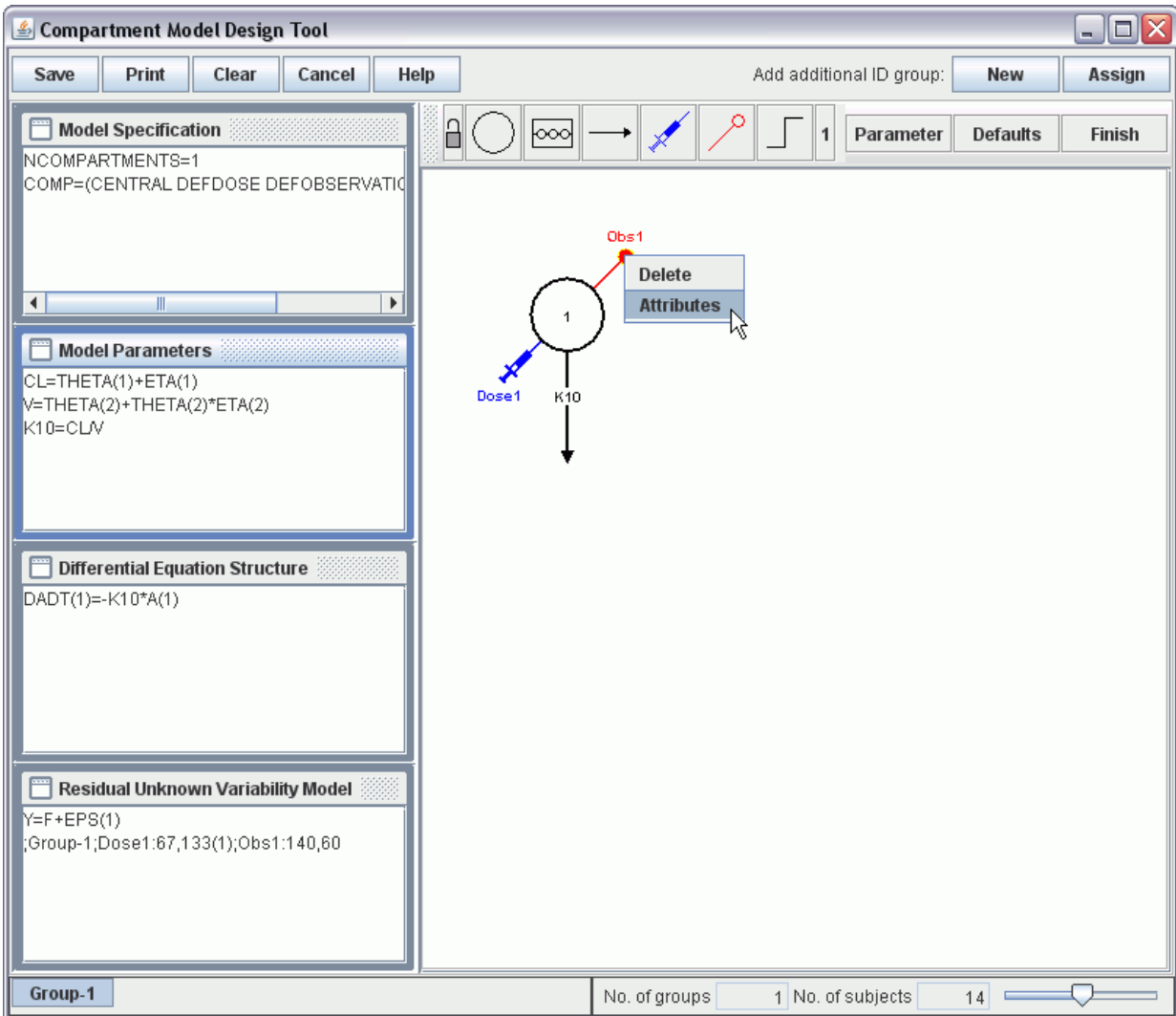
- *Defaults:* this allows the user to display various widely used defaults for population models:




- *Finish:* clicking on the Finish button allows the user to leave the Graphical Model Editor.

Right-clicking on the various elements of the canvas (**compartments**, **transfer rates**, **measurements** and **inputs**) allows the user to access various elements of the model. For example, right-clicking on the

measurement icon allows the user to either delete it or access its attributes:



- The Compartment attributes allow the user to specify forcing function, compartment attributes and optional compartment specific parameters.

Compartment Attributes 

Compartment name

Select forcing function: **Forcing Function**

Select compartment attributes:

☐ INITIALOFF ☐ NOOFF

☒ DEFDOSE ☒ DEFOBSERVATION

☐ NODOSE

Select optional compartment specific parameters:

Scaling: S1


Bioavailability: F1

Infusion Rate: R1

Infusion Duration: D1

Absorption Lag: ALAG1

OK **Cancel** **Help**


Forcing Function 

Name: A1

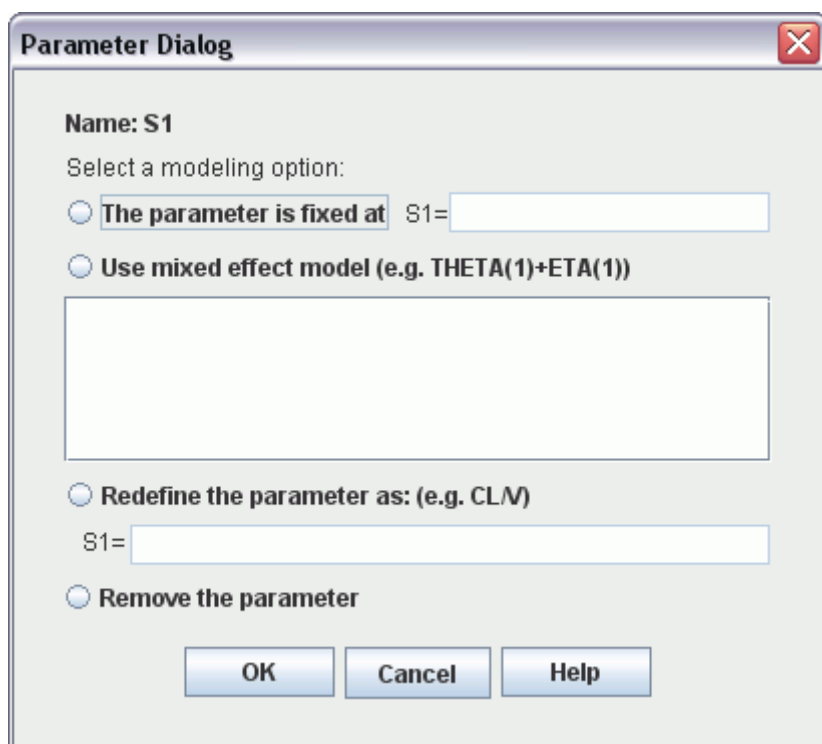
☒ **Turned Off**

☐ Equation for the forcing function:

FF1=

Add a data item to the function 

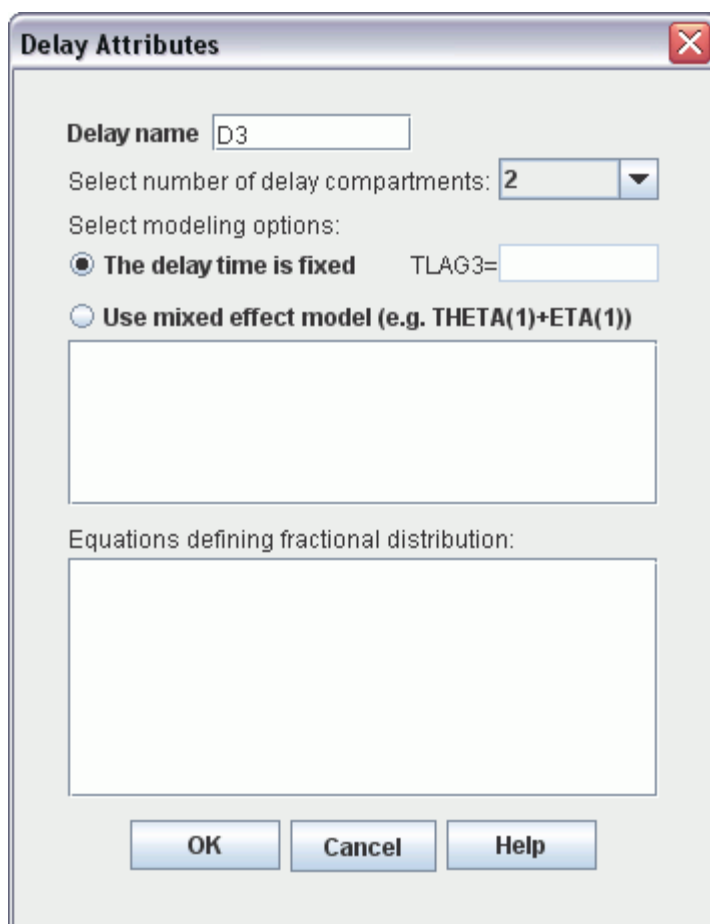
OK **Cancel** **Help**



The image shows a 'Parameter Dialog' window with a title bar and a close button. The window contains the following elements:

- Name:** S1
- Select a modeling option:**
 - ☐ **The parameter is fixed at** S1=
 - ☐ **Use mixed effect model (e.g. THETA(1)+ETA(1))**
 - ☐ **Redefine the parameter as: (e.g. CL/V)**
S1=
 - ☐ **Remove the parameter**
- Buttons:** OK, Cancel, Help

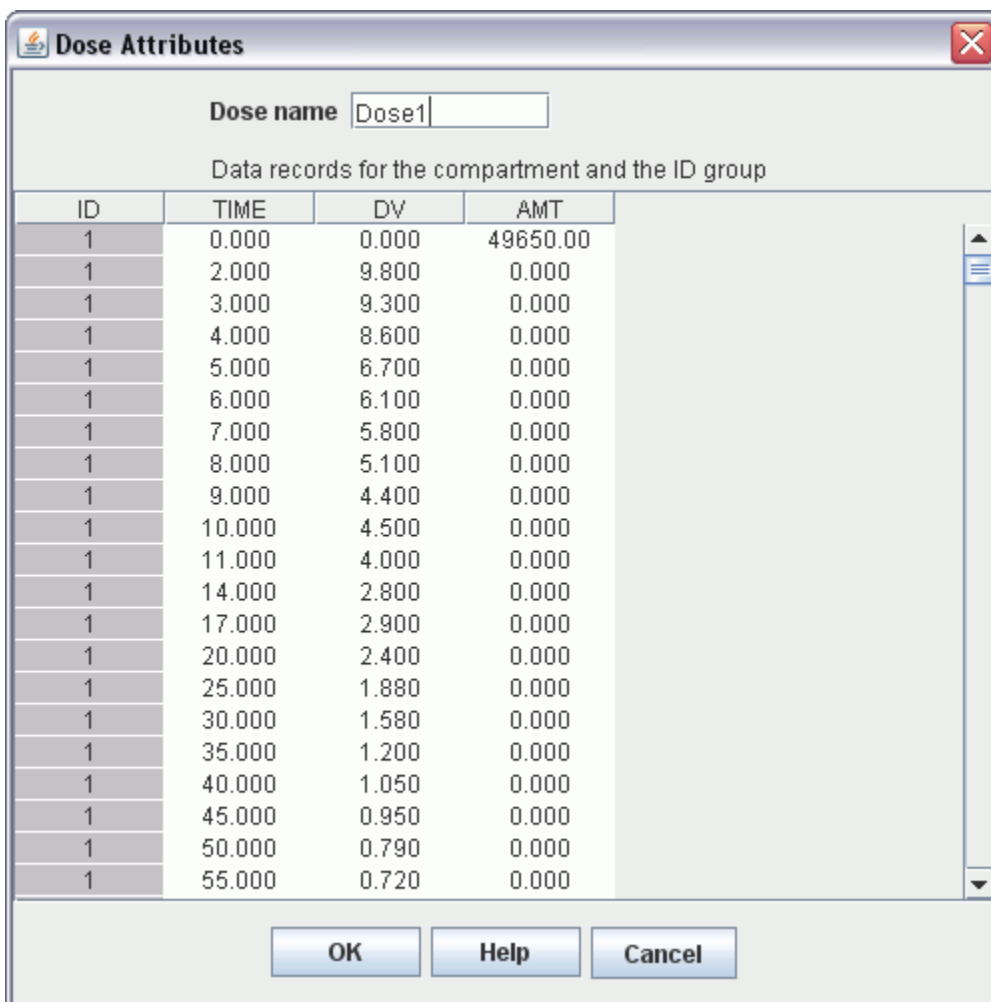
- The Delay attributes allow the user to specify number of compartments to simulate the delay, delay time and equations defining fractional distribution.



The image shows a 'Delay Attributes' dialog box with a title bar and a close button. It contains the following fields and controls:

- Delay name:** A text box containing 'D3'.
- Select number of delay compartments:** A dropdown menu showing '2'.
- Select modeling options:**
 - ☒ **The delay time is fixed** TLAG3= [text box]
 - ☐ **Use mixed effect model (e.g. THETA(1)+ETA(1))**
- Equations defining fractional distribution:** A large empty text box.
- Buttons:** 'OK', 'Cancel', and 'Help' at the bottom.

- For the Input, you can enter a new name and edit data for the compartment and the ID group:



Dose Attributes

Dose name:

Data records for the compartment and the ID group

ID	TIME	DV	AMT
1	0.000	0.000	49650.00
1	2.000	9.800	0.000
1	3.000	9.300	0.000
1	4.000	8.600	0.000
1	5.000	6.700	0.000
1	6.000	6.100	0.000
1	7.000	5.800	0.000
1	8.000	5.100	0.000
1	9.000	4.400	0.000
1	10.000	4.500	0.000
1	11.000	4.000	0.000
1	14.000	2.800	0.000
1	17.000	2.900	0.000
1	20.000	2.400	0.000
1	25.000	1.880	0.000
1	30.000	1.580	0.000
1	35.000	1.200	0.000
1	40.000	1.050	0.000
1	45.000	0.950	0.000
1	50.000	0.790	0.000
1	55.000	0.720	0.000

OK Help Cancel


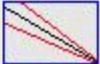


- The Measurement attributes allow the user to define various attributes of the Residual Unknown Variability for the experiment:

Residual Unknown Variability Model

Observation Name:

Select a residual unknown variability (RUV) model:

- F denotes the model function vector
- DV denotes the observed data vector
- Y, a random variable, represents the predicted observation
- Model must contain RUV parameter ETA
- Enter appropriate number in () following ETA (e.g. ETA(1))

Model Name	Expression	Weight
<input type="radio"/> Additive	$F + \text{ETA}$	
<input type="radio"/> Model-based Proportional	$F + F * \text{ETA}$	
<input type="radio"/> Data-Based Proportional	$F + \text{DV} * \text{ETA}$	
<input type="radio"/> Model-based Mixed	$F + F * \text{ETA} + \text{ETA}$	

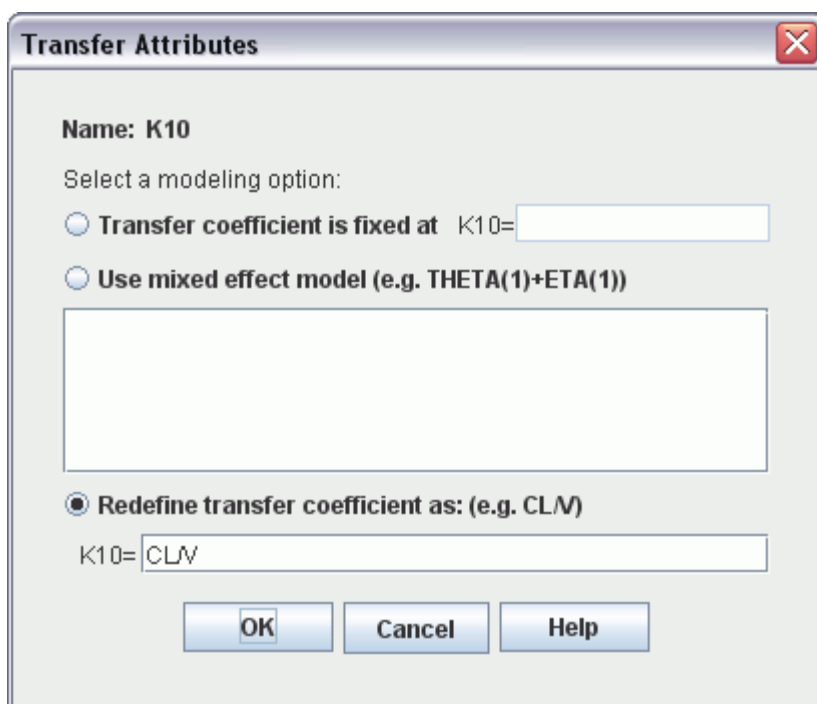
☒ **User Defined**

Enter additional equations used to define the RUV model

OK Cancel Help

Possible attributes for the RUV model are: Additive, Model-based Proportional, Data-Based Proportional and Model-based Mixed. Moreover, the user can enter a general error model as well.

- The Transfer attributes allow the user to enter specific mixed effects modeling characteristics for the Transfer Rate. More sophisticated mixed effects models can be entered as well.



Transfer Attributes

Name: K10

Select a modeling option:

☐ Transfer coefficient is fixed at K10=

☐ Use mixed effect model (e.g. THETA(1)+ETA(1))

☒ Redefine transfer coefficient as: (e.g. CL/V)

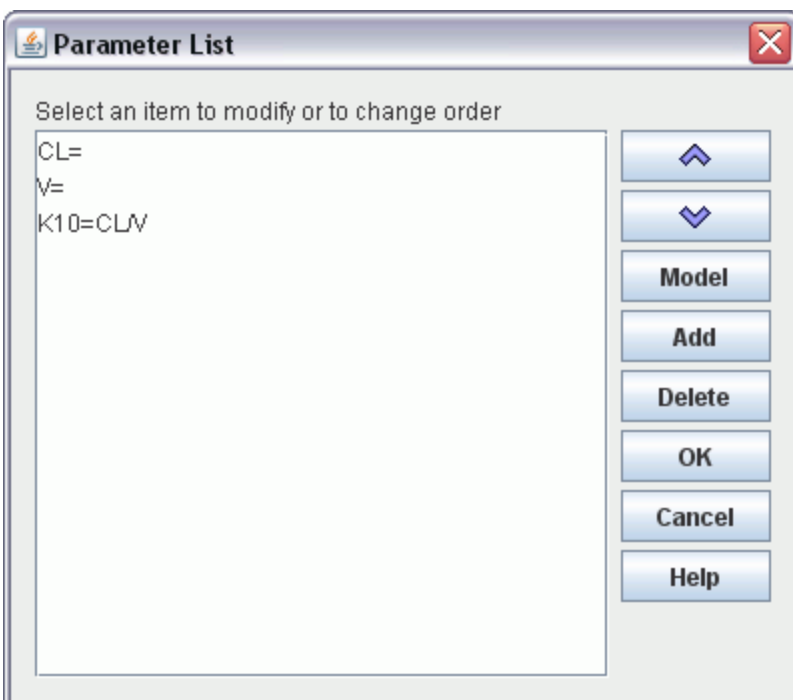
K10= CL/V

OK Cancel Help



Parameters

The Parameter List window displays a list of the undefined parameters in the model. The assumption is that these parameters now need to be associated with fixed and/or random effects, or covariates. The parameters need to be selected first, by clicking once on the corresponding line:






Next, by clicking on Model, a model definition window appears where the mixed effects model for the specific parameter can be defined for a population analyses:

Mixed Effects Model

Name: CL

Select a mixed-effects model:

- Model must contain fixed effect parameter THETA
- Model may contain random effect parameter ETA
- Enter appropriate number in () following parameter (e.g. THETA(1), ETA(2) etc.)

Model Name	Expression	Distribution
<input type="radio"/> Additive	THETA + ETA	Normal 
<input type="radio"/> Proportional	THETA * (1 + ETA)	Normal 
<input type="radio"/> Exponential	THETA * EXP(ETA)	Lognormal 
<input checked="" type="radio"/> User Defined		

CL=

Select a data item to add to the model

Edit the model: ☐ None conditional ☐ Conditional

OK Cancel Help




The available models are: **Additive**, **Proportional**, **Exponential** and **User Defined**. For example, by selecting Proportional, the following definition appears, and can be modified by the user:

Mixed Effects Model

Name: CL

Select a mixed-effects model:

- Model must contain fixed effect parameter THETA
- Model may contain random effect parameter ETA
- Enter appropriate number in () following parameter (e.g. THETA(1), ETA(2) etc.).

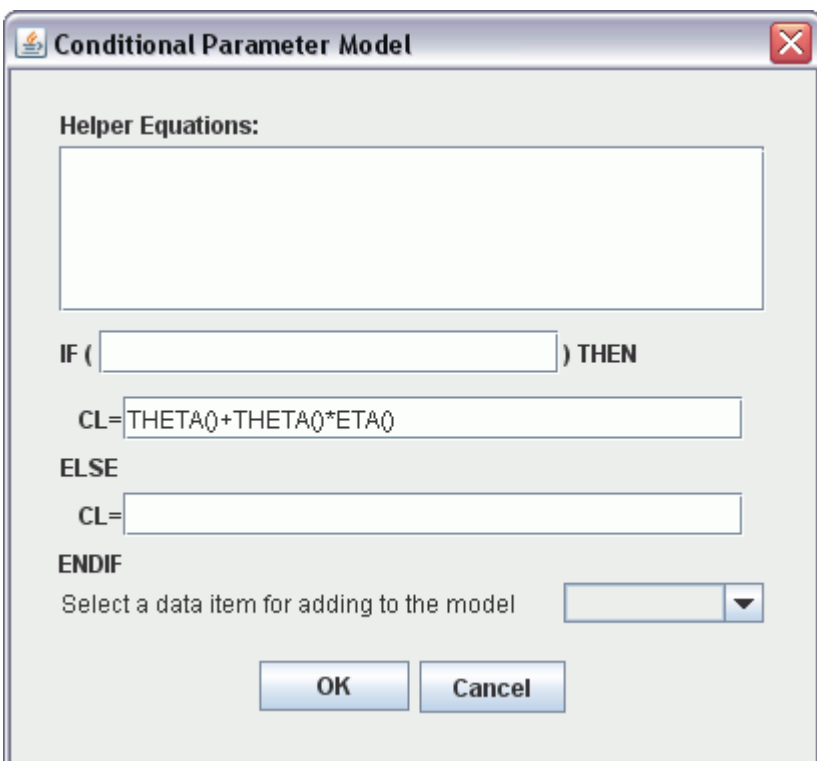
Model Name	Expression	Distribution
<input type="radio"/> Additive	THETA + ETA	Normal 
<input checked="" type="radio"/> Proportional	THETA * (1 + ETA)	Normal 
<input type="radio"/> Exponential	THETA * EXP(ETA)	Lognormal 
<input type="radio"/> User Defined	<div> CL=THETA0+THETA0*ETA0 </div>	

Select a data item to add to the model

Edit the model: ☐ None conditional ☐ Conditional

OK Cancel Help

Note that numerals indicating the sequence order of the fixed and random effects need to be specified. Lastly, if a conditional statement is associated with the model, the Conditional radio button must be selected. When this is done, the following window appears:



Conditional Parameter Model

Helper Equations:

IF () THEN

CL=

ELSE

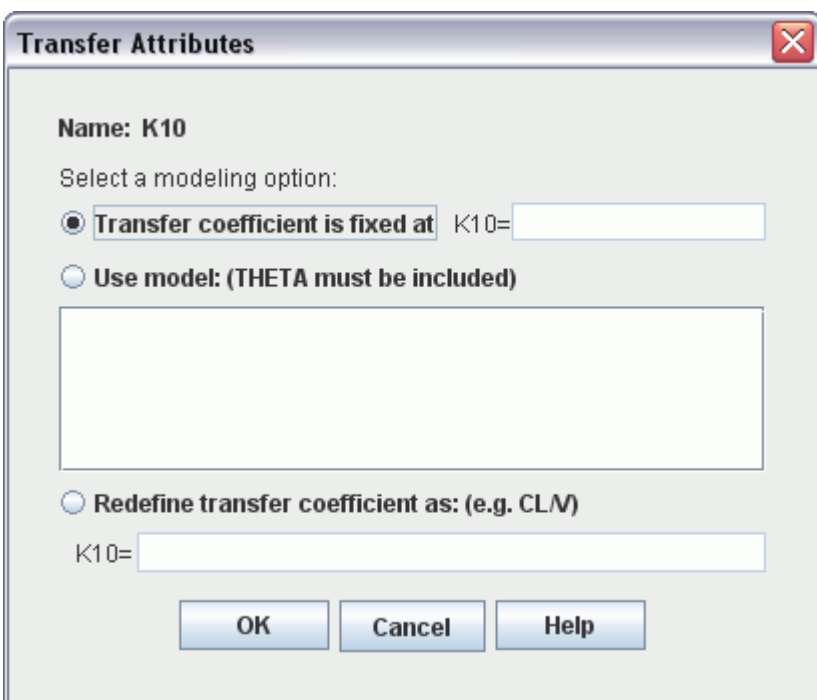
CL=

ENDIF

Select a data item for adding to the model ▼

OK Cancel

General conditional statements can then be defined. For an individual analyses the model definition window appears when a model is selected in the Parameter List window.



Transfer Attributes

Name: K10

Select a modeling option:

☒ Transfer coefficient is fixed at K10=

☐ Use model: (THETA must be included)

☐ Redefine transfer coefficient as: (e.g. CL/V)

K10=

OK Cancel Help

Defaults

The Defaults window allows the user to quickly and efficiently define standard mixed effects models. The window looks like this:

Default Parameter Model Selection

Select a default model for each parameter

Parameter Name	No Change	No Mixed Effects THETA	Additive THETA+ETA	Proportional THETA*(1+ETA)	Exponential THETA*EXP(ETA)
CL	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
V	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
K10	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>

OK Help Cancel

Mixed models can be defined quickly and are updated automatically in the Graphical Model Editor. For example, to define an additive model for CL and a proportional model for V, the corresponding boxes need to be selected:

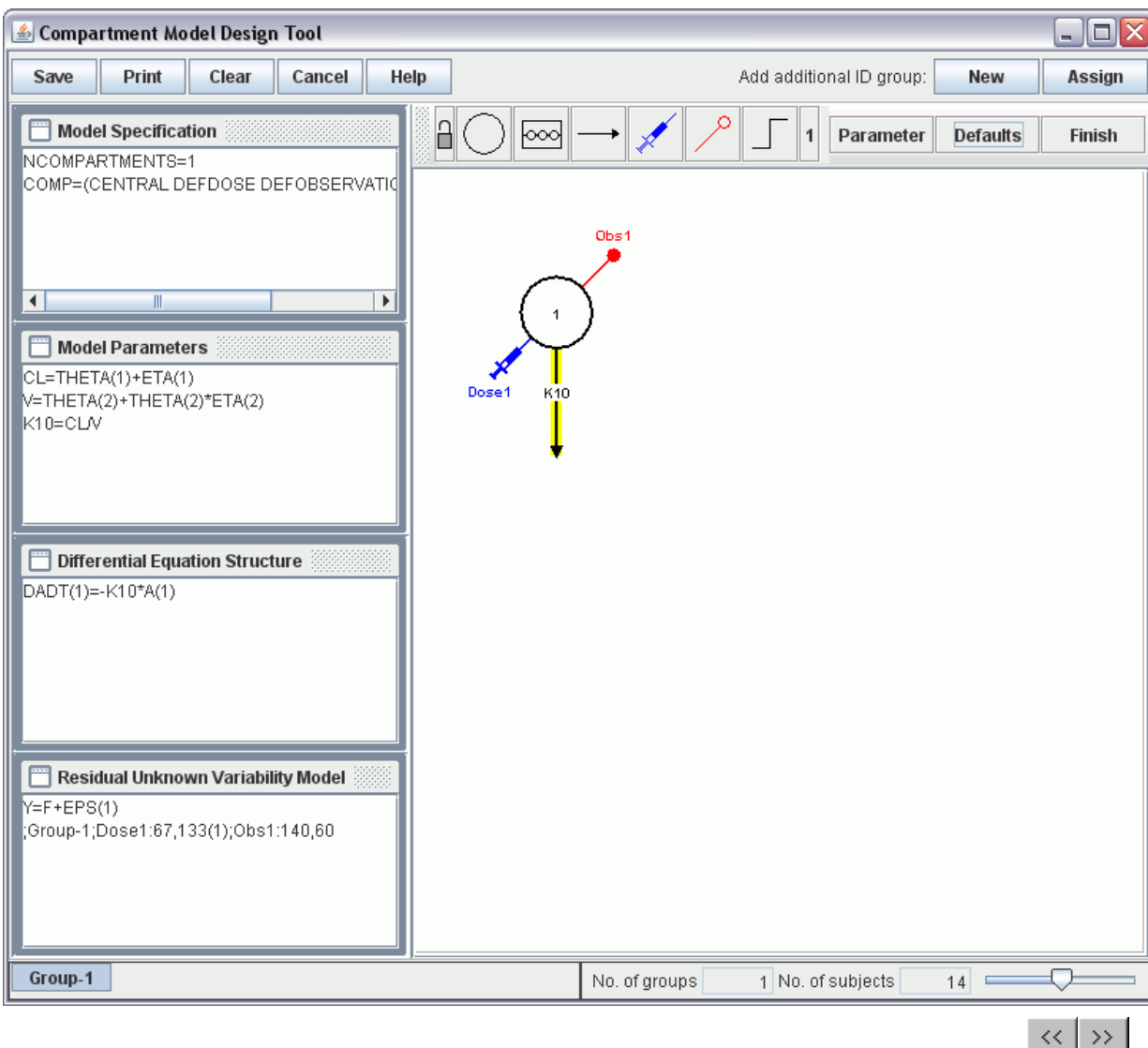
Default Parameter Model Selection

Select a default model for each parameter

Parameter Name	No Change	No Mixed Effects THETA	Additive THETA+ETA	Proportional THETA*(1+ETA)	Exponential THETA*EXP(ETA)
CL	<input type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
V	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>
K10	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>

OK Help Cancel

The model is automatically replicated in the Model Parameters window, where it is available for inspection.



Mixed Effects Model (Graphical Editor)

The statistical model to be defined in this window can be used to explicitly represents between-subject (BSV) variation. Options for defining a mixed effects model are accessed by clicking on relevant radio buttons. Pictorial representations of the associated probability densities assist the user in choosing a specific statistical model.

Mixed Effects Model

Name: K10

Select a mixed-effects model:

- Model must contain fixed effect parameter THETA
- Model may contain random effect parameter ETA
- Enter appropriate number in () following parameter (e.g. THETA(1), ETA(2) etc.).

Model Name	Expression	Distribution
<input type="radio"/> Additive	THETA + ETA	Normal
<input type="radio"/> Proportional	THETA * (1 + ETA)	Normal
<input type="radio"/> Exponential	THETA * EXP(ETA)	Lognormal

☒ **User Defined**

K10=CLM

Select a data item to add to the model

Edit the model: ☐ None conditional ☐ Conditional

OK **Cancel** **Help**

The model parameters are defined using NONMEM(R) compatible notation as follows:

- THETA(1), THETA(2), ... indicate the fixed effects of the mean, i.e. the model parameters that do not change between individuals. They are often the center of mass of the statistical distributions of the model parameters. They are deterministic;
- ETA(1), ETA(2), ... indicate the BSV random effects, i.e. random sources of variation at the between-subject level. They are random variables assumed to be Gaussian with mean zero and covariance of the random effects OMEGA;

For an individual subject, the BSV random effects, ETA(1), ETA(2), ... are not used.

For example, population linear Gaussian variation on a parameter LAMBDA would be modeled as:

$$\text{LAMBDA} = \text{THETA}(1) + \text{ETA}(1)$$

Gaussian variation on the apparent volume of distribution and log-normal variation on the clearance would be modeled as:

$$\text{CL} = \text{THETA}(1) * \text{EXP}(\text{ETA}(1))$$

$$\text{V} = \text{THETA}(2) + \text{ETA}(2)$$

As an example, we could build a log-normal model for population between-subject variation by entering the following equations:

$$\text{CL} = \text{THETA}(1) * \text{EXP}(\text{ETA}(1))$$

$$\text{V} = \text{THETA}(2) * \text{EXP}(\text{ETA}(2))$$



Residual Unknown Variability Model (Graphical Editor)





There are various possibilities for defining a Residual Unknown Variability model. These are accessed by selecting various radio buttons.

Residual Unknown Variability Model

Observation Name:

Select a residual unknown variability (RUV) model:

- F denotes the model function vector
- DV denotes the observed data vector
- Y, a random variable, represents the predicted observation
- Model must contain RUV parameter ETA
- Enter appropriate number in () following ETA (e.g. ETA(1))

Model Name	Expression	Weight
<input type="radio"/> Additive	$F + \text{ETA}$	
<input type="radio"/> Model-based Proportional	$F + F * \text{ETA}$	
<input type="radio"/> Data-Based Proportional	$F + \text{DV} * \text{ETA}$	
<input type="radio"/> Model-based Mixed	$F + F * \text{ETA} + \text{ETA}$	
<input checked="" type="radio"/> User Defined	<input type="text" value="Y=F+ETA(1)"/>	

Enter additional equations used to define the RUV model

OK Cancel Help

The model is defined using NONMEM(R) compatible notation as follows:

- EPS(1), EPS(2), ... indicate the RUV random effects, i.e. random sources of variation at the between-subject level. They are random variables assumed to be Gaussian with mean zero and covariance SIGMA;
- Y is the statistical model for the measurements in the DV data column; this is the variable that is directly associated with the data in the DV column. The association needs to be defined.
- F is the model for the population data, i.e. the model variable which is being measured and associated with the DV time course.

For example, Gaussian additive variation on the measurement would be modeled as:

$$Y = F + \text{EPS}(1)$$

Gaussian proportional error on the measurement would read:

$$Y = F * (1 + EPS(1))$$

In this particular instance, we have chosen an additive Gaussian error model. Other statistics are also possible, such as an exponential error model:

$$Y = F * EXP(EPS(1))$$



Prepare Input: Model Numerics from the Model Library

SPK allows the user to select models using the NONMEM(R) notation for compartmental pharmacokinetic models. For example, assume that we have selected ADVAN1, TRANS2 from the initial Analysis Selection window. This implies a one-compartment model parameterized as clearance and volume, where the rate constant is a derived variable. Note that all ADVANs except ADVAN8 are implemented in SPK as differential equations and are translated as ADVAN6, i.e. the differential equations are explicitly defined. At this point, all the user has to do is select the number of significant digits required in the computation of the model output. The default is five.

Steps:

1. Analysis Selection
2. Problem Identifier
3. Data File Selection
4. Data Labels
- 5. Model Library**
6. Model Specification
7. Model Parameters
8. Differential Equation Structure
9. Residual Unknown Variability Model
10. Fixed Effects
11. Random Effects Covariance
12. Residual Unknown Variability Covariance
13. Estimation Method Selection
14. Confirmation

Model Library

You have selected to use SUBROUTINE ADVAN6. You need to specify the number of significant digits in the computation for each compartment.

Significant digits

TRANS Subroutines

The options you have selected in NONMEM syntax

Click this button to enter Graphical Model Editor

After you have performed the requested operations, the "Next" button will highlight and you can select it and continue. You can navigate back and forth in the MDA interface using the "Back" and "Next" buttons. The "Confirm" button displays the NONMEM(R) control file generated by the MDA up to this step in the process. Clicking "Cancel" will abort the model definition, while selecting "Help" will bring you to the relevant Help topic.



Prepare Input: Model Specification

The Model Specification window allows the user to select specific attributes for the compartmental model. The content is already pre-filled if a library model is used. Otherwise, the user should click the "Attributes" button to select compartment attributes and then "Add" or "Change". Note that the default compartment for dosing (DEFDOSE) and the default compartment for the measurement (DEFOBSERVATION) have to be provided.

Model Design Agent Input File Generation Tool

Steps:

1. Analysis Selection
2. Problem Identifier
3. Data File Selection
4. Data Labels
5. Model Library
- 6. Model Specification**
7. Model Parameters
8. Differential Equation Structure
9. Residual Unknown Variability Model
10. Fixed Effects
11. Random Effects Covariance
12. Residual Unknown Variability Covariance
13. Estimation Method Selection
14. Confirmation

Model Specification

Enter the definition of each compartment: its name and attributes.
(Note: Attributes DEFDISE and DEFOBSERVATION are required.
Compartment name and other attributes are optional.)

NCOMPARTMENTS Name:

NEQUILIBRIUM

NPARAMETERS

List of the compartments you have entered in NONMEM syntax

COMP=(CENTRAL DEFOBSERVATION DEF

Clicking on **Attributes** will bring up a window where the compartmental attributes can be selected.

Attributes

Multiple attributes may be selected.

