



USER'S MANUAL



Statistical Tool for Agricultural Research

Version 1.0

July 2013

A NOTE TO THE READER:

An electronic copy of this user's manual comes with the STAR installer. The STAR User's Manual may be printed/copied and distributed to any number of users. STAR is a freeware developed for non-profit use. Hence, selling of either the software or the user's manual is prohibited.

Biometrics and Breeding Informatics
Plant Breeding, Genetics and Biotechnology Division
INTERNATIONAL RICE RESEARCH INSTITUTE

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Introduction

Statistical Tool for Agricultural Research (STAR) is a computer program for data management and basic statistical analysis of experimental data. It has a user-friendly graphical interface where items are accessible via drop-down menus. Its graphical interface was created using the Eclipse Rich Client Platform (RCP) and uses the R language and environment for statistical computing and graphics.

STAR has been developed primarily for the analysis of data from agricultural field trials, but many of the features can be used for analysis of data from other sources.

Feature Modules

STAR has the following modules:

- Data management with a spreadsheet
- Descriptive statistics
- Analysis of variance for experimental designs
- Correlation and linear regression analysis
- Graphics
- Utilities for randomization and electronic field book
- Non-parametric data analysis

About the User's Manual

The STAR user's manual provides step-by-step instructions on how to perform certain tasks of interest to users. Screen images have been included as deemed helpful.

Menu items, names of dialogs and form controls are in **bold** letters. Project names, filenames, variable names and directories are *italicized*. Menus appear in the form **File | Open**, which means “choose **Open** from the **File** menu”. All of the examples used in this manual are included when the STAR package is installed.

Getting Started

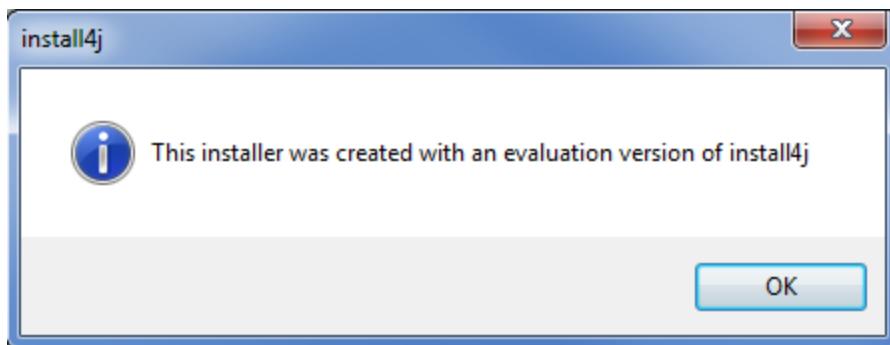
Installation

The installer of STAR and its required R packages can be downloaded from bbi.irri.org. To download the installers, click the links labeled as *STAR 1.0* and *R-Packages 1.0* at the right-hand side of the page.

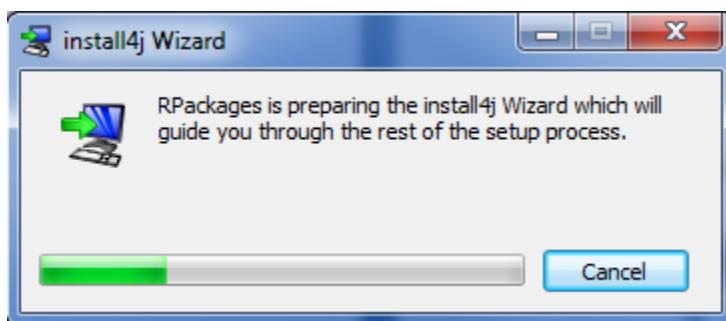
The screenshot shows the IRRI Biometrics and Breeding Informatics website. The top navigation bar includes links for Home, About Us, Products, Trainings, Research, and Contact Us. The 'About Us' section contains a brief description of the group's research support, consultation, and training services. The 'Training and consultation' section highlights enhancing capacity through efficient experiment and genetic design methods. The 'Research' section describes work in plant breeding trials, gene mapping, and selection. The 'Software development' section mentions developing user-friendly tools for data collection and management. On the right side, a 'Products Download' sidebar lists four items: 'Statistical Tool for Agricultural Research STAR 1.0' (highlighted with a red border), 'Plant Breeding Tools PBTools 1.0' (highlighted with a red border), 'STAR and PBTools required R Packages R-Packages1.0' (highlighted with a red border), and 'Android Tablet Application for Data Collection FieldLab V2.2'. Below the sidebar, there is a link to 'Interact with us on' followed by links to Facebook, Twitter, and Scribd.

User need to install *R-Packages* first before installing *STAR*. The steps to install the required R packages are as follows:

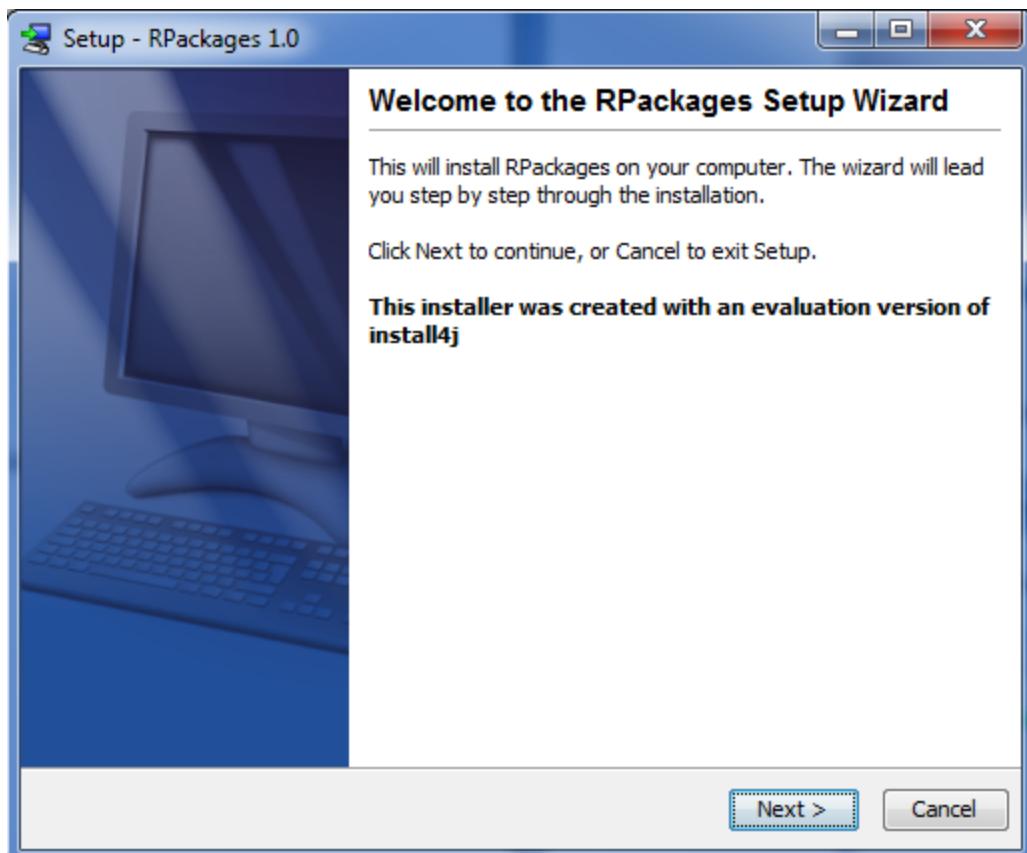
- Double-click the installer icon to launch the setup. A dialog as shown below is displayed. Click the **OK** button.



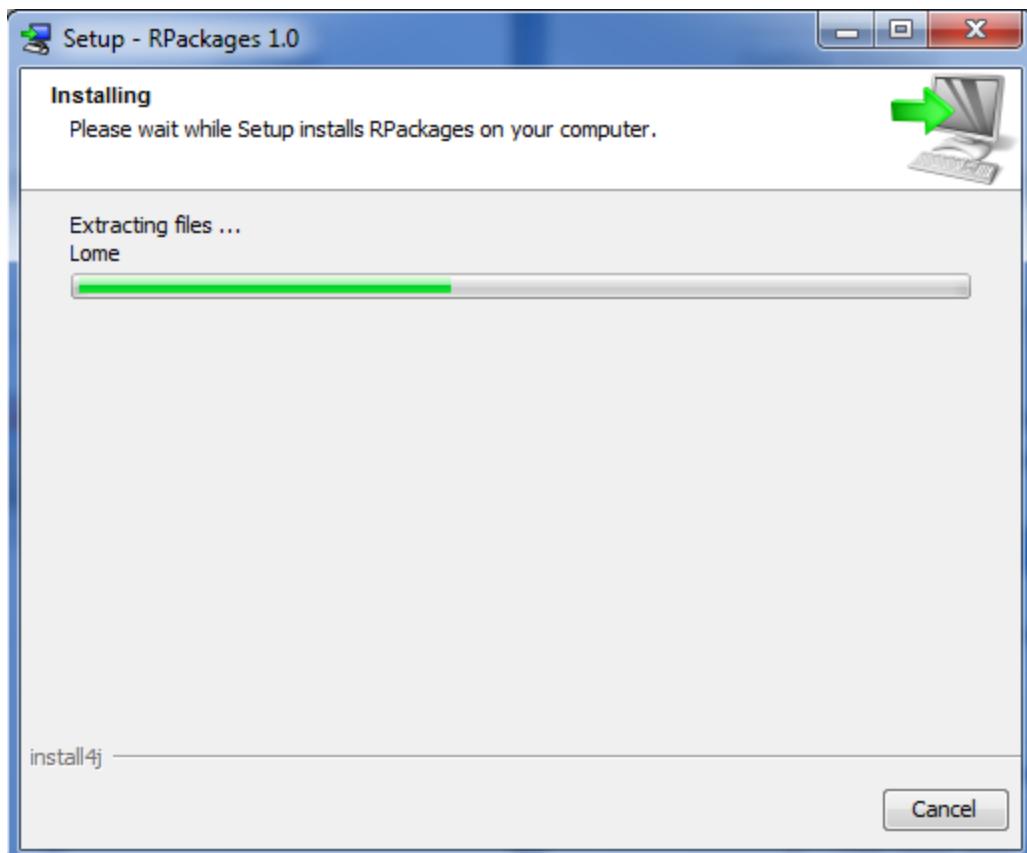
- The next step is the preparation of the wizard. A dialog with progress bar is displayed. Wait until the preparation is completed.



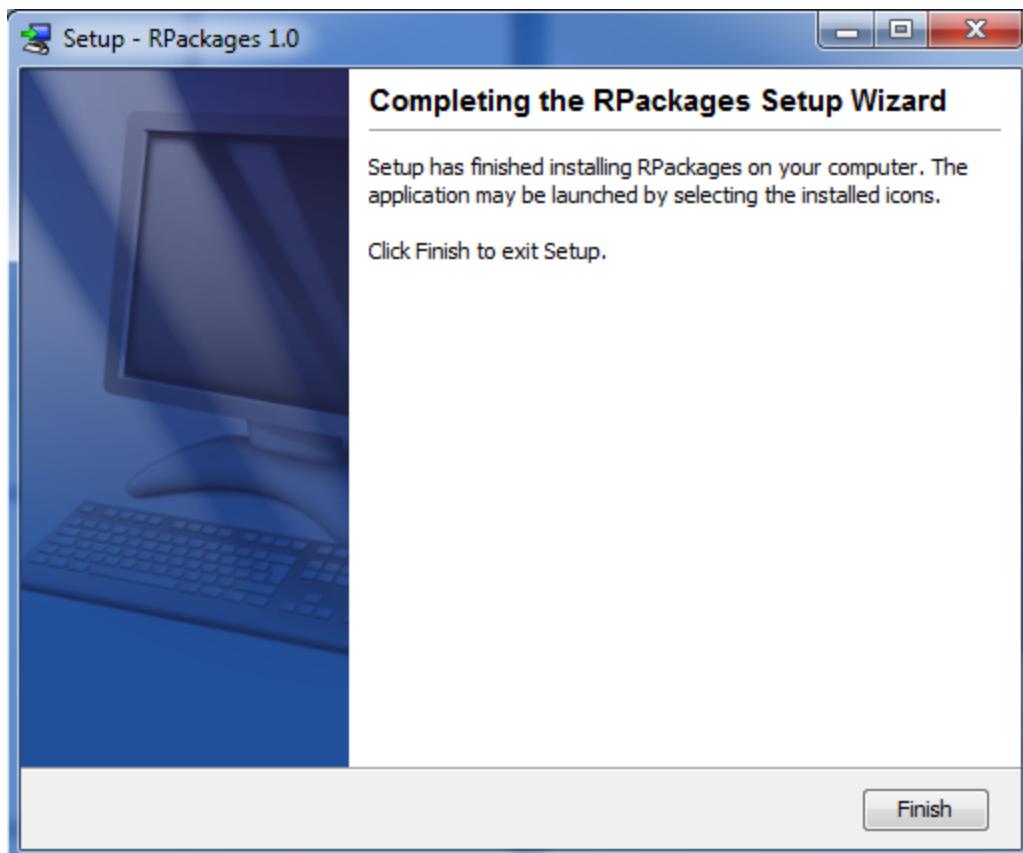
- When installing R Packages for the first time, the **Welcome** dialog as shown below is displayed. Click the **Next** button.



- Wait until the installation is completed.

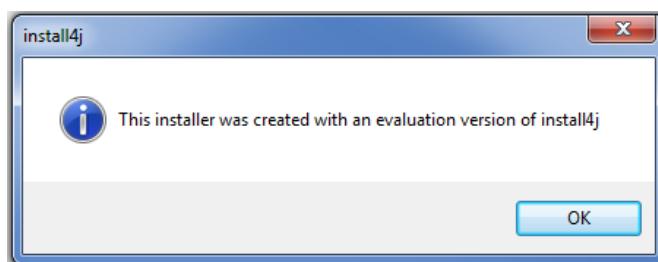


- Click the **Finish** button to exit Setup.

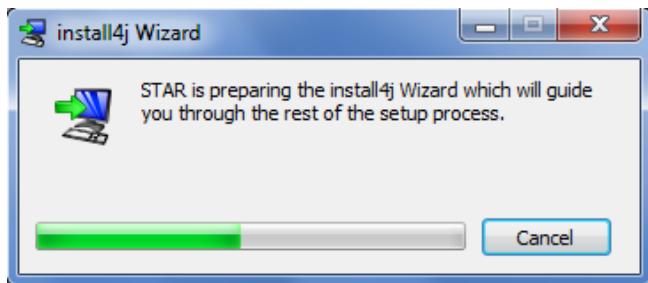


The steps to install STAR are as follows:

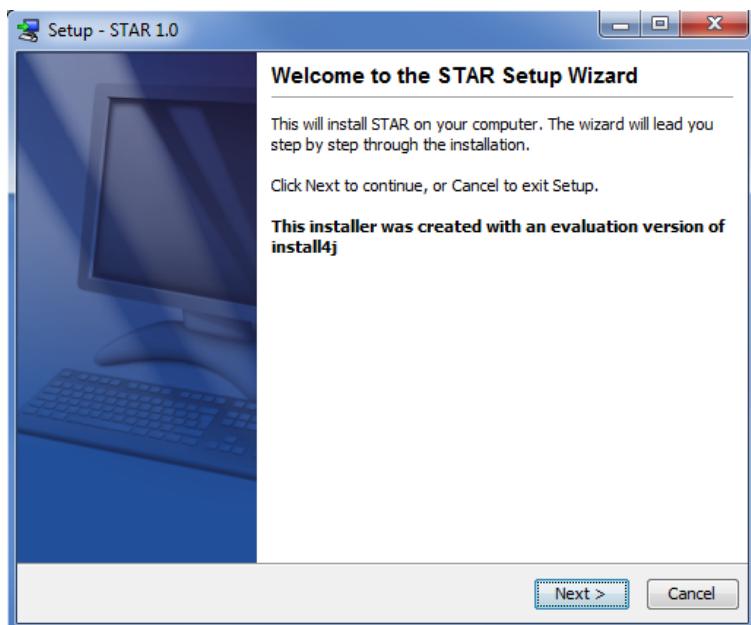
- Double-click the installer icon to launch the setup. A dialog as shown below is displayed. Click the **OK** button.



- The next step is the preparation of the wizard. A dialog with progress bar is displayed. Wait until the preparation is completed.

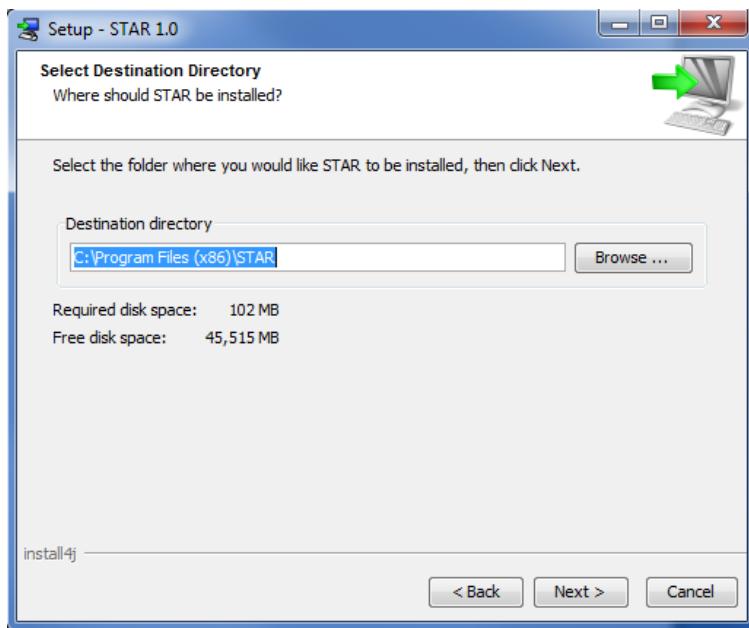


- When installing STAR for the first time, the **Welcome** dialog as shown below is displayed. Click the **Next** button.

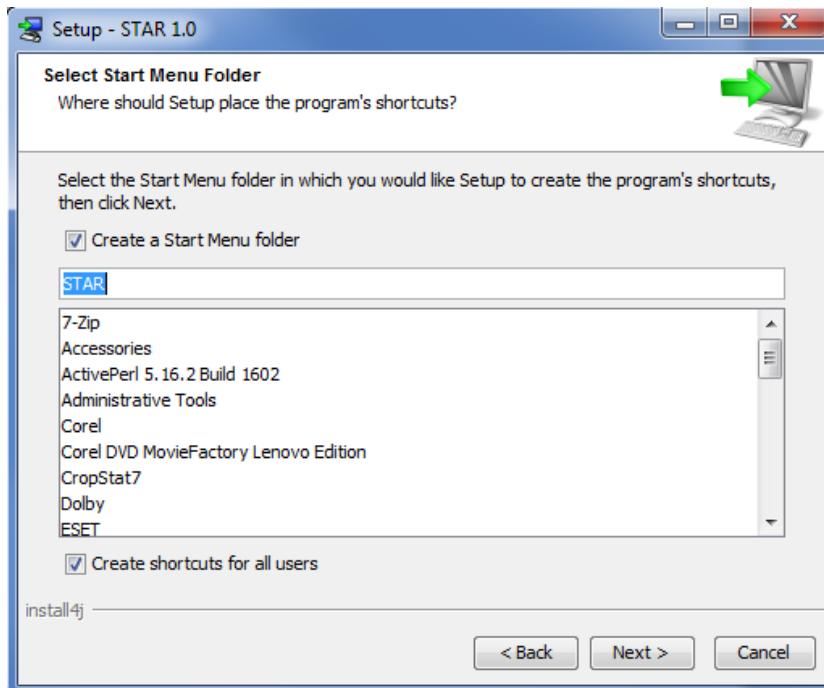


- Select the destination folder, preferably not in **C:\Program Files** as problems were encountered when STAR is installed in this location. Click the **Next** button.

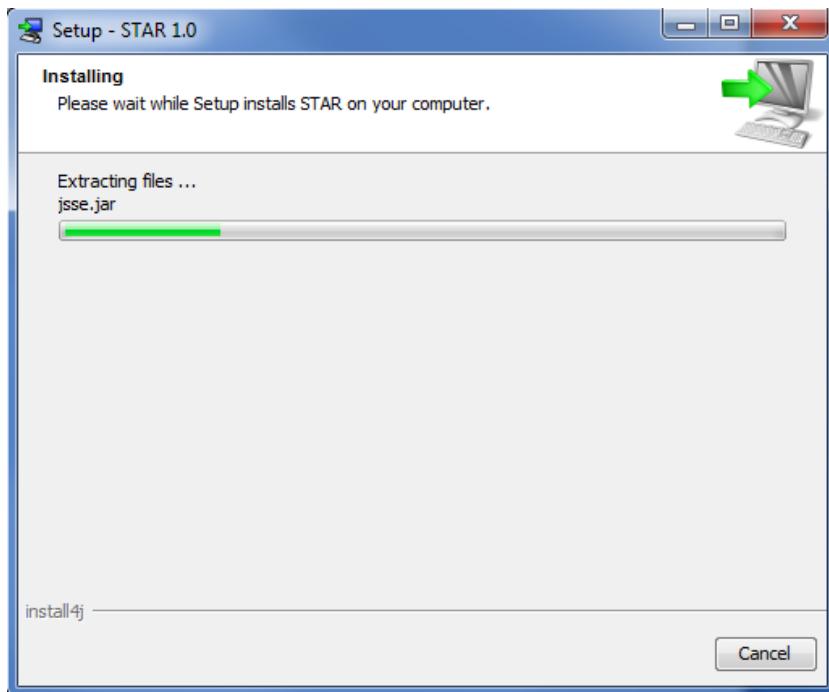
Change screen shot



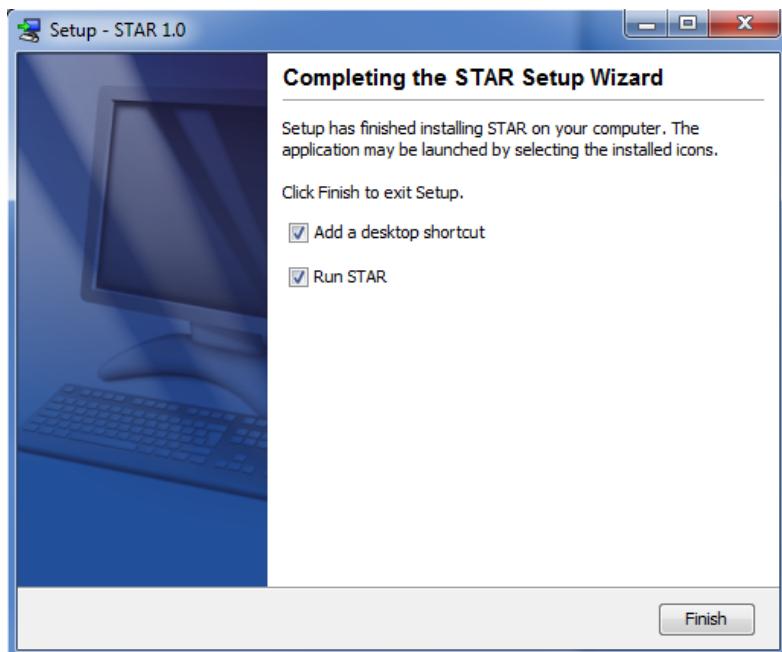
- Select which start menu folder you want to place the STAR icons in and click the **Next** button.



- Wait until the installation is completed.



- Finally, specify if you want to create a desktop icon and run STAR. Click the **Finish** button.



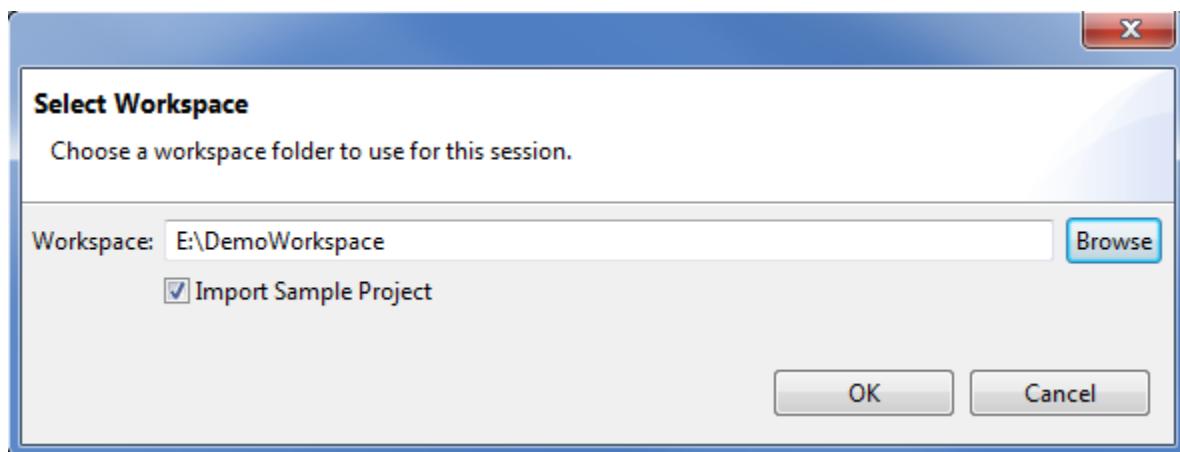
Launching STAR

To launch STAR, double-click the STAR shortcut icon on the desktop (if there is one) or click **Start** on the Windows task bar, choose **All Programs**, then click on the **STAR** folder and click the **STAR** icon.

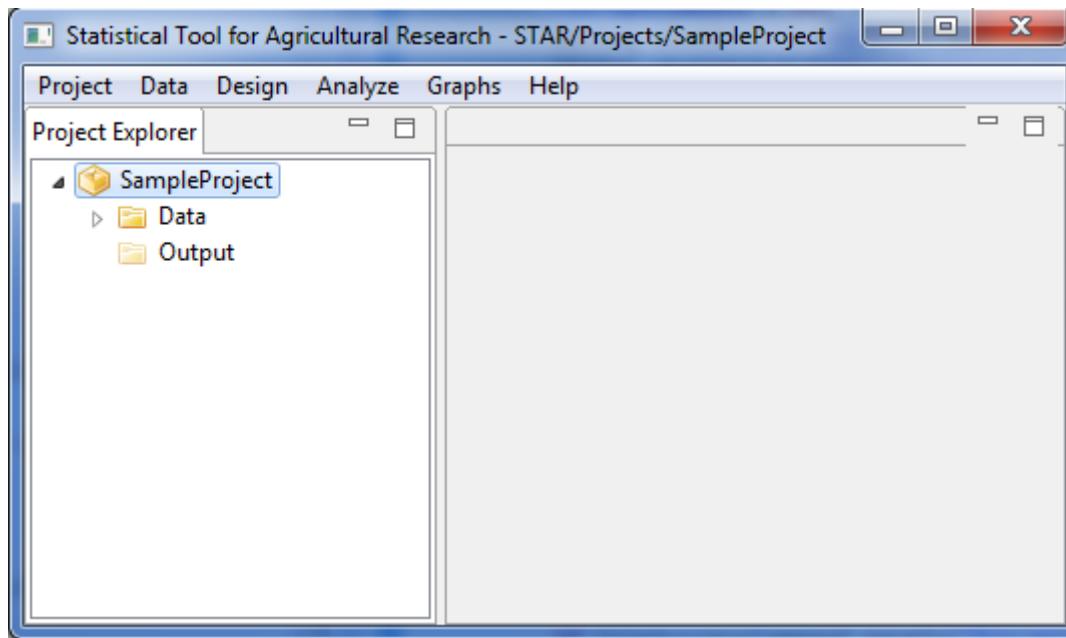
Upon launching, the splash image will appear.



When STAR is launched for the first time, the **Select Workspace** dialog is displayed. A default workspace folder is indicated in the **Workspace** entry box. To indicate a different workspace folder, click the **Browse** button and select the new workspace folder. By default, the checkbox **Import Sample Project** is selected. Then click the **OK** button.



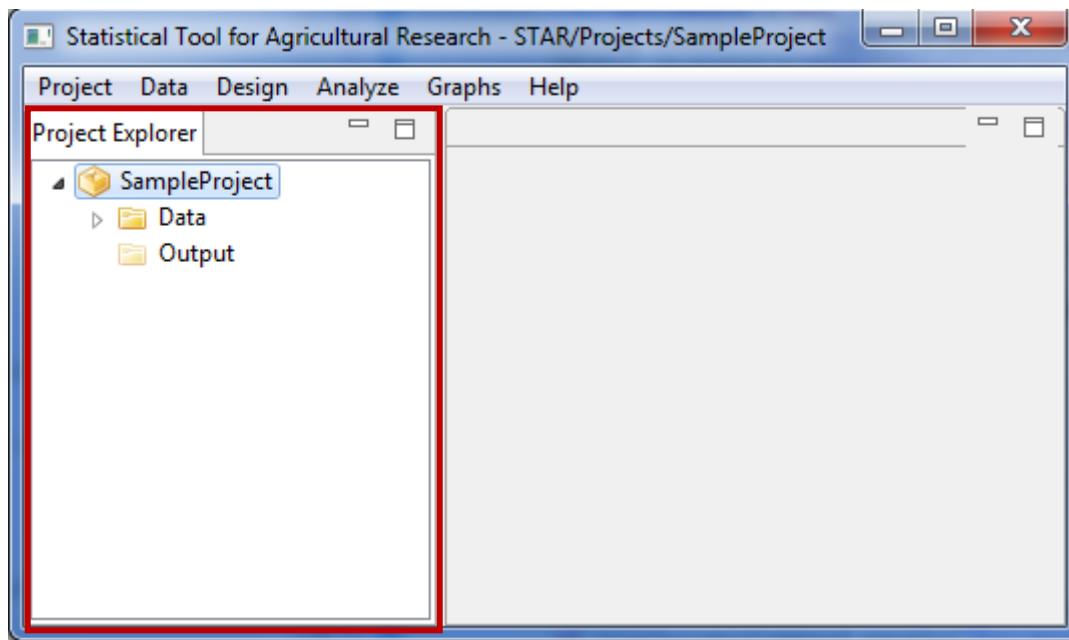
The main window of STAR will appear.



STAR main window has a menu bar and is divided into two panels, the **Project Explorer** panel located on the left-hand side and the **Editor Panel** on the right-hand side.

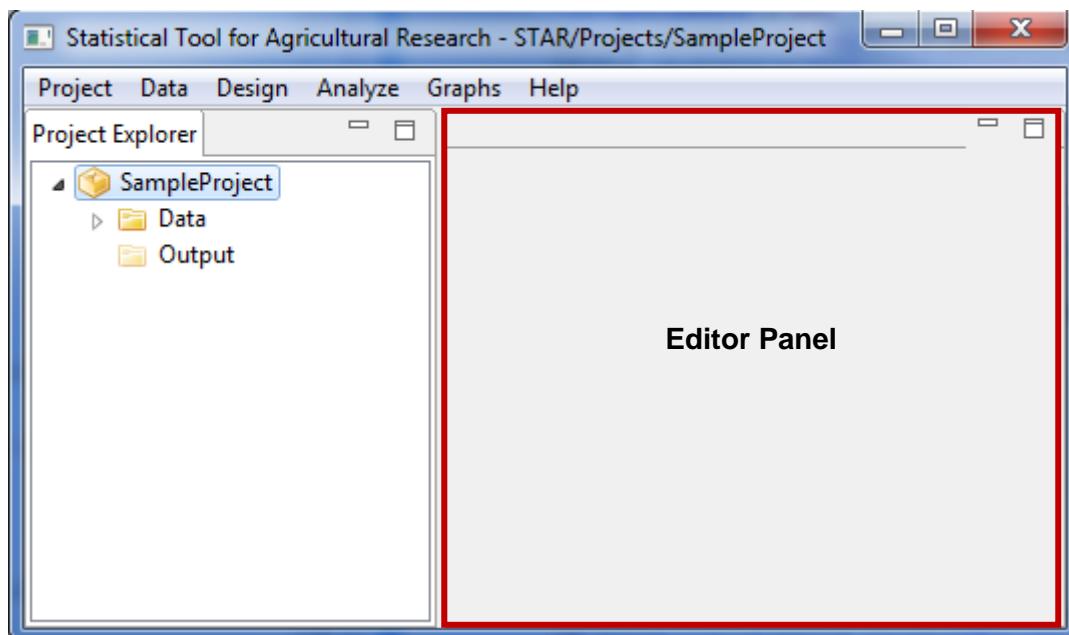
Project Explorer Panel

Project Explorer can be seen at the left-hand side of the main window. It serves as a file manager of the active project, where data and results of the analysis are displayed in a tree. It displays the last opened project from the previous STAR session. When STAR is opened for the first time, a default project names *SampleProject* is displayed with *Data* folder and *Output* folder inside it. The *Data* folder contains some sample datasets that will be used in this manual. The *Output* folder, on the other hand, will contain all output files that will be created when an analysis is performed.



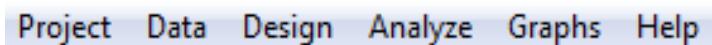
Editor Panel

Editor panel is located at the right-hand side of the main window. It consists of **Data Viewer** tab and the **Result Viewer** tab. By default, the editor panel is empty.

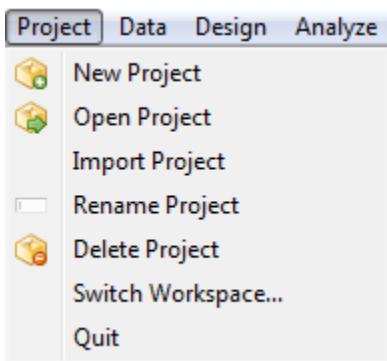


Menu Bar

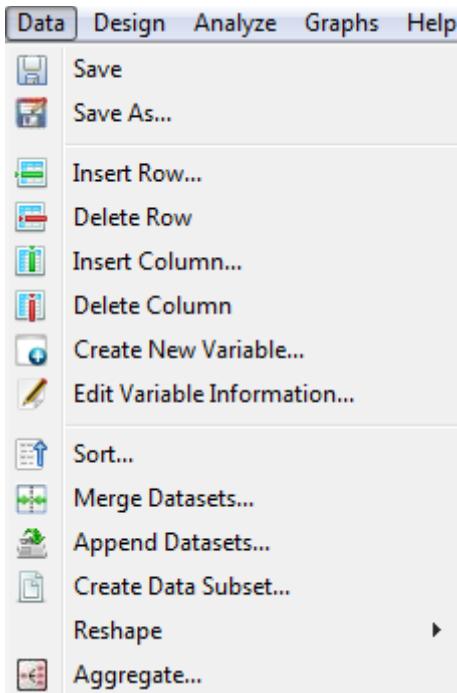
Most of the tasks that you perform in STAR start with menu selections. There are six drop-down menus available and this are:



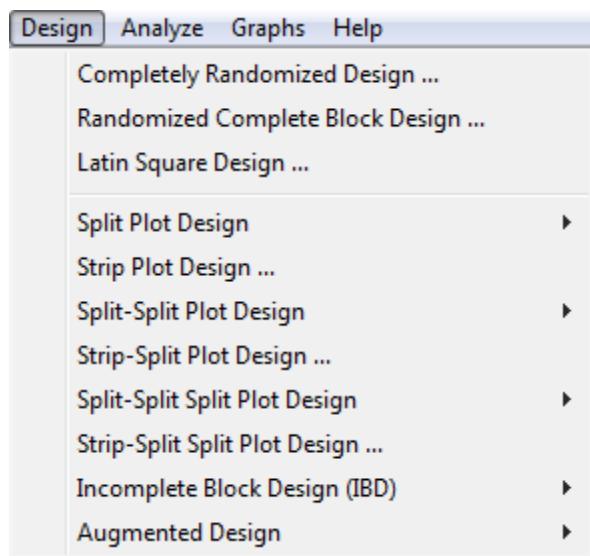
Project Menu contains functions for creating and managing project. This menu can also be used to quit or terminate sessions in STAR. It contains the following submenu items:



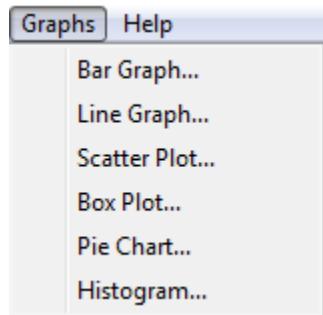
Data Menu contains functions for reading, managing and manipulating datasets. Items under this menu become visible only when a data in CSV format is displayed in the active tab of the editor panel. It contains the following submenu items:



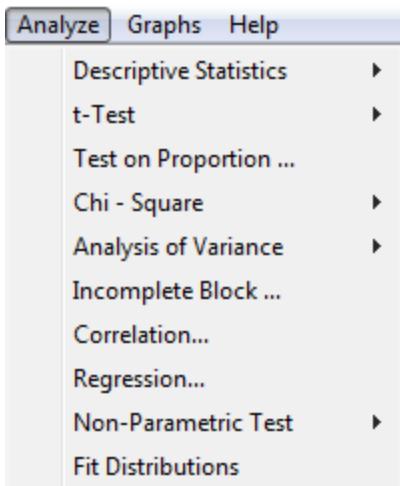
Design Menu contains functions for generating random assignment of factor levels for commonly used experimental design. It contains the following submenu items:



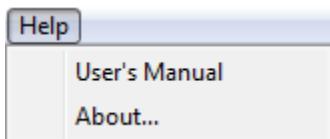
Graph Menu contains functions for creating the basic graphs. It contains the following submenu items:



Analyze Menu contains functions to perform statistical analysis. Items under this menu become visible only when a data in CSV format is displayed in the active tab of the editor panel. It contains the following submenu items:

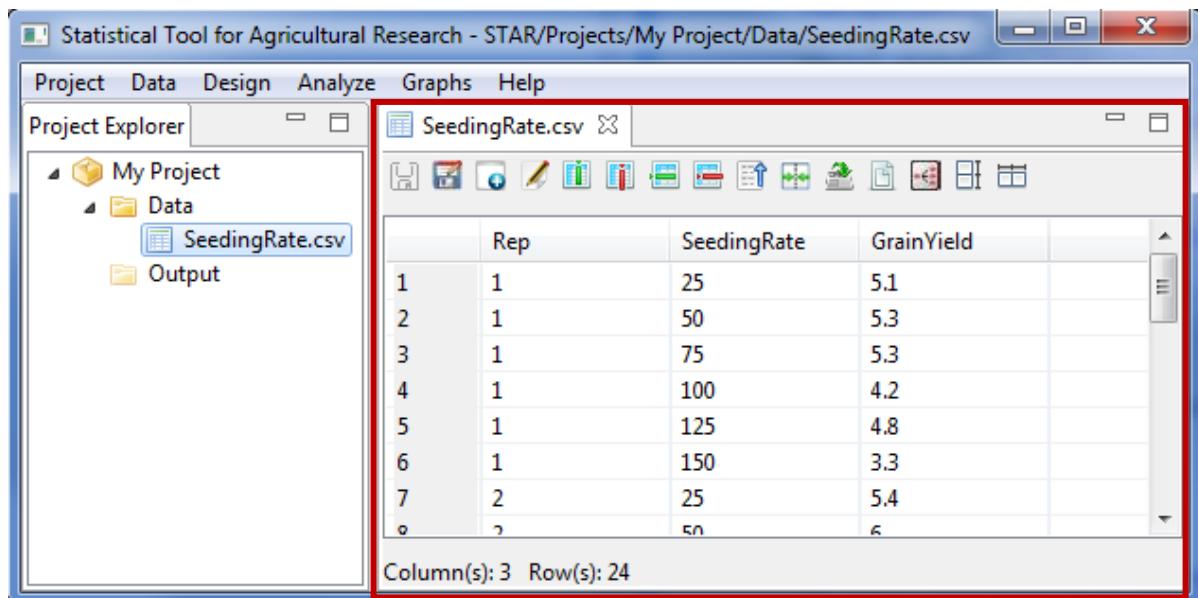


Help Menu used to access STAR's Help System or User's Manual. It contains the following submenu items:



Data Viewer

Data Viewer tab is displayed in the editor panel when a data in CSV format is double-clicked from the Project Explorer tree. It is used for viewing data in spread-sheet format, editing data values and performing data management. Several **Data Viewer** tabs can be seen simultaneously inside the **Editor Panel**. Each Data Viewer tab contains toolbars which can be used for managing the data. The toolbars have the same functionalities as the options under the **Data** menu.

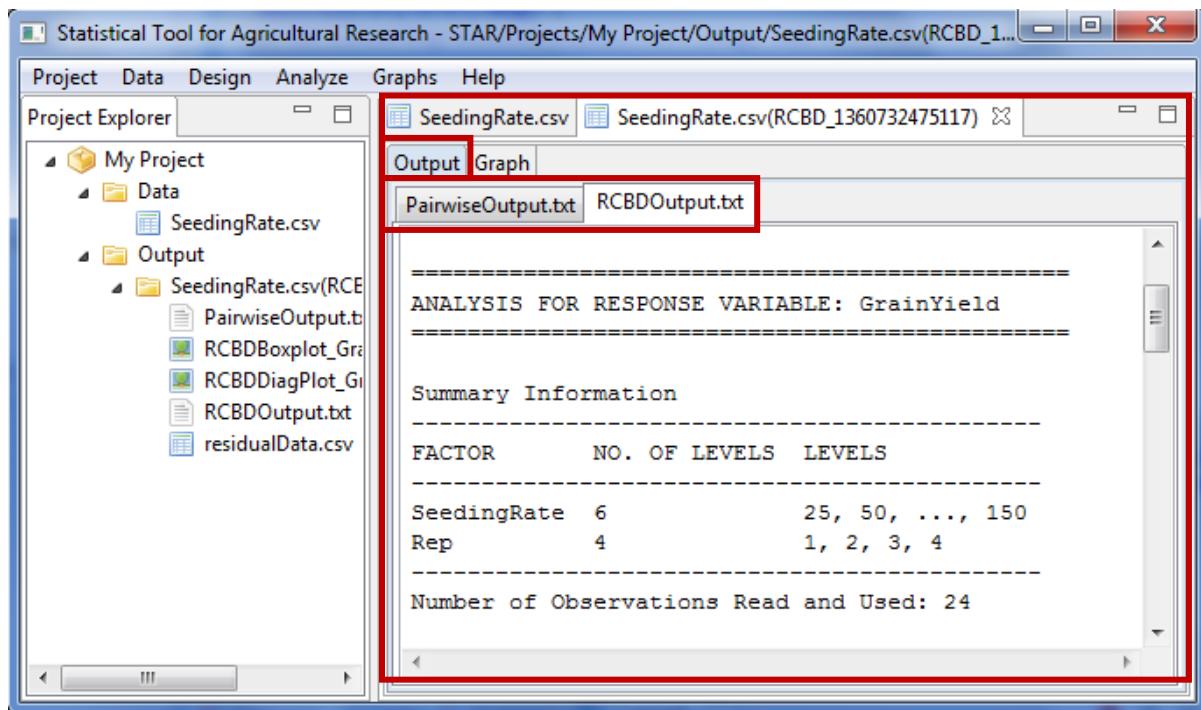


The name of the tab indicates the name of the dataset. When an asterisk appears in the tab

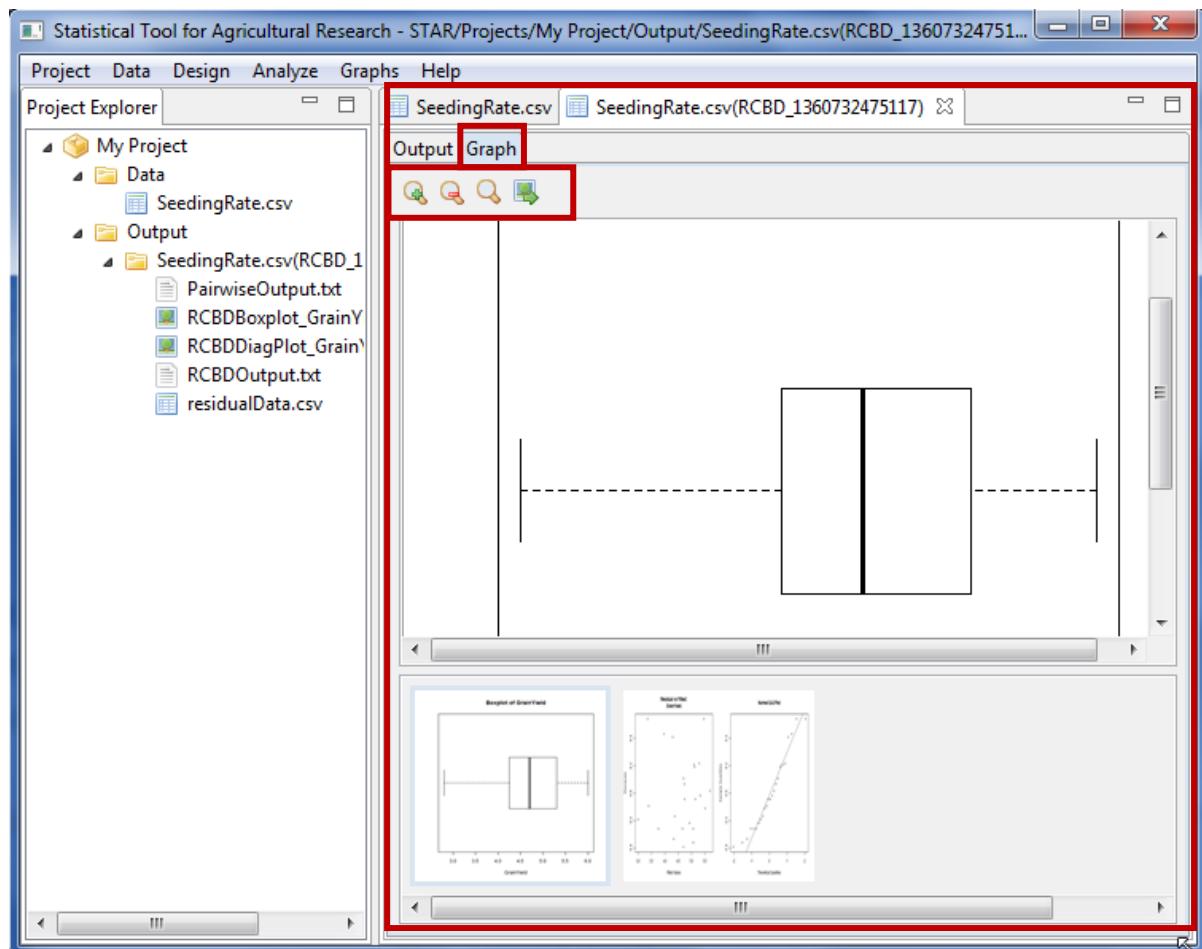
name it indicates that there has been modification made in the dataset and user needs to save the dataset for the modification to take effect. If a data with unsaved changes is used in an analysis or used in creating graphs, the original dataset will be used not the modified one. If a Data Viewer with unsaved changes is closed, the user will be prompted to save the changes.

Result Viewer

Results Viewer tab is displayed in the editor panel when an analysis is performed or by double-clicking a results folder inside the *Output* folder. Depending on the contents of the results folder, the Result Viewer may have an *Output* page and/or the *Graph* page.



All outputs in *txt* format are displayed in the *Output* page while all graphical outputs in *png* format are displayed in the *Graph* page. The *Graph* page has toolbars that can be used to minimize, maximize, and view the graph to normal size and to export graph to external sources. To view other graphs in the page, the left and right arrow keys can be used.

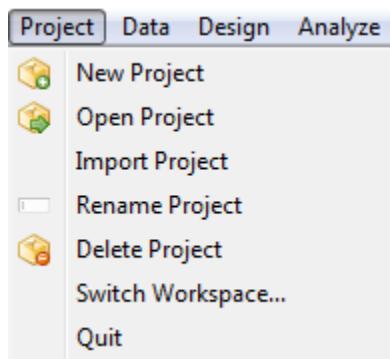


Project and File Management

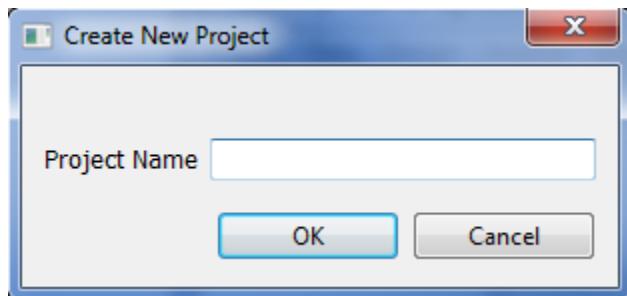
Creating New Project

Several projects can be created in STAR. However, only one project can be considered as the active project and is visible in the Project Explorer panel. The steps for creating new project are listed below.

- Select **Project | New Project** from the main menu.



- The **Create New Project** dialog box will appear. In the **Project Name** field, specify a name of the new project.

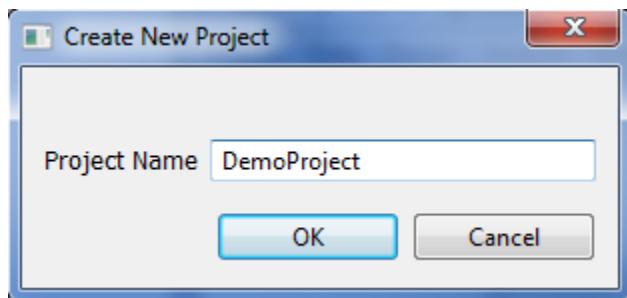


In naming a project, the following rules apply:

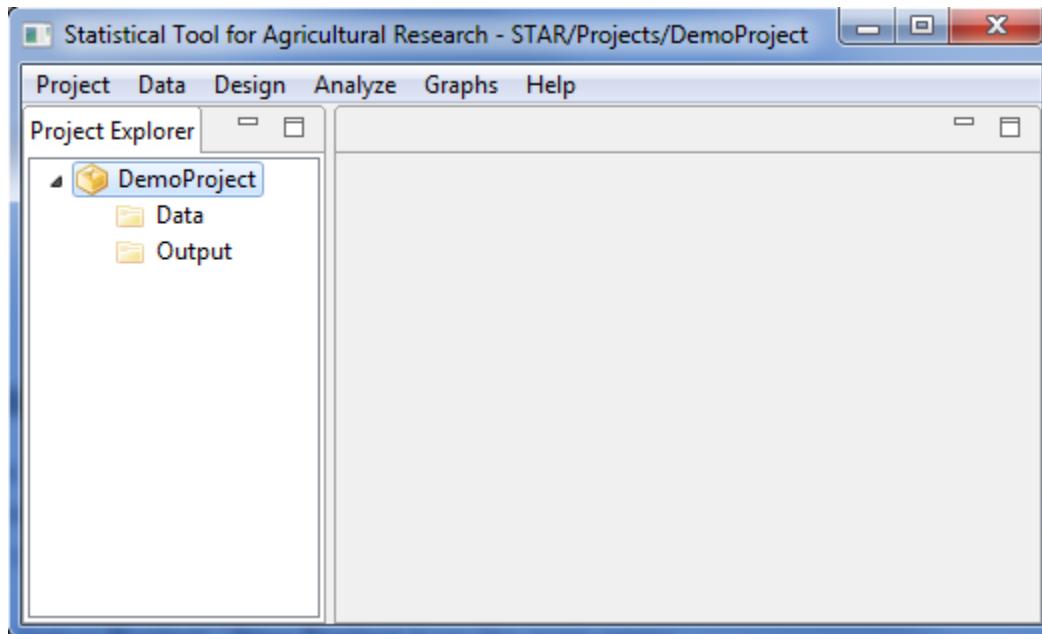
- The name must start with a letter. The remaining characters can be any letter, any digit, a period, underscore, blank or dash.

- The last character of the name should not be a period, underscore, blank or dash
- The length of the name should not be less than 4 characters.
- The name must be different from the existing project names.
- The name is not case sensitive.

For the example, type *DemoProject*. The completed dialog box will appear as shown below:



- Click the **OK** button. The new project named *DemoProject*, will now be displayed in the **Project Explorer** panel. By default, two empty folders under the project name will be automatically created, the *Data* and *Output* folders. Note that these folders cannot be deleted, rename or move to another location.

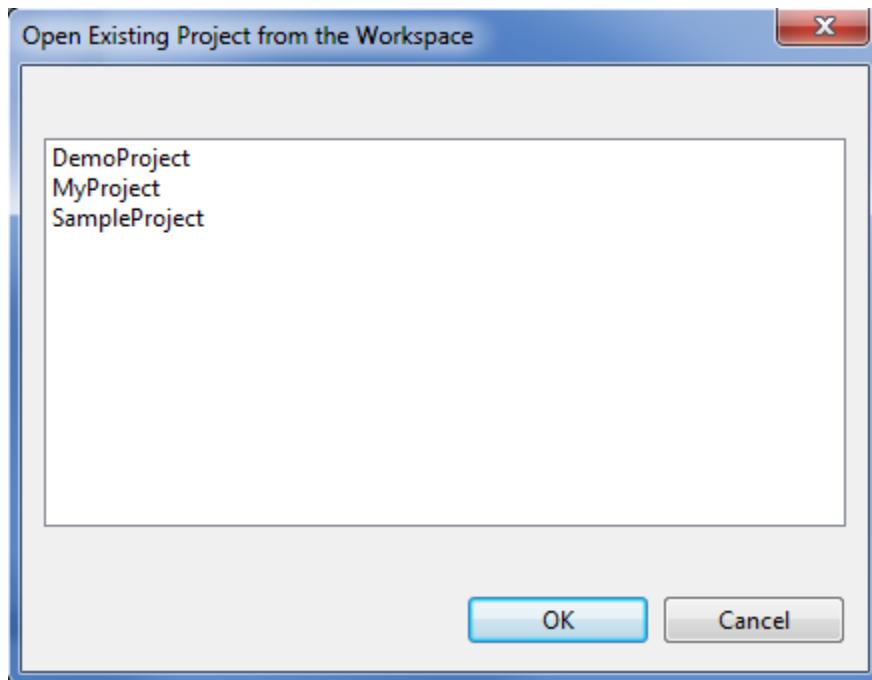


Note: As part of the examples, create another folder named *MyProject*.

Open Existing Project

The steps for opening existing project inside the STAR workspace are listed below.

- Select **Project | Open Project** from the main menu.
- The **Open Existing Project from the Workspace** dialog box will appear. The list of all existing projects in the workspace can be seen.

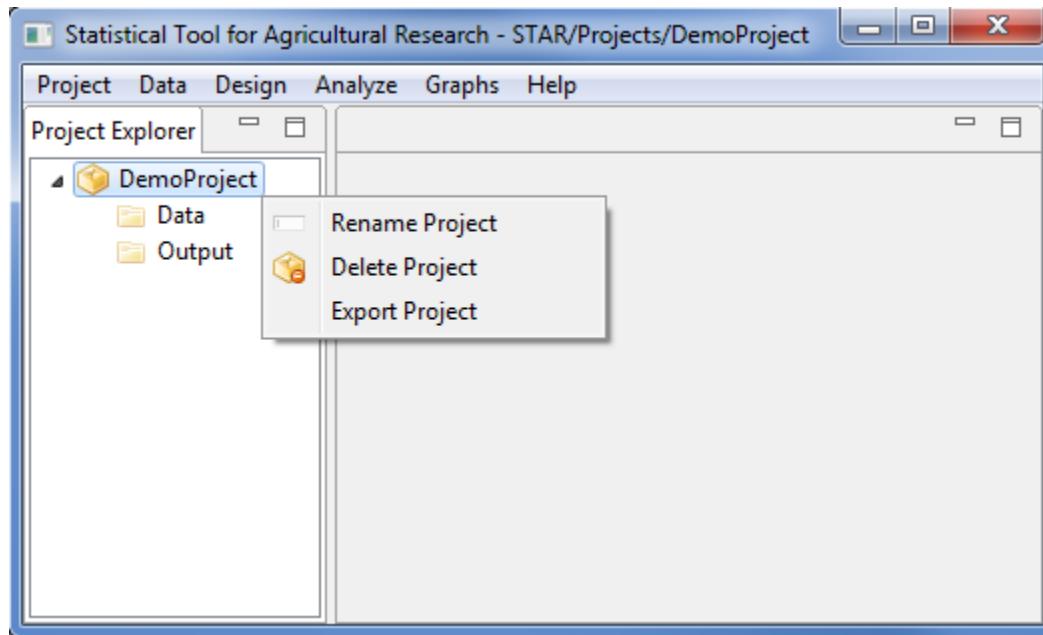


For the example, select the project named *DemoProject*. Click the **OK** button. *Demo Project* should now be the active project in the **Project Explorer**.

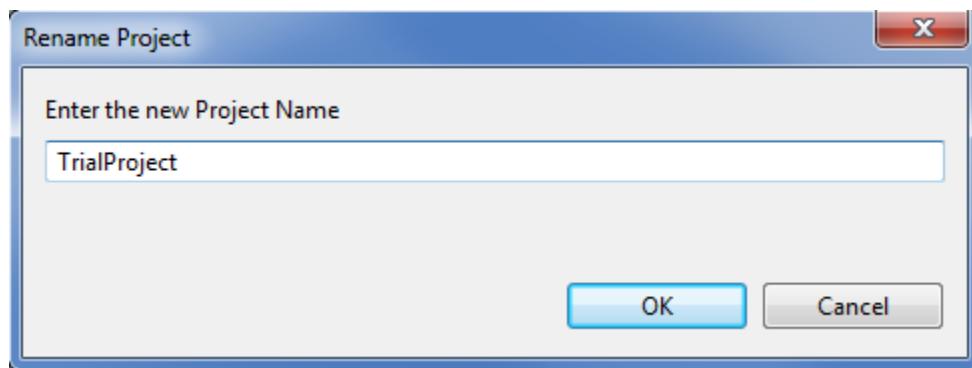
Renaming Project

The steps for renaming the active project are listed below.

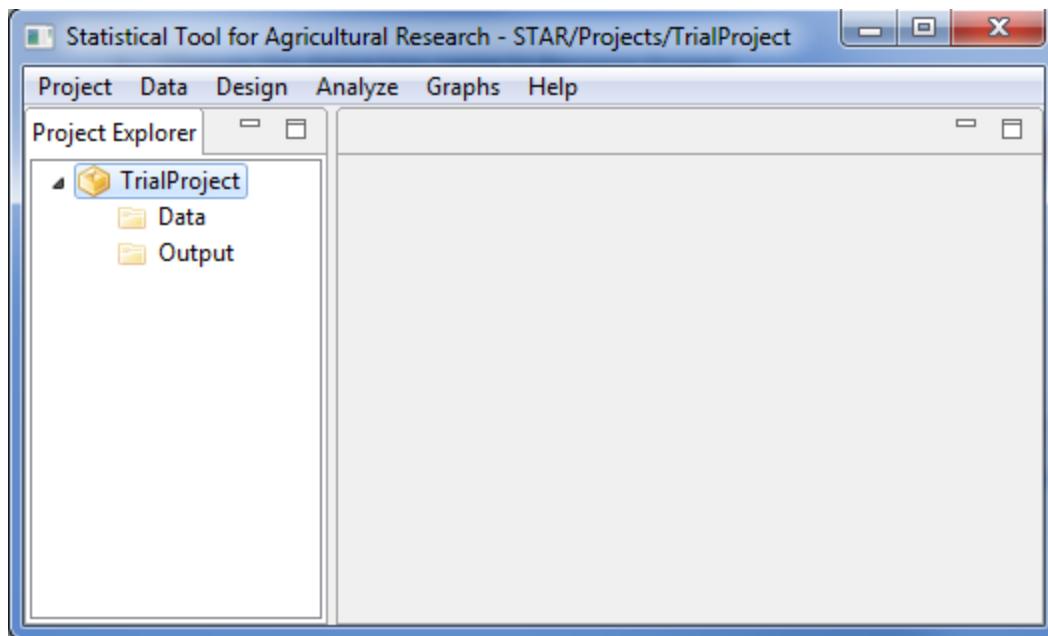
- Right-click on the active project, say *DemoProject*, then select **Rename Project** or select **Project | Rename Project** from the main menu.



- The **Rename Project** dialog box will appear. In the **New Project Name** field, specify a new project name, say *Trial Project*. Click the **OK** button.



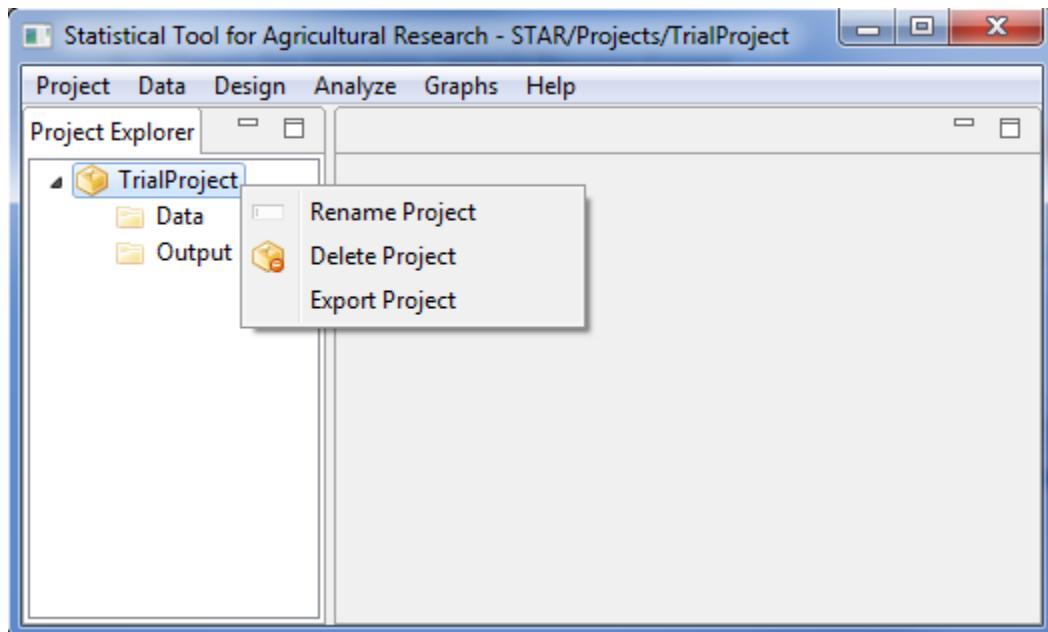
- The project should be displayed in the **Project Explorer** with the new name.



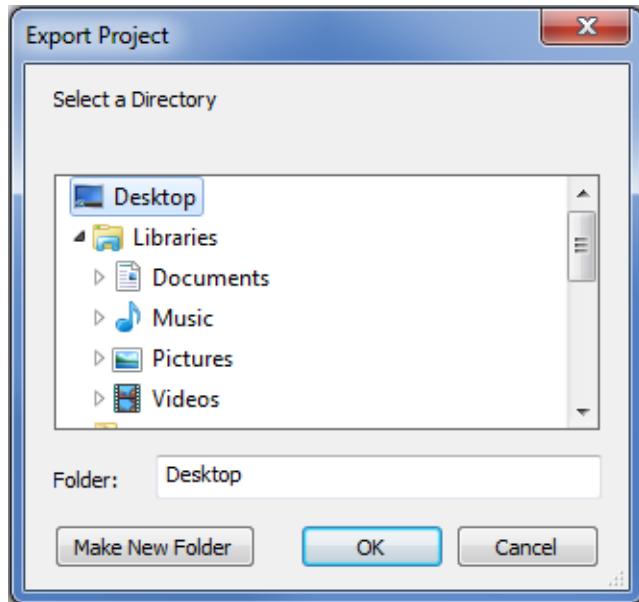
Exporting Project

If the user wants to save the active project to a different directory, the export project feature can be used. The steps are listed below.

- Right-click on the active project, say *TrialProject*, then select **Export Project**.



- The **Export Project** dialog box will appear. Select the directory where the active project will be saved. For the example, choose *Desktop*. Click the **OK** button.