☐ INITIALOFF

☒ NOOFF

☐ NODOSE

☐ EQUILIBRIUM

☐ EXCLUDE

☒ DEFOBSERVATION

☒ DEFDISE

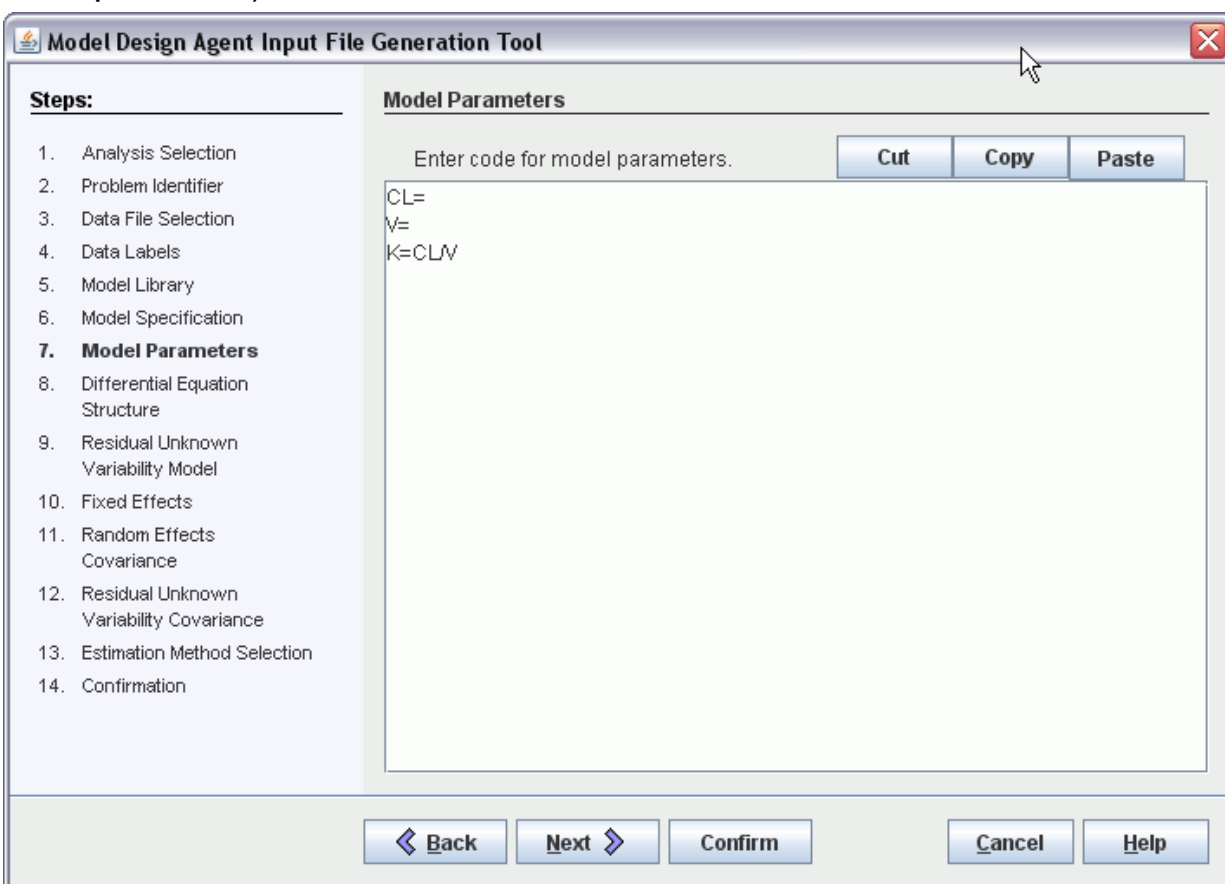
After you have performed the requested operations, the "Next" button will highlight and you can select it and continue. You can navigate back and forth in the MDA interface using the "Back" and "Next" buttons. The

"Confirm" button displays the NONMEM(R) control file generated by the MDA up to this step in the process. Clicking "Cancel" will abort the model definition, while selecting "Help" will bring you to the relevant Help topic.



Prepare Input: Model Parameters

This window allows the user to specify the model parameterization and the relationships between fixed and random effects and the kinetic parameters of the ODE model (to be defined on the following screen). If a model from the library was selected, the editor window will be already pre-filled with the left-hand side of the algebraic equations linking (in the example below) clearance and volume with fixed and random effects.



The statistical model to be defined in this window can be used to explicitly represents between-subject (BSV) variation. The model parameters are defined using NONMEM(R) compatible notation as follows:

- THETA(1), THETA(2), ... indicate the fixed effects of the mean, i.e. the model parameters that do not change between individuals. They are often the center of mass of the statistical distributions of the model parameters. They are deterministic;
- ETA(1), ETA(2), ... indicate the BSV random effects, i.e. random sources of variation at the between-subject level. They are random variables assumed to be Gaussian with mean zero and covariance of the random effects OMEGA;

For an individual subject, the BSV random effects, ETA(1), ETA(2), ... are not used.

For example, population linear Gaussian variation on a parameter LAMBDA would be modeled as:

$$\text{LAMBDA} = \text{THETA}(1) + \text{ETA}(1)$$

Gaussian variation on the apparent volume of distribution and log-normal variation on the clearance would be modeled as:

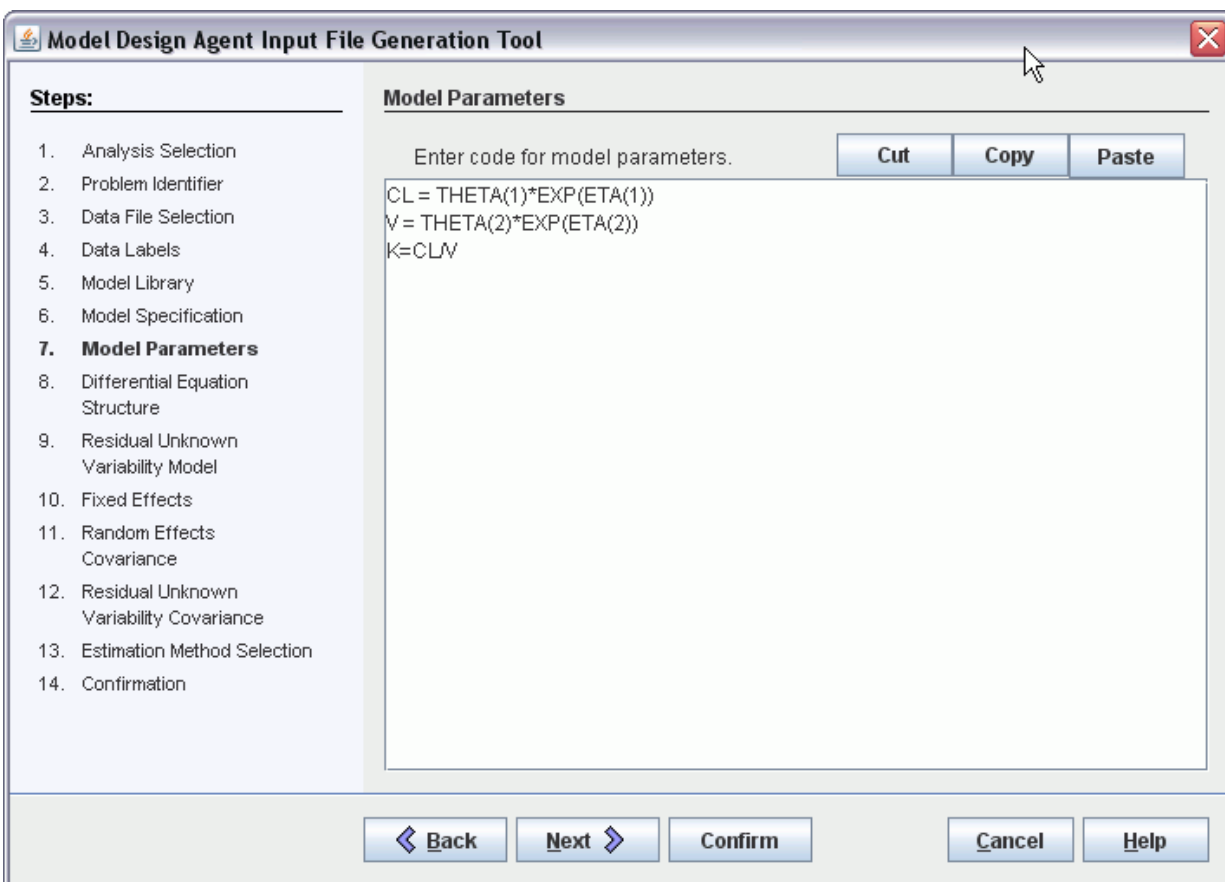
$$\text{CL} = \text{THETA}(1) * \text{EXP}(\text{ETA}(1))$$

$$\text{V} = \text{THETA}(2) + \text{ETA}(2)$$

As an example, we could build a log-normal model for population between-subject variation by entering the following equations:

$$\text{CL} = \text{THETA}(1) * \text{EXP}(\text{ETA}(1))$$

$$\text{V} = \text{THETA}(2) * \text{EXP}(\text{ETA}(2))$$



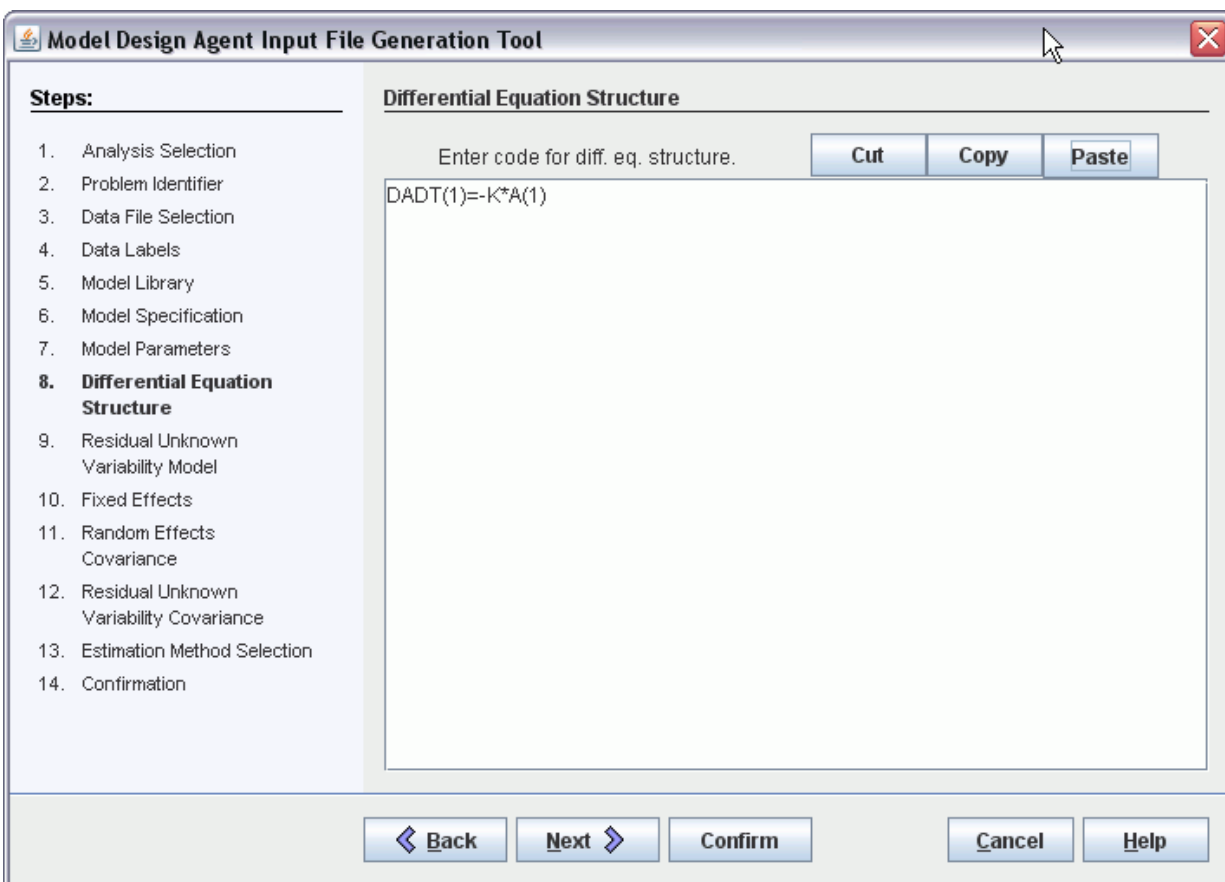
Other between-subject variation models are also possible. Note that the rate constant K is already defined as the ratio of clearance and volume.

After you have performed the requested operations, the "Next" button will highlight and you can select it and continue. You can navigate back and forth in the MDA interface using the "Back" and "Next" buttons. The "Confirm" button displays the NONMEM(R) control file generated by the MDA up to this step in the process. Clicking "Cancel" will abort the model definition, while selecting "Help" will bring you to the relevant Help topic.



Prepare Input: Differential Equation Structure

This window allows the user to define the differential equations for the model, assuming a model was selected from the library and/or ADVAN6 was used. If a model comes from the library, then the differential equations are pre-filled and all the user needs to do is check them to make sure they meet the needs of the analysis.

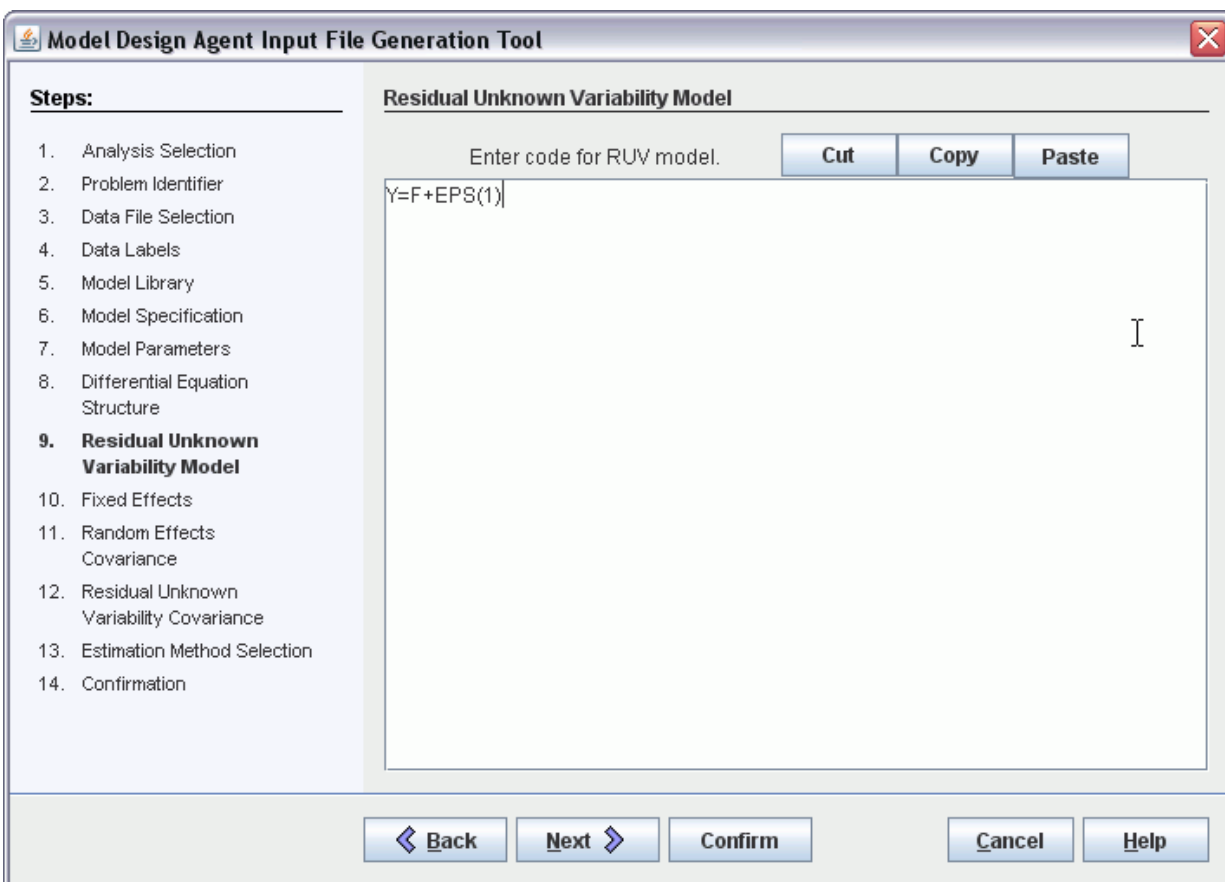


After you have performed the requested operations, the "Next" button will highlight and you can select it and continue. You can navigate back and forth in the MDA interface using the "Back" and "Next" buttons. The "Confirm" button displays the NONMEM(R) control file generated by the MDA up to this step in the process. Clicking "Cancel" will abort the model definition, while selecting "Help" will bring you to the relevant Help topic.



Prepare Input: Residual Unknown Variability Model

This window allows the user to define a model for the measurements that takes into account residual unknown variation (RUV).



The model is defined using NONMEM(R) compatible notation as follows:

- EPS(1), EPS(2), ... indicate the RUV random effects, i.e. random sources of variation at the between-subject level. They are random variables assumed to be Gaussian with mean zero and covariance SIGMA;
- Y is the statistical model for the measurements in the DV data column; this is the variable that is directly associated with the data in the DV column. The association needs to be defined.
- F is the model for the population data, i.e. the model variable which is being measured and associated with the DV time course.

For example, Gaussian additive variation on the measurement would be modeled as:

$$Y = F + \text{EPS}(1)$$

Gaussian proportional error on the measurement would read:

$$Y = F * (1 + \text{EPS}(1))$$

In this particular instance, we have chosen an additive Gaussian error model. Other statistics are also possible, such as an exponential error model:

$$Y = F * \text{EXP}(\text{EPS}(1))$$

After you have performed the requested operations, the "Next" button will highlight and you can select it and continue. You can navigate back and forth in the MDA interface using the "Back" and "Next" buttons. The "Confirm" button displays the NONMEM(R) control file generated by the MDA up to this step in the process. Clicking "Cancel" will abort the model definition, while selecting "Help" will bring you to the relevant Help topic.



Prepare Input: Fixed Effects

This step requires you to enter initial estimates for the fixed effects across the population. These are the THETA(1), THETA(2), ... parameters that you have entered earlier in the model equations. They represent model parameters that do not change across your population of subjects. This is the screen shot in question:

Model Design Agent Input File Generation Tool

Steps:

1. Analysis Selection
2. Problem Identifier
3. Data File Selection
4. Data Labels
5. Model Library
6. Model Specification
7. Model Parameters
8. Differential Equation Structure
9. Residual Unknown Variability Model
- 10. Fixed Effects**
11. Random Effects Covariance
12. Residual Unknown Variability Covariance
13. Estimation Method Selection
14. Confirmation

Fixed Effects

Enter initial estimates and bounds (except that FIXED is selected)
 - To get default bounds, press ENTER after entering initial estimate
 - Bounds influence stopping criteria (INF bounds not recommended)
 - Note: exponential expression may not be NONMEM compatible

Initial Estimate	<input type="text"/>	<input type="checkbox"/> FIXED	Add
Lower Bound	<input type="text"/>	<input type="checkbox"/> -INF	Change
Upper Bound	<input type="text"/>	<input type="checkbox"/> INF	Delete

List of fixed effect values and limits you have entered in NONMEM Syntax

Up
Down

You can enter initial estimates and bounds for the fixed effects across the population. Initial estimates, lower bound and upper bound must be entered separately for each fixed effect. The bounds are required, except when a fixed effect is designated as FIXED (which will cause it not to be adjusted during model optimization).

Note that, if you enter the value for the initial estimate and press the "Enter" key, default lower and upper bounds will appear equal to 1/10 and 10 times the initial estimate respectively, as shown below.

Model Design Agent Input File Generation Tool

Steps:

1. Analysis Selection
2. Problem Identifier
3. Data File Selection
4. Data Labels
5. Model Library
6. Model Specification
7. Model Parameters
8. Differential Equation Structure
9. Residual Unknown Variability Model
- 10. Fixed Effects**
11. Random Effects Covariance
12. Residual Unknown Variability Covariance
13. Estimation Method Selection
14. Confirmation

Fixed Effects

Enter initial estimates and bounds (except that FIXED is selected)
 - To get default bounds, press ENTER after entering initial estimate
 - Bounds influence stopping criteria (INF bounds not recommended)
 - Note: exponential expression may not be NONMEM compatible

Initial Estimate	<input type="text" value="4"/>	<input type="checkbox"/> FIXED	Add
Lower Bound	<input type="text" value=".4"/>	<input type="checkbox"/> -INF	Change
Upper Bound	<input type="text" value="40"/>	<input type="checkbox"/> INF	Delete

List of fixed effect values and limits you have entered in NONMEM Syntax

Up **Down**

Back **Next** **Confirm** **Cancel** **Help**

You will be asked to enter this information once for each fixed effect you have defined in the model equations. After entering Initial Estimate, Lower Bound and Upper Bound, you must press "Add". This will save your choices and associate them with the right fixed effect, as can be seen below:

Model Design Agent Input File Generation Tool

Steps:

1. Analysis Selection
2. Problem Identifier
3. Data File Selection
4. Data Labels
5. Model Library
6. Model Specification
7. Model Parameters
8. Differential Equation Structure
9. Residual Unknown Variability Model
- 10. Fixed Effects**
11. Random Effects Covariance
12. Residual Unknown Variability Covariance
13. Estimation Method Selection
14. Confirmation

Fixed Effects

Enter initial estimates and bounds (except that FIXED is selected)
 - To get default bounds, press ENTER after entering initial estimate
 - Bounds influence stopping criteria (INF bounds not recommended)
 - Note: exponential expression may not be NONMEM compatible

Initial Estimate	<input type="text" value="4"/>	<input type="checkbox"/> FIXED	Add
Lower Bound	<input type="text" value=".4"/>	<input type="checkbox"/> -INF	Change
Upper Bound	<input type="text" value="40"/>	<input type="checkbox"/> INF	Delete

List of fixed effect values and limits you have entered in NONMEM Syntax

1: (.4,4,40)	Up
	Down

Navigation:

You need to enter these values for all fixed effects. If you wish to change a set of values, you must highlight it in the list and then press "Change". At the end, the list of fixed effects will contain the required information, and the "Next" button will highlight to signal that it is time to move on to the next step. Double-clicking on a fixed effects list item will bring the values back up, so that changes can be made to either the initial value, or the bounds, or both.

Model Design Agent Input File Generation Tool

Steps:

1. Analysis Selection
2. Problem Identifier
3. Data File Selection
4. Data Labels
5. Model Library
6. Model Specification
7. Model Parameters
8. Differential Equation Structure
9. Residual Unknown Variability Model
- 10. Fixed Effects**
11. Random Effects Covariance
12. Residual Unknown Variability Covariance
13. Estimation Method Selection
14. Confirmation

Fixed Effects

Enter initial estimates and bounds (except that FIXED is selected)
 - To get default bounds, press ENTER after entering initial estimate
 - Bounds influence stopping criteria (INF bounds not recommended)
 - Note: exponential expression may not be NONMEM compatible

Initial Estimate: ☐ FIXED

Lower Bound: ☐ -INF

Upper Bound: ☐ INF

List of fixed effect values and limits you have entered in NONMEM Syntax

1:(.4,4,40)
2:(.4,20,40)

The bounds on the fixed effects determine (together with the user-requested number of significant digits) the stopping criteria for optimization. Bounds that are too wide can result in solutions that are less accurate, so it may be appropriate to use the default or make sure that the bounds do not increase too much.

After you have performed the requested operations, the "Next" button will highlight and you can select it and continue. You can navigate back and forth in the MDA interface using the "Back" and "Next" buttons. The "Confirm" button displays the NONMEM(R) control file generated by the MDA up to this step in the process. Clicking "Cancel" will abort the model definition, while selecting "Help" will bring you to the relevant Help topic.



Prepare Input: Random Effects Covariance

This section is where the covariance of the random effects ETA (which model the between subject variation, BSV) is defined and initial values chosen. Remember that ETA models RUV in individual analysis. There can be many ETA parameters, and their covariance structure can be

quite general. For example, a single exponential time course with Gaussian variation on the exponent proportional to 30% of the typical value would be modeled as:

$$\text{LAMBDA} = \text{THETA}(1) * (1 + \text{ETA}(1))$$

and the corresponding OMEGA value (in this case, OMEGA is a scalar) would be 0.09 (which is the square of 0.3). A single compartment pharmacokinetic model following a unitary pulse dose with linear Gaussian variation on the apparent volume of distribution equal to 50 volume units, and log-normal variation on the clearance proportional to 30% of the clearance typical value would be modeled as:

$$\text{CL} = \text{THETA}(1) * \text{EXP}(\text{ETA}(1))$$

$$\text{V} = \text{THETA}(2) + \text{ETA}(2)$$

where the corresponding OMEGA matrix would be diagonal 2 by 2 in the case of uncorrelated variations, and full 2 by 2 in the case of correlated variations. The OMEGA values would be $\text{OMEGA}(1,1)=2500$ (which is the square of 50) and $\text{OMEGA}(2,2)=0.09$.

The screenshot shows the 'Model Design Agent Input File Generation Tool' window. On the left is a 'Steps' list with 14 items, where '11. Random Effects Covariance' is highlighted. The main area is titled 'Random Effects Covariance' and contains the following text: 'Enter random effects covariance initial estimate. Bounds on random effects covariance and individual random effects set internally by SPK.' Below this text are three radio buttons: 'New block' (selected), 'Diagonal', and 'Full matrix'. To the right of these is an 'Add' button. Below the radio buttons is a 'Block size' dropdown menu set to '1' and an 'Enter data' button. Below that is a radio button for 'Constrained to be equal to preceding block'. To the right of this section are 'Change' and 'Delete' buttons. A horizontal line separates this section from the bottom section, which is titled 'Covariance blocks and initial estimates in NONMEM syntax' and contains a large empty text box. To the right of this box are 'Up' and 'Down' buttons. At the bottom of the window are five buttons: 'Back', 'Next', 'Confirm', 'Cancel', and 'Help'.

Every new OMEGA matrix is a new "block" (again in keeping with the NONMEM(R) notation). To start, one selects the "New block" radio button

and whether the matrix is "Diagonal" or "Full matrix". The next thing to do is to select the Block size, i.e. the size of the matrix. In this case, we are going to select a block of size 2 (since we have defined two random effects), and a diagonal matrix (which implies that the random effects are uncorrelated).

The screenshot shows a software window titled "Model Design Agent Input File Generation Tool". On the left is a "Steps:" sidebar with a list of 14 steps. Step 11, "Random Effects Covariance", is highlighted. The main area is titled "Random Effects Covariance" and contains the following elements:

- Instruction: "Enter random effects covariance initial estimate. Bounds on random effects covariance and individual random effects set internally by SPK."
- Radio buttons for matrix type: ☒ New block, ☒ Diagonal, ☐ Full matrix.
- A "Block size" dropdown menu with the value "2" selected, and an "Enter data" button to its right.
- A radio button for ☐ Constrained to be equal to preceding block.
- A large empty text box for "Covariance blocks and initial estimates in NONMEM syntax".
- Buttons on the right: "Add", "Change", "Delete", "Up", and "Down".
- Navigation buttons at the bottom: "Back", "Next", "Confirm", "Cancel", and "Help".

After the size of the block has been selected, the user should click on the "Enter data" button. The Matrix Entry Form appears.

Click cell to enter initial matrix diagonal elements.

	Initial Estimate	Value Fixed
1,1		<input type="checkbox"/>
2,2		<input type="checkbox"/>

☐ Entire block is fixed.

Done Add Change

Note that the form will be different depending on the size of the matrix. In this case, there are two rows corresponding to the 1,1 and 2,2 elements. These two numbers completely define the matrix. Note that the OMEGA values can also be fixed by checking the box next to the value, as shown below.

Click cell to enter initial matrix diagonal elements.

	Initial Estimate	Value Fixed
1,1	0.03	<input checked="" type="checkbox"/>
2,2		<input type="checkbox"/>

☐ Entire block is fixed.

Done Add Change

Your chosen values for OMEGA can be entered by clicking on the corresponding cell and typing in the value.

Diagonal Matrix Entry Form

Click cell to enter initial matrix diagonal elements.

	Initial Estimate	Value Fixed
1,1	0.03	<input type="checkbox"/>
2,2	0.03	<input type="checkbox"/>

☐ Entire block is fixed.

Done Add Change

After doing this, you need to press "Add" or "Change" to add or change these initial values:

Model Design Agent Input File Generation Tool

Steps:

1. Analysis Selection
2. Problem Identifier
3. Data File Selection
4. Data Labels
5. Model Library
6. Model Specification
7. Model Parameters
8. Differential Equation Structure
9. Residual Unknown Variability Model
10. Fixed Effects
- 11. Random Effects Covariance**
12. Residual Unknown Variability Covariance
13. Estimation Method Selection
14. Confirmation

Random Effects Covariance

Enter random effects covariance initial estimate.
Bounds on random effects covariance and individual random effects set internally by SPK.

☒ New block
 ☒ Diagonal
 ☐ Full matrix

Block size

☐ Constrained to be equal to preceding block

Covariance blocks and initial estimates in NONMEM syntax

```
$OMEGA DIAGONAL(2) 0.03 0.03
```

As can be seen, the screen below the entry buttons has displayed a description of the random effects covariance you have entered in NONMEM(R) syntax. In this case, we have entered an OMEGA matrix

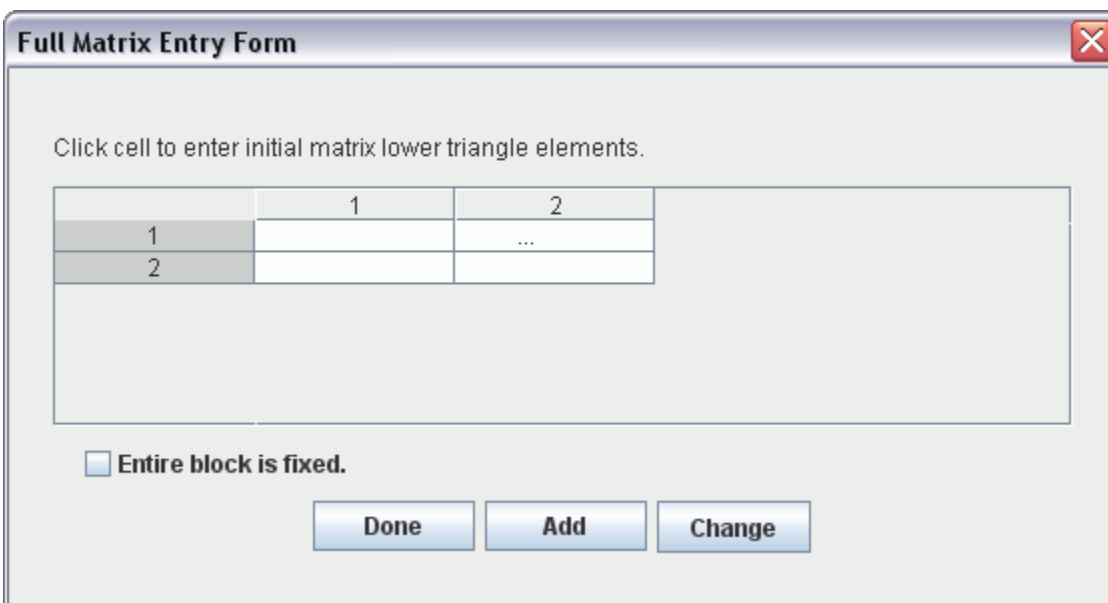
which is size 2, diagonal and with elements 1,1 and 2,2 both equal to 0.03.

We could also have chosen to enter a full two by two matrix. To do that, we would have to have selected a block of dimension two and we would check the radio button next to "Full matrix".

The screenshot shows the 'Model Design Agent Input File Generation Tool' window. On the left, a 'Steps:' list contains 14 items, with '11. Random Effects Covariance' highlighted. The main area is titled 'Random Effects Covariance' and contains the following elements:

- Instruction: 'Enter random effects covariance initial estimate. Bounds on random effects covariance and individual random effects set internally by SPK.'
- Three radio buttons: 'New block' (selected), 'Diagonal', and 'Full matrix'.
- A 'Block size' dropdown menu set to '2'.
- An 'Enter data' button.
- A radio button for 'Constrained to be equal to preceding block'.
- A text area labeled 'Covariance blocks and initial estimates in NONMEM syntax'.
- Buttons on the right: 'Add', 'Change', 'Delete', 'Up', and 'Down'.
- Buttons at the bottom: 'Back', 'Next', 'Confirm', 'Cancel', and 'Help'.

The user then clicks the "Enter data" button, as before. The Matrix Entry Form appears.



Full Matrix Entry Form

Click cell to enter initial matrix lower triangle elements.

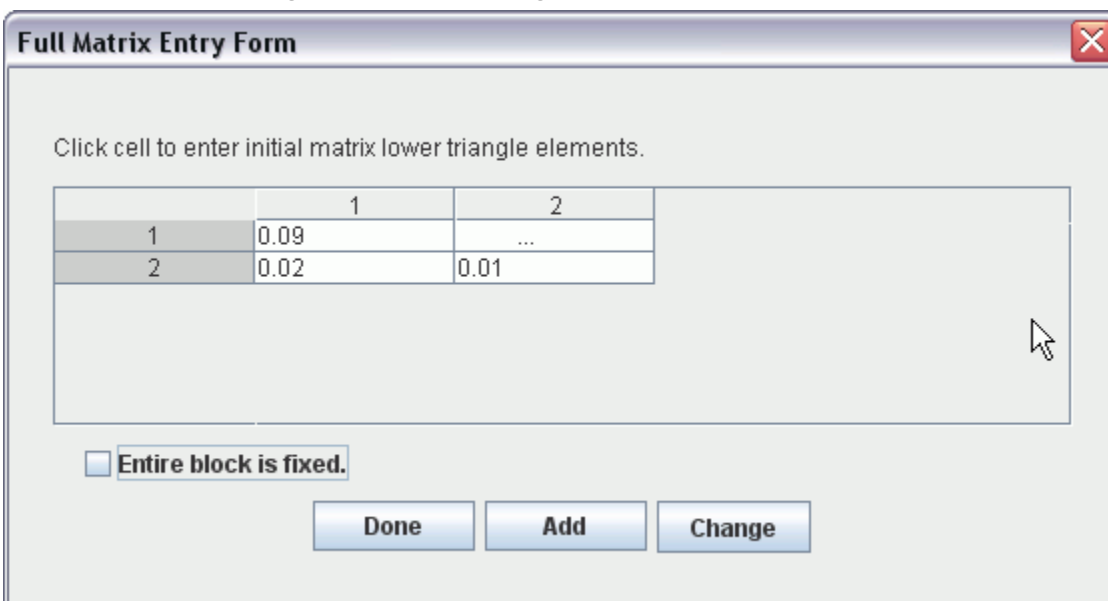
	1	2
1		...
2		

☐ Entire block is fixed.

Done Add Change

As before, the form will be different depending on the size of the matrix. In this case, there are two rows and two columns, and space to enter the (1,1), (2,1) and (2,2) elements (since the matrix is symmetric, the (2,1) element is identical to the (1,2) element). These three numbers completely define the matrix.

As before, the chosen values for OMEGA can be entered by clicking on the corresponding cell and typing in the value.



Full Matrix Entry Form

Click cell to enter initial matrix lower triangle elements.

	1	2
1	0.09	...
2	0.02	0.01

☐ Entire block is fixed.

Done Add Change

After doing this, you need to press "Add" or "Change" to finalize your entry.

Model Design Agent Input File Generation Tool

Steps:

1. Analysis Selection
2. Problem Identifier
3. Data File Selection
4. Data Labels
5. Model Library
6. Model Specification
7. Model Parameters
8. Differential Equation Structure
9. Residual Unknown Variability Model
10. Fixed Effects
- 11. Random Effects Covariance**
12. Residual Unknown Variability Covariance
13. Estimation Method Selection
14. Confirmation

Random Effects Covariance

Enter random effects covariance initial estimate.
Bounds on random effects covariance and individual random effects set internally by SPK.

☒ New block
 ☐ Diagonal
 ☒ Full matrix

Block size:

☐ Constrained to be equal to preceding block

Covariance blocks and initial estimates in NONMEM syntax

```
$OMEGA BLOCK(2) 0.09 0.02 0.01
```

Buttons: Add, Change, Delete, Up, Down

Navigation: Back, Next, Confirm, Cancel, Help

As it can be seen, the screen below the entry buttons has displayed a description of the random effects covariance you have entered in NONMEM(R) syntax. In this case, we have entered an OMEGA matrix which is size 2, full and with elements 1,1 equal to 0.09, 2,1 equal to 0.02 and 2,2 equal to 0.01.

After you have performed the requested operations, the "Next" button will highlight and you can select it and continue. You can navigate back and forth in the MDA interface using the "Back" and "Next" buttons. The "Confirm" button displays the NONMEM(R) control file generated by the MDA up to this step in the process. Clicking "Cancel" will abort the model definition, while selecting "Help" will bring you to the relevant Help topic.



Prepare Input: Residual Unknown Variability Covariance

This section of the MDA is where the matrix describing the residual unknown variation (RUV) can be defined and initial values chosen. This

is the covariance of the random effects EPS (which model the residual unknown variation, RUV).

The RUV appears at the level of the measurements, while the BSV appears at the level of the model parameters (although changes to this may be possible).

There can be many EPS parameters, and their covariance structure can be quite general. As with the OMEGA matrix, this is a covariance matrix, and it can be diagonal or full. For example, Gaussian, additive RUV on the measurement with constant variance would be modeled as:

$$Y = F + \text{EPS}(1)$$

On the other hand, Gaussian, additive RUV on the measurement with variance proportional to the magnitude of the measurement would be:

$$Y = F * (1 + \text{EPS}(1))$$

Lognormal RUV would be defined as:

$$Y = F * \text{EXP}(\text{EPS}(1))$$

Note that, when using the First Order approximation when fitting, the proportional and lognormal RUV are equivalent, since the exponential would be approximated by a proportional term. The SIGMA matrix defines the covariance of the RUV. For the examples above, the SIGMA matrix has different interpretations. For example, Gaussian, additive RUV on the measurement with constant standard deviation equal to 100 would be modeled as: $Y = F + \text{EPS}(1)$, and SIGMA would be equal to 10000 (the square of 100, since SIGMA is in variance units). An additive RUV with standard deviation proportional to 10% of the measurement would be modeled with a SIGMA equal to 0.01 (which is the square of 0.1). When fitting, these values are only starting (initial guesses) values, to be modified during and after data fitting, and when simulating they are taken as the true value for the population to be simulated. Note also that SIGMA is a full matrix, so more complicated error structures are feasible as well. For example, a RUV structure with error that is characterized by both a proportional and a linearly additive term would be modeled as:

$$Y = F * (1 + \text{EPS}(1)) + \text{EPS}(2)$$

In this case, the SIGMA matrix is going to be 2 by 2 and with values determined by the magnitudes of the error terms. For example, if the RUV is proportional to 10% of the measurement and has a noise "floor" of standard deviation equal to 100, then SIGMA(1,1) is going to be 0.01 and SIGMA(2,2) is 10000. The cross-covariance term, SIGMA(1,2) or

SIGMA(2,1), can be zero in case of uncorrelated noise or nonzero in case some information is available from the data and the model can be fit.

Model Design Agent Input File Generation Tool

Steps:

1. Analysis Selection
2. Problem Identifier
3. Data File Selection
4. Data Labels
5. Model Library
6. Model Specification
7. Model Parameters
8. Differential Equation Structure
9. Residual Unknown Variability Model
10. Fixed Effects
11. Random Effects Covariance
- 12. Residual Unknown Variability Covariance**
13. Estimation Method Selection
14. Confirmation

Residual Unknown Variability Covariance

Enter residual unknown variability covariance initial estimate.
Bounds on residual unknown variability covariance set internally by SPK.

☒ **New block**
☒ **Diagonal**
☐ Full matrix

Dimension:

☐ Constrained to be equal to preceding block

Covariance blocks and initial estimates in NONMEM syntax

As we have seen for the OMEGA matrix, every new SIGMA matrix is a new "block" (in keeping with the NONMEM(R) notation). To start, one selects the "New block" radio button and whether the matrix is "Diagonal" (only non diagonal elements are nonzero) or "Full matrix" (all matrix elements are nonzero – note that SIGMA is symmetric). The next thing to do is to select the Block size, i.e. the size of the matrix. In this case, we are going to select a block of size 1, and a diagonal matrix. The Entry Form will appear:

Click cell to enter initial matrix diagonal elements.

	Initial Estimate	Value Fixed
1,1		<input type="checkbox"/>

☐ Entire block is fixed.

Done Add Change

Note that the form will be different depending on the size of the matrix. In this case, there is only one row, corresponding to the only SIGMA element to be defined. This number will define the matrix completely. Note that the SIGMA values can also be fixed by checking the box next to the value. Fixing the values will cause them not to be changed during estimation. Your chosen values for SIGMA can be entered by clicking on the corresponding cell and typing in the value.

Click cell to enter initial matrix diagonal elements.

	Initial Estimate	Value Fixed
1,1	0.01	<input type="checkbox"/>

☐ Entire block is fixed.

Done Add Change

After doing this, press "Add" or "Change" to finalize your entry.

Model Design Agent Input File Generation Tool

Steps:

1. Analysis Selection
2. Problem Identifier
3. Data File Selection
4. Data Labels
5. Model Library
6. Model Specification
7. Model Parameters
8. Differential Equation Structure
9. Residual Unknown Variability Model
10. Fixed Effects
11. Random Effects Covariance
- 12. Residual Unknown Variability Covariance**
13. Estimation Method Selection
14. Confirmation

Residual Unknown Variability Covariance

Enter residual unknown variability covariance initial estimate.
Bounds on residual unknown variability covariance set internally by SPK.

☒ New block
 ☒ Diagonal
 ☐ Full matrix

Dimension:

☐ Constrained to be equal to preceding block

Covariance blocks and initial estimates in NONMEM syntax

```
$SIGMA DIAGONAL(1) 0.01
```

Buttons: Add, Change, Delete, Up, Down

Navigation: Back, Next, Confirm, Cancel, Help

As can be seen above, the screen below the entry buttons displays a description of the residual unknown variability covariance you have entered in NONMEM(R) syntax. In this case, we have entered a SIGMA matrix which is size 1 (scalar) and with element 1,1 equal to 0.01. Again, for comparison, a SIGMA values of 0.01 in the case of proportional error implies a standard deviation of 0.1, or 10%, on the measurements.

After you have performed the requested operations, the "Next" button will highlight and you can select it and continue. You can navigate back and forth in the MDA interface using the "Back" and "Next" buttons. The "Confirm" button displays the NONMEM(R) control file generated by the MDA up to this step in the process. Clicking "Cancel" will abort the model definition, while selecting "Help" will bring you to the relevant Help topic.



Prepare Input: Simulation

SPK allows the user to simulate data conditional on a model. If Simulation has been selected at the start (under Analysis Selection):

Model Design Agent Input File Generation Tool

Steps:

- Analysis Selection**
- Problem Identifier
- Data File Selection
- Data Labels
- Model Equations
- Fixed Effects
- Random Effects Covariance
- Residual Unknown Variability Covariance
- Simulation
- Confirmation

Analysis Selection

Select Analysis Type:
☒ **Population** ☐ **Individual** ☐ **Identifiability** seed:

Choose: ☐ **Parameter estimation** ☒ **Data simulation**

Select Population-level Model:
☒ **Parametric** ☐ **Two-stage** ☐ **Nonparametric**

Select Model Type: Select Model Editor
☐ **Analytic/algebraic model** ☒ **Text model editor**
☒ **SUBROUTINE ADVAN1** ☐ **Graphical model editor**

Select Statistics Option:
☐ **Compute statistics of parameter estimates**

Optional NONMEM Compatible Output: ☐ **Tables** ☐ **Scatterplots**

Reload Previous SPK Model or Job XML Input:

then the following screen will be shown instead of the Method Selection screen:

Steps:

1. Analysis Selection
2. Problem Identifier
3. Data File Selection
4. Data Labels
5. Model Equations
6. Fixed Effects
7. Random Effects Covariance
8. Residual Unknown Variability Covariance
- 9. Simulation**
10. Estimation Method Selection
11. Estimate Statistics
12. Confirmation

Simulation

Enter an integer number as the seed for the random source.
The number should be between 0 and 21474836447.

Seed Number for Random Source

Repeatedly run the problem. In each run, use the simulated data obtained from the previous run as the current random source.
If you want the parameters to be estimated from each simulated dataset, select the "Parameter Estimation" option in the first step.

Number of Sub-Problems to Run

Click the "Enter" button to continue.

The \$SIMULATION record you have entered.

The user is required to select a seed number (to replicate the run if needed) and a subproblem number.

After you have performed the requested operations, the "Next" button will highlight and you can select it and continue. You can navigate back and forth in the MDA interface using the "Back" and "Next" buttons. The "Confirm" button displays the NONMEM(R) control file generated by the MDA up to this step in the process. Clicking "Cancel" will abort the model definition, while selecting "Help" will bring you to the relevant Help topic.



Prepare Input: Estimation Method Selection

The Method Selection screen allows you to select various methods for estimation of the fixed effects and the BSV and RUV covariances. The presence of many methods is due to the fact that the maximum likelihood problem for nonlinear mixed effects does not have a closed-form solution with respect to the unknown parameters, due to the nonlinear fashion in which the fixed and random effects enter the problem. Thus,

approximation methods have to be used to linearize the model function and approximate the likelihood function w.r.t. the original problem. If you have selected **Parametric** in the opening window, the methods available from the computational server include, in increasing order of accuracy:

1. The **First Order method** linearizes the mathematical model of the measurements around a value of zero for the BSV random effects. While the approximation to the expected value of the measurement is linear, the approximation to the second order moment (RUV) is zero order. This is considered a rather crude approximation, but it is very computationally efficient, and so it is still widely used in practice. The First Order method is equivalent to the NONMEM(R) First Order, or FO, method.
2. The **Expected Hessian method** linearizes the model for the expected value of the measurements around a suitable individual estimate for the BSV random effects. In principle, a linear approximation (the default method) or a zero-order approximation (this approach is not currently available in the SPK system) can be used for the RUV. Expected Hessian is more accurate than the First Order method, but also more computationally expensive. The Expected Hessian method is equivalent to the NONMEM(R) First Order Conditional Estimation (FOCE) method with INTERACTION.
3. The **Laplace approximation** turns the integration problem of the marginal likelihood into an optimization problem using Laplace's approximation to the integral. It is considered marginally more accurate than the Expected Hessian method, but it is also considerably more computationally expensive. The Laplace approximation is equivalent to NONMEM(R)'s conditional estimation method with selection of the LAPLACIAN option.

The selection of the desired method is done by clicking on the corresponding radio button. Checking "Obtain individual estimates" will also return the individual parameter estimates for the random effects (POSTHOC option in NONMEM(R)). Checking "Make Automatic Error Recovery" will instruct SPK to gracefully recover from errors such as failure in parametric optimization or integration (it roughly has the same effect as NONMEM(R) NOABORT option).

Model Design Agent Input File Generation Tool

Steps:

1. Analysis Selection
2. Problem Identifier
3. Data File Selection
4. Data Labels
5. Model Library
6. Model Specification
7. Model Parameters
8. Differential Equation Structure
9. Residual Unknown Variability Model
10. Fixed Effects
11. Random Effects Covariance
12. Residual Unknown Variability Covariance
- 13. Estimation Method Selection**
14. Confirmation

Estimation Method Selection

Select an estimation method and available option(s) on the right.

☒ **First Order**
☐ **Expected Hessian**
☐ **Laplace Approximation**
☐ **Standard Two-Stage**
☐ **Iterative Two-Stage**
☐ **Global Two-Stage**

☐ **Obtain individual estimat...**
☐ **RUV depends on random effec...**
☐ **Center random effec...**
☐ **Make automatic error recove...**
☐ **Use MAP Bayesian Objecti...**

Enter Cov for THETA

Enter or select values for the following options.

Significant digits (stopping criterion) 3
Maximum number of iterations 450 ☒
Summary print iteration interval 5 ☒

Method and options expressed in NONMEM syntax

```
$ESTIMATION METHOD=0 SIGDIGITS=3 MAXEVALS=450 PRINT=5
```

If you have selected Two Stage on the opening window, your choices include:

1. The **Standard Two Stage** approach, where every subject's data are fit separately and the population parameters are defined as the sample average (THETAs) and sample covariance (OMEGAs) of the individual estimates. The SIGMAS are calculated as the sample averages of the individual SIGMAS estimates.
2. The **Iterative Two Stage** approach, where every subject's data are fit separately, but the population parameters (again defined as the sample average (THETAs) and sample covariance (OMEGAs) of the individual estimates) are used as population priors for the individual estimation, using a Maximum A Posteriori (MAP) approach.
3. The **Global Two Stage** approach, where every subject's data are fit separately, and an iterative scheme similar to the Iterative Two Stage is applied to the individual parameter estimates and the individual asymptotic covariance matrices, thus returning refined population estimates.

Model Design Agent Input File Generation Tool

Steps:

1. Analysis Selection
2. Problem Identifier
3. Data File Selection
4. Data Labels
5. Model Library
6. Model Specification
7. Model Parameters
8. Differential Equation Structure
9. Residual Unknown Variability Model
10. Random Effects
11. Residual Unknown Variability Covariance
- 12. Estimation Method Selection**
13. Confirmation

Estimation Method Selection

Select a two-stage method and MAP Bayesian objective

☐ First Order
 ☐ Obtain individual estimat...

☐ Expected Hessian
 ☐ RUV depends on random effec...

☐ Laplace Approximation
 ☐ Center random effec...

☒ **Standard Two-Stage**
☐ Make automatic error recove...

☐ Iterative Two-Stage
 ☐ Use MAP Bayesian Objecti...

☐ Global Two-Stage

Enter or select values for the following options.

Significant digits (stopping criterion)

Maximum number of iterations ☒

Summary print iteration interval ☒

Method and options expressed in NONMEM syntax

`$ESTIMATION METHOD=0 SIGDIGITS=3 MAXEVALS=450 PRINT=5`

Other estimation variables that can be set in this screen include:

- The number of significant digits in the estimate: the default number is 3. A choice of a higher number will require longer computation time, while a lower number will sacrifice accuracy for computational speed.
- The maximum allowable number of function evaluations: these are the evaluations of the maximum likelihood functions to be performed by the computational engine. This number can be varied at will. In general, noisier, less reliable data may require more function evaluations for the estimation to be successful, while better data may not require as much computational effort. This may not hold for all data sets.
- The Iteration summaries print out interval steps number indicates the number of iterations after which a report should be given to the user. Usually, this choice is 5, meaning that a report should be given about the optimization status every 5 function evaluations.

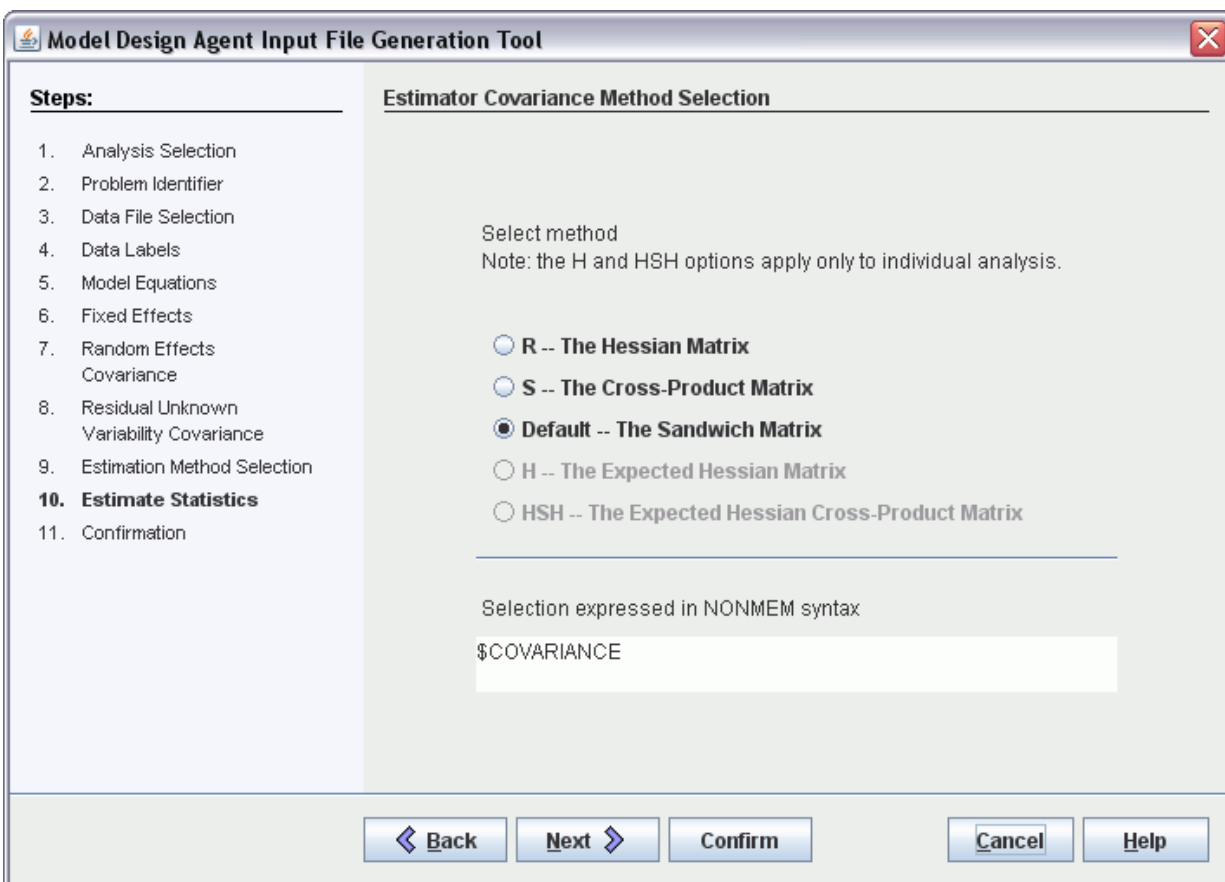
Note that, after you have entered the required variables, you will see that the screen below the entry buttons has displayed a description of the requirements you have entered (method and other variables) in NONMEM(R) syntax. This is meant to facilitate comparison between SPK and NONMEM(R) output. In the case displayed in the screen shot above, we have selected the First Order method and have requested 3 significant digits, at most 450 function evaluations and a printout of the optimization status every 5 function evaluations. If the method you selected is not available in NONMEM(R), then the First Order estimation is displayed.

After you have performed the requested operations, the "Next" button will highlight and you can select it and continue. You can navigate back and forth in the MDA interface using the "Back" and "Next" buttons. The "Confirm" button displays the NONMEM(R) control file generated by the MDA up to this step in the process. Clicking "Cancel" will abort the model definition, while selecting "Help" will bring you to the relevant Help topic.

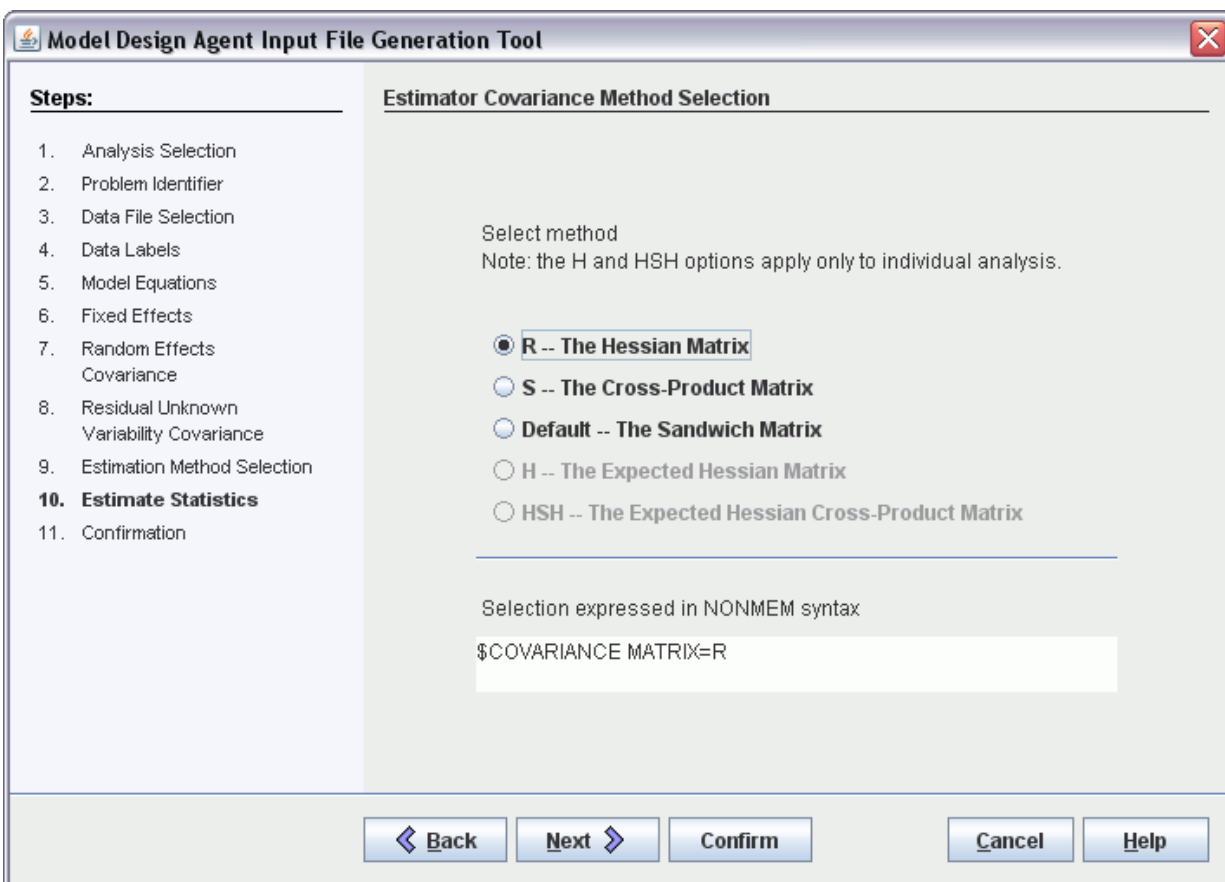


Prepare Input: Estimator Covariance Method

The Estimator Covariance Method Selection screen is where the user selects the procedure to be employed when calculating the reliability of the parametric estimate. This applies to THETA, OMEGA and SIGMA estimates since they are all estimated together and simultaneously. Just like with the optimization problem, there is not a single way to calculate the estimate precision. Thus, three methods are provided, which the user can select. Note that no method is absolutely reliable, and one method may provide well-defined answers while another may not. Serious divergence between methods usually indicates that the precision of the estimates is not well determined.



The screen shot above and the one below indicate the result (in NONMEM(R) syntax) of selecting two different options for the calculation of the covariance. In the estimation report, covariance information will be given as standard errors of the estimates.



After you have performed the requested operations, the "Next" button will highlight and you can select it and continue. You can navigate back and forth in the MDA interface using the "Back" and "Next" buttons. The "Confirm" button displays the NONMEM(R) control file generated by the MDA up to this step in the process. Clicking "Cancel" will abort the model definition, while selecting "Help" will bring you to the relevant Help topic.



Prepare Input: Table Output

In this section, the user can specify which kind of tabular output the system should return after the estimation step is completed. The options in this window apply only if one wants to generate NONMEM(R)-compatible tables, since SPK tables can be usually generated from the report window.

Normally, data values (DV), population predictions (PRED), residuals, i.e. the difference between data and model (RES) and weighted residuals

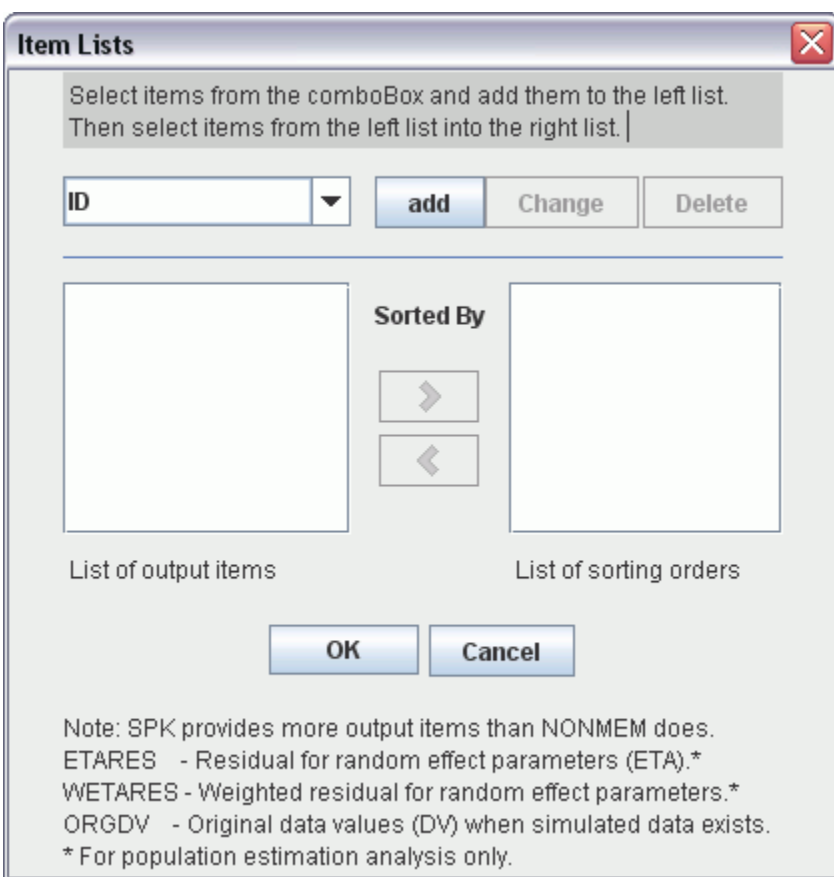
(i.e. the difference between data and model weighted by the covariance of the measurements) are appended to the output table by default.

This is the starting screen for the Table Output definition:

The screenshot shows a software window titled "Model Design Agent Input File Generation Tool". On the left is a "Steps:" sidebar with a list of 13 steps. Step 11, "Table Output", is highlighted. The main area is titled "Table Output" and contains the following elements:

- Instructional text: "Enter the output file name and select a header format. The data items are listed as columns and the order of the rows may be sorted. If No Append is selected, data values, population prediction, residuals and weighted residuals (i.e. DV, PRED, RES, WRES) will not be automatically in the output."
- A "File Name" text input field.
- Three radio buttons for header format: "No Append", "No Header", and "One Header".
- A "Select items and sorting orders" section with a "Make Selection" button.
- A list box labeled "List of tables you have selected in NONMEM syntax" which is currently empty.
- Buttons "Add", "Change", and "Delete" on the right side of the main area.
- Buttons "Up" and "Down" on the right side of the list box.
- A bottom navigation bar with buttons: "Back", "Next", "Confirm", "Cancel", and "Help".

By clicking on **Make Selection**, items to be plotted and their sorting orders can be defined. This is the screen that becomes available when Make Selection is invoked:



In addition to DV, PRED, WRES and RES, SPK also provides:

- ETARES, the residuals for the random effect parameters. These are the differences between the individual ETAs (random effects) and their average;
- WETARES, the weighted residuals for the random effect parameters. These are the differences between the individual ETAs (random effects) and their average, weighted by the corresponding OMEGA elements;
- ORGDV, the original data values (DV) in the data file when simulated data are generated.

Any combination of input and output variables can be selected. For example, in the screen shot below, we have selected to return DV and PRED, sorted by subject ID:

Item Lists

Select items from the comboBox and add them to the left list.
Then select items from the left list into the right list.

TIME

▼

add

Change

Delete

DV

PRED

ID

Sorted By

ID

➤

➤

List of output items

List of sorting orders

OK

Cancel

Note: SPK provides more output items than NONMEM does.

ETARES - Residual for random effect parameters (ETA).*

WETARES - Weighted residual for random effect parameters.*

ORGDV - Original data values (DV) when simulated data exists.

* For population estimation analysis only.

After selecting OK, we are returned to the screen below – one still needs to select **Add** for the table output to be saved and be displayed in NONMEM(R) format.

Model Design Agent Input File Generation Tool

Steps:

1. Analysis Selection
2. Problem Identifier
3. Data File Selection
4. Data Labels
5. Model Equations
6. Fixed Effects
7. Random Effects Covariance
8. Residual Unknown Variability Covariance
9. Estimation Method Selection
10. Estimate Statistics
- 11. Table Output**
12. Plot Output
13. Confirmation

Table Output

Enter the output file name and select a header format. The data items are listed as columns and the order of the rows may be sorted. If No Append is selected, data values, population prediction, residuals and weighted residuals (i.e. DV, PRED, RES, WRES) will not be automatically in the output.

File Name

☐ No Append ☐ No Header ☐ One Header

Select items and sorting orders

List of tables you have selected in NONMEM syntax

\$TABLE DV PRED ID BY ID

After you have performed the requested operations, the "Next" button will highlight and you can select it and continue. You can navigate back and forth in the MDA interface using the "Back" and "Next" buttons. The "Confirm" button displays the NONMEM(R) control file generated by the MDA up to this step in the process. Clicking "Cancel" will abort the model definition, while selecting "Help" will bring you to the relevant Help topic.



Prepare Input: Plot Output

SPK offers basic and extended plotting capabilities. The options in this window apply only if one wants to generate NONMEM(R)-compatible plots, since SPK plots can be usually generated from the report window. The screen below is the starting point to define plot output following the Estimation step:

Model Design Agent Input File Generation Tool

Steps:

1. Analysis Selection
2. Problem Identifier
3. Data File Selection
4. Data Labels
5. Model Equations
6. Fixed Effects
7. Random Effects Covariance
8. Residual Unknown Variability Covariance
9. Estimation Method Selection
10. Estimate Statistics
11. Table Output
- 12. Plot Output**
13. Confirmation

Plot Output

Enter the range of the data for plotting. The default starting number is 1. Up to 900 data points may be plotted. Lines along $X = 0$, $Y = 0$ or $X = Y$ may be added to the plot. Select items for X, Y and parameters to plot.

Plot Data From To

☐ $X = 0$ Line ☐ $Y = 0$ Line ☐ $X = Y$ Line

Select Data Items For Plotting.

List of plots you have selected in MNONMEM syntax

In the instance below, the data are plotted from 1 to 64 (the maximum number of data records in this instance), and we have asked for the x-axis, the y-axis and the identity line to be displayed.

Model Design Agent Input File Generation Tool

Steps:

1. Analysis Selection
2. Problem Identifier
3. Data File Selection
4. Data Labels
5. Model Equations
6. Fixed Effects
7. Random Effects Covariance
8. Residual Unknown Variability Covariance
9. Estimation Method Selection
10. Estimate Statistics
11. Table Output
- 12. Plot Output**
13. Confirmation

Plot Output

Enter the range of the data for plotting. The default starting number is 1. Up to 900 data points may be plotted. Lines along $X = 0$, $Y = 0$ or $X = Y$ may be added to the plot. Select items for X, Y and parameters to plot.

Plot Data From To

☒ $X = 0$ Line ☒ $Y = 0$ Line ☒ $X = Y$ Line

Select Data Items For Plotting.

List of plots you have selected in MNONMEM syntax

Plotting variables are selected similarly to the tabular output variables by clicking on Make Selection. The following screen appears:

Item Lists

Select items from the comboBox and add them to the lists. The buttons are shared. You need to select a current list to work on.

Select current list

☒ List 1
☐ List 2
☐ List 3

ID

▼

Add

Change

Delete

List 1: ordinate Y

List 2: abscissa X

List 3: plot for each

OK

Cancel

Note: SPK provides more output items than NONMEM does.

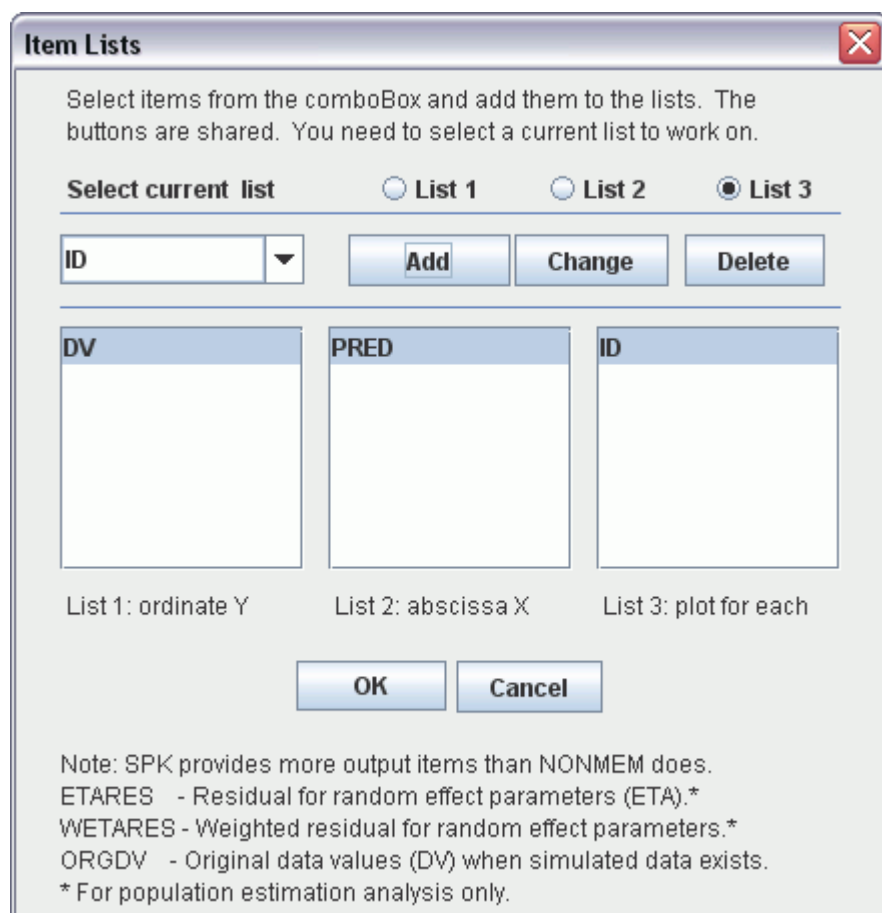
ETARES - Residual for random effect parameters (ETA).*

WETARES - Weighted residual for random effect parameters.*

ORGDV - Original data values (DV) when simulated data exists.

* For population estimation analysis only.

For example, one can ask to plot the predictions (PRED) on the x-axis and the data values (DV) on the y-axis, plotted for each subject ID:



The dialog box is titled "Item Lists" and contains instructions: "Select items from the comboBox and add them to the lists. The buttons are shared. You need to select a current list to work on." Below this, there are three radio buttons for "List 1", "List 2", and "List 3", with "List 3" selected. A horizontal line separates this from a section with a dropdown menu labeled "ID" and three buttons: "Add", "Change", and "Delete". Below this is another horizontal line, followed by three empty list boxes labeled "DV", "PRED", and "ID". At the bottom of these boxes are labels: "List 1: ordinate Y", "List 2: abscissa X", and "List 3: plot for each". At the bottom of the dialog are "OK" and "Cancel" buttons. A note at the very bottom explains that SPK provides more output items than NONMEM does, listing ETARES, WETARES, and ORGDV, and stating that these are for population estimation analysis only.

Select items from the comboBox and add them to the lists. The buttons are shared. You need to select a current list to work on.

Select current list ☐ List 1 ☐ List 2 ☒ List 3

ID Add Change Delete

DV PRED ID

List 1: ordinate Y List 2: abscissa X List 3: plot for each

OK Cancel

Note: SPK provides more output items than NONMEM does.
ETARES - Residual for random effect parameters (ETA).*
WETARES - Weighted residual for random effect parameters.*
ORGDV - Original data values (DV) when simulated data exists.
* For population estimation analysis only.

In the example above, "List 1", "2" and "3" correspond to the ordinate, abscissa and splitting variable respectively. After clicking on OK, one is returned to the screen below:

Model Design Agent Input File Generation Tool

Steps:

1. Analysis Selection
2. Problem Identifier
3. Data File Selection
4. Data Labels
5. Model Equations
6. Fixed Effects
7. Random Effects Covariance
8. Residual Unknown Variability Covariance
9. Estimation Method Selection
10. Estimate Statistics
11. Table Output
- 12. Plot Output**
13. Confirmation

Plot Output

Enter the range of the data for plotting. The default starting number is 1. Up to 900 data points may be plotted. Lines along $X = 0$, $Y = 0$ or $X = Y$ may be added to the plot. Select items for X, Y and parameters to plot.

Plot Data From To

☒ X = 0 Line ☒ Y = 0 Line ☒ X = Y Line

Select Data Items For Plotting.

List of plots you have selected in MNONMEM syntax

After clicking "Add", the plot variables are saved and displayed in NONMEM(R) syntax:

Model Design Agent Input File Generation Tool

Steps:

1. Analysis Selection
2. Problem Identifier
3. Data File Selection
4. Data Labels
5. Model Equations
6. Fixed Effects
7. Random Effects Covariance
8. Residual Unknown Variability Covariance
9. Estimation Method Selection
10. Estimate Statistics
11. Table Output
- 12. Plot Output**
13. Confirmation

Plot Output

Enter the range of the data for plotting. The default starting number is 1. Up to 900 data points may be plotted. Lines along $X = 0$, $Y = 0$ or $X = Y$ may be added to the plot. Select items for X, Y and parameters to plot.

Plot Data From To

☒ X = 0 Line ☒ Y = 0 Line ☒ X = Y Line

Select Data Items For Plotting.

List of plots you have selected in MNONMEM syntax

`$SCATTERPLOT DV VS PRED BY ID FROM 1 TO 64 UNI`

Another plot can be added, for example, by selecting to plot DV and PRED against TIME, splitted by ID:

Item Lists

Select items from the comboBox and add them to the lists. The buttons are shared. You need to select a current list to work on.

Select current list

List 1

List 2

List 3

ID

Add

Change

Delete

DV

PRED

TIME

ID

List 1: ordinate Y

List 2: abscissa X

List 3: plot for each

OK

Cancel

Note: SPK provides more output items than NONMEM does.

ETARES - Residual for random effect parameters (ETA).*

WETARES - Weighted residual for random effect parameters.*

ORGDV - Original data values (DV) when simulated data exists.

* For population estimation analysis only.

The resulting selection is as follows:

Model Design Agent Input File Generation Tool

Steps:

1. Analysis Selection
2. Problem Identifier
3. Data File Selection
4. Data Labels
5. Model Equations
6. Fixed Effects
7. Random Effects Covariance
8. Residual Unknown Variability Covariance
9. Estimation Method Selection
10. Estimate Statistics
11. Table Output
- 12. Plot Output**
13. Confirmation

Plot Output

Enter the range of the data for plotting. The default starting number is 1. Up to 900 data points may be plotted. Lines along $X = 0$, $Y = 0$ or $X = Y$ may be added to the plot. Select items for X, Y and parameters to plot.

Plot Data From To

☒ X = 0 Line ☒ Y = 0 Line ☒ X = Y Line

Select Data Items For Plotting.