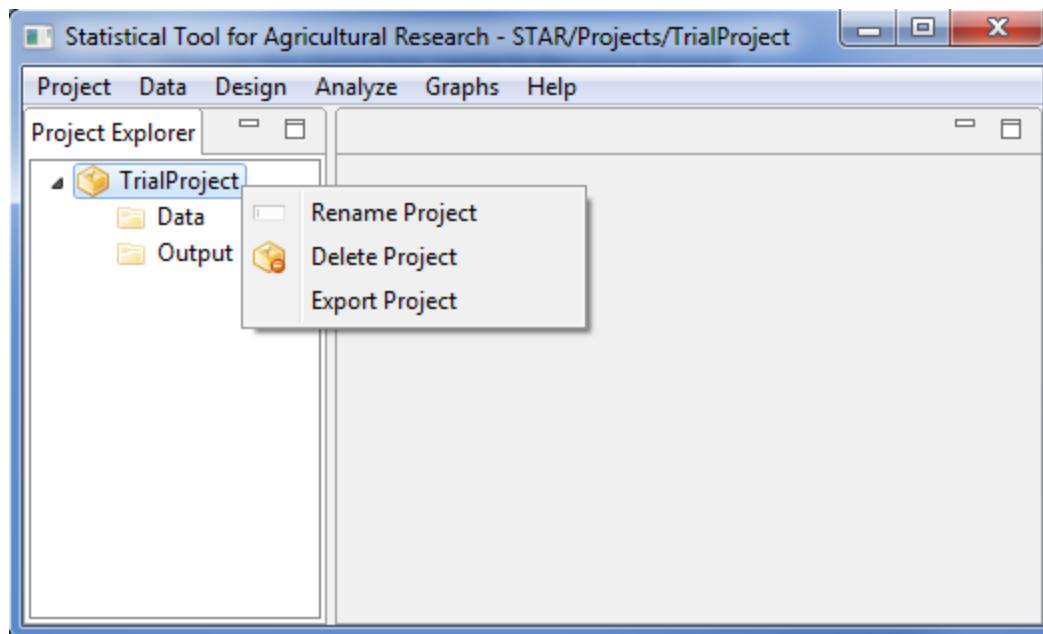


- The *TrialProject* folder is now on the desktop.

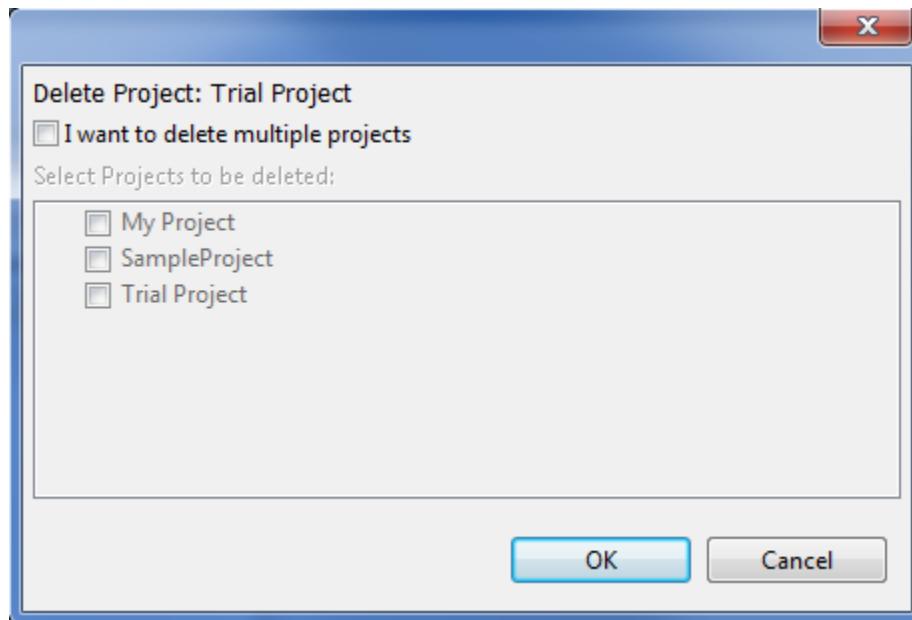
Deleting Project

The steps for deleting an existing project inside the STAR workspace are listed below.

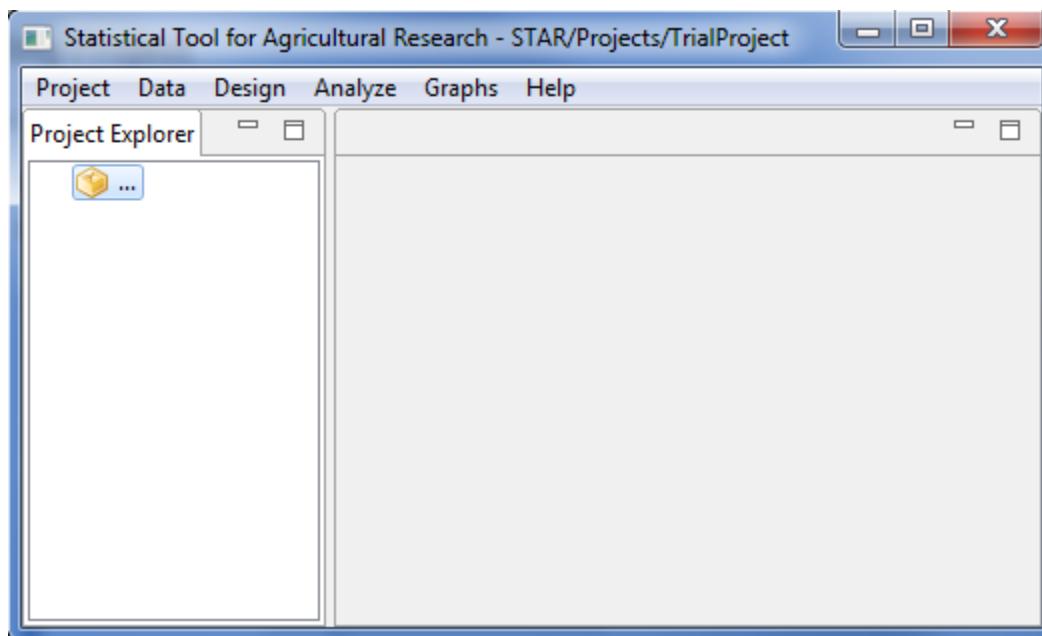
- Right-click on the active project, say *TrialProject* then select **Delete Project** or select **Project | Delete Project** from the main menu.



- Another dialog will be displayed. Click on the check box labeled **I want to delete multiple projects** if multiple projects are to be deleted. Then select from the list the projects to be deleted. For the example, delete only *TrialProject* by clicking the **OK** button.



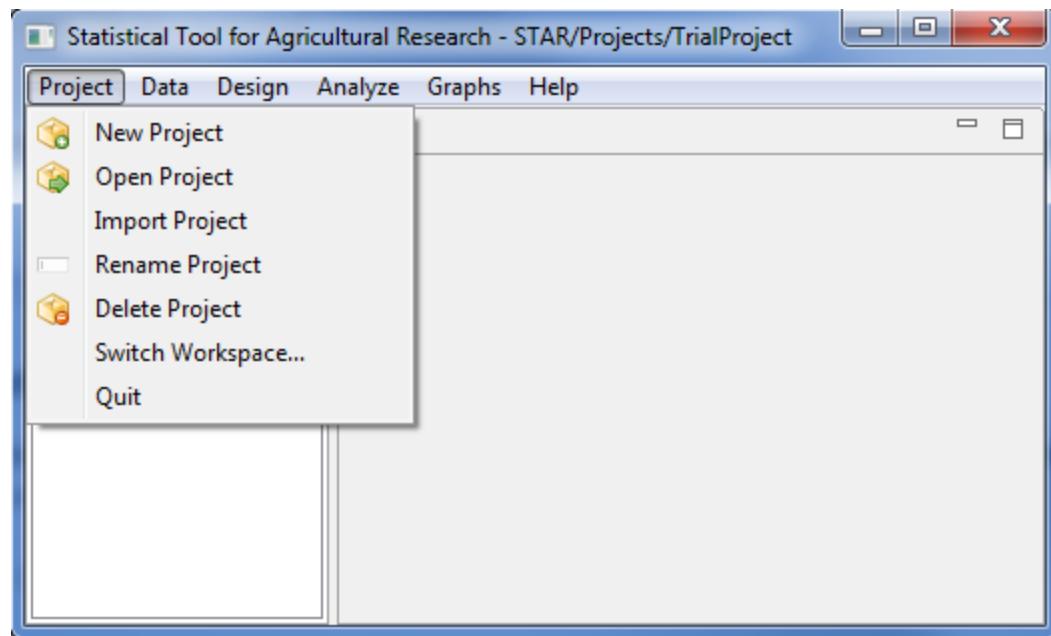
- Since *TrialProject* is now deleted from the STAR workspace, there is no active project displayed in the Project Explorer as shown below.



Importing Project

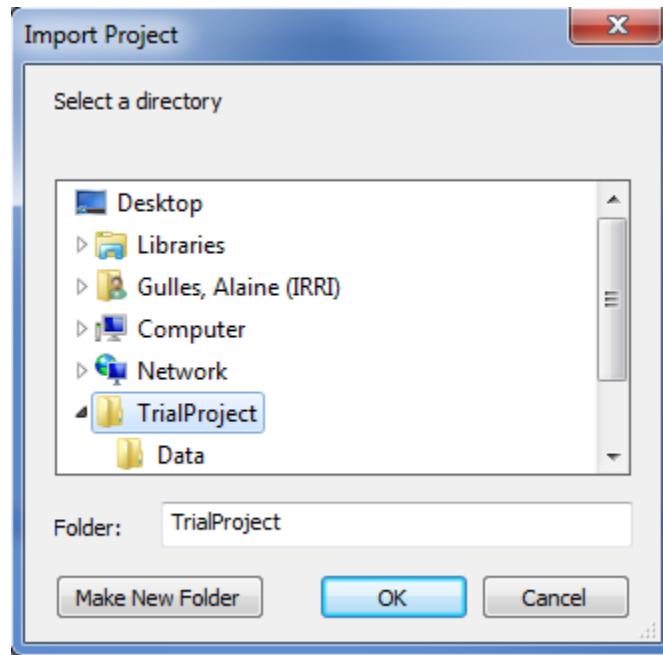
Projects, as long as it is a valid STAR project, can be saved inside the STAR workspace by using the import project feature. The steps are listed below.

- Click **Project | Import Project** from the main menu.



- Select the project folder that will be imported.

For the example, select *TrialProject* folder on the desktop. Click the **OK** button.



- The *TrialProject* is now the active project in the **Project Explorer**.

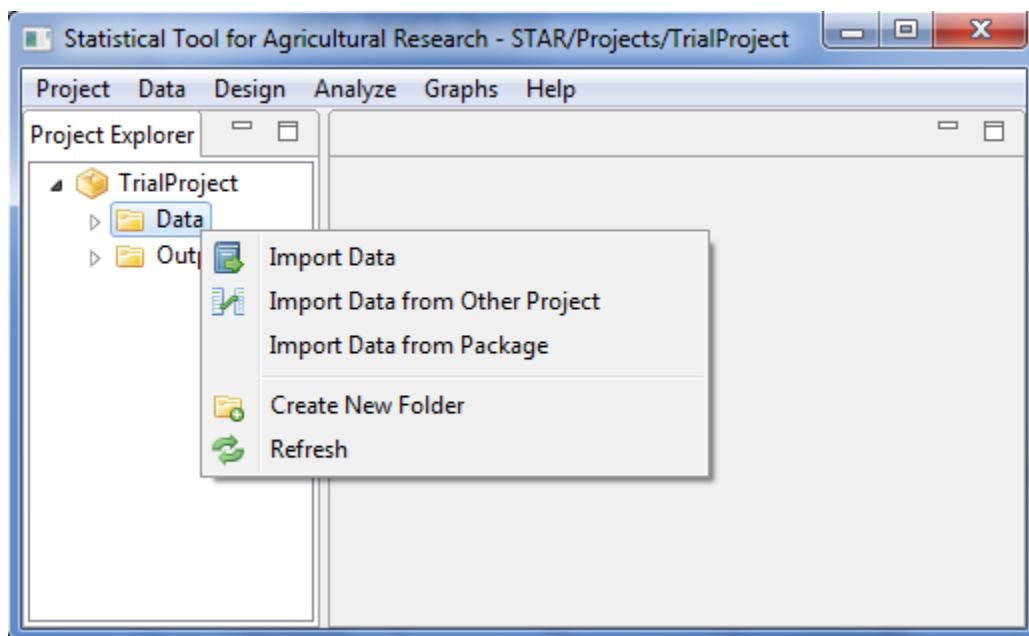
Importing Data from External Source

There are three file formats that STAR accepts to import from external source namely:

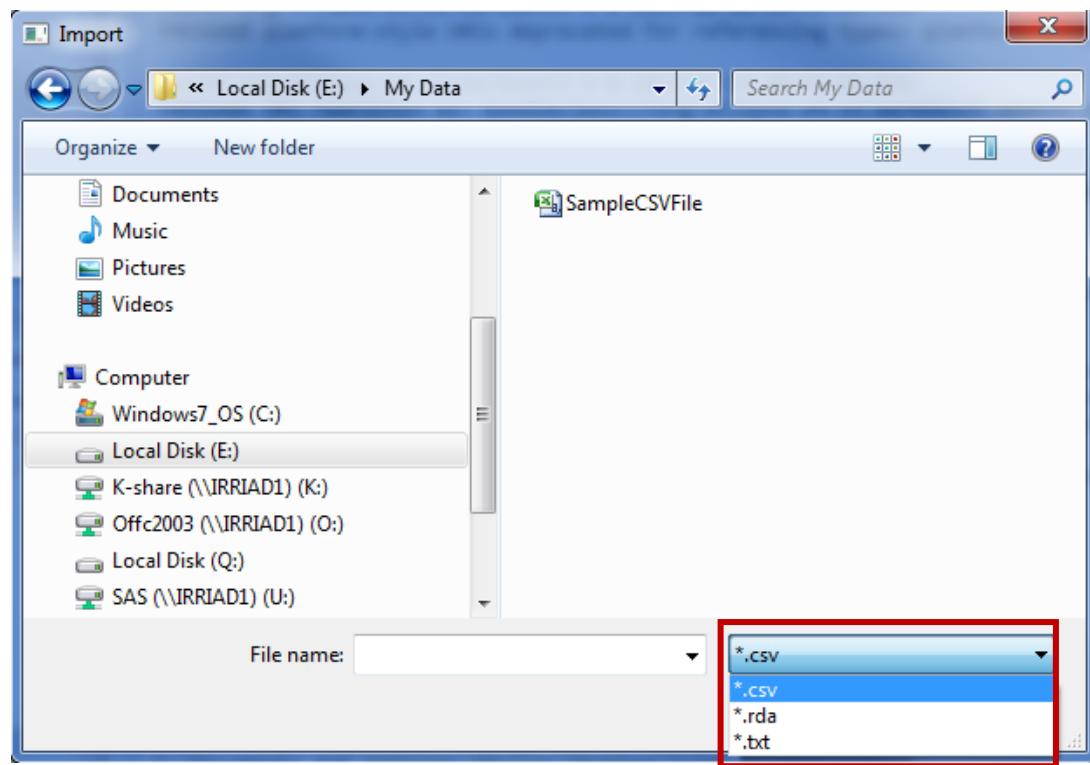
- i. R datasets. These are datasets that were saved in the R environment and have an extension .rda, .Rda, .RDA, or .Rdata;
- ii. text files. These are datasets with extension .txt whose file delimiter can be a tab, space, comma or a semi-colon; and
- iii. comma-separated value files. These are datasets with extension .csv.

The general steps for importing data from external source are listed below:

- On the **Project Explorer** panel, right-click the *Data* folder of the project named *TrialProject*. A pop-up menu will appear. Choose **Import Data**.

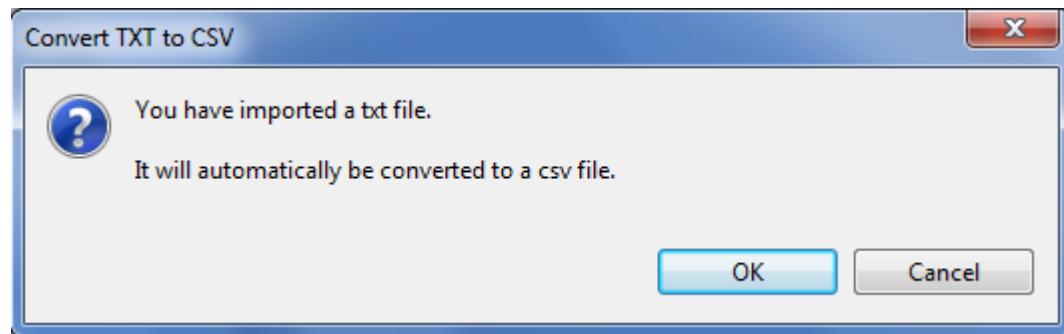


- The **Import** dialog box will appear. Choose the appropriate file type to be imported in the File of Types drop-down box. The default file type is ***.csv**. Go to the directory where the file to be imported is located. Select the file or type the file name on the **File name** text box.

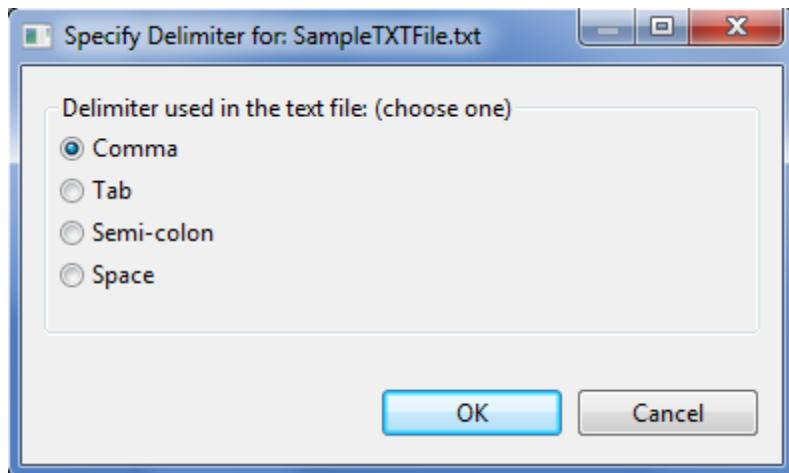


- Click the **Open** button.

If the ***.txt** or the ***.rda** file type is chosen, a message dialog box will appear indicating that the text or r data files will be automatically converted to a csv file. Click the **OK** button.



Further, if the ***.txt** file type is chosen, the **Specify Delimiter** dialog box will appear. Choose the appropriate delimiter of the text file to be open then click the **OK** button.

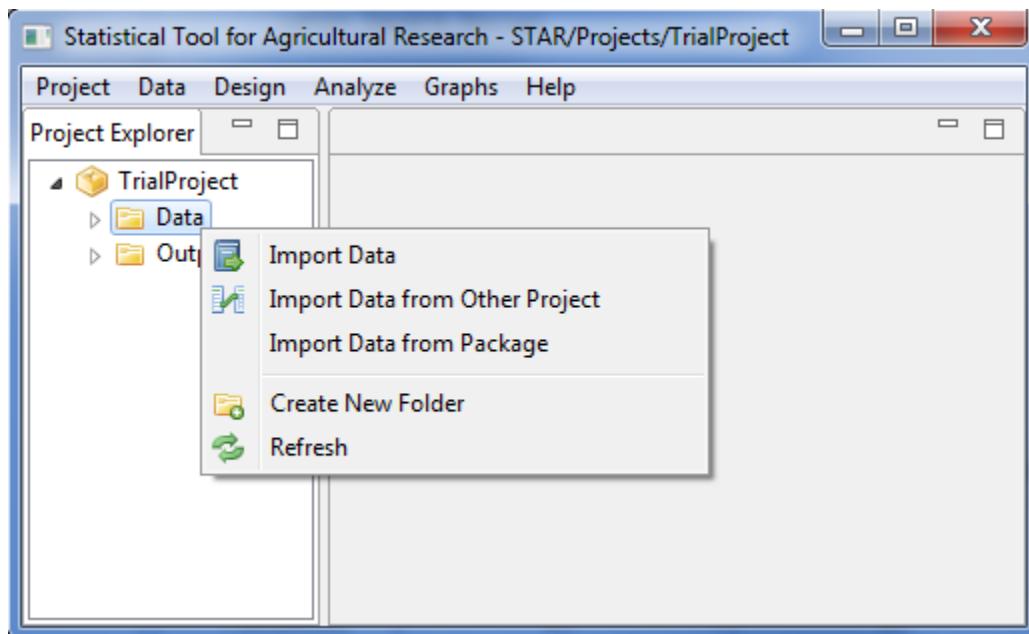


- The newly imported data will now be displayed inside the *Data* folder of the active project in the **Project Explorer**. To view the data in a spreadsheet format, double-click the icon of the data file.

Importing Data from Other Project

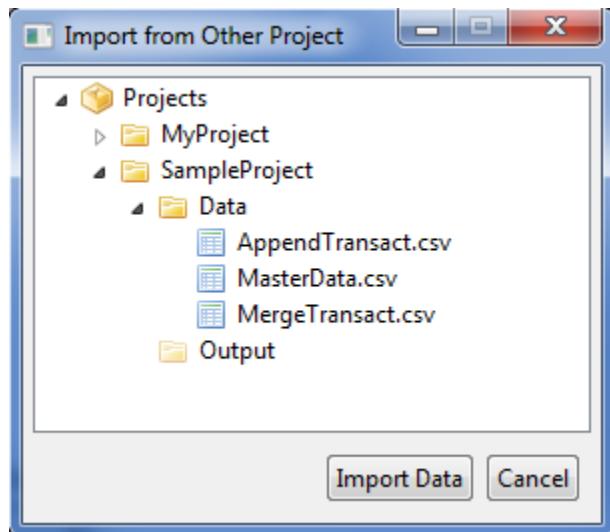
The steps for importing data from other project are listed below:

- On the **Project Explorer** panel, right-click the *Data* folder of the project named *TrialProject*. A pop-up menu will appear. Choose **Import Data from Other Project**.

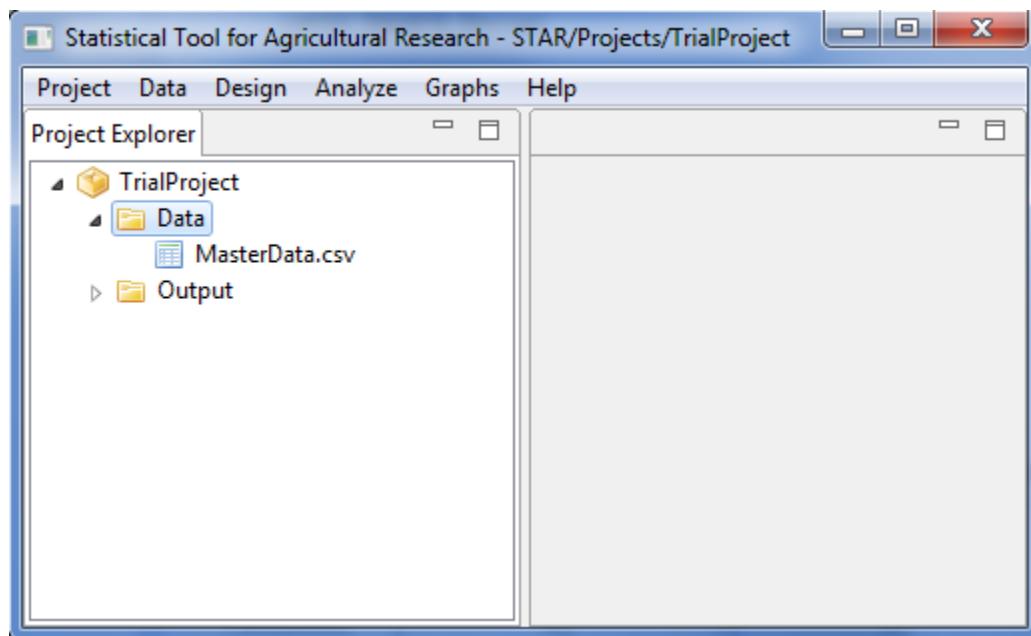


- The **Import from Other Project** dialog box will appear. This dialog box contains all existing projects in STAR. Select one or several project folders, one or several folders within projects or one or several data files. Choose the data files to be imported.

For the example, choose *MasterData.csv* from *Projects | SampleProject | Data*.



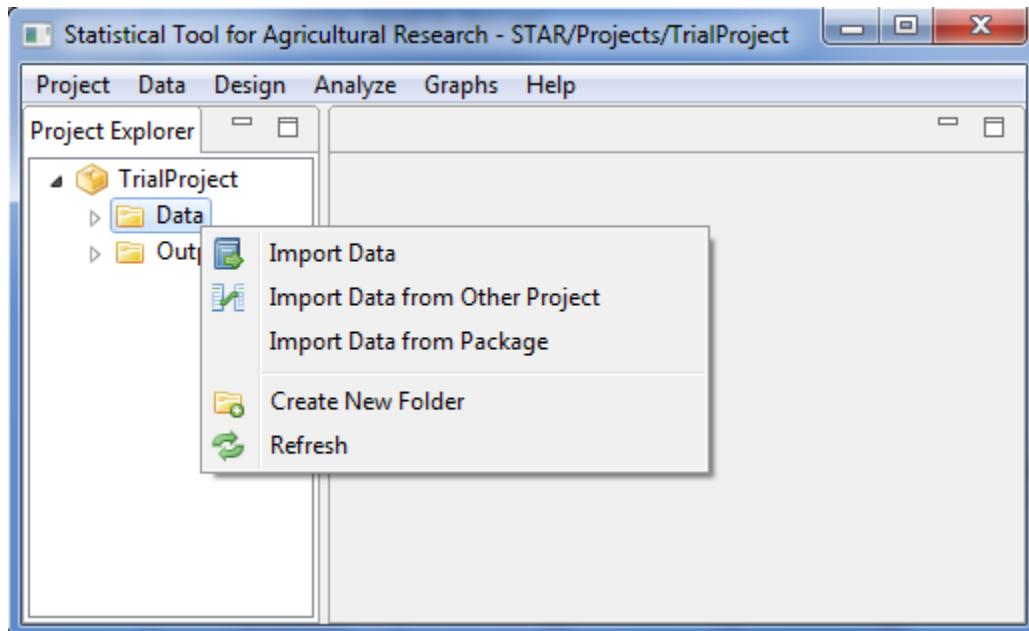
- Click the **Import Data** button. The new imported data file will now be displayed inside the *Data* folder of the active project in the **Project Explorer** panel. To view the data in a spreadsheet format, double-click the icon of the data file.



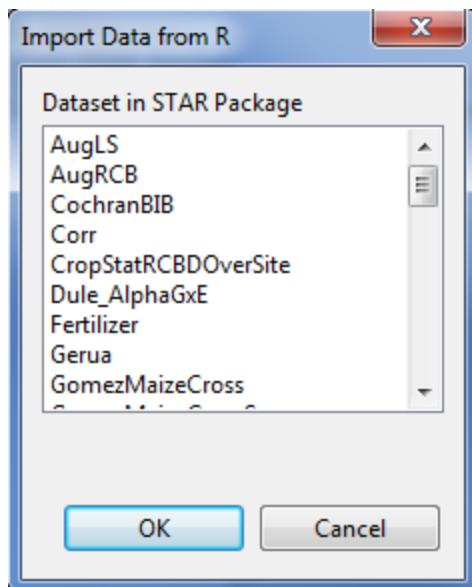
Importing Data from Package

Datasets in STAR package of R can be imported. The steps to import data from R package are listed below:

- On the **Project Explorer** panel, right-click the *Data* folder of the project named *TrialProject*. A pop-up menu will appear. Choose **Import Data from Package**.

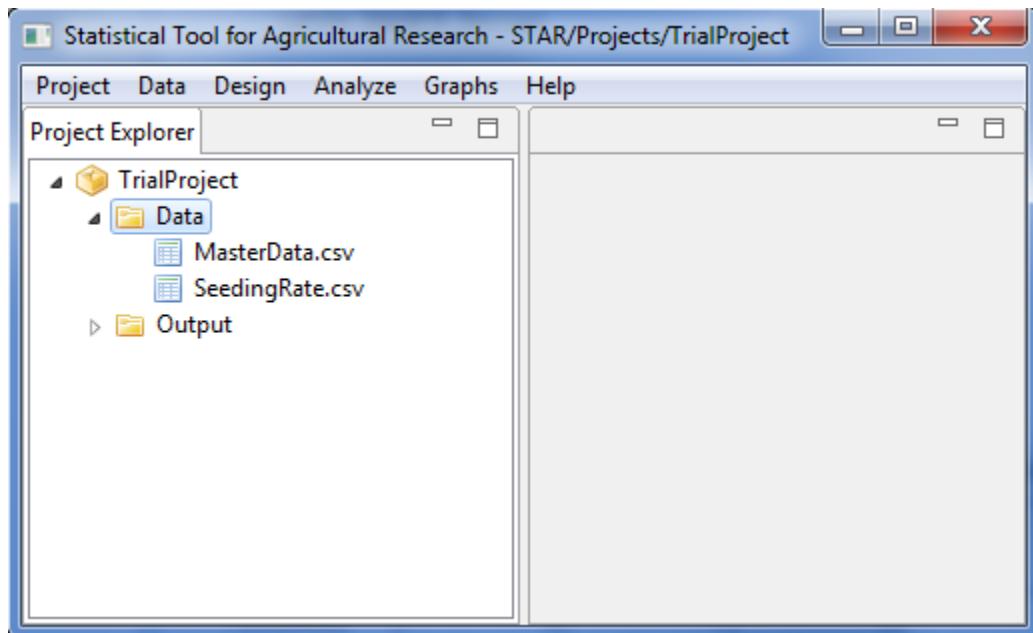


- The **Import Data from R** dialog box will appear. This dialog box contains all existing data file in STAR R package. Select one or several data files. Choose the data files to be imported.



For the example, choose *SeedingRate*.

- Click the **OK** button. The new imported data file will now be displayed inside the *Data* folder of the active project in the **Project Explorer** panel. To view the data in a spreadsheet format, double-click the icon of the data file.



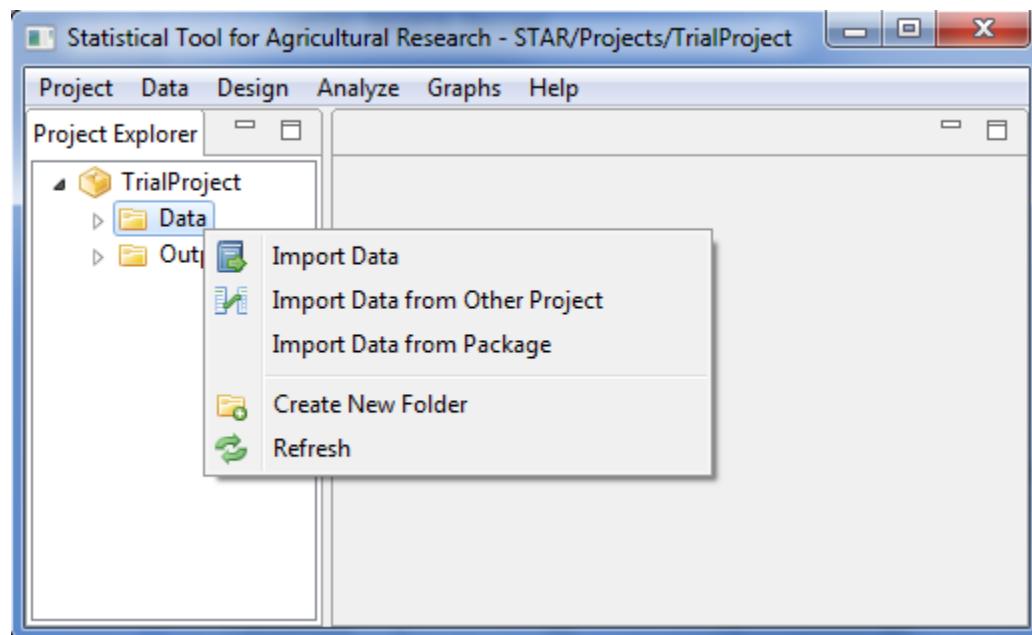
Creating New Folder

To organize the data files imported in a project or results of an analysis, user may want to create a sub folder inside the *Data* folder or inside the *Output* folder.

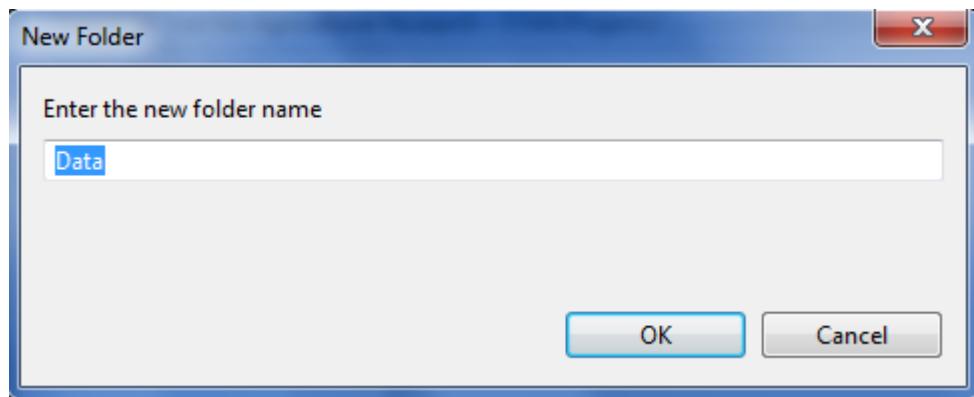
The steps in creating a sub folder are listed below:

- On the **Project Explorer** panel, right-click the folder where you want to create the sub folder. A pop-up menu will appear. Choose **Create New Folder**.

For the example, right-click the *Data* folder of the project named *TrialProject*.



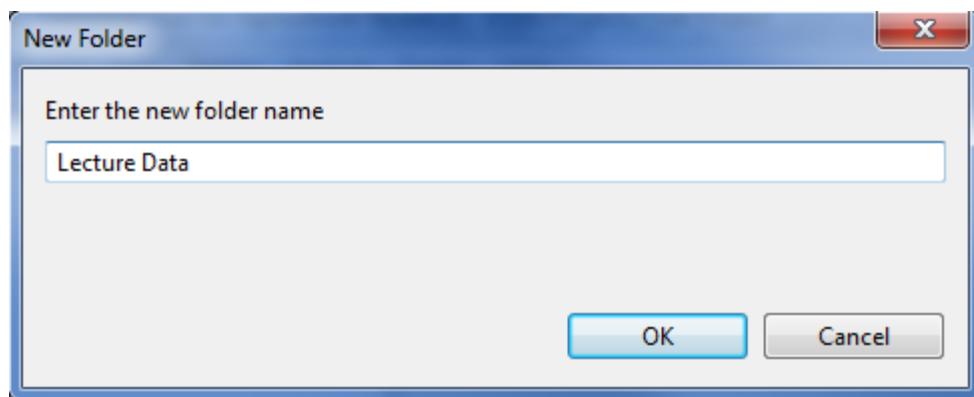
- The **New Folder** dialog box will appear. In the **Enter the new folder name** field, specify the name for the new folder. If the sub folder will be created within the *Data* folder, the default folder name is *Data*. If the sub folder will be created within the *Output* folder, the default folder name is *Output*.



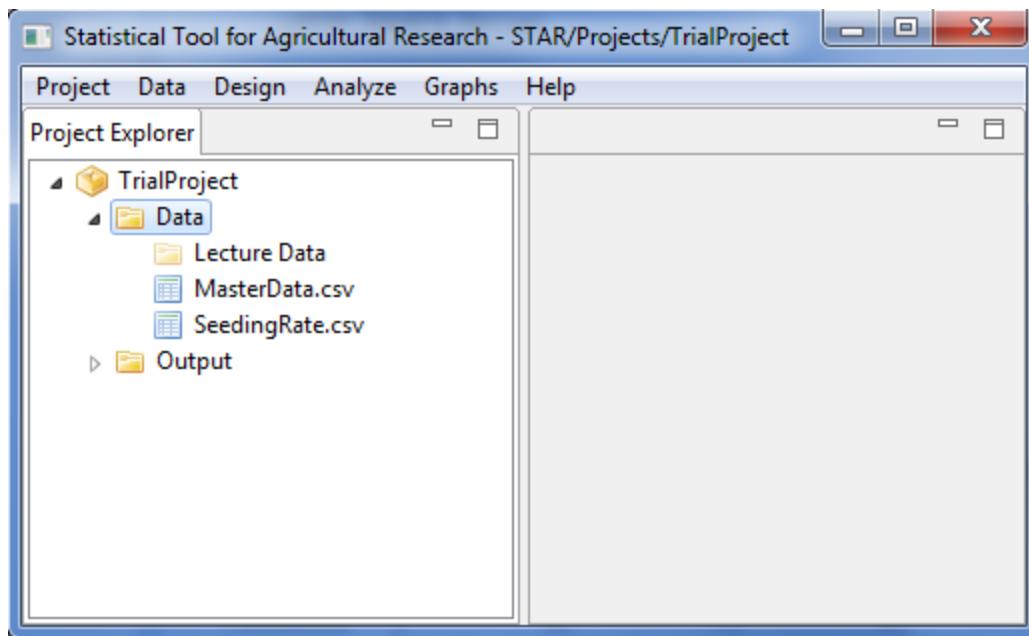
In naming a folder, the following rules apply:

- The name must start with a letter. The remaining characters can be any letter, any digit, a period, underscore, blank or dash.
- The last character of the name should not be a period, underscore, blank or dash.
- The length of the name should not be less than 4 characters.
- The name must be different from the existing folder names inside a parent folder.
- The name is not case sensitive.

For the example, type *Lecture Data* as the new folder name.



- A new sub-folder inside *Data* folder is now created and can be seen in the Project Explorer.



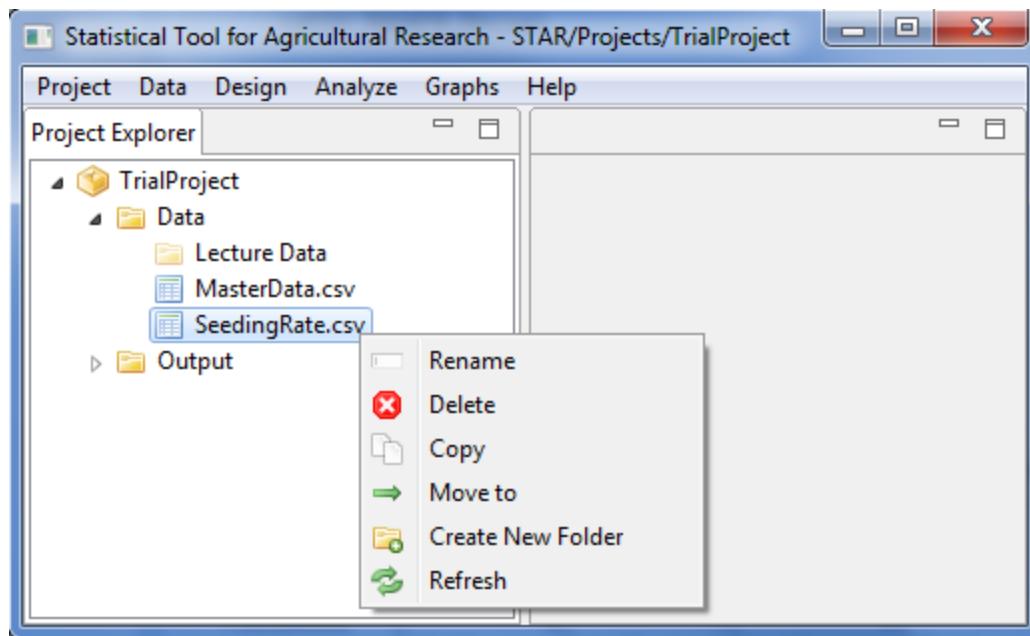
The user can create several sub folders within the *Data* folder or *Output* folder. If the sub folders are created within the *Data* folder, user can import data set to the sub folder, rename, copy, delete and move the sub folder.

Copying File/Folder

The steps to copy data files to other location are listed below:

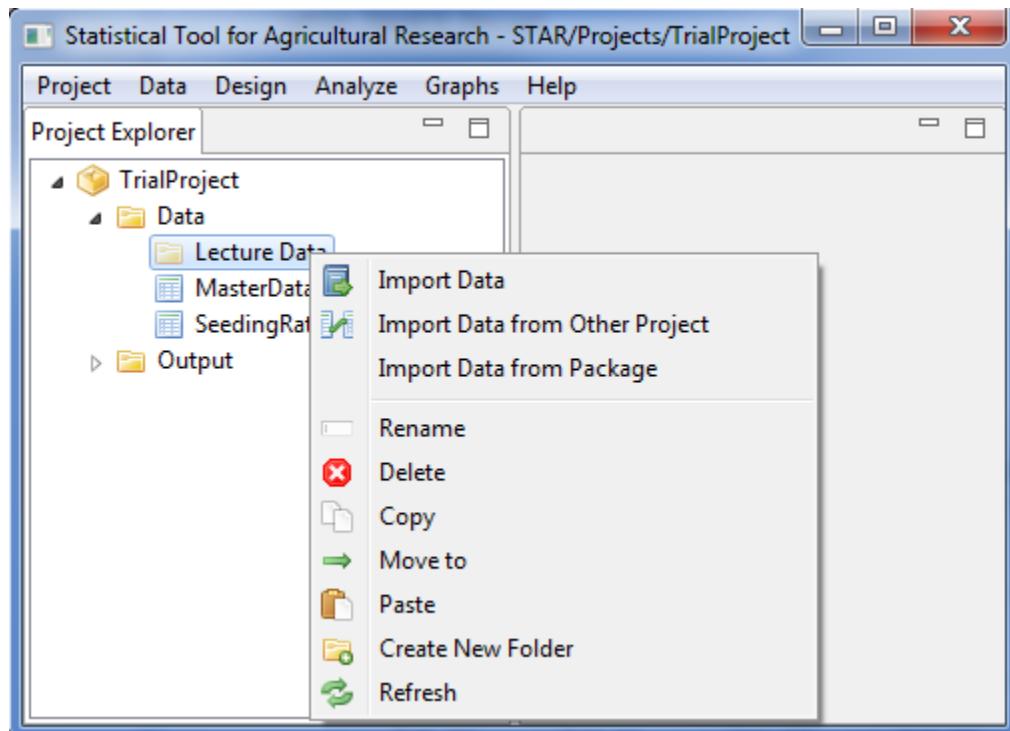
- On the **Project Explorer** panel, right-click the file you want to copy. A pop-up menu will appear. Choose **Copy**.

For the example, right-click *SeedingRate.csv* inside the *Data* folder of the project named *TrialProject*.

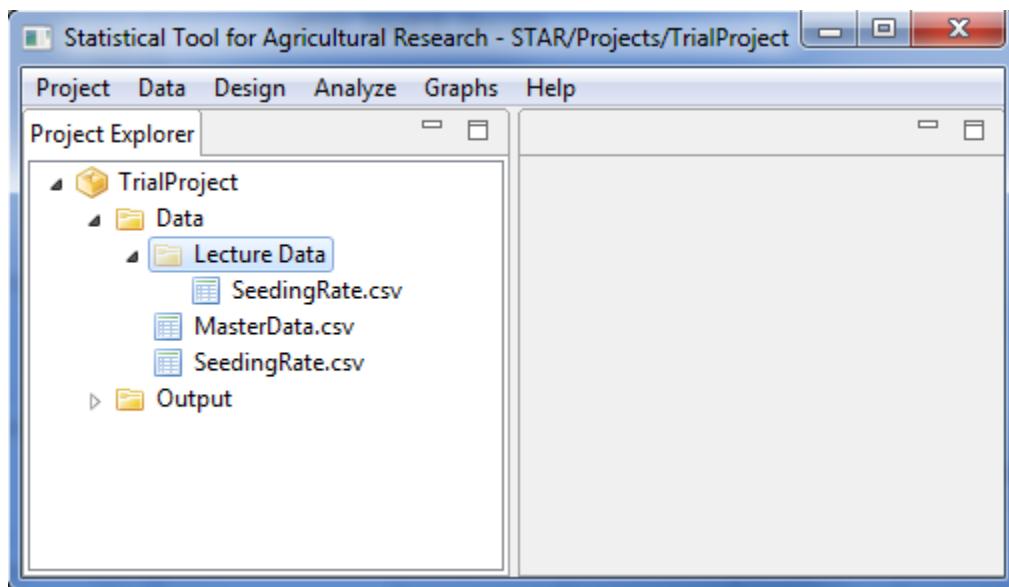


- Go to the desired destination folder, which can be within or outside STAR workspace, then right-click then choose **Paste**.

For the example, right-click on the *Lecture Data* folder then choose **Paste**.



- The file is now copied inside the destination folder.



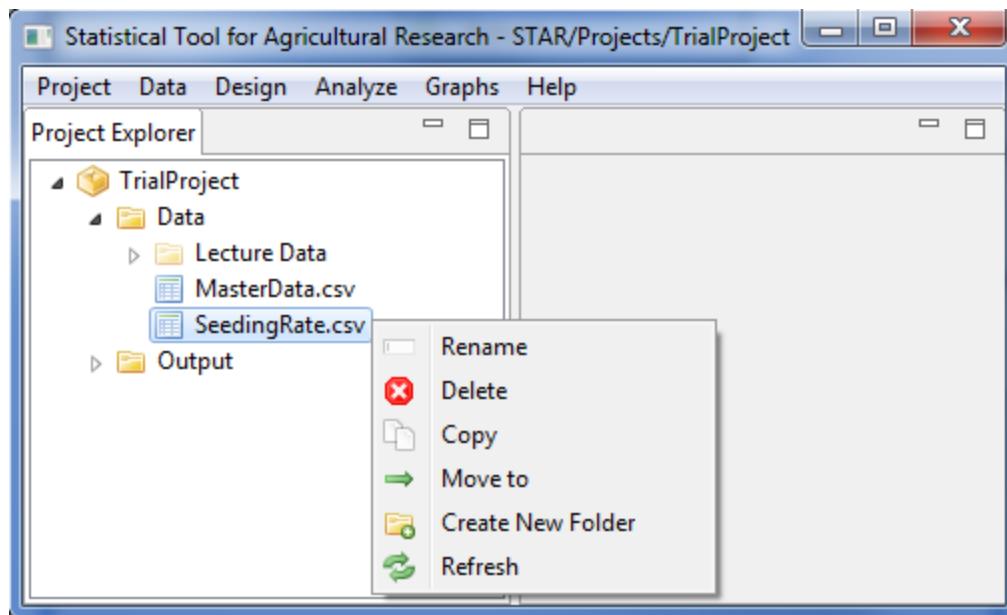
These steps also apply when copying the sub- folders within the *Data* and *Output* folders.

Renaming File/Folder

The steps to rename files are listed below:

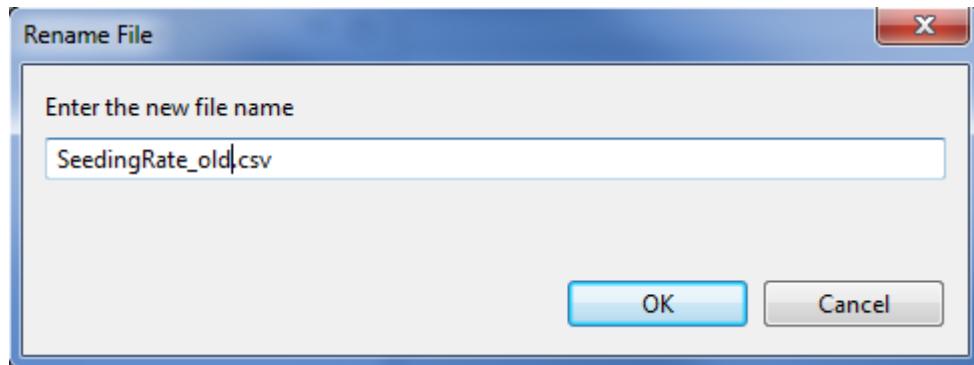
- On the **Project Explorer** panel, right click the file to rename. A pop-up menu will appear. Choose **Rename**.

For the example, right-click *SeedingRate.csv* inside the *Data* folder of the project named *TrialProject*.

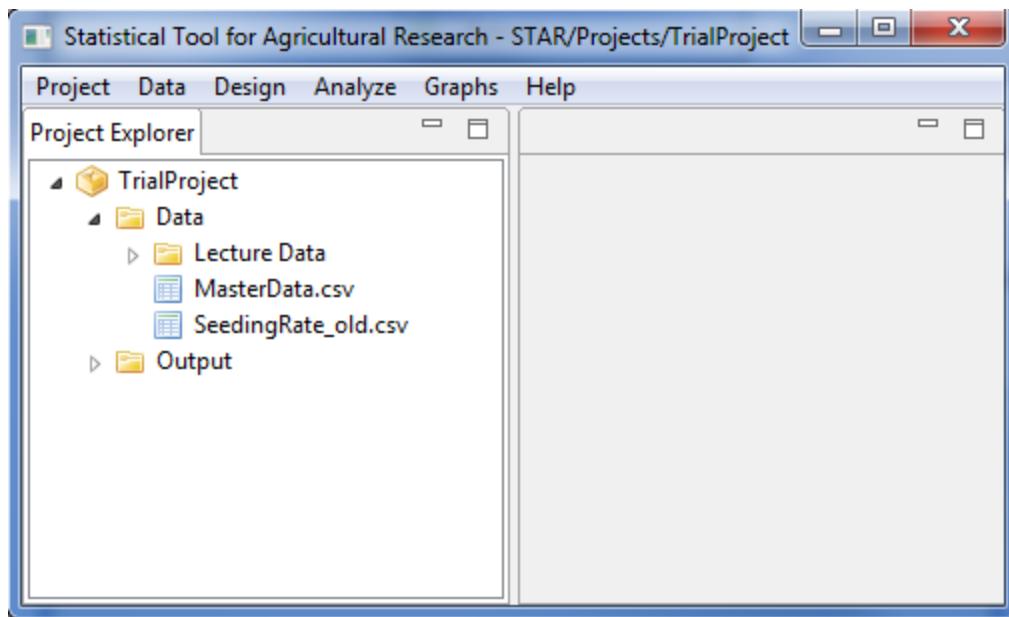


- The **Rename File** dialog box will appear. In the **Enter the new file name** field, specify the new filename.

For the example, set the new filename to *SeedingRate_old.csv*. The completed dialog box should appear as shown below:



- Click the **OK** button. The renamed data file should appear in the **Project Explorer** panel.



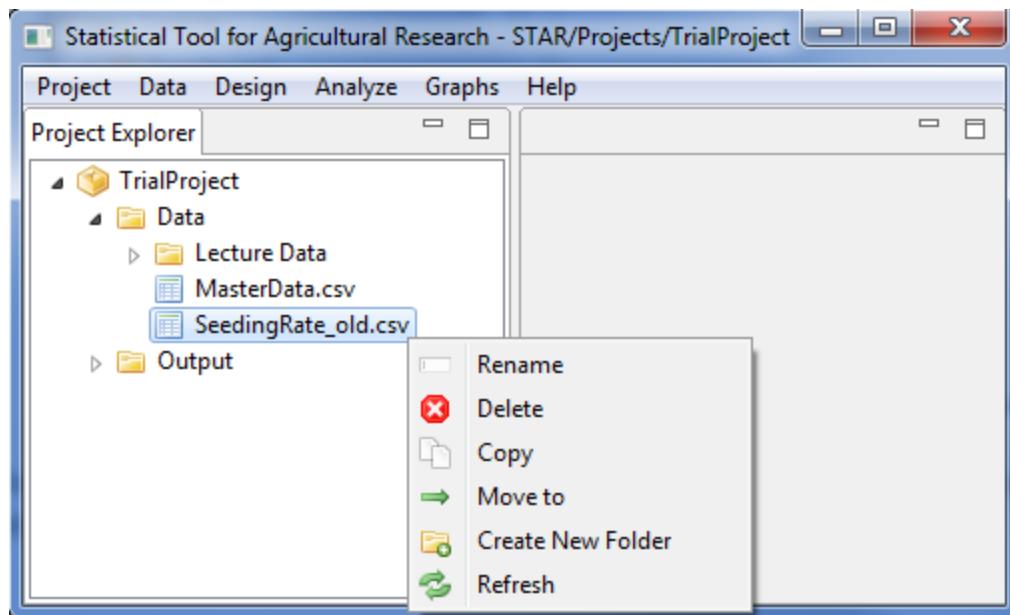
These steps also apply when renaming the sub- folders within the *Data* and *Output* folders.

Moving File/Folder

The steps to move data files to other location in the STAR workspace are listed below:

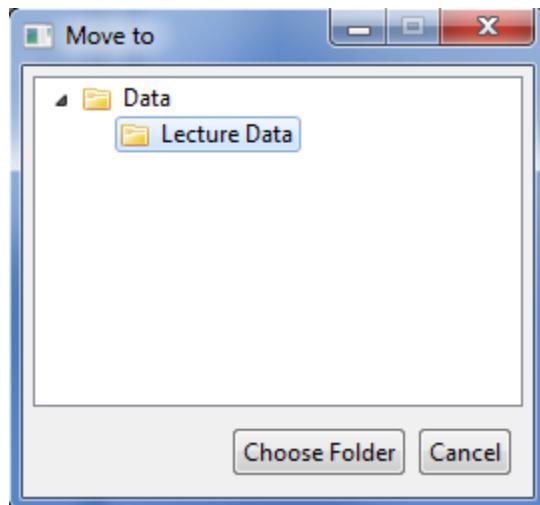
- On the **Project Explorer** panel, right click the file to you want to move. A pop-up menu will appear. Choose **Move to**.

For the example, right-click *SeedingRate_old.csv* inside the *Data* folder of the project named *TrialProject*.

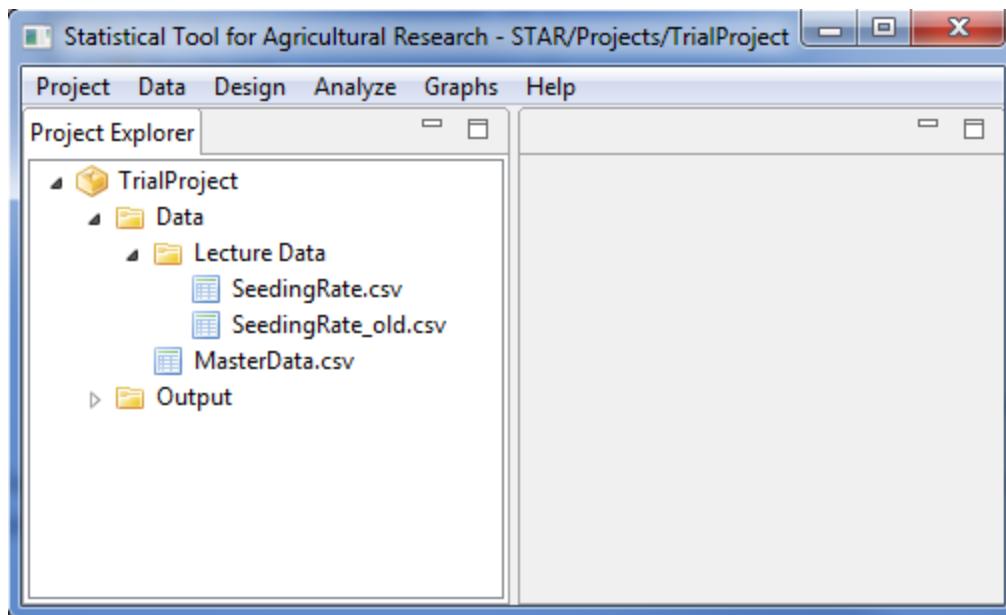


- The **Move to** dialog box will appear. Select the destination folder.

For the example, choose the *Lecture Data* folder inside the *Data* folder.



- Click the **Choose Folder** button. The file is now moved to the destination folder.



These steps also apply when moving the sub-folders within the *Data* and *Output* folder.

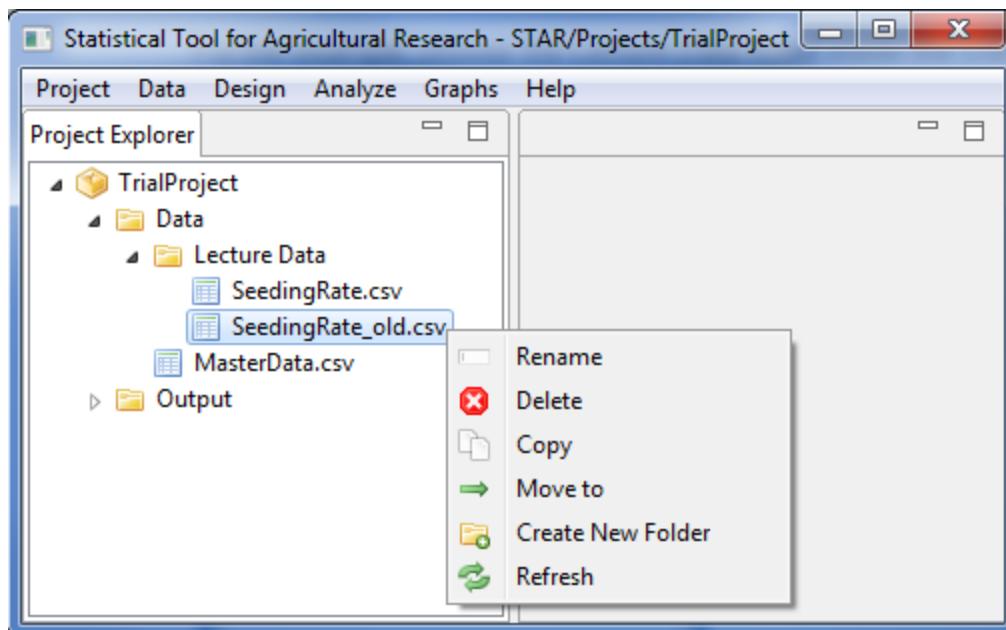
Deleting File/Folder

Files to be deleted must be close before following the steps listed below. However, if a user wants to delete a folder, all items inside the folder to be deleted must be close before deleting the folder. Note that the default folders created (*Data* folder and *Output* folder) cannot be deleted.

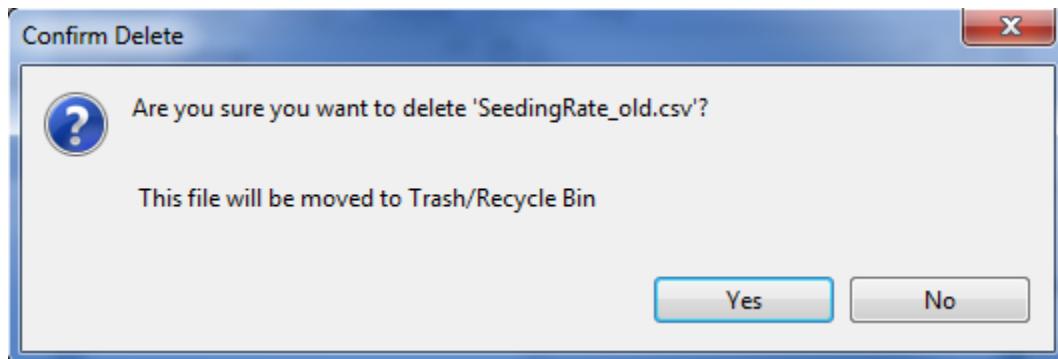
The steps to delete data files are listed below:

- On the **Project Explorer** panel, right click the file to you want to delete. A pop-up menu will appear. Choose **Delete**.

For the example, right-click *SeedingRate_old.csv* inside the *Lecture Data* of the *Data* folder of the project named *Trial Project*.



- The **Confirm Delete** message box will appear.



- Click the **Yes** button to delete.

These steps also apply when deleting the sub-folders within the *Data* and *Output* folder.

Switching Workspace

Workspace is a location where projects, data and output will be saved.

The steps to switch workspace are listed below:

- Click **Project | Switch Workspace....**. The **Select Workspace** dialog box will appear as shown below:

■

For the example, right-click *SeedingRate_old.csv* inside the *Lecture Data* of the *Data* folder of the project named *Trial Project*. Choose **Delete**.

Data Manipulation

Insert Row(s)

The steps to insert row(s) are listed below:

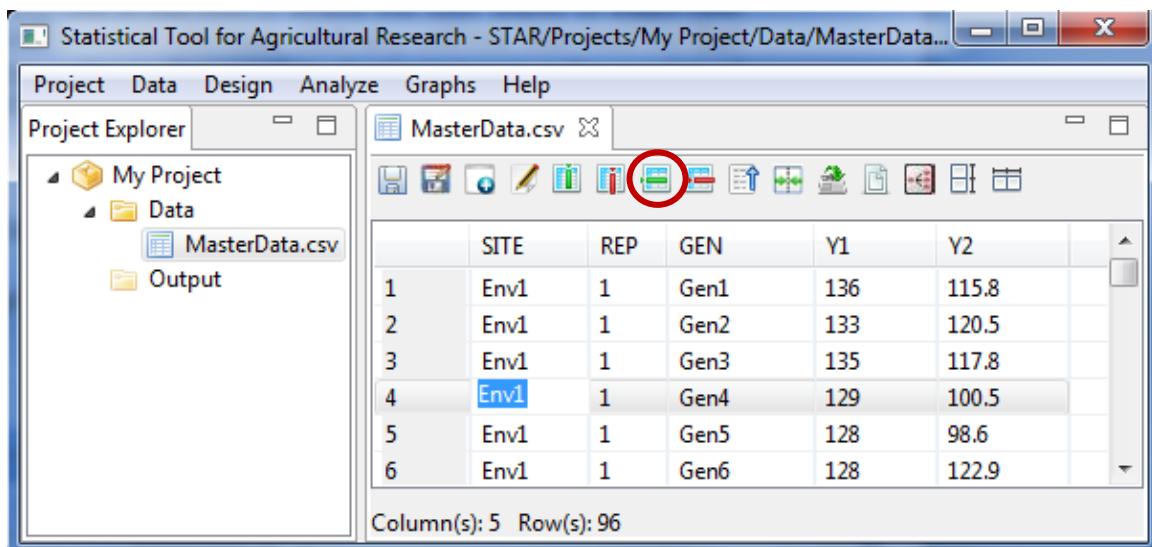
- On the **Project Explorer** panel, double-click the file where new row(s) will be inserted to open it and view it in the Data Viewer tab.

For the example, using the project named *MyProject*, import the data *MasterData.csv* from the *Data* folder of the project named *SampleProject*. To import data from the *SampleProject*, see *Importing Data from Other Project* section of this user's manual.

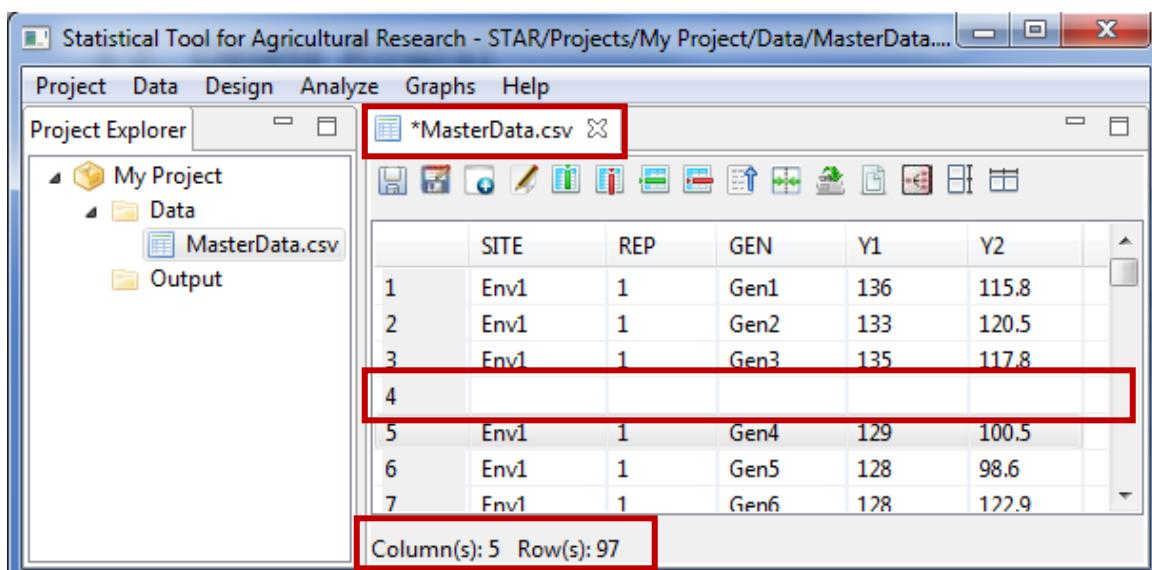
- Select any row(s) or any cell in the row(s) where new row(s) are to be inserted above it. To select several cells/rows, click any cell/row, then hold the **Ctrl** key and click on another cell/row. The number of selected rows is the number of row that will be inserted.

For the example, select the 4th row.

- Click **Data | Insert Row...** from the menu bar of the main window or click on the  Insert Row icon in the **Data Viewer** toolbar.



- The data now contains the newly inserted row.



If there is no row selected before executing the Insert Row function, the user will be prompted if the user wants to insert a row after the last row of the data or not.

Delete Row(s)

The steps to delete row(s) are listed below:

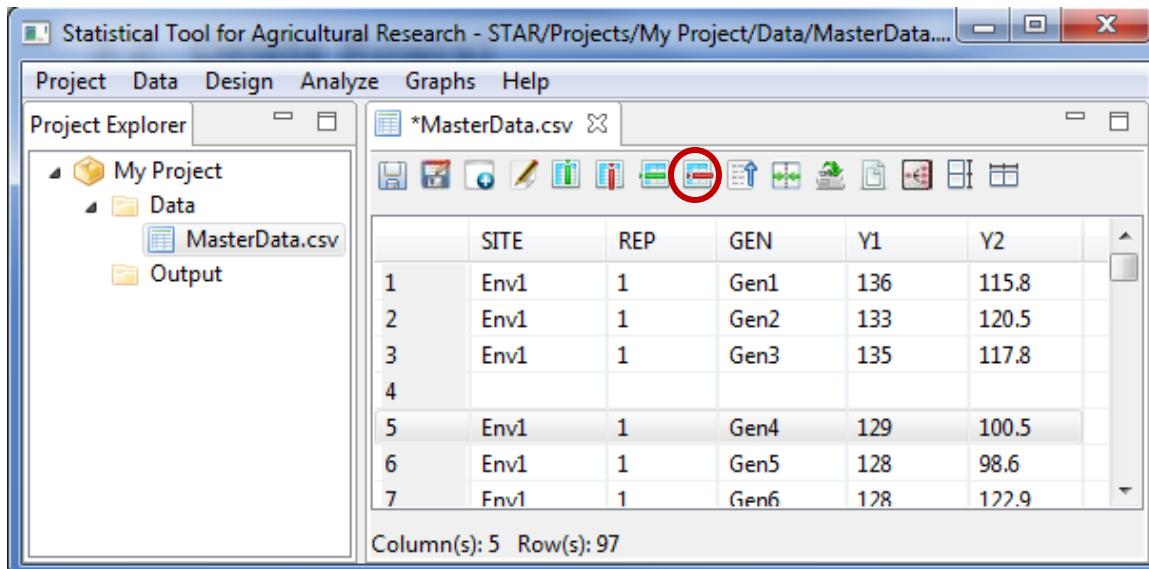
- On the **Project Explorer** panel, double-click the file where rows will be deleted to open it and view it in the Data Viewer tab.

For the example, use the modified and unsaved *MasterData.csv* in the project named *MyProject* created from the previous section that is displayed in the Data Viewer.

- Select any row(s) or any cell in the row(s) that will be deleted. To select several cells/rows, click any cell/row, then hold the Ctrl key and click on another cell/row. The number of selected rows is the number of row that will be deleted.

For the example, select the 4th row.

- Click **Data | Delete Row** from the menu bar of the main window or click on the  Delete Row icon in the Data Viewer tool bar.



- The **Delete Row** dialog box will appear. Confirm that the row deletion is desired by clicking the **Yes** button.
- The changes made should be reflected in the Data Viewer tab.

For the example, close the modified *MasterData.csv* and do not save the changes.

Inserting Column(s)

The steps to delete row(s) are listed below:

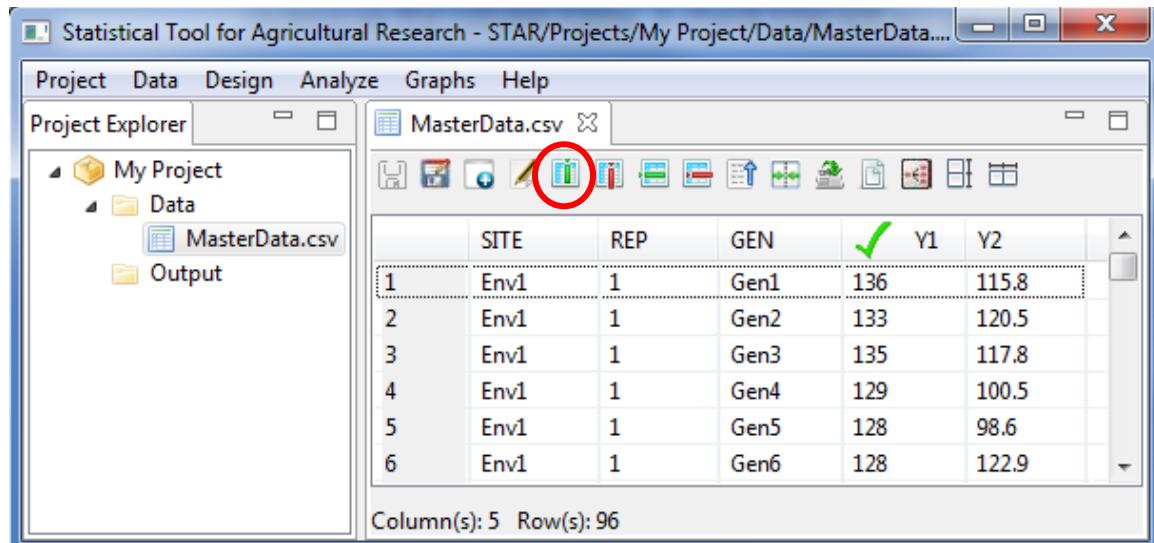
- On the **Project Explorer** panel, double-click the file where new columns will be inserted to open it and view it in the Data Viewer tab.

For the example, using the project named *MyProject*, import the data *MasterData.csv* from the *Data* folder of the project named *SampleProject*. To import data from the *SampleProject*, see *Importing Data from Other Project* section of this user's manual.

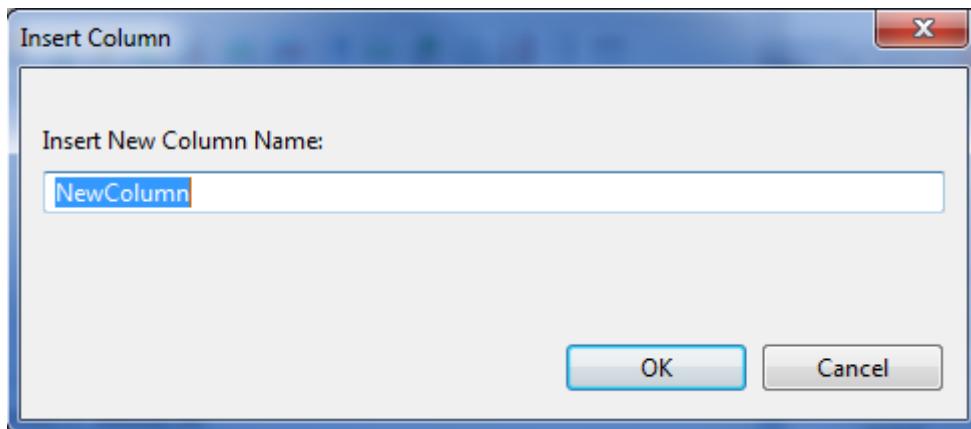
- Select a column where the new column will be inserted before it by clicking on the column name. A check icon will appear on the column header.

For the example, select the column named *Y1*.

- Click **Data | Insert Column...** from the menu bar of the main window or click on the  in the Data Viewer tool bar.



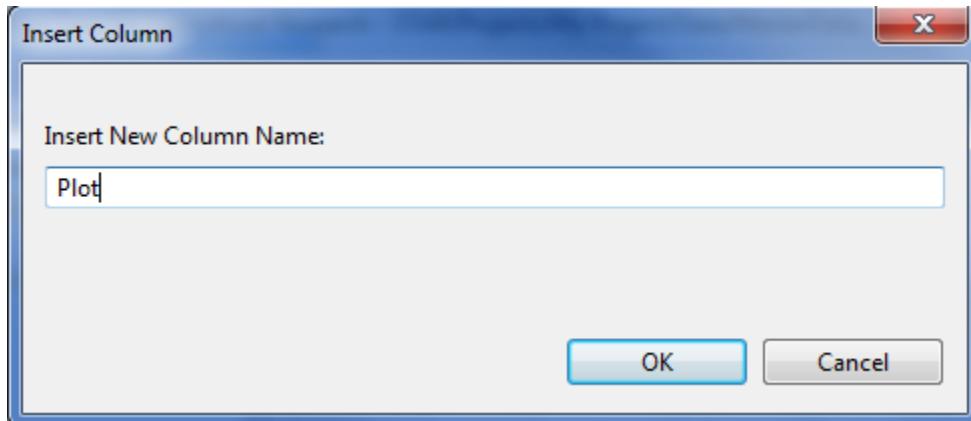
- The **Insert Column** dialog box will appear. In the **Insert New Column Name** field, specify a new name for the inserted column. The default new column name is *NewColumn*.



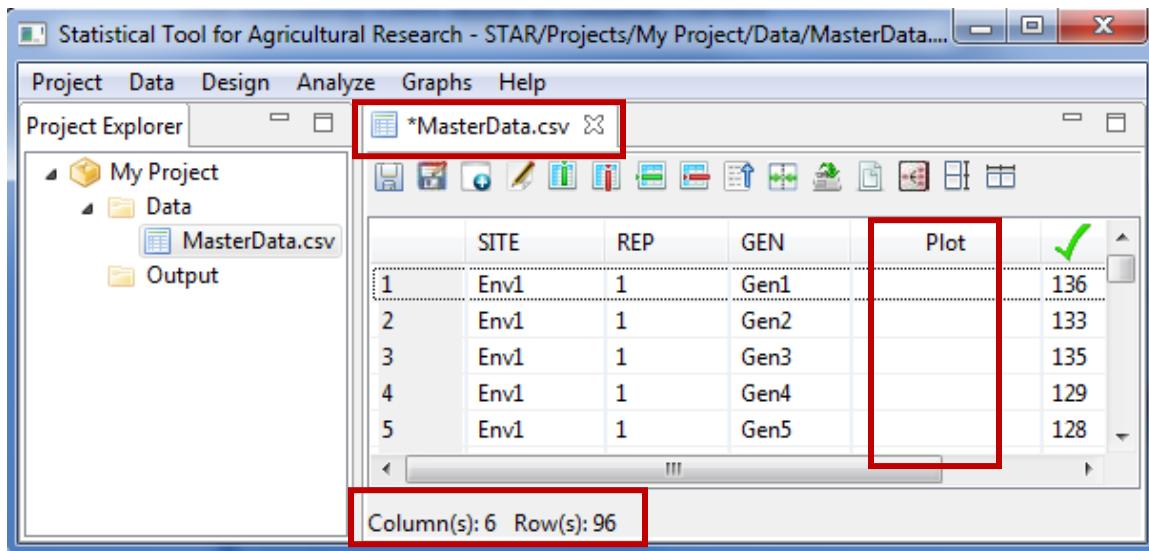
In naming the column, the following rules apply:

- The name must start with a letter while the remaining characters can be any letter, any digit, a period or underscore.
- The name must be different from the existing column names in the data.
- The name is case sensitive.

For the example, type *Plot*. The completed dialog box will appear as shown below:



- Click the **OK** button.



- The data now contains the newly inserted column named *Plot*.

Deleting Column(s)

The steps to delete row(s) are listed below:

- On the **Project Explorer** panel, double-click the file where columns will be deleted to open it and view it in the Data Viewer tab.

For the example, use the modified and unsaved *MasterData.csv* in the project named *MyProject* created from the previous section that is displayed in the Data Viewer tab.

- Select the column or one of the columns to be deleted by clicking on the column name. A check icon will appear on the column header.

For the example, select the column named *Plot*.

- Click **Data | Delete Column...** from the main window or click on the Insert Column icon in the Data Viewer tool bar.
- Click the **OK** button.

Create New Variables

New variables can be created in the active data set by transforming existing variables or collapsing categories of two or more existing variables.

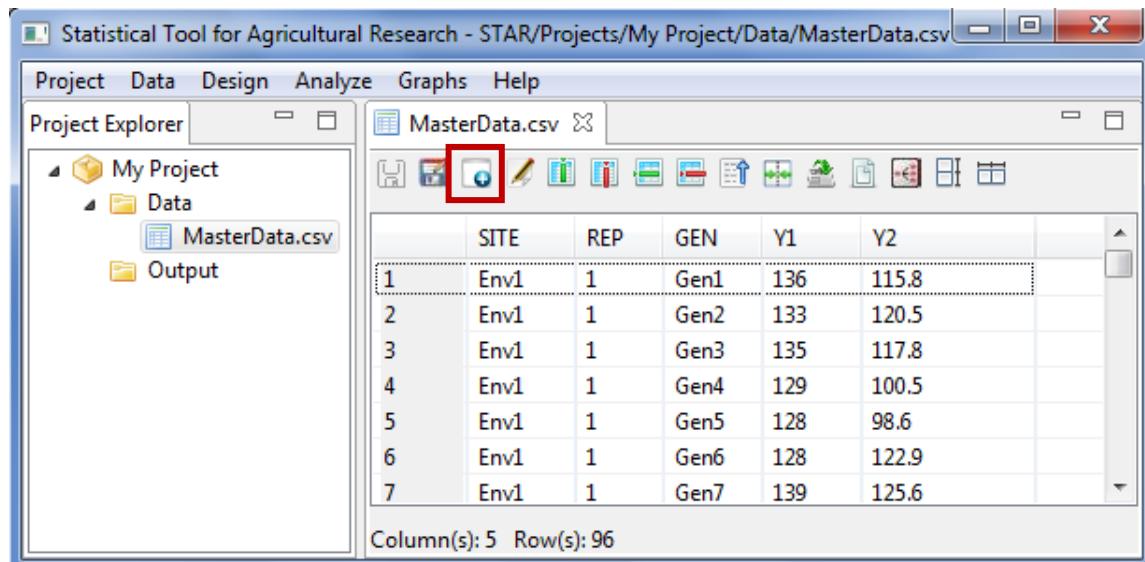
For transformations, there are six available functions, namely: logarithm, natural logarithm, square root, power, exponential and standardized. For logarithm, natural logarithm, square root and power transformation, the variables to be transformed should not contain negative values. For logarithm and natural logarithm transformation, values of the variable to be transformed will be incremented by 1 if it contains values equal to 0. For square root and power transformation, values of the variable will be incremented by 0.5 if it contains values equal to 0.

The steps to create new variables are listed below:

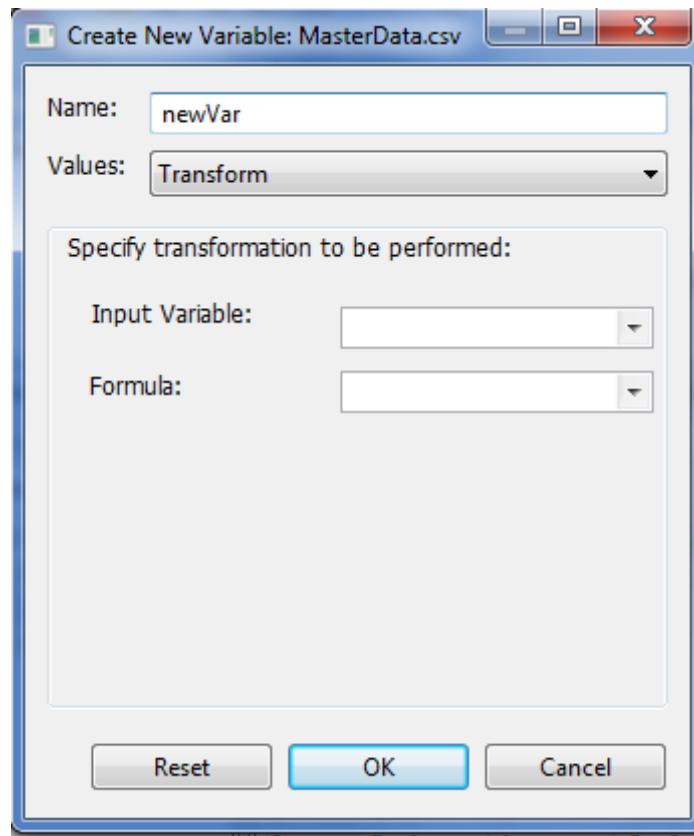
- On the **Project Explorer** panel, double-click the file to be used to open it and view it in the Data Viewer tab.

For the example, using the project named *MyProject*, import the data *MasterData.csv* from the *Data* folder of the project named *SampleProject*. To import data from the *SampleProject*, see *Importing Data from Other Project* section of this user's manual.

- To create new variables, click **Data | Create New Variable** from the main window or click on the Create New Variable icon  in the Data Viewer toolbar.



The **Create New Variable** dialog box will appear.



- Specify the required fields and appropriate options.

Name

This is the name of the new variable to be created. The default variable name is *newVar*. In naming the column, the following rules apply:

- The name must start with a letter while the remaining characters can be any letter, any digit, a period or underscore.
- Each column name must be unique; duplication is not allowed.
- Column name is case sensitive

Values

There are two options to determine the values of the new variable. The user can either transform any existing numeric variables or concatenate the values of any variables in the data set. The default is *Transform*.

Input Variable

If *transformation* is selected in the **Value** drop-down box, this drop-down box will be visible. This box pertains to the variable where the transformation will be performed. All numeric variables of the active data will be displayed in the drop-down box.

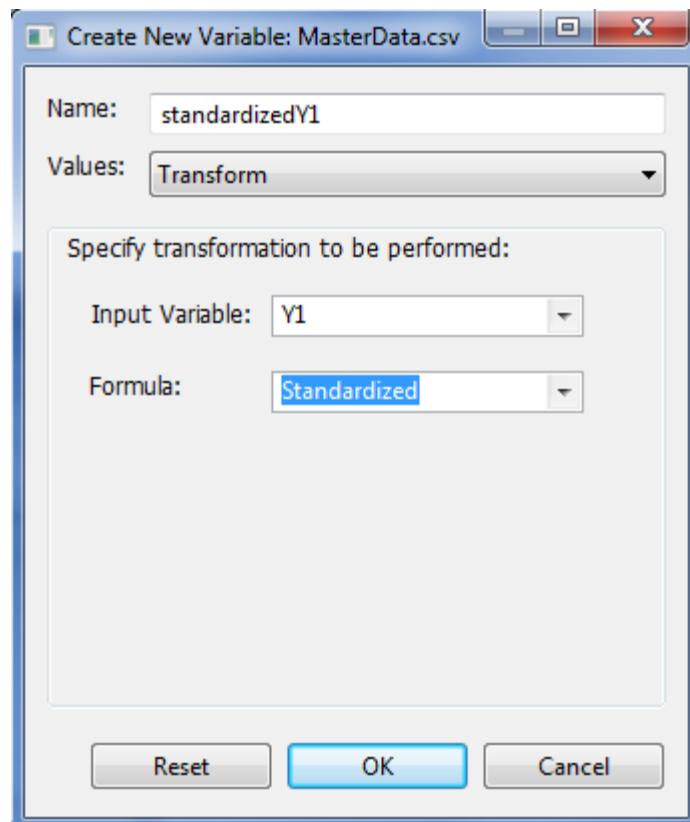
Formula

If *transformation* is selected in the **Value** drop-down box, this drop-down box will be visible. This box pertains to the formula that will be used when the value in the **Input Variable** is transformed. Transformation options available are logarithm, natural logarithm, square root, power, exponential and standardized.

Checkbox Table

If *Concatenate Columns* is selected in the **Value** drop-down box, this table will be visible. This table lets the user specify the columns to concatenate by ticking at least two column names. All columns of the active data will be displayed in the table.

For the example, suppose we want to standardize the variable Y1. The completed dialog box should appear as shown below:

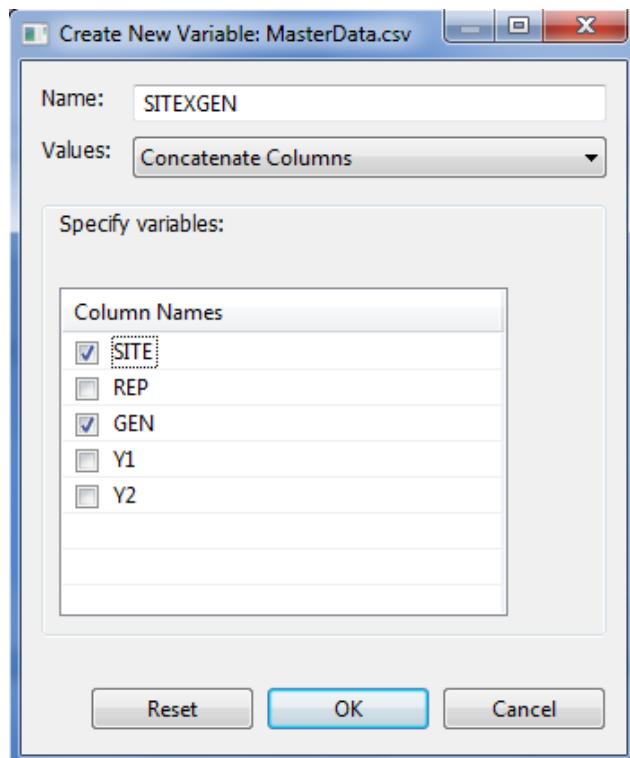


- Click the **OK** button. The data set with the transformed variable is displayed in the Data Viewer tab.

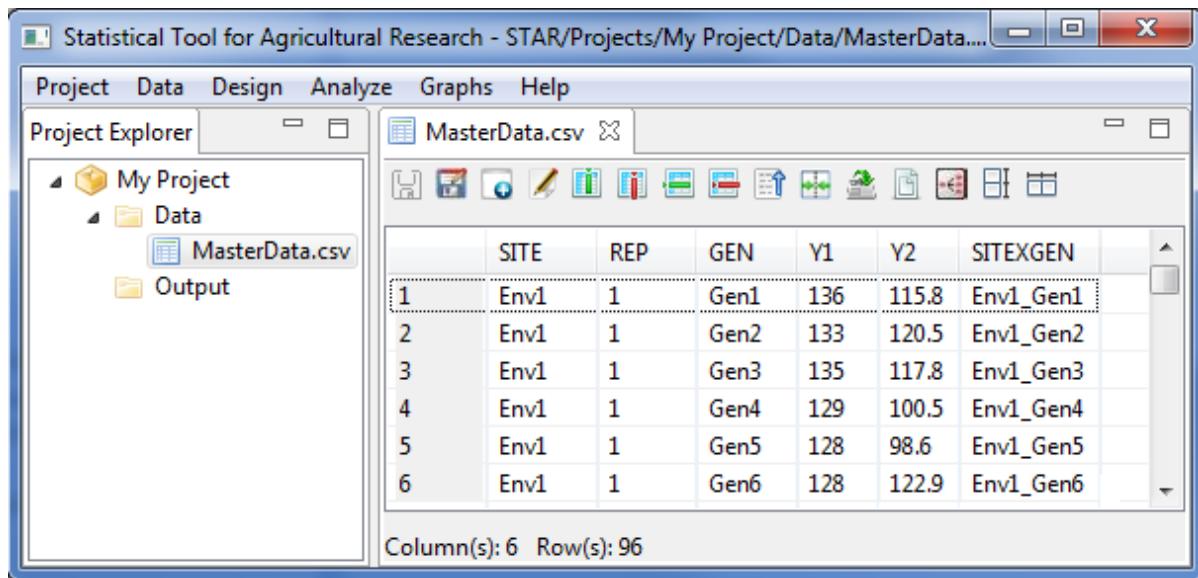
The screenshot shows the main window of the Statistical Tool for Agricultural Research. The menu bar includes Project, Data, Design, Analyze, Graphs, and Help. The Project Explorer tab is selected, showing a project named 'My Project' with a 'Data' folder containing 'MasterData.csv'. The Data Viewer tab is also selected, displaying the contents of 'MasterData.csv'. The table in the viewer shows six columns: SITE, REP, GEN, Y1, Y2, and 'standardizedY1'. The data rows show values for Env1 across six generations (Gen1 to Gen6) with corresponding Y1 and Y2 values and their standardized version. The status bar at the bottom indicates 'Column(s): 6 Row(s): 96'.

	SITE	REP	GEN	Y1	Y2	standardizedY1
1	Env1	1	Gen1	136	115.8	0.3472559098263
2	Env1	1	Gen2	133	120.5	0.1603218873403
3	Env1	1	Gen3	135	117.8	0.2849445689977
4	Env1	1	Gen4	129	100.5	-0.088923475974
5	Env1	1	Gen5	128	98.6	-0.151234816802
6	Env1	1	Gen6	128	122.9	-0.151234816802

Suppose we want to create a new variable by concatenating the values of two variables. The completed dialog box should appear as shown below:



- Click the **OK** button. The transform variable is displayed in the Data Viewer tab.



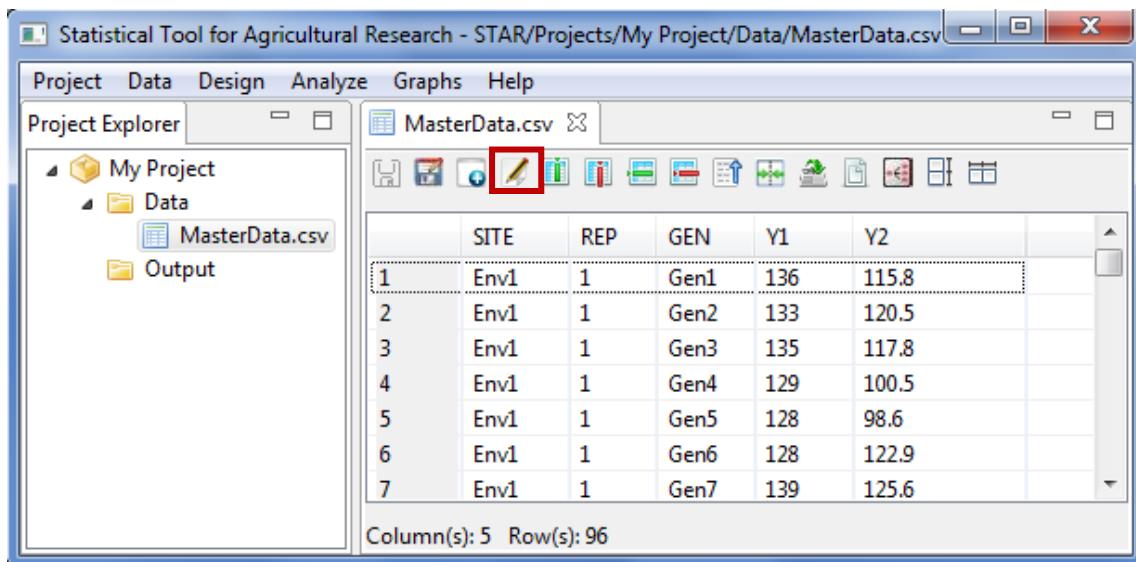
Edit Variable Information

The steps to edit the variable information are listed below:

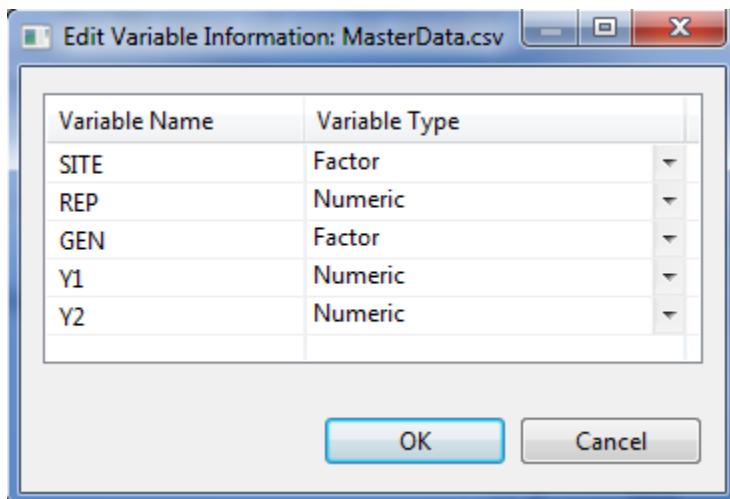
- On the **Project Explorer** panel, double-click the file to be used to open it and view it in the Data Viewer tab.

For the example, using the project named *MyProject*, import the data *MasterData.csv* from the *Data* folder of the project named *SampleProject*. To import data from the *SampleProject*, see *Importing Data from Other Project* section of this user's manual.

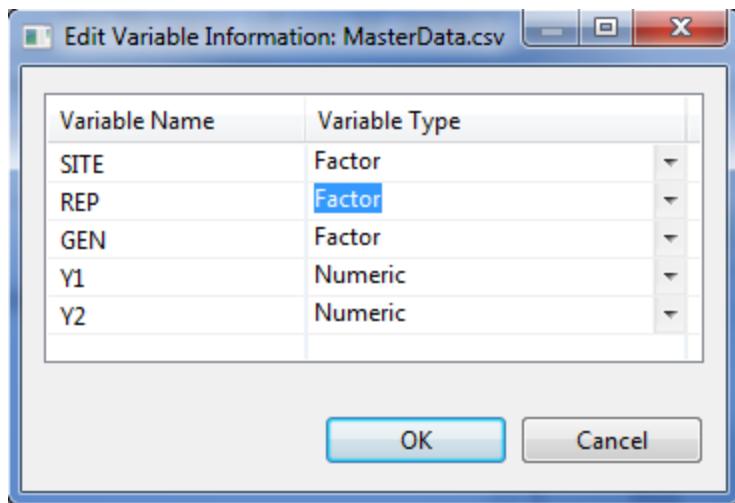
- To edit variable information, click **Data | Edit Variable Information** from the main window of STAR or click on the Edit Variable Information icon in the Data Viewer toolbar.



- The **Edit Variable Information** dialog box will appear. The variables in the active data set are classified as either a factor or numeric variable. The user can modify the variable type of the variables in the data set.



For the example, change the Variable Type of *REP* from Numeric to Factor. The complete dialog box should appear as shown below:



- Click the **OK** button.

Sorting

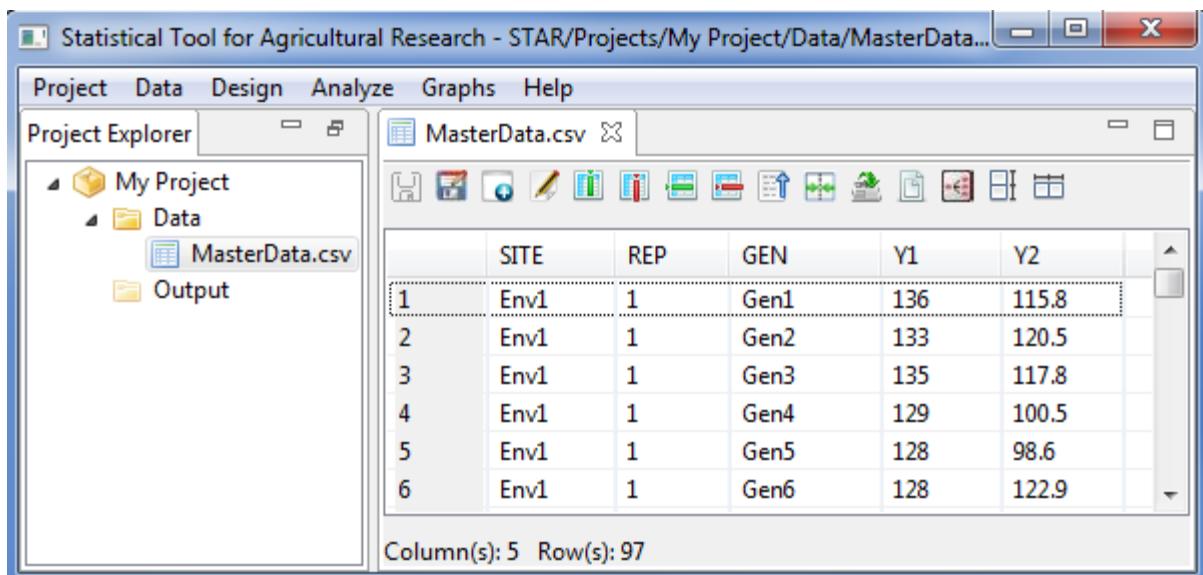
Re-arranging or sorting the rows or cases of the data file is often useful and sometimes necessary for certain types of analysis. The **Sort Cases Menu** can be used to sort rows based on the value of one or more sorting variables.

The steps to re-arrange the data set based on the value of one or more sorting variables are listed below:

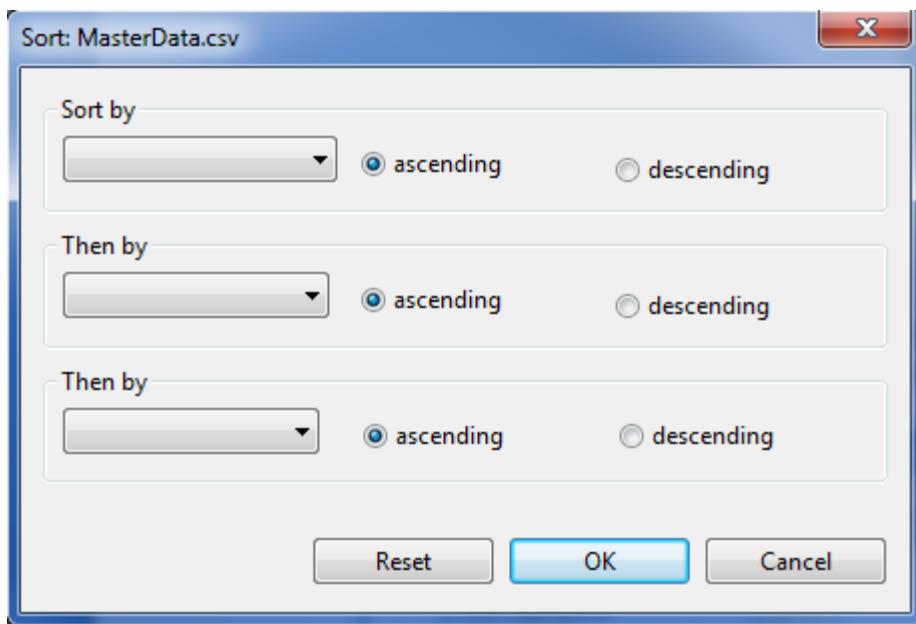
- On the **Project Explorer** panel, double-click the file to be used to open it and view it in the Data Viewer tab.

For the example, using the project named *MyProject*, import the data *MasterData.csv* from the *Data* folder of the project named *SampleProject*. The data file is arranged by *SITE*, *REP* then by *GEN*.

To import data from the *SampleProject*, see *Importing Data from Other Project* section of this user's manual.

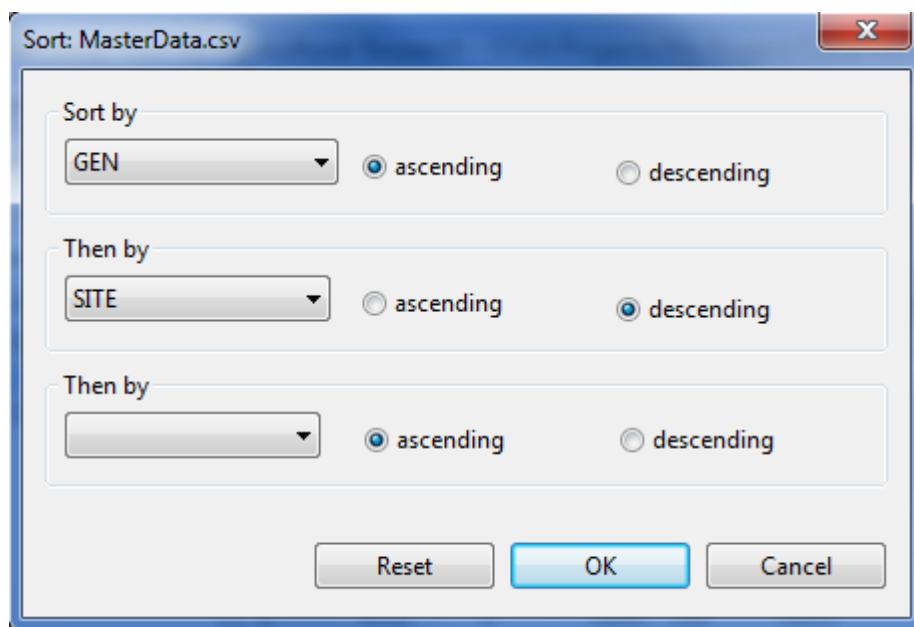


- Choose **Data | Sort...** from the main window or click on the Sort icon  in the Data Viewer tool bar. The **Sort** dialog box will appear.



- Specify up to three variables as the basis for sorting and the order of sorting. Click the drop-down list box to identify the sorting variables. The rows can be re-arranged or sorted in ascending or descending order, with ascending order as the default option. If two or three variables are selected, rows are sorted for each variable within categories of the preceding variables. For character variables, uppercase letters precede their lowercase counterparts.

For the example, suppose we want to re-arrange the content of the data *MasterData.csv*, by ascending order of the variable *GEN* then by descending order of the variable *SITE*. The completed dialog box should appear as shown below:



- Click the **OK** button to sort the active data. The **Sort** dialog box is closed and the sorted data is saved in the parent folder of the active data and displayed in the Data Viewer tab.

The Data Viewer tab shows the sorted data in a table. The Project Explorer on the left lists 'My Project' > 'Data' > 'MasterData.csv' and 'MasterData_sorted.csv'. The table displays the following data:

	SITE	REP	GEN	Y1	Y2
1	Env3	1	Gen1	143	112.8
2	Env3	2	Gen1	134	115.5
3	Env3	3	Gen1	113	154.2
4	Env3	4	Gen1	121	163.5
5	Env2	1	Gen1	136	143.5
6	Env2	2	Gen1	144	130.6

Column(s): 5 Row(s): 96

Merge Datasets

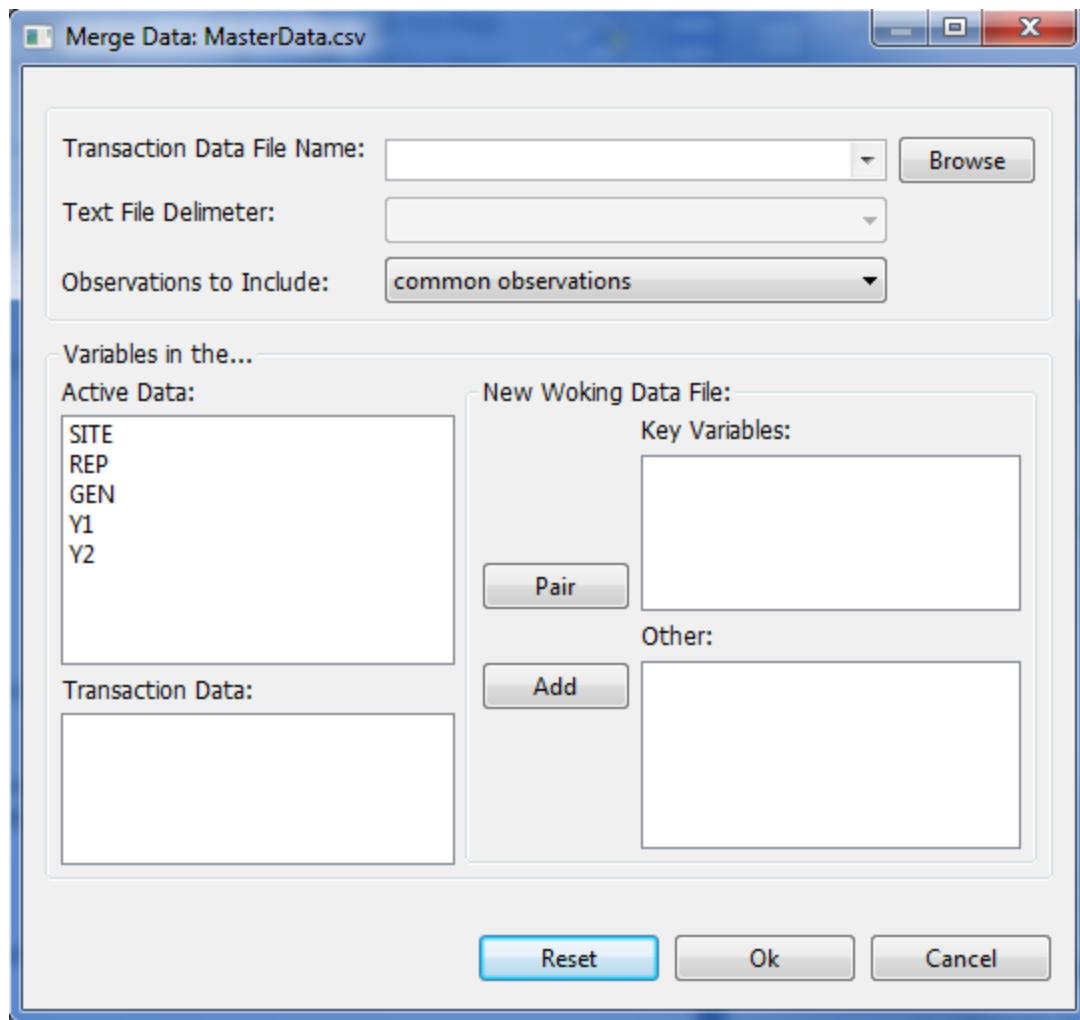
The **Merge** submenu can be used to combine the active data file (known as the master data) with another data file (referred as the transaction data) that contains the same cases or rows but different variables.

The steps to merge datasets are listed below:

- On the **Project Explorer** panel, using the project named *MyProject*, import the data files *MasterData.csv* and *MergeTransact.csv* from the *Data* folder of the project named *SampleProject*. Double-click the file *MasterData.csv* to open it and view it in the Data Viewer.

To import data from the *SampleProject*, see *Importing Data from Other Project* section of this user's manual.

- Choose **Data | Merge Datasets...** or click on the Merge Datasets icon  in the Data Viewer toolbar. The **Merge Data** dialog box will appear.



- Specify the required fields and appropriate options.

Transaction File Name

Specify this file by selecting a file using the drop-down combo box or by locating it using the **Browse** button. The files included in the drop-down combo box are files inside the *Data* folder not in its sub-folder. Only .txt and .csv data file format can be selected as the transaction file.

Text File Delimeter

If the transaction file selected is a text file, the delimeter should be specified. Four delimiters are available, namely: comma, space, tab and semi-colon.

Observations to Include

This option pertains to how rows or cases will be included in the new merged data file. The options available are to include common observations (default value), all

observations in the active data, all observations in the transaction data and all observations.

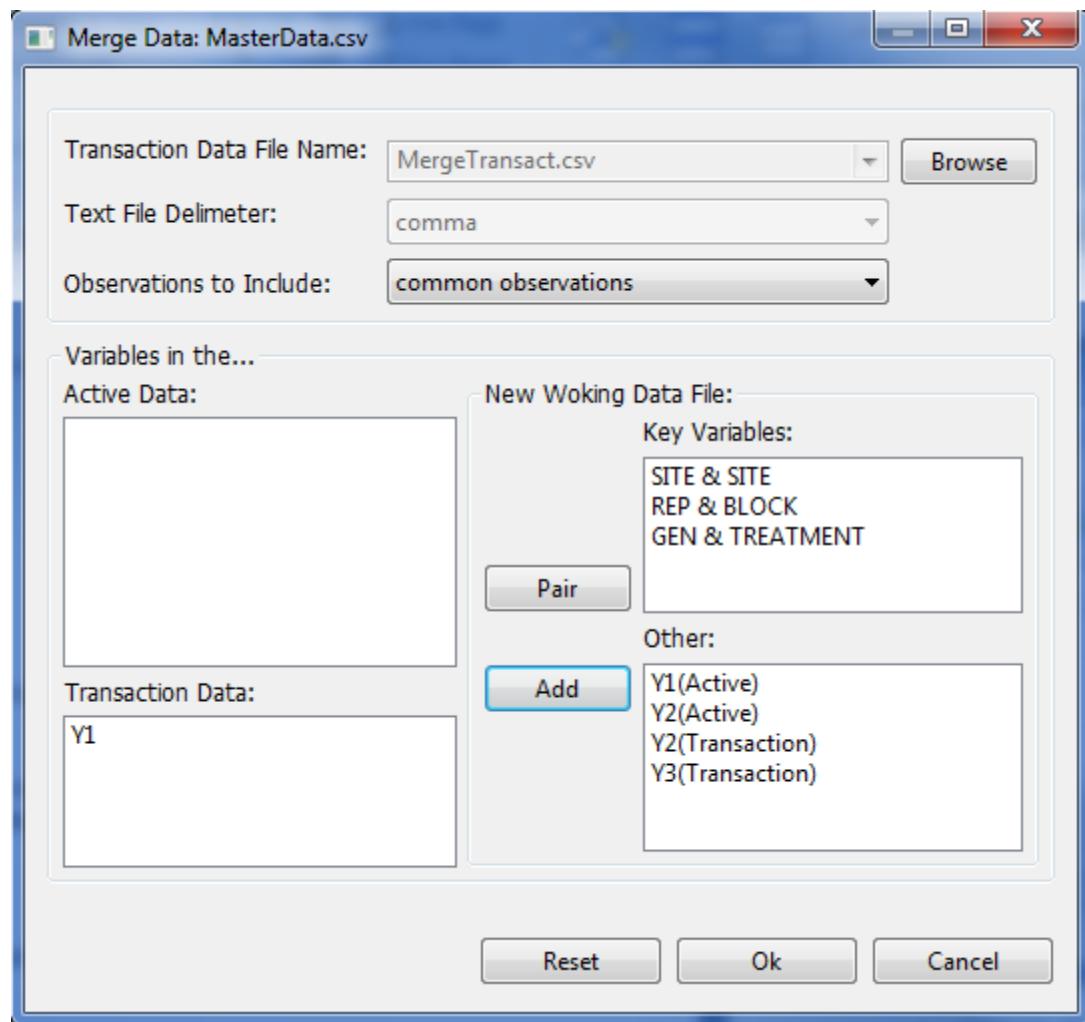
Key Variables

These are pair(s) of variables that are present in the active and transaction files and will be the basis for the merging. Variables can be paired by clicking one variable in the active data and clicking one variable in the transaction data then clicking the **Pair** button. If the pair of variables has different column names, the new merged data file that will be created will use the column name of the active data.

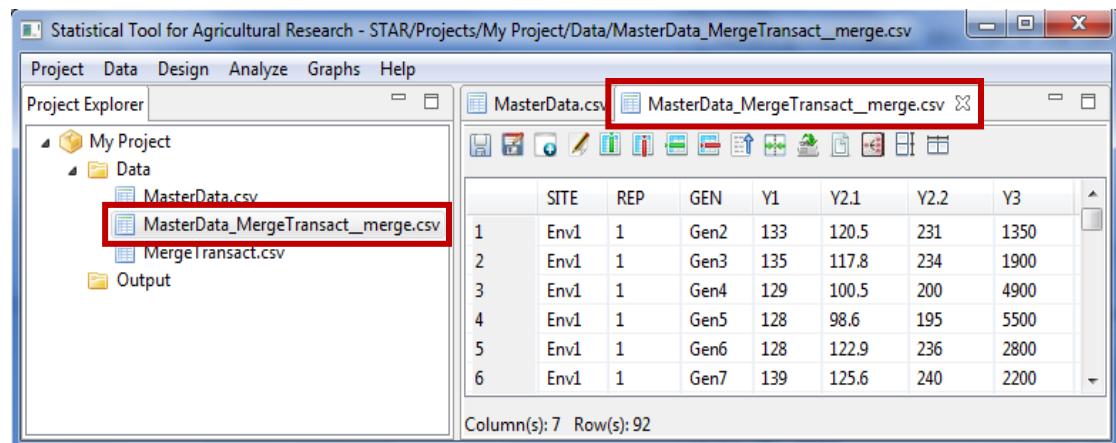
Other

These are the other variables the user wants to include in the merged data file. Variables can be added by selecting at least one variable in the active data and/or in the transaction data then clicking the **Add** button. If columns in this list have the same name, **.1** will be appended to the column name coming from the active data and **.2** to the one from the transaction data.

For the example, select *MergeTransact.csv* file as the transaction data file from the drop-down combo box. The completed dialog box should appear as shown below:



- Click the **OK** button. The merged data is saved in the parent folder of the active data and displayed in the Data Viewer tab. The default filename of the merged data set follows the format `<activeDataFilename>_<TransactionDataFilename>_merge.csv`.



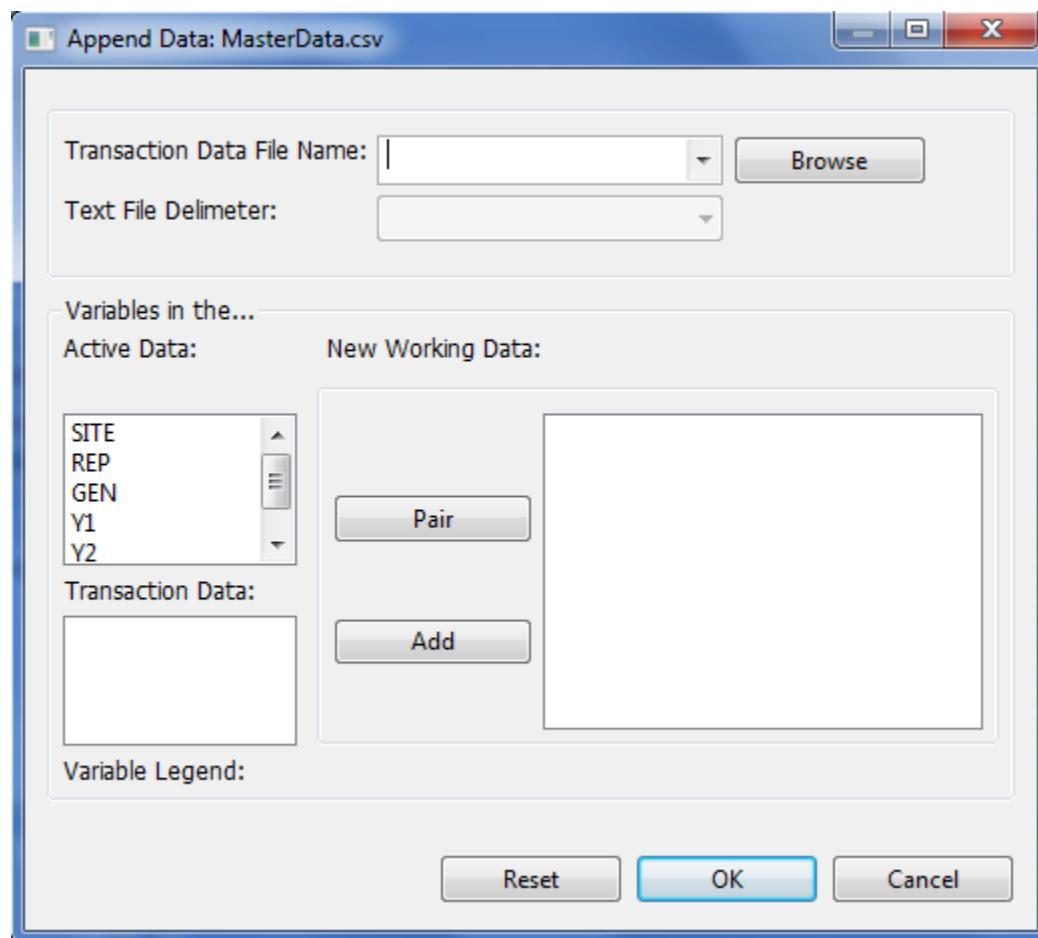
Append Datasets

The Append submenu can be used combine two data files with the same variables but different cases.

- On the **Project Explorer** panel, using the project named *MyProject*, import the data files *MasterData.csv* and *AppendTransact.csv* from the *Data* folder of the project named *SampleProject*. Double-click the file *MasterData.csv* to open it and view it in the Data Viewer.

To import data from the *SampleProject*, see *Importing Data from Other Project* section of this user's manual.

- Choose **Data | Append Datasets...** or click on the Append Datasets icon  in the Data Viewer toolbar. The Append Data dialog box will appear.



- Specify the required fields and appropriate options.

Transaction File Name

Specify this file by selecting a file using the drop-down combo box or by locating it using the **Browse** button. The files included in the drop-down combo box are files inside the *Data* folder not in its sub-folder. Only *.txt* and *.csv* data file format can be selected as the transaction file.

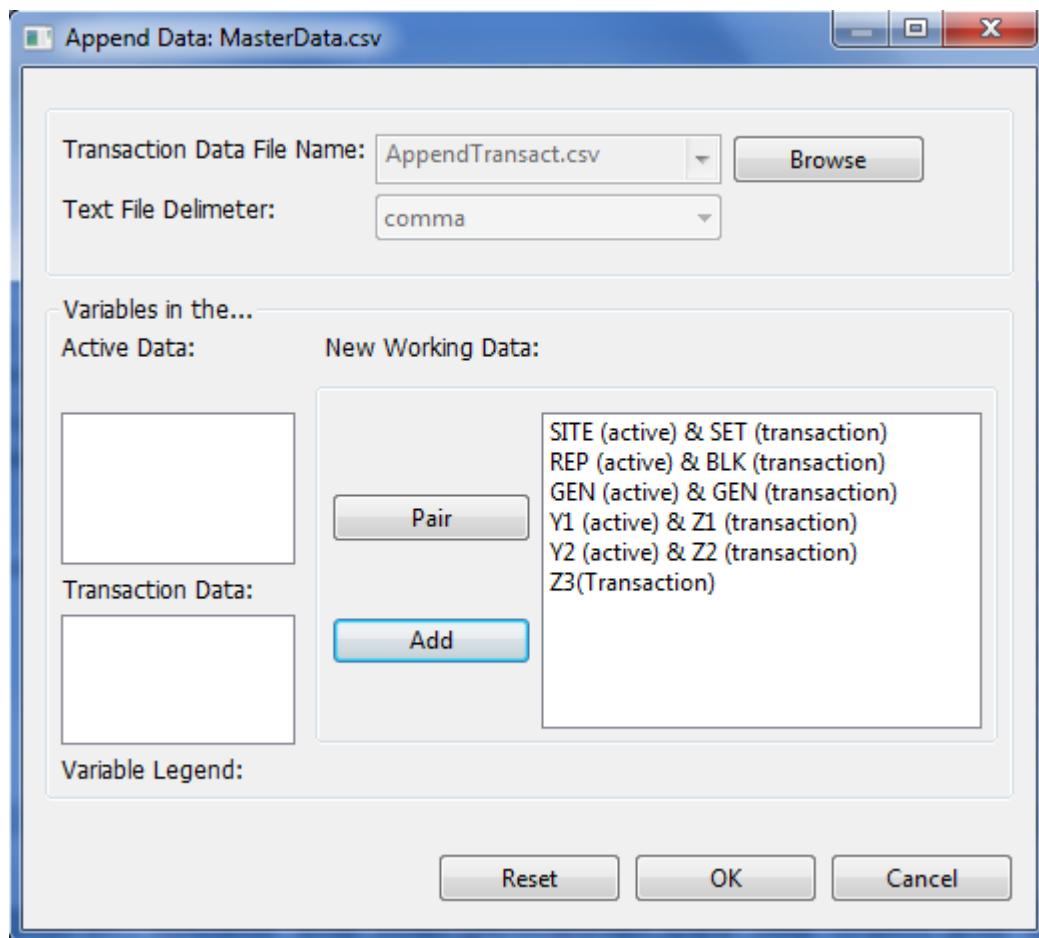
Text File Delimeter

If the transaction file selected is a text file, the delimeter should be specified. Four delimeters are available, namely: comma, space, tab and semi-colon

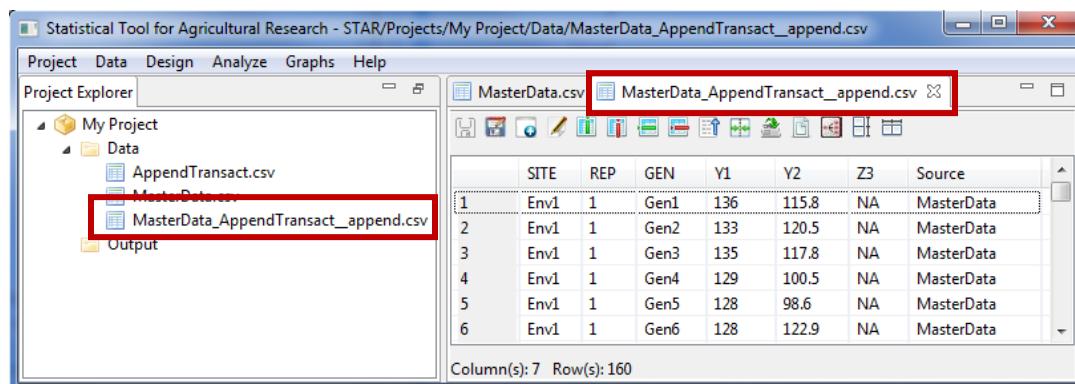
New Working Data

This is the list of variables or paired variables that will be included in the new data set. Variables can be paired by clicking one variable in the active data and clicking one variable in the transaction data then clicking the **Pair** button. Other variables can be added to this list by clicking the variable then clicking the **Add** button. For paired variables in this list, the appended data file that will be created will use the column name of the active data. For non-paired variables, **.1** will be appended to the column name coming from the active data and **.2** to the one from the transaction data.

For the example, select *AppendTransact.csv* file as the transaction data file from the drop-down combo box. The completed dialog box should appear as illustrated below:



- Click the **OK** button. The appended data is saved in the parent folder of the active data and displayed in the Data Viewer tab. The appended data will contain an additional column named *Source* which indicates where the data came from. The default filename of the appended data set follows the format `<activeDataFilename>_<TransactionDatafilename>_merge.csv`.



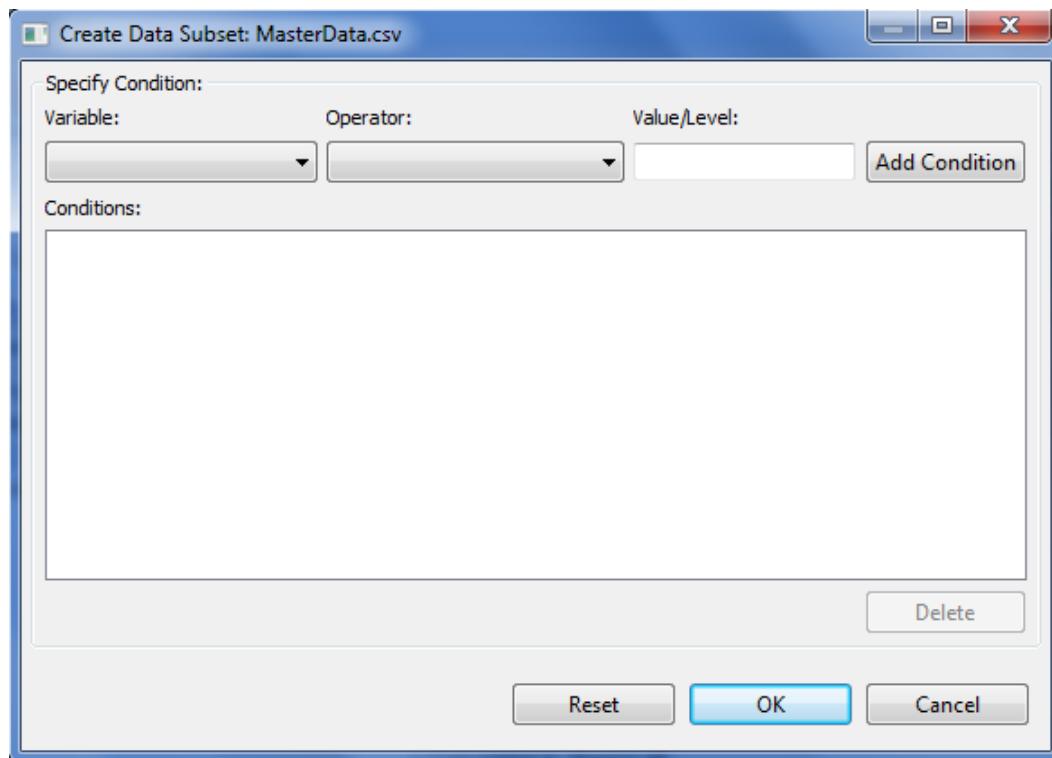
Creating Data Subset

The steps in creating a subset of a dataset are listed below:

- On the **Project Explorer** panel, using the project named *My Project*, import the data file *MasterData.csv* from the *Data* folder of the project named *SampleProject*. Double-click the file to open it and view it in the Data Viewer.

To import data from the *SampleProject*, see *Importing Data from Other Project* section of this user manual.

- Choose **Data | Create Data Subset...** or click on the Create Data Subset icon  in the Data Viewer toolbar. The **Create Data Subset** dialog box will appear.



- Specify the required fields and appropriate options.

Variable

This drop-down list box lists all the variables in the active data set. User can specify the variable by clicking the drop-down list box and selecting the variable of interest.

Operator

This drop-down list box lists the available relational operators that can be used. The seven available operators that can be used are: equal (==), not equal (!=), at least (\geq), at most (\leq), greater than (>), less than (<) and within the range. User can specify the variable by clicking the drop-down list box and selecting the operator of interest.

Value/Level

Specify the level or value of the variable specified. If the operator specified is *within range*, user must specify two values separated by comma. Otherwise, user should specify only one value/level.

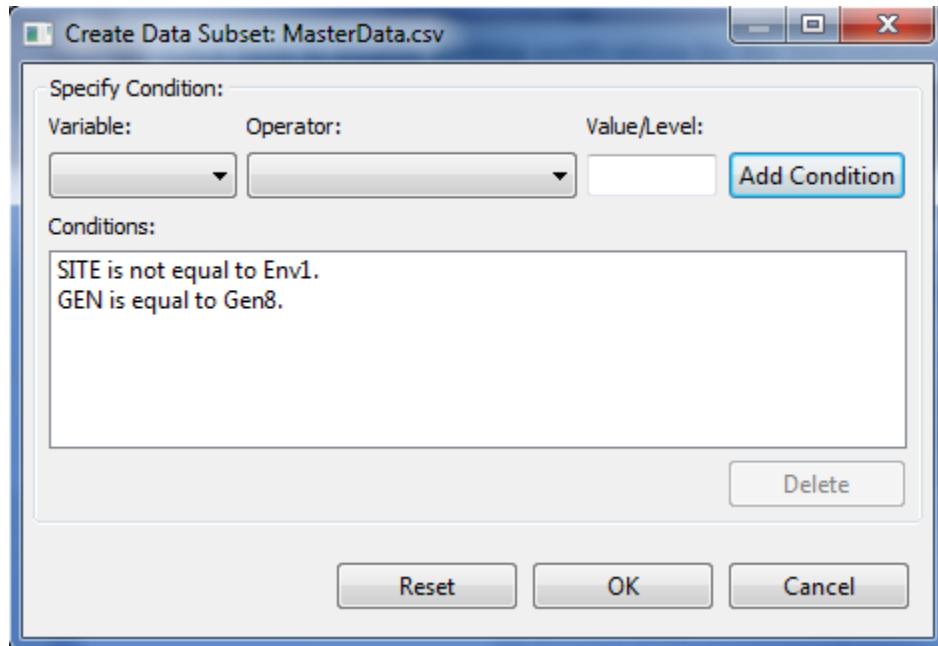
Add Condition

After specifying the conditional expression, user needs to click this button for the expression to be included in the **Conditions** list box.

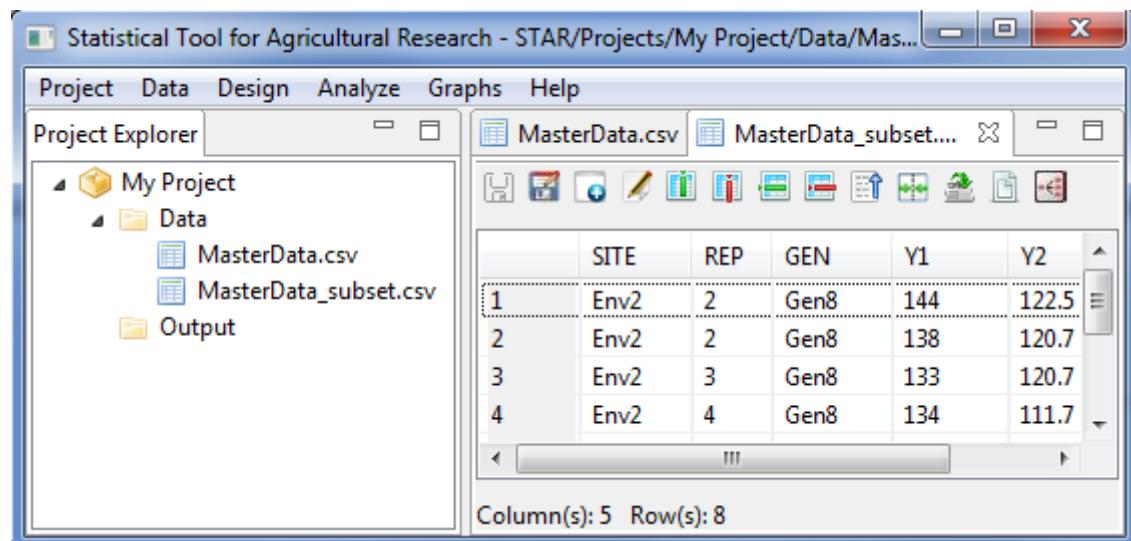
Conditions

All the conditional expressions specified in this list box will be used when sub setting the active data set.