List of plots you have selected in MNONMEM syntax

```
$SCATTERPLOT DV VS PRED BY ID FROM 1 TO 64 UN
$SCATTERPLOT DV PRED VS TIME BY ID FROM 1 TO 6
```

After you have performed the requested operations, the "Next" button will highlight and you can select it and continue. You can navigate back and forth in the MDA interface using the "Back" and "Next" buttons. The "Confirm" button displays the NONMEM(R) control file generated by the MDA up to this step in the process. Clicking "Cancel" will abort the model definition, while selecting "Help" will bring you to the relevant Help topic.

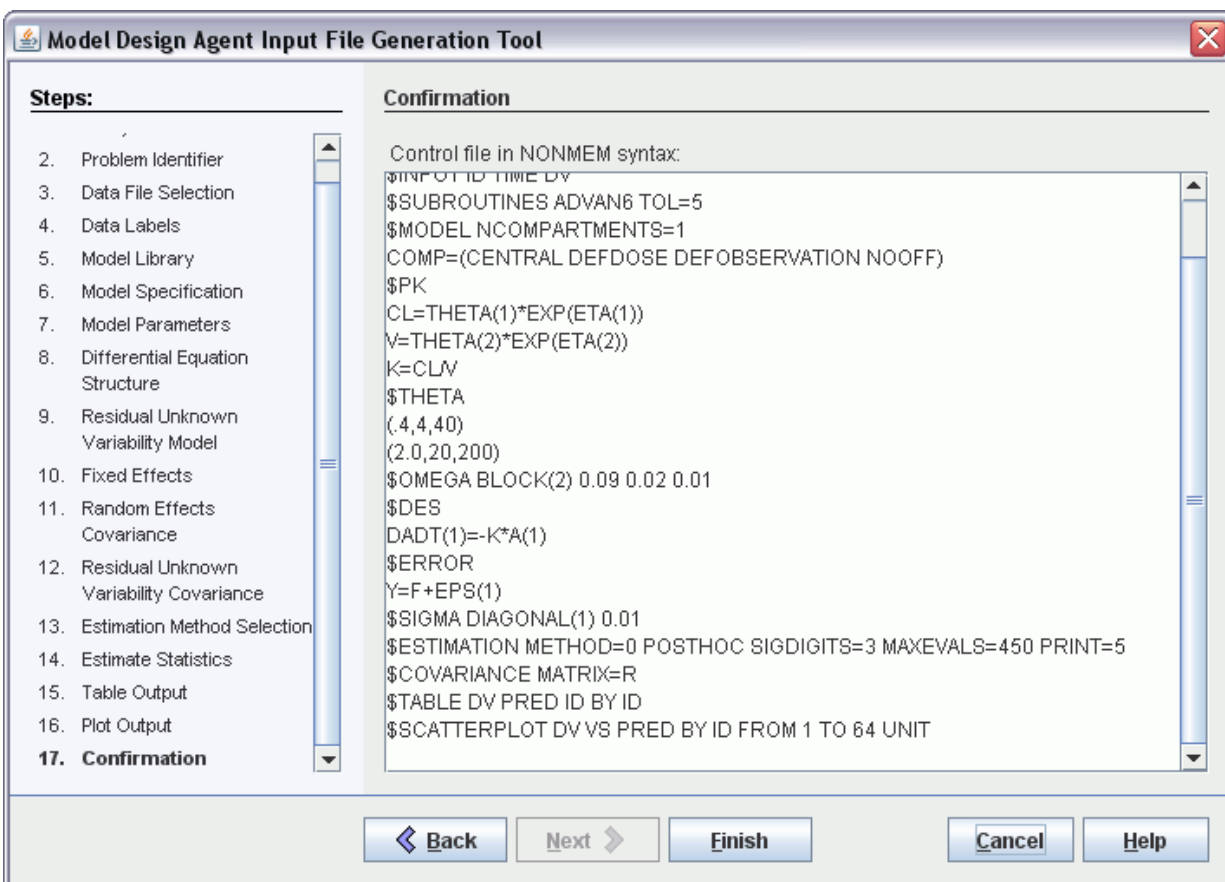


Prepare Input: Confirmation

The problem has now been completely defined, and if you reached this step your model has all the required information.

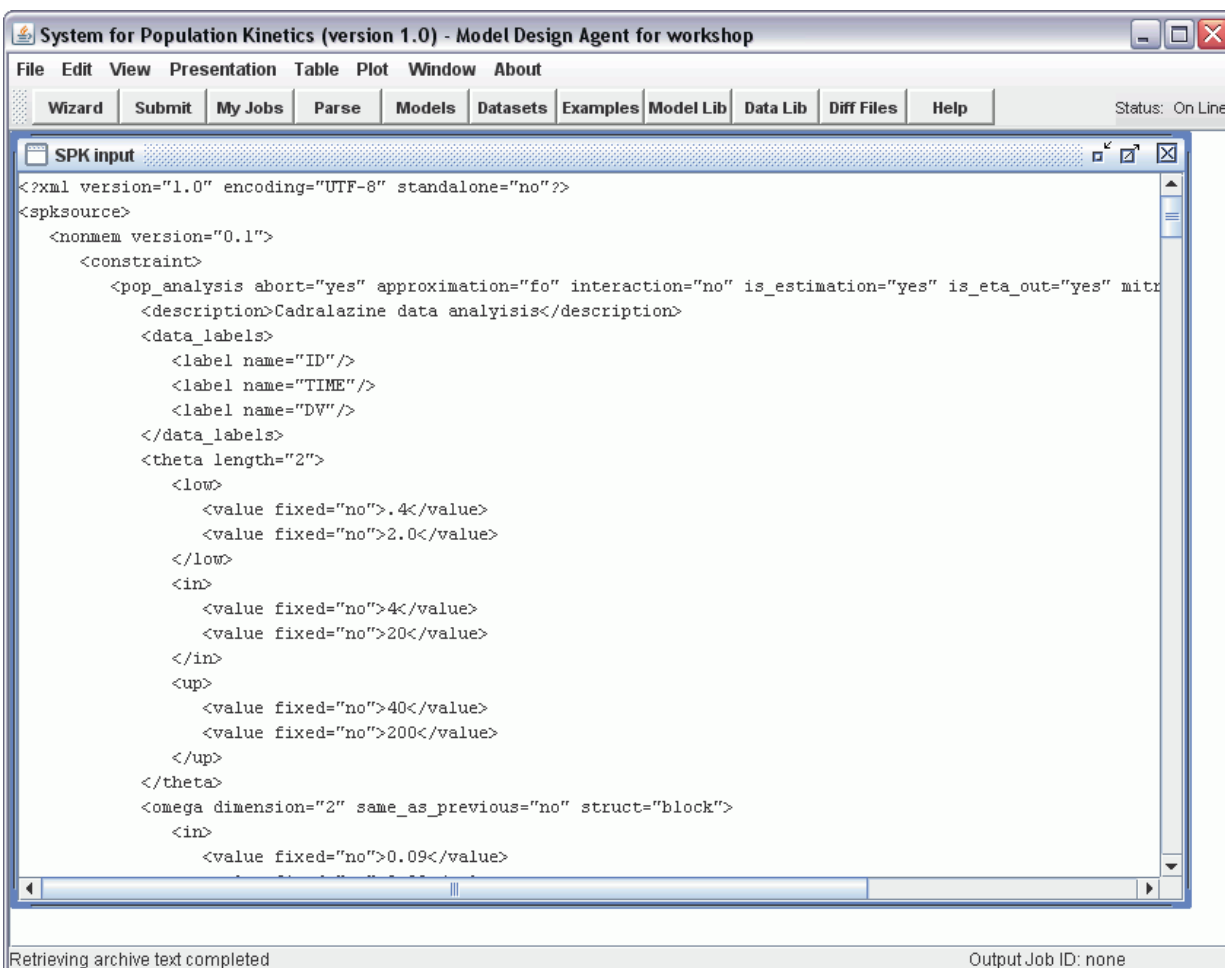
It is time now to finalize the model structure before submission to the computational library.

The model information is shown in NONMEM(R) format, since at this time system functionality is comparable to NONMEM(R). Commands which are not compatible with NONMEM(R) will be flagged in future versions.



If you would like to change the model specification, simply use the "Back" button to return to the appropriate screen.

If the model is satisfactory, you should click the "Finish" button, which finalizes the model structure and starts the translation in XML, which is the modeling language spoken by the computational kernel. Then, the system will present the XML translation of your model file.

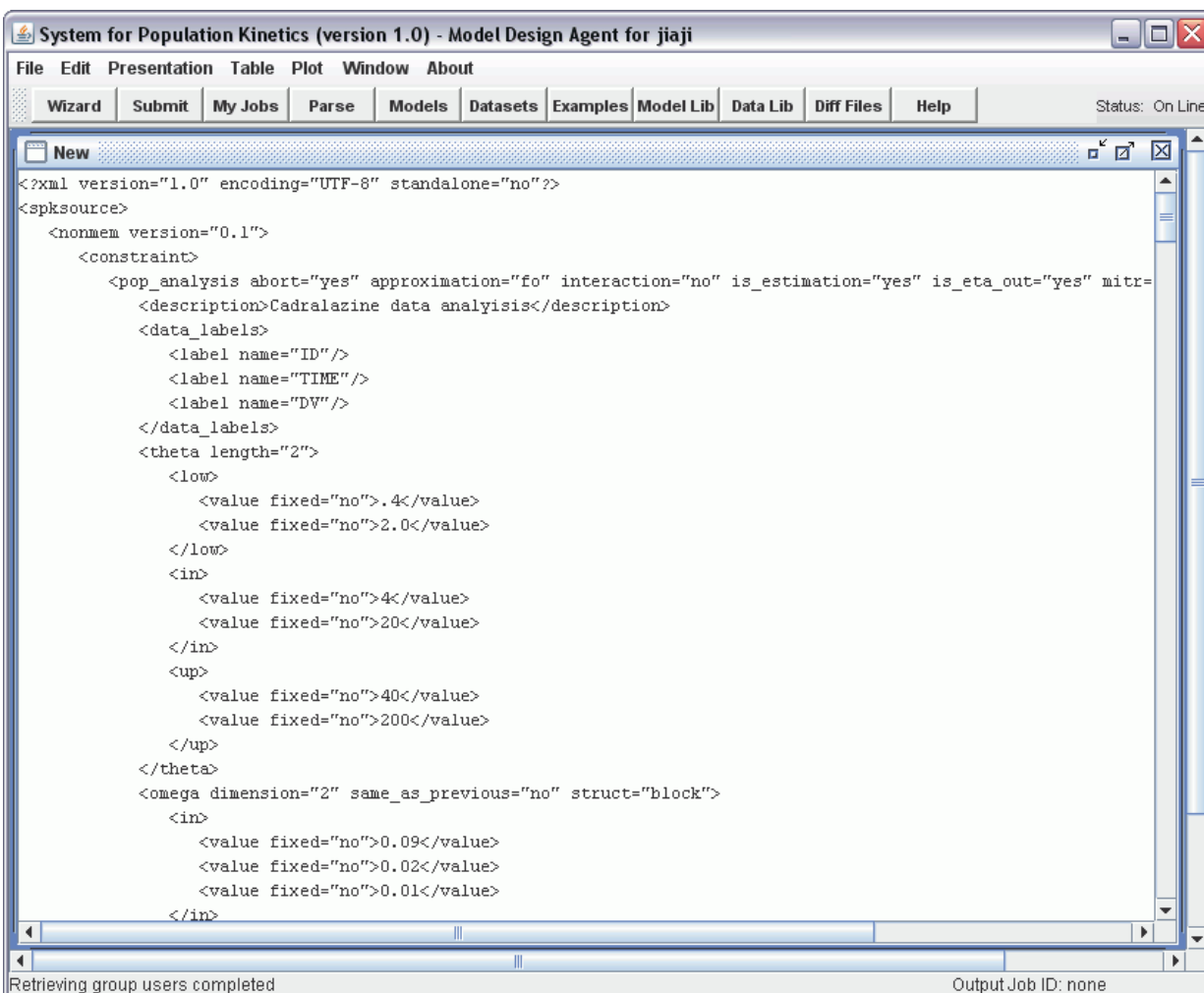


At this point, the model file is ready to be submitted to the computational library by clicking on "Submit Job" (the second button from the top left). Please note that you should now either submit the job or save it locally, or the whole process will be lost.



Submit Job

This action sends the XML model code to the computational server for execution. Submit is the second button from the left in the MDA main window.



This button, when activated, brings up a dialog box, the **Job Submission Dialog**.

In this dialog there are three tabbed panes for "Model", "Dataset" and "Job", respectively.

The "Model" and the "Dataset" panes allow the user to specify the names and descriptors of the model and the dataset used in the job.

The "Job" pane displays the analysis method for the job and allows the user to enter a short job abstract.

More specifically, you are asked whether the job you are submitting contains:

- A new model (as defined by the NONMEM(R) control file), which applies when the model you have defined is completely new and it has not been derived from a previous model (a model name must be entered if this is the case);

- A new version of an existing model, which applies when your model has been derived from a previous model by changing some options (e.g., the between-subject variability options, the initial parameter values, etc.). The most common case when this may occur is when the same dataset is analyzed with different models, to compare modeling strategies. You will be asked to select the model of which this one is a derivative version, and the version number is automatically updated by the system.
- An existing version of an existing model: this may apply, for example, when the model is exactly the same as a previous model, and the dataset being analyzed is changed.

If the job is a likelihood evaluation job, only the job pane appears (since the parent job's model and dataset are used automatically). In this case, the user must choose among the available likelihood integration methods. Each integrator provides a different approximation to the negative logarithm of the likelihood near the (approximate) optimal value provided by the estimation method.

Job Submission Dialog

Model | Dataset | Job

☒ New model (NONMEM control file)
☐ New version of an existing model
☐ Existing version of an existing model

model name (<=20 characters)
 Cadralazine SPKHelp

model description (<= 100characters)
 [Empty text box]

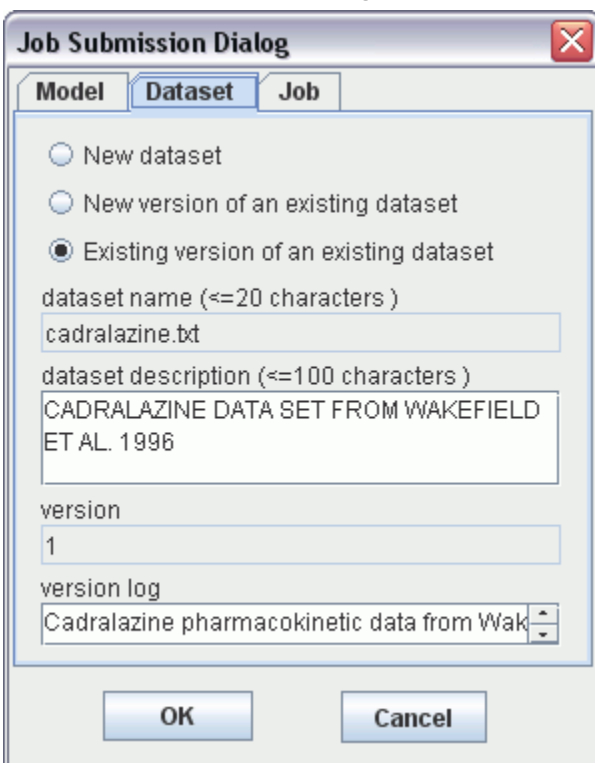
version
 1

version log
 [Empty text box with scroll arrows]

OK Cancel

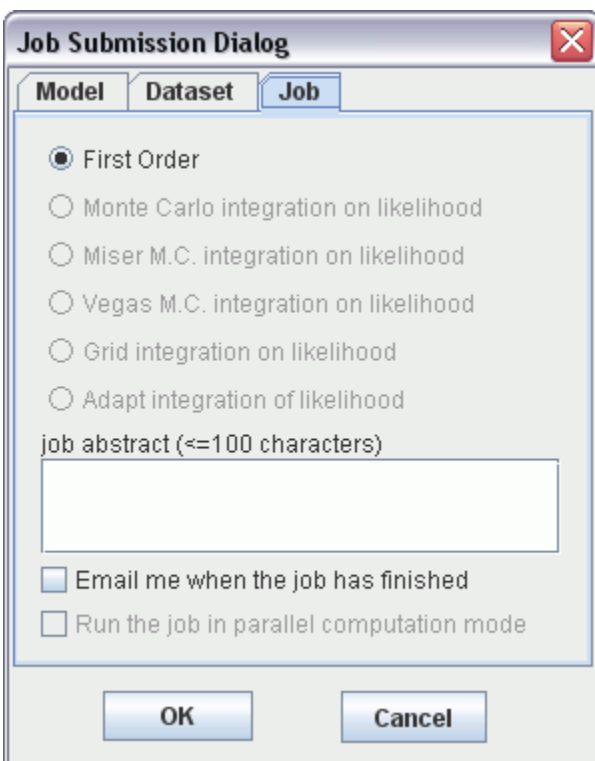
The second tab of the Job Submission Dialog regards the dataset which is associated with the job you are submitting. Again, there are three cases:

- A new dataset: this situation applies when the dataset you wish to analyze is completely new and it has not been derived from a previous dataset;
- A new version of an existing dataset, which applies when your dataset has been derived from a previous dataset by changing some data (e.g., removing a sample value, or a subject, or modifying input rates, etc.). The most common case when this may occur is when your purpose is to measure the effect of removing outlying observations. You will be asked to select the dataset of which this one is a derivative version, and the version number is automatically updated by the system.
- An existing version of an existing dataset: this applies, for example, when this dataset is exactly the same as a previous dataset, and you are analyzing it with a new model.



The image shows a 'Job Submission Dialog' window with three tabs: 'Model', 'Dataset', and 'Job'. The 'Dataset' tab is selected. It contains three radio buttons: 'New dataset', 'New version of an existing dataset', and 'Existing version of an existing dataset'. The 'Existing version of an existing dataset' option is selected. Below the radio buttons are four text input fields: 'dataset name (<=20 characters)' with the value 'cadralazine.txt', 'dataset description (<=100 characters)' with the value 'CADRALAZINE DATA SET FROM WAKEFIELD ET AL. 1996', 'version' with the value '1', and 'version log' with the value 'Cadralazine pharmacokinetic data from Wak'. At the bottom are 'OK' and 'Cancel' buttons.

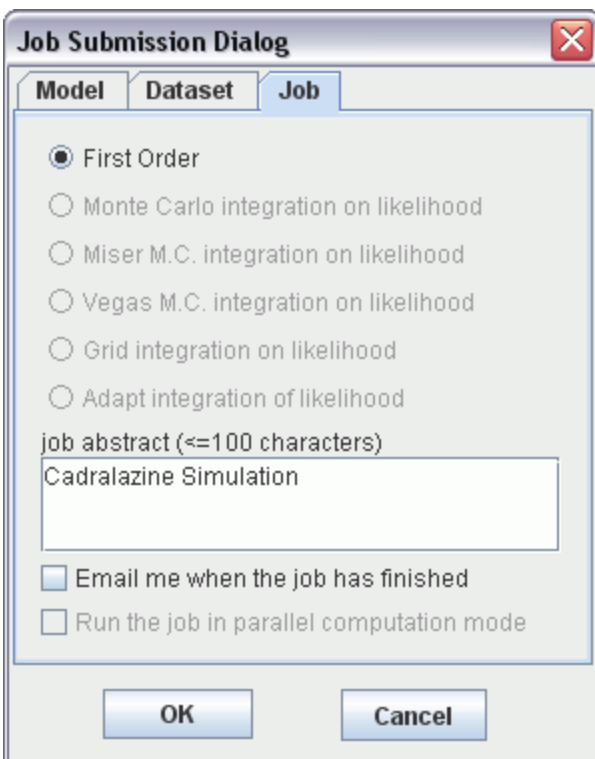
For new models and datasets, you will be asked to enter a descriptive name and a short description. It pays to be as descriptive as possible.



The Job Submission Dialog box has three tabs: Model, Dataset, and Job. The Job tab is selected. It contains a list of radio buttons for integration methods: First Order (selected), Monte Carlo integration on likelihood, Miser M.C. integration on likelihood, Vegas M.C. integration on likelihood, Grid integration on likelihood, and Adapt integration of likelihood. Below these is a text field for 'job abstract (<=100 characters)'. At the bottom are two checkboxes: 'Email me when the job has finished' and 'Run the job in parallel computation mode'. OK and Cancel buttons are at the bottom right.

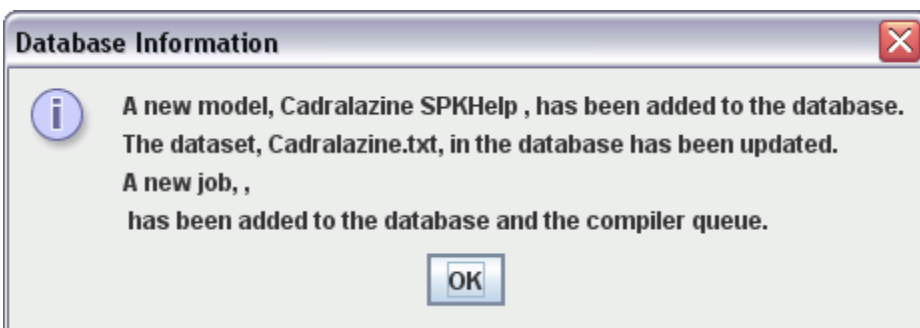
The Job Description you provide here will be visible when you access the database (see under **My Jobs**). It will be editable later from the Job information page (again, see under **My Jobs**).

If the job had been a simulation job, then the following would appear:



This is the same Job Submission Dialog box as above, but the 'job abstract (<=100 characters)' text field now contains the text 'Cadralazine Simulation'. All other elements, including the selected 'First Order' radio button and the checkboxes, remain the same.

After you click OK on the Job Submission Dialog, the job is sent to the computational kernel. Lastly, you are told that your model is queued for execution:

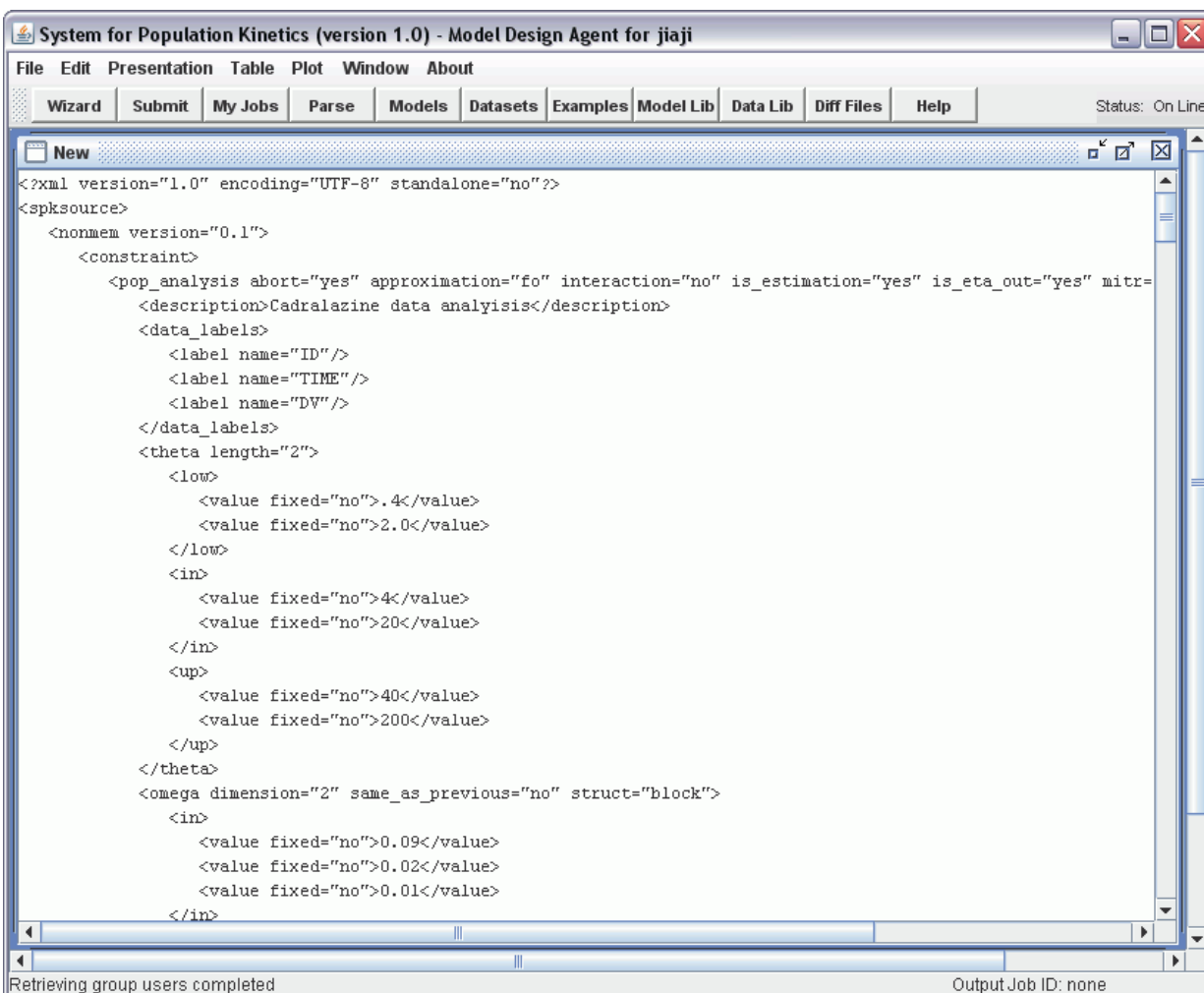


Congratulations! You have completed your SPK run submission! When you click OK, you are returned to the MDA.



My Jobs and Job Information Page

Every job sent to the SPK computational server through the MDA is logged in the user's personal database. This database can be accessed by clicking on **My Jobs**. This is the third button from the left in the MDA main window.



By clicking on **My Jobs**, the user accesses a personal database where every job is stored and assigned a Job ID, a Submission Time, a Status Code, a Model Version, a Dataset Version and a Job Abstract.

Job List - /workshop							
Job ID	Submission Time	Status Code	Model Version	Dataset Version	Job Abstract		cut
2206	Thu 2006-08-24 13:22:45...	Successful Run	OneComp ODE CL,V.4	Phenobarbital Pop.1	Phenobarbital SLO*WT on CL and V and...		<input type="checkbox"/>
2205	Thu 2006-08-24 12:46:37...	Successful Run	OneComp ODE CL,V.3	Phenobarbital Pop.1	Phenobarbital SLO*WT on CL and V mod...		<input type="checkbox"/>
2204	Thu 2006-08-24 12:29:46...	Successful Run	OneComp ODE CL,V.2	Phenobarbital Pop.1	Phenobarbital INT+SLO*WT on CL and V...		<input type="checkbox"/>
2203	Thu 2006-08-24 11:57:00...	Successful Run	OneComp ODE CL,V.1	Phenobarbital Pop.1	Phenobarbital base model run		<input type="checkbox"/>
2195	Wed 2006-08-23 18:43:01...	Successful Run	OneComp Algebr C...	Cadralazine Pop.1	MC on Expected Hessian Cadralazine data		<input type="checkbox"/>
2193	Wed 2006-08-23 18:31:17...	Successful Run	OneComp Algebr C...	Cadralazine Pop.1	MC on First Order Cadralazine data		<input type="checkbox"/>
2192	Wed 2006-08-23 18:19:29...	Successful Run	OneComp Algebr C...	Cadralazine Pop.1	Expected Hessian Analysis Cadralazin...		<input type="checkbox"/>
2191	Wed 2006-08-23 18:14:15...	Successful Run	OneComp Algebr C...	Cadralazine Pop.1	First Order Analysis Cadralazine data		<input type="checkbox"/>
2136	Tue 2006-08-22 16:54:56...	Successful Run	OneComp LinAbs K...	Theophylline Pop...	Theophylline F0 from STS Starting Va...		<input type="checkbox"/>
2131	Tue 2006-08-22 14:34:50...	Successful Run	OneComp LinAbs K...	Theophylline Pop.1	Theophylline F0 from STS analysis - ...		<input type="checkbox"/>
2121	Tue 2006-08-22 12:45:06...	Successful Run	OneComp LinAbs K...	Theophylline Pop...	Theophylline ITS analysis - subsampled		<input type="checkbox"/>
2120	Tue 2006-08-22 12:43:52...	Successful Run	OneComp LinAbs K...	Theophylline Pop...	Theophylline STS analysis - subsampled		<input type="checkbox"/>

Search Jobs

Group member

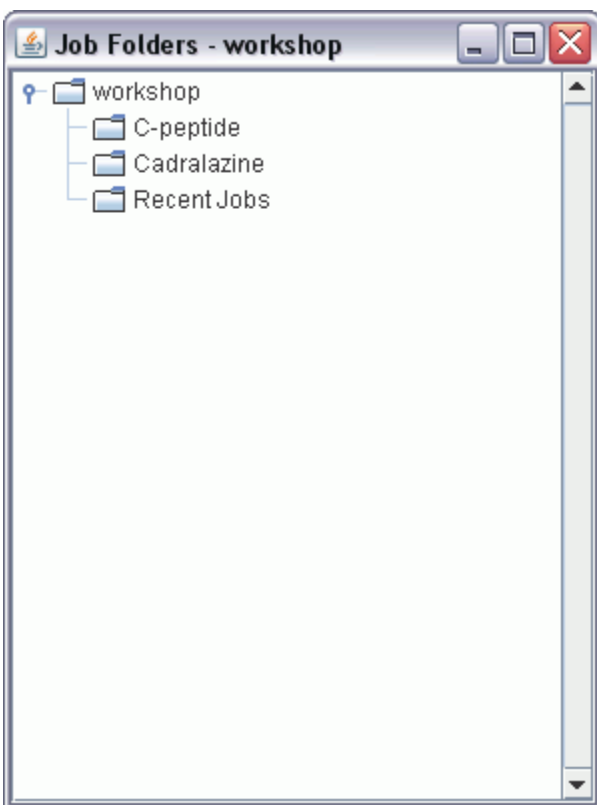
workshop

Total found

38

Previous Page

Next Page



The **Search Jobs** button allows the user to refine the job list by specifying search terms or job numbers. The **Group member** drop-down menu allows one user to see jobs that belong to other members of the Group. Users can establish groups by contacting the SPK administrator. Users can select jobs on the list by clicking on the corresponding line. Selecting, for example, Job ID 310, a Job Information window is accessed:

The screenshot shows a window titled "Job Information - vicini". It contains the following fields and buttons:

- Owner:** vicini **Job ID:** 310
- Folder:** /
- Share With username:** [text box] **Share Job** button
- Method:** First Order **Single** **Abort Job** button
- Model:** SINGLE EXPONENTIAL **Version:** 3
- Dataset:** cadralazine.txt **1**
- Abstract:** CADRALAZINE **Update** button

View Current Job:

- Model** **Dataset** **XML In** **XML Out**
- History** **Parent** **Trace** **Results**

Create New Job:

- ☒ Set the current job as the parent job of the new job.
- Initialize parameters from current job input. **From Input** button
- Initialize parameters from current job output. **From Output** button
- Continue current job's parameter estimation. **Warm Start** button
- Evaluate likelihood of current job estimation. **Likelihood** button
- Create a parametric job from two-stage job. **Create Job** button

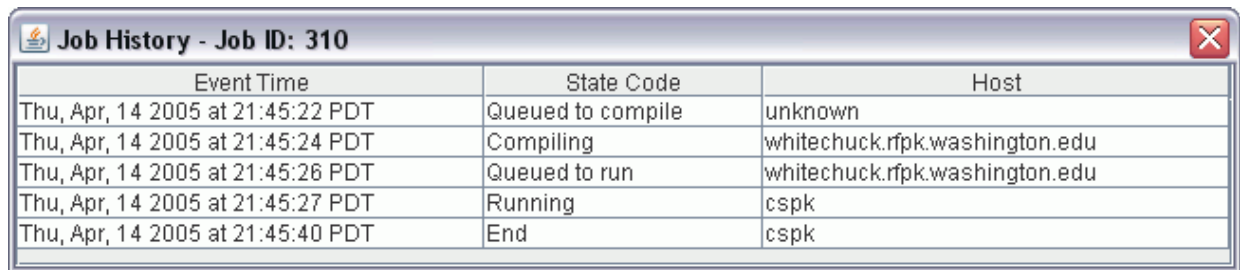
Various information regarding the job is displayed in this window. In addition, the job can be shared with another user (a blue-tinted job number will appear in that user's job list). The Model and Dataset used in the job appear (with a version number) and the job abstract is also listed (this can be edited).

There are eight options for viewing information related to the current job and up to five options for creating a new job from the current job:

Information retrieval options are:

- **Model:** clicking on this button brings up the NONMEM(R) control file for this job in the MDA editor window.
- **Dataset:** selecting this option visualizes the data file in the MDA editor window.

- **XML In:** selecting this option visualizes the input XML file in the MDA editor window.
- **XML Out:** selecting this option visualizes the output XML file in the MDA editor window.
- **History:** selecting this option visualizes the time history of the job from submission to completion, and allows to determine how much time was spent in the compilation and execution of the job.



Event Time	State Code	Host
Thu, Apr, 14 2005 at 21:45:22 PDT	Queued to compile	unknown
Thu, Apr, 14 2005 at 21:45:24 PDT	Compiling	whitechuck.rfpk.washington.edu
Thu, Apr, 14 2005 at 21:45:26 PDT	Queued to run	whitechuck.rfpk.washington.edu
Thu, Apr, 14 2005 at 21:45:27 PDT	Running	cspk
Thu, Apr, 14 2005 at 21:45:40 PDT	End	cspk

- **Parent:** this option opens the Job Information Window of the corresponding parent job, if one exists.
- **Trace/Status:** trace allows user to watch real-time optimizer trace for parameter estimation jobs, or status allows user to watch job completion progress for likelihood profiling jobs.
- **Results:** this option requests the MDA to load the output values (parameter estimates, model predictions) from the current job. After parsing the job output XML, the Summary Report is displayed first. The Summary Report for the file we have defined is below:

System for Population Kinetics (version 1.0) - Model Design Agent for vicini

File Edit View Presentation Table Plot Window About

Wizard Submit My Jobs Parse Models Datasets Examples Model Lib Data Lib Diff Files Help Status: On Line

310 Summary Report

Summary Report

Job Identification number: 310
Job Description: CADRALAZINE

Time of Job Submission: Thu, Apr, 14 2005 at 21:45:22 PDT
Time of Job Completion: Thu, Apr, 14 2005 at 21:45:40 PDT
SPK Computing Time: 10.0 s
Computation Mode: single

Analysis Type: population
Analysis Method: First Order

Model Name: SINGLE EXPONENTIAL Model Version: 3
Model Description: ONE COMPARTMENT MODEL WITH CLEARANCE PARAMETRIZATION
Model Version Log: CADRALAZINE MODEL FOR HELP FILE

Dataset Name: cadralazine.txt Dataset Version: 1
Dataset Description: CADRALAZINE DATA SET FROM WAKEFIELD ET AL. 1996
Dataset Version Log: Cadralazine pharmacokinetic data from Wakefield et al. 1996

Error Messages:
None

Warning Messages:
None

Minimum Value of Objective Function: -43.9216

Parameter Estimation Result:

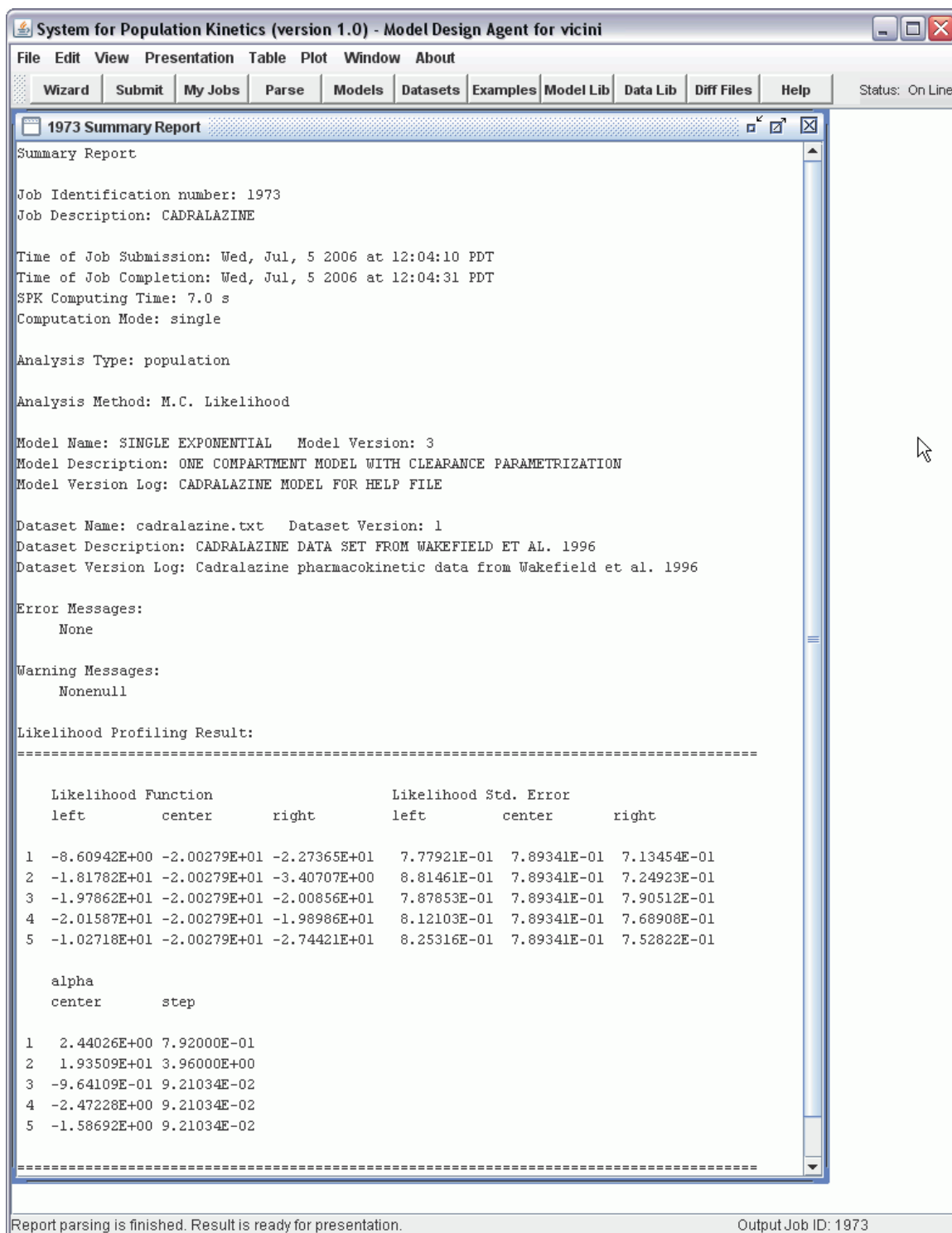
Parameter	Estimate	Std. Error	Coef. of Var.	95% Confidence Interval		Variability*
				L-bound	U-bound	
THETA						
1	2.44E+00	2.20E-01	9.01E+00	2.00E+00	2.88E+00	
2	1.94E+01	8.39E-01	4.34E+00	1.77E+01	2.10E+01	
OMEGA						
1,1	1.45E-01	6.72E-02	4.62E+01	1.09E-02	2.80E-01	3.81E-01
2,2	7.12E-03	1.53E-02	2.15E+02	-2.36E-02	3.78E-02	8.44E-02
SIGMA						
1,1	4.18E-02	1.36E-02	3.24E+01	1.47E-02	6.90E-02	2.04E-01

*For OMEGA, this column indicates BSV in standard deviation units.
For SIGMA, this column indicates RUV in standard deviation units.