For the example, the completed dialog box should appear as shown below:



- Click the **OK** button. The new data is saved in the parent folder of the active data and displayed in the Data Viewer tab. The default filename of the new data set follows the format <activeDataFilename>_subset.csv



Reshaping

The **Reshape submenu** can be used to restructure or reshape your active data set to follow the structure of the data set appropriate for the STAR procedure you want to use.

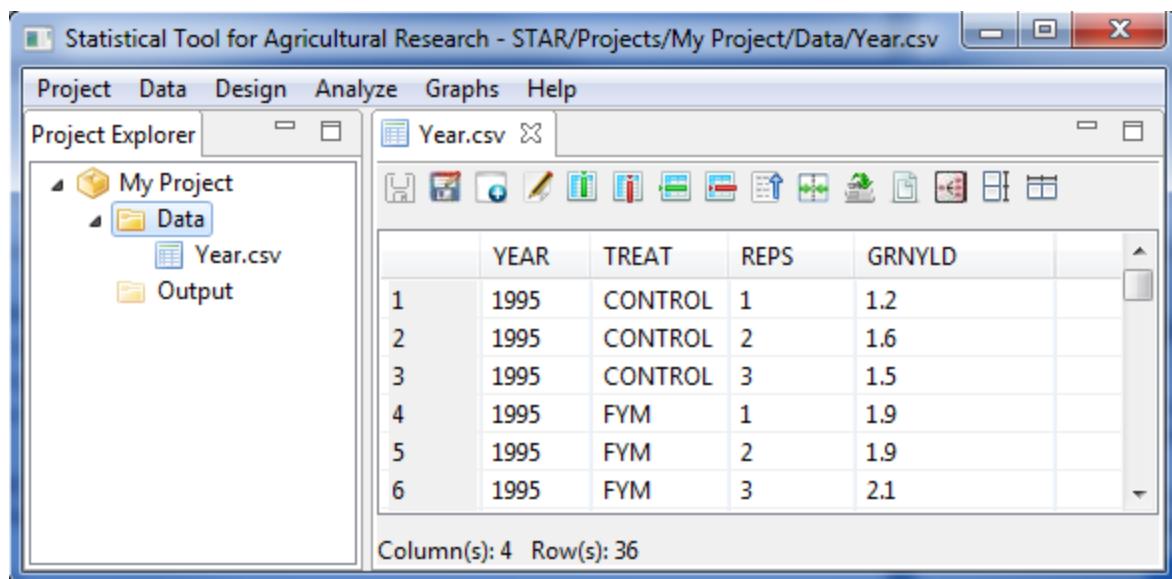
Reshaping Data from Long (Serial) to Wide (Parallel) Format

Reshaping data from long (serial) to wide (parallel) involves re-arranging a data file, such that, repeated measurements are in separate columns.

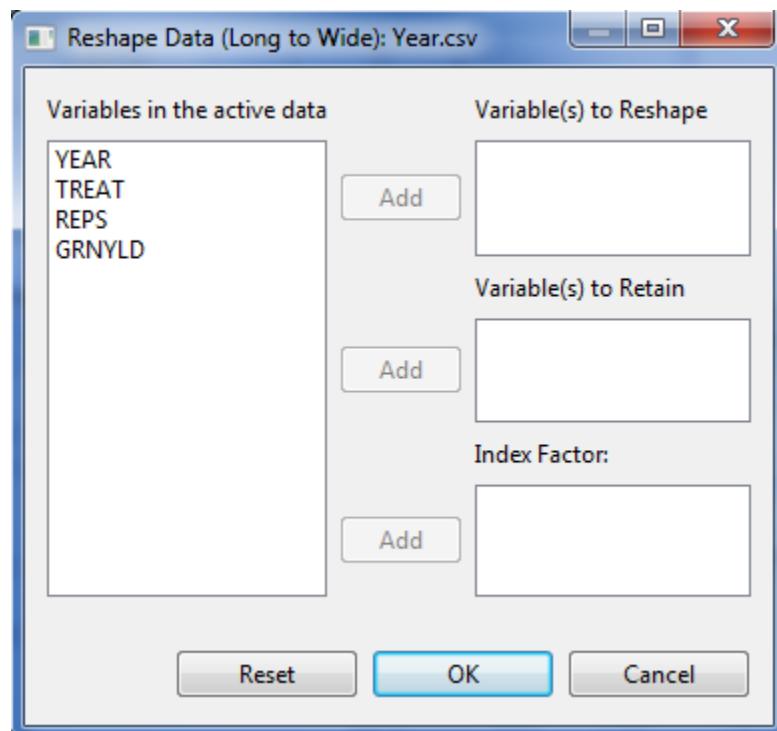
The steps for reshaping the data from long to wide format are listed below:

- On the **Project Explorer** panel, using the project named *My Project*, import the data files *Year* from package. Double-click the file to open it and view it in the Data Viewer.

To import data from the *SampleProject*, see *Importing Data from Other Project* section of this user manual.



- Click **Data | Reshape | Long (Serial) to Wide (Parallel) ...** from the main window or click on the Reshape to Wide icon  in the Data Viewer tool bar. The **Reshape Data (Long to Wide)** dialog box will automatically appear as shown below.



- Specify the required fields and appropriate options.

Variables to be Reshape

This pertains to the list of variable(s) which is to be divided into two or more columns and saved to different variables in terms of the levels of the index factor.

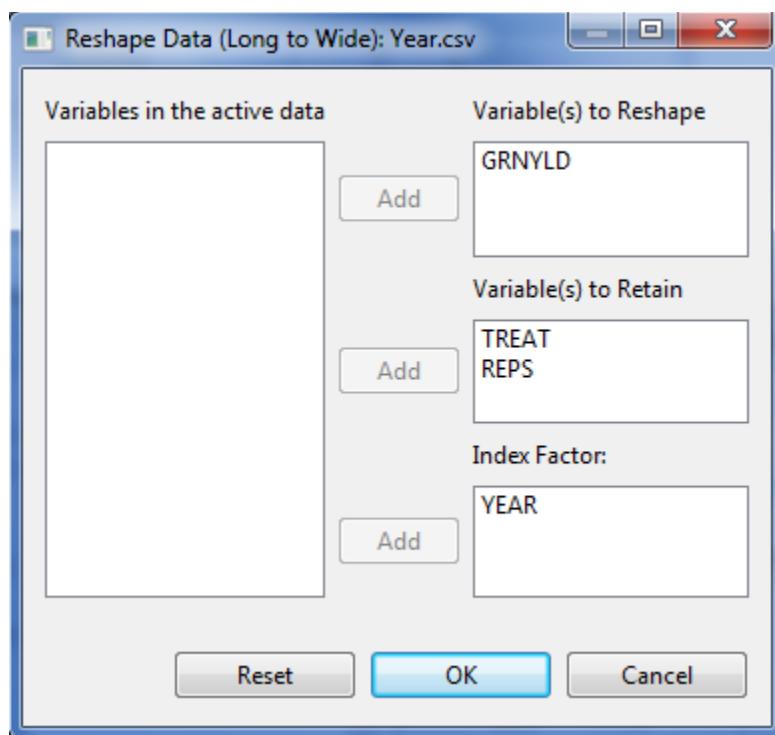
Variables to be Retained

This pertains to variable(s) to be retained to describe the individual cases or observations.

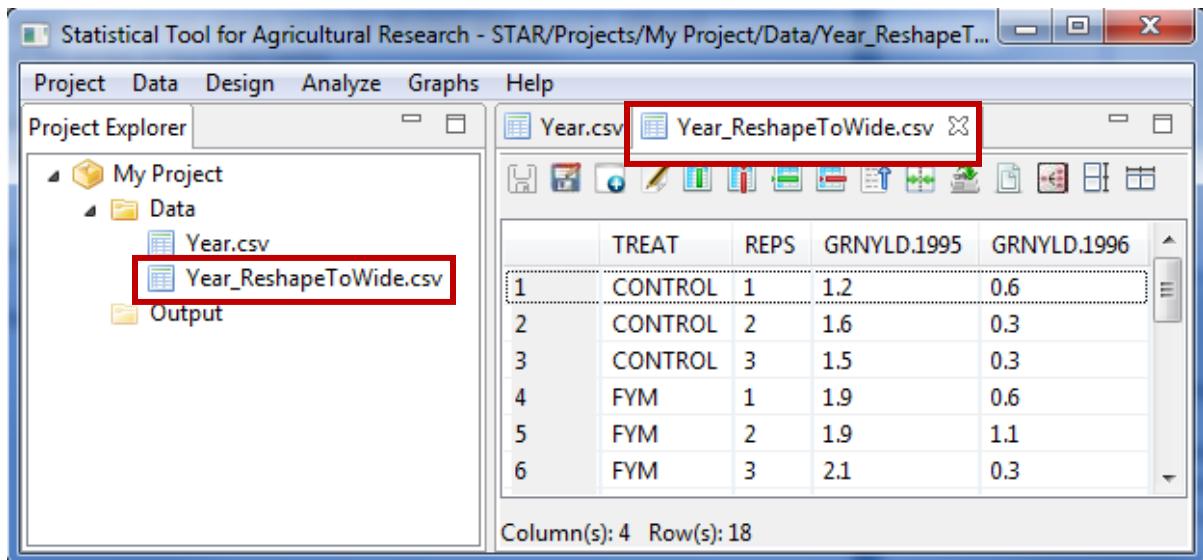
Index Factor

This pertains to variable(s) which will determine the groupings of the values of the variable(s) to be transposed

For the example, the completed **Reshape Data (Long to Wide)** dialog box should now look like this:



- Click the **Ok** button. The restructured data set is saved in the parent folder of the active data and displayed in the Data Viewer tab. The default filename of the restructured data set follows the format <activeDataFilename>_ReshapeToWide.csv.



Reshape Data from Wide to Long Format

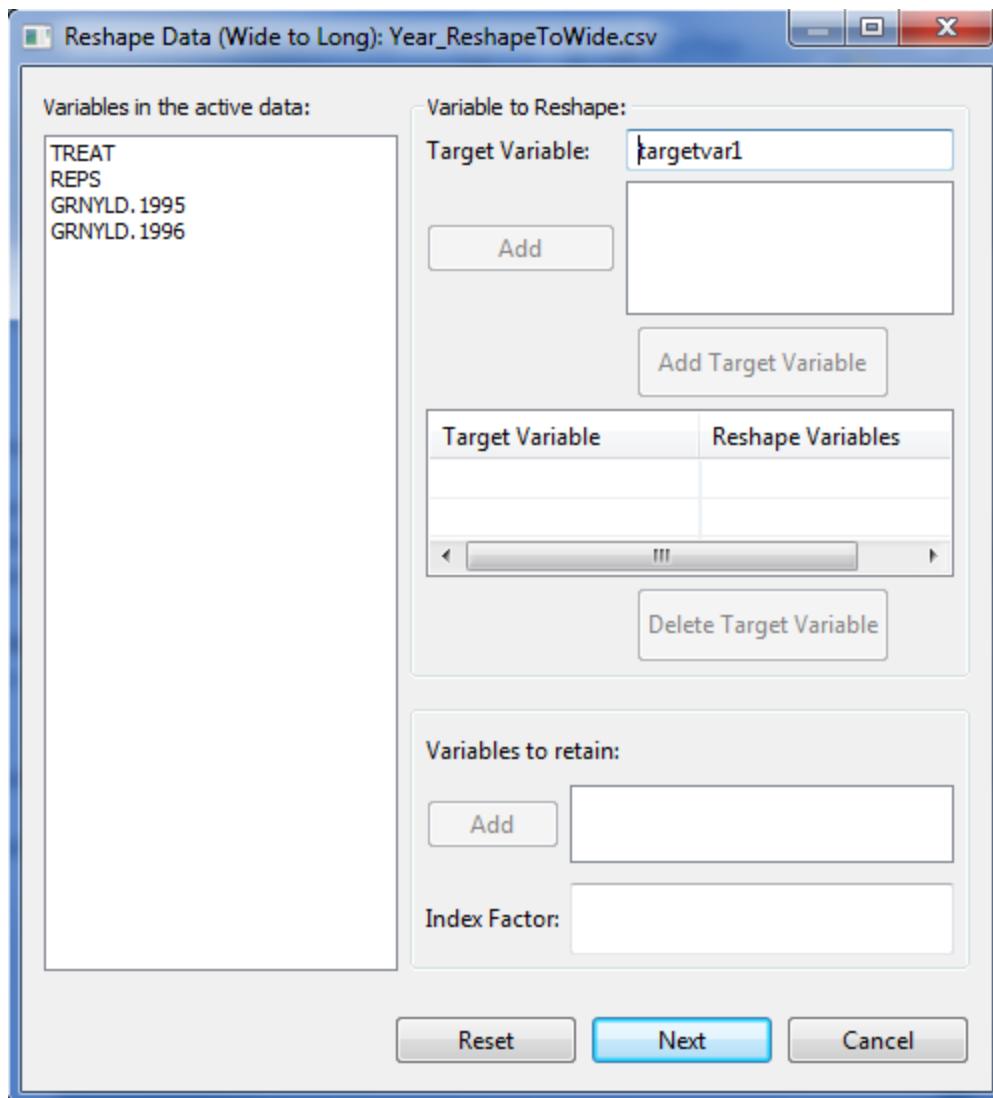
Manipulating data from wide (parallel) to long (serial) refers to re-arranging a multivariate into a univariate data. For instance, different columns representing measurements taken for a response variable over a period of time can be combined to form a single column, with the time variable used as an additional identifier variable.

The steps for reshaping the data from wide to long format are listed below:

- On the **Project Explorer**, double-click the file to be reshaped to open and view it in the Data Viewer tab.

For the example, locate the *Year_ReshapeToWide.csv* file from the *Data* folder of the project named *MyProject*. This file was generated from the section *Reshape Data from Long to Wide Format* of this user's manual.

- Click **Data | Reshape | From Wide (Parallel) to Long (Serial) ...** from the main window or click on the Reshape to Long icon  in the Data Viewer tool bar. The **Reshape Data (Wide to Long)** dialog box will appear.



- Specify the required fields and appropriate options:

Variable to be Reshape

These are the variables that will be combined to form one variable. Click the variables in the list of variables in the active data while holding the Ctrl key then click the **Add** button. Moreover, the user should specify as the target variable the name of the variable to be created. The default target variable name is *targetvar1*. Then click the **Add Target Variable**. In specifying the name of the target variable, the following rules apply:

- The name must start with a letter. The remaining characters can be any letter, any digit, a period or underscore.
- Each column name must be unique; duplication is not allowed.
- Column name is case sensitive

User can create at least one target variable. This target variable should be unique and the length of the *Reshape Variables* should be the equal for all target variables to be created.

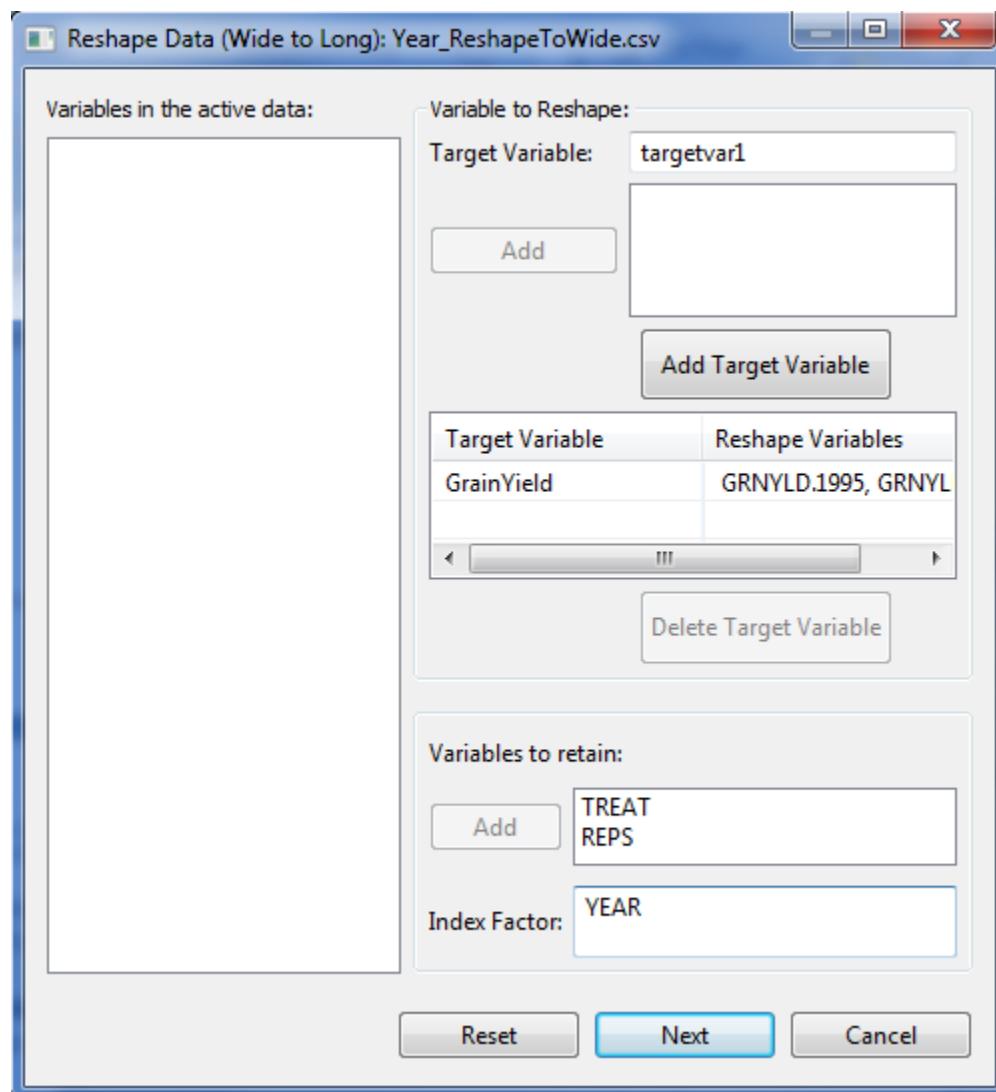
Variables to be Retained

These are the variables that will be included in the restructured data set and pertains to variables that describe the individual cases.

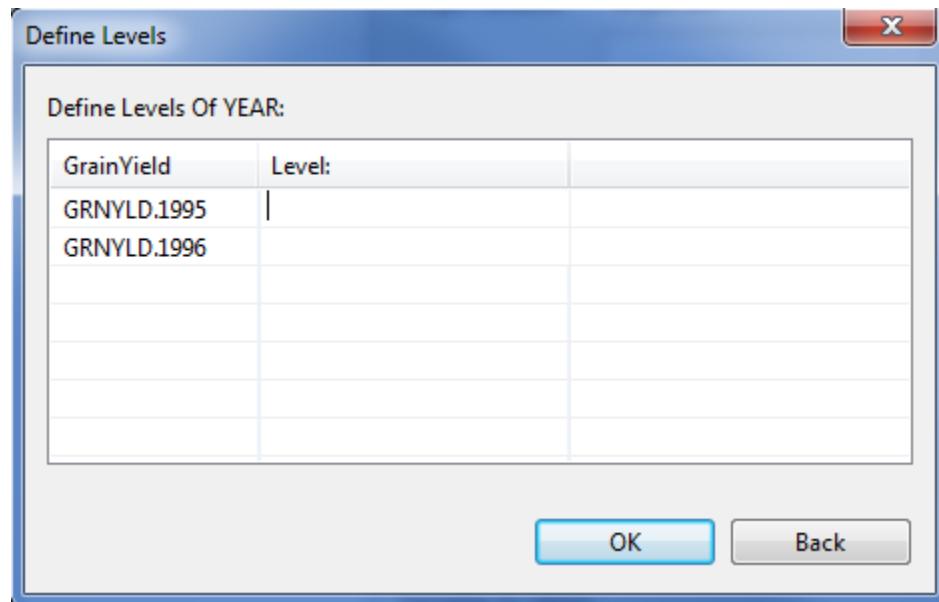
Index Factor

This is the name of the grouping variables that will be created.

For the *example*, the completed dialog box should appear as shown below:

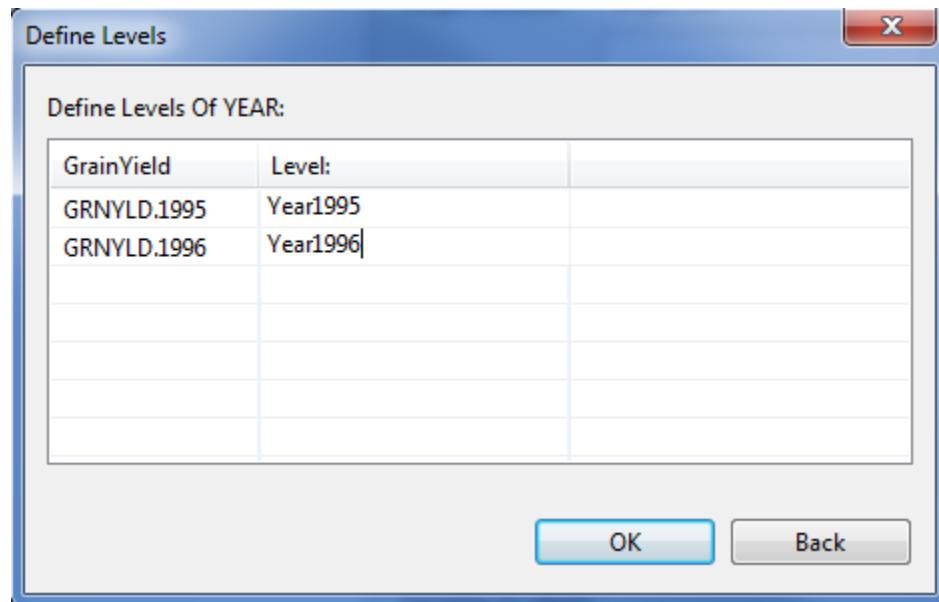


- Click the **Next** button to proceed. The **Define Levels** dialog box will appear.

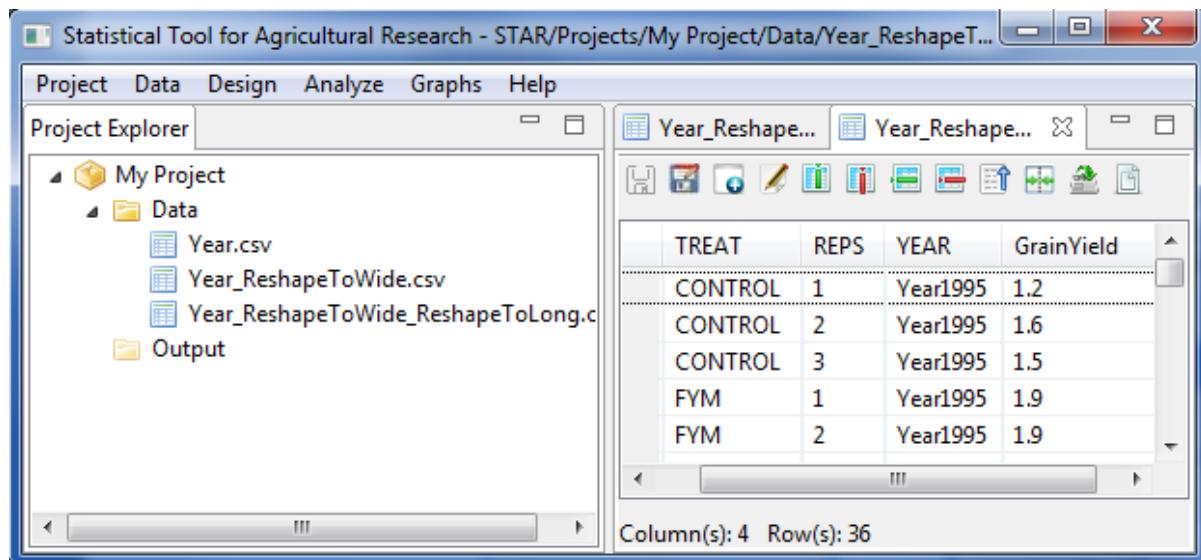


- Specify the required fields.

For the example, the complete dialog box should appear as shown below:



- Click the **OK** button. The restructured data set is saved in the parent folder of the active data and displayed in the Data Viewer tab. The default filename of the restructured data set follows the format <activeDataFilename>_ReshapeToLong.csv.



Aggregate

The **Aggregate submenu** aggregates group of observations into single observation and creates a new, aggregated data file or creates new columns in the active data file that contain the aggregated data. Observations are aggregated based on the value of one or more grouping variables.

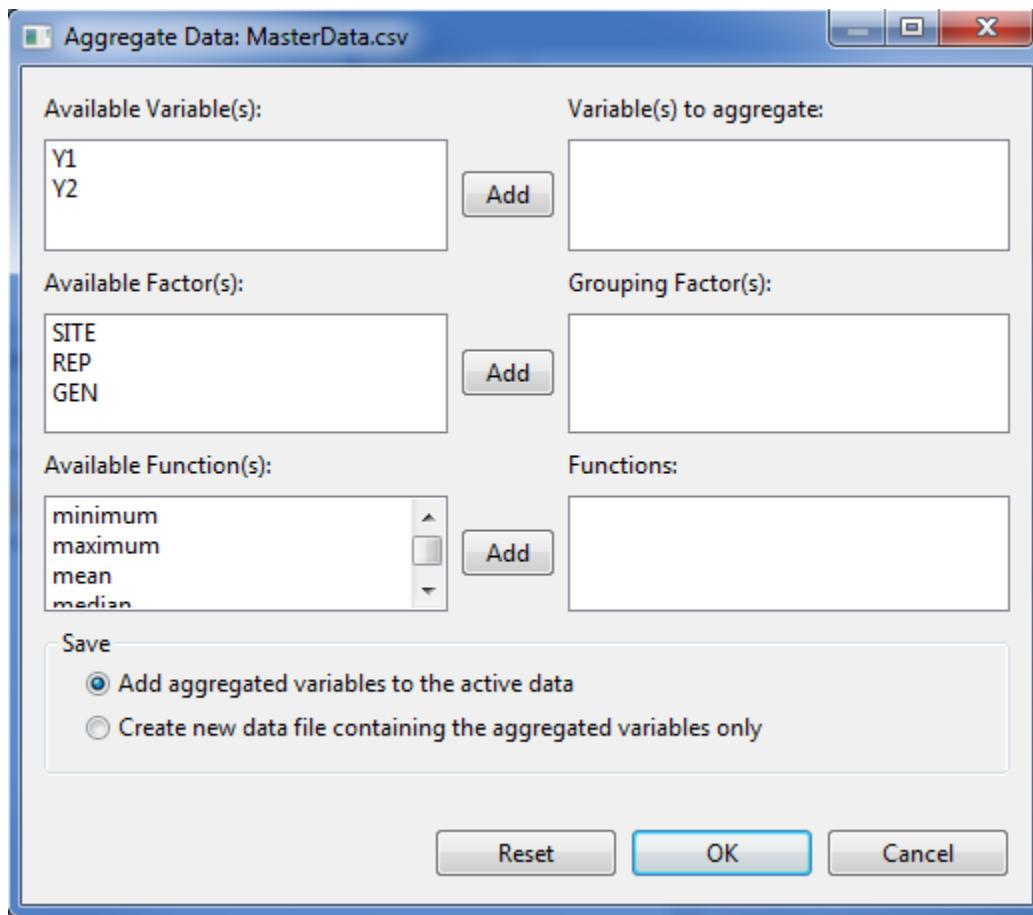
The steps for aggregating the data are listed below:

- On the **Project Explorer**, double-click the file to be used to open and view it in the Data Viewer tab.

For the example, using the project named *MyProject*, import the data file *MasterData.csv* from the *Data* folder of the project named *SampleProject*. To import data from the *SampleProject*, see *Importing Data from Other Project* section of this user's manual.

Opening the data for the first time, *REP* field is regarded by STAR as numerical variable. To change its type, go to **Data | Edit Variable Information** and change the *Variable Type* of *REP* from *Numeric* to *Factor*.

- Choose **Data | Aggregate...** or click on the Aggregate Data icon in the Data Viewer tool bar.



- Specify the required fields and appropriate options.

Variable(s) to Aggregate

This is the list of variables whose values will be summarized using the selected functions. At least one entry is needed and should come from the **Available Variable(s)** list box.

Grouping Factor(s)

This field is optional. If specified, it will summarize the values per category of the grouping factor. Entries should come from the **Available Factor(s)** list box.

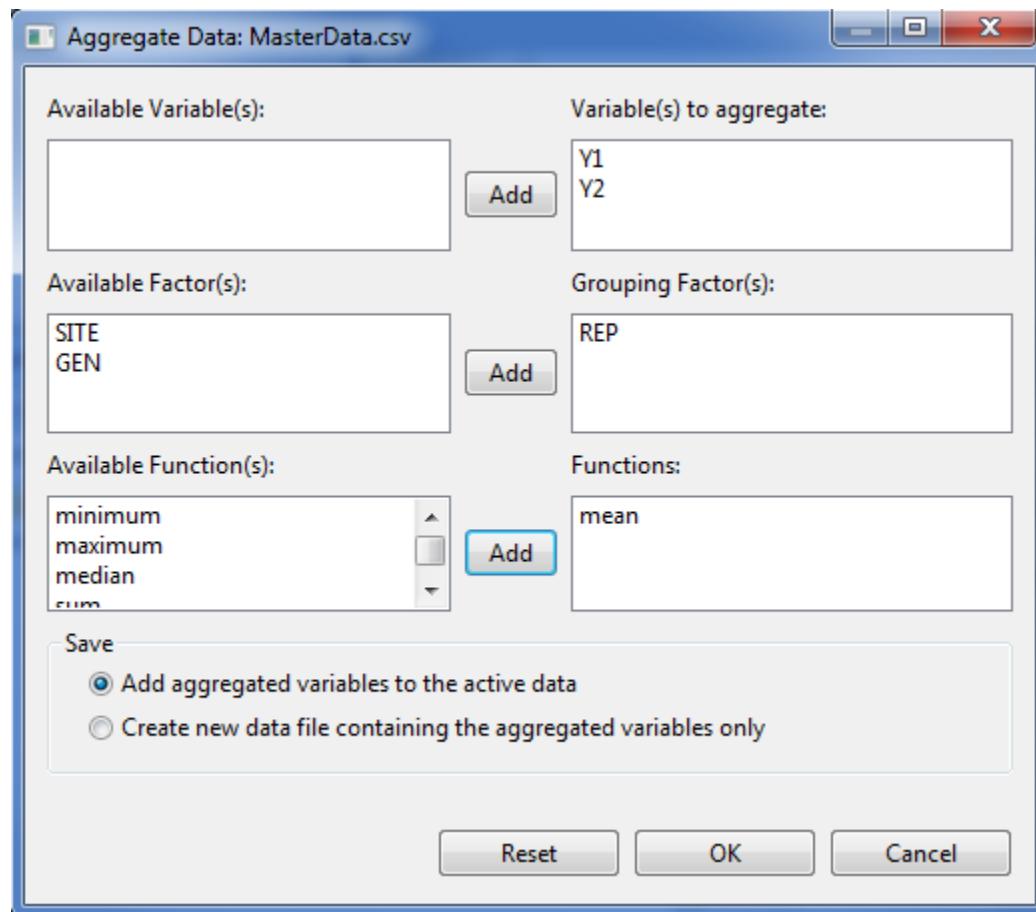
Functions

At least one function should be specified. Available functions are minimum, maximum, mean, median, sum, variance and standard deviation.

Save

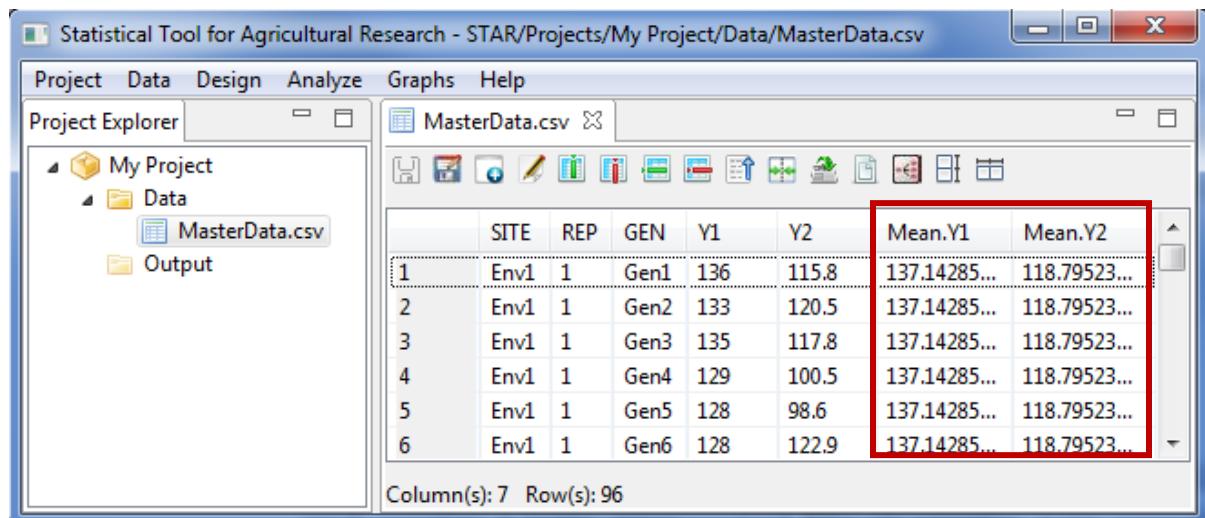
Specify how the aggregated data will be saved. User can either add aggregated variables to the active data (default options) or create a new data file containing the aggregated variables only. If user chooses the default option, the resulting data file is not aggregated. Each observations with the save value(s) of the grouping variable(s) will receive the same values of the new aggregated variables. If user chooses the option create a new data file containing the aggregated variables only, the new data files contains one observation for each category of the grouping variables.

For the example, suppose we want to compute the mean of the variables *Y1* and *Y2* for each level of *REP*. The completed dialog box should appear as shown below:

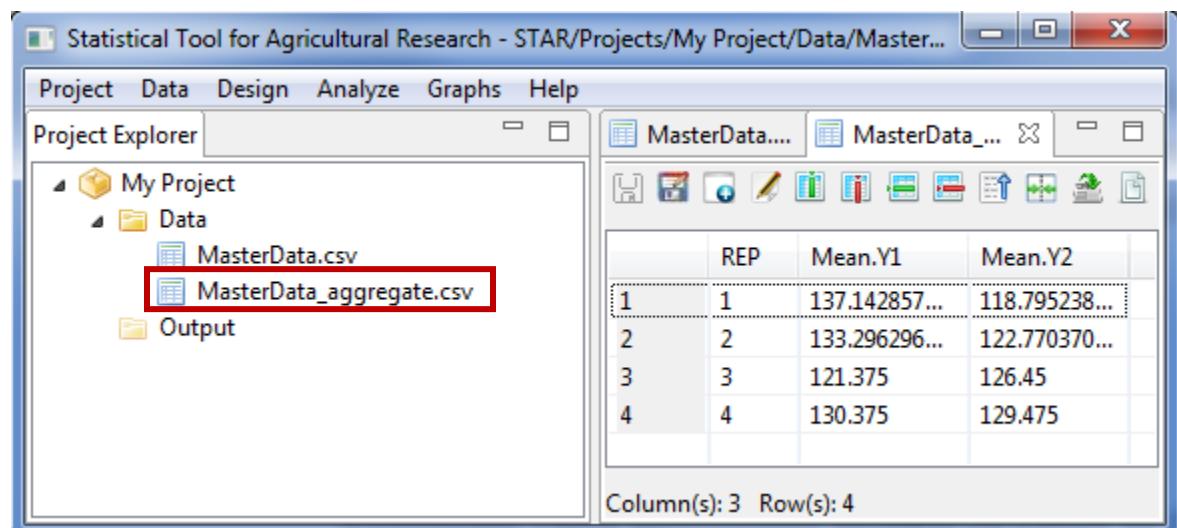


- Click the **OK** button.

If the user chooses the save option: *add aggregated variables to the active data* (default option), the active data is saved with the additional column(s) and displayed in the Data Viewer. The default column name(s) which contain the aggregate data follows the format *<Function>.< Variable to aggregate >*.



If the user chooses the save option: *create a new data file containing the aggregated variables only*, the aggregated data file is saved in the parent folder of the active data and displayed in the Data Viewer. The default column name(s) which contain the aggregate data follows the format <Function>.<Variable name to aggregate> and the default filename of the aggregated data set follows the format <activeDataFilename>_aggregate.csv.



Randomization and Layout

The **Design Menu** allows user to generate randomization and layout for single- and multi-factor designs. If the menu is used for the first-time in the active project, a *Randomization* folder will be created inside the *Output* folder. Sub-folders will be created inside the *Randomization* folder where the generated field book in csv format and a text file will be saved. The default sub-folder name follows the format <design>_<time stamp>.

Completely Randomized Design

The randomization that will be generated is for balanced design. Equal number of replicates will be generated for each level of the factor or treatment combination.

The steps to generate randomization are listed below:

- To perform randomization, click **Design | Completely Randomized Design....** The **Randomization and Layout** dialog box will appear.
- Specify the required fields and appropriate options.

Number of Factors

Define the number of factors to be generated with default and minimum value equal to 1 and maximum value equal to 10. The number of factors specified will define the number of rows of the table inside the **Factor Definition** frame. To change the default value, user can either type a value inside the spin box or click the up-arrow key of the spin box to increase the value, down-arrow key, otherwise.

Factor Definition Frame

Name

Contain the default name for each factor which can be change. In specifying the factor name, the following rules apply:

- name should not contain any space;
- must begin with a letter or a period (.) ;
- succeeding characters can be a combination of letters, numbers, period (.) and underscore (_); and

- name must be different from other factor names already specified.

Factor ID

Contain the default code for each factor. User can change the factor ID by typing the desired factor ID. Factor ID should consist of 1 to 4 letters only and should be unique.

Levels

Contain the level for each factor. User can change the level of the factor by either typing a value inside the spin box or clicking the up-arrow key of the spin box to increase the value, down-arrow key, otherwise. The default and minimum value of the levels is equal to 2 while the maximum value of the levels is 500.

Number of Replicates

Define the number of replicates to be generated for each level of the factor or for each treatment combination. The default and minimum value is equal to 2.

Number of Field Rows

Define the number of rows in the field layout for each trial. The default and minimum value is equal to one.

Number of Trial

Define the number of trials to be generated. The default and minimum value is equal to one.

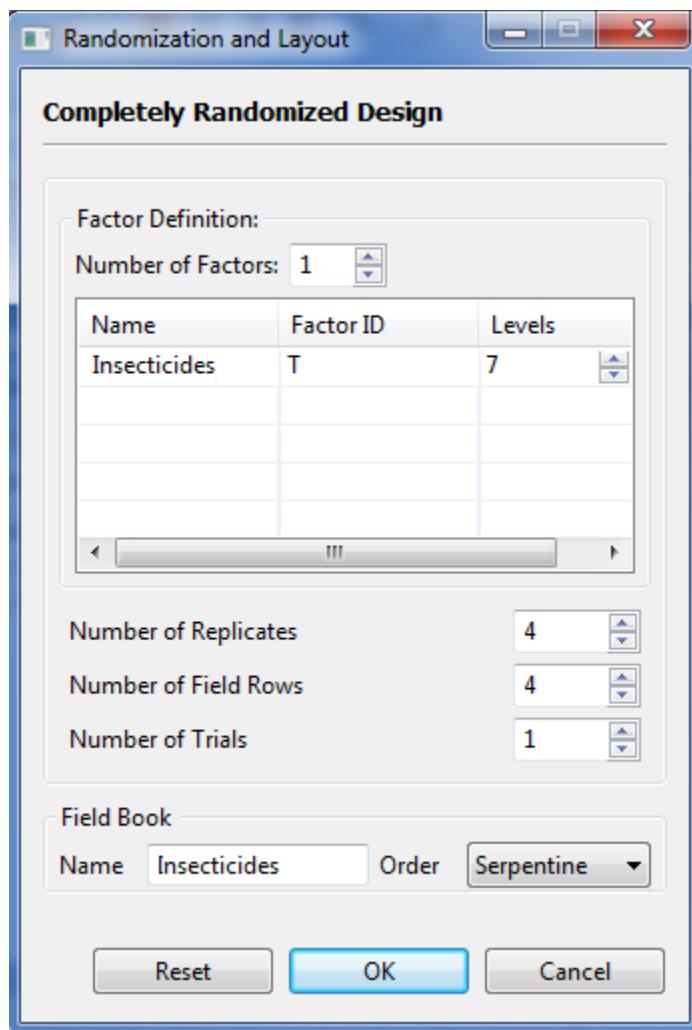
Field Book Filename

This field is required and it specifies the file name where the result of the randomization will be saved. The default filename is *fieldbookCRD*.

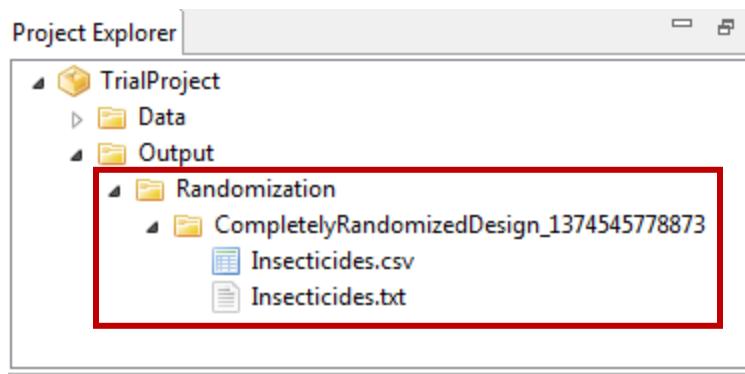
Field Book Order

Define how the plot number will be arranged. There are two options available: *Plot Order* (default value) and *Serpentine*.

For the example, suppose we want to generate a randomization for an experiment whose aim is to compare the effects of seven different foliar and granular insecticides on the grain yield of a certain rice variety. The experiment will be conducted in completely randomized design with four replicates. The completed dialog box should appear as shown below:



- Click the **OK** button to generate the randomization. The **Randomization** dialog box will be minimized and STAR will automatically display the csv data file and the txt file created in the Data Viewer tab.



Sample *txt* file displayed in the Data Viewer tab is shown below:

DESIGN PROPERTIES:
Single Factor
Completely Randomized Design

DESIGN PARAMETERS:
Number of Trials = 1
Number of Replicates = 4
Treatment Name = Insecticides
Treatment Levels = T1, T2, T3, ..., T7

Layout for Completely Randomized Design

Trial = 1

1	2	3	4	5	6	7
T2	T7	T3	T6	T4	T5	T1
8	9	10	11	12	13	14
T2	T1	T1	T3	T2	T1	T5
15	16	17	18	19	20	21
T6	T5	T7	T5	T2	T6	T4
22	23	24	25	26	27	28
T3	T6	T4	T4	T7	T7	T3

**Note: Cells contain plot numbers on top, treatments/entries below

Sample csv data file displayed in the Data Viewer tab is shown below:

The screenshot shows a software interface with two tabs labeled "Randomization\Completel..." at the top. Below the tabs is a toolbar with various icons. The main area is a data viewer containing a table with six columns: Trial, Insecticides, PlotNum, FieldRow, FieldColumn, and an unlabeled column represented by a vertical ellipsis. The data consists of 8 rows, each with values corresponding to the columns. At the bottom of the data viewer, it says "Column(s): 5 Row(s): 28".

	Trial	Insecticides	PlotNum	FieldRow	FieldColumn	
1	1	T1	1	1	1	
2	1	T5	2	1	2	
3	1	T3	3	1	3	
4	1	T7	4	1	4	
5	1	T7	5	1	5	
6	1	T2	6	1	6	
7	1	T4	7	1	7	
8	1	T2	8	2	7	

Randomized Complete Block Design

The steps to generate randomization in are listed below:

- To perform randomization, click **Design | Randomized Complete Block Design**. The **Randomization and Layout** dialog box will appear.
- Specify the required fields and appropriate options.

Number of Factors

Define the number of factors to be generated with default and minimum value equal to 1 and maximum value equal to 10. The number of factors specified will define the number of rows of the table inside the **Factor Definition** frame. To change the default value, user can either type a value inside the spin box or click the up-arrow key of the spin box to increase the value, down-arrow key, otherwise.

Factor Definition Frame

Name

Contain the default name for each factor which can be change. In specifying the factor name, the following rules apply:

- name should not contain any space;
- must begin with a letter or a period (.) ;
- succeeding characters can be a combination of letters, numbers, period (.) and underscore (_); and

- name must be different from other factor names already specified.

Factor ID

Contain the default code for each factor. User can change the factor ID by typing the desired factor ID. Factor ID should consist of 1 to 4 letters only and should be unique.

Levels

Contain the level for each factor. User can change the level of the factor by either typing a value inside the spin box or clicking the up-arrow key of the spin box to increase the value, down-arrow key, otherwise. The default and minimum value of the levels is equal to 2 while the maximum value of the levels is 500.

Number of Blocks

Define the number of blocks to be generated. The default and minimum value is equal to 2.

Number of Rows per Block

Define the number of rows per block. The default and minimum value is equal to 2.

Number of Field Rows

Define the number of rows in the field layout for each trial. The default and minimum value is equal to one.

Number of Trial

Define the number of trials to be generated. The default and minimum value is equal to one.

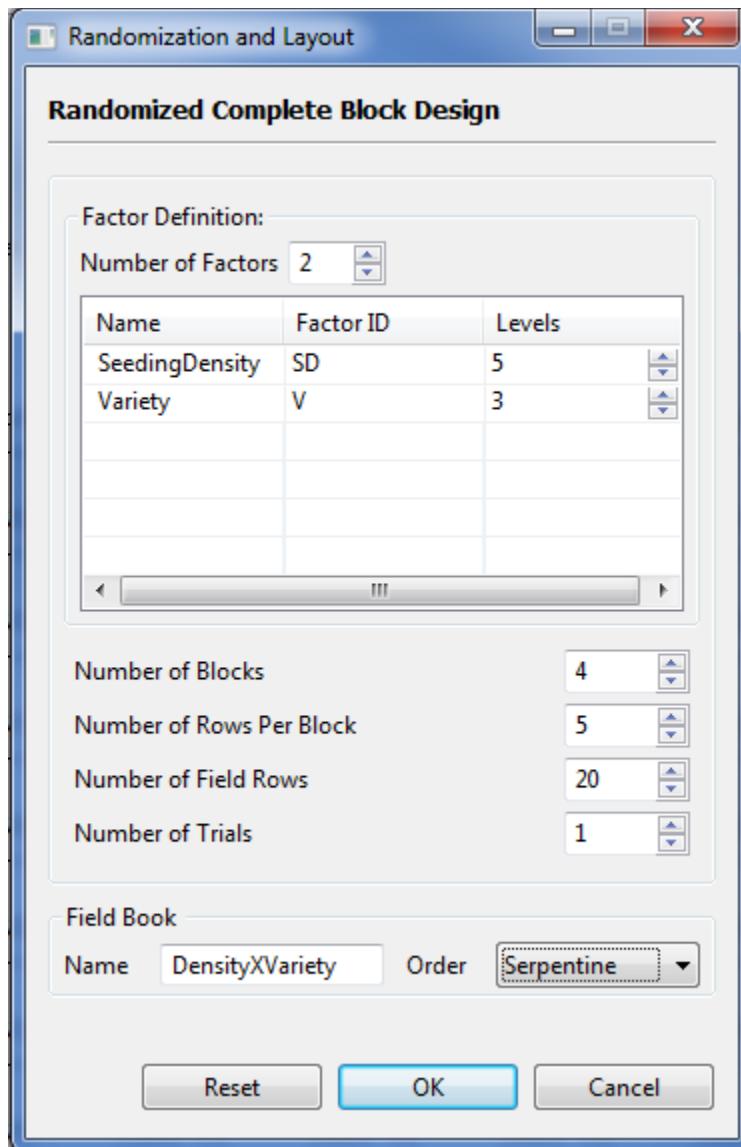
Field Book Filename

This field is required and it specifies the file name where the result of the randomization will be saved. The default filename is *fieldbookRCBD*.

Field Book Order

Define how the plot number will be arranged. There are two options available: *Plot Order* (default value) and *Serpentine*.

For the example, suppose we want to generate a randomization for an experiment whose aim is to compare the effects of five seeding densities on the on grain yield of three rice varieties. The experiment will be conducted in randomized complete block design with four blocks in one trial. The completed dialog box should appear as shown below:



- Click the **OK** button to generate the randomization. The **Randomization and Layout** dialog box will be minimized and STAR will automatically display the csv data file and the *txt* file created in the Data Viewer tab.

Sample *txt* file displayed in the Data Viewer tab is shown below:

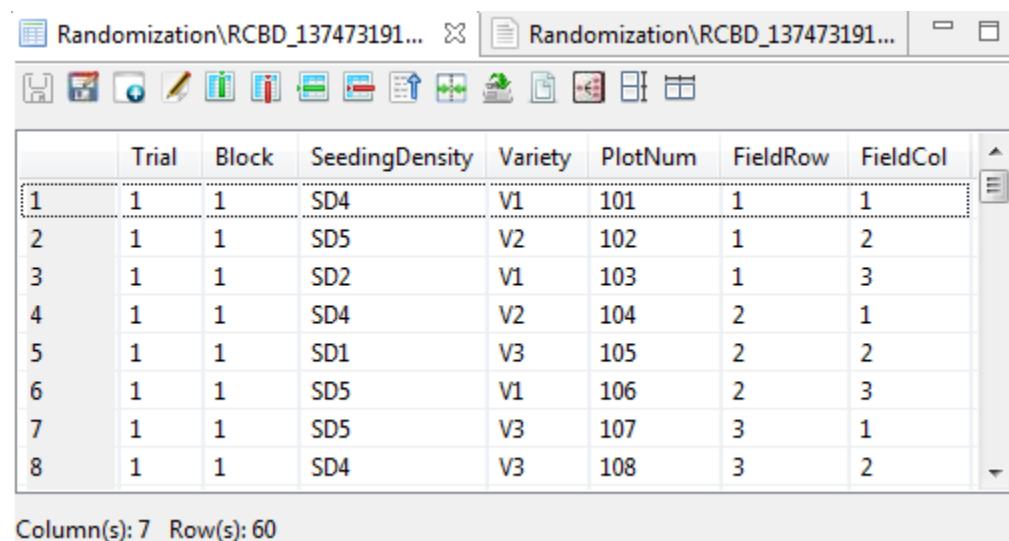
```
DESIGN PROPERTIES:  
    Factorial Design  
    Randomized Complete Block Design  
  
DESIGN PARAMETERS:  
    Number of Trials = 1  
    Number of Blocks = 4  
    Factor 1 = SeedingDensity  
    Levels = SD1, SD2, SD3, SD4, SD5  
    Factor 2 = Variety  
    Levels = V1, V2, V3  
  
    Number of Field Row = 20  
    Number of Field Column = 3  
  
Layout for Randomized Complete Block Design
```

```
Trial = 1  
  
          FieldCol1   FieldCol2   FieldCol3  
          +-----+-----+-----+  
FieldRow1 |       101|       102|       103|  
          |SD4 V1   |SD5 V2   |SD2 V1   |  
          +-----+-----+-----+  
FieldRow2 |       104|       105|       106|  
          |SD4 V2   |SD1 V3   |SD5 V1   |  
          +-----+-----+-----+  
FieldRow3 |       107|       108|       109|  
          |SD5 V3   |SD4 V3   |SD1 V1   |  
          +-----+-----+-----+  
FieldRow4 |       110|       111|       112|  
          |SD1 V2   |SD2 V3   |SD3 V2   |  
          +-----+-----+-----+  
FieldRow5 |       113|       114|       115|  
          |SD3 V3   |SD2 V2   |SD3 V1   |  
          +-----+-----+-----+  
FieldRow6 |       201|       202|       203|  
          |SD1 V1   |SD4 V1   |SD5 V1   |  
          +-----+-----+-----+  
FieldRow7 |       204|       205|       206|  
          |SD1 V2   |SD4 V2   |SD3 V1   |  
          +-----+-----+-----+  
FieldRow8 |       207|       208|       209|  
          |SD1 V3   |SD3 V3   |SD2 V1   |  
          +-----+-----+-----+  
FieldRow9 |       210|       211|       212|  
          |SD2 V3   |SD3 V2   |SD2 V2   |  
          +-----+-----+-----+  
FieldRow10|       213|       214|       215|  
          |SD5 V2   |SD4 V3   |SD5 V3   |  
          +-----+-----+-----+  
FieldRow11|       301|       302|       303|  
          |SD5 V3   |SD4 V2   |SD2 V1   |
```

FieldRow12	304	305	306
	SD5 V1	SD5 V2	SD2 V2
FieldRow13	307	308	309
	SD3 V2	SD1 V1	SD1 V3
FieldRow14	310	311	312
	SD3 V3	SD3 V1	SD4 V3
FieldRow15	313	314	315
	SD1 V2	SD4 V1	SD2 V3
FieldRow16	401	402	403
	SD4 V2	SD5 V3	SD2 V3
FieldRow17	404	405	406
	SD3 V1	SD4 V1	SD1 V3
FieldRow18	407	408	409
	SD5 V2	SD4 V3	SD2 V1
FieldRow19	410	411	412
	SD3 V2	SD1 V1	SD5 V1
FieldRow20	413	414	415
	SD3 V3	SD2 V2	SD1 V2

**Note: Cells contain plot numbers on top, treatments/entries below

Sample csv data file displayed in the Data Viewer tab is shown below:



	Trial	Block	SeedingDensity	Variety	PlotNum	FieldRow	FieldCol
1	1	1	SD4	V1	101	1	1
2	1	1	SD5	V2	102	1	2
3	1	1	SD2	V1	103	1	3
4	1	1	SD4	V2	104	2	1
5	1	1	SD1	V3	105	2	2
6	1	1	SD5	V1	106	2	3
7	1	1	SD5	V3	107	3	1
8	1	1	SD4	V3	108	3	2

Column(s): 7 Row(s): 60

Latin Square Design

The steps to generate randomization are listed below:

- To perform randomization, click **Design | Latin Square Design....** The **Randomization and Layout** dialog box will appear.
- Specify the required fields and appropriate options.

Number of Factors

Define the number of factors to be generated with default and minimum value equal to 1 and maximum value equal to 10. The number of factors specified will define the number of rows of the table inside the **Factor Definition** frame. To change the default value, user can either type a value inside the spin box or click the up-arrow key of the spin box to increase the value, down-arrow key, otherwise.

Factor Definition Frame

Name

Contain the default name for each factor which can be change. In specifying the factor name, the following rules apply:

- name should not contain any space;
- must begin with a letter or a period (.) ;
- succeeding characters can be a combination of letters, numbers, period (.) and underscore (_); and
- name must be different from other factor names already specified.

Factor ID

Contain the default code for each factor. User can change the factor ID by typing the desired factor ID. Factor ID should consist of 1 to 4 letters only and should be unique.

Levels

Contain the level for each factor. User can change the level of the factor by either typing a value inside the spin box or clicking the up-arrow key of the spin box to increase the value, down-arrow key, otherwise. The default and minimum value of the levels is equal to 2. The maximum levels of the factor or treatment combination should be equal to 11.

Number of Trial

Define the number of trials to be generated. The default value and minimum value is equal to one.

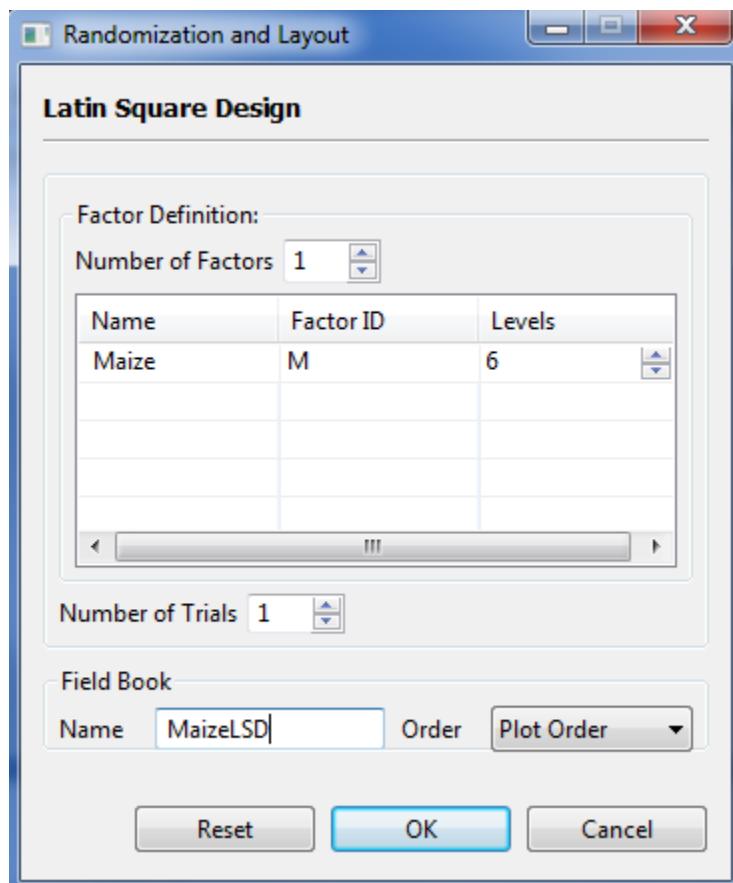
Field Book Filename

This field is required and it specifies the file name where the result of the randomization will be saved. The default filename is *fieldbookLSD*.

Field Book Order

Define how the plot number will be arranged. There are two options available: *Plot Order* (default value) and *Serpentine*.

For the example, suppose we want to generate a randomization for an experiment to be laid out in Latin Square design whose aim is to compare the grain yield of five promising maize hybrids and a check variety. The completed dialog box should appear as shown below:



- Click the **OK** button to generate the randomization. The **Randomization and Layout** dialog box will be minimized and STAR will automatically display the *csv* data file and the *txt* file created in the Data Viewer tab.

Sample *txt* file displayed in the Data Viewer is shown below:

DESIGN PROPERTIES:
Single Factor
Latin Square Design

DESIGN PARAMETERS:
Number of Trials = 1
Treatment Name = Maize
Treatment Levels = M1, M2, M3, ..., M6

Layout for Latin Square Design

Trial = 1

1	2	3	4	5	6
M6	M3	M2	M4	M1	M5
7	8	9	10	11	12
M5	M2	M1	M3	M6	M4
13	14	15	16	17	18
M1	M4	M3	M5	M2	M6
19	20	21	22	23	24
M2	M5	M4	M6	M3	M1
25	26	27	28	29	30
M3	M6	M5	M1	M4	M2
31	32	33	34	35	36
M4	M1	M6	M2	M5	M3

**Note: Cells contain plot numbers on top, treatments/entries below

Sample csv data file displayed in the Data Viewer is shown below:

	Trial	Row	Column	Maize	PlotNum
1	1	1	1	M1	1
2	1	1	2	M6	2
3	1	1	3	M4	3
4	1	1	4	M5	4
5	1	1	5	M2	5
6	1	1	6	M3	6
7	1	2	1	M3	7
8	1	2	2	M2	8

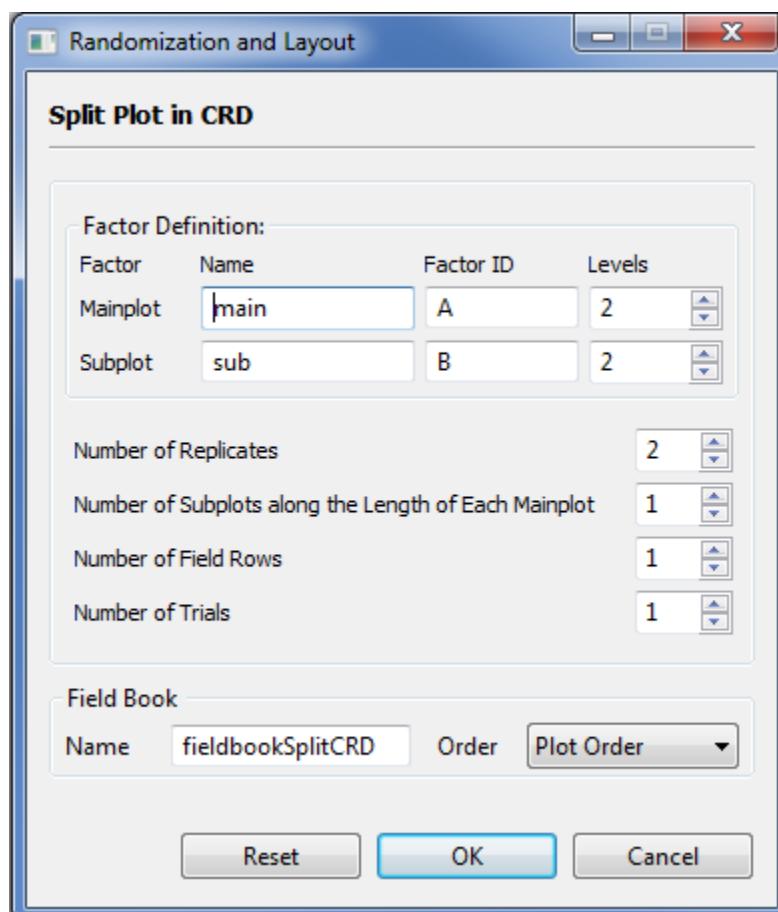
Split Plot Design

This design can be generated for experiments where the main plot is arranged in completely randomized design, randomized complete block design and Latin square design.

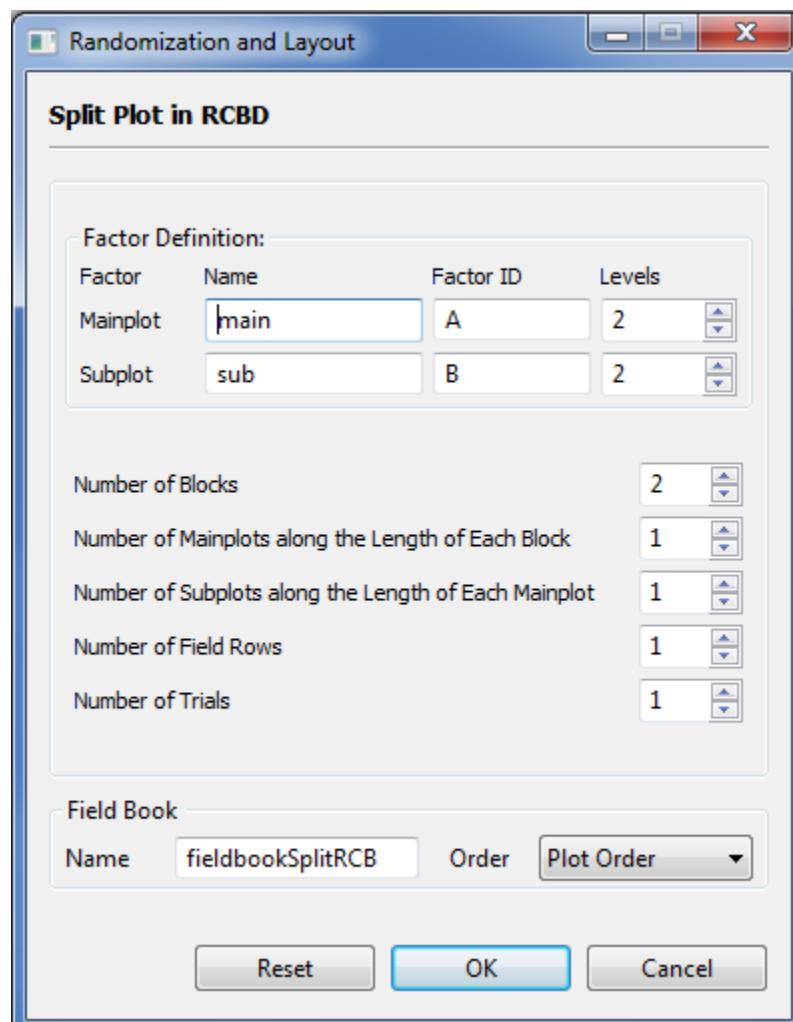
The steps to generate randomization are listed below:

- Click **Design | Split Plot Design** from the main window. Choose the appropriate design for the main plot.
- The **Randomization and Layout** dialog box will appear.