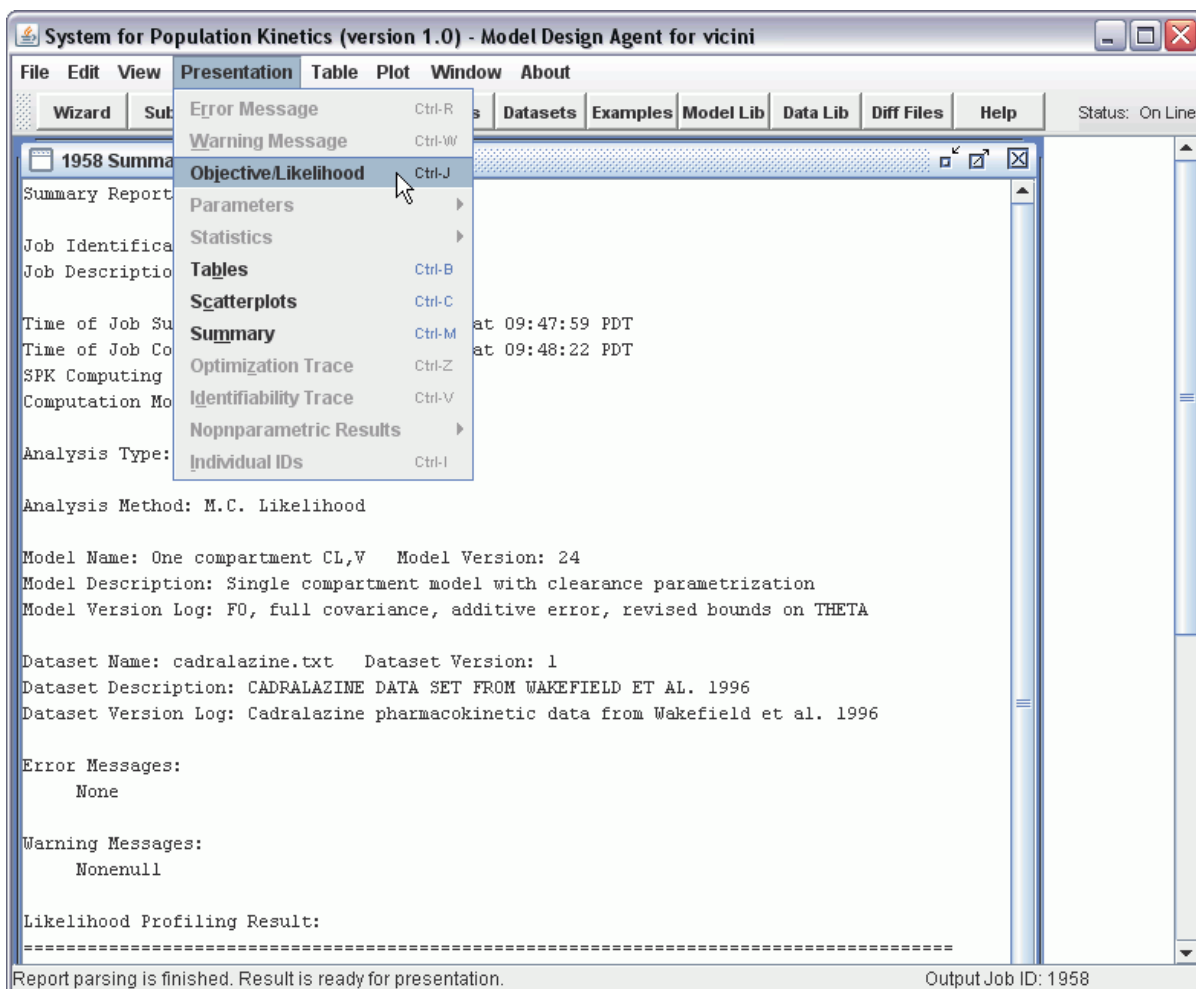
Report parsing is finished. Result is ready for presentation. Output Job ID: 310

The Summary Report displays important information about the job, such as optimal parameter estimates, their coefficients of variation, lower and upper bound of the 95% confidence interval, and so on. If the job was a likelihood evaluation job, then the report only shows the

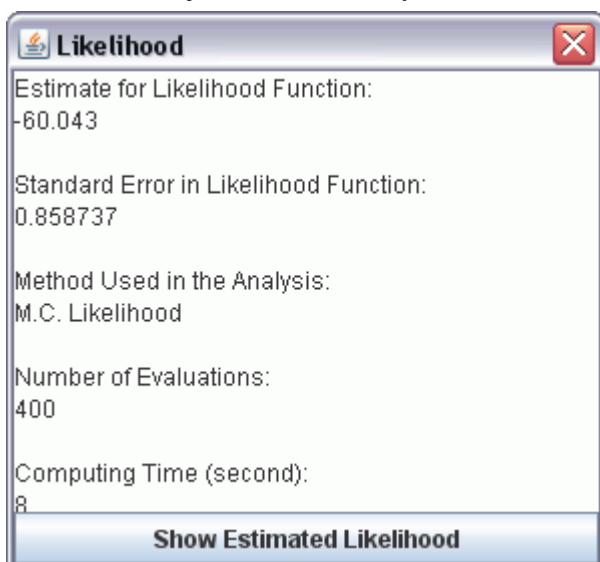
value of the integrated likelihood and its standard error from the Monte Carlo analysis, as shown below.



Graphical output from a Monte Carlo run can be accessed by going to the "Presentation" menu and selecting "Objective/Likelihood":



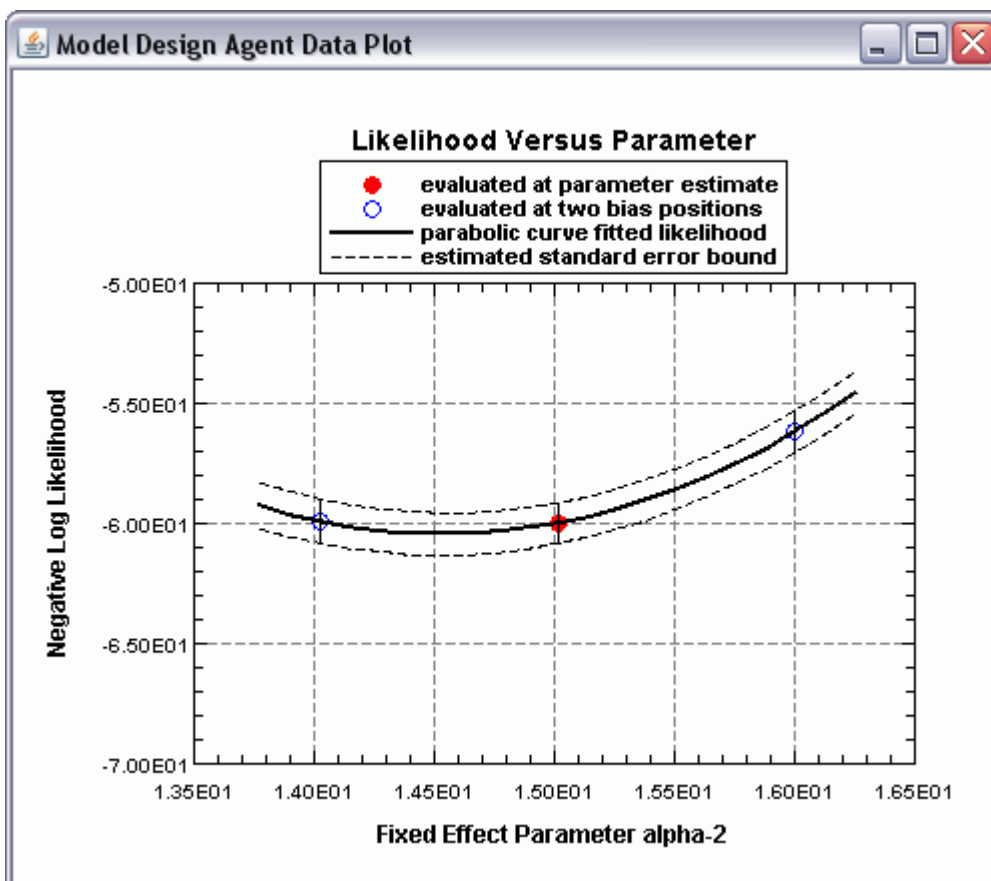
This opens a window that summarizes the results of the likelihood evaluation job, an example of which is shown below.



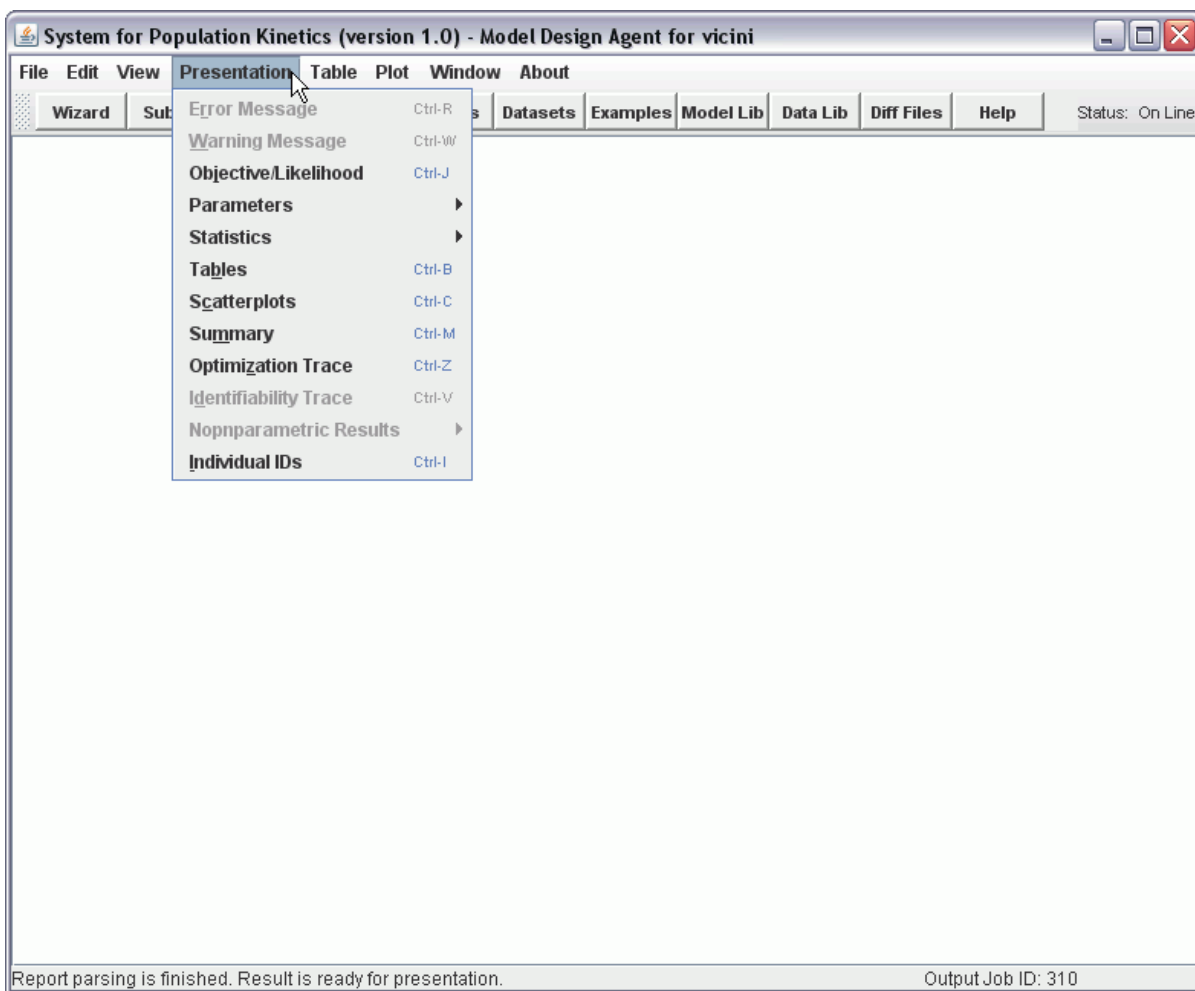
Clicking on "Show Estimated Likelihood" provides access to a series of plots that profile the Monte Carlo likelihood against each one of the fixed effects:



The user can select one or more of these plots. An example of profiling is shown below.



Other elements of the computational output can be accessed using the Presentation menu from the MDA:



The MDA allows to create new jobs from the Job Information page, which is shown below.

Job Information - vicini

Owner: vicini Job ID: 310

Folder: /

Share With username: **Share Job**

Method: First Order Single **Abort Job**

Name: SINGLE EXPONENTIAL Version: 3

Model: SINGLE EXPONENTIAL

Dataset: cadralazine.txt 1

Abstract: CADRALAZINE **Update**

View Current Job:

Model **Dataset** **XML In** **XML Out**

History **Parent** **Trace** **Results**

Create New Job:

☒ Set the current job as the parent job of the new job.

Initialize parameters from current job input. **From Input**

Initialize parameters from current job output. **From Output**

Continue current job's parameter estimation. **Warm Start**

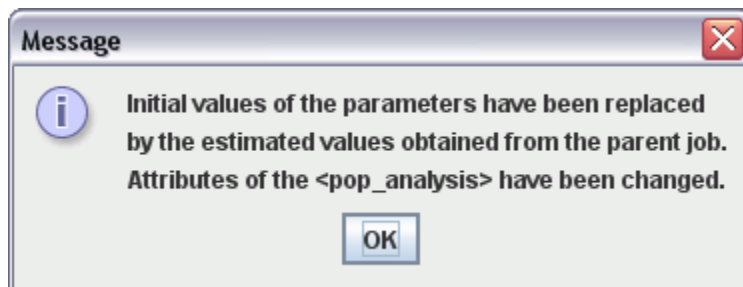
Evaluate likelihood of current job estimation. **Likelihood**

Create a parametric job from two-stage job. **Create Job**

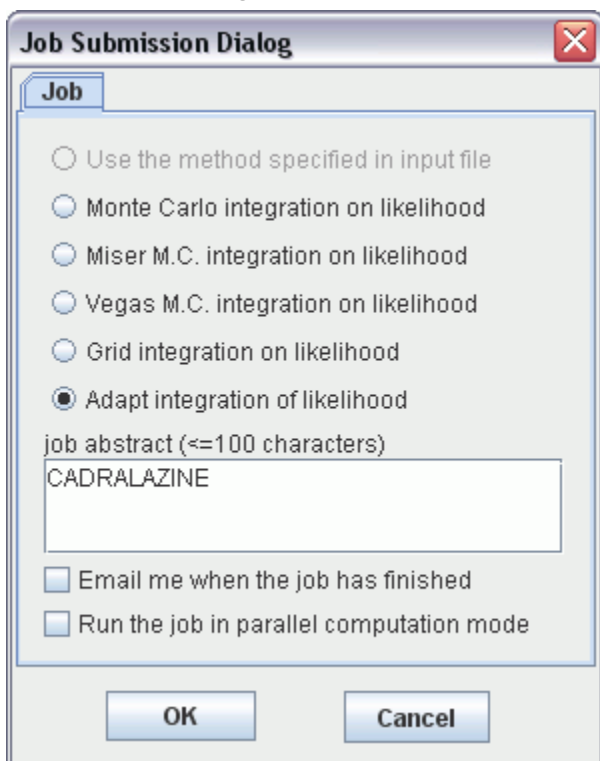
Under **Create New Job** there are a series of possibilities for the user to create a new job using elements of an existing job. Checking next to "Set the current job as the parent job of the new job" keeps track of which job was used to generate (is the parent) of the new job.

- **From Input:** this option allows you to generate a new job using the existing job as a template. When selecting this option, the Input File Generation Tool opens up, and all fields are pre-filled with the corresponding elements from the current job:

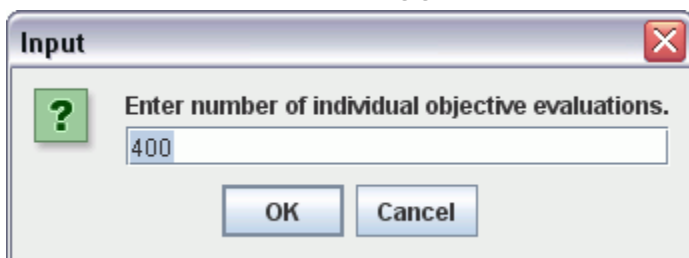
- **From Output:** same as "From Input", except that this option allows you to generate a new job using the results of the existing job as a template. When selecting this option, the Input File Generation tool opens again, but the fields are pre-filled with the output of the preceding job.
- **Warm Start:** this option restarts a job that has been aborted or has used its maximum number of function evaluations. Values relating to the current state of the optimization are periodically saved and used to restart the job if this option is used.
- **Likelihood:** this option allows for Monte Carlo integration of the likelihood following a successful job run. After selecting this option, the user will see this window:



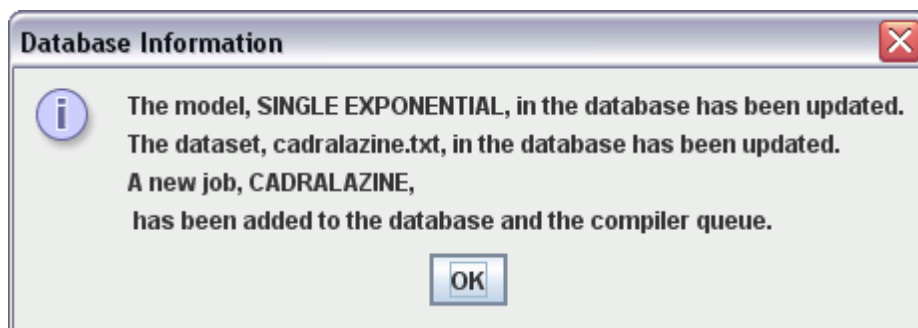
The purpose of this window is to alert the user to the fact that the output of the job is going to be used to initialize a likelihood integration routine that will provide the profile of the likelihood function at the optimal parameter estimates for the job. This triggers a job submission, where the user is asked to select between various likelihood integration options:



The ADAPT integrator is usually selected as the default, since it is presumed to be faster and more reliable. By clicking OK, the user starts the submission process. The accuracy of the integration depends on the number of functions evaluations used in the calculations. The user can set this number in this window, which is pre-filled with values suggested from the size of the random effects:



The job can then be submitted just like any other job:



- **Create Job:** this option allows to seed a parametric population analysis from two-stage results. In other words, it initializes a population run by using output from a two-stage method parameter estimation. This is only available if the current job used a two-stage method.



Parse Report

The MDA user has the option to view the output as an XML job file or to parse the output and view a summary report. Parsing the report also allows access to plotting and tabling functionality.

Every job is associated with an XML file that contains all information about that job. While the structure of these XML files is somewhat fluid, they are built and updated with compatibility in mind, so ideally the MDA should be able to process both old and new XML files.

XML is a text-based format, so it can be exchanged using email and/or FTP (please note that some email clients format this file, so email may not always work reliably (compressing the file before email may work best)).

Clicking the **Parse** button is a way to process and display the output or the input associated with a particular XML job file. Parse is the fourth button from the left in the MDA main window. When the user has selected My Jobs and the database list appears:

Printed Documentation

The image shows two windows from a software application. The top window, titled 'Job List - /workshop', displays a table of job execution details. The bottom window, titled 'Job Folders - workshop', shows a hierarchical tree view of the file system.

Job List - /workshop

Job ID	Submission Time	Status Code	Model Version	Dataset Version	Job Abstract	cut
2206	Thu 2006-08-24 13:22:45...	Successful Run	OneComp ODE CL,V.4	Phenobarbital Pop.1	Phenobarbital SLO*WT on CL and V and...	<input type="checkbox"/>
2205	Thu 2006-08-24 12:46:37...	Successful Run	OneComp ODE CL,V.3	Phenobarbital Pop.1	Phenobarbital SLO*WT on CL and V mod...	<input type="checkbox"/>
2204	Thu 2006-08-24 12:29:46...	Successful Run	OneComp ODE CL,V.2	Phenobarbital Pop.1	Phenobarbital INT+SLO*WT on CL and V...	<input type="checkbox"/>
2203	Thu 2006-08-24 11:57:00...	Successful Run	OneComp ODE CL,V.1	Phenobarbital Pop.1	Phenobarbital base model run	<input type="checkbox"/>
2195	Wed 2006-08-23 18:43:01...	Successful Run	OneComp Algebr C...	Cadralazine Pop.1	MC on Expected Hessian Cadralazine data	<input type="checkbox"/>
2193	Wed 2006-08-23 18:31:17...	Successful Run	OneComp Algebr C...	Cadralazine Pop.1	MC on First Order Cadralazine data	<input type="checkbox"/>
2192	Wed 2006-08-23 18:19:29...	Successful Run	OneComp Algebr C...	Cadralazine Pop.1	Expected Hessian Analysis Cadralazin...	<input type="checkbox"/>
2191	Wed 2006-08-23 18:14:15...	Successful Run	OneComp Algebr C...	Cadralazine Pop.1	First Order Analysis Cadralazine data	<input type="checkbox"/>
2136	Tue 2006-08-22 16:54:56...	Successful Run	OneComp LinAbs K...	Theophylline Pop...	Theophylline F0 from STS Starting Va...	<input type="checkbox"/>
2131	Tue 2006-08-22 14:34:50...	Successful Run	OneComp LinAbs K...	Theophylline Pop.1	Theophylline F0 from STS analysis - ...	<input type="checkbox"/>
2121	Tue 2006-08-22 12:45:06...	Successful Run	OneComp LinAbs K...	Theophylline Pop...	Theophylline ITS analysis - subsampled	<input type="checkbox"/>
2120	Tue 2006-08-22 12:43:52...	Successful Run	OneComp LinAbs K...	Theophylline Pop...	Theophylline STS analysis - subsampled	<input type="checkbox"/>

Search Jobs Group member: **workshop** Total found: **38** Previous Page Next Page

Job Folders - workshop

- workshop
 - C-peptide
 - Cadralazine
 - Recent Jobs

the user can select one job from the list. The following window (or a similar one) will appear:

Job Information - vicini

Owner: vicini Job ID: 313

Folder: /

Share With username: **Share Job**

Method: Simulation Only Single **Abort Job**

Model: SINGLE EXPONENTIAL Version: 6

Dataset: cadralazine.txt Version: 1

Abstract: CADRALAZINE Simulation **Update**

View Current Job:

Model **Dataset** **XML In** **XML Out**

History **Parent** **Trace** **Results**

Create New Job:

☒ Set the current job as the parent job of the new job.

Initialize parameters from current job input. **From Input**

Initialize parameters from current job output. **From Output**

Continue current job's parameter estimation. **Warm Start**

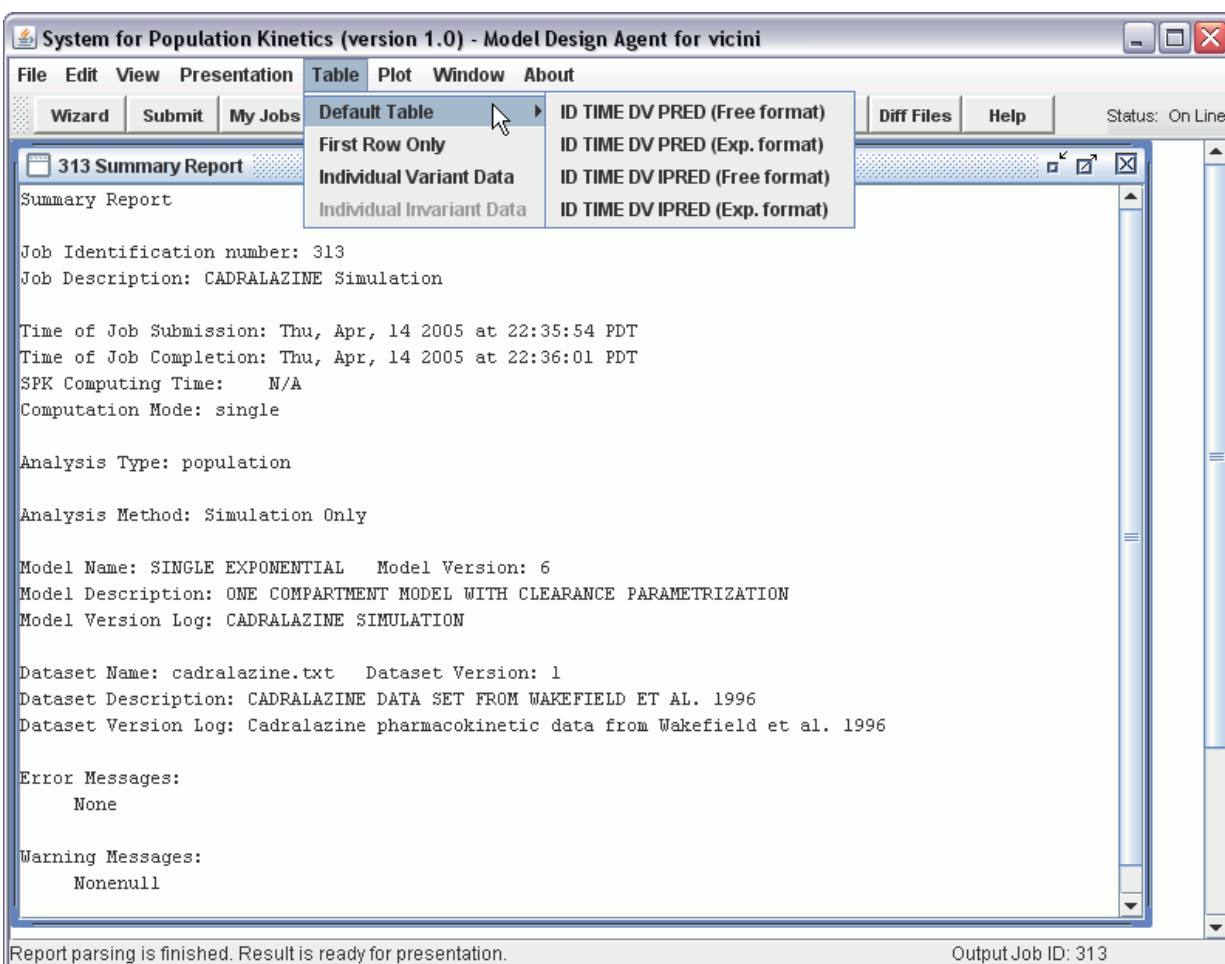
Evaluate likelihood of current job estimation. **Likelihood**

Create a parametric job from two-stage job. **Create Job**

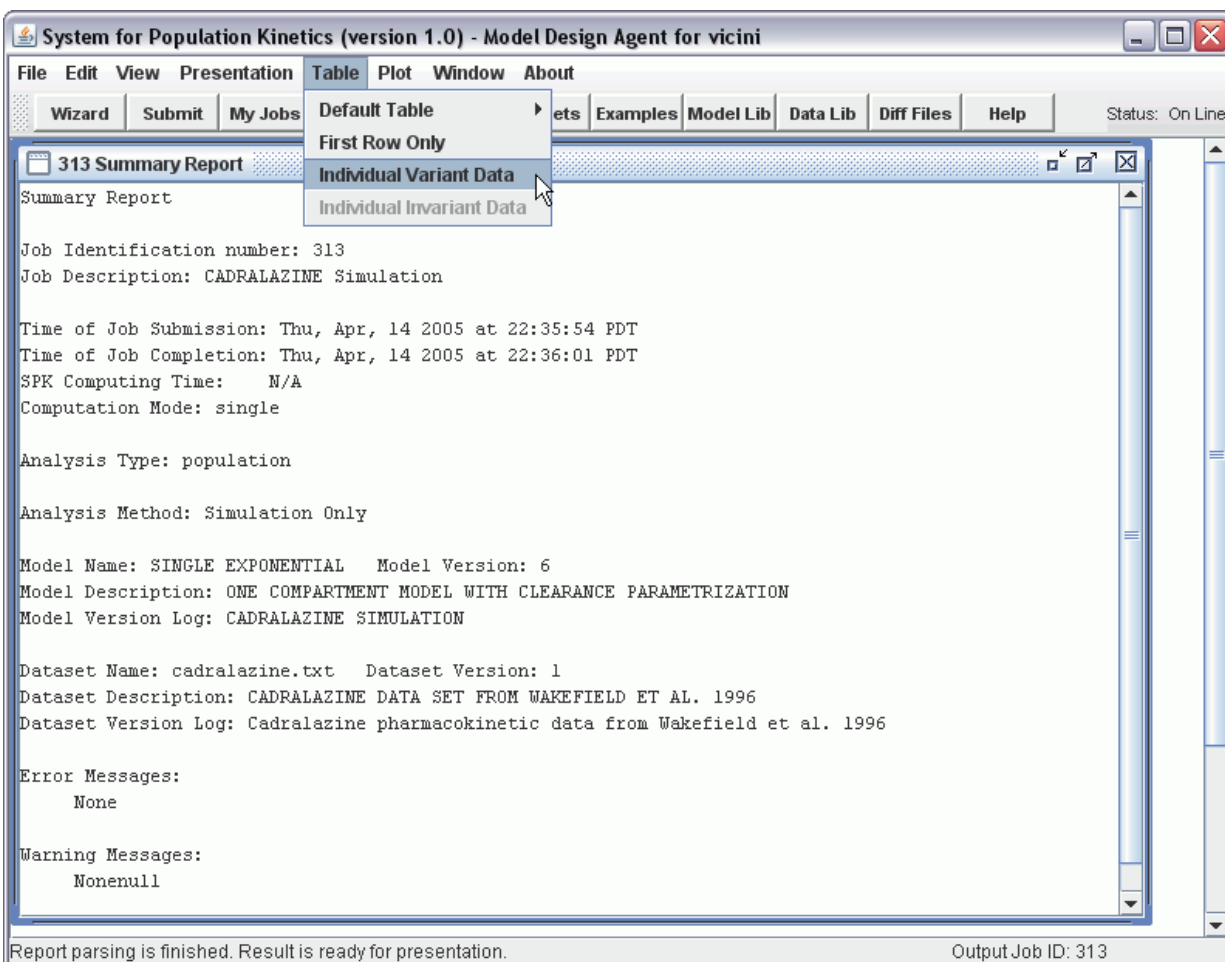
If one clicks on the "Output" button, the XML file describing this model's output will appear in the MDA's editor window, instead of being processed automatically. The user can then check the report for accuracy and inconsistencies that may be causing a problem with the MDA processing the output. Clicking on "Parse Report" will then load the results in memory for processing. This is also a possible way through which users can share models between themselves (they only need to email each other the XML file).

Tabular and plotting output are possible.

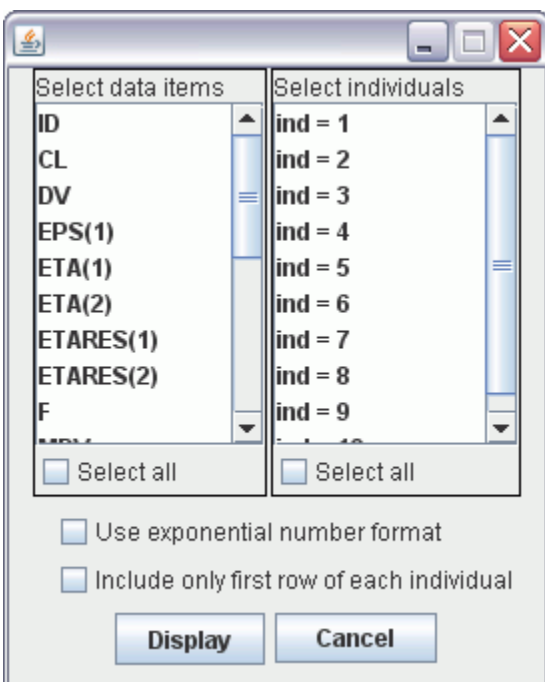
Tabular output: There are default tabular outputs or a custom table can be built using the entire report.



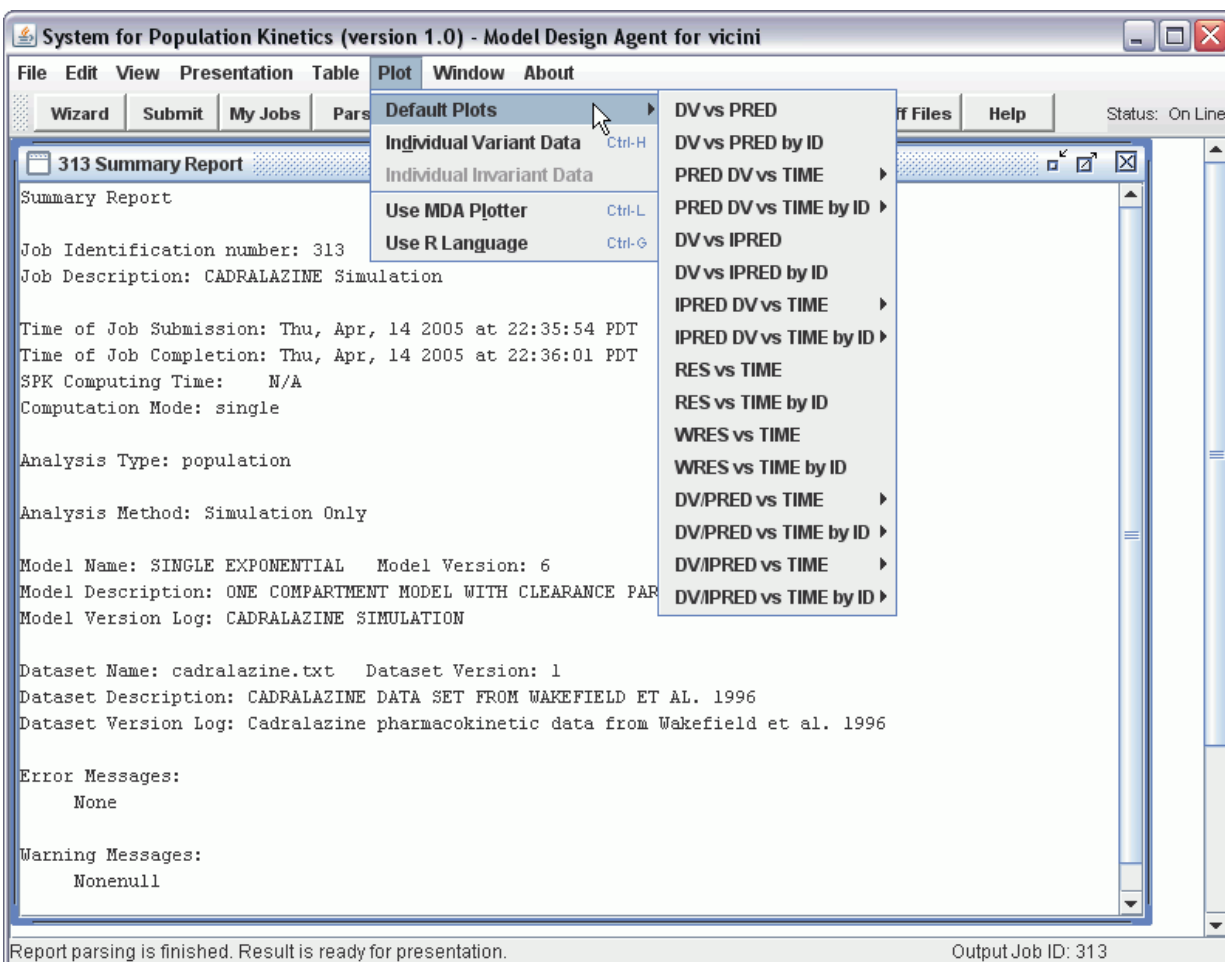
The "First Row Only" option is useful to display ID-specific information without repetition (if the variable of interest does not change between IDs).