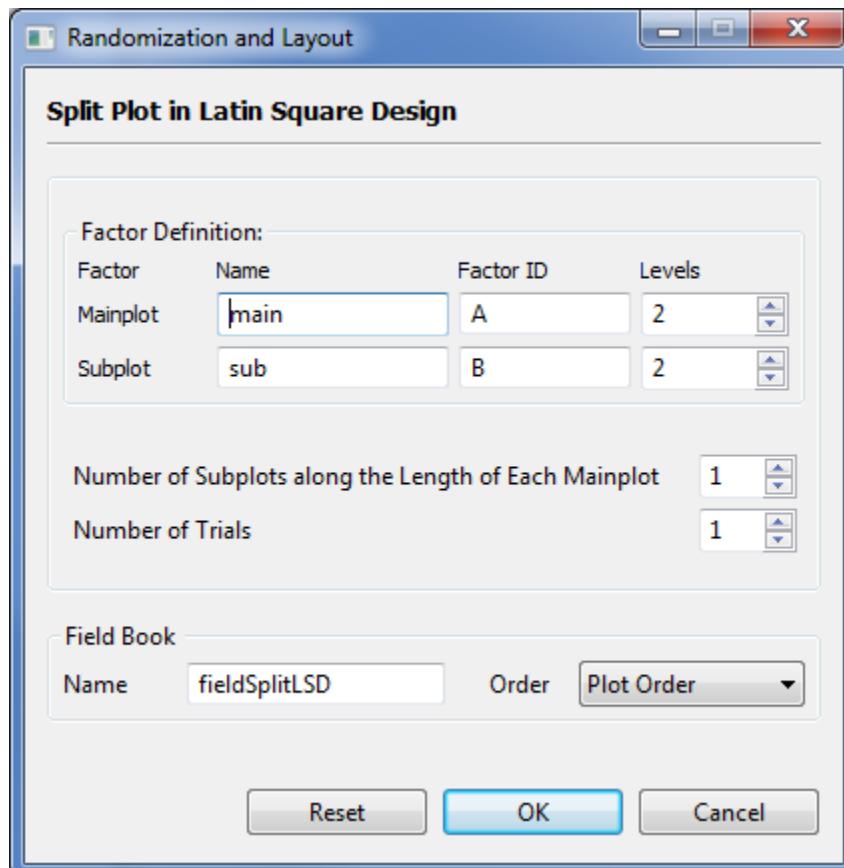
When the main plot is arranged in completely randomized design, the default **Randomization and Layout** dialog box is shown below:



When the main plot is arranged in randomized complete block design, the default **Randomization and Layout** dialog box is shown below:



When the main plot is arranged in Latin Square design, the default **Randomization and Layout** dialog box is shown below:



- Specify the required field and appropriate options.

Factor Definition Frame

Name

Contain the default name for each factor which can be change. In specifying the factor name, the following rules apply:

- name should not contain any space;
- must begin with a letter or a period (.) ;
- succeeding characters can be a combination of letters, numbers, period (.) and underscore (_); and
- name must be different from other factor names already specified.

Factor ID

Contain the default code for each factor. User can change the factor ID by typing the desired factor ID. Factor ID should consist of 1 to 4 letters only and should be unique.

Levels

Contain the level for each factor. User can change the level of the factor by either typing a value inside the spin box or clicking the up-arrow key of the spin box to increase the value, down-arrow key, otherwise. The default and minimum value of the levels is equal to 2 while the maximum value of the levels is 500. When the main plot is arranged in Latin Square design, the maximum value of the levels of the main plot factor is 11.

Number of Replicates

Applicable only if completely randomized design is chosen. These define the number of replicates to be generated per trial. The default and minimum value is equal to 2.

Number of Blocks

Applicable only if randomized complete block design is chosen. These define the number of blocks to be generated. The default value and minimum value is equal to 2.

Number of Mainplots along the Length of Each Block

Applicable only if randomized complete block design is chosen. These define the number of mainplots along the length of each block. The default and minimum value is equal to one.

Number of Subplots along the Length of Each Mainplot

These define the number of subplots along the length of each mainplot. The default and minimum value is equal to one.

Number of Field Rows

Applicable only if completely randomized or randomized complete block design is chosen. Define the total number of rows in the field layout for each trial. The default and minimum value is equal to one.

Number of Trial

Define the number of trials to be generated. The default value and minimum value is equal to one.

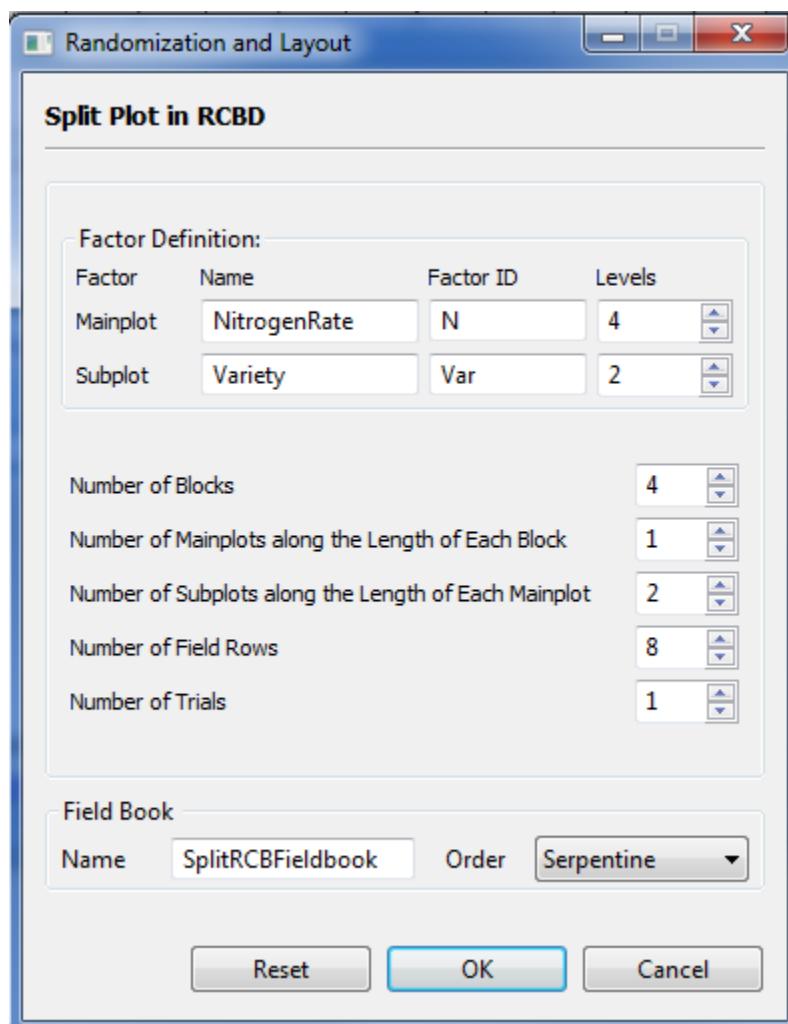
Field Book Filename

This field is required and it specifies the file name where the result of the randomization will be saved.

Field Book Order

Define how the plot number will be arranged. There are two options available: *Plot Order* (default value) and *Serpentine*.

For this example, suppose we want to generate a randomization for an experiment whose aim is to compare the effects of four nitrogen rates on grain yield of five rice varieties. The experiment will be conducted using Split Plot with four blocks. Nitrogen rates will be assigned as the mainplot factor and will be laid out in randomized complete block design; and the varieties as the subplot factor. The completed dialog box should appear as below:



- Click the **OK** button to generate the randomization. The **Randomization and Layout** dialog box will be minimized and STAR will automatically display the csv data file and the *txt* file created in the Data Viewer tab.

Sample *txt* displayed in the Data Viewer is shown below:

DESIGN PROPERTIES:

Split Plot Design
Randomized Complete Block Design

DESIGN PARAMETERS:

Number of Trials = 1
Number of Blocks = 4
Mainplot Factor = NitrogenRate
Levels = N1, N2, N3, N4
Subplot Factor = Variety
Levels = Var1, Var2

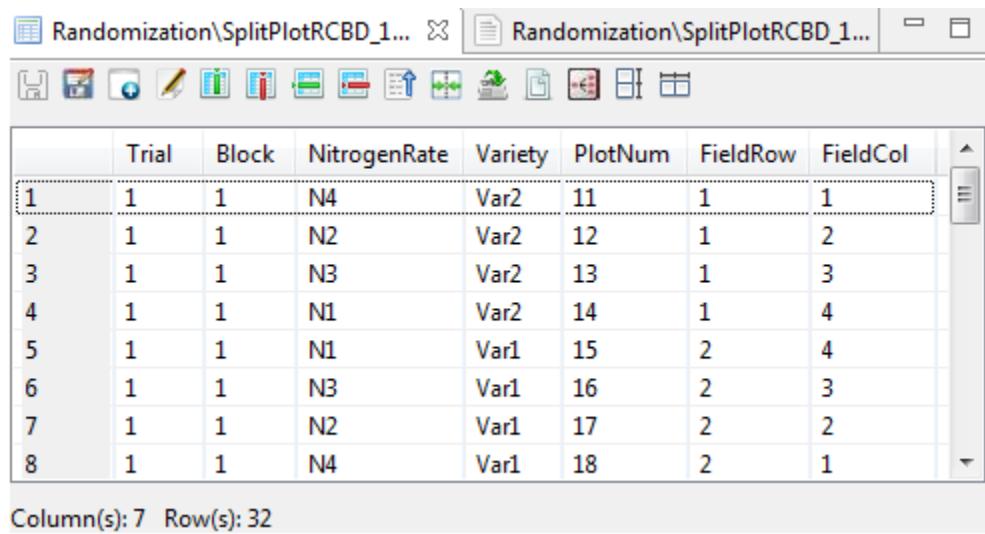
Layout for Split Plot in Randomized Complete Block Design:

Trial = 1

	FieldCol1	FieldCol2	FieldCol3	FieldCol4
FieldRow1	11 N4 Var2	12 N2 Var2	13 N3 Var2	14 N1 Var2
FieldRow2	18 N4 Var1	17 N2 Var1	16 N3 Var1	15 N1 Var1
FieldRow3	21 N3 Var2	22 N4 Var2	23 N2 Var1	24 N1 Var2
FieldRow4	28 N3 Var1	27 N4 Var1	26 N2 Var2	25 N1 Var1
FieldRow5	31 N4 Var1	32 N2 Var2	33 N1 Var2	34 N3 Var2
FieldRow6	38 N4 Var2	37 N2 Var1	36 N1 Var1	35 N3 Var1
FieldRow7	41 N2 Var1	42 N3 Var1	43 N4 Var2	44 N1 Var2
FieldRow8	48 N2 Var2	47 N3 Var2	46 N4 Var1	45 N1 Var1

**Note: Cells contain plot numbers on top, treatments/entries below

Sample csv data file displayed in the Data Viewer is shown below:



The screenshot shows a software interface titled "Randomization\SplitPlotRCBD_1...". Below the title bar is a toolbar with various icons. The main area is a data grid containing 8 rows of data. The columns are labeled: Trial, Block, NitrogenRate, Variety, PlotNum, FieldRow, and FieldCol. The data is as follows:

	Trial	Block	NitrogenRate	Variety	PlotNum	FieldRow	FieldCol
1	1	1	N4	Var2	11	1	1
2	1	1	N2	Var2	12	1	2
3	1	1	N3	Var2	13	1	3
4	1	1	N1	Var2	14	1	4
5	1	1	N1	Var1	15	2	4
6	1	1	N3	Var1	16	2	3
7	1	1	N2	Var1	17	2	2
8	1	1	N4	Var1	18	2	1

Column(s): 7 Row(s): 32

Strip Plot Design

The steps to generate randomization are listed below:

- Choose **Design | Strip Plot Design...** from the main window. The **Randomization and Layout** dialog box will appear.
- Specify the required fields and appropriate options.

Factor Definition Frame

Name

Contain the default name for each factor which can be change. In specifying the factor name, the following rules apply:

- name should not contain any space;
- must begin with a letter or a period (.);
- succeeding characters can be a combination of letters, numbers, period (.) and underscore (_); and
- name must be different from other factor names already specified.

Factor ID

Contain the default code for each factor. User can change the factor ID by typing the desired factor ID. Factor ID should consist of 1 to 4 letters only and should be unique.

Levels

Contain the level for each factor. User can change the level of the factor by either typing a value inside the spin box or clicking the up-arrow key of the spin box to increase the value, down-arrow key, otherwise. The default and minimum value of the levels is equal to 2 while the maximum value of the levels is 500.

Number of Blocks

These define the number of blocks to be generated. The default value and minimum value is equal to 2.

Number of Field Rows

Define the total number of rows in the field layout for each trial. The default and minimum value is equal to 2.

Number of Trial

Define the number of trials to be generated. The default value and minimum value is equal to one.

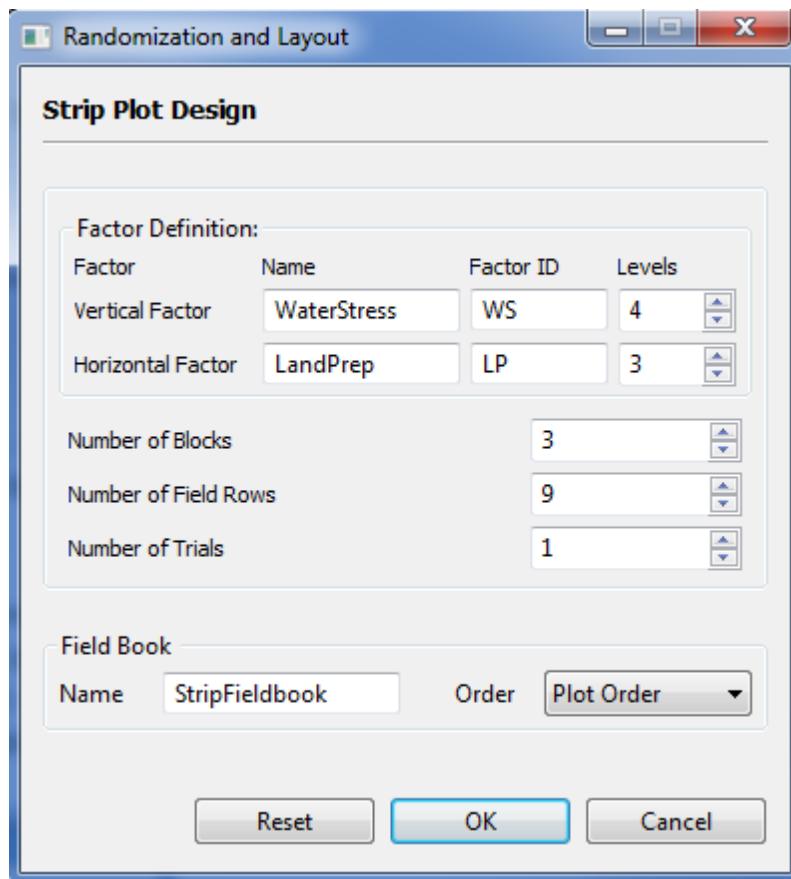
Field Book Filename

This field is required and it specifies the file name where the result of the randomization will be saved. The default filename is *fieldbookStrip*.

Field Book Order

Define how the plot number will be arranged. There are two options available: *Plot Order* (default value) and *Serpentine*.

For this example, suppose we want to generate a randomization for an experiment to be conducted using Strip Plot, with land preparation (with 3 levels) as the horizontal factor and water stress (with four levels) as the vertical factor. Three blocks will be used. The completed dialog box should appear as shown below:



- Click the **OK** button to generate the randomization. The **Randomization and Layout** dialog box will be minimized and STAR will automatically display the csv data file and *txt* file created in the Data Viewer tab.

Sample *txt* file displayed in the Data Viewer is shown below:

DESIGN PROPERTIES:

Strip Plot Design

DESIGN PARAMETERS:

Number of Trials = 1
Number of Blocks = 3
Vertical Factor = WaterStress
Levels = WS1, WS2, WS3, WS4
Horizontal Factor = LandPrep
Levels = LP1, LP2, LP3

Layout for Strip Plot:

Trial = 1

	FieldCol1	FieldCol2	FieldCol3	FieldCol4
FieldRow1	101 WS3 LP1	102 WS2 LP1	103 WS4 LP1	104 WS1 LP1
FieldRow2	105 WS3 LP3	106 WS2 LP3	107 WS4 LP3	108 WS1 LP3
FieldRow3	109 WS3 LP2	110 WS2 LP2	111 WS4 LP2	112 WS1 LP2
FieldRow4	201 WS4 LP3	202 WS1 LP3	203 WS3 LP3	204 WS2 LP3
FieldRow5	205 WS4 LP1	206 WS1 LP1	207 WS3 LP1	208 WS2 LP1
FieldRow6	209 WS4 LP2	210 WS1 LP2	211 WS3 LP2	212 WS2 LP2
FieldRow7	301 WS3 LP1	302 WS1 LP1	303 WS4 LP1	304 WS2 LP1
FieldRow8	305 WS3 LP3	306 WS1 LP3	307 WS4 LP3	308 WS2 LP3
FieldRow9	309 WS3 LP2	310 WS1 LP2	311 WS4 LP2	312 WS2 LP2

**Note: Cells contain plot numbers on top, treatments/entries below

Sample csv data file displayed in the Data Viewer is shown below:

	Trial	Block	WaterStress	LandPrep	PlotNum	FieldRow	FieldCol
1	1	1	WS3	LP1	101	1	1
2	1	1	WS2	LP1	102	1	2
3	1	1	WS4	LP1	103	1	3
4	1	1	WS1	LP1	104	1	4
5	1	1	WS3	LP3	105	2	1
6	1	1	WS2	LP3	106	2	2
7	1	1	WS4	LP3	107	2	3
8	1	1	WS1	LP3	108	2	4

Column(s): 7 Row(s): 36

Split-Split Plot Design

This design can be generated for experiments where the main plot is arranged in completely randomized design, randomized complete block design and Latin square design.

The steps to generate randomization are listed below:

- Click **Design | Split-Split Plot Design** from the main window. Choose the appropriate design for the main plot.
- The appropriate **Randomization and Layout** dialog box will appear depending on how the main plot will be arranged.
- Specify the required field and appropriate options.

Factor Definition Frame

Name

Contain the default name for each factor which can be change. In specifying the factor name, the following rules apply:

- name should not contain any space;
- must begin with a letter or a period (.);

- succeeding characters can be a combination of letters, numbers, period(.) and underscore(_); and
- name must be different from other factor names already specified.

Factor ID

Contain the default code for each factor. User can change the factor ID by typing the desired factor ID. Factor ID should consist of 1 to 4 letters only and should be unique.

Levels

Contain the level for each factor. User can change the level of the factor by either typing a value inside the spin box or clicking the up-arrow key of the spin box to increase the value, down-arrow key, otherwise. The default and minimum value of the levels is equal to 2 while the maximum value of the levels is 500. When the main plot is arranged in Latin Square design, the maximum value of the levels of the main plot factor is 11.

Number of Replicates

Applicable only if completely randomized design is chosen. These define the number of replicates to be generated. The default and minimum value is equal to 2.

Number of Blocks

Applicable only if randomized complete block design is chosen. These define the number of blocks to be generated. The default and minimum value is equal to 2.

Number of Mainplots along the Length of Each Block

Applicable only if randomized complete block design is chosen. These define the number of main plots along the length of each block. The default and minimum value is equal to one.

Number of Subplots along the Length of Each Mainplot

Define the number of subplots along the length of each mainplot. The default and minimum value is equal to one.

Number of Sub-subplots along the Length of Each Subplot

Define the number of sub-subplots along the length of each subplot. The default and minimum value is equal to one.

Number of Field Rows

Applicable only if completely randomized or randomized complete block design is chosen. Define the total number of rows in the field layout for each trial. The default and minimum value is equal to one.

Number of Trial

Define the number of trials to be generated. The default value and minimum value is equal to one.

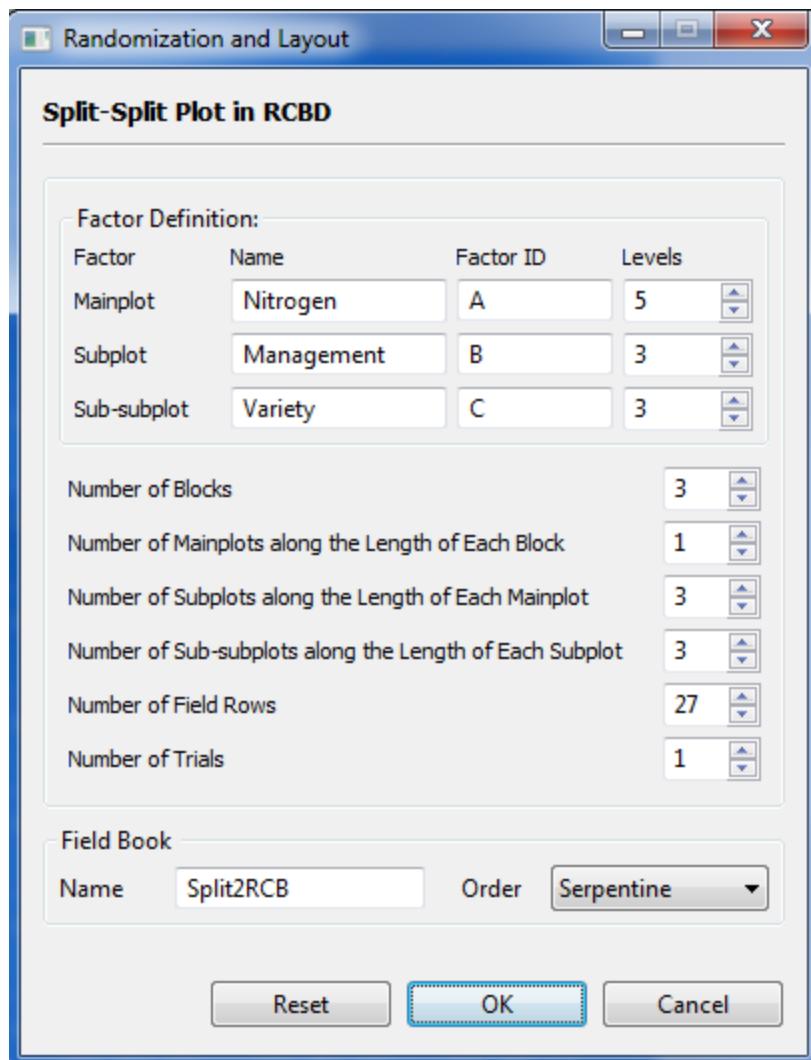
Field Book Filename

This field is required and it specifies the file name where the result of the randomization will be saved.

Field Book Order

Define how the plot number will be arranged. There are two options available: *Plot Order* (default value) and *Serpentine*.

For this example, suppose we want to generate a randomization for an experiment whose aim is to compare the effects of five nitrogen rates and three management practices on the grain yield of three rice varieties which will be conducted using Split-Split Plot with three blocks. Nitrogen rates will be assigned as the mainplot factor and will be arranged in randomized complete block design, management practices as the subplot factor and varieties as the sub-subplot factor. The completed dialog box should appear as shown below:



- Click the **OK** button to generate the randomization. The **Randomization and Layout** dialog box will be minimized and STAR will automatically display the csv data file created in the Data Viewer.

Sample *txt* data file displayed in the Data Viewer is shown below:

```
DESIGN PROPERTIES:  
Split-Split Plot Design  
Randomized Complete Block Design  
  
DESIGN PARAMETERS:  
Number of Trials = 1  
Number of Blocks = 3  
Mainplot Factor = Nitrogen  
Levels = A1, A2, A3, A4, A5  
Subplot Factor = Management  
Levels = B1, B2, B3  
Sub-subplot Factor = Variety  
Levels = C1, C2, C3
```

Layout for Split-Split Plot in Randomized Complete Block Design:

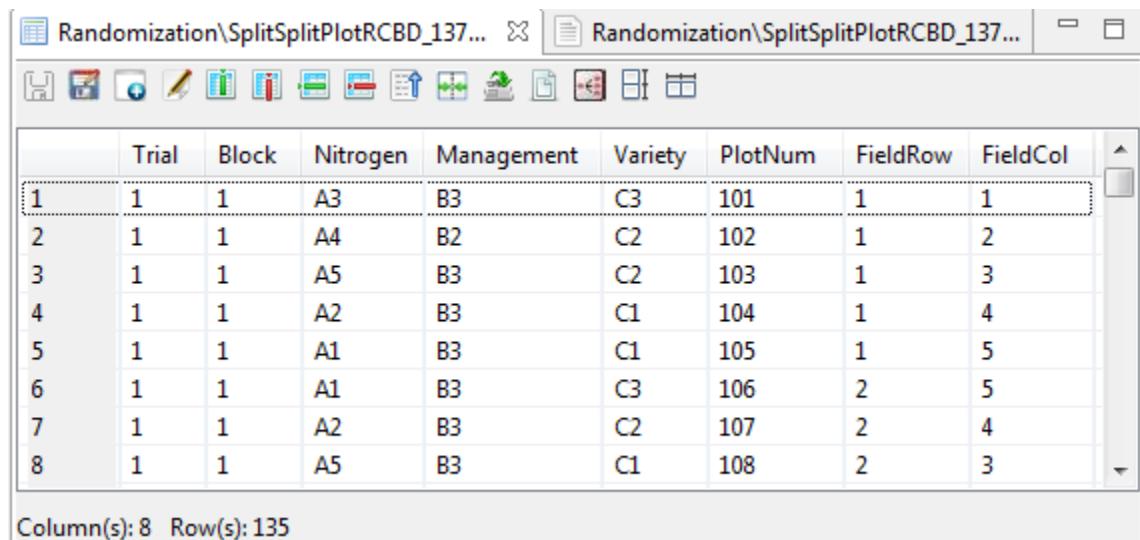
Trial = 1

	FieldCol1	FieldCol2	FieldCol3	FieldCol4	FieldCol5
FieldRow1	101	102	103	104	105
	A3 B3 C3	A4 B2 C2	A5 B3 C2	A2 B3 C1	A1 B3 C1
FieldRow2	110	109	108	107	106
	A3 B3 C2	A4 B2 C1	A5 B3 C1	A2 B3 C2	A1 B3 C3
FieldRow3	111	112	113	114	115
	A3 B3 C1	A4 B2 C3	A5 B3 C3	A2 B3 C3	A1 B3 C2
FieldRow4	120	119	118	117	116
	A3 B2 C2	A4 B3 C2	A5 B2 C2	A2 B1 C3	A1 B1 C3
FieldRow5	121	122	123	124	125
	A3 B2 C1	A4 B3 C1	A5 B2 C3	A2 B1 C1	A1 B1 C1
FieldRow6	130	129	128	127	126
	A3 B2 C3	A4 B3 C3	A5 B2 C1	A2 B1 C2	A1 B1 C2
FieldRow7	131	132	133	134	135
	A3 B1 C2	A4 B1 C3	A5 B1 C2	A2 B2 C3	A1 B2 C3
FieldRow8	140	139	138	137	136
	A3 B1 C1	A4 B1 C2	A5 B1 C3	A2 B2 C2	A1 B2 C2
FieldRow9	141	142	143	144	145
	A3 B1 C3	A4 B1 C1	A5 B1 C1	A2 B2 C1	A1 B2 C1
FieldRow10	201	202	203	204	205
	A1 B1 C1	A3 B2 C3	A5 B2 C2	A2 B2 C3	A4 B1 C1
FieldRow11	210	209	208	207	206
	A1 B1 C3	A3 B2 C2	A5 B2 C1	A2 B2 C1	A4 B1 C2
FieldRow12	211	212	213	214	215
	A1 B1 C2	A3 B2 C1	A5 B2 C3	A2 B2 C2	A4 B1 C3
FieldRow13	220	219	218	217	216
	A1 B2 C3	A3 B3 C1	A5 B1 C3	A2 B3 C1	A4 B2 C2
FieldRow14	221	222	223	224	225
	A1 B2 C1	A3 B3 C2	A5 B1 C1	A2 B3 C3	A4 B2 C3
FieldRow15	230	229	228	227	226
	A1 B2 C2	A3 B3 C3	A5 B1 C2	A2 B3 C2	A4 B2 C1
FieldRow16	231	232	233	234	235
	A1 B3 C3	A3 B1 C3	A5 B3 C3	A2 B1 C2	A4 B3 C3
FieldRow17	240	239	238	237	236
	A1 B3 C2	A3 B1 C2	A5 B3 C2	A2 B1 C3	A4 B3 C2
FieldRow18	241	242	243	244	245
	A1 B3 C1	A3 B1 C1	A5 B3 C1	A2 B1 C1	A4 B3 C1
FieldRow19	301	302	303	304	305
	A2 B3 C3	A4 B1 C2	A1 B3 C1	A3 B2 C2	A5 B2 C3

FieldRow20	310	309	308	307	306
	A2 B3 C1	A4 B1 C3	A1 B3 C2	A3 B2 C3	A5 B2 C2
FieldRow21	311	312	313	314	315
	A2 B3 C2	A4 B1 C1	A1 B3 C3	A3 B2 C1	A5 B2 C1
FieldRow22	320	319	318	317	316
	A2 B2 C1	A4 B2 C1	A1 B2 C1	A3 B1 C3	A5 B3 C3
FieldRow23	321	322	323	324	325
	A2 B2 C2	A4 B2 C3	A1 B2 C2	A3 B1 C1	A5 B3 C1
FieldRow24	330	329	328	327	326
	A2 B2 C3	A4 B2 C2	A1 B2 C3	A3 B1 C2	A5 B3 C2
FieldRow25	331	332	333	334	335
	A2 B1 C1	A4 B3 C2	A1 B1 C3	A3 B3 C1	A5 B1 C2
FieldRow26	340	339	338	337	336
	A2 B1 C3	A4 B3 C1	A1 B1 C2	A3 B3 C3	A5 B1 C3
FieldRow27	341	342	343	344	345
	A2 B1 C2	A4 B3 C3	A1 B1 C1	A3 B3 C2	A5 B1 C1

**Note: Cells contain plot numbers on top, treatments/entries below

Sample csv data file displayed in the Data Viewer is shown below:



	Trial	Block	Nitrogen	Management	Variety	PlotNum	FieldRow	FieldCol
1	1	1	A3	B3	C3	101	1	1
2	1	1	A4	B2	C2	102	1	2
3	1	1	A5	B3	C2	103	1	3
4	1	1	A2	B3	C1	104	1	4
5	1	1	A1	B3	C1	105	1	5
6	1	1	A1	B3	C3	106	2	5
7	1	1	A2	B3	C2	107	2	4
8	1	1	A5	B3	C1	108	2	3

Column(s): 8 Row(s): 135

Strip-Split Plot Design

The steps to generate randomization are listed below:

- Choose **Design | Strip-Split Plot Design...** from the main window. The **Randomization** dialog box will appear.
- Specify the required fields and appropriate options.

Factor Definition

Name

Contain the default name for each factor. User can change the factor name by typing the desired factor name. In specifying the factor name, the following rules apply:

- name should not contain any space;
- must begin with a letter or a period (.) ;
- succeeding characters can be a combination of letters, numbers, period (.) and underscore (_); and
- name must be different from other factor names already specified.

Factor ID

Contain the default code for each factor. User can change the factor ID by typing the desired factor ID. Factor ID should consist of 1 to 4 letters only and should be unique.

Levels

Contain the level for each factor. User can change the level of the factor by either typing a value inside the spin box or clicking the up-arrow key of the spin box to increase the value, down-arrow key, otherwise. The default and minimum value of the levels is equal to 2 while the maximum value of the levels is 500.

Number of Blocks

Define the number of blocks to be generated. The default value and minimum value is equal to 2.

Number of Subplots along the Length of Each VxH plot

These define the number of subplots along the length of VxH plot. The default and minimum value is equal to one.

Number of Field Rows

Define the total number of rows in the field layout for each trial. The default and minimum value is equal to 2.

Number of Trial

Define the number of trials to be generated. The default value and minimum value is equal to one.

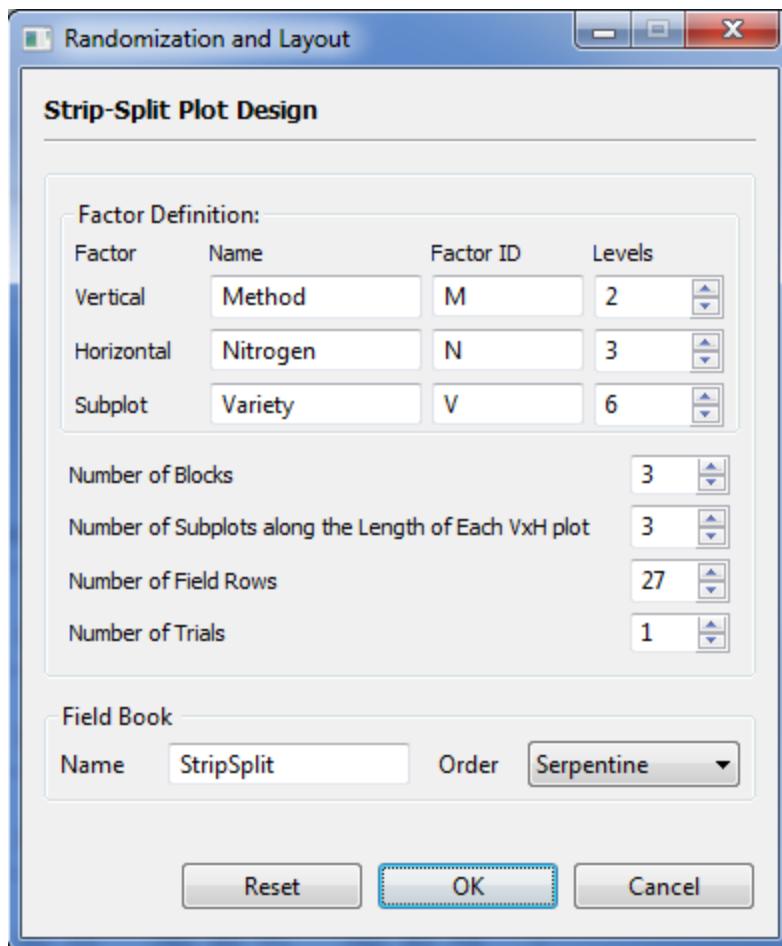
Field Book Filename

This field is required and it specifies the file name where the result of the randomization will be saved. The default filename is *fieldbookStripSplit*.

Field Book Order

Define how the plot number will be arranged. There are two options available: *Plot Order* (default value) and *Serpentine*.

For this example, suppose we want to generate a randomization for an experiment to be conducted using Strip-Split Plot, with planting methods (with 2 levels) as vertical factor, nitrogen rates (with 3 levels) as the horizontal factor and rice variety (with 6 levels) as the subplot factor. Three blocks will be used. The completed dialog box should appear as shown below:



- Click the **OK** button to generate the randomization. The **Randomization and Layout** dialog box will be minimized and STAR will automatically display the csv data file and the *txt* file created in the Data Viewer.

Sample *txt* file displayed in the Data Viewer is shown below:

```
DESIGN PROPERTIES:  
    Strip-Split Plot Design  
  
DESIGN PARAMETERS:  
    Number of Trials = 1  
    Number of Blocks = 3  
    Vertical Factor = Method  
    Levels = M1, M2  
    Horizontal Factor = Nitrogen  
    Levels = N1, N2, N3  
    Subplot Factor = Variety  
    Levels = V1, V2, V3, ..., V6
```

Layout for Strip-Split Plot

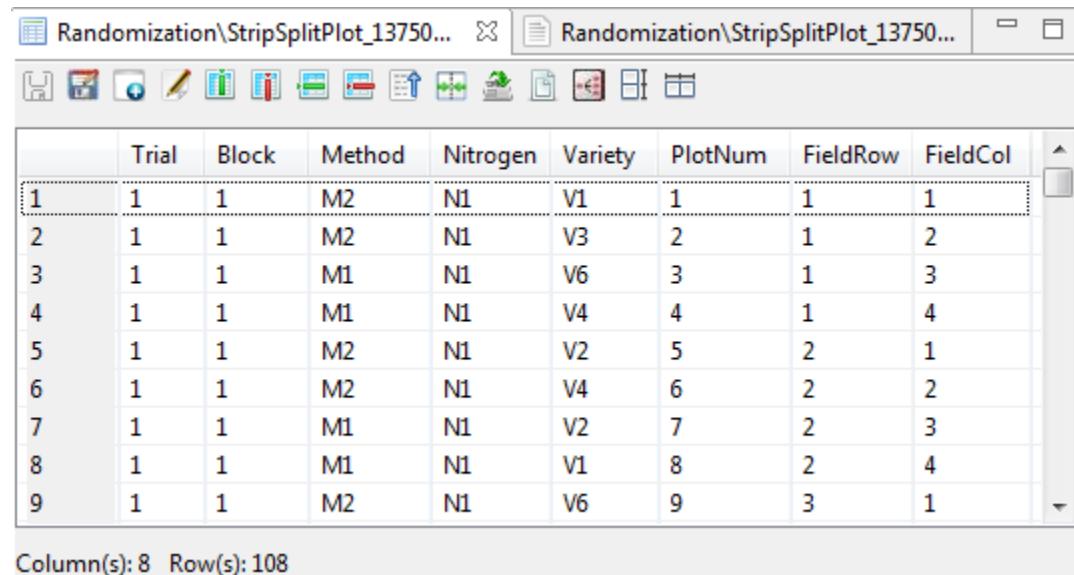
Trial = 1

	FieldCol1	FieldCol2	FieldCol3	FieldCol4
FieldRow1	101	102	103	104
	M2 N1 V1	M2 N1 V3	M1 N1 V6	M1 N1 V4
FieldRow2	108	107	106	105
	M2 N1 V2	M2 N1 V4	M1 N1 V2	M1 N1 V1
FieldRow3	109	110	111	112
	M2 N1 V6	M2 N1 V5	M1 N1 V5	M1 N1 V3
FieldRow4	116	115	114	113
	M2 N3 V2	M2 N3 V3	M1 N3 V6	M1 N3 V1
FieldRow5	117	118	119	120
	M2 N3 V6	M2 N3 V5	M1 N3 V3	M1 N3 V5
FieldRow6	124	123	122	121
	M2 N3 V1	M2 N3 V4	M1 N3 V4	M1 N3 V2
FieldRow7	125	126	127	128
	M2 N2 V2	M2 N2 V5	M1 N2 V1	M1 N2 V3
FieldRow8	132	131	130	129
	M2 N2 V3	M2 N2 V4	M1 N2 V6	M1 N2 V4
FieldRow9	133	134	135	136
	M2 N2 V1	M2 N2 V6	M1 N2 V2	M1 N2 V5
FieldRow10	201	202	203	204
	M1 N3 V1	M1 N3 V2	M2 N3 V6	M2 N3 V3
FieldRow11	208	207	206	205
	M1 N3 V4	M1 N3 V5	M2 N3 V2	M2 N3 V4
FieldRow12	209	210	211	212
	M1 N3 V6	M1 N3 V3	M2 N3 V1	M2 N3 V5
FieldRow13	216	215	214	213
	M1 N1 V2	M1 N1 V1	M2 N1 V6	M2 N1 V2
FieldRow14	217	218	219	220
	M1 N1 V3	M1 N1 V5	M2 N1 V5	M2 N1 V3
FieldRow15	224	223	222	221
	M1 N1 V4	M1 N1 V6	M2 N1 V4	M2 N1 V1
FieldRow16	225	226	227	228
	M1 N2 V4	M1 N2 V2	M2 N2 V3	M2 N2 V4
FieldRow17	232	231	230	229
	M1 N2 V3	M1 N2 V6	M2 N2 V1	M2 N2 V5

FieldRow18	233	234	235	236
	M1 N2 V5	M1 N2 V1	M2 N2 V6	M2 N2 V2
FieldRow19	301	302	303	304
	M1 N1 V5	M1 N1 V3	M2 N1 V6	M2 N1 V2
FieldRow20	308	307	306	305
	M1 N1 V4	M1 N1 V1	M2 N1 V4	M2 N1 V3
FieldRow21	309	310	311	312
	M1 N1 V2	M1 N1 V6	M2 N1 V1	M2 N1 V5
FieldRow22	316	315	314	313
	M1 N2 V1	M1 N2 V2	M2 N2 V2	M2 N2 V5
FieldRow23	317	318	319	320
	M1 N2 V5	M1 N2 V6	M2 N2 V1	M2 N2 V6
FieldRow24	324	323	322	321
	M1 N2 V3	M1 N2 V4	M2 N2 V3	M2 N2 V4
FieldRow25	325	326	327	328
	M1 N3 V6	M1 N3 V2	M2 N3 V2	M2 N3 V4
FieldRow26	332	331	330	329
	M1 N3 V1	M1 N3 V4	M2 N3 V3	M2 N3 V1
FieldRow27	333	334	335	336
	M1 N3 V3	M1 N3 V5	M2 N3 V5	M2 N3 V6

**Note: Cells contain plot numbers on top, treatments/entries below

Sample csv data file displayed in the Data Viewer is shown below:



	Trial	Block	Method	Nitrogen	Variety	PlotNum	FieldRow	FieldCol
1	1	1	M2	N1	V1	1	1	1
2	1	1	M2	N1	V3	2	1	2
3	1	1	M1	N1	V6	3	1	3
4	1	1	M1	N1	V4	4	1	4
5	1	1	M2	N1	V2	5	2	1
6	1	1	M2	N1	V4	6	2	2
7	1	1	M1	N1	V2	7	2	3
8	1	1	M1	N1	V1	8	2	4
9	1	1	M2	N1	V6	9	3	1

Column(s): 8 Row(s): 108

Split-Split-Split Plot Design

This design can be generated for experiments where the main plot is arranged in completely randomized, randomized complete block and Latin square design.

The steps to generate randomization are listed below:

- Click **Design | Split-Split-Split Plot Design** from the main window. Choose the appropriate design for the main plot.
- The appropriate **Randomization and Layout** dialog box will appear depending on how the main plot will be arranged.
- Specify the required field and appropriate options.

Factor Definition Frame

Name

Contain the default name for each factor which can be change. In specifying the factor name, the following rules apply:

- name should not contain any space;
- must begin with a letter or a period (.) ;
- succeeding characters can be a combination of letters, numbers, period (.) and underscore (_); and
- name must be different from other factor names already specified.

Factor ID

Contain the default code for each factor. User can change the factor ID by typing the desired factor ID. Factor ID should consist of 1 to 4 letters only and should be unique.

Levels

Contain the level for each factor. User can change the level of the factor by either typing a value inside the spin box or clicking the up-arrow key of the spin box to increase the value, down-arrow key, otherwise. The default and minimum value of the levels is equal to 2 while the maximum value of the levels is 500. When the main plot is arranged in Latin Square design, the maximum value of the levels of the main plot factor is 11.

Number of Replicates

Applicable only if completely randomized design is chosen. These define the number of replicates to be generated. The default and minimum value is equal to 2.

Number of Blocks

Applicable only if randomized complete block design is chosen. These define the number of blocks to be generated. The default and minimum value is equal to 2.

Number of Mainplots along the Length of Each Block

Applicable only if randomized complete block design is chosen. These define the number of main plots along the length of each block. The default and minimum value is equal to one.

Number of Subplots along the Length of Each Mainplot

Define the number of subplots along the length of each main plot. The default and minimum value is equal to one.

Number of Sub-subplots along the Length of Each Subplot

Define the number of sub-subplots along the length of each subplot. The default and minimum value is equal to one.

Number of Sub-sub-subplots along the Length of Each Sub-subplot

Define the number of sub-sub-subplots along the length of each sub-subplot. The default and minimum value is equal to one.

Number of Field Rows

Applicable only if completely randomized or randomized complete block design is chosen. Define the total number of rows in the field layout for each trial. The default and minimum value is equal to one.

Number of Trial

Define the number of trials to be generated. The default value and minimum value is equal to one.

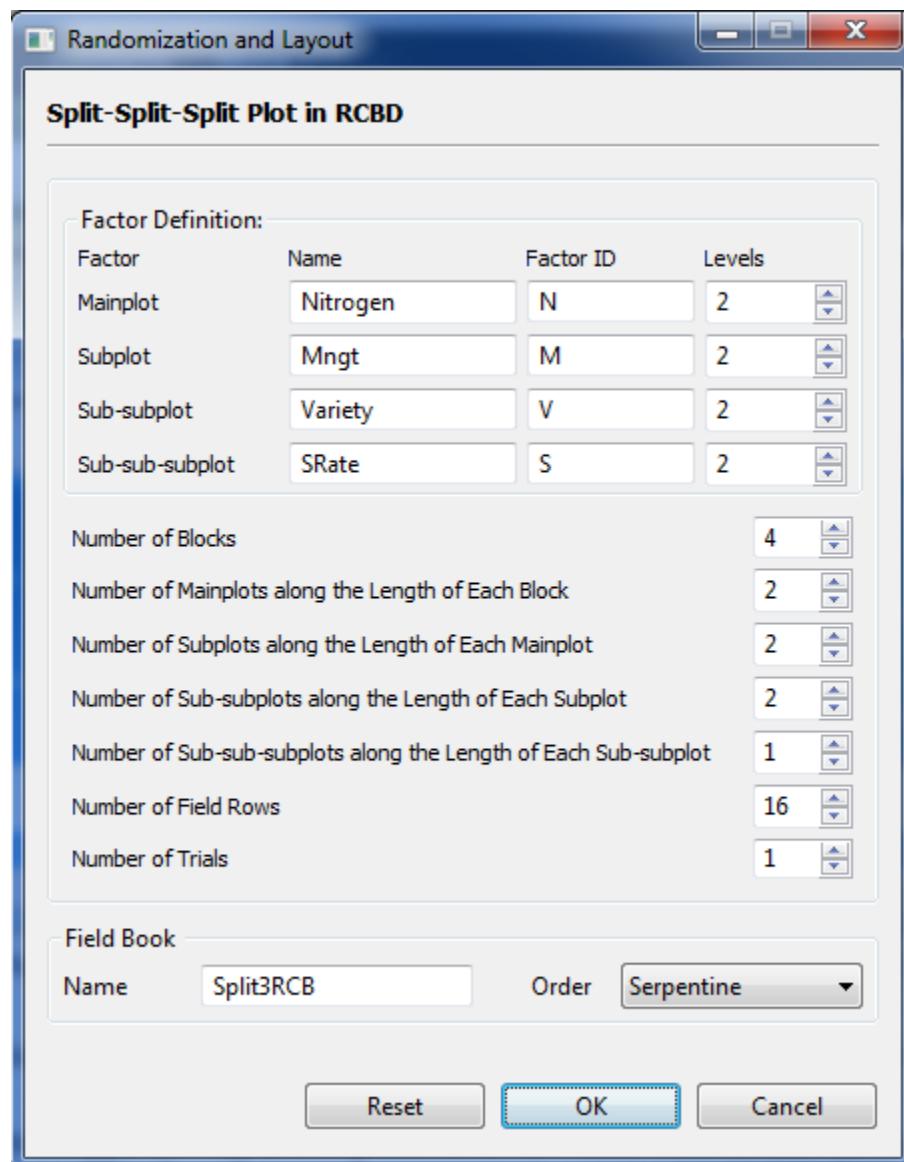
Field Book Filename

This field is required and it specifies the file name where the result of the randomization will be saved.

Field Book Order

Define how the plot number will be arranged. There are two options available: *Plot Order* (default value) and *Serpentine*.

For this example, suppose we want to generate a randomization for an experiment whose aim is to compare the effects of two nitrogen rates, two management practices and two seeding rate on the grain yield of two rice varieties which will be conducted using Split-Split-Split Plot with four blocks. Nitrogen rates will be assigned as the mainplot factor and will be arranged in randomized complete block design, management practices as the subplot factor, varieties as the sub-subplot factor and seeding rate as the sub-sub-subplot factor. The completed dialog box should appear as shown below:



- Click the **OK** button to generate the randomization. The **Randomization and Layout** dialog box will be minimized and STAR will automatically display the csv data file and the *txt* file created in the Data Viewer tab.

Sample *txt* file displayed in the Data Viewer is shown below:

```

DESIGN PROPERTIES:
    Split-Split-Split Plot Design
    Randomized Complete Block Design

DESIGN PARAMETERS:
    Number of Trials = 1
    Number of Blocks = 4
    Mainplot Factor = Nitrogen
    Levels = N1, N2
    Subplot Factor = Mngt
    Levels = M1, M2
    Sub-subplot Factor = Variety
    Levels = V1, V2
    Sub-sub-subplot Factor = SRate
    Levels = S1, S2

```

Layout for Split-Split-Split Plot in Randomized Complete Block Design:

Trial = 1

	FieldCol1	FieldCol2	FieldCol3	FieldCol4
FieldRow1	101 N2 M2 V2 S1	102 N2 M2 V2 S2	201 N1 M1 V1 S1	202 N1 M1 V1 S2
FieldRow2	104 N2 M2 V1 S1	103 N2 M2 V1 S2	204 N1 M1 V2 S2	203 N1 M1 V2 S1
FieldRow3	105 N2 M1 V1 S2	106 N2 M1 V1 S1	205 N1 M2 V1 S2	206 N1 M2 V1 S1
FieldRow4	108 N2 M1 V2 S1	107 N2 M1 V2 S2	208 N1 M2 V2 S2	207 N1 M2 V2 S1
FieldRow5	109 N1 M2 V2 S2	110 N1 M2 V2 S1	209 N2 M1 V2 S1	210 N2 M1 V2 S2
FieldRow6	112 N1 M2 V1 S2	111 N1 M2 V1 S1	212 N2 M1 V1 S1	211 N2 M1 V1 S2
FieldRow7	113 N1 M1 V1 S2	114 N1 M1 V1 S1	213 N2 M2 V2 S1	214 N2 M2 V2 S2
FieldRow8	116 N1 M1 V2 S1	115 N1 M1 V2 S2	216 N2 M2 V1 S2	215 N2 M2 V1 S1
FieldRow9	301 N1 M2 V2 S2	302 N1 M2 V2 S1	401 N2 M2 V2 S1	402 N2 M2 V2 S2
FieldRow10	304 N1 M2 V1 S2	303 N1 M2 V1 S1	404 N2 M2 V1 S1	403 N2 M2 V1 S2
FieldRow11	305 N1 M1 V2 S1	306 N1 M1 V2 S2	405 N2 M1 V1 S1	406 N2 M1 V1 S2
FieldRow12	308 N1 M1 V1 S1	307 N1 M1 V1 S2	408 N2 M1 V2 S2	407 N2 M1 V2 S1

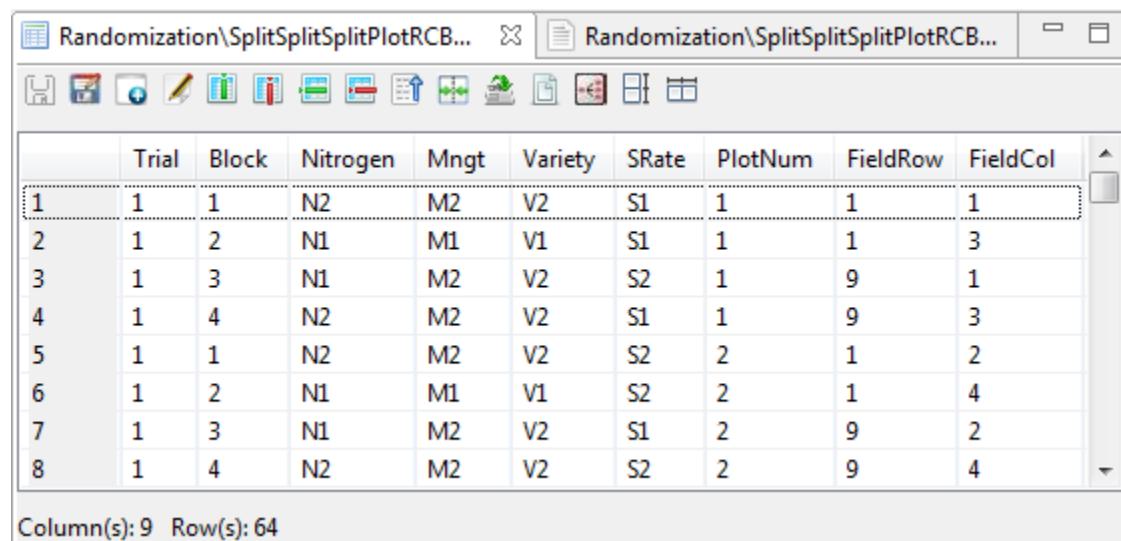
```

FieldRow13 | 309 | 310 | 409 | 410 |
| N2 M1 V2 S2 | N2 M1 V2 S1 | N1 M1 V1 S1 | N1 M1 V1 S2 |
+-----+-----+-----+-----+
FieldRow14 | 312 | 311 | 412 | 411 |
| N2 M1 V1 S2 | N2 M1 V1 S1 | N1 M1 V2 S1 | N1 M1 V2 S2 |
+-----+-----+-----+-----+
FieldRow15 | 313 | 314 | 413 | 414 |
| N2 M2 V1 S2 | N2 M2 V1 S1 | N1 M2 V1 S1 | N1 M2 V1 S2 |
+-----+-----+-----+-----+
FieldRow16 | 316 | 315 | 416 | 415 |
| N2 M2 V2 S2 | N2 M2 V2 S1 | N1 M2 V2 S1 | N1 M2 V2 S2 |
+-----+-----+-----+-----+

```

**Note: Cells contain plot numbers on top, treatments/entries below

Sample csv data file displayed in the Data Viewer is shown below:



	Trial	Block	Nitrogen	Mngt	Variety	SRate	PlotNum	FieldRow	FieldCol
1	1	1	N2	M2	V2	S1	1	1	1
2	1	2	N1	M1	V1	S1	1	1	3
3	1	3	N1	M2	V2	S2	1	9	1
4	1	4	N2	M2	V2	S1	1	9	3
5	1	1	N2	M2	V2	S2	2	1	2
6	1	2	N1	M1	V1	S2	2	1	4
7	1	3	N1	M2	V2	S1	2	9	2
8	1	4	N2	M2	V2	S2	2	9	4

Column(s): 9 Row(s): 64

Strip-Split-Split Plot Design

The steps to generate randomization are listed below:

- Choose **Design | Strip-Split-Split Plot Design** from the main window. The **Randomization and Layout** dialog box will appear.
- Specify the required fields and appropriate options.

Factor Definition

Name

Contain the default name for each factor. User can change the factor name by typing the desired factor name. In specifying the factor name, the following rules apply:

- name should not contain any space;

- must begin with a letter or a period (.);
- succeeding characters can be a combination of letters, numbers, period (.) and underscore (_); and
- name must be different from other factor names already specified.

Factor ID

Contain the default code for each factor. User can change the factor ID by typing the desired factor ID. Factor ID should consist of 1 to 4 letters only and should be unique.

Levels

Contain the level for each factor. User can change the level of the factor by either typing a value inside the spin box or clicking the up-arrow key of the spin box to increase the value, down-arrow key, otherwise. The default and minimum value of the levels is equal to 2 while the maximum value of the levels is 500.

Number of Blocks

Define the number of blocks to be generated. The default value and minimum value is equal to 2.

Number of Subplots along the Length of Each VxH plot

These define the number of subplots along the length of VxH plot. The default and minimum value is equal to one.

Number of Sub-subplots along the Length of Each Subplot

These define the number of sub-subplots along the length of subplot. The default and minimum value is equal to one.

Number of Field Rows

Define the total number of rows in the field layout for each trial. The default and minimum value is equal to 2.

Number of Trial

Define the number of trials to be generated. The default value and minimum value is equal to one.

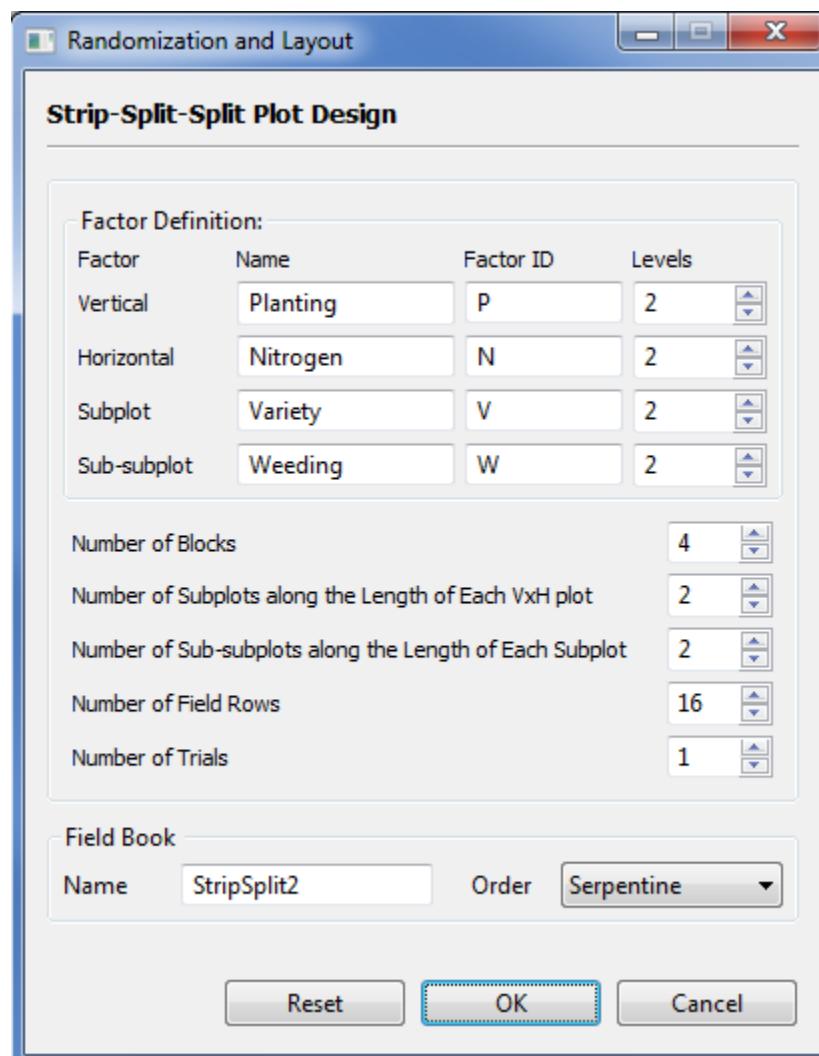
Field Book Filename

This field is required and it specifies the file name where the result of the randomization will be saved. The default filename is *fieldbookStripSplit2*.

Field Book Order

Define how the plot number will be arranged. There are two options available: *Plot Order* (default value) and *Serpentine*.

For this example, suppose we want to generate a randomization for an experiment to be conducted using Strip-Split-Split Plot, with planting methods (with 2 levels) as vertical factor, nitrogen rates (with 2 levels) as the horizontal factor, rice variety (with 2 levels) as the subplot factor and weeding method (with and without as levels) as sub-subplot. Four blocks will be used. The completed dialog box should appear as shown below:



- Click the **OK** button to generate the randomization. The **Randomization and Layout** dialog box will be minimized and STAR will automatically display the *csv* data file and the *txt* file created in the Data Viewer tab.

Sample *txt* file displayed in the Data Viewer is shown below:

```
DESIGN PROPERTIES:
    Strip-Split-Split Plot Design

DESIGN PARAMETERS:
    Number of Trials = 1
    Number of Blocks = 4
    Vertical Factor = Planting
    Levels = P1, P2
    Horizontal Factor = Nitrogen
    Levels = N1, N2
    Subplot Factor = Variety
    Levels = V1, V2
    Sub-subplot Factor = Weeding
    Levels = W1, W2
```

Layout for Strip-Split-Split Plot:

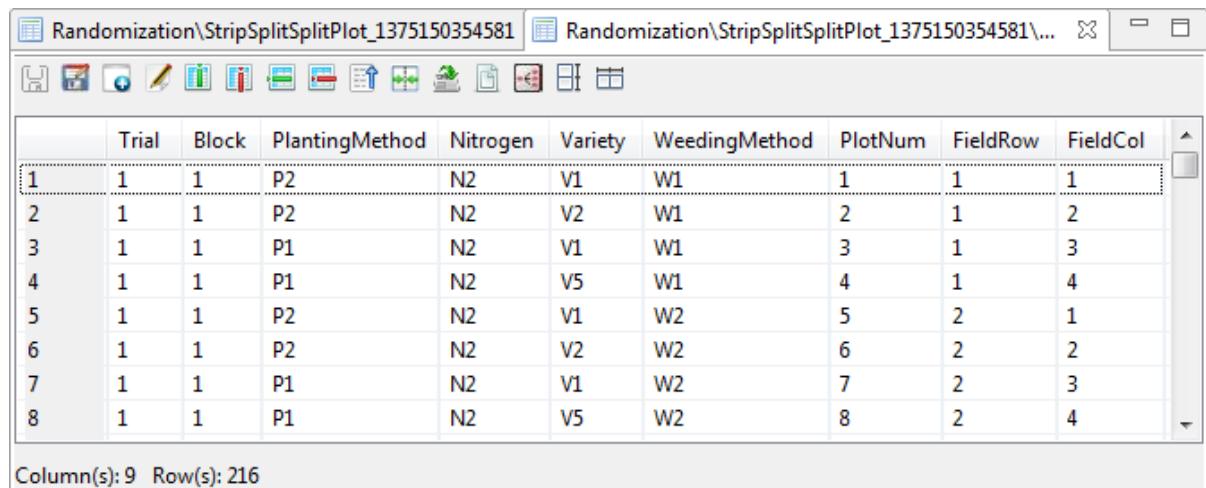
Trial = 1

	FieldCol1	FieldCol2	FieldCol3	FieldCol4
FieldRow1	101 P2 N2 V2 W2	102 P1 N2 V1 W2	201 P2 N1 V2 W1	202 P1 N1 V2 W1
FieldRow2	104 P2 N2 V2 W1	103 P1 N2 V1 W1	204 P2 N1 V2 W2	203 P1 N1 V2 W2
FieldRow3	105 P2 N2 V1 W1	106 P1 N2 V2 W1	205 P2 N1 V1 W1	206 P1 N1 V1 W2
FieldRow4	108 P2 N2 V1 W2	107 P1 N2 V2 W2	208 P2 N1 V1 W2	207 P1 N1 V1 W1
FieldRow5	109 P2 N1 V1 W2	110 P1 N1 V1 W2	209 P2 N2 V1 W1	210 P1 N2 V2 W2
FieldRow6	112 P2 N1 V1 W1	111 P1 N1 V1 W1	212 P2 N2 V1 W2	211 P1 N2 V2 W1
FieldRow7	113 P2 N1 V2 W2	114 P1 N1 V2 W2	213 P2 N2 V2 W2	214 P1 N2 V1 W2
FieldRow8	116 P2 N1 V2 W1	115 P1 N1 V2 W1	216 P2 N2 V2 W1	215 P1 N2 V1 W1
FieldRow9	301 P2 N2 V1 W1	302 P1 N2 V2 W1	401 P2 N2 V2 W1	402 P1 N2 V1 W2
FieldRow10	304 P2 N2 V1 W2	303 P1 N2 V2 W2	404 P2 N2 V2 W2	403 P1 N2 V1 W1
FieldRow11	305	306	405	406

	P2 N2 V2 W2	P1 N2 V1 W2	P2 N2 V1 W1	P1 N2 V2 W2
FieldRow12	308	307	408	407
	P2 N2 V2 W1	P1 N2 V1 W1	P2 N2 V1 W2	P1 N2 V2 W1
FieldRow13	309	310	409	410
	P2 N1 V1 W2	P1 N1 V2 W1	P2 N1 V1 W2	P1 N1 V2 W1
FieldRow14	312	311	412	411
	P2 N1 V1 W1	P1 N1 V2 W2	P2 N1 V1 W1	P1 N1 V2 W2
FieldRow15	313	314	413	414
	P2 N1 V2 W1	P1 N1 V1 W1	P2 N1 V2 W2	P1 N1 V1 W2
FieldRow16	316	315	416	415
	P2 N1 V2 W2	P1 N1 V1 W2	P2 N1 V2 W1	P1 N1 V1 W1

**Note: Cells contain plot numbers on top, treatments/entries below

Sample csv data file displayed in the Data Viewer is shown below:



	Trial	Block	PlantingMethod	Nitrogen	Variety	WeedingMethod	PlotNum	FieldRow	FieldCol
1	1	1	P2	N2	V1	W1	1	1	1
2	1	1	P2	N2	V2	W1	2	1	2
3	1	1	P1	N2	V1	W1	3	1	3
4	1	1	P1	N2	V5	W1	4	1	4
5	1	1	P2	N2	V1	W2	5	2	1
6	1	1	P2	N2	V2	W2	6	2	2
7	1	1	P1	N2	V1	W2	7	2	3
8	1	1	P1	N2	V5	W2	8	2	4

Column(s): 9 Row(s): 216

Balanced Incomplete Block Design

The steps to generate randomization for Balanced Incomplete Block Design are listed below:

- Click **Design | Incomplete Block Design | Balanced Incomplete Block Design...** from the main window. The **Randomization and Layout** dialog box will appear.
- Specify the required field and appropriate options.