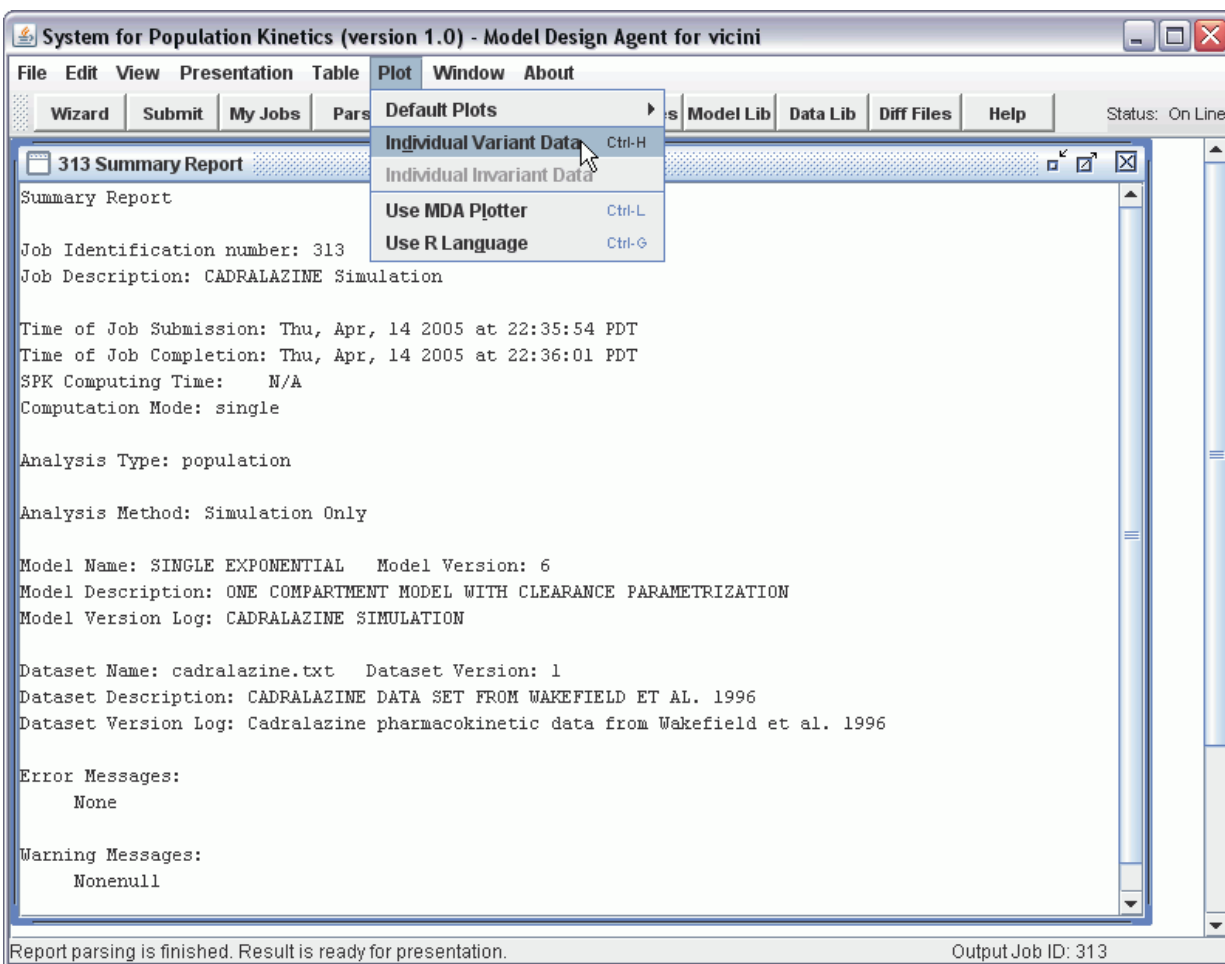
The "Individual Variant Data" option and the "Individual Invariant Data" option allow to build custom tables that may be specific to a certain ID or to a certain group of subjects or variables of interest.



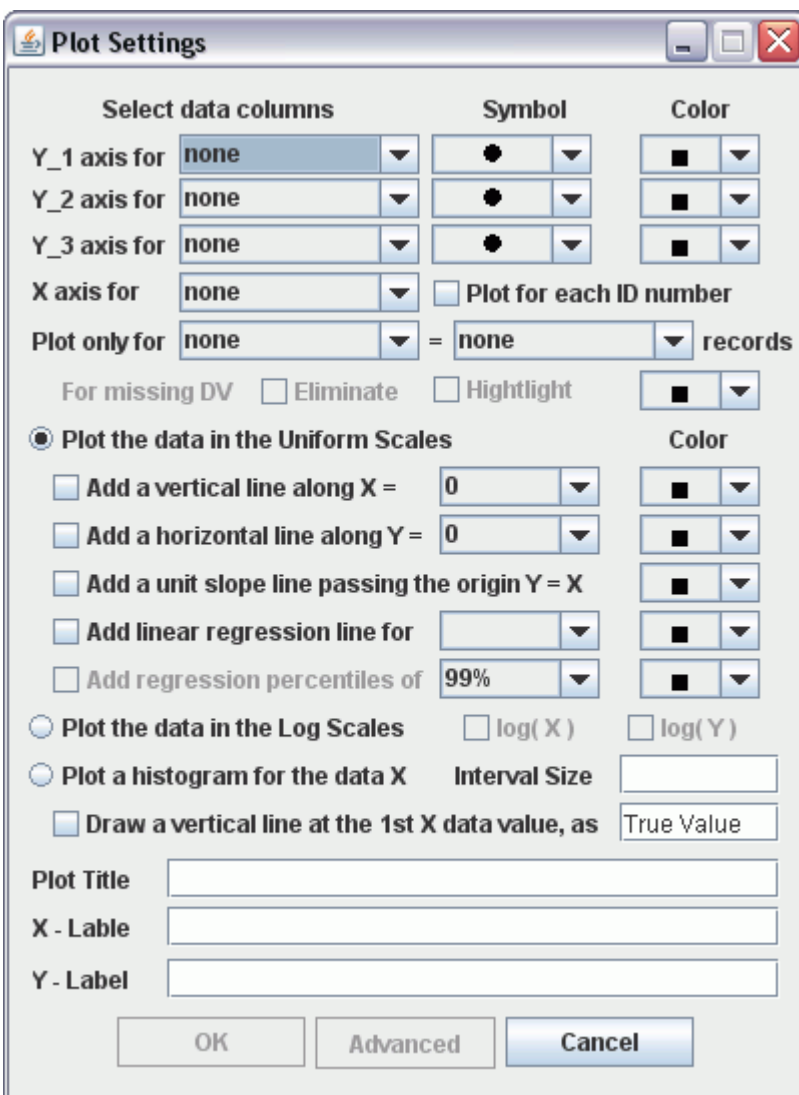
Plotting output: Default plots are available or a custom plot can be built using the entire report.



The "Individual Variant Data" option and the "Individual Invariant Data" option display the values for all the variables defined in the entire job. If a default variable has not been modified, its value is not displayed.



The "Use MDA Plotter" option allows the user to build custom plots that may be specific to a certain ID or to a certain group of subjects or variables of interest.



Plot Settings

Select data columns	Symbol	Color
Y_1 axis for: none	•	■
Y_2 axis for: none	•	■
Y_3 axis for: none	•	■
X axis for: none	<input type="checkbox"/> Plot for each ID number	
Plot only for: none	= none	records

For missing DV ☐ Eliminate ☐ Highlight ■

☒ **Plot the data in the Uniform Scales**

	Color
<input type="checkbox"/> Add a vertical line along X = 0	■
<input type="checkbox"/> Add a horizontal line along Y = 0	■
<input type="checkbox"/> Add a unit slope line passing the origin Y = X	■
<input type="checkbox"/> Add linear regression line for	■
<input type="checkbox"/> Add regression percentiles of 99%	■

☐ **Plot the data in the Log Scales** ☐ log(X) ☐ log(Y)

☐ **Plot a histogram for the data X** Interval Size

☐ Draw a vertical line at the 1st X data value, as True Value

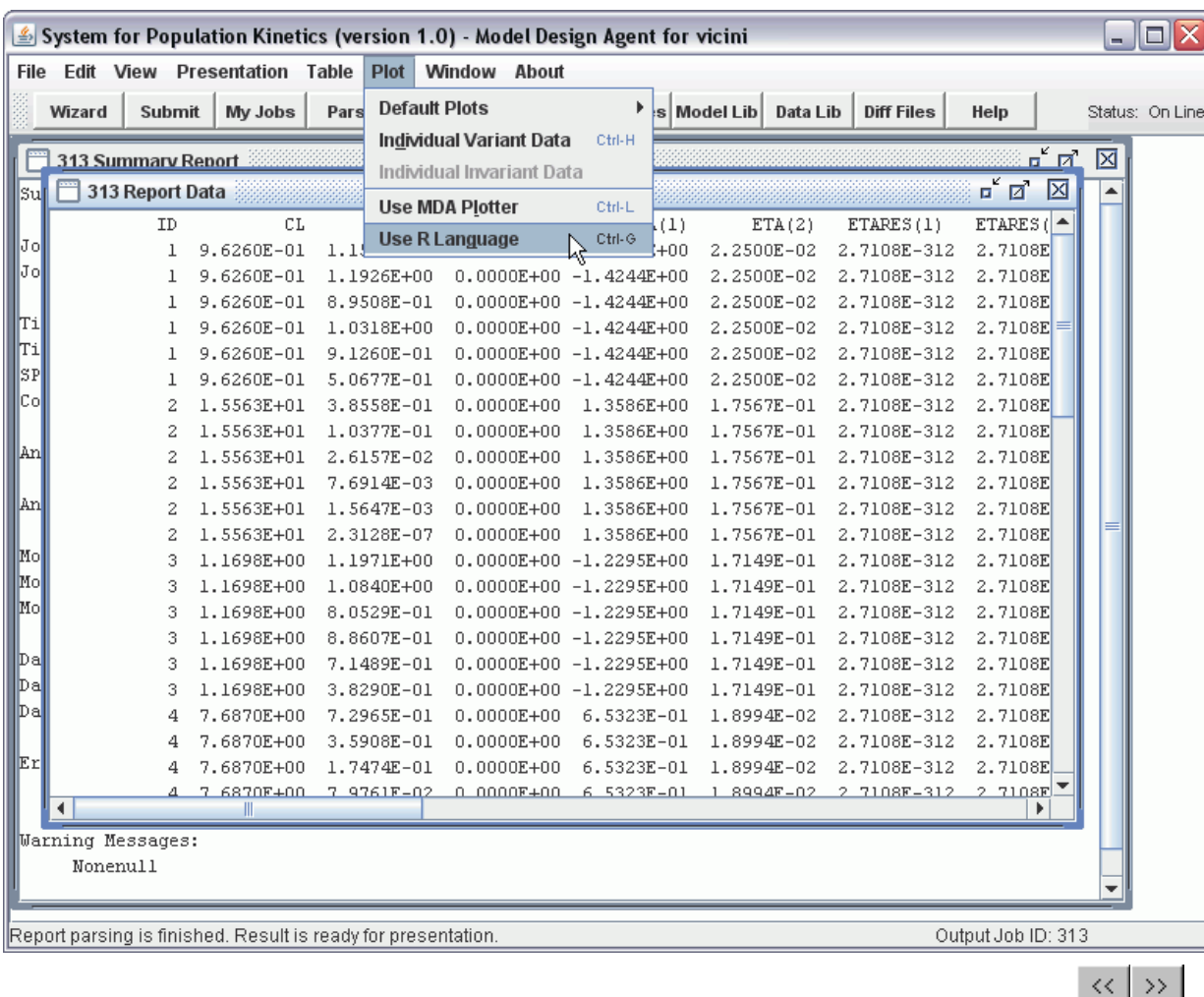
Plot Title

X - Lable

Y - Label

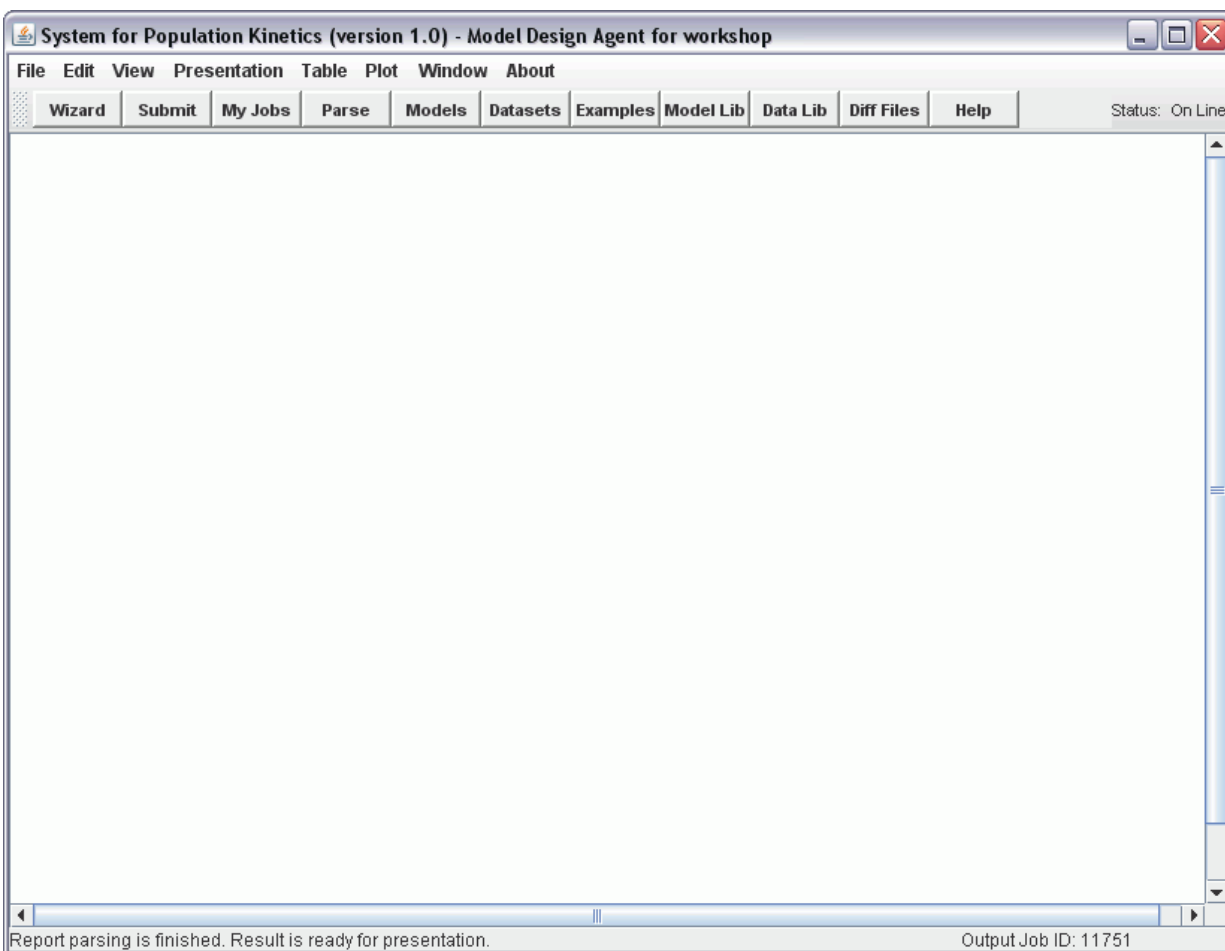
OK Advanced Cancel

The "Use R Language" option provides an escape to the R programming environment. The login page at MySPK has instructions for installing R.



My Models

Normally, the user will want to access full jobs from the database via the **My Jobs** button. There are some instances when the user would like to inspect models or datasets separately. Clicking on the **Models** option (the fifth button from the left in the MDA main window) allows the MDA user to select models from the database.



When selecting My Models, a list of all models generated by a user appears:

Model ID	Model Name	No. of Versions	Last Revised Time	Description
2489	C-peptide model with	1	PST 2007.09.25.06.10.39	2-compartment C-peptide model
517	OneComp ODE CL,V	4	PST 2006.08.24.13.22.45	ODE single compartment model for phenobarbital data
516	OneComp Algebr CL,V	2	PST 2006.08.23.18.19.29	Algebraic single exponential model for cadralazine...
515	Two Compartment CL,V	1	PST 2006.08.23.16.06.21	Two compartment model with clearances and volume
511	OneComp LinAbs K,V	8	PST 2006.08.22.16.54.56	One compartment with linear absorption K, KA
509	Two Compartment K,V	7	PST 2006.08.23.15.57.03	Two compartment model with rate constants and volume
506	One Exponential K, V	10	PST 2006.08.18.11.01.54	Single Exponential model for cadralazine data

List ☒ Versions ☐ Jobs Group member: workshop Total found: 7 Previous Page Next Page

Every version of each model is stored separately in the database. Details referring to each model can be displayed in two ways. When the **Jobs** bullet is chosen and a model is selected, all jobs that have used that model are displayed in the Job List window. When the **Versions** bullet is chosen and a model is selected, all versions of that model are displayed. For example, this model has five versions:

Version List - Model ID: 511			
Revision	Author	Revised Time	Log Message
1	Paolo_Vic...	PST 2006.08.21.13.13.14	Model for Workshop Module 04
2	Paolo_Vic...	PST 2006.08.21.14.36.48	New set of starting values
3	Paolo_Vic...	PST 2006.08.22.12.39.16	OneComp LinAbs K,V for STS
4	Paolo_Vic...	PST 2006.08.22.12.40.09	OneComp LinAbs K,V for ITS
5	Paolo_Vic...	PST 2006.08.22.12.43.52	OneComp LinAbs K,V for STS Reduced Sampling
6	Paolo_Vic...	PST 2006.08.22.12.45.06	OneComp LinAbs K,V for ITS RSS
7	Paolo_Vic...	PST 2006.08.22.14.34.50	FO estimation from STS results
8	Paolo_Vic...	PST 2006.08.22.16.54.56	FO estimates from subsampled data set

Every version is described by a log and has a revision time stamp associated with it. When a particular model is selected from the list, that model opens in the MDA editor window:

```

$PROBLEM Theophylline Two Stage
$DATA TheophyllineReducedB.txt
$INPUT ID AMT TIME DV WT
$SUBROUTINES ADVAN6 TOL=5
$MODEL NCOMPARTMENTS=2
COMP=(DEPOT INITIALOFF DEFDOSE)
COMP=(CENTRAL DEFOBSERVATION NOOFF)
$PK
K = (THETA(1)+ETA(1))
KA = (THETA(2)+ETA(2))
V = (THETA(3)+ETA(3))
S2 =V
$THETA
(.008,0.080898,0.8)
(.09,2.81573,9.)
(.03,0.480753,3.)
$OMEGA BLOCK(3) 0.000328609 0.0109367 6.21474 0.000202169 -0.0373281 0.00492866
$DES
DADT(1)=-KA*A(1)
DADT(2)=KA*A(1)-K*A(2)
$ERROR
Y=F+EPS(1)
$SIGMA DIAGONAL(1) 0.381914
$ESTIMATION METHOD=0 POSTHOC SIGDIGITS=3 MAXEVALS=450 PRINT=5
$COVARIANCE

```

Retrieving archive text completed Output Job ID: 11751

This model can be processed by clicking on **Prepare Input**:

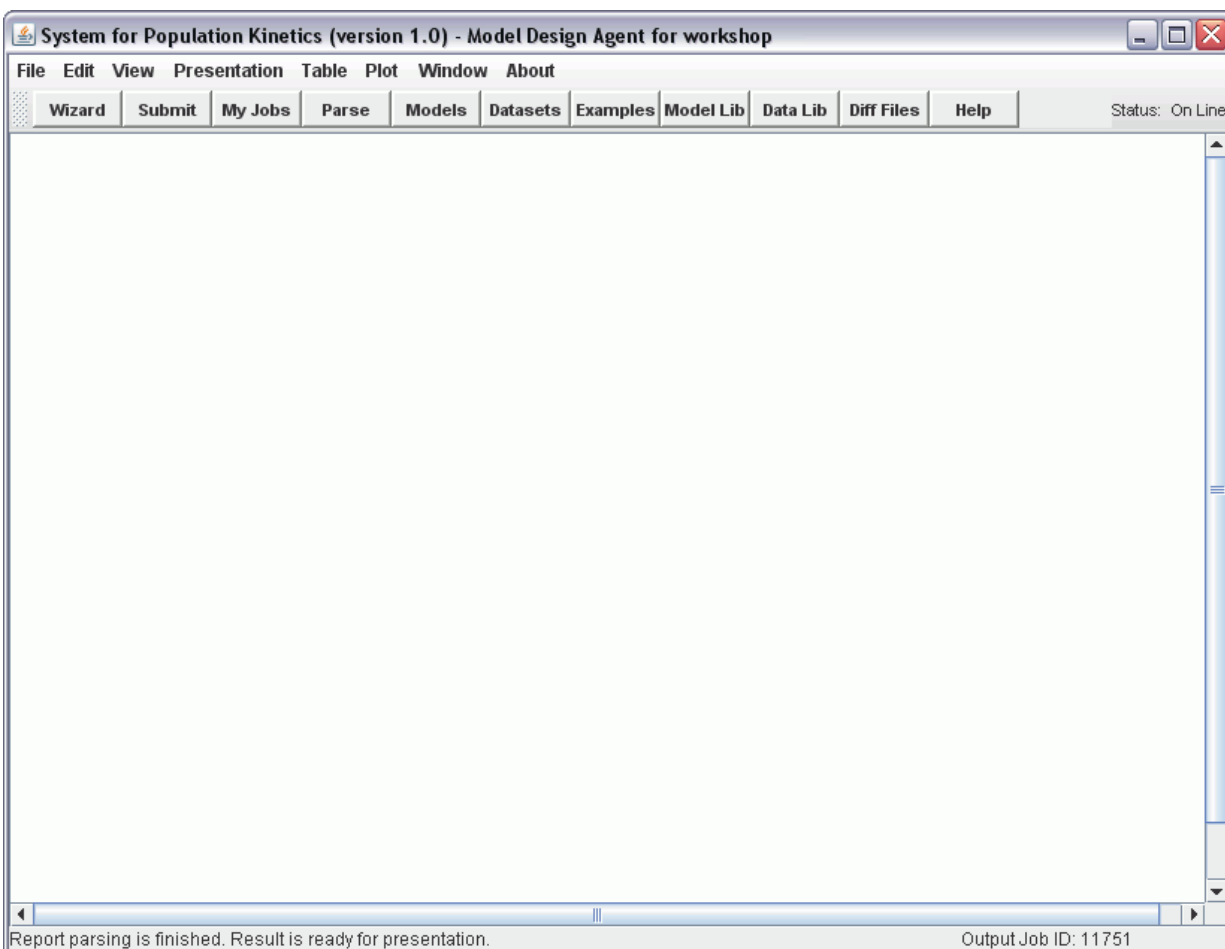
and then selecting "Load Model or Input". The user will also be presented with choices about where the model information should come from (the alternatives are to read the text in the editor or load a model from the file system):



My Datasets

Normally, the user will want to access full jobs from the database via the **My Jobs** button. There are some instances when the user would like to inspect datasets separately. Clicking on the **Datasets** option (the sixth

button from the left in the MDA main window) allows the MDA user to select datasets from the database.



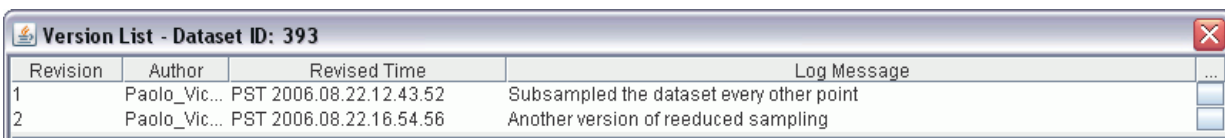
When selecting My Datasets, a list of all datasets belonging to a user appears:

Dataset ID	Dataset Name	No. of Versions	Last Revised Time	Description
397	Phenobarbital Pop	1	PST 2006-08-24 11:57:00	Phenobarbital population dataset
396	Cadralazine Pop	1	PST 2006-08-23 18:14:15	Cadralazine population dataset
393	Theophylline Pop RSS	2	PST 2006-08-22 16:54:56	Theophylline dataset from Dataset Library with re...
392	Theophylline Pop	1	PST 2006-08-22 12:39:16	Theophylline population dataset from Dataset Library
390	Theophylline Sub01	1	PST 2006-08-21 13:13:14	Theophylline dataset Subject 01
387	Cpeptide Population	2	PST 2007-09-25 06:10:39	Cpeptide population data
385	Cpeptide Sub01	1	PST 2006-08-18 14:00:40	Cpeptide data for Subject 01
382	Cadralazine Px10	1	PST 2006-08-18 11:01:54	Cadralazine data for Patient 10
381	Cadralazine Px09	1	PST 2006-08-18 11:01:11	Cadralazine data for Patient 09
380	Cadralazine Px08	1	PST 2006-08-18 11:00:19	Cadralazine data for Patient 08
379	Cadralazine Px07	1	PST 2006-08-18 10:59:24	Cadralazine data for Patient 07
378	Cadralazine Px06	1	PST 2006-08-18 10:58:45	Cadralazine data for Patient 06

List ☒ Versions ☐ Jobs Group member: workshop Total found: 17 Previous Page Next Page

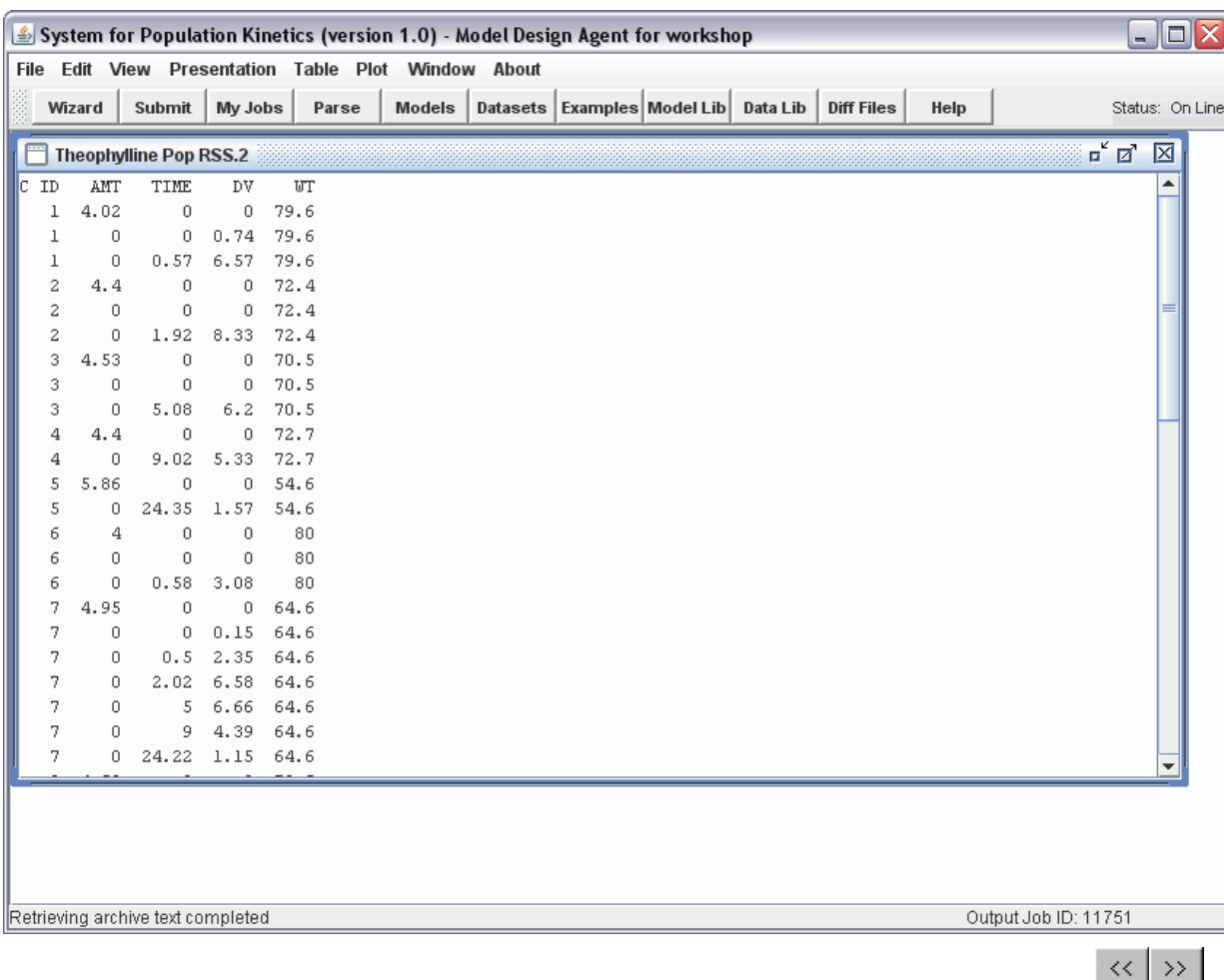
Every version of each dataset is stored separately in the database. Details referring to each dataset can be displayed in two ways. When the **Jobs** bullet is chosen and a dataset is selected, all jobs that have used that dataset are displayed in the Job List window. When the **Versions**

bullet is chosen and a dataset is selected, all versions of that dataset are displayed:



Revision	Author	Revised Time	Log Message
1	Paolo_Vic...	PST 2006.08.22.12.43.52	Subsampled the dataset every other point
2	Paolo_Vic...	PST 2006.08.22.16.54.56	Another version of reeduced sampling

Every version is described by a log and has a revision time stamp associated with it. When a version is selected, that dataset becomes visible in the MDA editor window:

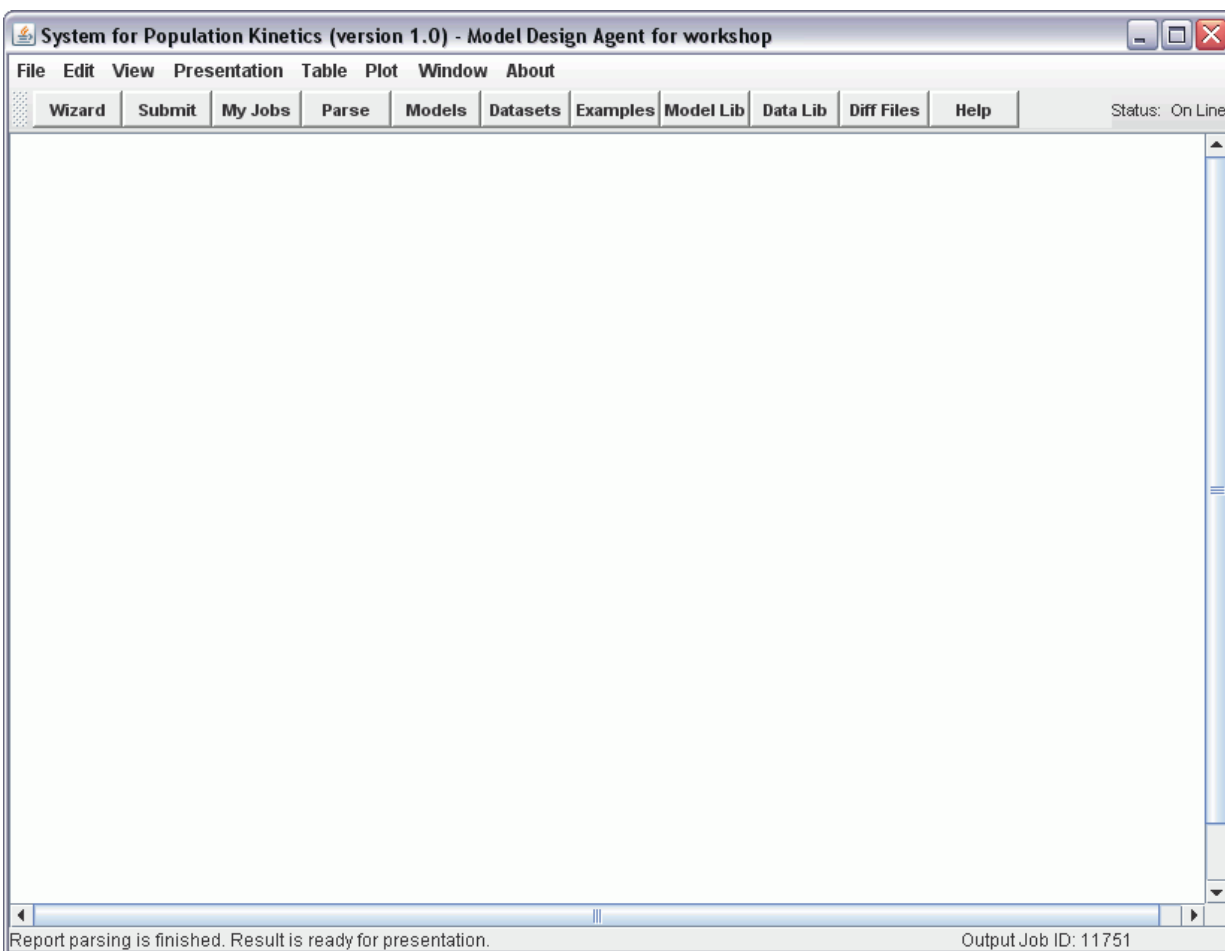


Theophylline Pop RSS.2					
C	ID	AMT	TIME	DV	WT
1	1	4.02	0	0	79.6
1	1	0	0	0.74	79.6
1	1	0	0.57	6.57	79.6
2	2	4.4	0	0	72.4
2	2	0	0	0	72.4
2	2	0	1.92	8.33	72.4
3	3	4.53	0	0	70.5
3	3	0	0	0	70.5
3	3	0	5.08	6.2	70.5
4	4	4.4	0	0	72.7
4	4	0	9.02	5.33	72.7
5	5	5.86	0	0	54.6
5	5	0	24.35	1.57	54.6
6	6	4	0	0	80
6	6	0	0	0	80
6	6	0	0.58	3.08	80
7	7	4.95	0	0	64.6
7	7	0	0	0.15	64.6
7	7	0	0.5	2.35	64.6
7	7	0	2.02	6.58	64.6
7	7	0	5	6.66	64.6
7	7	0	9	4.39	64.6
7	7	0	24.22	1.15	64.6

Retrieving archive text completed Output Job ID: 11751

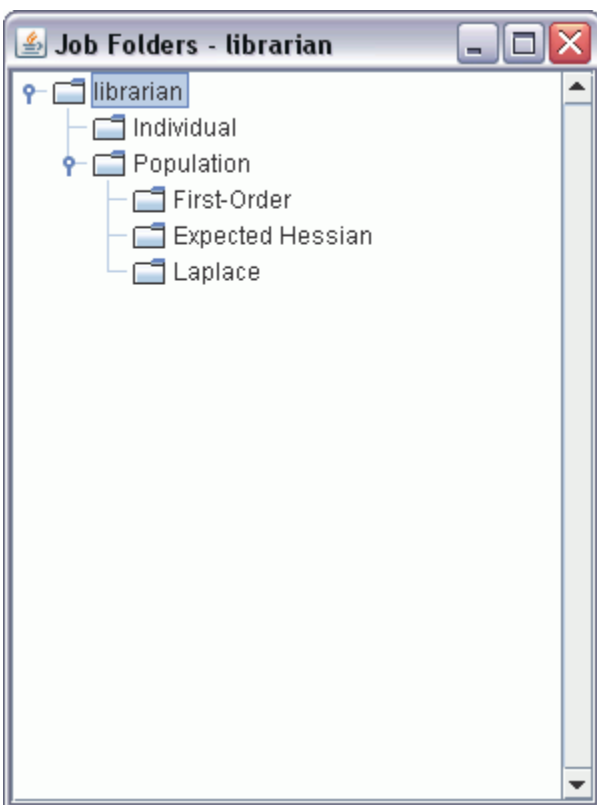
Job Examples

RFPK scientists have made available a series of sample jobs to familiarize users with the SPK system. These jobs are available to all users by clicking on the "Examples" button in the main MDA screen:



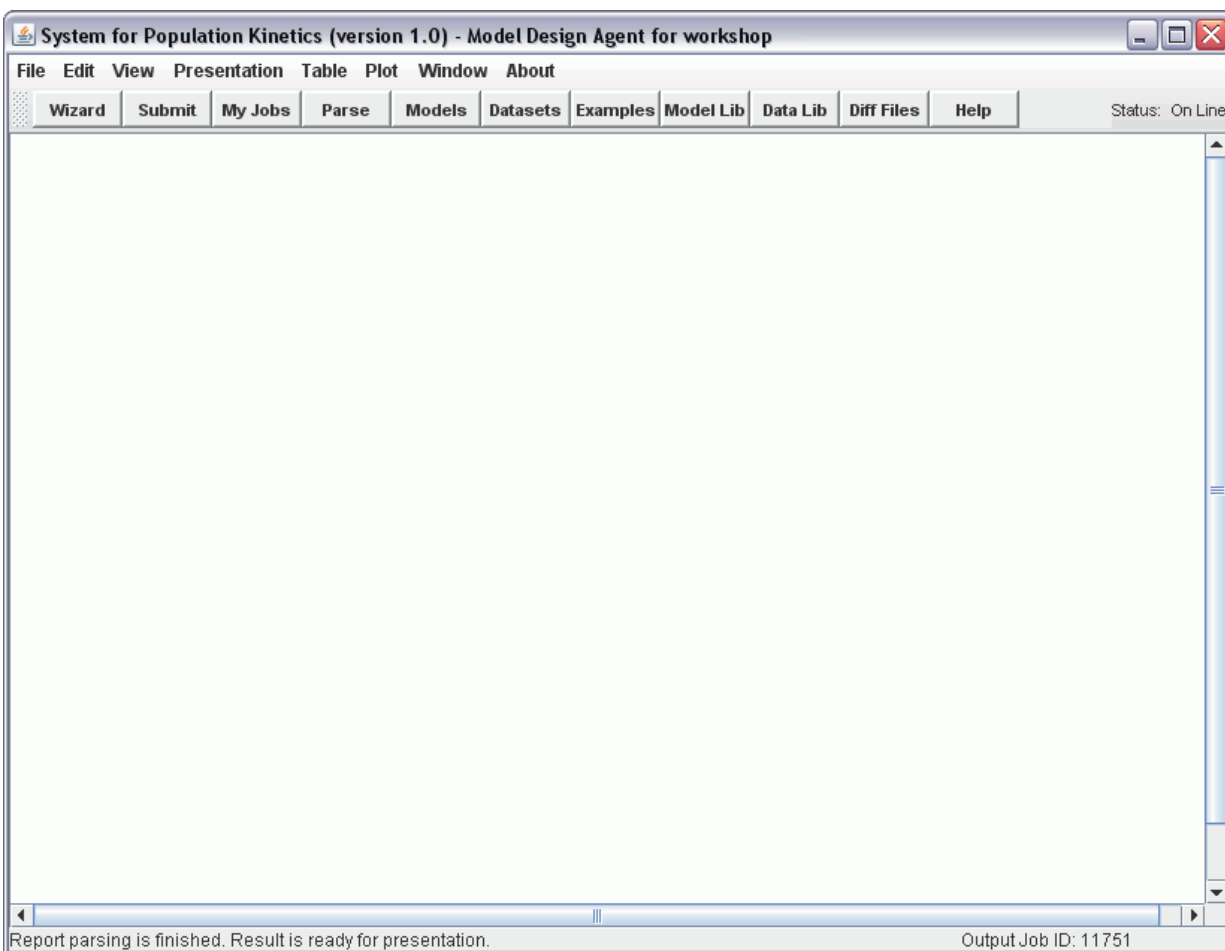
The examples are brought up and can be inspected or used to create new jobs. They are available to all users and can be modified by anyone (the modified version belongs to the user that modifies it).

Job List - /librarian							
Job ID	Submission Time	Status Code	Model Version	Dataset Version	Job Abstract		cut
1181	Wed 2005-11-30 23:51:36...	Successful Run	1CMT CL, V.4	PHENOBARBITAL.1	POP018 PHENOBARBODE1 DE 1CMT XB 2F 2...		<input type="checkbox"/>
1180	Wed 2005-11-30 23:47:39...	Successful Run	LOGISTIC.1	ORANGETREES.1	POP017 ORANGETREES AN LOGISTIC NA 3F...		<input type="checkbox"/>
1179	Wed 2005-11-30 23:43:56...	Successful Run	2CMT KA, KE, CL.1	THEOPHYLLINE.1	POP016 THEOPHODE DE 2CMT BD 3F 3R F ...		<input type="checkbox"/>
1174	Wed 2005-11-30 23:29:32...	Successful Run	CIRCADIAN.1	MARES.1	POP011 MARES1 AN 1SIN1COS NA 3F 2R D...		<input type="checkbox"/>
Search Jobs Group member <u>workshop</u> Total found 43 Previous Page Next Page							



Model Library

RFPK scientists have made available a series of sample models to familiarize users with the SPK system. These models are available to all users by clicking on the "Model Lib" button in the main MDA screen:



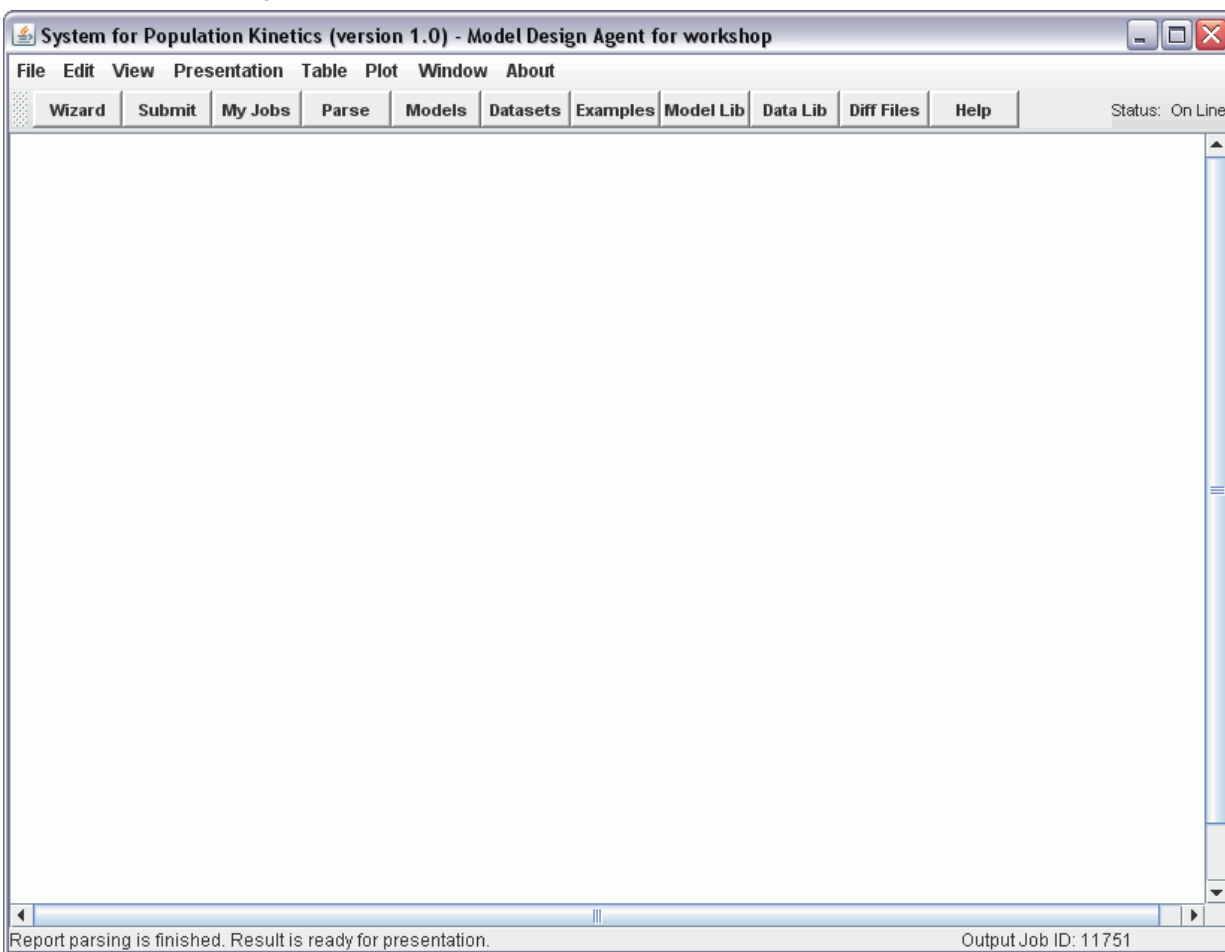
The examples are accessible and can be inspected or used to create new jobs as indicated elsewhere.

Model ID	Model Name	No. of Versions	Last Revised Time	Description
221	LOGISTIC	1	PST 2005.11.30.23.47.39	Logistic growth equation
220	2CMT KA, KE, CL	1	PST 2005.11.30.23.43.56	TWO COMPARTMENTS WITH KA, KE, CL PARAMETERIZATION
219	1CMT CL, V	4	PST 2005.11.30.23.51.34	SINGLE COMPARTMENT WITH CLEARANCE, VOLUME PARAMETE...
218	CIRCADIAN	2	PST 2005.11.30.23.31.10	mixed-effect model
217	POLYNOMIAL REGRESSIO	2	PST 2005.11.30.23.24.20	Pinheiro, J. C. and Bates, D. M. (2000), Mixed-Eff...
216	1EXP CL, V	8	PST 2005.11.30.23.26.00	SINGLE EXPONENTIAL DECAY, CLEARANCE AND VOLUME PAR...
215	RAIL	1	PST 2005.11.30.23.01.21	Pinheiro JC and Bates DM (2000), Mixed-Effects Mod...
214	BENNETT5	1	PST 2005.11.30.22.31.11	NIST BENNETT5 http://www.itl.nist.gov/div898/strd/...
213	RAT43	1	PST 2005.11.30.22.29.10	NIST RAT43 http://www.itl.nist.gov/div898/strd/nls...
212	ECKERLE4	1	PST 2005.11.30.22.26.42	NIST ECKERLE4 http://www.itl.nist.gov/div898/strd/...
211	MGH10	1	PST 2005.11.30.22.24.40	NIST MGH10 http://www.itl.nist.gov/div898/strd/nls...
210	RAT42	1	PST 2005.11.30.22.21.46	NIST RAT42 http://www.itl.nist.gov/div898/strd/nls...

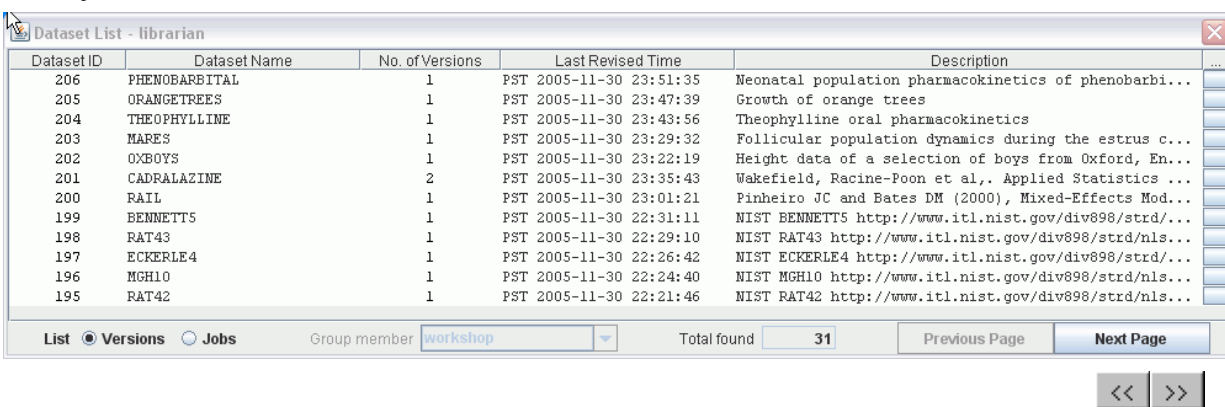
List ☒ Versions ☐ Jobs
 Group member: workshop
 Total found: 31
 Previous Page Next Page

Dataset Library

RFPK scientists have made available a series of sample datasets to familiarize users with the SPK system. These datasets are available to all users by clicking on the "Dataset Lib" button in the main MDA screen:

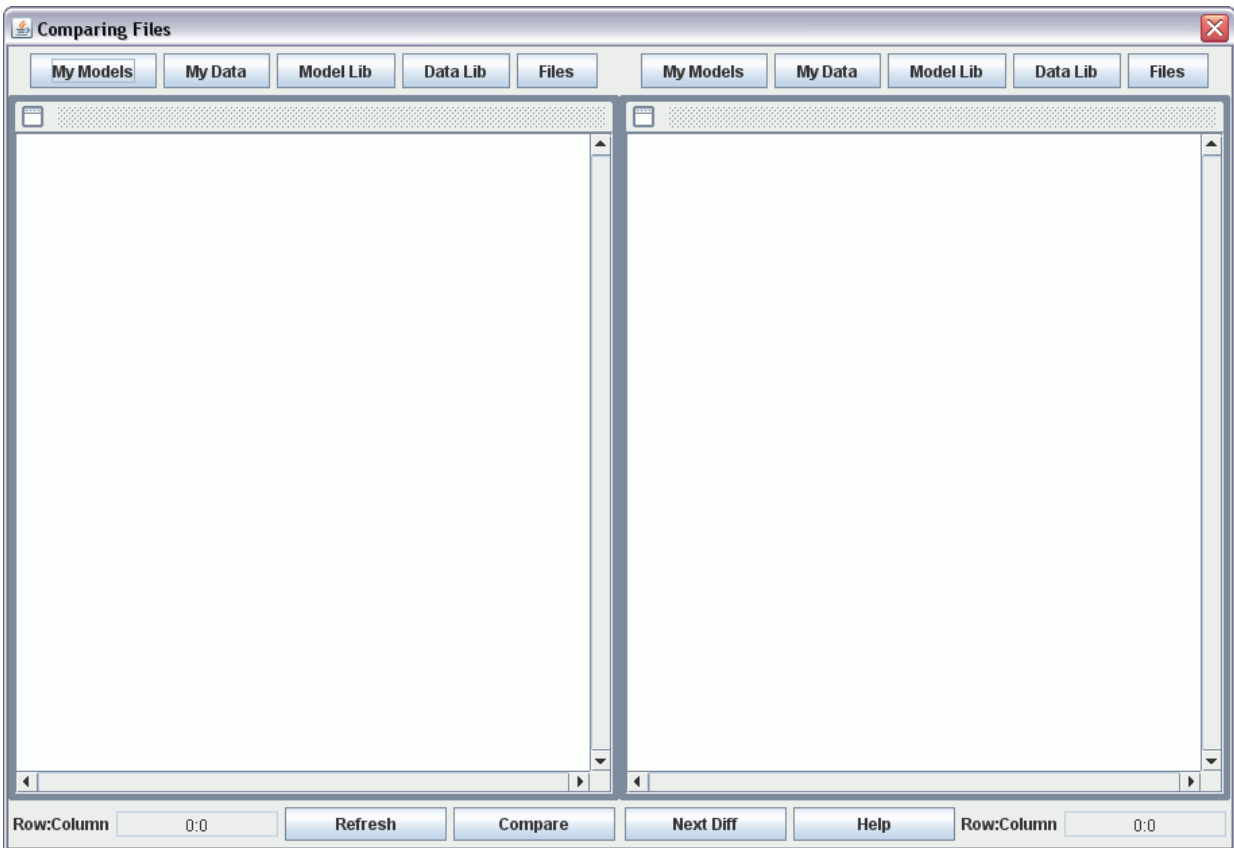


The examples are accessible and can be inspected or used to create new jobs as indicated elsewhere.



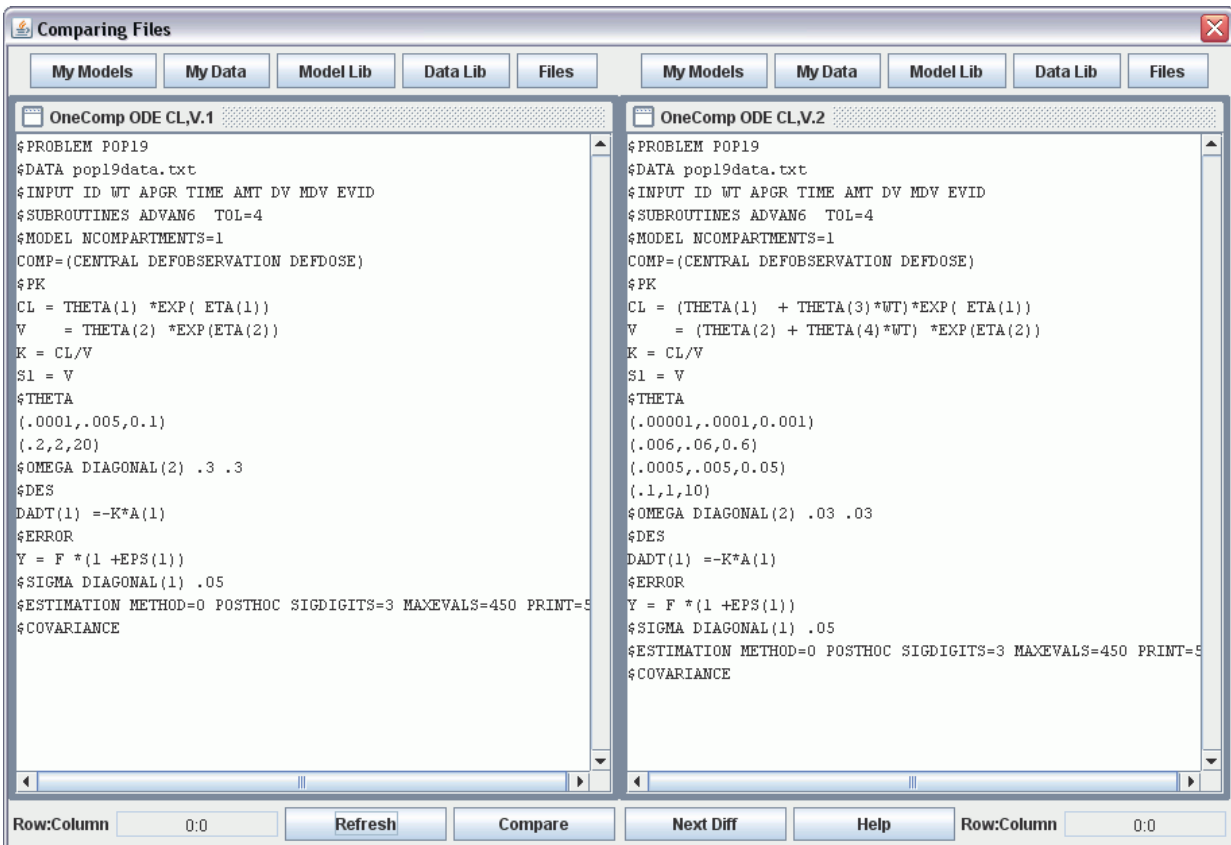
Compare Files

This option allows to compare files that are residing in different portions of the database. When clicking Diff Files button from the main MDA window, the following screen appears:

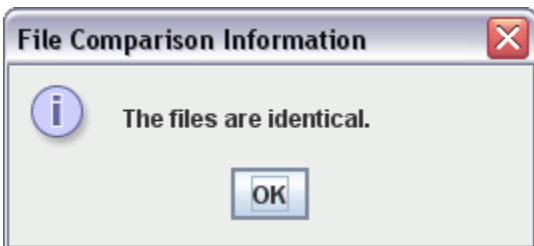


My Models and My Data select files in the individual (personal) sections of the database, Model Lib and Data Lib select files from the library while Files selects files from the local hard drive.

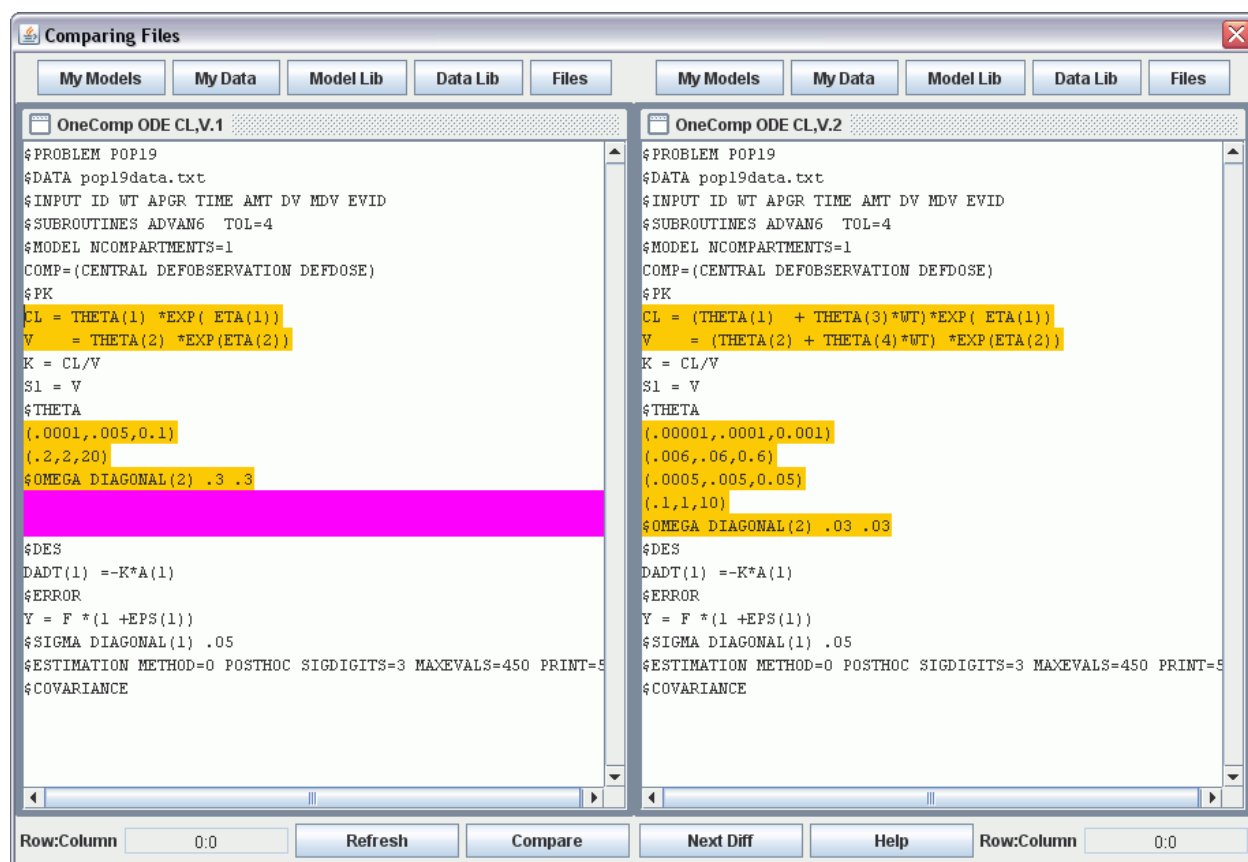
Selecting two files provides the following prompt:



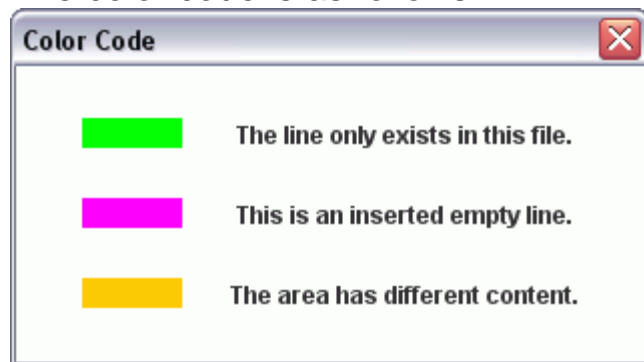
If two files are identical, then the result is:



If the files are different, like in this case, differences are highlighted:

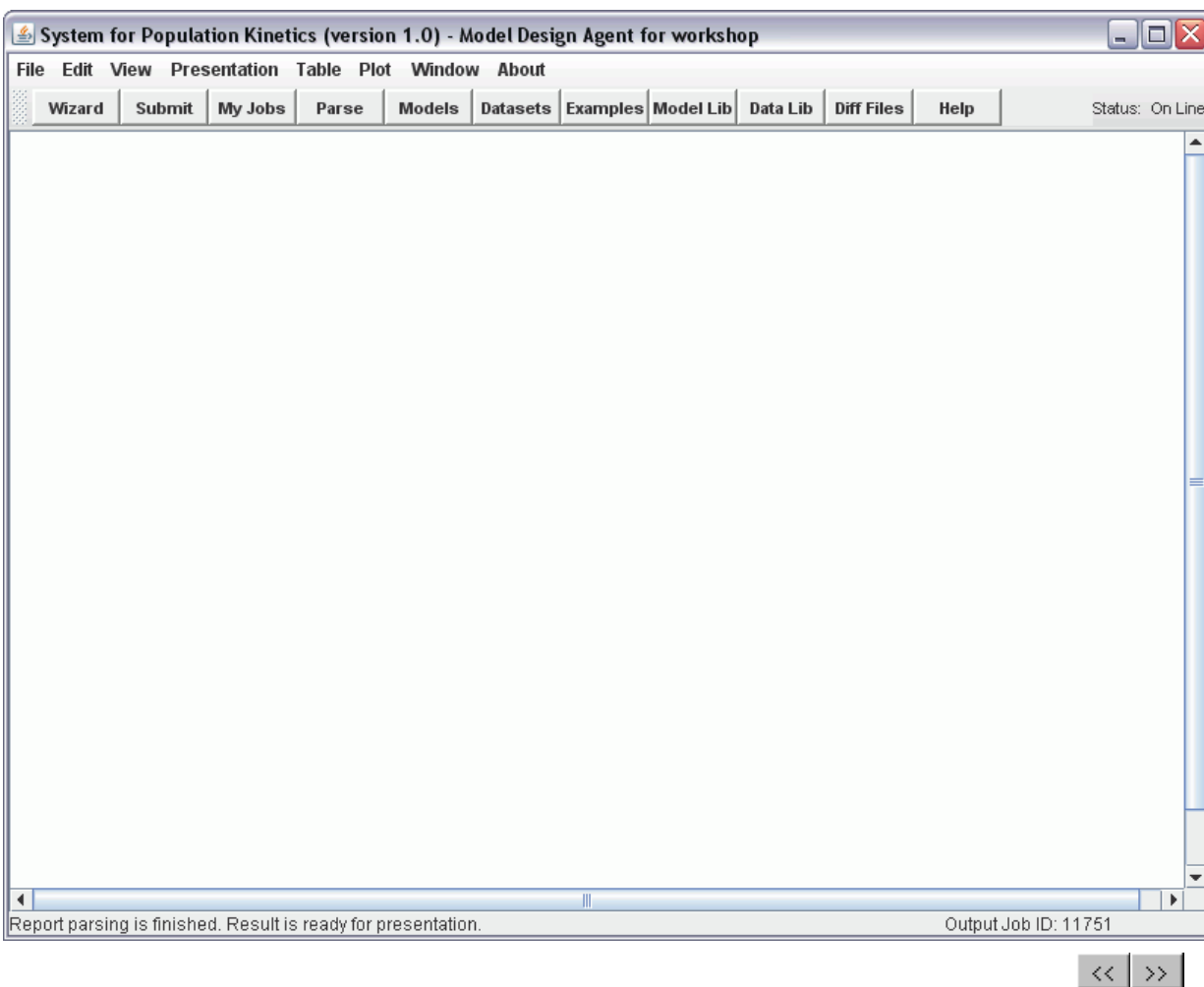


The color code is as follows:



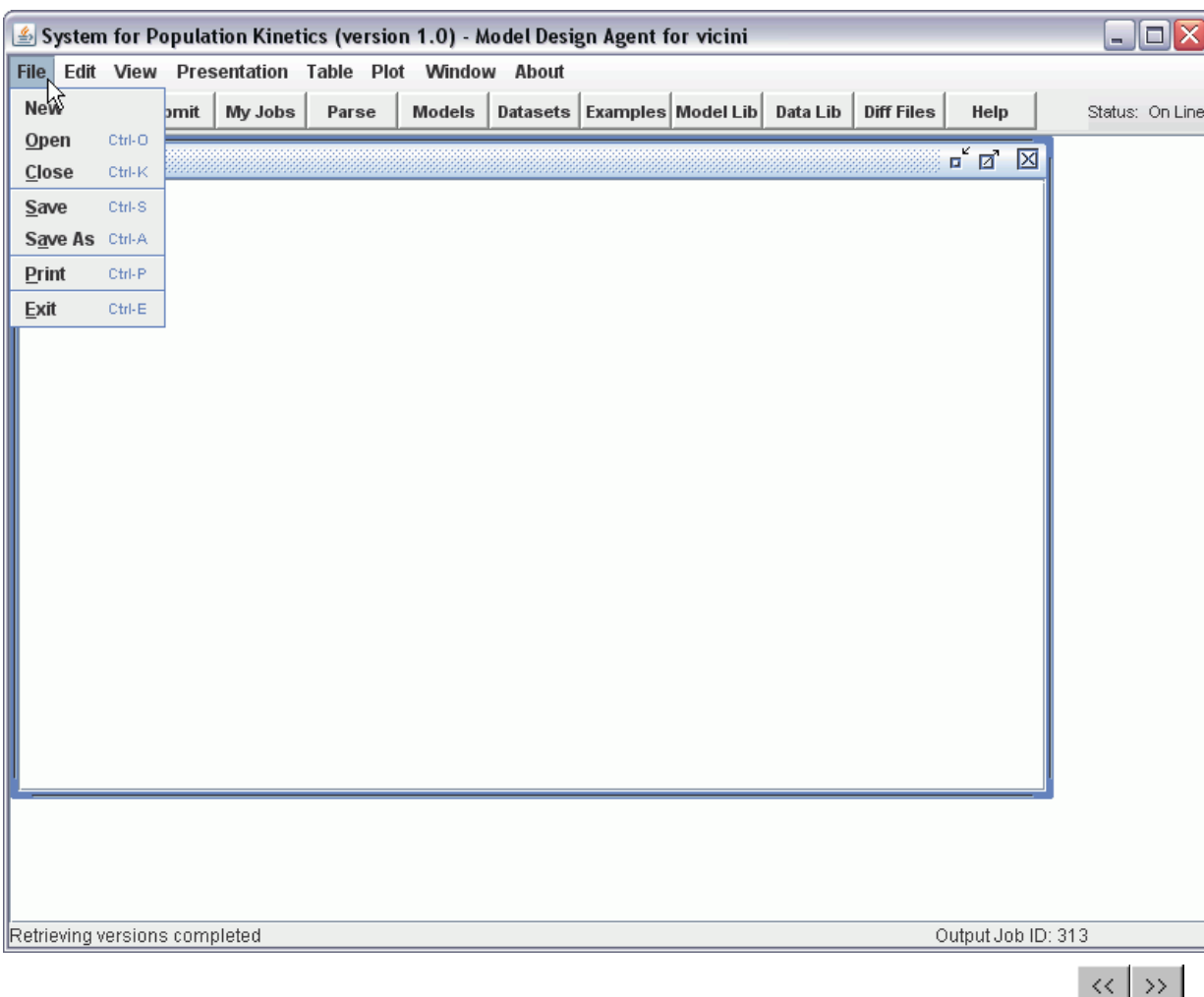
Help

Clicking on the Help button on the main screen brings up the main Introduction panel; clicking on the Help button from every other screen accesses the relevant help topic.



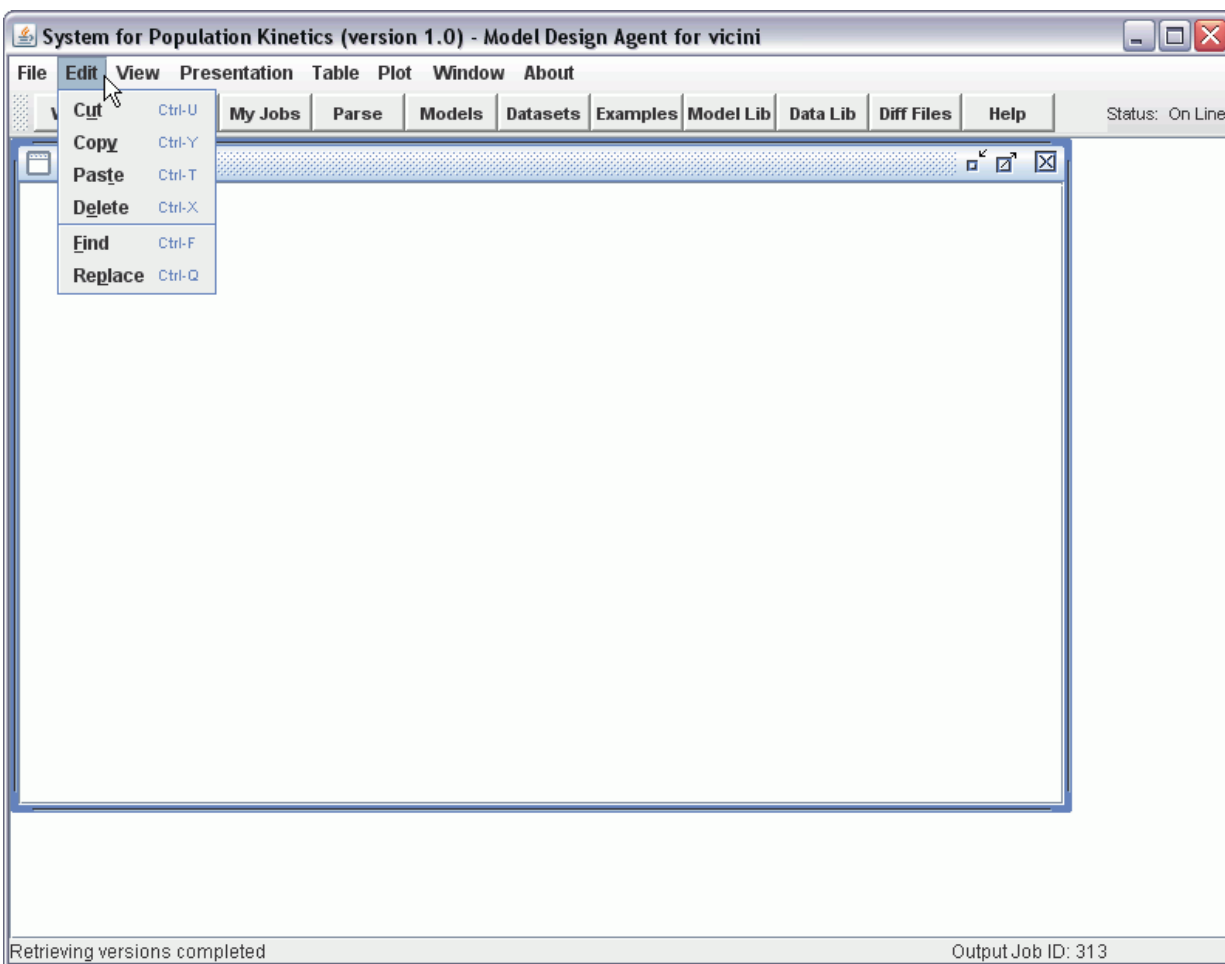
File

This option in the MDA editor window provides the basic file editing capabilities (New, Open, Close, Save, Save As, Print, Exit). Note that selecting Exit closes the MDA.