Number of Treatments

Define the number of treatments (trmt) to be included in the randomization. The default and minimum value is 3. The entry should be a greater than the entry for the plots per block.

Plots per Block (block size)

These define the number of replicates to be generated. The default value and minimum value is equal to 2. The entry should be less than the number of treatments.

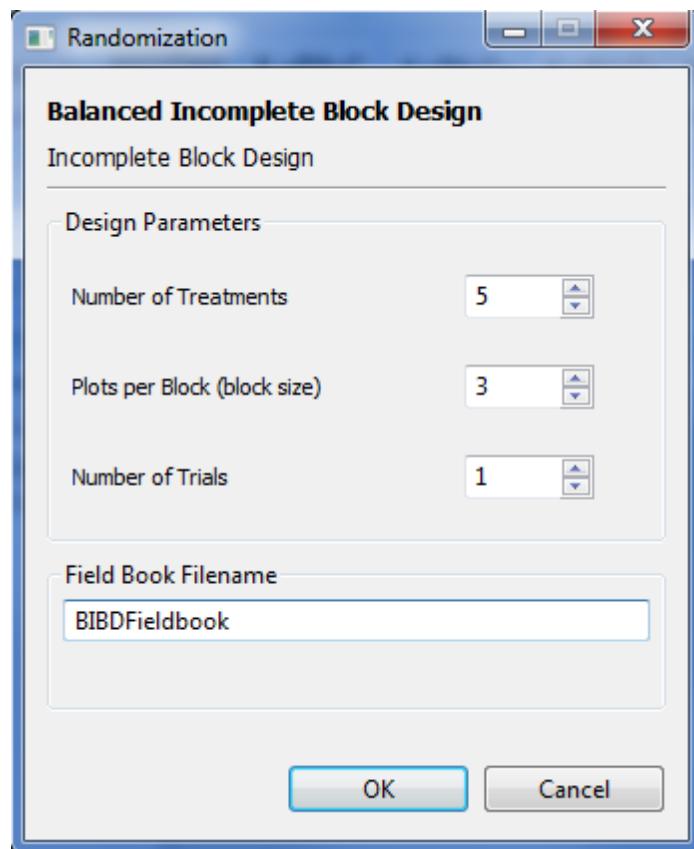
Number of Trial

Define the number of trials to be generated. The default value and minimum value is equal to one.

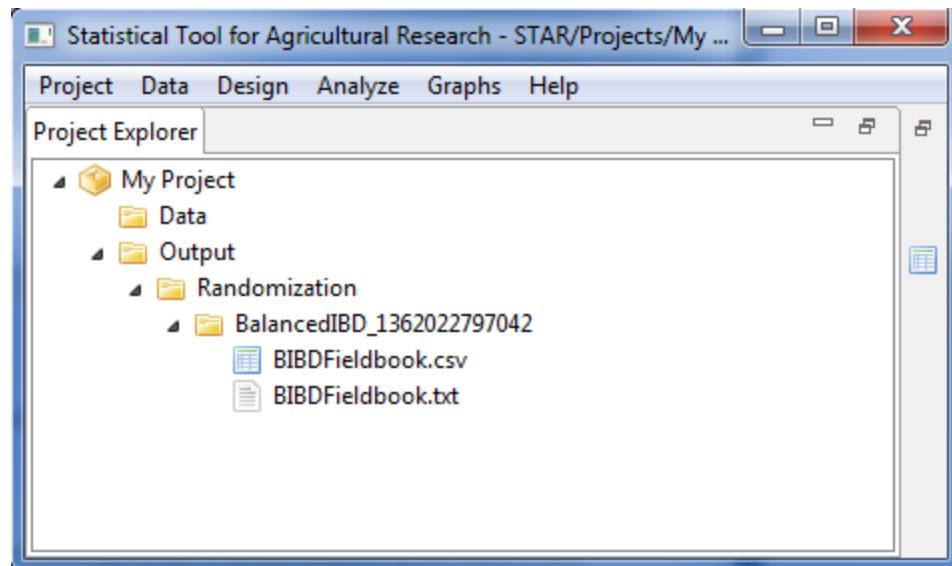
Field Book Filename

This field is required and it specifies the file name where the result of the randomization will be saved.

For the example, the completed dialog box should appear as below:



- Click the **OK** button to generate the randomization. The **Randomization and Layout** dialog box will be minimized and STAR will automatically display the csv data file created in the Data Viewer tab.



Sample csv file displayed in the Data Viewer is shown below:

The screenshot shows the 'Data View' window of the software. The title bar reads 'Statistical Tool for Agricultural Research - STAR/Projects/My Project...'. The menu bar includes Project, Data, Design, Analyze, Graphs, and Help. The left pane is a 'Project Explorer' tree view with nodes for Project, Data, Output, Randomization, and a specific folder 'BalancedIBD_1362022797042' containing 'BIBDFieldbook.csv' and 'BIBDFieldbook.txt'. The right pane displays a table with four columns: Trials, Blocks, Treatment, and PlotNum. The data in the table is as follows:

Trials	Blocks	Treatment	PlotNum
1	1	T5	1
1	1	T1	2
1	1	T4	3
1	2	T1	1
1	2	T3	2

Below the table, it says 'Column(s): 4 Row(s): 30'.

To view the text file created, double click the text file to view it in the **Result Viewer**. Sample *txt* file that was created is shown below:

The screenshot shows the 'Result Viewer' window of the software. The title bar reads 'Statistical Tool for Agricultural Research - STAR/Projects/My Project...'. The left pane is a 'Project Explorer' tree view with nodes for My Project, Data, Output, Randomization, and a specific folder 'BalancedIBD_1362022797042' containing 'BIBDFieldbook.csv' and 'BIBDFieldbook.txt'. The right pane displays the contents of the 'BIBDFieldbook.txt' file, which contains the following text:

```
DESIGN PROPERTIES:  
    Balanced Incomplete Block Design  
  
DESIGN PARAMETERS:  
    Number of Trials = 1  
    Number of Treatments = 5  
    Plots per Block (Block Size) = 3  
    Number of Blocks = 10  
    Number of Replicates = 6  
    Lambda = 3
```

Lattice Design

The steps to generate randomization for Lattice design are listed below:

- Click **Design | Incomplete Block Design | Lattice Design...** from the main window. The **Randomization and Layout** dialog box will appear.
- Specify the required fields and appropriate options.

Number of Treatments

Define the number of treatments (trmt) to be included in the randomization. The default and minimum value is 9 while the maximum value is 144. The entry should be a perfect square.

Number of Replicates

These define the number of replicates to be generated. The default value and minimum value is equal to 2. If the \sqrt{trmts} is odd, the maximum number of replicates is $\sqrt{trmt} + 1$. If the \sqrt{trmts} is even, the maximum number of replicates is 5 if the treatment is equal to 4, otherwise the maximum number of replicates is 3.

Number of Field Rows

Define the total number of rows in the field layout for each trial. The default and minimum value is equal to 1.

Number of Trial

Define the number of trials to be generated. The default value and minimum value is equal to one.

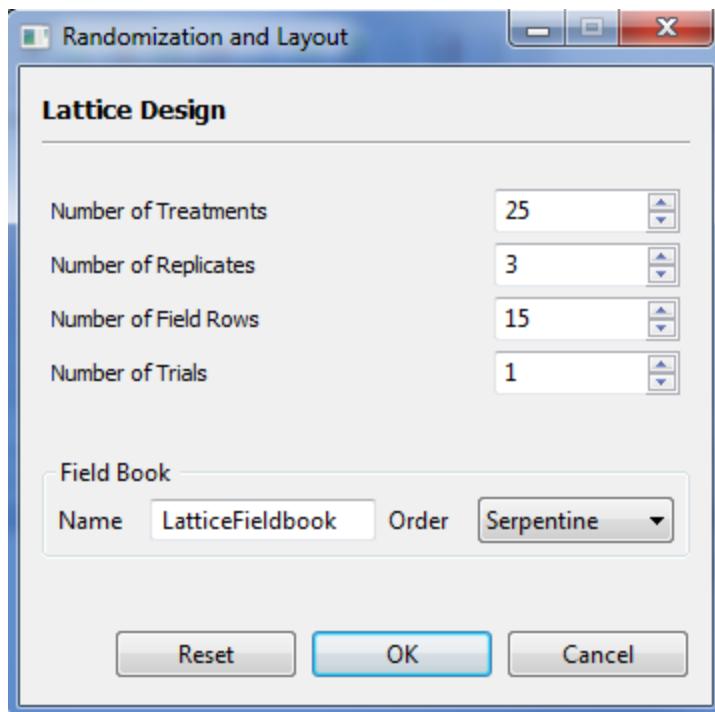
Field Book Filename

This field is required and it specifies the file name where the result of the randomization will be saved. The default filename is *fieldbookLattice*.

Field Book Order

Define how the plot number will be arranged. There are two options available: *Plot Order* (default value) and *Serpentine*.

For this example, suppose we want to generate a randomization for an experiment that will be conducted using Lattice design with 25 treatments in three replicates. The completed dialog box should appear as shown below:



- Click the **OK** button to generate the randomization. The **Randomization and Layout** dialog box will be minimized and STAR will automatically display the csv data file and the *txt* file created in the Data Viewer tab.

Sample *txt* file displayed in the Data Viewer is shown below:

DESIGN PROPERTIES:
Incomplete Block Design
5 x 5 Partially Balanced Lattice Design

DESIGN PARAMETERS:
Number of Trials = 1
Number of Treatments = 25
Number of Replicates = 3
Plots per Block (Block Size) = 5
Block per Replicate = 5
Number of Field Row = 15
Number of Field Column = 5

Layout for Lattice Design

```
Trial = 1

      FieldCol1   FieldCol2   FieldCol3   FieldCol4   FieldCol5
      +-----+-----+-----+-----+
FieldRow1 |       101|     102|     103|     104|     105|
           |T16    |T4     |T25    |T22    |T14    |
           +-----+-----+-----+-----+
FieldRow2 |       110|     109|     108|     107|     106|
           |T9     |T10    |T1     |T20    |T2     |
           +-----+-----+-----+-----+
```

FieldRow3	111	112	113	114	115
	T6	T15	T12	T19	T8
	+-----+	+-----+	+-----+	+-----+	+-----+
FieldRow4	120	119	118	117	116
	T13	T18	T21	T17	T11
	+-----+	+-----+	+-----+	+-----+	+-----+
FieldRow5	121	122	123	124	125
	T3	T24	T5	T7	T23
	+-----+	+-----+	+-----+	+-----+	+-----+
FieldRow6	201	202	203	204	205
	T5	T12	T1	T25	T21
	+-----+	+-----+	+-----+	+-----+	+-----+
FieldRow7	210	209	208	207	206
	T3	T6	T9	T16	T13
	+-----+	+-----+	+-----+	+-----+	+-----+
FieldRow8	211	212	213	214	215
	T23	T8	T2	T14	T11
	+-----+	+-----+	+-----+	+-----+	+-----+
FieldRow9	220	219	218	217	216
	T7	T19	T20	T22	T17
	+-----+	+-----+	+-----+	+-----+	+-----+
FieldRow10	221	222	223	224	225
	T24	T15	T10	T4	T18
	+-----+	+-----+	+-----+	+-----+	+-----+
FieldRow11	301	302	303	304	305
	T13	T24	T12	T20	T14
	+-----+	+-----+	+-----+	+-----+	+-----+
FieldRow12	310	309	308	307	306
	T3	T15	T1	T22	T11
	+-----+	+-----+	+-----+	+-----+	+-----+
FieldRow13	311	312	313	314	315
	T6	T10	T25	T17	T23
	+-----+	+-----+	+-----+	+-----+	+-----+
FieldRow14	320	319	318	317	316
	T16	T18	T5	T19	T2
	+-----+	+-----+	+-----+	+-----+	+-----+
FieldRow15	321	322	323	324	325
	T9	T4	T21	T7	T8
	+-----+	+-----+	+-----+	+-----+	+-----+

**Note: Cells contain plot numbers on top, treatments/entries below

Sample csv data file displayed in the Data Viewer is shown below:

Trial	Rep	Block	Treatment	PlotNum	FieldRow	FieldCol
1	1	1	T16	101	1	1
2	1	1	T4	102	1	2
3	1	1	T25	103	1	3
4	1	1	T22	104	1	4
5	1	1	T14	105	1	5
6	1	1	T9	110	2	1
7	1	1	T10	109	2	2
8	1	1	T1	108	2	3

Alpha Lattice Design

The steps to generate randomization for Alpha Lattice Design are listed below:

- Click **Design | Incomplete Block Design | Alpha Lattice Design...** from the main window. The **Randomization** dialog box will appear.
- Specify the required field and appropriate options.

Number of Treatments

Define the number of treatments to be included in the randomization. The default and minimum value is 9.

Number of Replicates

Define the number of replicates to be generated per trial. The default and minimum value is 2 while the maximum is equal to 4. If number of replicates (r) is equal to 2, the block size (k) should be less than or equal to the number of blocks (s). If r = 3, and s is an odd number, $k \leq s$. If r = 3, and s is an even number, $k \leq s - 1$. If r = 4, and s is an odd number but multiple of 3, $k \leq s$. The number of blocks can be computed as the number of treatments /block size.

Plots per Block (block size)

Define the number of plots per block or the block size. The default and minimum value is 3

Number of Field Rows

Define the total number of rows in the field layout for each trial. The default and minimum value is equal to 3.

Number of Trial

Define the number of trials to be generated. The default value and minimum value is equal to one.

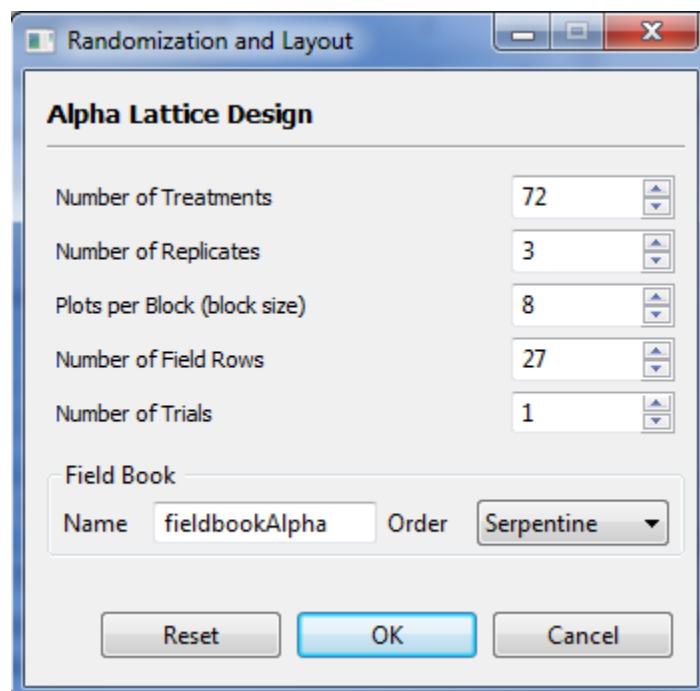
Field Book Filename

This field is required and it specifies the file name where the result of the randomization will be saved. The default filename is *fieldbookAlpha*.

Field Book Order

Define how the plot number will be arranged. There are two options available: *Plot Order* (default value) and *Serpentine*.

For this example, suppose we want to generate a randomization for an experiment that will be conducted using Alpha Lattice design with 72 entries grouped into 8 with three replicates. The completed dialog box should appear as illustrated below:



- Click the **OK** button to generate the randomization. The **Randomization and Layout** dialog box will be minimized and STAR will automatically display the csv data file and the *txt* file created in the Data Viewer tab.

Sample *txt* file displayed in the Data Viewer is shown below:

DESIGN PROPERTIES:

Incomplete Block Design
Alpha Lattice Design

DESIGN PARAMETERS:

Number of Trials = 1
Number of Treatments = 72
Number of Replicates = 3
Plots per Block (Block Size) = 8
Block per Replicate = 9

Layout for Alpha Lattice Design

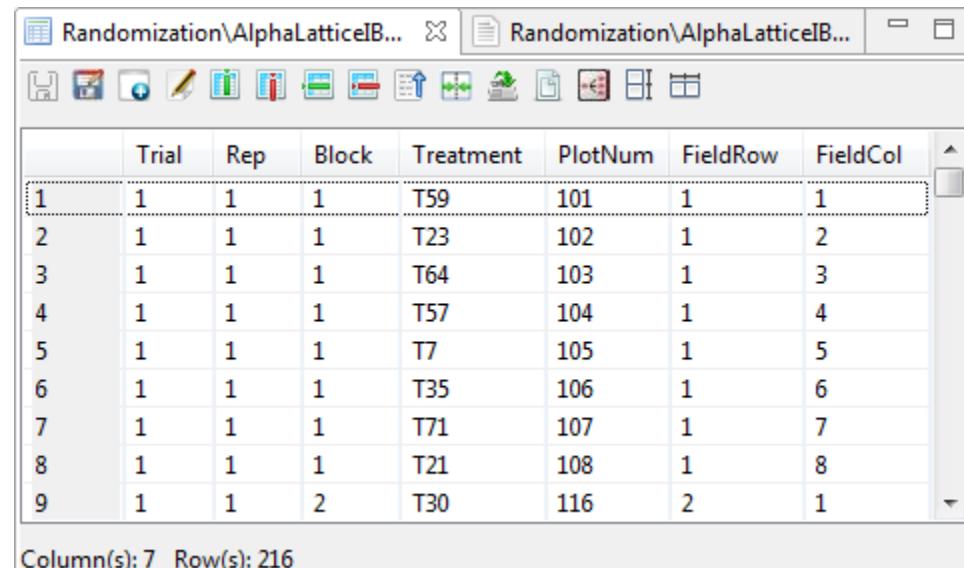
Trial = 1

	FieldCol1	FieldCol2	FieldCol3	FieldCol4	FieldCol5	FieldCol6	FieldCol7	FieldCol8
FieldRow1	101	102	103	104	105	106	107	108
	T59	T23	T64	T57	T7	T35	T71	T21
FieldRow2	116	115	114	113	112	111	110	109
	T30	T1	T34	T26	T46	T33	T18	T49
FieldRow3	117	118	119	120	121	122	123	124
	T63	T56	T39	T47	T69	T27	T42	T60
FieldRow4	132	131	130	129	128	127	126	125
	T37	T2	T43	T62	T15	T5	T61	T24
FieldRow5	133	134	135	136	137	138	139	140
	T68	T14	T66	T48	T70	T41	T10	T72
FieldRow6	148	147	146	145	144	143	142	141
	T36	T55	T58	T45	T3	T29	T12	T11
FieldRow7	149	150	151	152	153	154	155	156
	T8	T25	T40	T28	T52	T16	T32	T4
FieldRow8	164	163	162	161	160	159	158	157
	T31	T9	T51	T53	T54	T20	T67	T50
FieldRow9	165	166	167	168	169	170	171	172
	T22	T65	T6	T13	T19	T38	T44	T17
FieldRow10	201	202	203	204	205	206	207	208
	T35	T22	T26	T47	T62	T10	T4	T51
FieldRow11	216	215	214	213	212	211	210	209
	T60	T7	T48	T67	T38	T30	T52	T12
FieldRow12	217	218	219	220	221	222	223	224
	T11	T28	T66	T37	T13	T46	T54	T27
FieldRow13	232	231	230	229	228	227	226	225
	T36	T18	T50	T23	T8	T44	T15	T42
FieldRow14	233	234	235	236	237	238	239	240
	T64	T17	T5	T9	T70	T56	T34	T58
FieldRow15	248	247	246	245	244	243	242	241
	T61	T57	T31	T19	T72	T55	T63	T16
FieldRow16	249	250	251	252	253	254	255	256
	T45	T68	T20	T65	T25	T33	T71	T43
FieldRow17	264	263	262	261	260	259	258	257
	T3	T41	T6	T49	T21	T24	T40	T69

FieldRow18	265	266	267	268	269	270	271	272
	T32	T14	T2	T29	T39	T1	T59	
FieldRow19	301	302	303	304	305	306	307	308
	T40	T56	T53	T71	T66	T30	T61	T44
FieldRow20	316	315	314	313	312	311	310	309
	T25	T62	T39	T12	T6	T70	T23	T54
FieldRow21	317	318	319	320	321	322	323	324
	T49	T59	T43	T72	T47	T13	T36	T67
FieldRow22	332	331	330	329	328	327	326	325
	T55	T65	T27	T9	T8	T14	T26	T21
FieldRow23	333	334	335	336	337	338	339	340
	T7	T4	T11	T68	T34	T2	T42	T19
FieldRow24	348	347	346	345	344	343	342	341
	T20	T22	T69	T1	T58	T57	T52	T37
FieldRow25	349	350	351	352	353	354	355	356
	T3	T15	T31	T32	T10	T60	T17	T33
FieldRow26	364	363	362	361	360	359	358	357
	T51	T45	T24	T63	T28	T48	T64	T18
FieldRow27	365	366	367	368	369	370	371	372
	T38	T50	T16	T41	T46	T29	T5	T35

**Note: Cells contain plot numbers on top, treatments/entries below

Sample csv data file displayed in the Data Viewer is shown below:



	Trial	Rep	Block	Treatment	PlotNum	FieldRow	FieldCol
1	1	1	1	T59	101	1	1
2	1	1	1	T23	102	1	2
3	1	1	1	T64	103	1	3
4	1	1	1	T57	104	1	4
5	1	1	1	T7	105	1	5
6	1	1	1	T35	106	1	6
7	1	1	1	T71	107	1	7
8	1	1	1	T21	108	1	8
9	1	1	2	T30	116	2	1

Column(s): 7 Row(s): 216

Augmented Randomized Complete Block Design

The steps to generate randomization for augmented randomized complete block design are listed below:

- Click **Design | Augmented Design | Randomized Complete Block Design...** from the main window. The **Randomization and Layout** dialog box will appear.
- Specify the required fields and appropriate options.

Number of Replicated Treatments

Define the number of replicated treatments to be included in the randomization. The default and minimum value is 2 while the maximum value is 500.

Number of Blocks

Define the number of blocks to be generated. The default and minimum value is 2.

Number of Unreplicated Treatments

Define the number of unreplicated treatments to be included in the randomization. The default and minimum value is 2 while the maximum value is 2000.

Number of Field Rows

Define the number of rows in the field layout. Number should be greater than or equal to the number of blocks. The default and minimum value is equal to 1.

Number of Trials

Define the number of trials to be generated. The default and minimum value is 1.

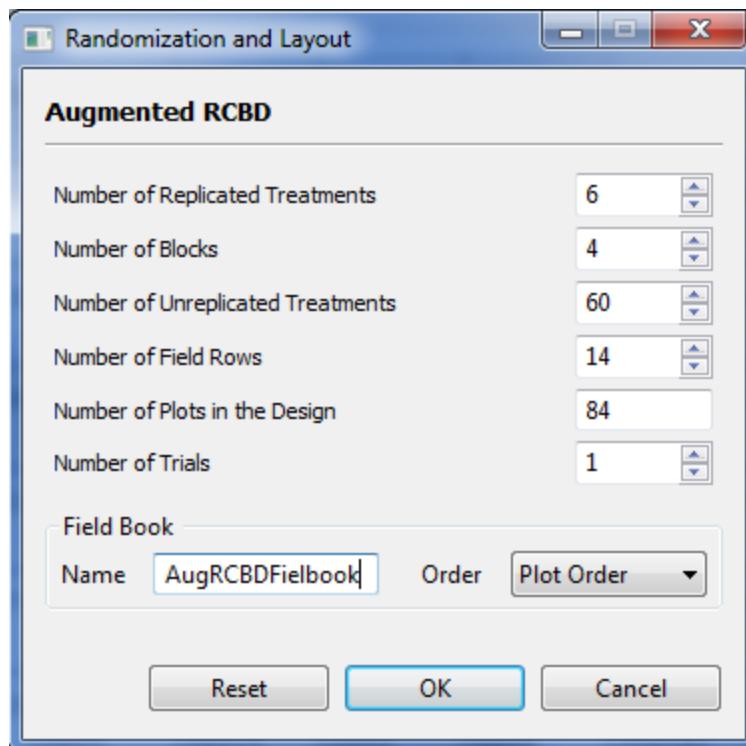
Field Book Filename

This field is required and it specifies the file name where the result of the randomization will be saved. The default filename is *fieldbookAugRCBD*.

Field Book Order

Define how the plot number will be arranged. There are two options available: *Plot Order* (default value) and *Serpentine*.

For this example, suppose we want to generate a randomization for an experiment which will be conducted using augmented randomized complete block design involving four blocks. The experiment will use six replicated treatments and 60 unreplicated treatments (test entries). The completed dialog box should appear as shown below:



- Click the **OK** button to generate the randomization. The **Randomization and Layout** dialog box will be minimized and STAR will automatically display the csv data file and the *txt* file created in the Data Viewer tab.

Sample *txt* file displayed in the Data Viewer is shown below:

```

DESIGN PROPERTIES:
    Augmented Randomized Complete Block Design (Augmented RCBD)

DESIGN PARAMETERS:
    Number of Trials = 1
    Number of Replicated Treatments = 6
    Levels of Replicated Treatments = check1, check2, check3, ..., check6
    Number of Replicates = 4
    Number of Unreplicated Treatments = 60
    Levels of UnReplicated Treatments = new1, new2, new3, ..., new60
    Number of Field Row = 14
  
```

Layout for Augmented Randomized Complete Block Design

```

Trial = 1

+-----+-----+-----+-----+-----+
FieldRow1 |     101|     102|     103|     104|     105|     106|
|new14   |new7  |check3 |check5 |new15  |new9   |
+-----+-----+-----+-----+-----+
FieldRow2 |     107|     108|     109|     110|     111|     112|
|check4  |new8  |new6  |check2 |new5   |check6 |
+-----+-----+-----+-----+-----+
  
```

FieldRow3	113	114	115	116	117	118
	new3	new17	new2	new16	new10	new13
FieldRow4	119	120	121	122	123	124
	new11	new18	check1	new4	new12	new1
FieldRow5	201	202	203	204	205	206
	new4	new14	new15	new2	new13	check3
FieldRow6	207	208	209	210	211	212
	new1	new7	new10	new8	check6	check5
FieldRow7	213	214	215	216	217	218
	new16	new3	new18	new9	new6	check1
FieldRow8	219	220	221	222	223	224
	check2	new12	new11	check4	new5	new17
FieldRow9	301	302	303	304	305	306
	new7	new9	new4	new1	new5	new8
FieldRow10	307	308	309	310	311	312
	check6	new11	new2	check5	new10	check1
FieldRow11	313	314	315	316	317	318
	new12	check4	check3	new3	check2	new6
FieldRow12	401	402	403	404	405	406
	new3	new8	check4	new7	check5	check6
FieldRow13	407	408	409	410	411	412
	new10	new2	new9	new11	new12	check1
FieldRow14	413	414	415	416	417	418
	new4	check3	check2	new1	new6	new5

**Note: Cells contain plot numbers on top, treatments/entries below

Sample csv data file displayed in the Data Viewer is shown below:

The screenshot shows a software window titled "Randomization\Augmente...". The main area contains a table with columns: Trial, Block, Treatment, PlotNum, FieldRow, and FieldCol. The table has 8 rows of data. The last row is highlighted with a dashed border. Below the table, status text indicates "Column(s): 6 Row(s): 84".

	Trial	Block	Treatment	PlotNum	FieldRow	FieldCol
1	1	1	new14	101	1	1
2	1	1	new7	102	1	2
3	1	1	check3	103	1	3
4	1	1	check5	104	1	4
5	1	1	new15	105	1	5
6	1	1	new9	106	1	6
7	1	1	check4	107	2	1
8	1	1	new8	108	2	2

Augmented Latin Square Design

The steps to generate randomization for augmented Latin square design are listed below:

- Click **Design | Augmented Design | Latin Square Design...** from the main window. The **Randomization and Layout** dialog box will appear.
- Specify the required fields and appropriate options.

Number of Replicated Treatments

Define the number of replicated treatments to be included in the randomization. The default and minimum value is 2 while the maximum value is 11.

Number of Unreplicated Treatments

Define the number of unreplicated treatments to be included in the randomization. The default and minimum value is 2 while the maximum value is 2000.

Number of Field Rows

Define the number of rows in the field layout. Number should be greater than or equal to the number of replicated treatments. The default and minimum value is equal to 2.

Number of Trials

Define the number of trials to be generated. The default and minimum value is 1.

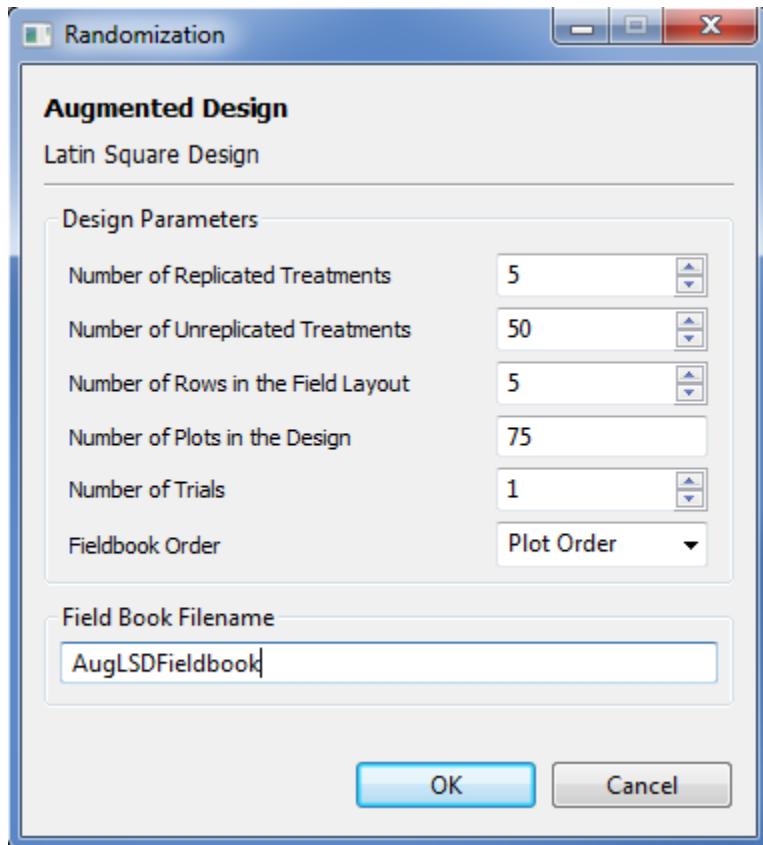
Field Book Filename

This field is required and it specifies the file name where the result of the randomization will be saved. The default filename is *fieldbookAugLSD*.

Field Book Order

Define how the plot number will be arranged. There are two options available: *Plot Order* (default value) and *Serpentine*.

For this example, suppose we want to generate a randomization for an experiment which will be conducted using augmented latin square design. The experiment will use five replicated treatment and 50 unreplicated treatments (test entries). The completed dialog box should appear as illustrated below:



- Click the **OK** button to generate the randomization. The **Randomization and Layout** dialog box will be minimized and STAR will automatically display the csv data file and txt file created in the Data Viewer tab.

Sample *txt* file displayed in the Data Viewer is shown below:

DESIGN PROPERTIES:

Augmented Latin Square Design (Augmented LSD)

DESIGN PARAMETERS:

```
Number of Trials = 1
Number of Replicated Treatments = 5
Levels of Replicated Treatments = check1, check2, check3, check4,
check5
Number of Unreplicated Treatments = 50
Levels of UnReplicated Treatments = new1, new2, new3, ..., new50
Number of Field Row = 15
Number of Field Column = 5
```

Layout for Augmented Latin Square Design

Trial = 1

	FieldCol1	FieldCol2	FieldCol3	FieldCol4	FieldCol5
FieldRow1	1 check2	2 new20	3 new15	4 new8	5 check4
FieldRow2	6 new7	7 new44	8 new45	9 check5	10 new46
FieldRow3	11 new5	12 check1	13 check3	14 new9	15 new35
FieldRow4	16 check3	17 new25	18 check4	19 new19	20 check5
FieldRow5	21 new6	22 check2	23 new23	24 new31	25 new32
FieldRow6	26 new43	27 new22	28 new1	29 check1	30 new11
FieldRow7	31 new37	32 check3	33 check5	34 new42	35 check1
FieldRow8	36 new50	37 new26	38 new34	39 check2	40 new13
FieldRow9	41 check4	42 new16	43 new14	44 new48	45 new49
FieldRow10	46 new30	47 new21	48 check1	49 new27	50 new29
FieldRow11	51 new3	52 new39	53 new24	54 new33	55 check2
FieldRow12	56 check5	57 check4	58 new10	59 check3	60 new17
FieldRow13	61 new47	62 new41	63 new4	64 check4	65 new2
FieldRow14	66 check1	67 new18	68 new28	69 new38	70 check3

FieldRow15	71	72	73	74	75
	new12	check5	check2	new40	new36

**Note: Cells contain plot numbers on top, treatments/entries below

Sample csv data file displayed in the Data Viewer is shown below:

The screenshot shows a software interface titled "Randomization\AugmentedL...". The main window displays a data grid with the following columns: Trial, Row, Column, Treatment, PlotNum, FieldRow, and FieldCol. The data consists of 8 rows of experimental entries. The "Treatment" column contains values like "check2", "new20", "new15", etc. The "PlotNum" column contains values like 1, 2, 3, etc. The "FieldRow" and "FieldCol" columns both contain values 1, 2, and 3. Below the grid, a status bar indicates "Column(s): 7 Row(s): 75".

Trial	Row	Column	Treatment	PlotNum	FieldRow	FieldCol
1	1	1	check2	1	1	1
2	1	1	new20	2	1	2
3	1	1	new15	3	1	3
4	1	1	new8	4	1	4
5	1	1	check4	5	1	5
6	1	1	new7	6	2	1
7	1	1	new44	7	2	2
8	1	1	new45	8	2	3

Graphs

Bar Graph

Bar graphs are useful for visualizing frequencies, sums, and statistics such as means and medians. The bar graphs that are created here can come from raw data or from pre-computed summary information.

The steps to create a bar graph are listed below:

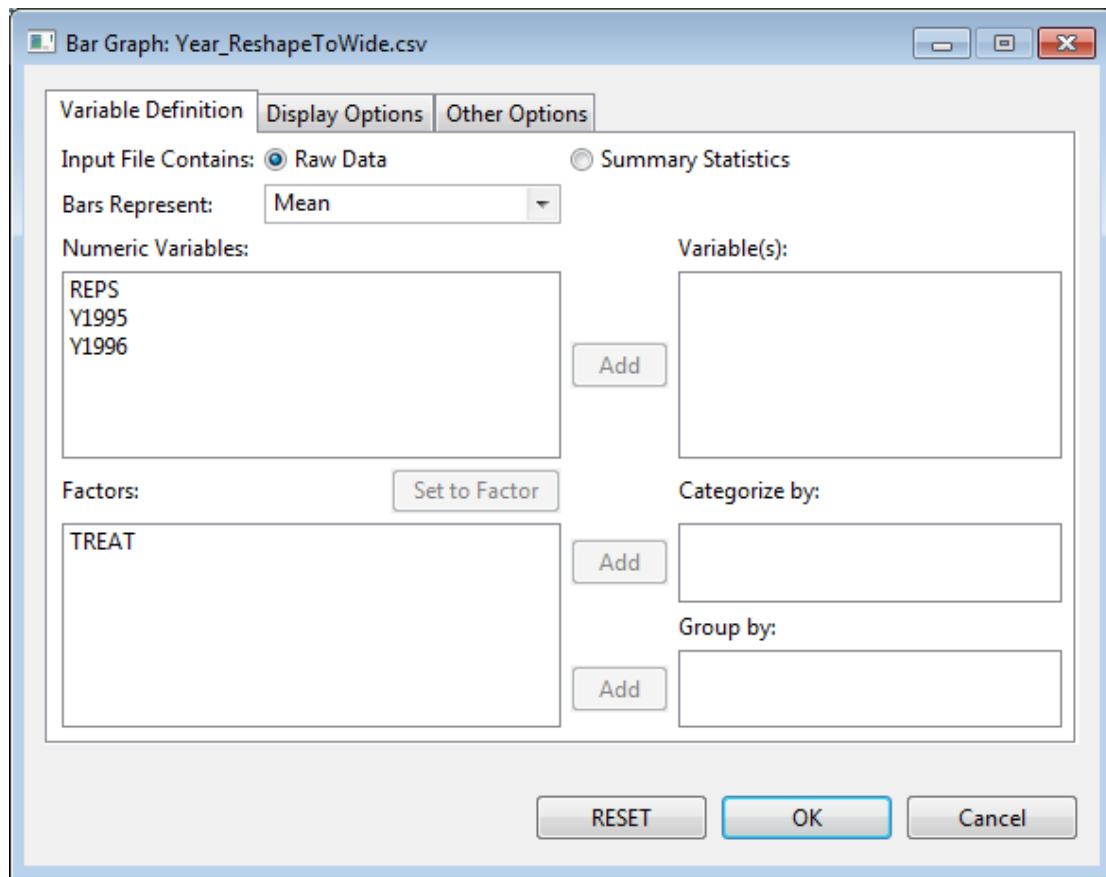
- On the **Project Explorer** panel, double-click the file to be used to open it and view it in the Data Viewer tab.

For the example, using the project named *TrialProject*, select the data file *Year_ReshapeToWide.csv*. Double-click the file to open it and view it in the Data Viewer.

- Click **Graphs | Bar Graph....** The **Bar Graph** dialog box will appear.

The file *Year_ReshapeToWide.csv* was created in the **Reshaping data from long (serial) to wide (parallel)** section of this user manual.

- Click **Graphs | Bar Graph....** The **Bar Graph** dialog box will appear.



- Specify the inputs for the required fields and desired options.

Variable Definition Tab

Input File Contains

There are two options available, **Raw Data** (default option) and **Summary Statistics**.

Bars Represent

This item is enabled if the **Input File Contains Raw Data** option is selected. Four options are available for creating the bars: **Frequency**, **Mean**, **Median**, and **Sum**.

Variable(s)

At least one entry should be specified for the graph to be created. Entries should come from the **Numeric Variables** dialog box.

Categorize by

This field is required. The factor specified will define the labels for the bars and, if input file contains raw data, the categories for which values are computed.

Group by

This field is optional. If a factor is specified, a bar graph is going to be generated per category of the factor. Entries should come from the **Factors** list box.

Display Options Tab

Main Title

This field will contain the title for the graph.

Category Axis Label

This field will contain the label for the factor. If two or more numeric variables are specified in the graph, checking the **Display variable names** box will add the names of the numeric variables onto the category axis.

Value Axis

The **Label** field will contain the label for the numeric variable(s). The **Range** will contain the suggested minimum (**Lower Limit**) and maximum (**Upper Limit**) values for the axis. If not specified (*Auto*), these are determined from the data.

Draw box around plot

If checked, the graph will be enclosed in a box.

Show legend

If checked, a legend will be added to the graph. The legend may be placed in any of nine positions within the graph: *bottom*, *bottom-left*, *bottom-right*, *center*, *left*, *right*, *top*, *top-left*, *top-right*. The legend may or may not have a title.

This option is useful if there are two or more numeric variables used in the graph and the **Display variable names** is unchecked.

Display multiple graphs in a page

If checked, several graphs will be displayed on a single page, based on the specified number of rows and columns and orientation. At most 5 rows and 5 columns of graphs can be fitted into a single page, arranged either from *Top-to-bottom* or *Left-to-right*.

Other Options Tab

Orientation

Bars can either be drawn vertically or horizontally.

Style

This option is useful if several numeric variables are selected. Bars can be clustered (side-by-side) or stacked.

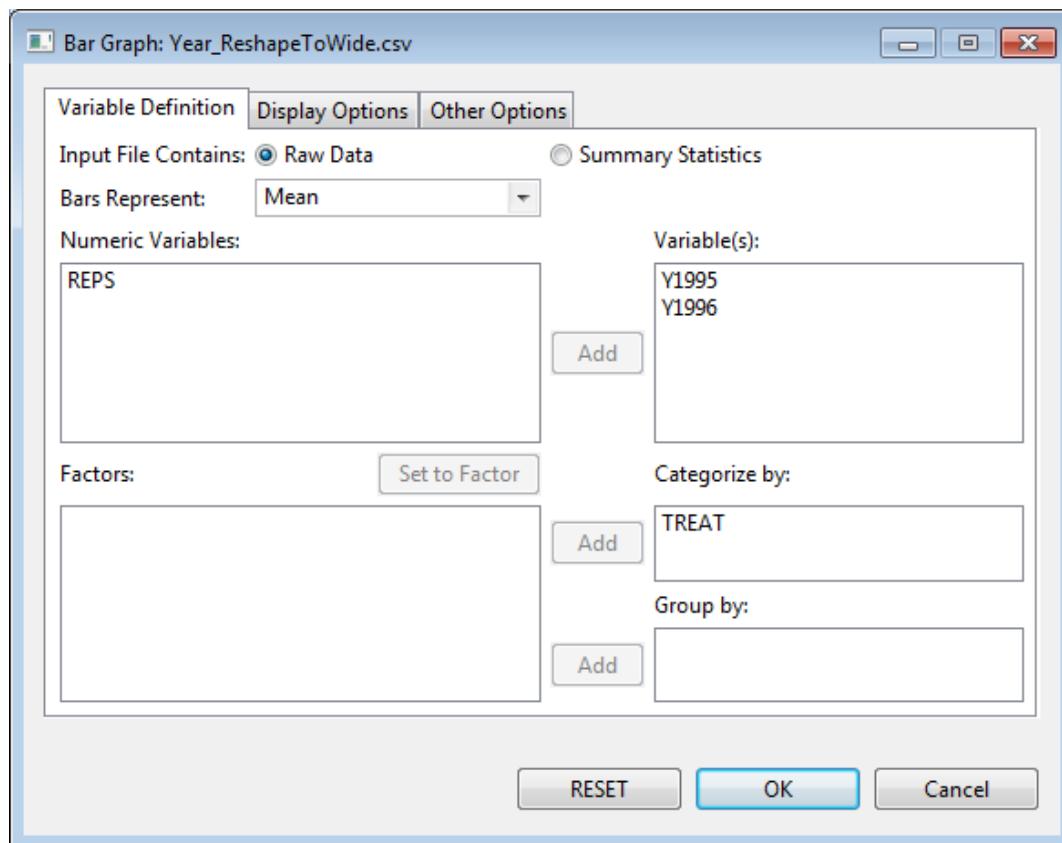
Color and Fill

Different colors (solid fill pattern) have been pre-selected to distinguish bars for different numeric variables. The default settings may be changed in this section/

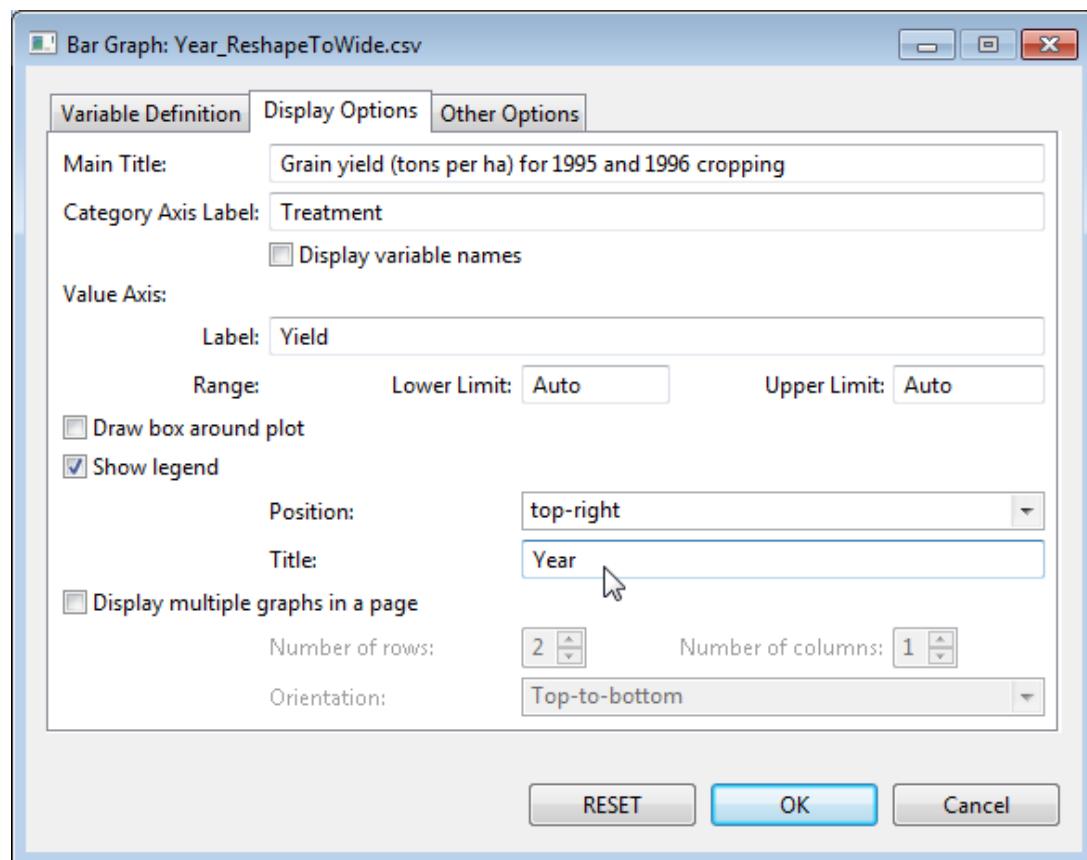
Display Error Bars

If the bars represent means to be computed from raw data, error bars may be added based on one of three options: **confidence level** (default: 95%), **standard error** (with multiplier 1, 2, or 3), and **standard deviation** (with multiplier 1, 2, or 3).

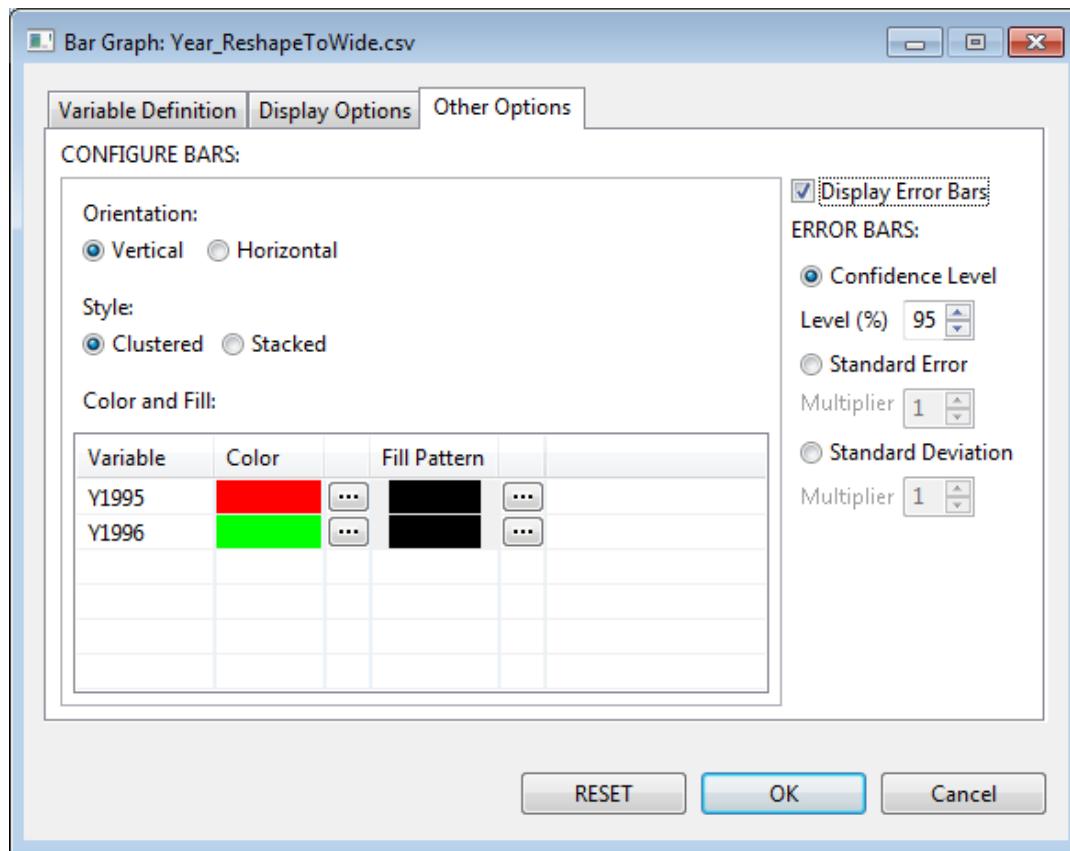
For the example, suppose we want to create a bar graph of the means of Y1995 and Y1996 with error bars, the completed **Variable Definition** tab should appear as illustrated:



Items in the **Display Options** tab may be supplied as illustrated:

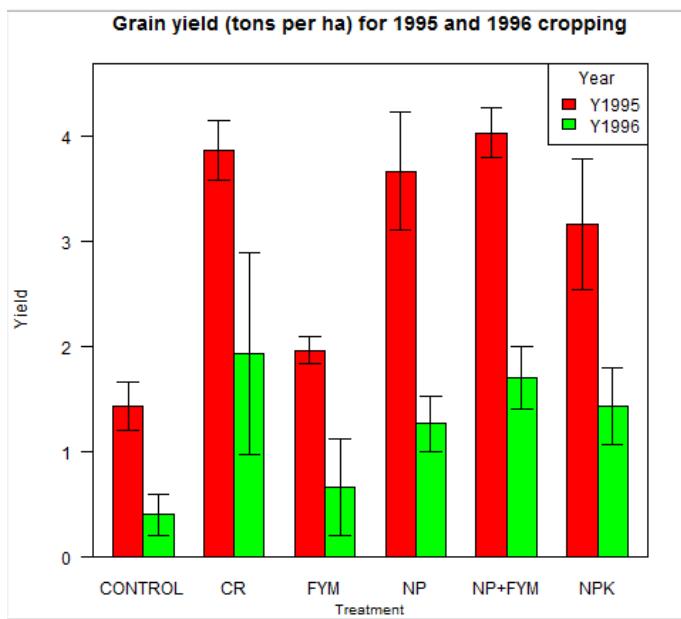


Items in the **Other Options** tab may be supplied as illustrated:



- Click the **OK** button to create the graph. The **Bar Graph** dialog box will be minimized and the Result Viewer will be activated.

Sample graph as displayed in the *Graph* page of the Result Viewer:



Box Plot

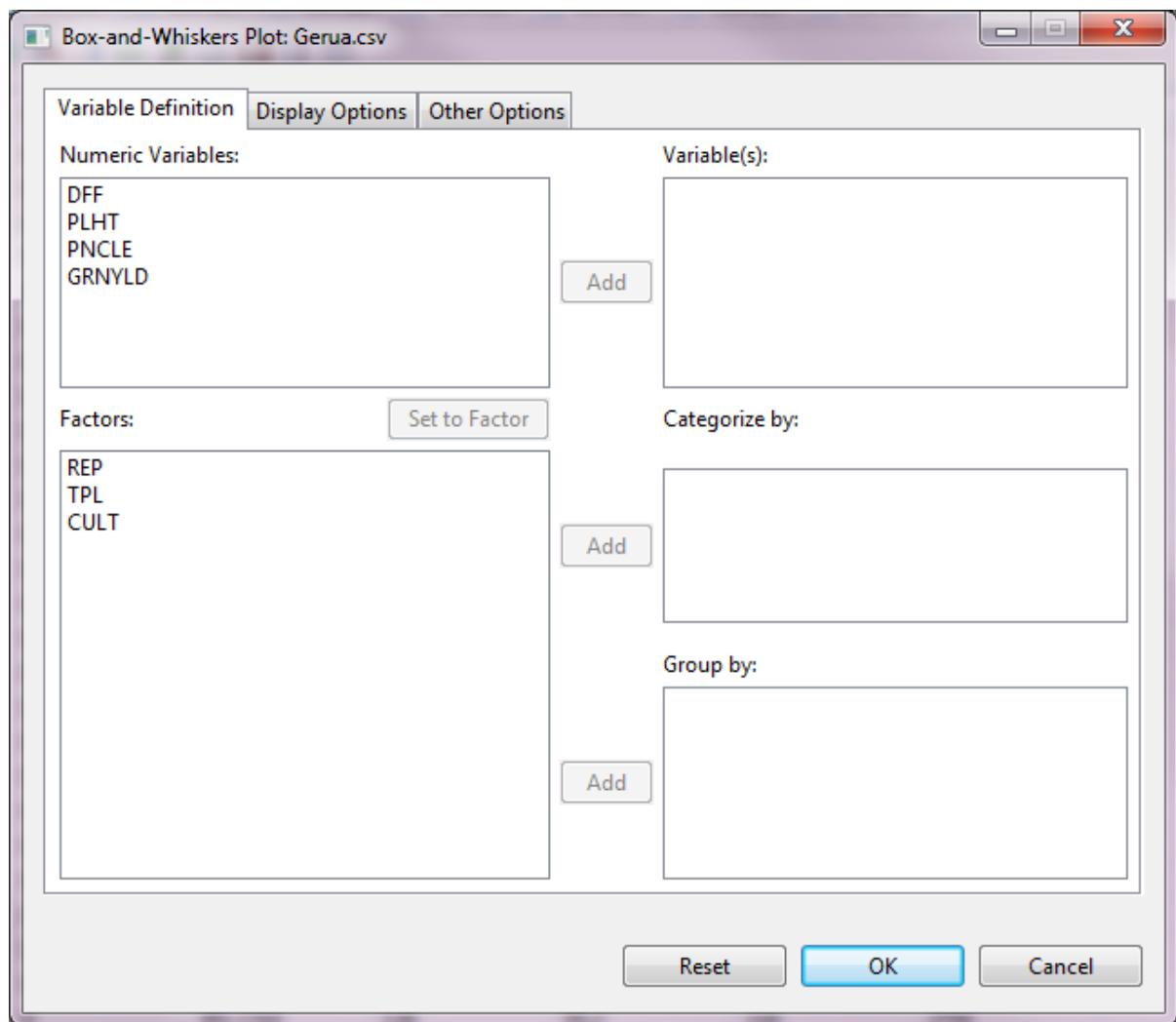
Box plots are useful for displaying distributional properties of data.

The steps to create a box plot are listed below:

- On the **Project Explorer**, double-click the file to be used for the analysis to open and view it in the Data Viewer.

For the example, using the project named *My Project*, import the data *Gerua* from STAR Package. Double-click the file to open and view it in the Data Viewer tab.

- Click **Graphs | Box Plot....** The **Box Plot** (or Box-and-Whiskers Plot) dialog box will appear.



- Specify the inputs for the required fields and desired options.

Variable Definition Tab

Variable(s)

At least one entry should be specified for the graph to be created. Entries should come from the **Numeric Variables** dialog box.

Categorize by

This field, if specified, will define the labels and sub-grouping for the box plots.

Group by

This field is optional. If a factor is specified, a graph is going to be generated per category of the factor. Entries should come from the **Factors** list box.

Display Options Tab

Main Title

This field will contain the title for the graph.

Category Axis Label

This field will contain the label for the factor.

Value Axis

The label and limits for the numeric variable(s) can be edited here. Default axis label is the name of the numeric variable(s). Lower and upper limits, if not specified, are determined from the data.

Orientation

Plots can be displayed vertically (default) or horizontally.

Draw box around plot

If checked, the graph will be enclosed in a box.

Display multiple graphs in a page

If checked, several graphs will be displayed on a single page, based on the specified number of rows and columns and orientation. At most 5 rows and 5 columns of graphs can be fitted into a single page, arranged either from *Top-to-bottom* or *Left-to-right*.

Other Options Tab

BOX

Color for the box outline and fill, as well as the size of the line used for the box may be edited here.

WHISKERS

Color, type and width for the line representing the whiskers may be edited here.

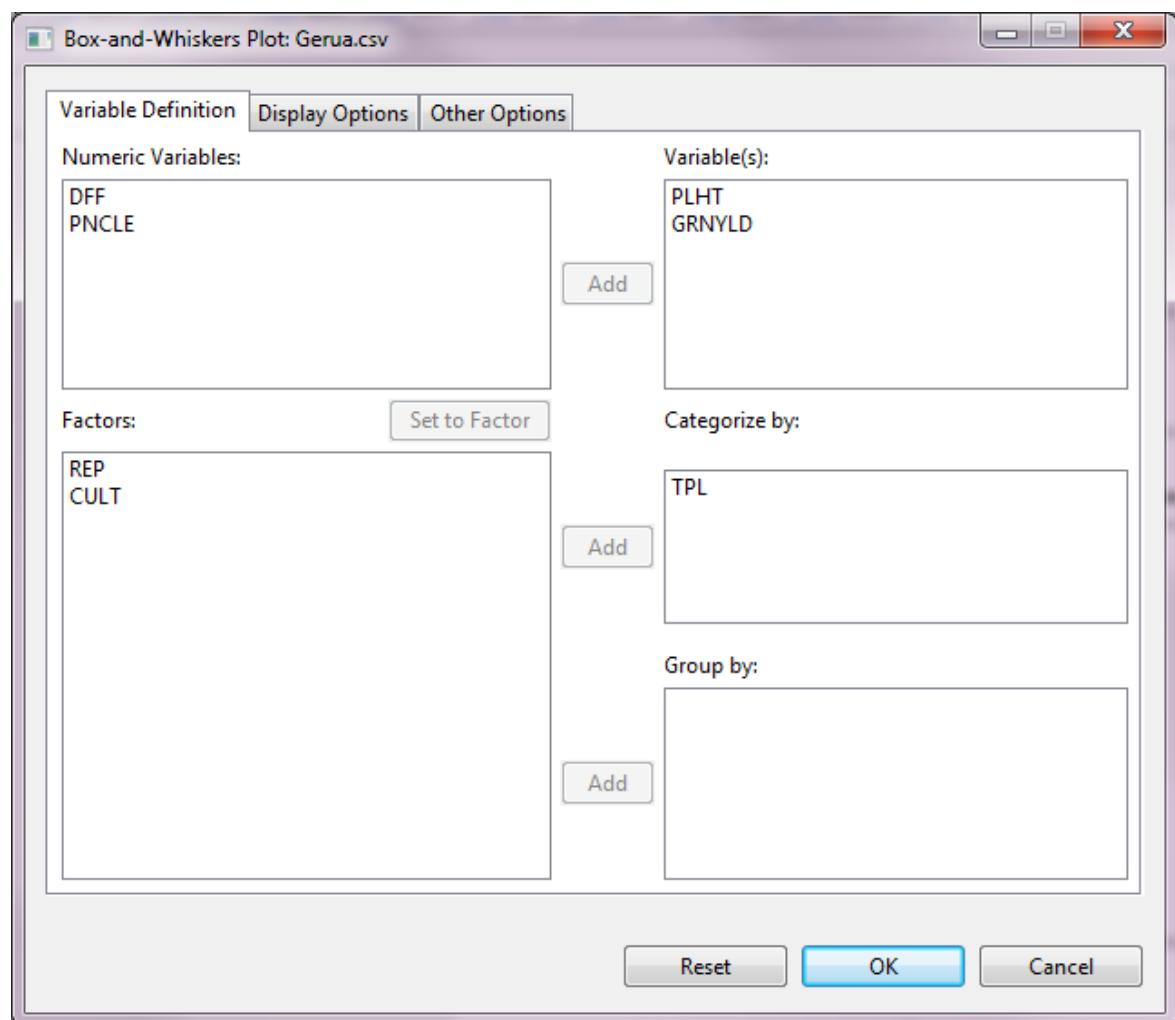
MEDIAN

Color, type and width for the line representing the median may be edited here.

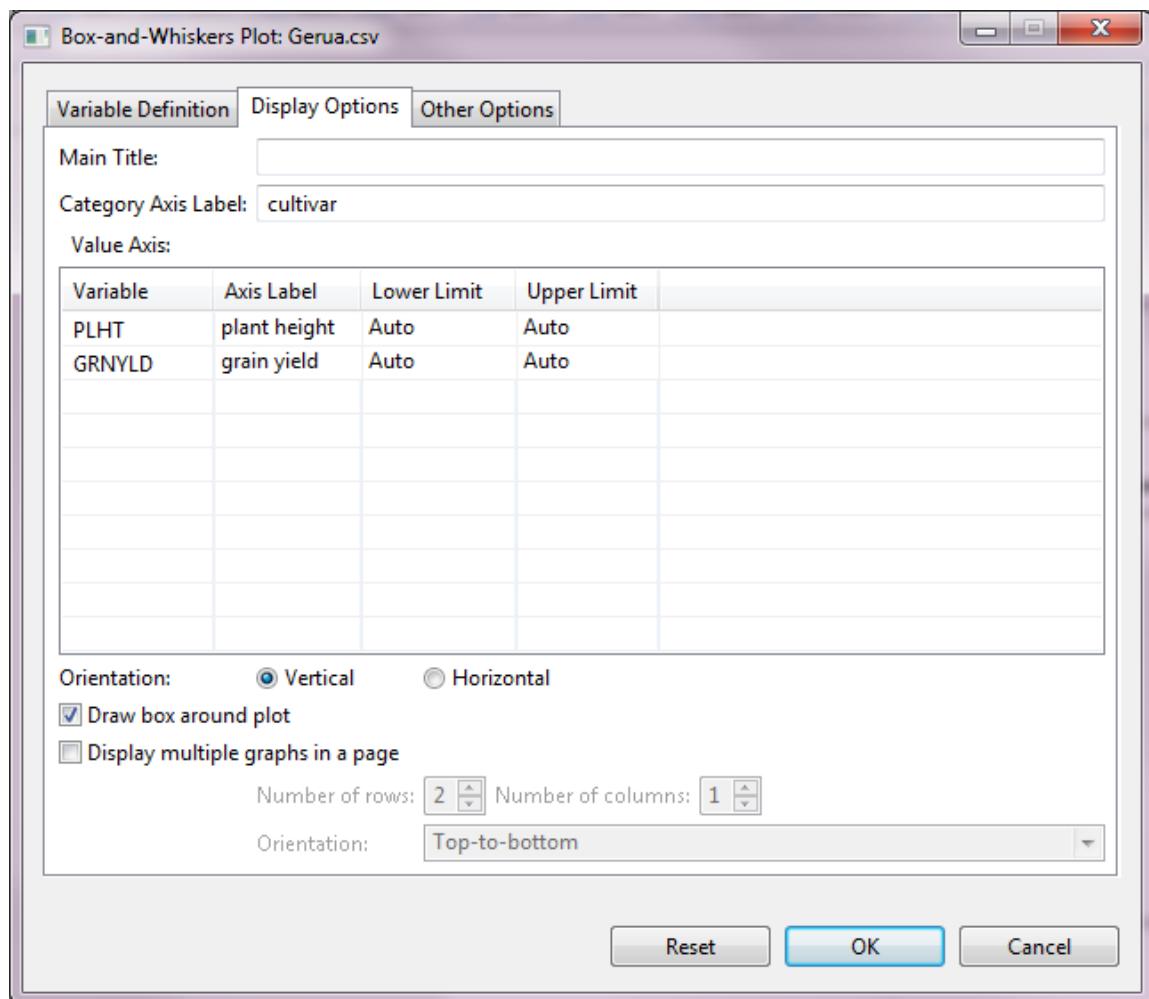
OUTLIERS

Color, symbol and size for the representing the outliers may be edited here.

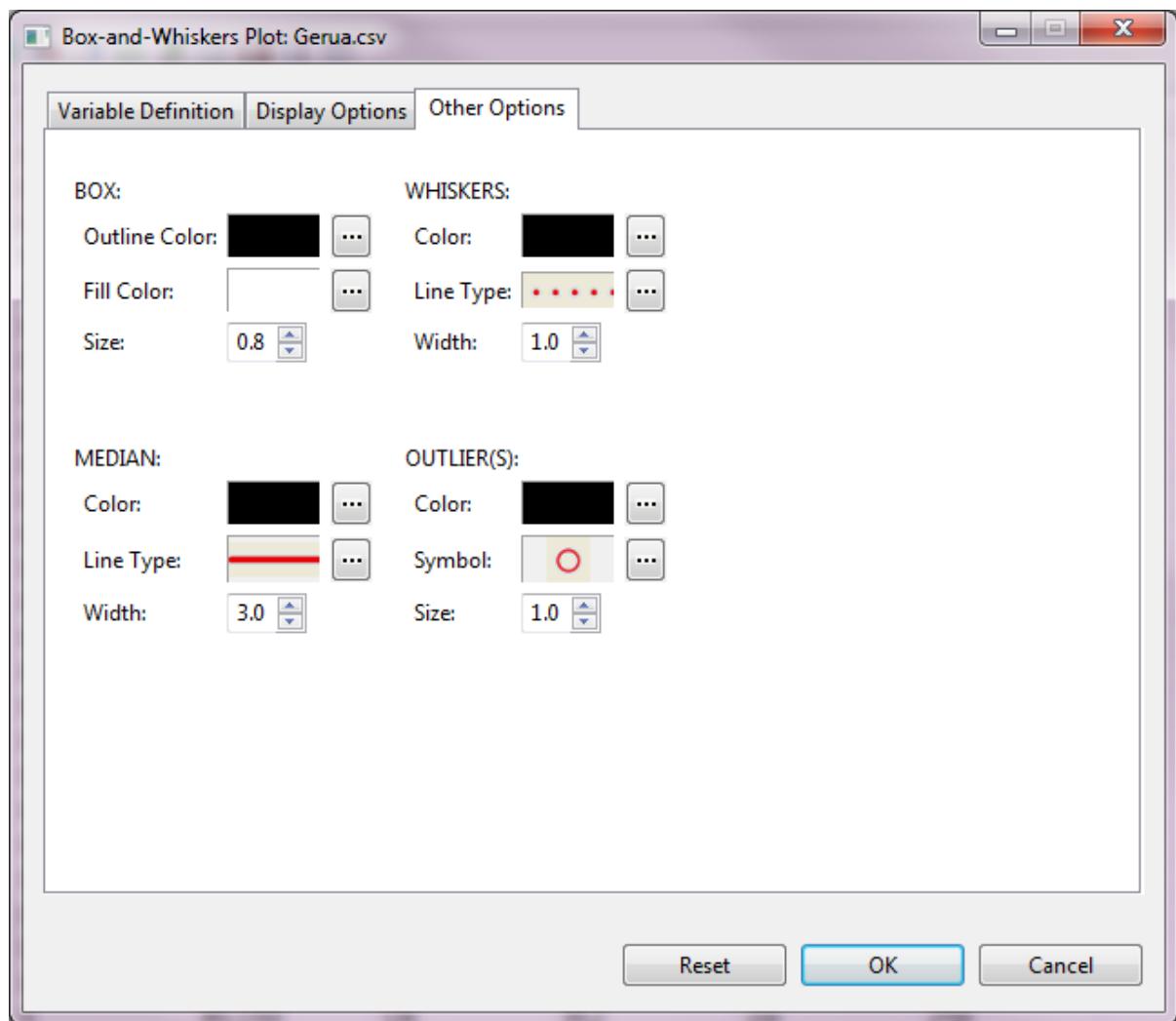
For the example, suppose we want to create box plots for the plant height (*PLHT*) and grain yield (*GRNYLD*) variables. The completed **Variable Definition** tab should appear as illustrated:



Items in the **Display Options** tab may be supplied as illustrated:

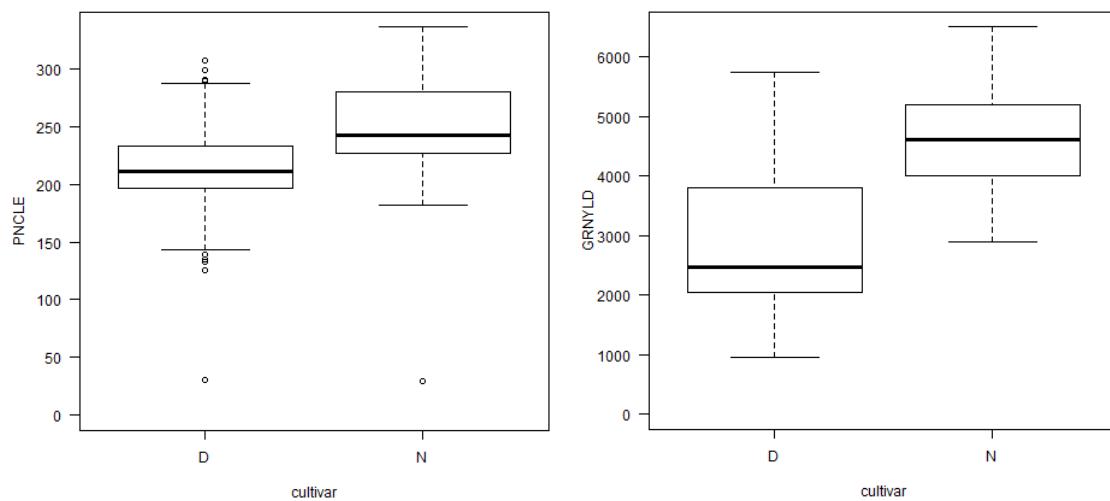


Items in the **Other Options** tab may be supplied as illustrated:

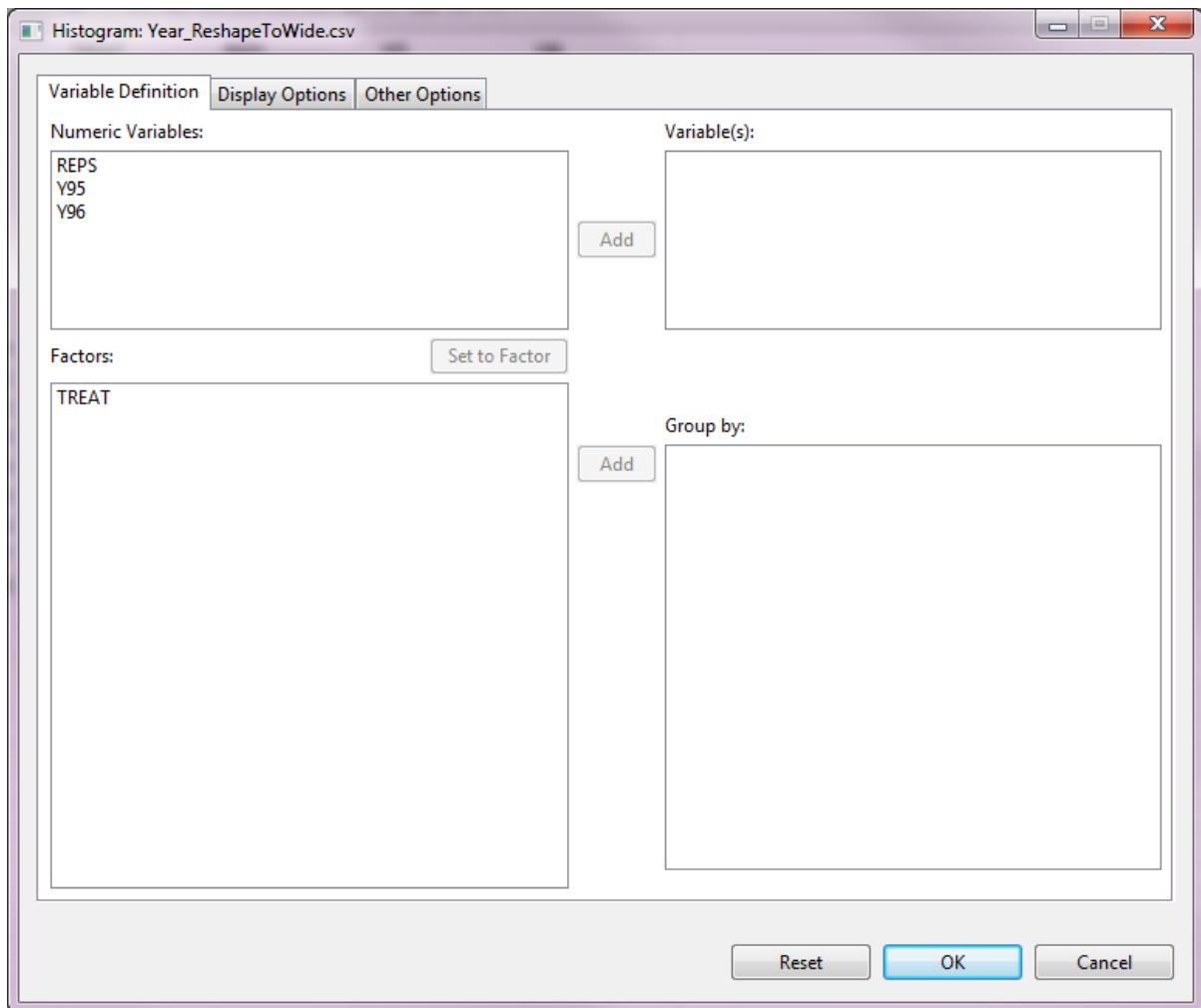


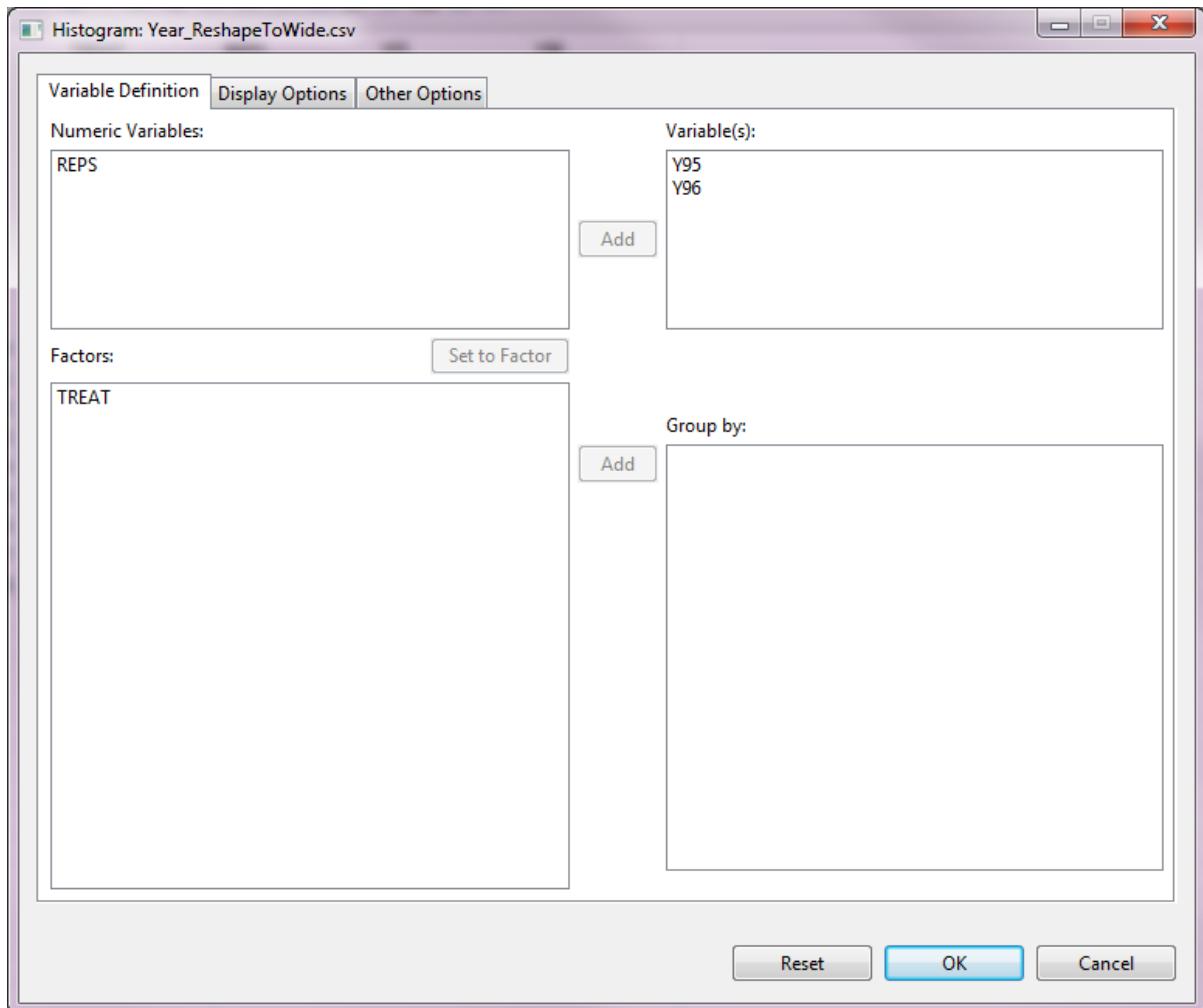
- Click the **OK** button to create the graph. The **Box Plot** dialog box will be minimized and the Result Viewer will be activated.

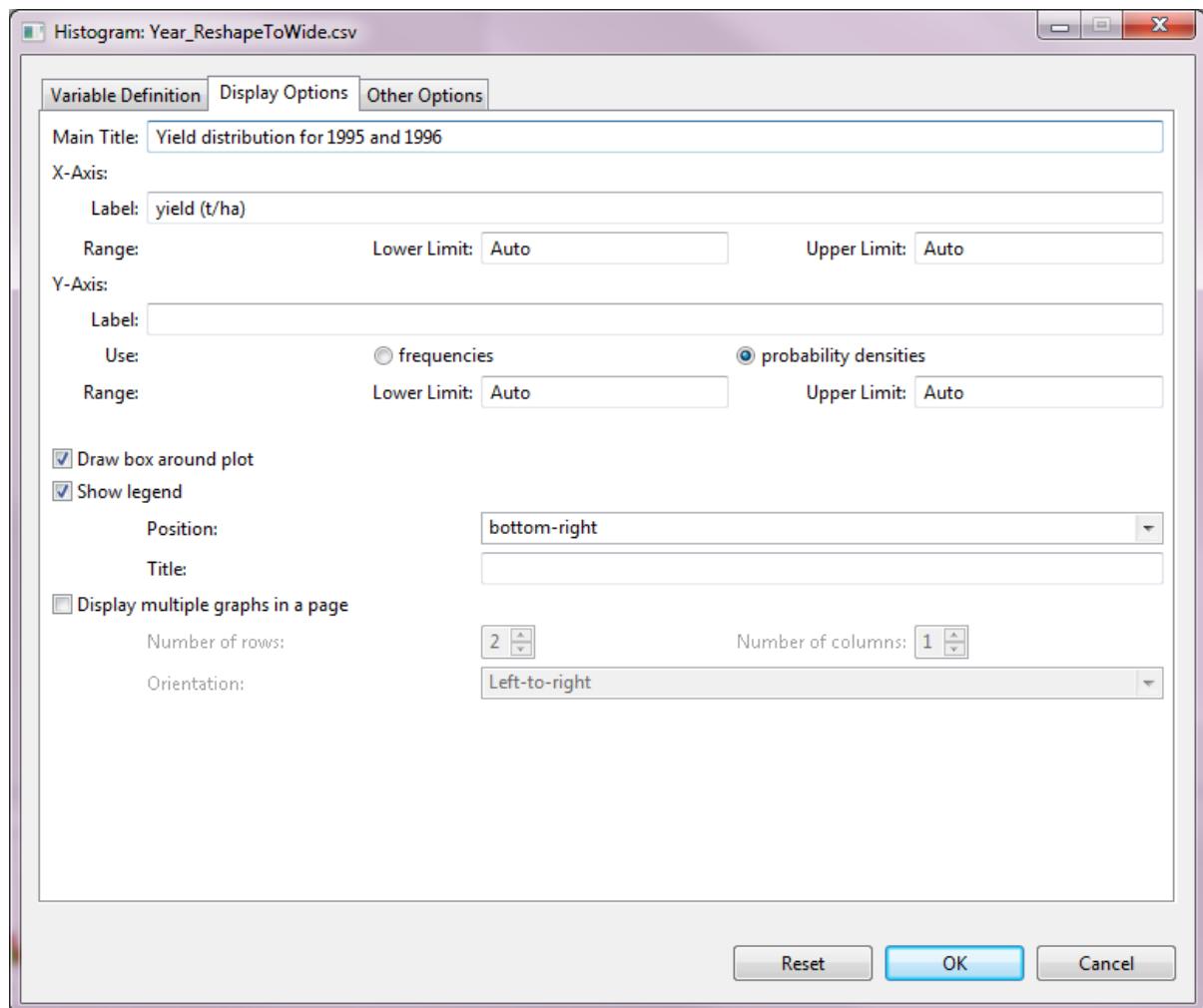
Sample graph as displayed in the *Graph* page of the Result Viewer:

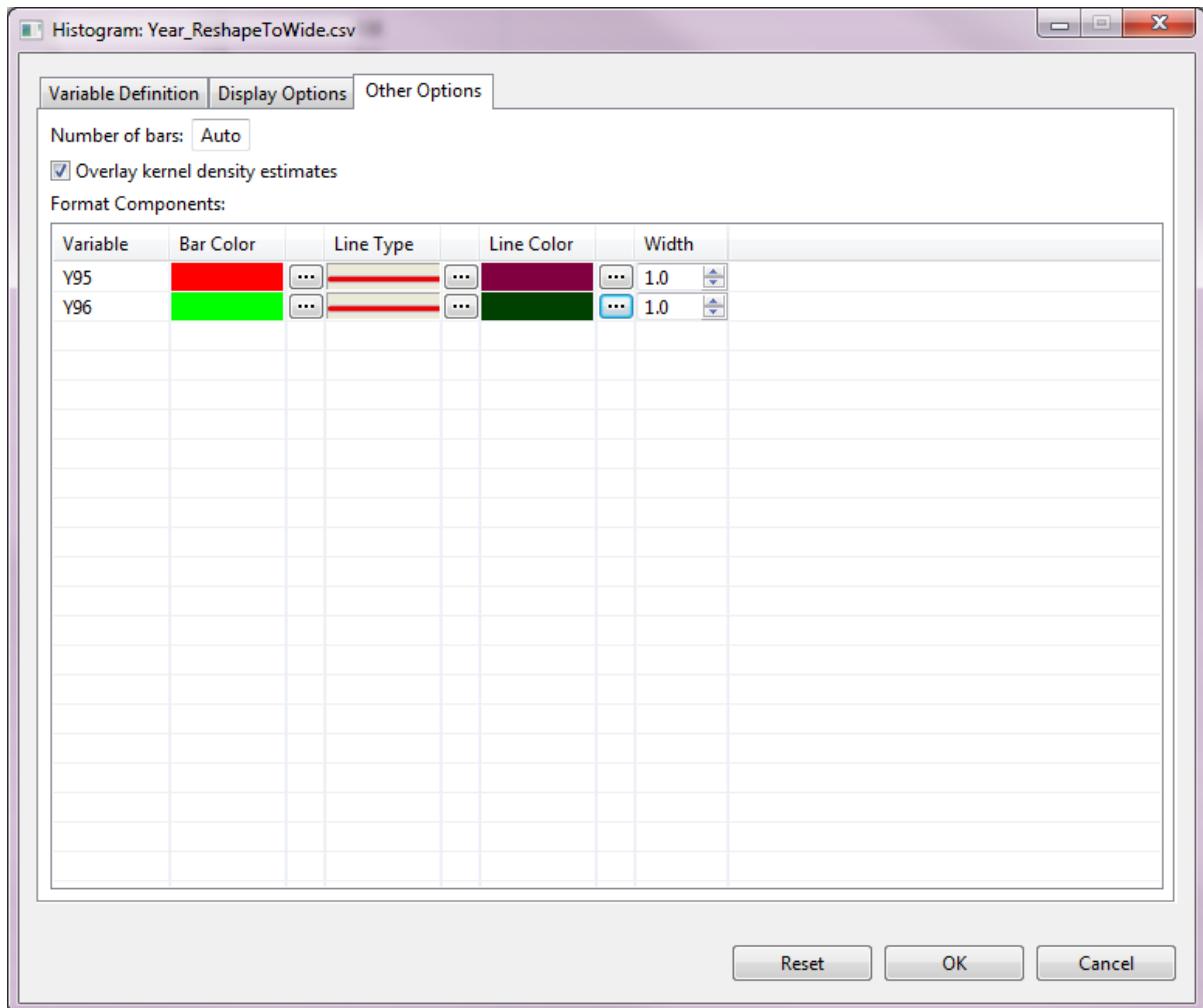


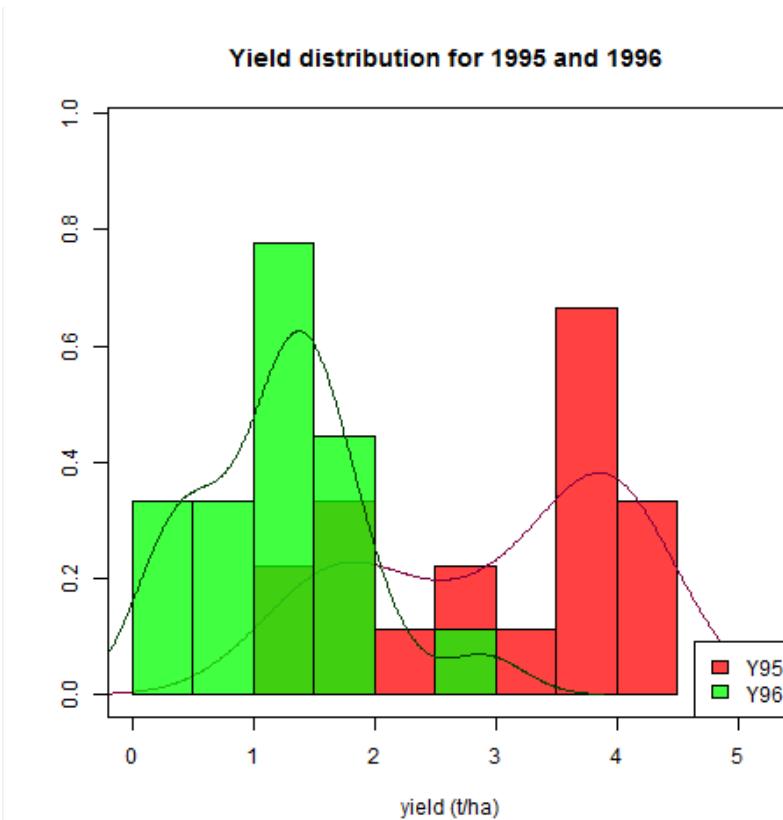
Histogram











Line Graph

Line graphs are useful for displaying trends using either raw data or statistics.

The steps to create a line graph are listed below:

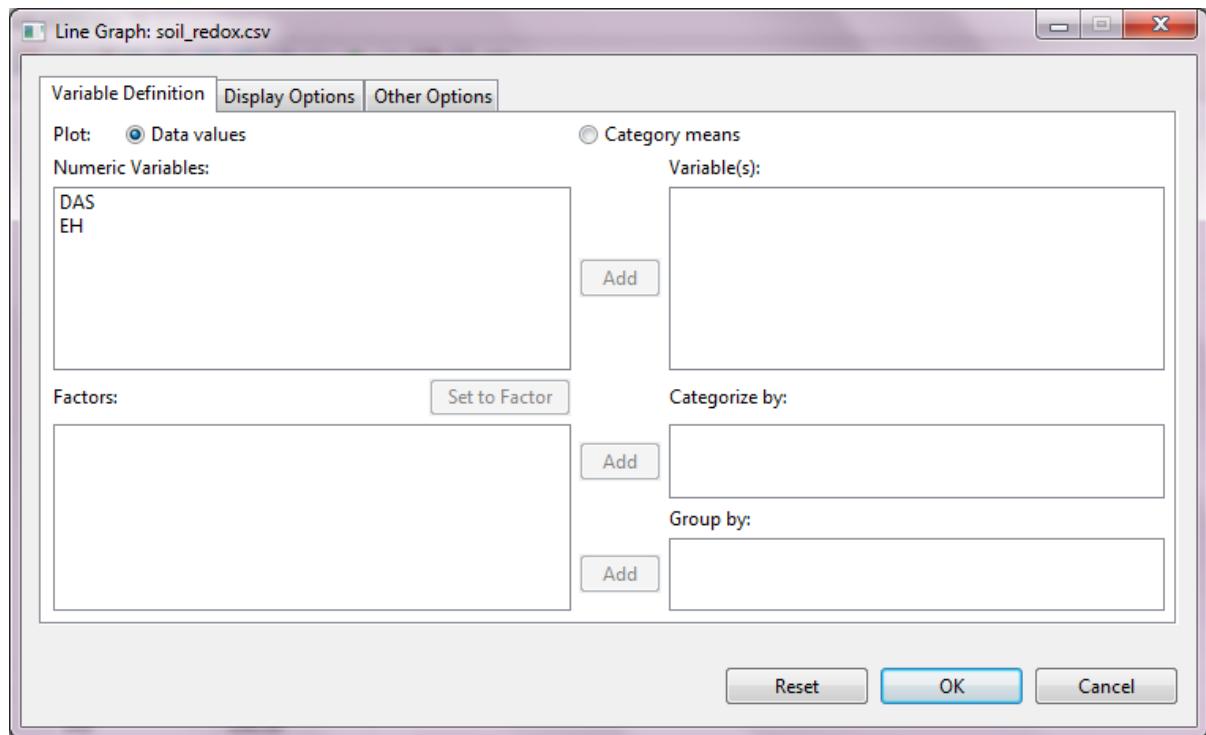
- On the **Project Explorer**, double-click the file to be used for the analysis to open and view it in the Data Viewer

On the Project Explorer, using the project named *My Project*, import the data *soil_redox* from STAR Package. Double-click the file to open and view it in the Data Viewer tab.

The file contains the data of number of days after seeding (DAS) and soil redox potential (EH). Based on this data, a line graph can be created to examine the

behavior of soil redox potential assess over time (days) after seeding, on the average.

- Click **Graphs | Line Graph....** The **Line Graph** dialog box will appear.



- Specify the inputs for the required fields and desired options.

Variable Definition Tab

Plot

There are two options available, **Data values** (default option) and **Category means**. If the default option is used, the values from the raw data are plotted directly.

Variable(s)

At least one entry should be specified for the graph to be created. Entries should come from the **Numeric Variables** dialog box.

Categorize by

If specified, will determine the categories for which means are computed, if category means are to be plotted. If data values are to be plotted, this will just define the grids in the category axis. If not specified, only data values are plotted.

Group by

This field is optional. If a factor is specified, a line graph is going to be generated per category of the factor. Entries should come from the **Factors** list box.

Display Options Tab

Main Title

This field will contain the title for the graph.

Horizontal Axis Label

This field will contain the label for the factor.

Vertical Axis

The **Label** field will contain the label for the numeric variable(s). The **Range** will contain the suggested minimum (**Lower Limit**) and maximum (**Upper Limit**) values for the axis. If not specified (*Auto*), these are determined from the data.

Draw box around plot

If checked, the graph will be enclosed in a box.

Display line labels

If checked, the name(s) of the numeric variable(s) are displayed on the right side of the corresponding line(s).

This option is useful if there are two or more numeric variables used in the graph and the **Display variable names** is unchecked.

Show legend

If checked, a legend will be added to the graph. The legend may be placed in any of nine positions within the graph: *bottom*, *bottom-left*, *bottom-right*, *center*, *left*, *right*, *top*, *top-left*, *top-right*. The legend may or may not have a title.

This option is useful if there are two or more numeric variables used in the graph and the **Display variable names** is unchecked.

Display multiple graphs in a page

If checked, several graphs will be displayed on a single page, based on the specified number of rows and columns and orientation. At most 5 rows and 5 columns of

graphs can be fitted into a single page, arranged either from *Top-to-bottom* or *Left-to-right*.

Other Options Tab

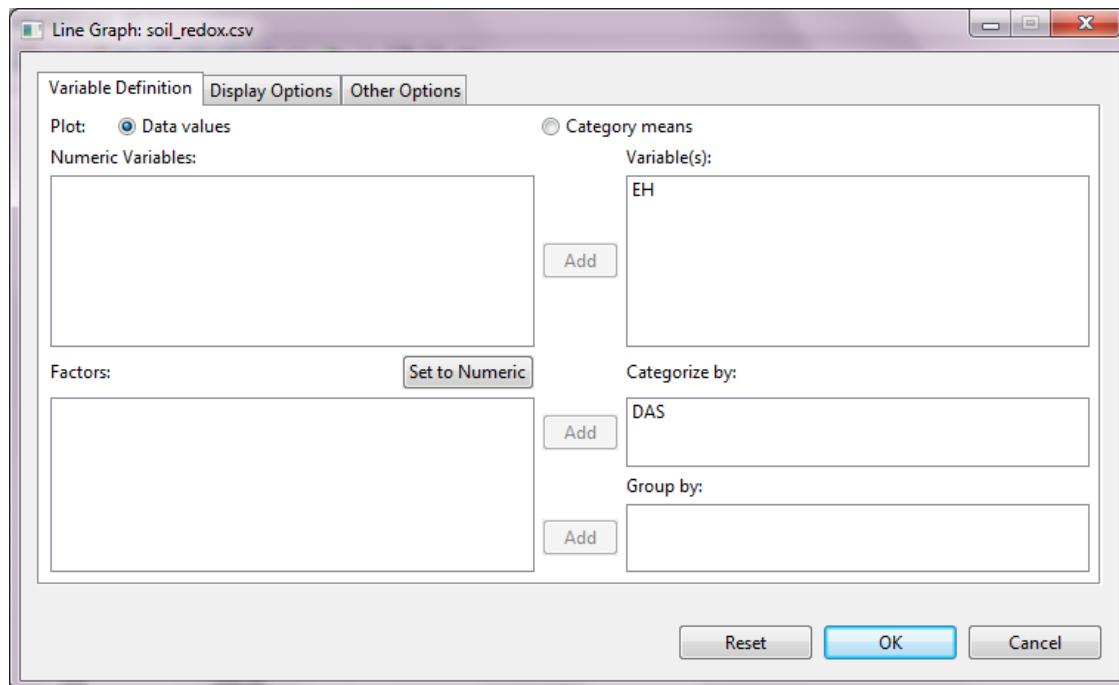
Format Components (lines and points)

Formats of lines and points (if any) can be edited here. Under *Type*, available options are *lines only*, *overplot* (overlapping lines and points), or *both* (non-overlapping lines and points). Default color, width and type for lines, as well as symbol and size for points can be changed.

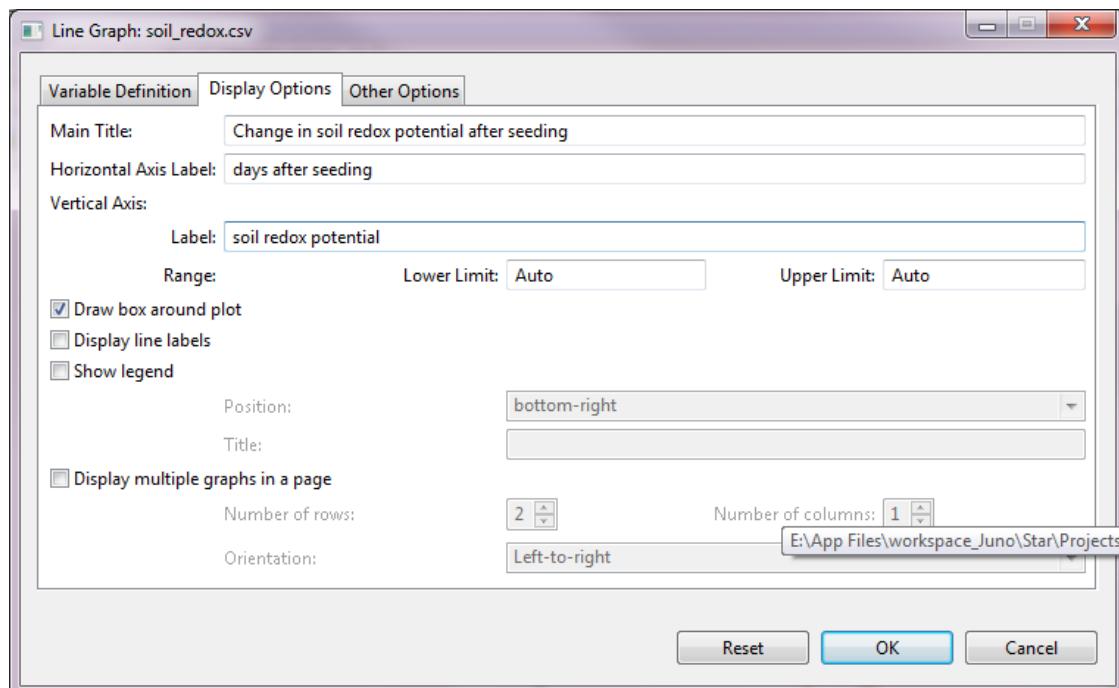
Display Error Bars

If category means are plotted, error bars may be added based on one of two options: **confidence level** (default: 95%) and **standard error** (with multiplier 1, 2, or 3).

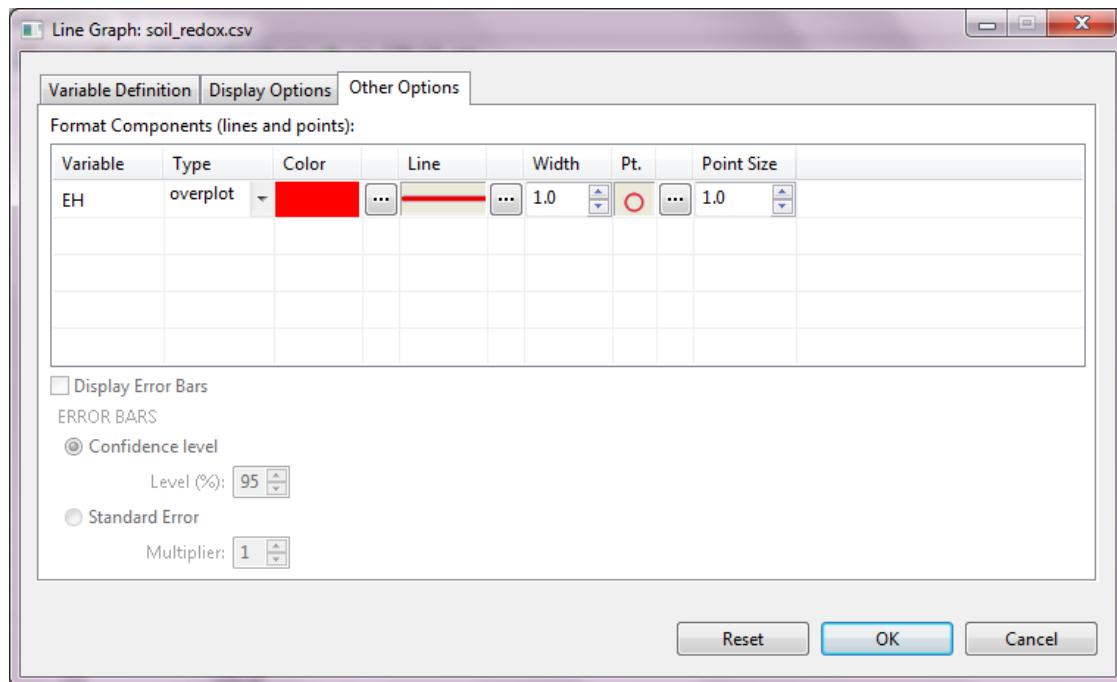
For the example, the **Variable Definition** tab should appear as illustrated:



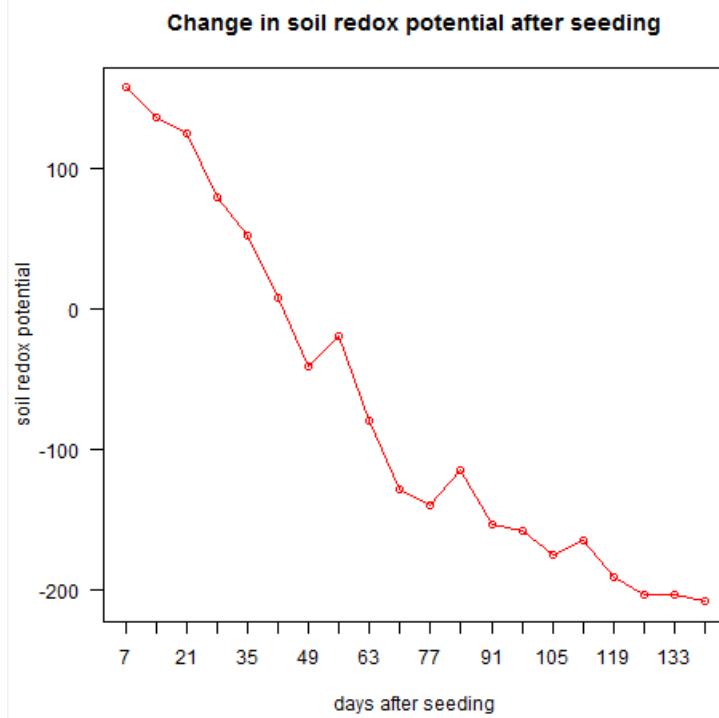
Items in the **Display Options** tab may be supplied as illustrated:



Components in the **Other Options** tab may be edited:



Sample graph as displayed in the *Graph* page of the Result Viewer:



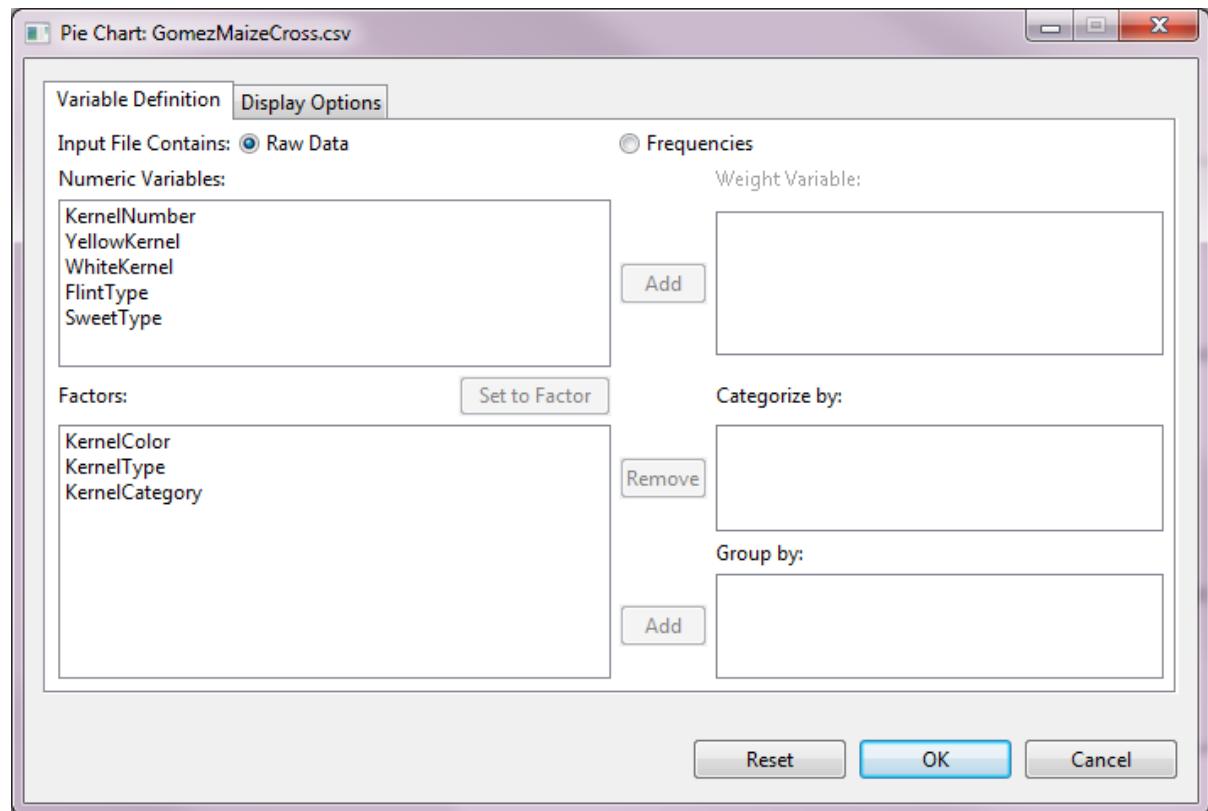
Pie Chart

Pie charts are useful for presenting how a data set is divided into different sections or groups. In STAR, pie charts can be created from raw data or summaries (containing frequencies).

The steps to create a pie chart are listed below:

- On the **Project Explorer**, double-click the file to be used for the analysis to open and view it in the Data Viewer

*On the Project Explorer, using the project named *My Project*, import the data *GomezMaizeCross* from STAR Package. Double-click the file to open and view it in the Data Viewer tab.*
- Click **Graphs | Pie Chart....** The **Pie Chart** dialog box will appear.



- Specify the inputs for the required fields and desired options.

Variable Definition Tab

Input file contains

There are two options available, **Raw Data** (default option) and **Frequencies**. If the default option is used, the percentages (or frequencies) are determined for the category variable, otherwise, values from the frequencies are plotted directly.

Weight Variable

This item is enabled if **Input file contains Frequencies** is selected. This will contain the frequencies variable.

Categorize by

This will determine the sections for partitioning the pie. This field is required.

Group by

This field is optional. If a factor is specified, a pie chart is going to be generated per category of the factor. Entries should come from the **Factors** list box.

Display Options Tab

Main Title

This field will contain the title for the graph.

Format slices

In this section, changes to the formats of the slices may be made.

Under **Labels**, available options are: none, counts, percentages, levels, both counts and levels and both levels and percentages.

Draw box around plot

If checked, the graph will be enclosed in a box.

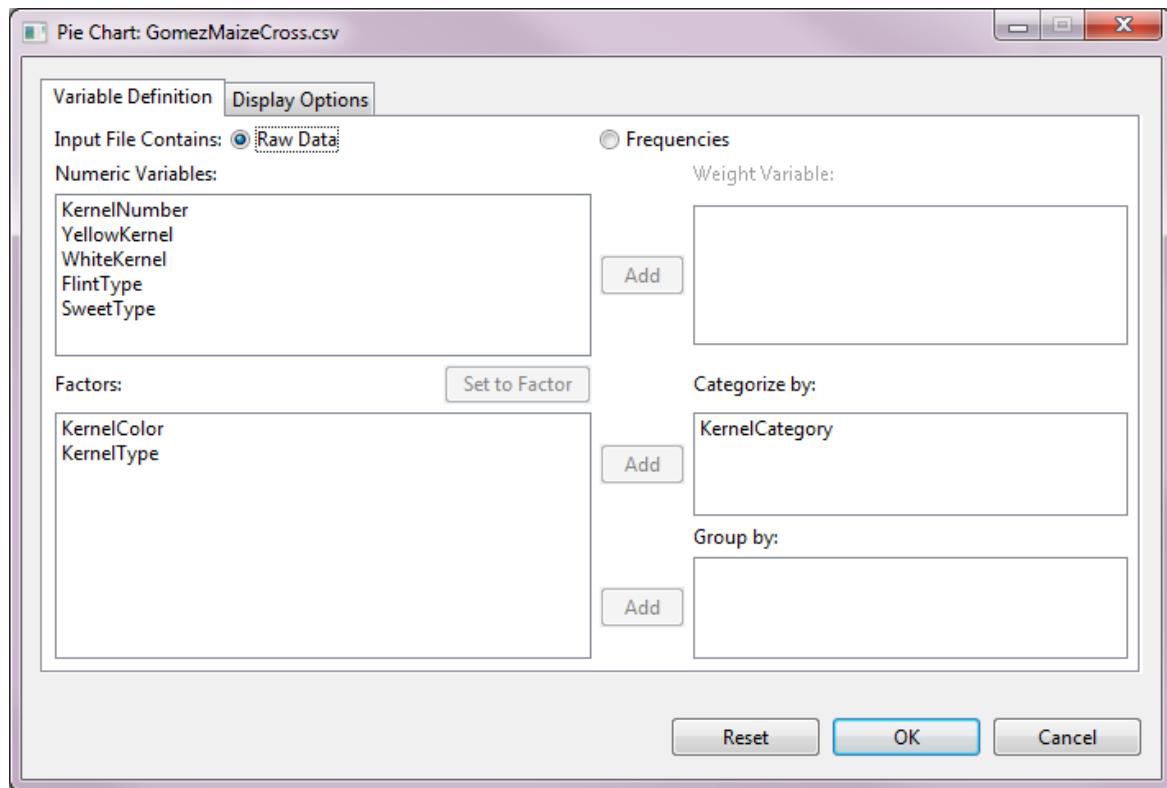
Show legend

If checked, a legend will be added to the graph. The legend may be placed in any of nine positions within the graph: *bottom*, *bottom-left*, *bottom-right*, *center*, *left*, *right*, *top*, *top-left*, *top-right*. The legend may or may not have a title.

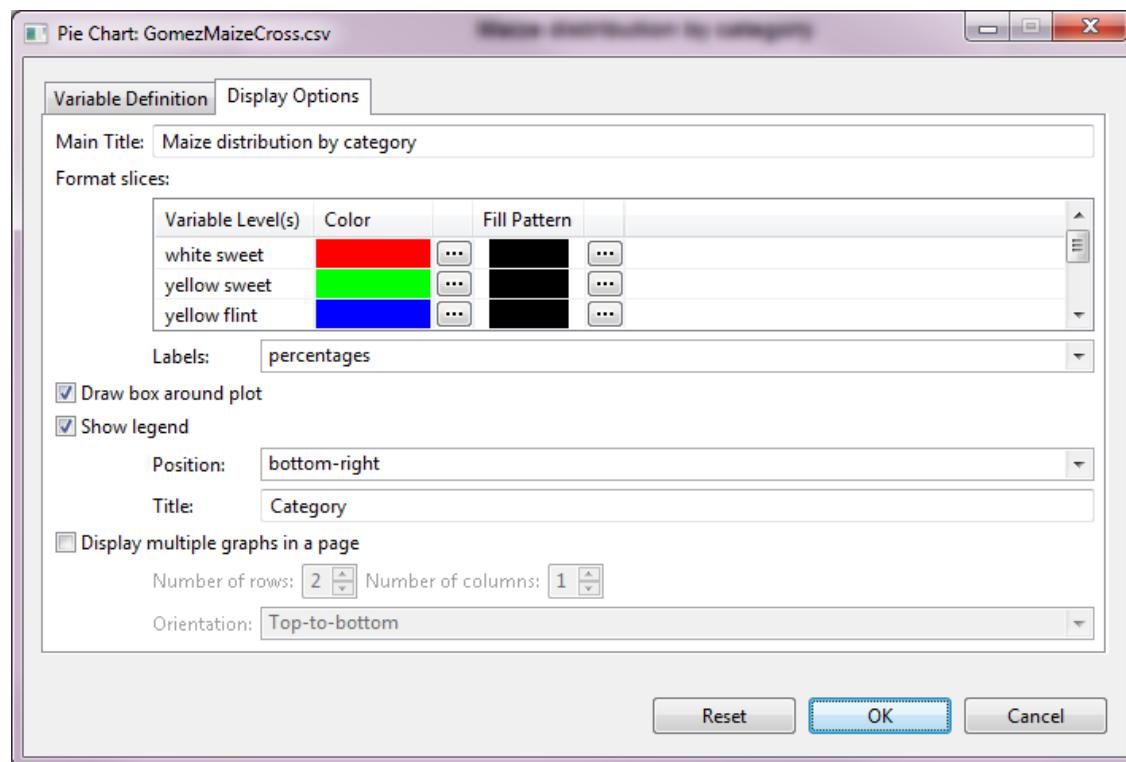
Display multiple graphs in a page

If checked, several graphs will be displayed on a single page, based on the specified number of rows and columns and orientation. At most 5 rows and 5 columns of graphs can be fitted into a single page, arranged either from *Top-to-bottom* or *Left-to-right*.

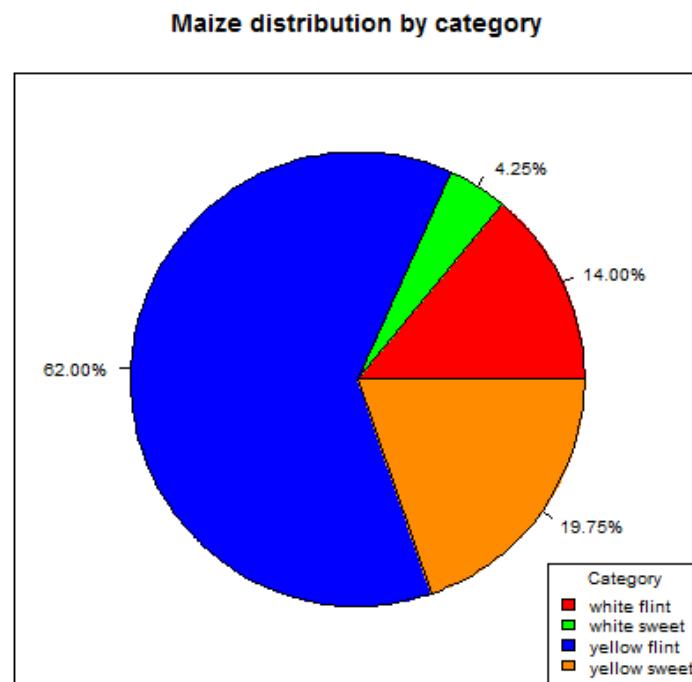
For the example, the **Variable Definition** tab should appear as illustrated:



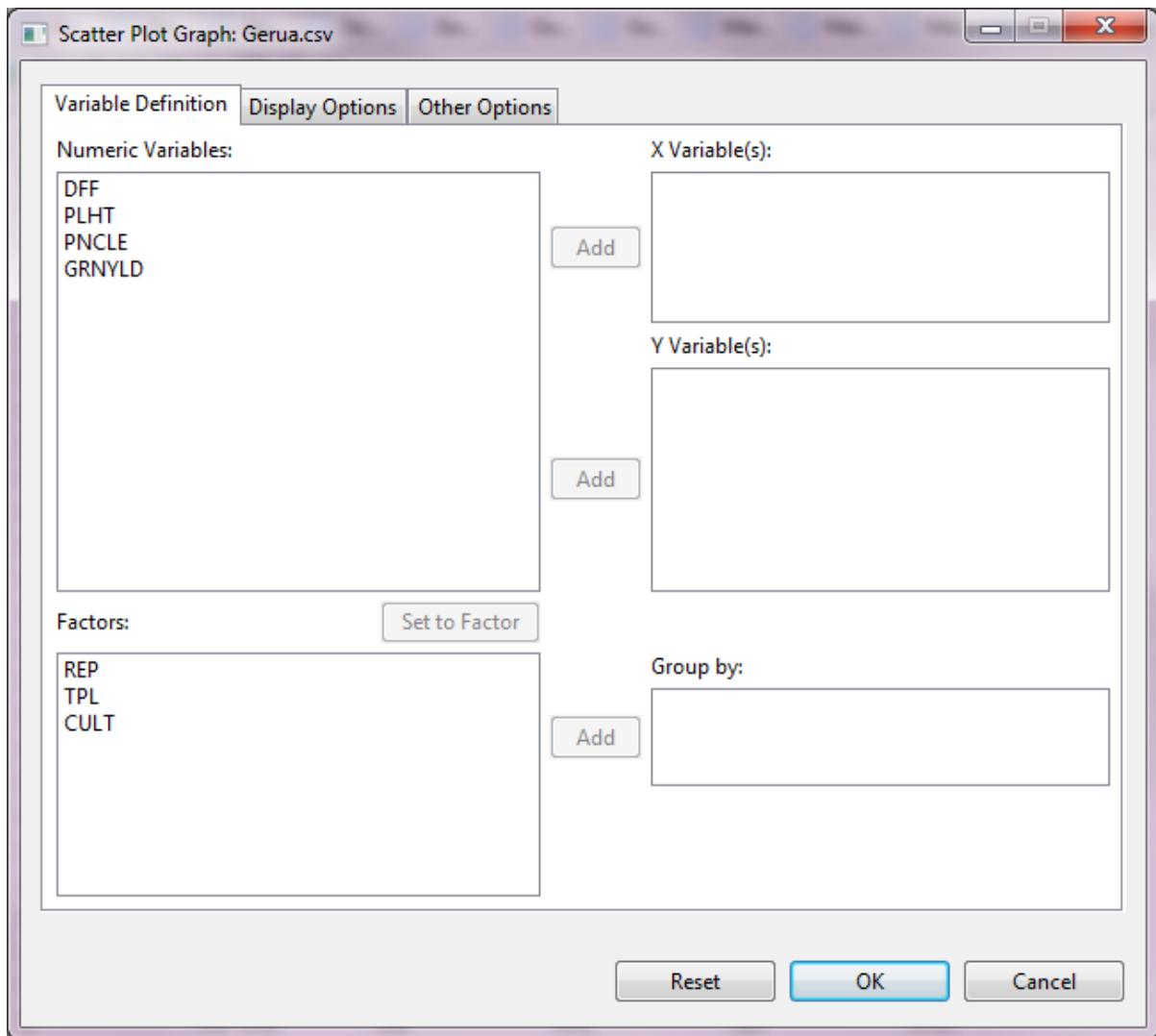
The **Display Options** Tab may be edited:

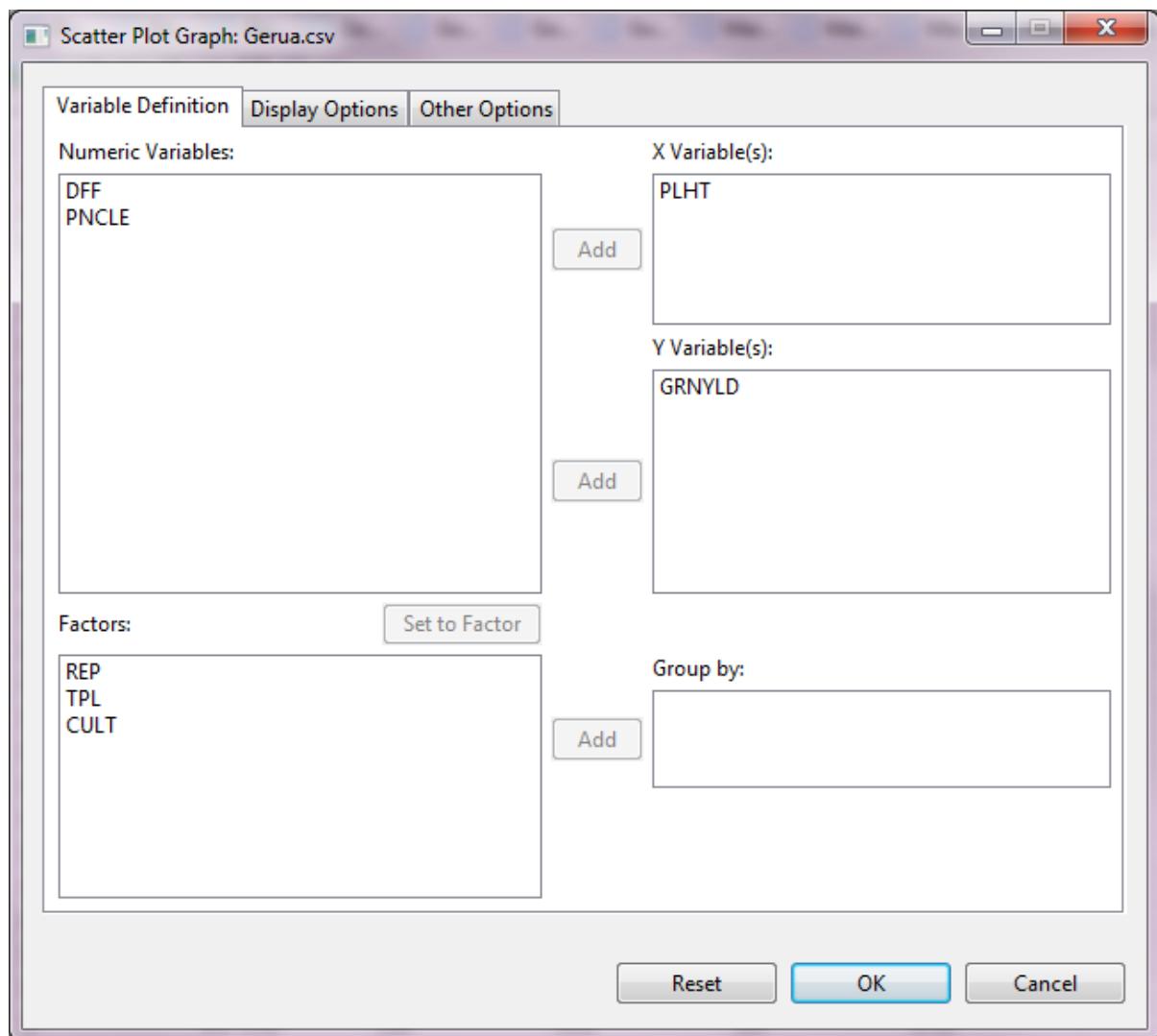


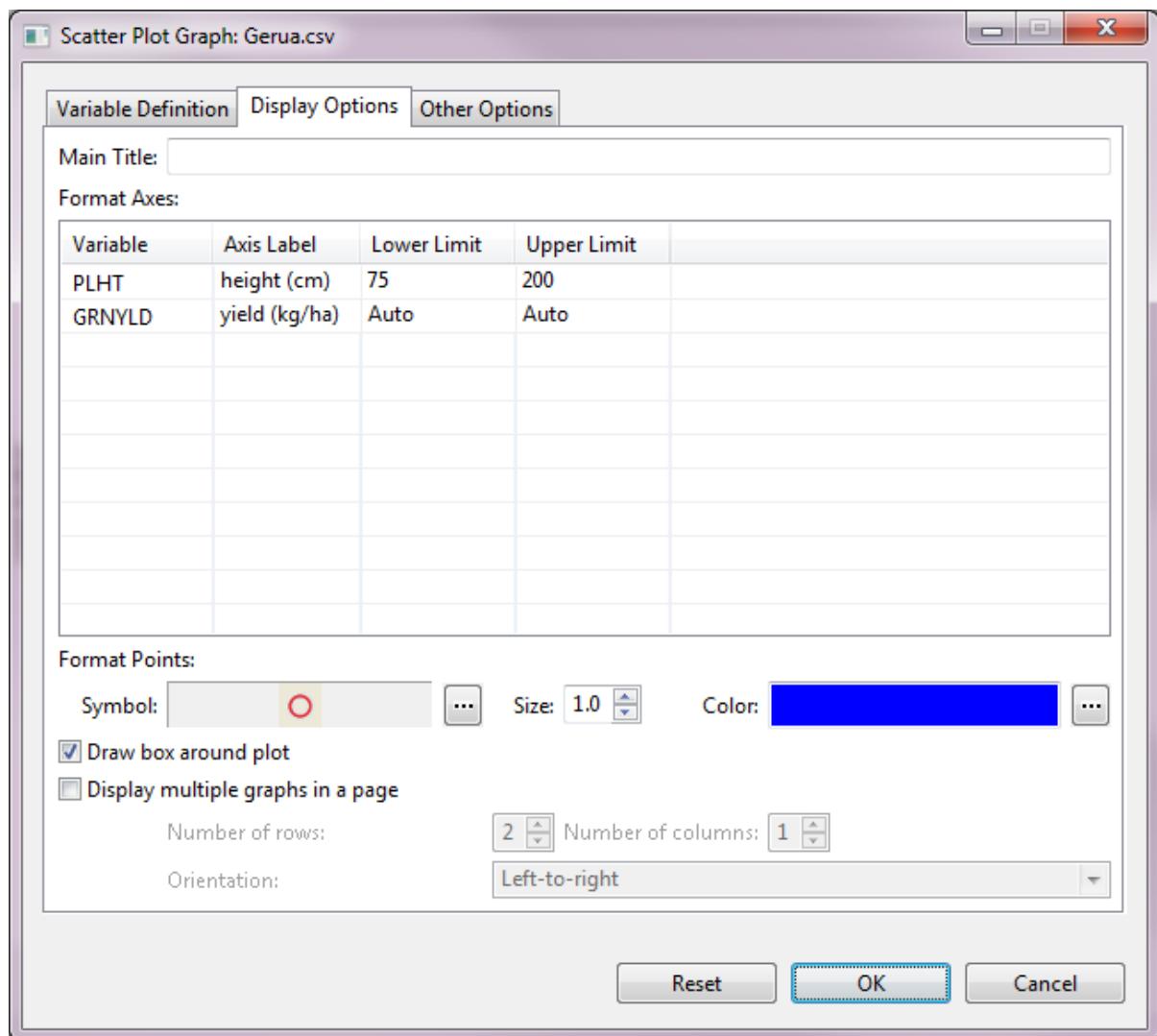
Sample graph as displayed in the *Graph* page of the Result Viewer:

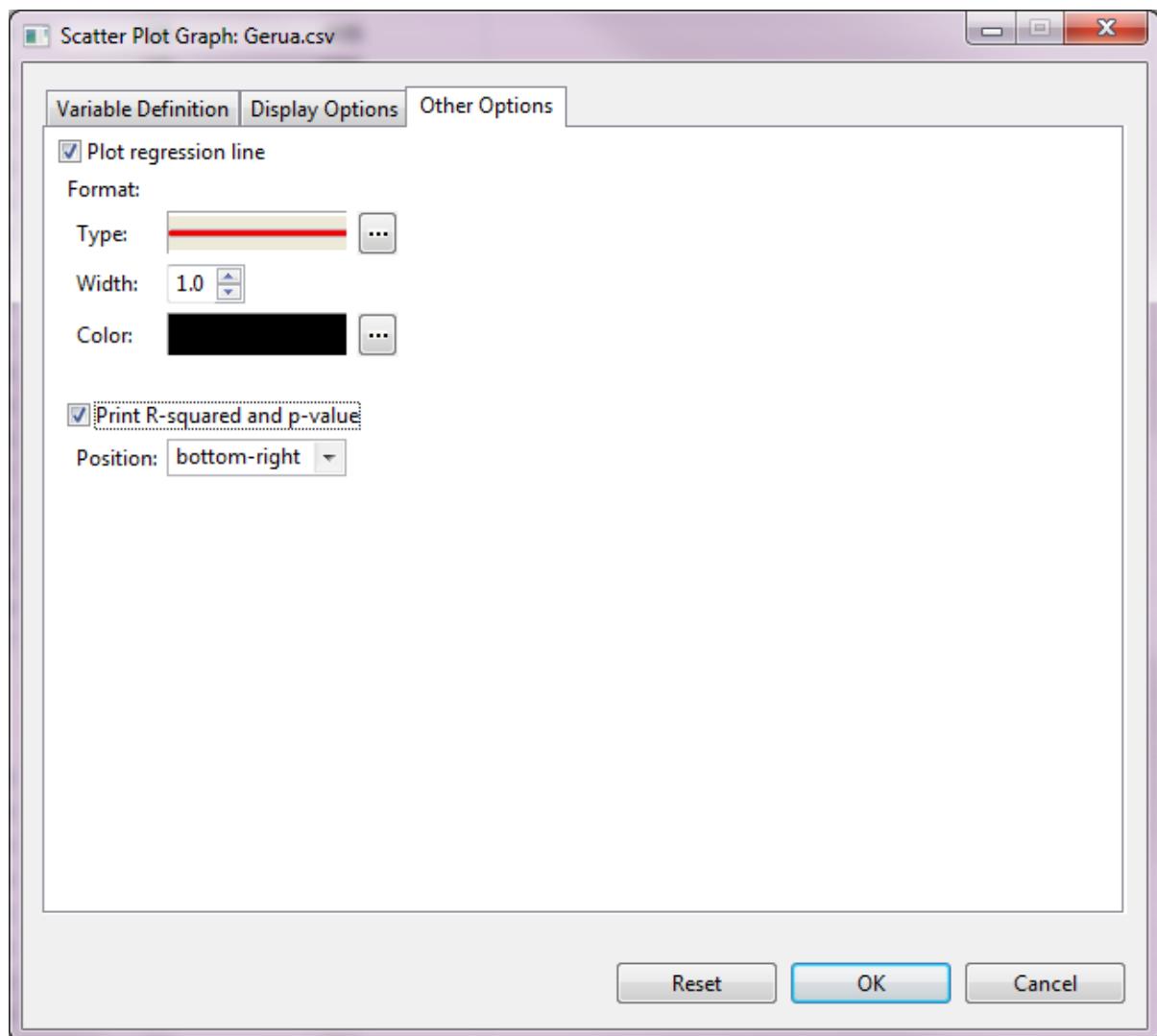


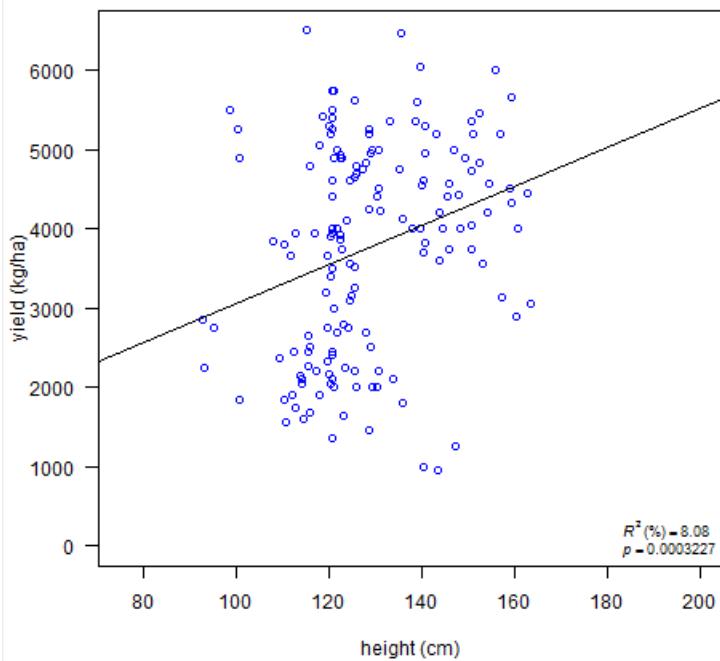
Scatter Plot











Descriptive Statistics

The **Descriptive** procedure performs univariate summary statistics for several variables and/or per levels of grouping variable(s).