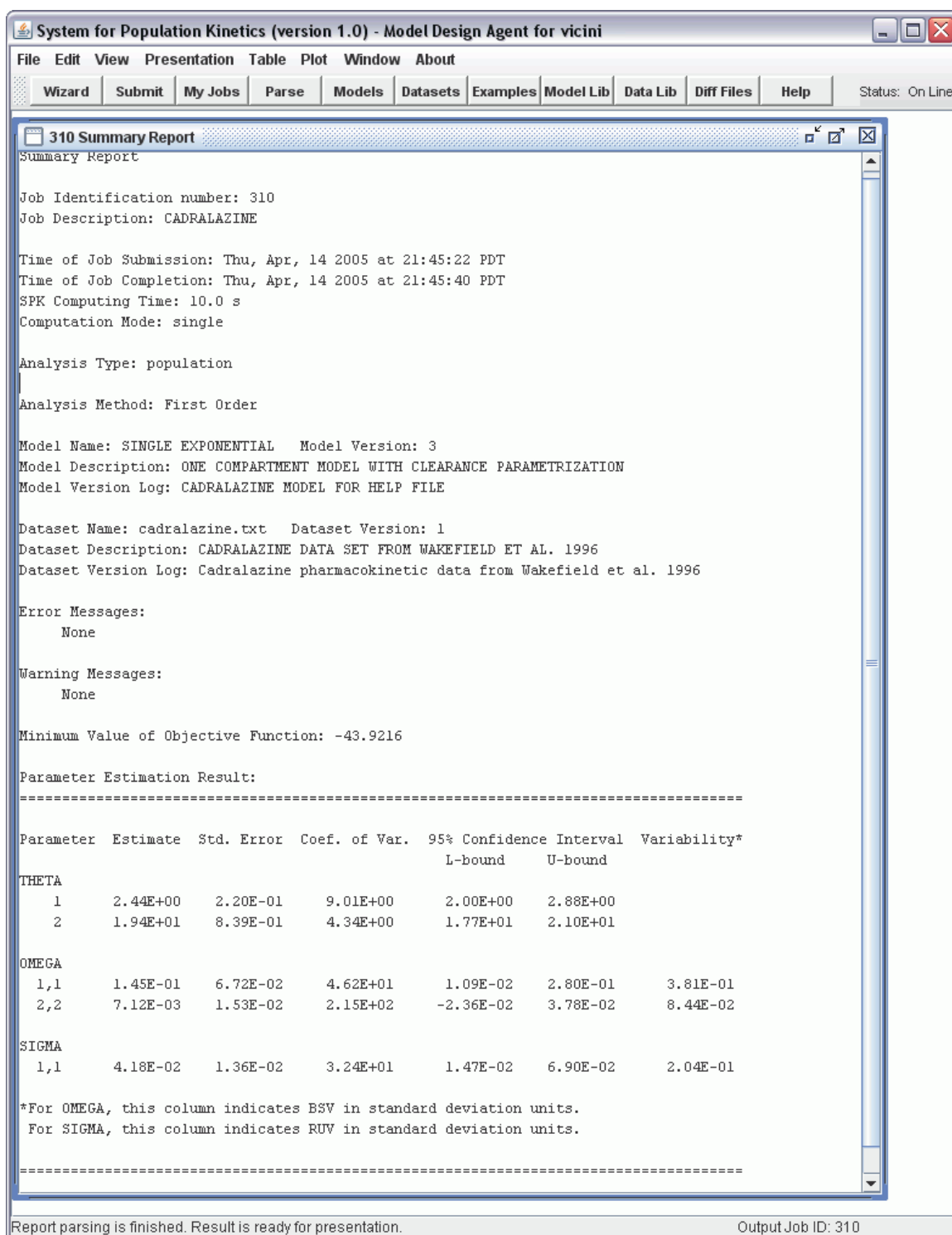
Edit

This option in the MDA editor window provides the basic file editing capabilities (Cut, Copy, Paste, Delete, Find and Replace):



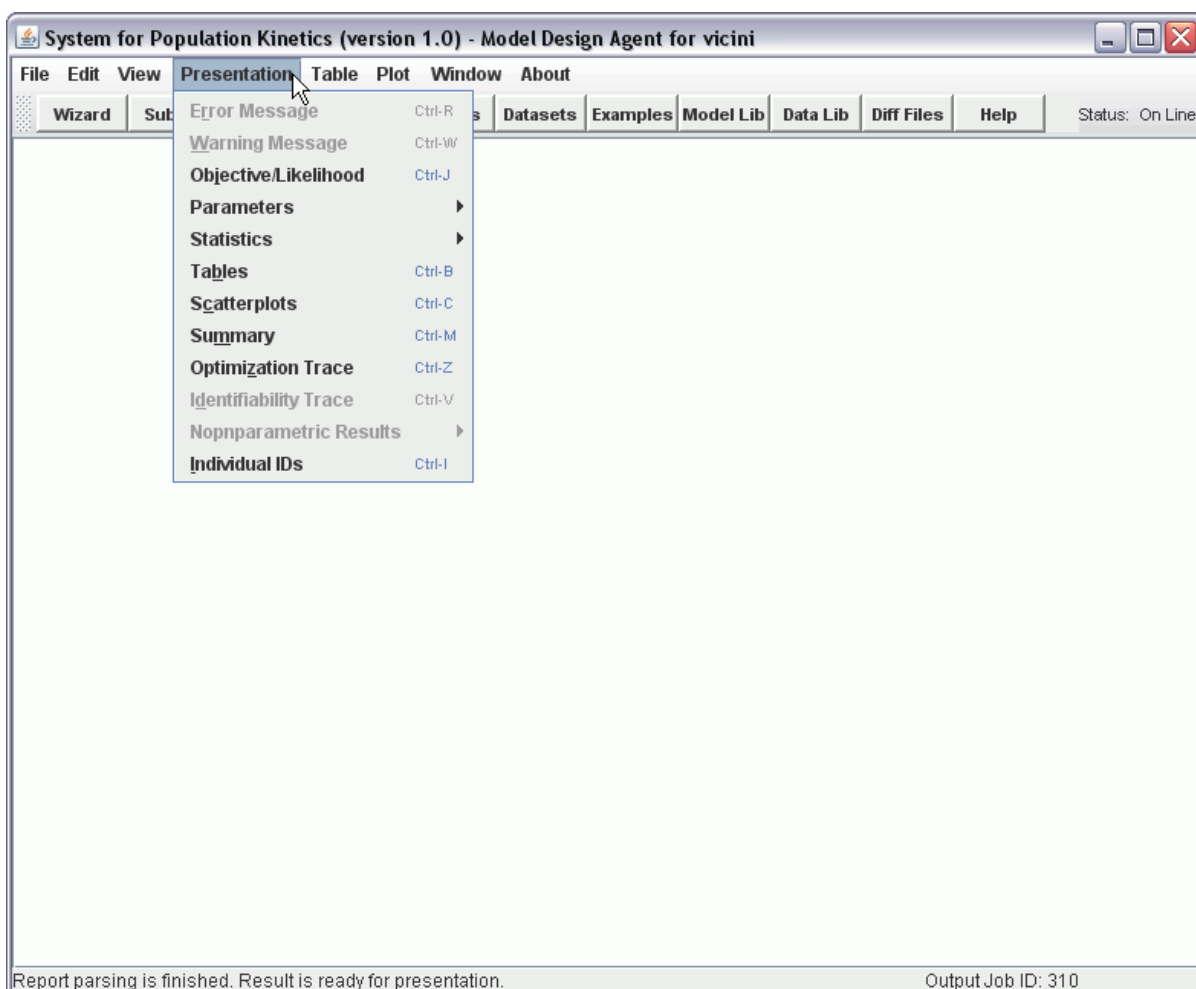
Presentation

An example Summary Report is shown below:



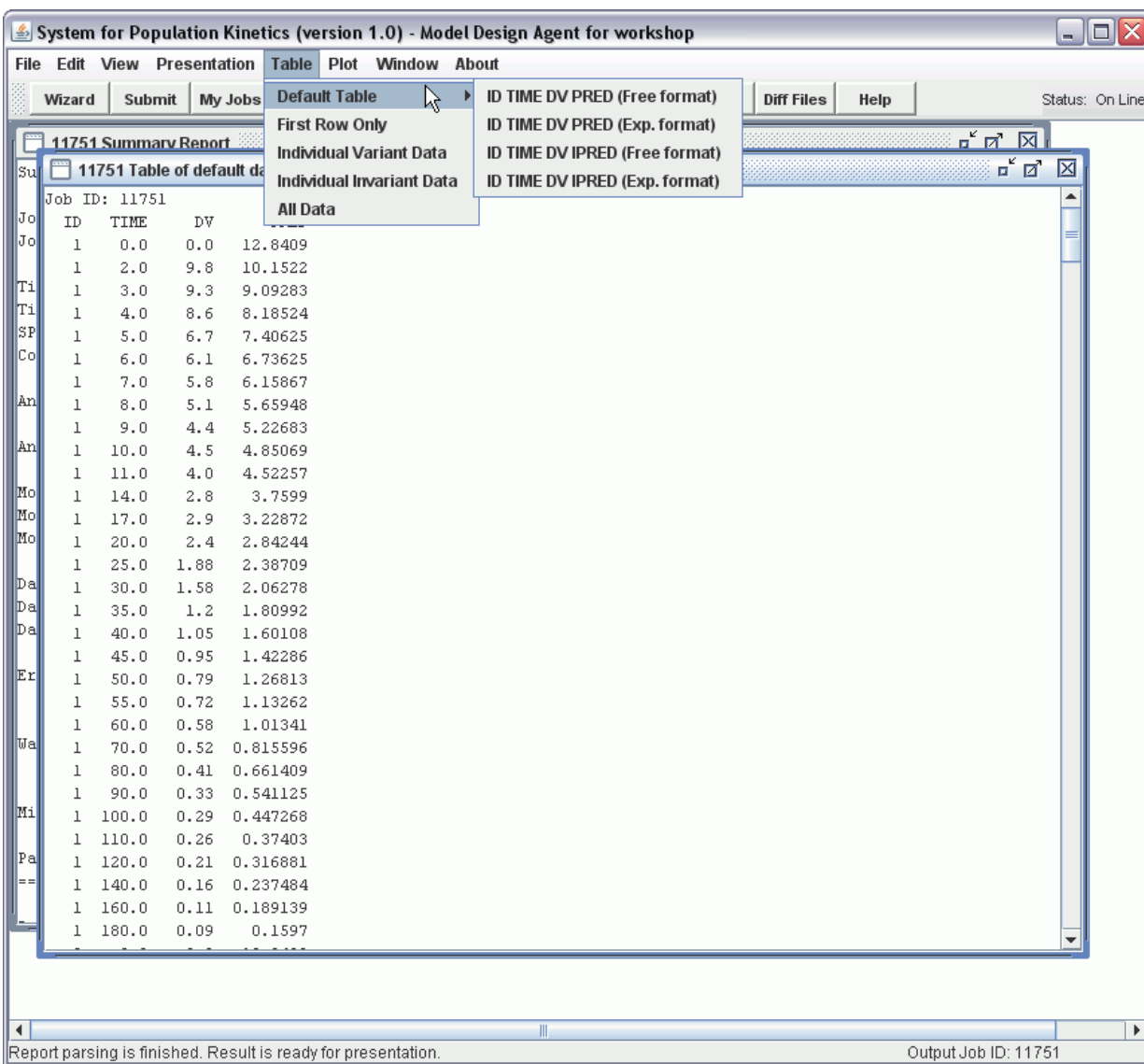
The Summary Report displays important information about the job, such as optimal parameter estimates, their coefficients of variation, lower and upper bound of the 95% confidence interval, and so on.

Other elements of the computational output can be accessed using the Presentation menu from the MDA:



Table

Default tables are available or a custom table can be built using the entire report. Tables can be requested once the report has been loaded. Default tables include TIME versus both PRED and IPRED for each ID. They are provided both in free format and exponential (scientific) format.



The option "First Row Only" provides values for each variable once for ID. It is useful when it is needed to display individual parameter values only once

System for Population Kinetics (version 1.0) - Model Design Agent for workshop

File Edit View Presentation Table Plot Window About

Wizard Submit My Jobs Parse Models Datasets Examples Model Lib Data Lib Diff Files Help Status: On Line

11751 Summary Report

11751 Table of default dataset

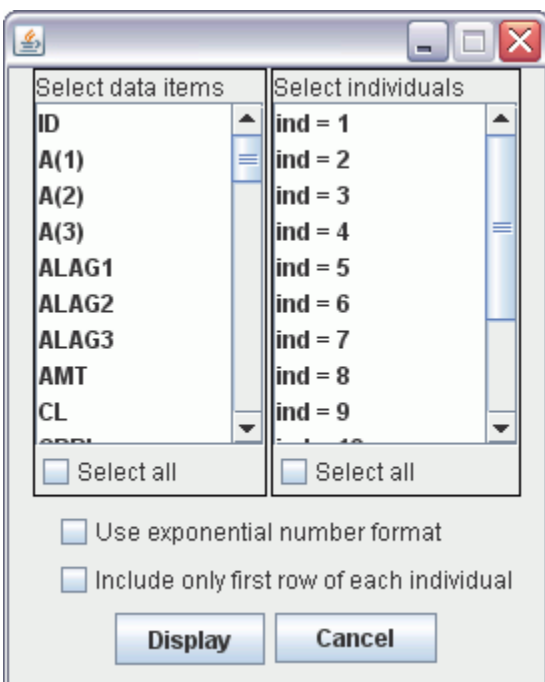
11751 Report Data (First row only)

Job ID: 11751

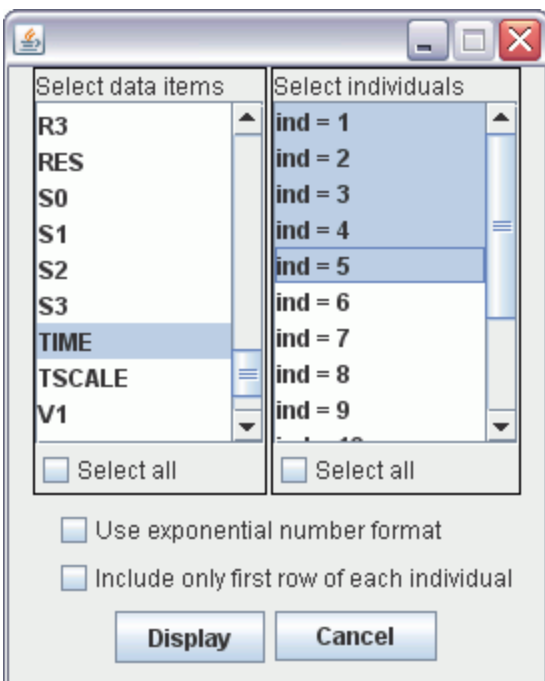
ID	A(1)	A(2)	A(3)	ALAG1	ALAG2	ALAG3	AMT	
1	4.9650E+04	0.0000E+00	0.0000E+00	0.0000E+00	0.0000E+00	0.0000E+00	4.9650E+04	2.923
2	4.9650E+04	0.0000E+00	0.0000E+00	0.0000E+00	0.0000E+00	0.0000E+00	4.9650E+04	2.844
3	4.9650E+04	0.0000E+00	0.0000E+00	0.0000E+00	0.0000E+00	0.0000E+00	4.9650E+04	2.270
4	4.9650E+04	0.0000E+00	0.0000E+00	0.0000E+00	0.0000E+00	0.0000E+00	4.9650E+04	2.465
5	4.9650E+04	0.0000E+00	0.0000E+00	0.0000E+00	0.0000E+00	0.0000E+00	4.9650E+04	2.111
6	4.9650E+04	0.0000E+00	0.0000E+00	0.0000E+00	0.0000E+00	0.0000E+00	4.9650E+04	3.551
7	4.9650E+04	0.0000E+00	0.0000E+00	0.0000E+00	0.0000E+00	0.0000E+00	4.9650E+04	2.047
8	5.4000E+04	0.0000E+00	0.0000E+00	0.0000E+00	0.0000E+00	0.0000E+00	5.4000E+04	1.917
9	4.3800E+04	0.0000E+00	0.0000E+00	0.0000E+00	0.0000E+00	0.0000E+00	4.3800E+04	2.455
10	5.4000E+04	0.0000E+00	0.0000E+00	0.0000E+00	0.0000E+00	0.0000E+00	5.4000E+04	3.022
11	5.4000E+04	0.0000E+00	0.0000E+00	0.0000E+00	0.0000E+00	0.0000E+00	5.4000E+04	2.367
12	4.9200E+04	0.0000E+00	0.0000E+00	0.0000E+00	0.0000E+00	0.0000E+00	4.9200E+04	1.684
13	5.9400E+04	0.0000E+00	0.0000E+00	0.0000E+00	0.0000E+00	0.0000E+00	5.9400E+04	2.655
14	5.5800E+04	0.0000E+00	0.0000E+00	0.0000E+00	0.0000E+00	0.0000E+00	5.5800E+04	3.551

Report parsing is finished. Result is ready for presentation. Output Job ID: 11751

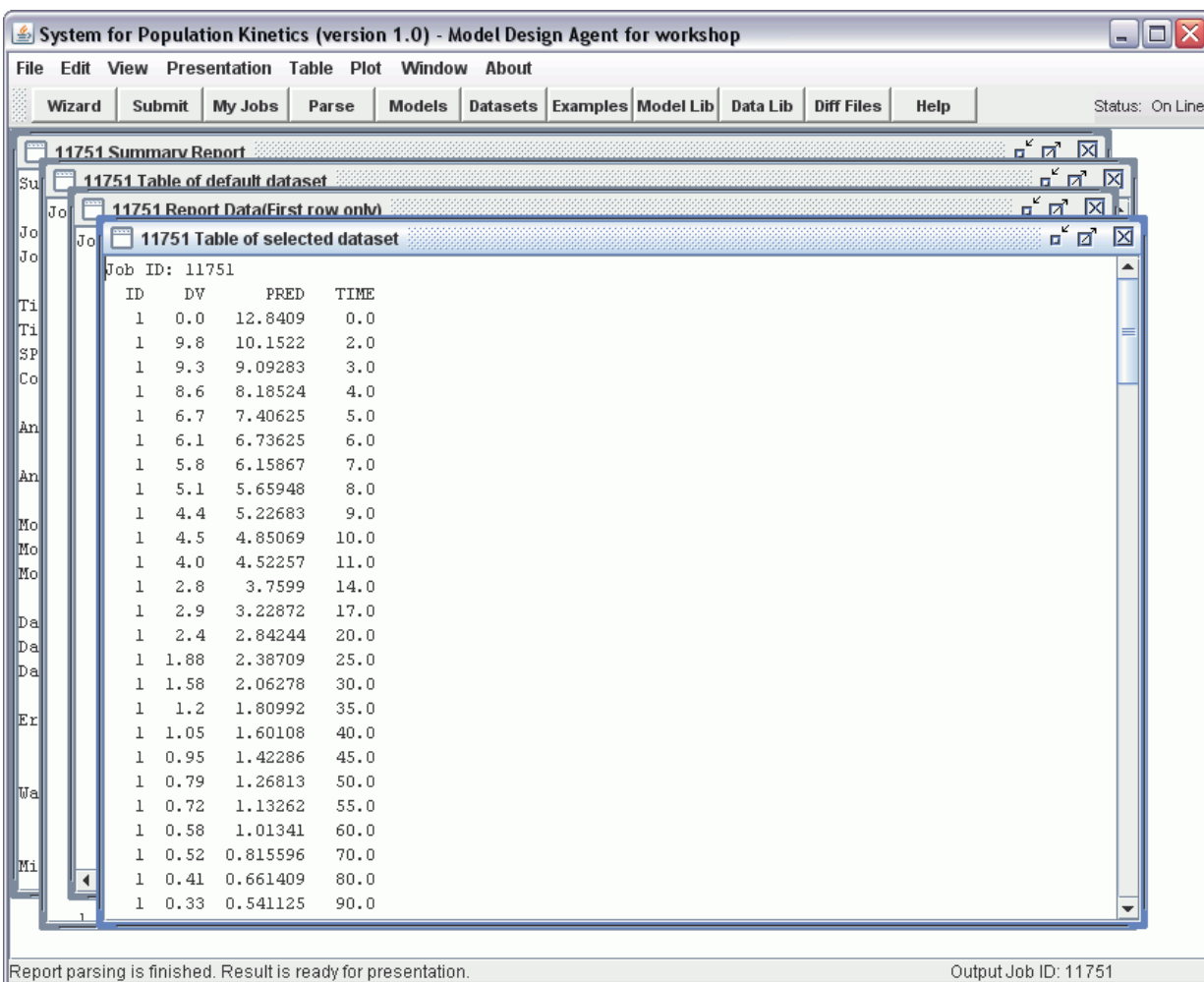
The "Selected Dataset" option allows the user to build custom plots that may be specific to a certain ID or to a certain group of subjects or variables of interest.



For example, the user could choose to plot the data (DV) and the predictions (PRED) for the first five individuals, listed by ID (the CTRL key should be used to select multiple items):

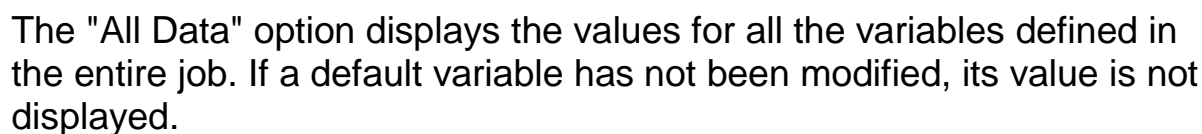


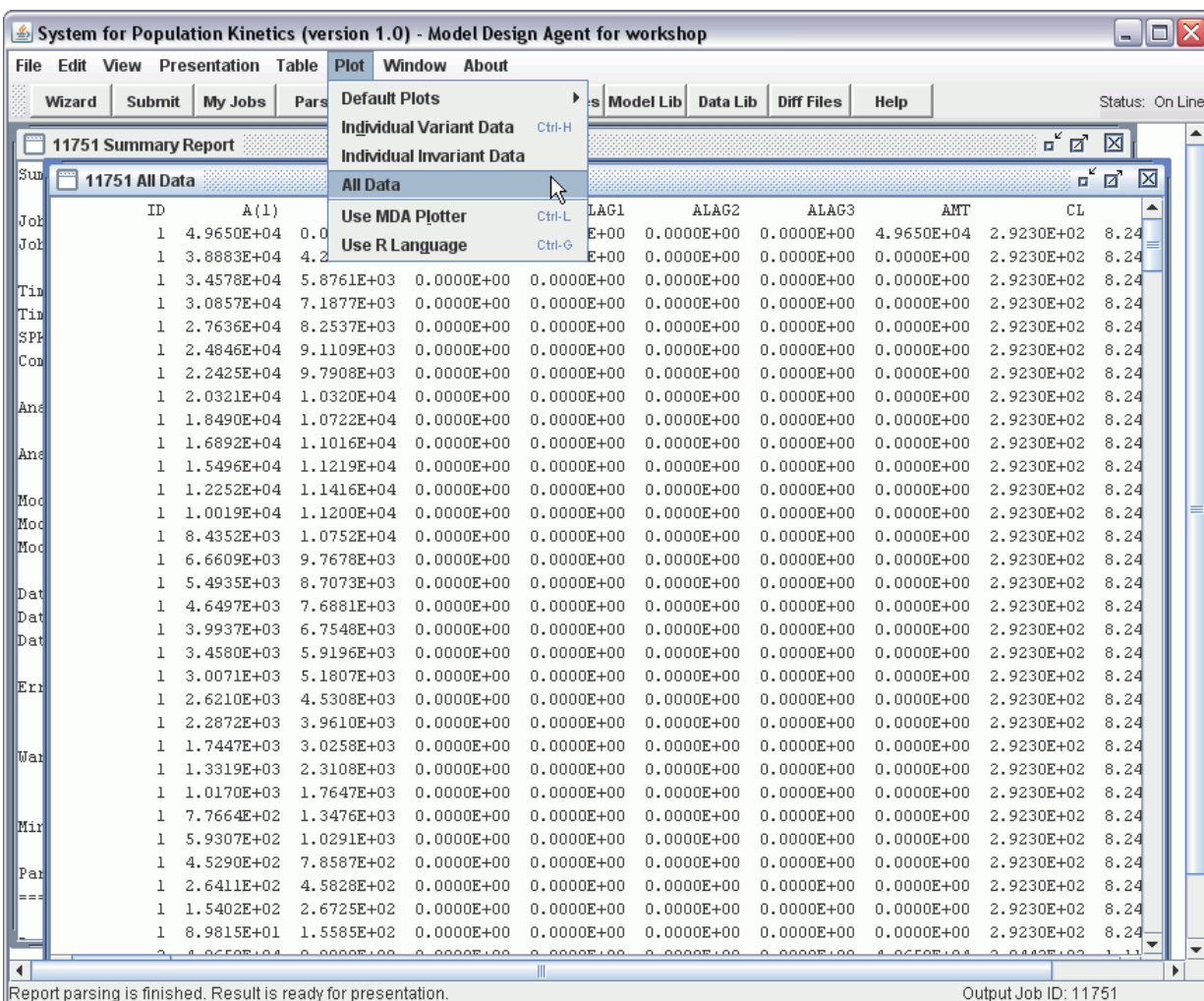
The result is displayed in the MDA window:



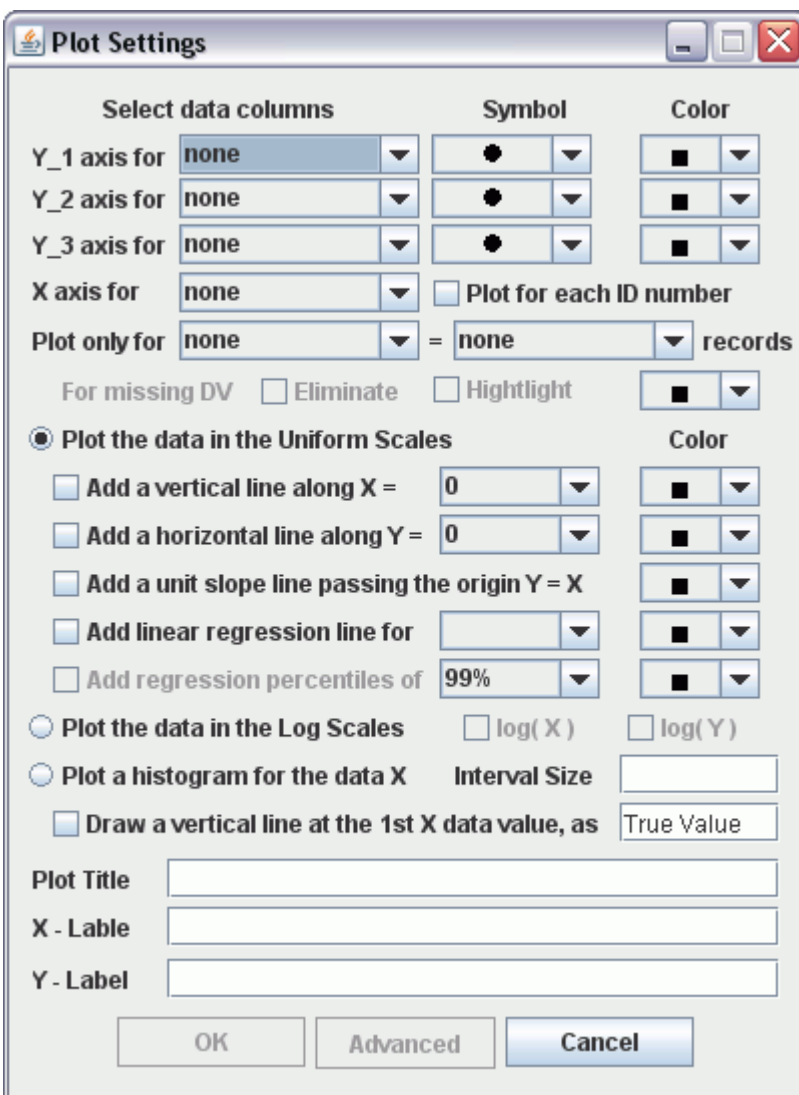
Plot

Default plots are available or a custom plot can be built using the entire report. The "Individual Variant Data", the "Individual Invariant Data" or the "All Data" should be selected before plots are requested.





The "Use MDA Plotter" option allows the user to build custom plots that may be specific to a certain ID or to a certain group of subjects or variables of interest.



Plot Settings

Select data columns	Symbol	Color
Y_1 axis for: none	●	■
Y_2 axis for: none	●	■
Y_3 axis for: none	●	■
X axis for: none	<input type="checkbox"/> Plot for each ID number	
Plot only for: none	= none	records

For missing DV ☐ Eliminate ☐ Highlight ■

☒ **Plot the data in the Uniform Scales**

	Color
<input type="checkbox"/> Add a vertical line along X = 0	■
<input type="checkbox"/> Add a horizontal line along Y = 0	■
<input type="checkbox"/> Add a unit slope line passing the origin Y = X	■
<input type="checkbox"/> Add linear regression line for	■
<input type="checkbox"/> Add regression percentiles of 99%	■

☐ **Plot the data in the Log Scales** ☐ log(X) ☐ log(Y)

☐ **Plot a histogram for the data X** Interval Size:

☐ Draw a vertical line at the 1st X data value, as True Value

Plot Title:

X - Lable:

Y - Label:

OK Advanced Cancel

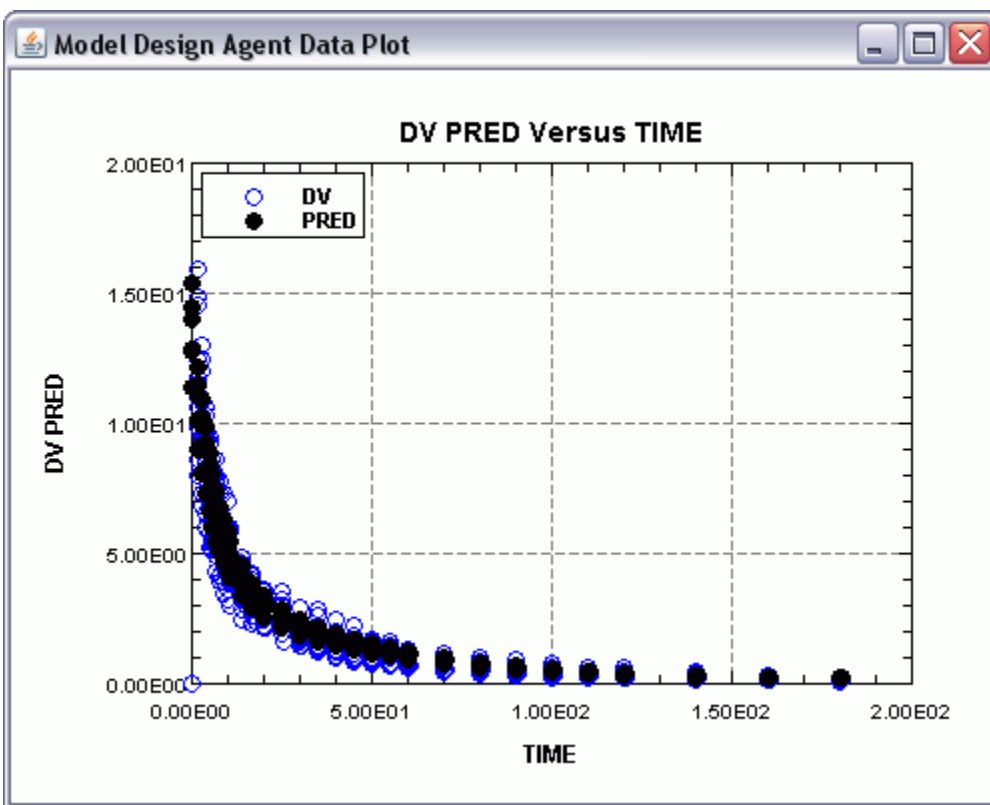
For example, the user could choose to plot the data (DV) as empty blue circles and the predictions (PRED) as black full circles, against TIME:

Plot Settings

Select data columns	Symbol	Color
Y_1 axis for DV	○	Blue
Y_2 axis for PRED	●	Black
Y_3 axis for none	●	Black
X axis for TIME	<input type="checkbox"/> Plot for each ID number	
Plot only for none	= none	records
For missing DV	<input type="checkbox"/> Eliminate	<input type="checkbox"/> Highlight
<input checked="" type="radio"/> Plot the data in the Uniform Scales		Color
<input type="checkbox"/> Add a vertical line along X = 0		Black
<input type="checkbox"/> Add a horizontal line along Y = 0		Black
<input type="checkbox"/> Add a unit slope line passing the origin Y = X		Black
<input type="checkbox"/> Add linear regression line for DV		Black
<input type="checkbox"/> Add regression percentiles of 99%		Black
<input type="radio"/> Plot the data in the Log Scales	<input type="checkbox"/> log(X)	<input type="checkbox"/> log(Y)
<input type="radio"/> Plot a histogram for the data X	Interval Size	
<input type="checkbox"/> Draw a vertical line at the 1st X data value, as	True Value	
Plot Title	DV PRED Versus TIME	
X - Lable	TIME	
Y - Label	DV PRED	

OK Advanced Cancel

The result is as follows:



Another interesting plot could be WRES versus TIME:

Plot Settings

Select data columns	Symbol	Color
Y_1 axis for WRES	○	Blue
Y_2 axis for none	●	Black
Y_3 axis for none	●	Black
X axis for TIME	<input type="checkbox"/> Plot for each ID number	
Plot only for none	= none	records

For missing DV ☐ Eliminate ☐ Highlight ☐

☒ Plot the data in the Uniform Scales

	Color
<input type="checkbox"/> Add a vertical line along X = 0	Black
<input type="checkbox"/> Add a horizontal line along Y = 0	Black
<input type="checkbox"/> Add a unit slope line passing the origin Y = X	Black
<input type="checkbox"/> Add linear regression line for WRES	Black
<input type="checkbox"/> Add regression percentiles of 99%	Black

☐ Plot the data in the Log Scales ☐ log(X) ☐ log(Y)

☐ Plot a histogram for the data X Interval Size

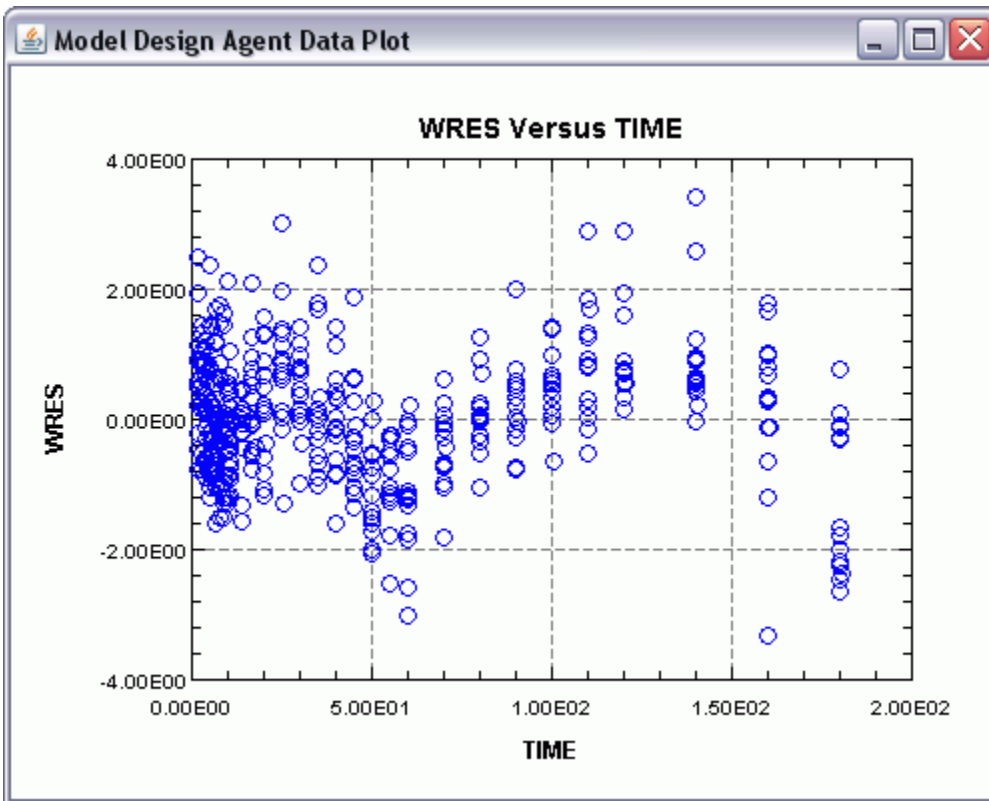
☐ Draw a vertical line at the 1st X data value, as True Value

Plot Title WRES Versus TIME

X - Lable TIME

Y - Label WRES

OK Advanced Cancel



Plots can be sent to a printer by right-clicking on the plot window and selecting **Print**, or can be saved in either PNG or JPG format by right-clicking and selecting **Save**.

It is also possible to plot histograms, together with relevant statistics (mean, median, etc.):

Plot Settings

Select data columns	Symbol	Color
Y_1 axis for: none	●	■
Y_2 axis for: none	●	■
Y_3 axis for: none	●	■
X axis for: WRES	<input type="checkbox"/> Plot for each ID number	
Plot only for: none	= none	records

For missing DV ☐ Eliminate ☐ Highlight ■

☐ Plot the data in the Uniform Scales

	Color
<input type="checkbox"/> Add a vertical line along X = 0	■
<input type="checkbox"/> Add a horizontal line along Y = 0	■
<input type="checkbox"/> Add a unit slope line passing the origin Y = X	■
<input type="checkbox"/> Add linear regression line for	■
<input type="checkbox"/> Add regression percentiles of 99%	■

☐ Plot the data in the Log Scales ☐ log(X) ☐ log(Y)

☒ Plot a histogram for the data X Interval Size: 3.37E-01

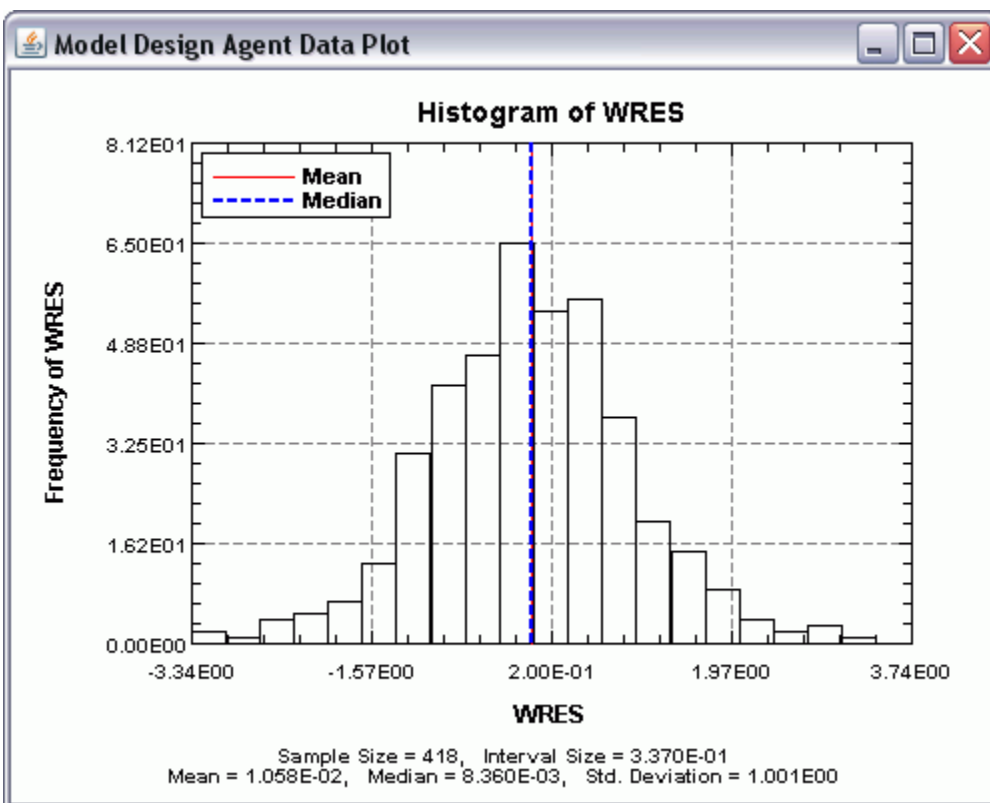
☐ Draw a vertical line at the 1st X data value, as True Value

Plot Title: Histogram of WRES

X - Lable: WRES

Y - Label: Frequency of WRES

OK Advanced Cancel



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