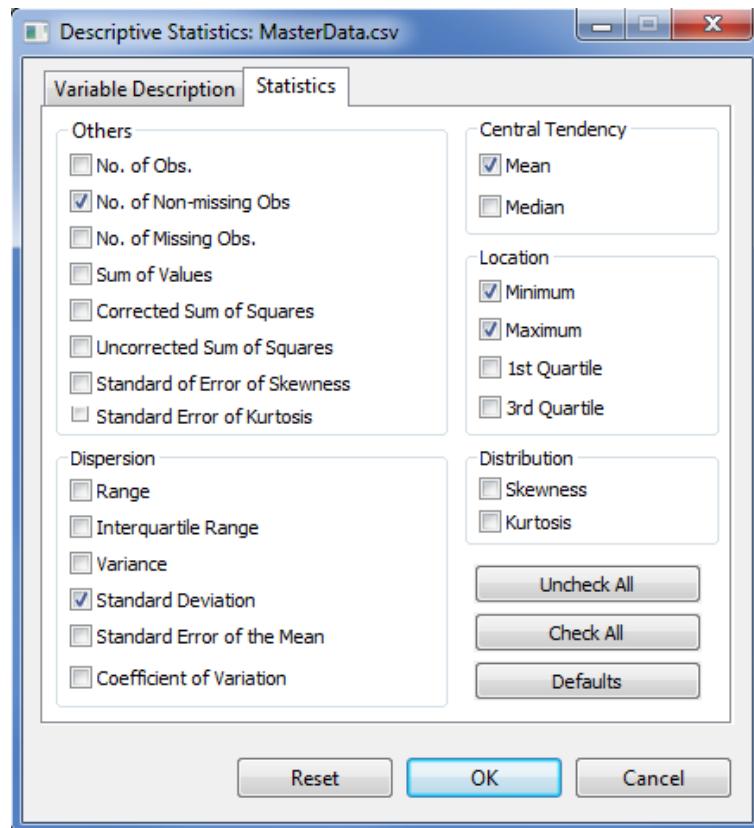
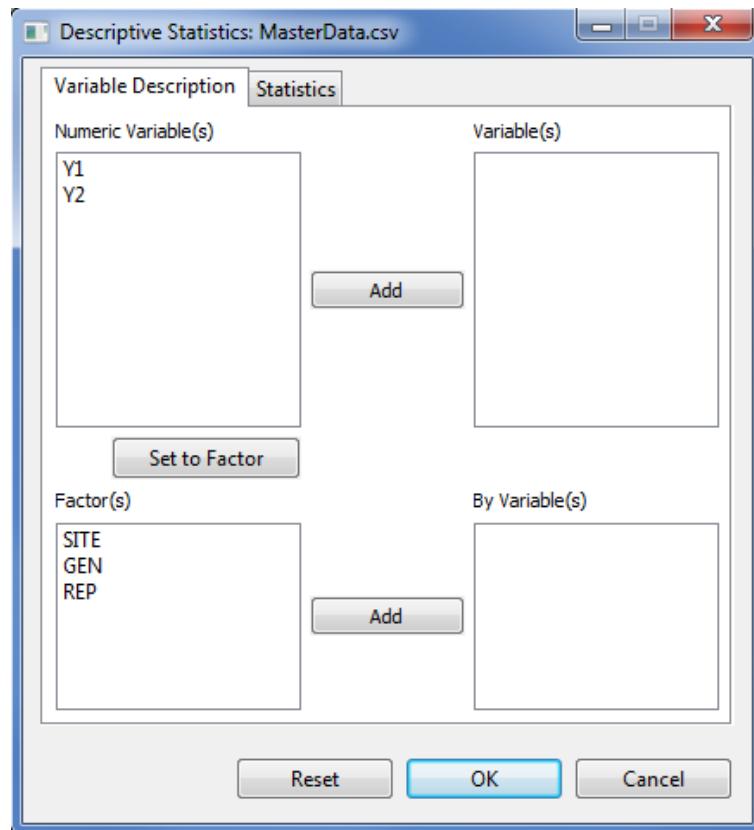
The steps to obtain numerical descriptive measures are listed below:

- On the **Project Explorer** panel, double-click the file to be used for the analysis to open it and view it in the Data Viewer tab.

For the example, using the project named *MyProject*, import the data *MasterData.csv* from the *Data* folder of the project named *SampleProject*. To import data from the *SampleProject*, see *Importing Data from Other Project* section of this user's manual.

Opening the data for the first time, *REP* field is regarded by STAR as numerical variable. To change its type, choose the variable *REP* and click on the **Set to Factor** button.

- Click **Analyze | Descriptive Statistics | Descriptive....** The **Descriptive Statistics** dialog box will appear.



- Specify the required field and appropriate options for the analysis.

Variable Description Tab

This tab lets the user identify the variables and grouping variable(s) where descriptive statistics will be computed.

Variable(s)

At least one entry is needed for the analysis to proceed. Entries should come from the **Numeric Variable(s)** list box.

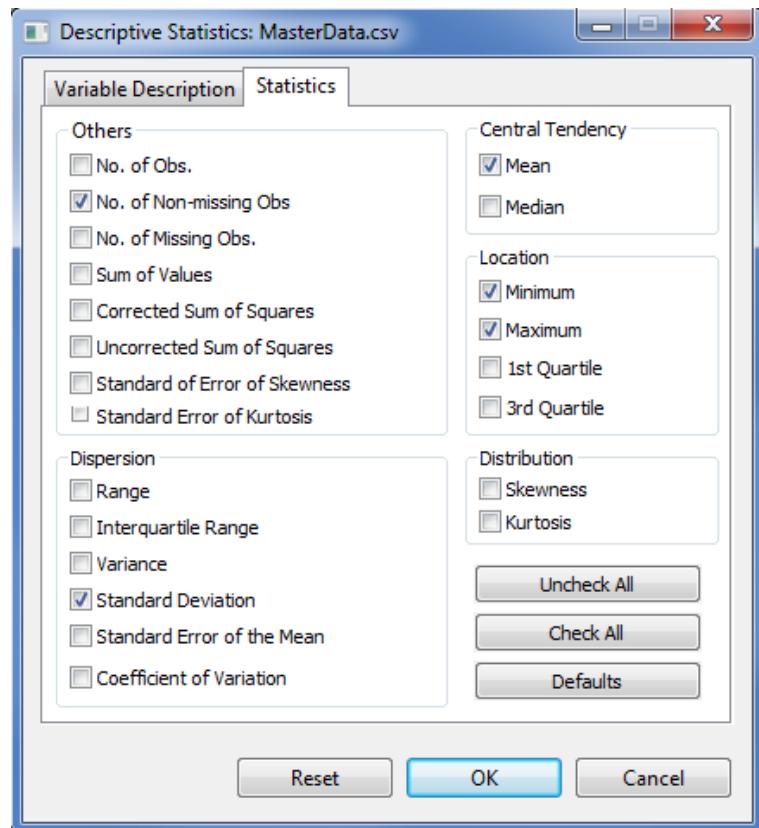
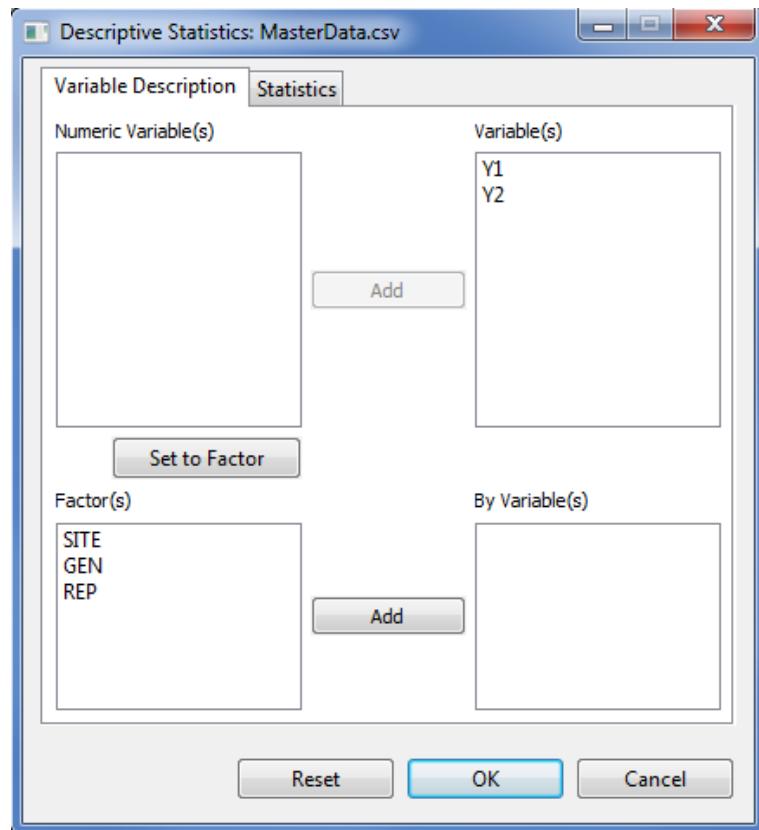
By Variable(s)

This field is optional. If a **By Variable(s)** is specified, it will generate descriptive statistic per category of the **By Variable**. Entries should come from the **Factor(s)** list box.

Statistics Tab

This tab lets the user identify the numerical descriptive measures to be displayed. By default, the procedure will display five statistics, namely: number of non-missing observations (NNMissObs), minimum (min), maximum (max), mean, and standard deviation (stdDev). To request for all statistics, click the **Check All** button of the **Statistics** tab. User may click on the **Uncheck All** button to remove previously selected items and start with a new selection. At least one statistics should be checked to the analysis to proceed.

For the example, suppose we want to compute the descriptive statistics of variables Y1 and Y2. The completed **Variable Description** tab and **Statistics** tab should appear as shown below:

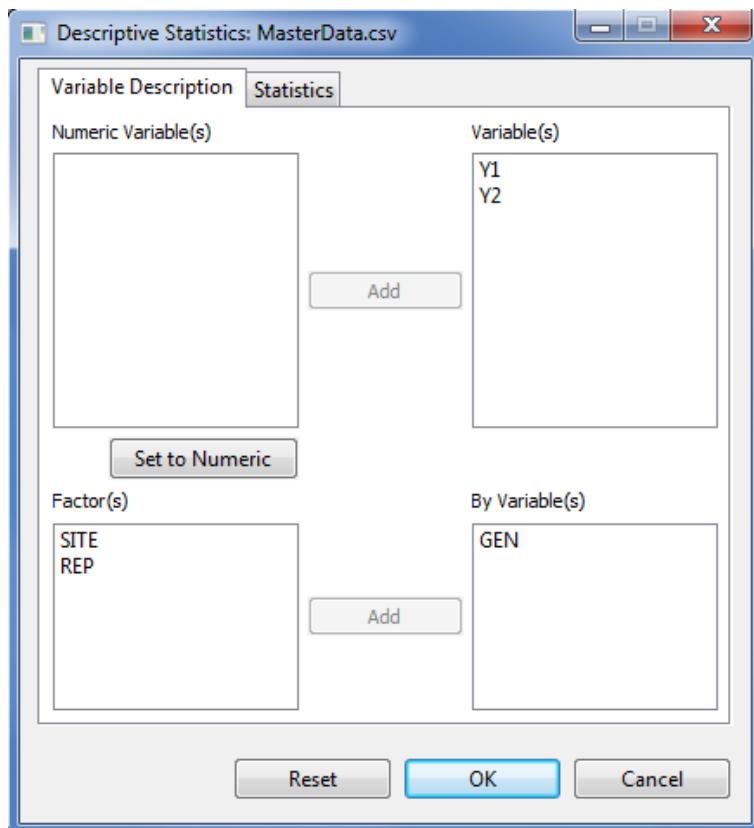


- Click the **OK** button to generate the summary statistics. The **Descriptive Statistics** dialog box will be minimize and STAR activates the **Output** page of the **Result Viewer** tab. Sample output of the descriptive statistics is shown below:

Descriptive Statistics

Variable	N_NonMissObs	Min	Max	Mean	StdDev
Y1	96	14.00	151.00	130.43	16.05
Y2	96	92.60	163.50	124.50	15.05

Suppose we want to compute the descriptive statistics for variables Y1 and Y2 per level of GEN. The completed **Variable Description** tab should appear as shown below:



- Click the **OK** button to generate the summary statistics. Sample output of the descriptive statistics is shown below:

Descriptive Statistics

Variable	GEN	N_NonMissObs	Min	Max	Mean	StdDev
Y1	Gen1	12	113.00	144.00	132.33	10.50
Y1	Gen2	12	106.00	150.00	134.17	11.07
Y1	Gen3	12	116.00	148.00	132.42	9.46
Y1	Gen4	12	14.00	151.00	122.92	36.36
Y1	Gen5	12	106.00	145.00	129.42	11.84
Y1	Gen6	12	121.00	143.00	133.25	6.84
Y1	Gen7	12	109.00	149.00	130.00	12.05
Y1	Gen8	12	106.00	144.00	128.92	12.26
Y2	Gen1	12	92.60	163.50	128.87	20.06
Y2	Gen2	12	95.20	149.30	119.24	14.21
Y2	Gen3	12	93.10	148.40	120.09	15.03
Y2	Gen4	12	100.50	150.70	124.54	16.45
Y2	Gen5	12	98.60	160.70	125.22	16.83
Y2	Gen6	12	110.20	130.60	119.24	5.54
Y2	Gen7	12	117.90	159.30	130.05	13.78
Y2	Gen8	12	111.70	150.90	128.72	13.98

Cross Tabulation

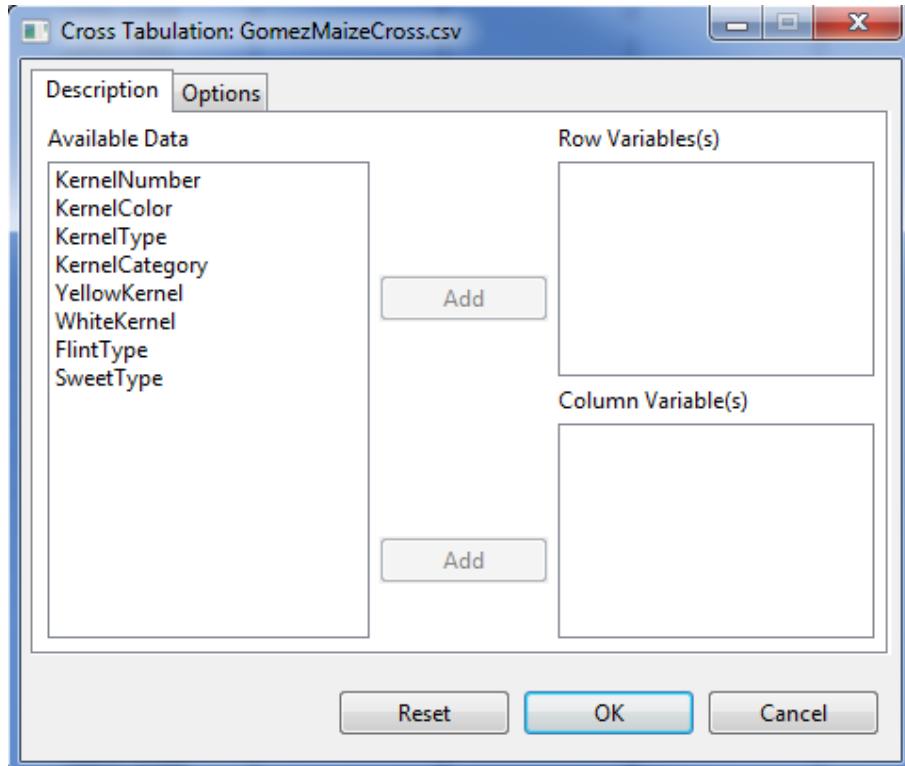
The cross tabulation forms two-way tables. By default, the observed frequency is displayed.

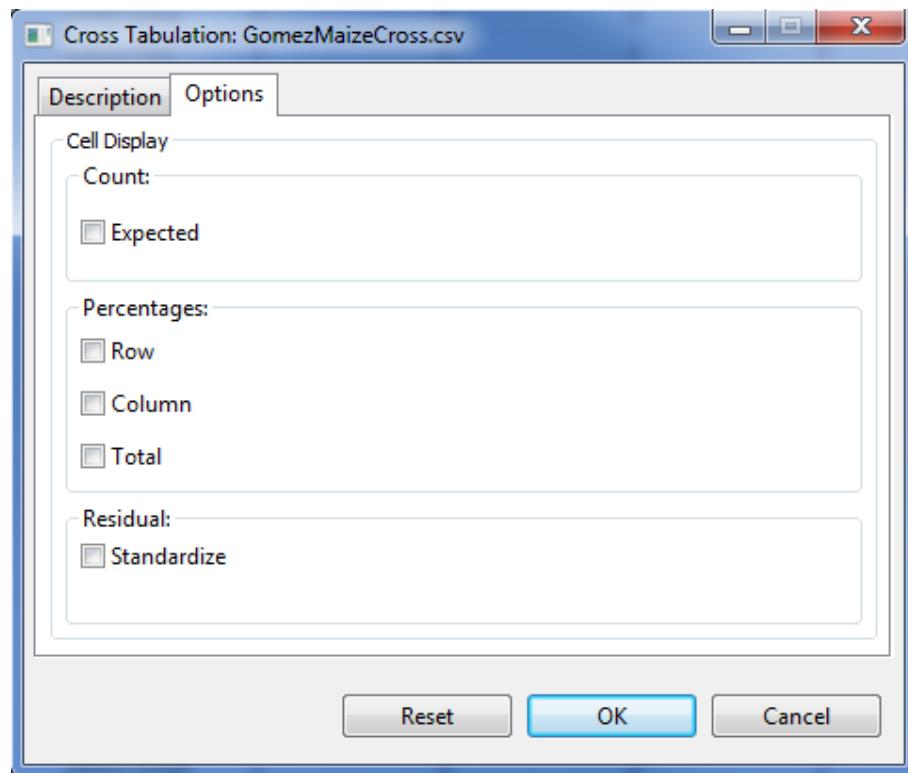
The steps to perform Cross Tabulation are listed below:

- On the **Project Explorer** panel, double-click the file to be used for analysis to open it and view it in the Data Viewer tab.

For the example, using the project named *MyProject*, import the data *GomezMaizeCross.csv* from the package. To import data from the package, see *Importing Data from Package* section of this user's manual.

- To generate cross table, from the main window click **Analyze | Descriptive Statistics | Cross Tabulation....** The **Cross Tabulation** dialog box will appear.





- Specify the required field and the appropriate options for the analysis.

Description Tab

This tab lets the user identify the variables where cross tabulation will be performed.

Row Variable(s)

At least one entry is need for the analysis to proceed.

Column Variable(s)

At least one entry is need for the analysis to proceed.

Options Tab

This tab lets the user identify the additional output that will be displayed.

Expected Count

If this option is selected, the expected frequency will be displayed.

Row Percentages

If this option is selected, the row percentage will be displayed.

Column Percentages

If this option is selected, the column percentage will be displayed.

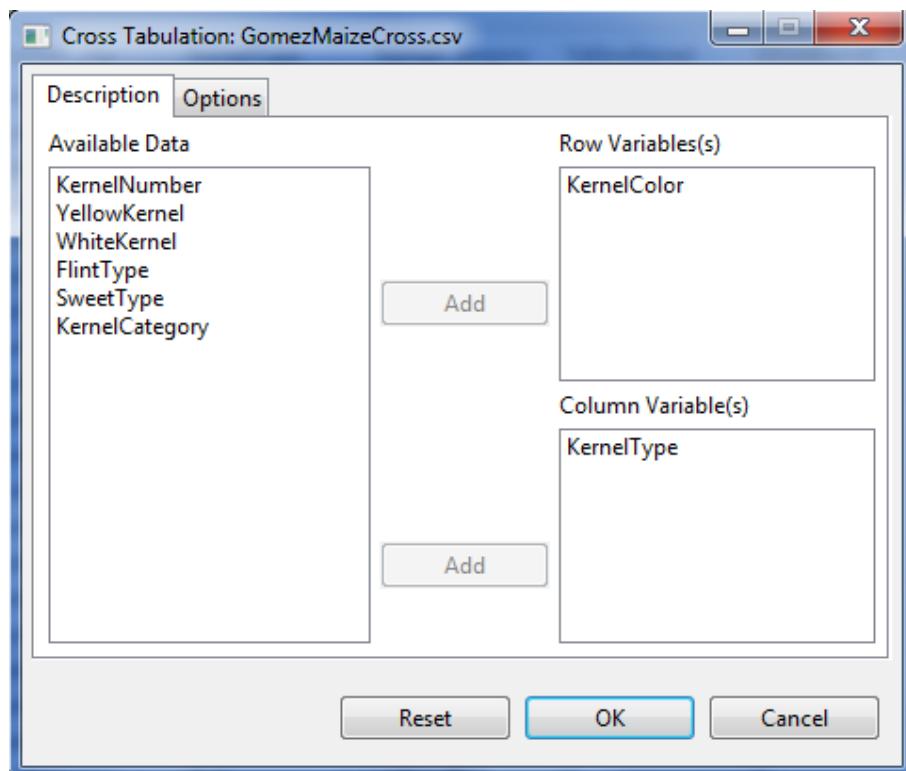
Total Percentages

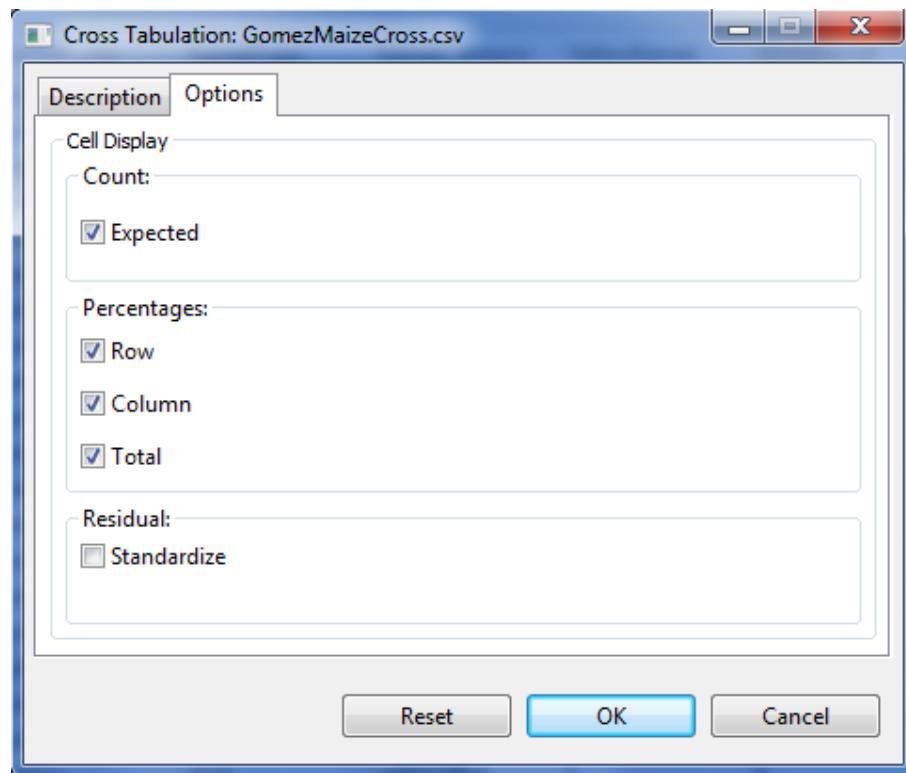
If this option is selected, the total percentage will be displayed.

Standardize Residual

If this option is selected, the standardize residual will be displayed.

For the example, the completed **Variable Description** tab and **Options** tab should appear as shown below:





- Click the **OK** button. The **Cross Tabulation** dialog box will be minimized and STAR activates the **Output** page of the **Result Viewer** tab. Sample output of the analysis is shown below:

CROSS TABULATION

Table of KernelColor by KernelType

		KernelType		
		flint	sweet	Total
white	Obs Freq	1121	34	146
	Expected Freq	110.9600	35.0400	146.0000
	% within KernelColor	76.7123	23.2877	100.0000
	% within KernelType	18.4211	17.7083	
	% of Total	14.0000	4.2500	18.2500
yellow	Obs Freq	496	158	654
	Expected Freq	497.0400	156.9600	654.0000
	% within KernelColor	75.8410	24.1590	100.0000
	% within KernelType	81.5789	82.2917	
	% of Total	62.0000	19.7500	81.7500
Total	Obs Freq	608	192	800
	Expected Freq	608.0000	192.0000	800.0000
	% within KernelType	100.0000	100.0000	
	% of Total	76.0000	24.0000	100.0000

Normality Test

The Test for Normality menu display normality test for at least one numeric variable. There are five procedures available in this menu, namely: Shapiro-Wilk, Shapiro-Francia, Lilliefors (Kolmogorov-Smirnov), Cramer-Von Mises and the Anderson-Darling test for normality.

The Shapiro-Wilk test for normality can be used if the number of non-missing observations is between 3 and 5000. While the Shapiro-Francia test for normality can be used if the number of non-missing observations is between 5 and 5000. The Lilliefors test for normality can be used if the number of non-missing observations is greater than 4. The Cramer-Von Mises and the Anderson-Darling test for normality can both be used if the number of non-missing observations is greater than 7.

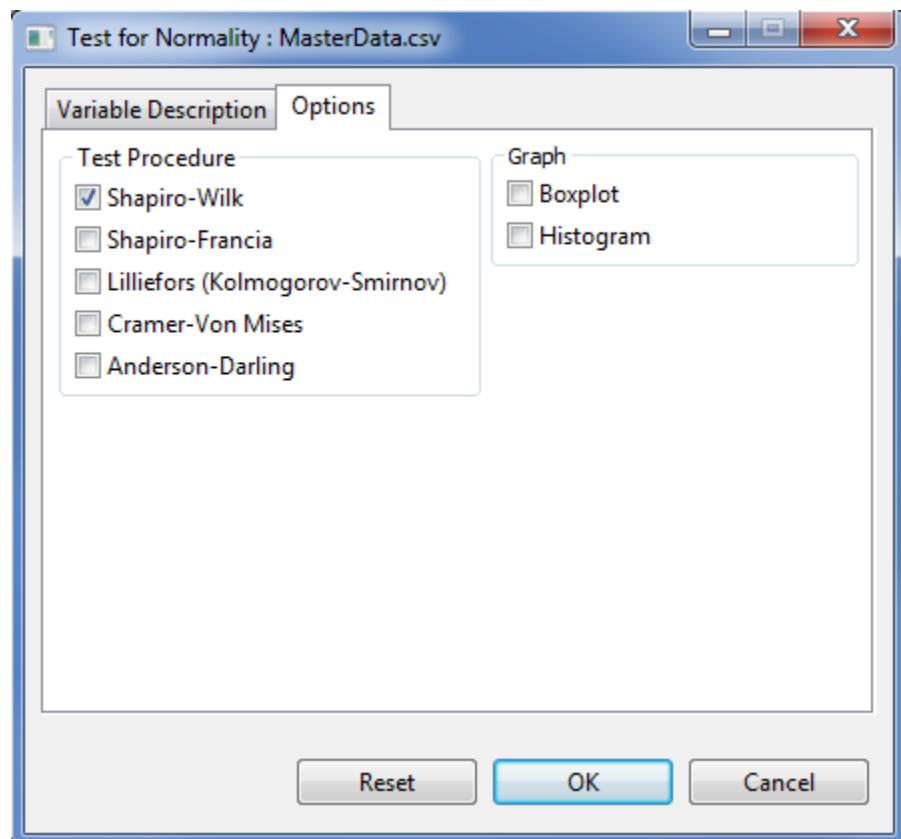
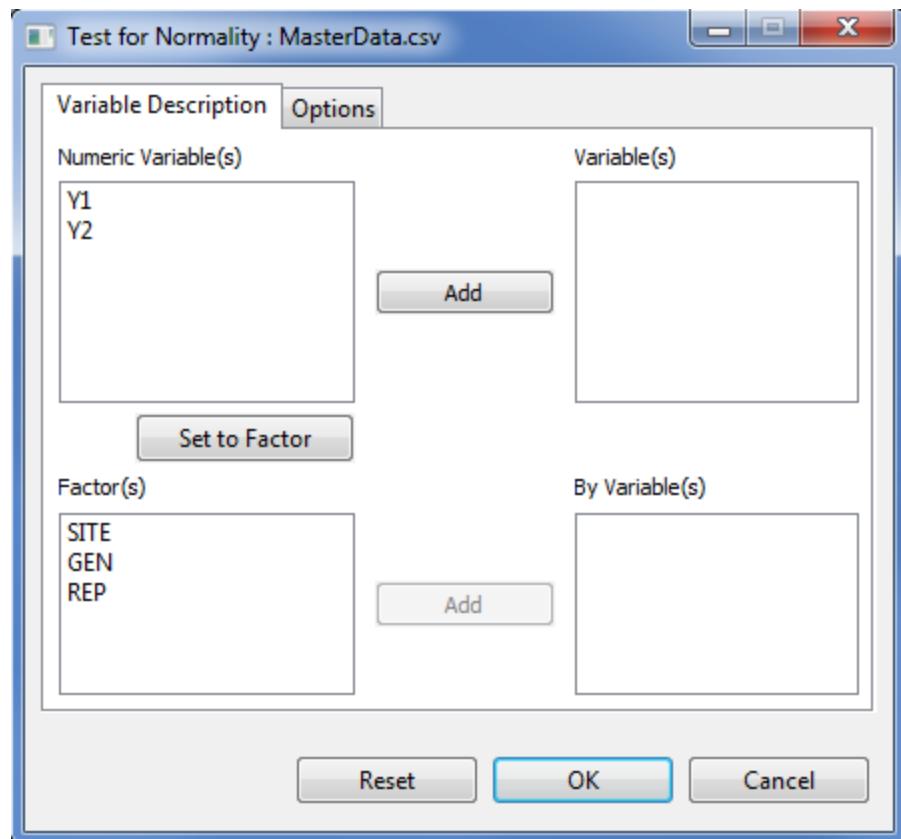
The steps to perform test for normality are listed below:

- On the **Project Explorer** panel, double-click the file to be used for the analysis to open it and view it in the Data Viewer tab.

For the example, using the project named *MyProject*, import the data *MasterData.csv* from the *Data* folder of the project named *SampleProject*. To import data from the *SampleProject*, see *Importing Data from Other Project* section of this user's manual.

Opening the data for the first time, *REP* field is regarded by STAR as numerical variable. To change its type, choose the variable *REP* and click on the **Set to Factor** button.

- Click **Analyze | Descriptive Statistics | Normality Test....** The **Normality Test** dialog box will appear.



- Specify the required field and appropriate options for the analysis.

Variable Description Tab

This tab lets the user identify the variables and grouping variable(s) where test for normality will be performed.

Variables

At least one entry should be specified for the analysis to proceed. Entries for this list box should come from the **Numeric Variable(s)** list box.

By Variables

This field is optional. If a by variable(s) is specified, it will perform test for normality per level of the **By Variable(s)**. Entries for this list box should come from the **Factor(s)** list box.

Options Tab

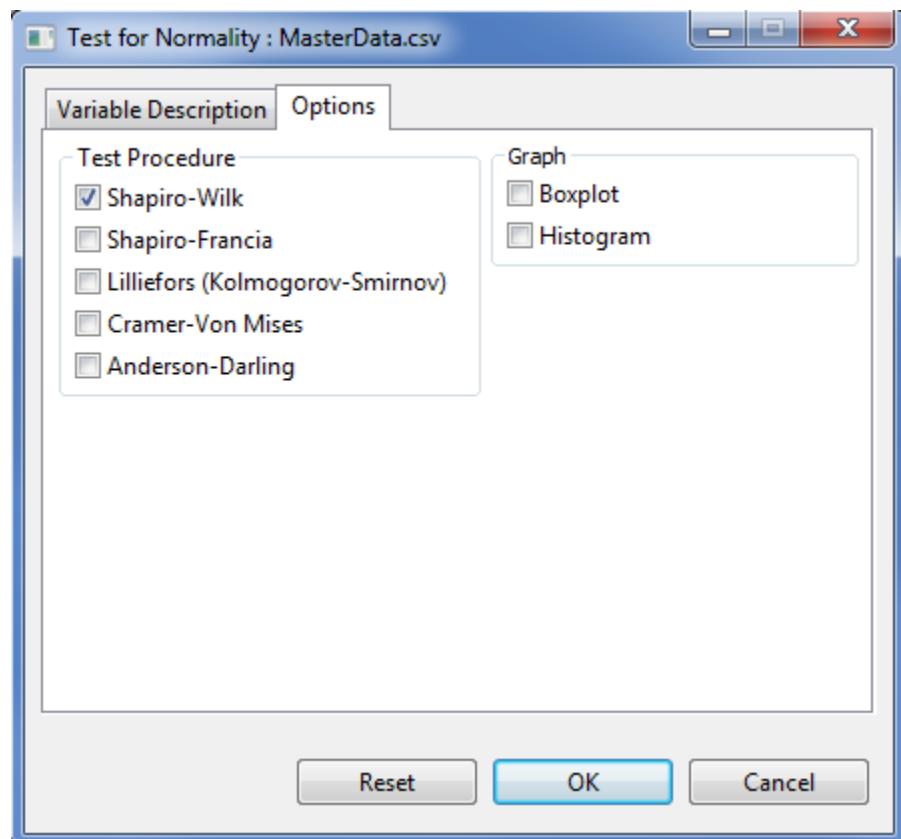
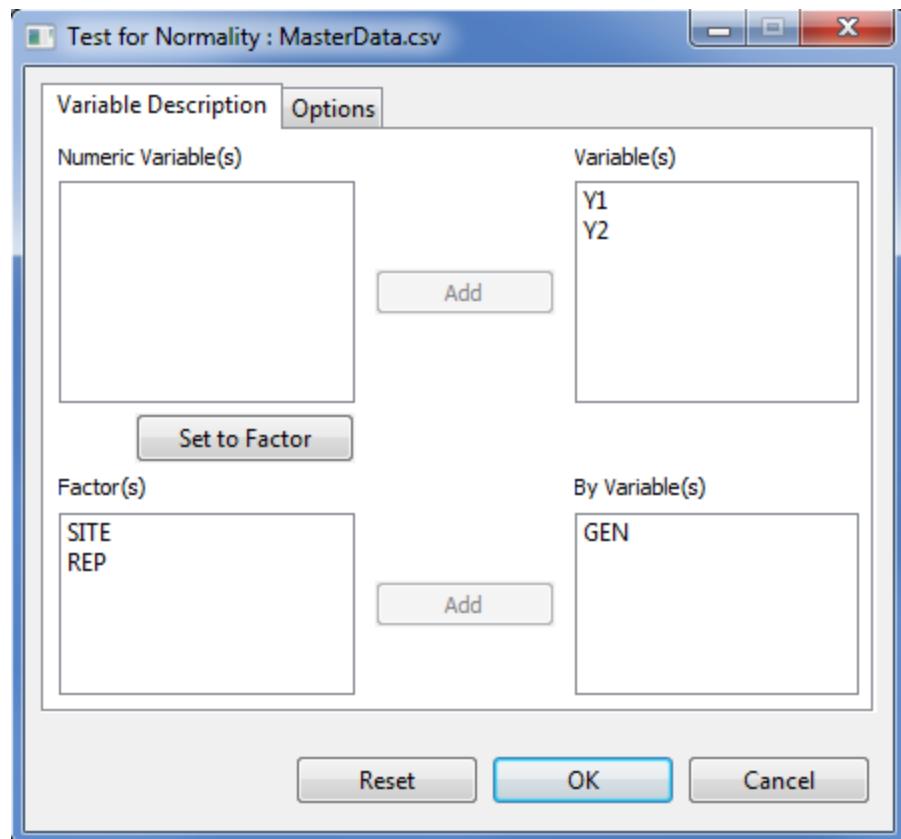
Test Procedure

This option is required. At least one test procedure should be selected for the analysis to proceed. By default, the Shapiro-Wilk test is selected.

Graph

The user has the option to display the box plot and the histogram.

For the example, suppose we want to perform normality test using Shapiro-Wilk test for variables *Y1* and *Y2* per level of *GEN*. The completed **Variable Description** tab and **Option** tab should appear as shown below:



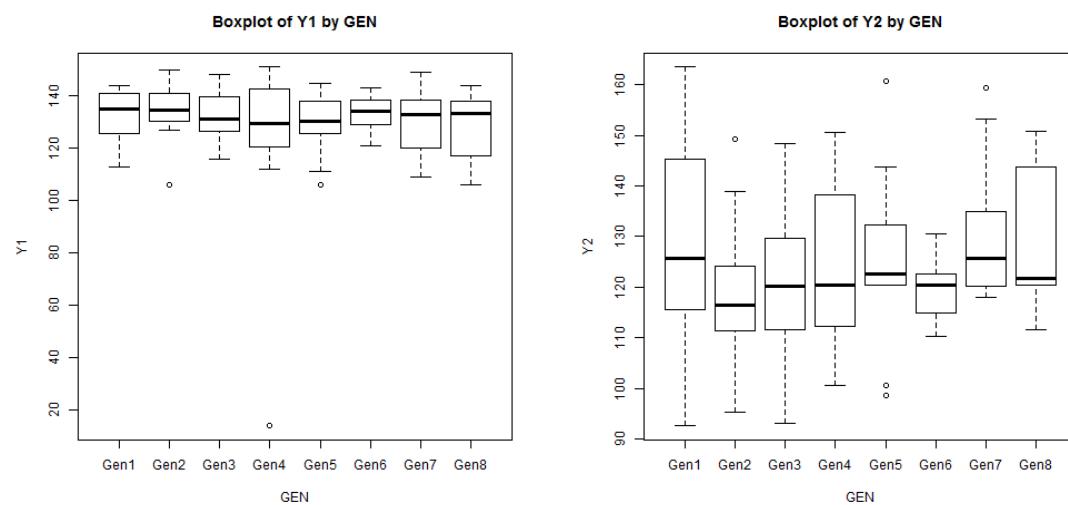
- Click the **OK** button to perform the test. The **Normality Test** dialog box will be minimized and STAR activates the **Output** page of the **Result Viewer** tab.

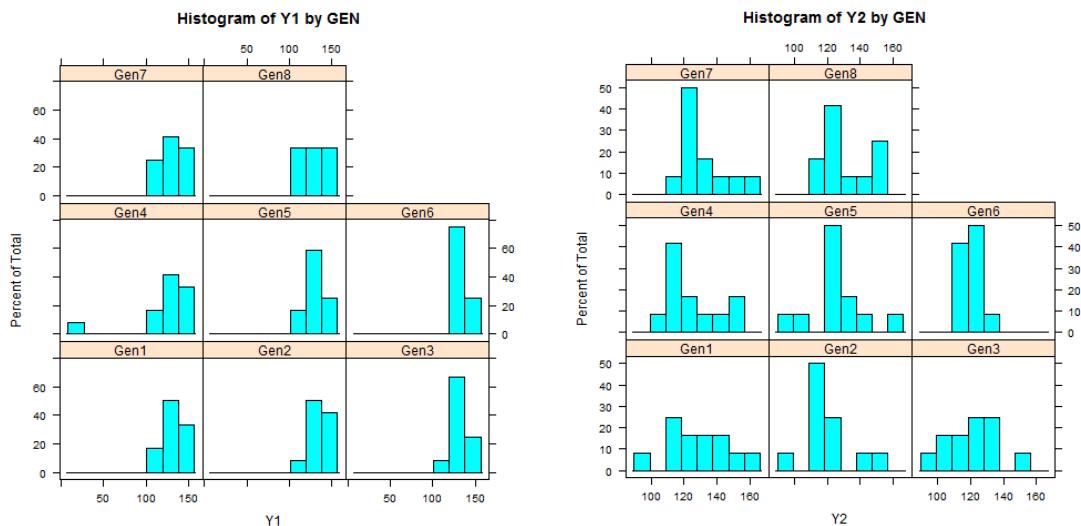
Sample text output displayed in the **Output** page.

Test for Normality

Grp	Level	Variable	Method	Statistics	Prob
GEN	Gen1	Y1	Shapiro-Wilk	0.8914	0.1228
GEN	Gen2	Y1	Shapiro-Wilk	0.8947	0.1353
GEN	Gen3	Y1	Shapiro-Wilk	0.9560	0.7259
GEN	Gen4	Y1	Shapiro-Wilk	0.6460	0.0003
GEN	Gen5	Y1	Shapiro-Wilk	0.9268	0.3474
GEN	Gen6	Y1	Shapiro-Wilk	0.9645	0.8454
GEN	Gen7	Y1	Shapiro-Wilk	0.9618	0.8097
GEN	Gen8	Y1	Shapiro-Wilk	0.9020	0.1681
GEN	Gen1	Y2	Shapiro-Wilk	0.9700	0.9107
GEN	Gen2	Y2	Shapiro-Wilk	0.9341	0.4251
GEN	Gen3	Y2	Shapiro-Wilk	0.9811	0.9876
GEN	Gen4	Y2	Shapiro-Wilk	0.9200	0.2860
GEN	Gen5	Y2	Shapiro-Wilk	0.9314	0.3956
GEN	Gen6	Y2	Shapiro-Wilk	0.9450	0.5658
GEN	Gen7	Y2	Shapiro-Wilk	0.8047	0.0106
GEN	Gen8	Y2	Shapiro-Wilk	0.8613	0.0508

Sample graphical output displayed in the **Graph** page.





Homogeneity of Variances

The Homogeneity of Variances menu perform test for equally of variances across groups. There are two procedures available in this menu, namely: Bartlett's test and the Levene's test.

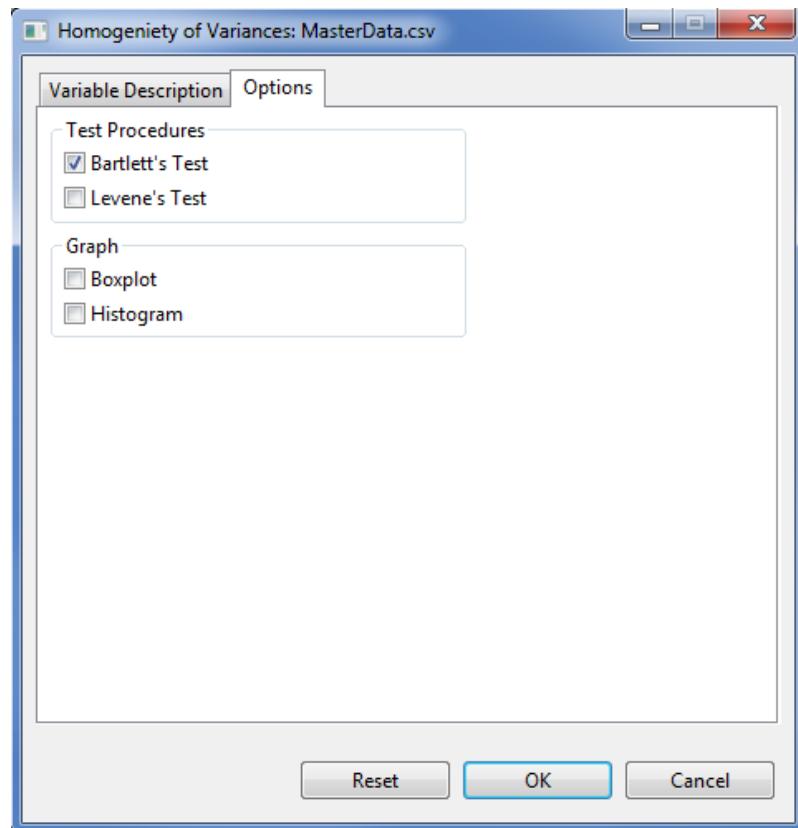
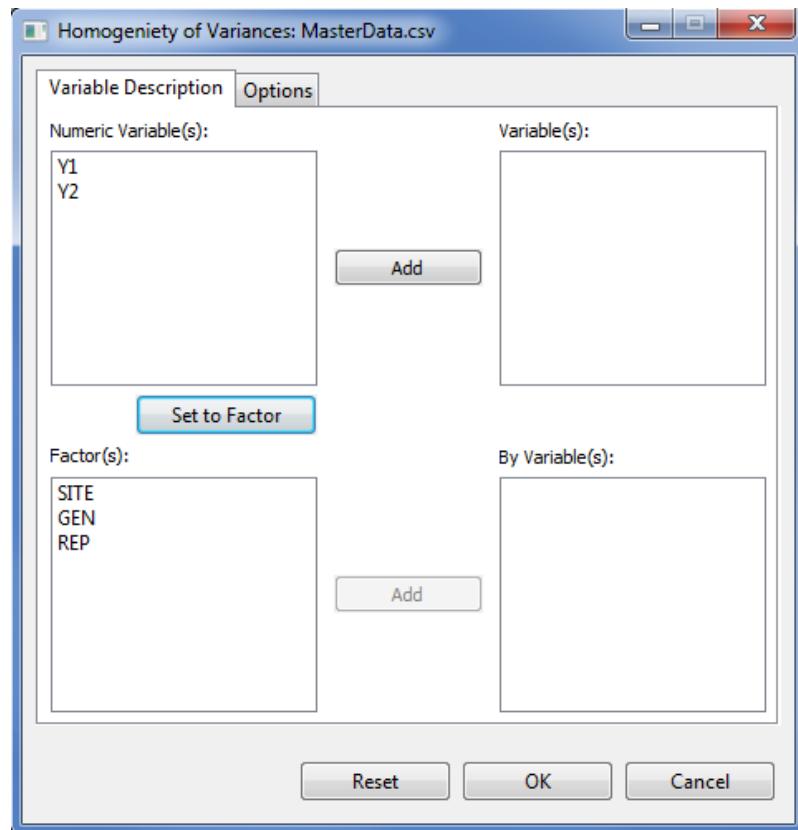
The steps to perform the test are listed below:

- On the **Project Explorer** panel, double-click the file to be used for the analysis to open it and view it in the Data Viewer tab.

For the example, using the project named *MyProject*, import the data *MasterData.csv* from the *Data* folder of the project named *SampleProject*. To import data from the *SampleProject*, see *Importing Data from Other Project* section of this user's manual.

Opening the data for the first time, *REP* field is regarded by STAR as numerical variable. To change its type, choose the variable *REP* and click on the **Set to Factor** button.

- Click **Analyze | Descriptive Statistics | Homogeneity of Variance....** The **Homogeneity of Variance** dialog box will appear.



- Specify the required field and appropriate options for the analysis.

Variable Description Tab

This tab lets the user identify the variables and grouping variable(s) where test for homogeneity of variances will be performed.

Variables

At least one entry should be specified for the analysis to proceed. Entries must come from the **Numeric Variable(s)** list box.

By Variables

At least one entry should be specified for the analysis to proceed. Entries specified here should contain two or more levels and must come from the **Factor(s)** list box.

Options Tab

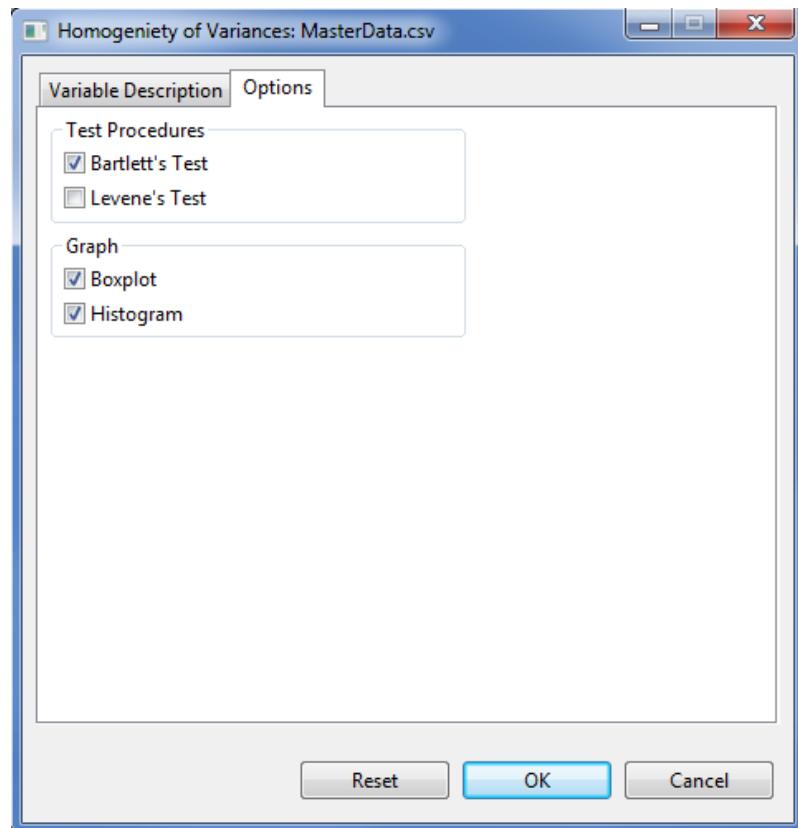
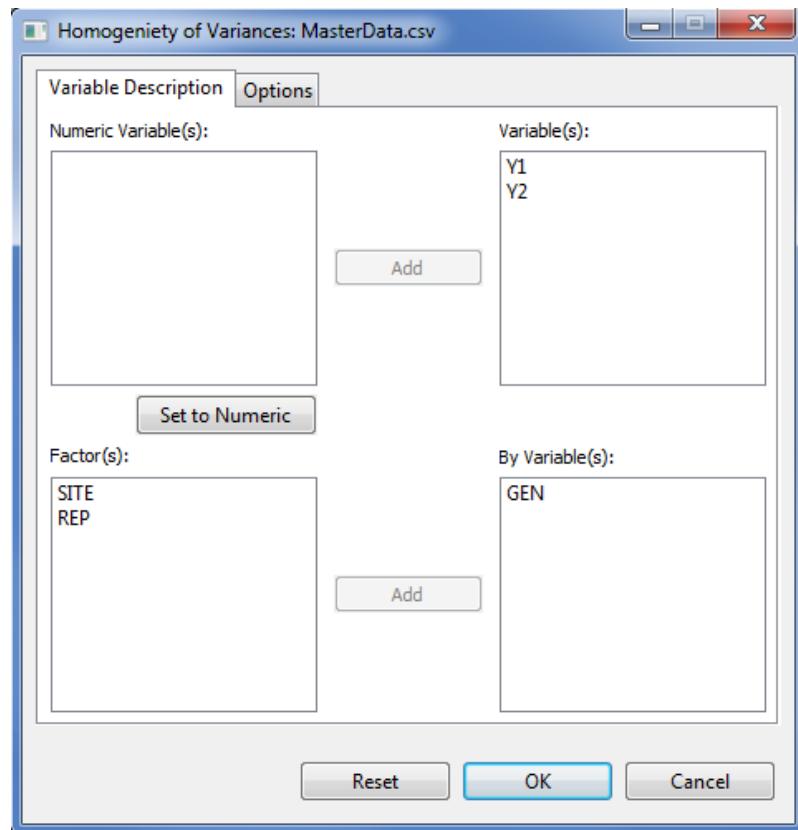
Test Procedure

At least one test procedure should be selected for the analysis to proceed. By default, the Bartlett's test for homogeneity of variances is selected.

Graph

The user has the option to display the box plot and the histogram.

For the example, suppose we want to determine whether the variances are equal among the levels of *GEN* for variables *Y1* and *Y2*. The completed **Variable Description** tab and completed **Option** tab should appear as below:

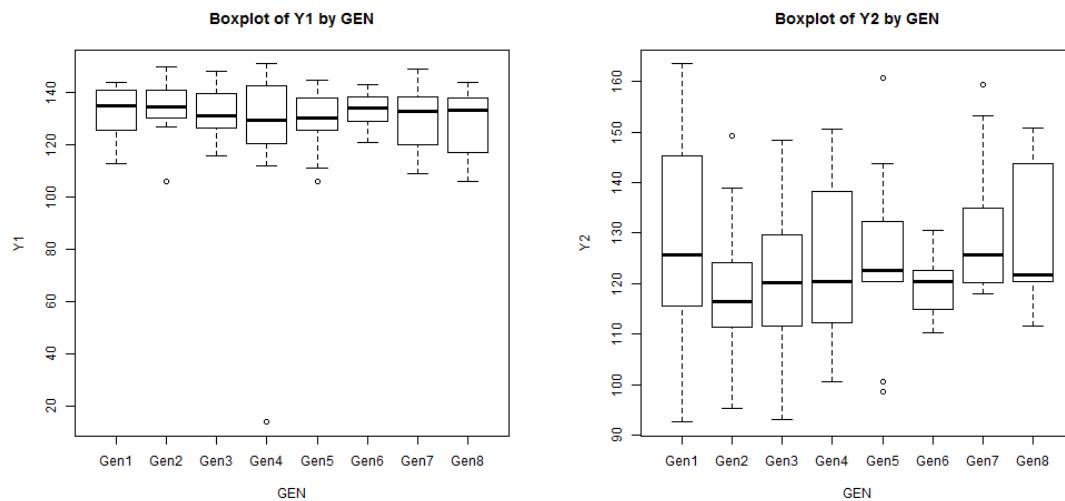


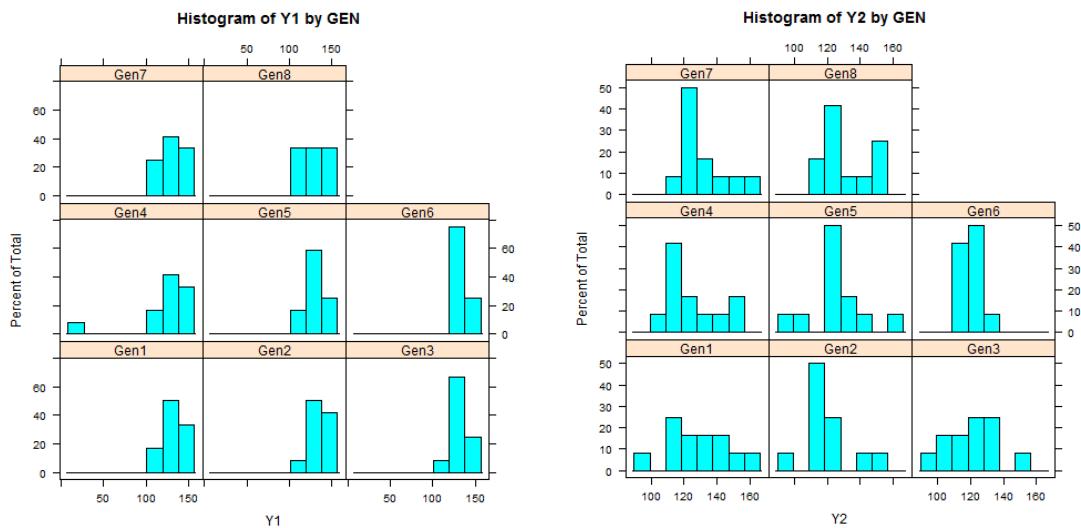
- Click the **OK** button to perform the test. The **Homogeneity of Variances** dialog box will be minimized and STAR activates the **Output** page of the **Result Viewer** tab.

Sample text output as displayed in the **Output** page:

Test for Homogeneity of Variances					
Grp	Variable	Method	DF	Statistics	Prob
GEN	Y1	bartlett	7	49.91	0.0000
GEN	Y2	bartlett	7	15.00	0.0359

Sample graphical output displayed in the **Graph** page.





Fitting Distributions

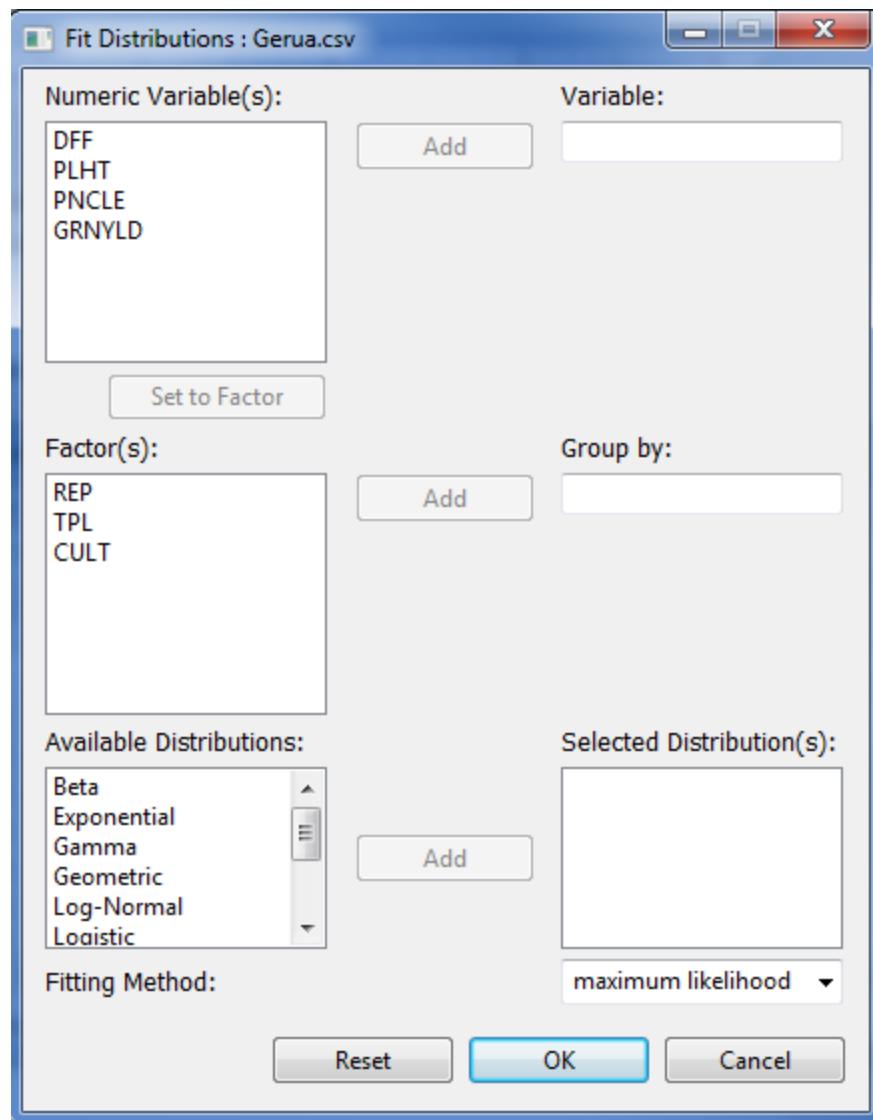
The One Sample *t*-test procedure determine whether the mean of one variable differ from the hypothesized value. It assumes that the samples are randomly taken from the population of interest and that the observations are obtained from a normal distribution.

The steps to fit a distribution are listed below:

- On the **Project Explorer** panel, double-click the file to be used for the analysis to open it and view it in the Data Viewer tab.

For the example, using the project named *MyProject*, import the data *Gerua* from the package. To import data from the package, see *Importing Data from package* section of this user's manual.

- Click **Analyze | Fit Distributions....** The **Fit Distributions** dialog box will appear.



- Specify the required field and appropriate options for the analysis.

Variable

This field is required.

Group by

This field is required.

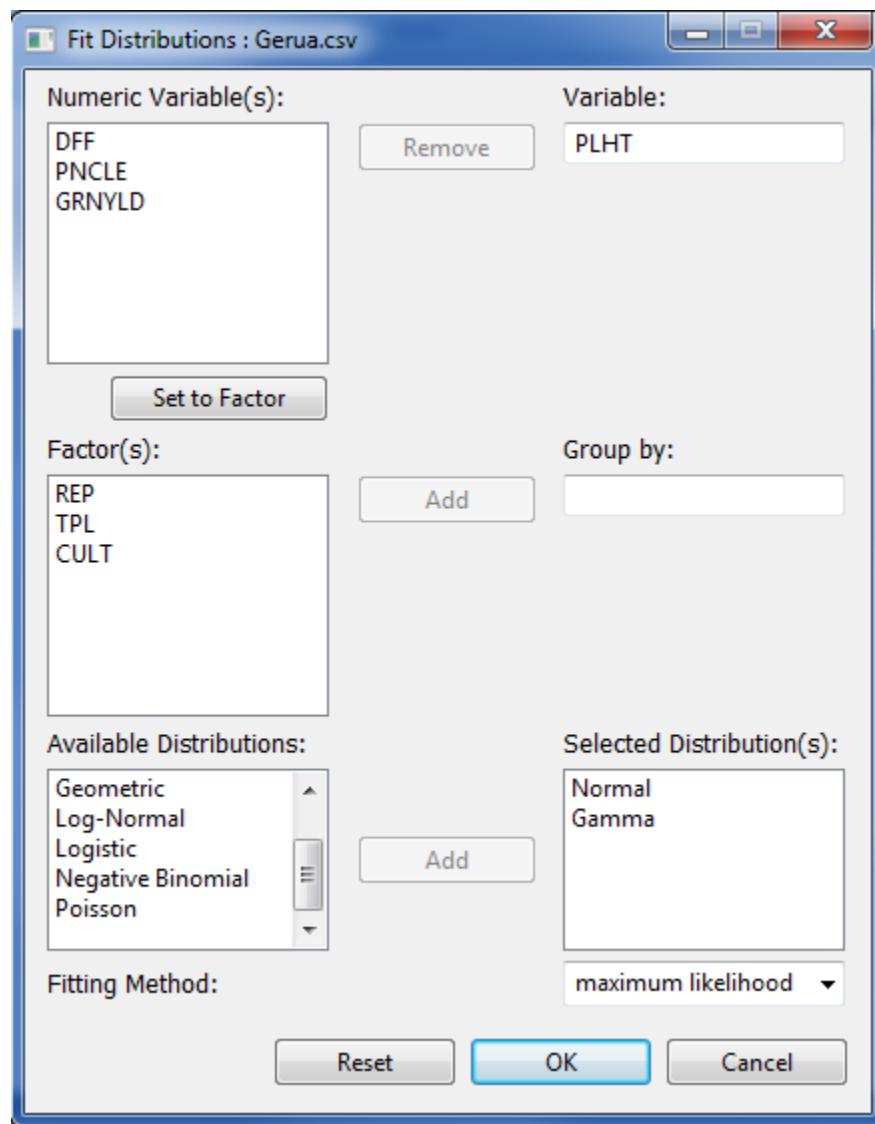
Selected Distribution(s)

This field is required.

Fitting Method

This field is required.

For the example, the completed dialog box should appear as below:



- Click the **OK** button to fit the distributions. The **Fit Distributions** dialog box will be minimized and STAR activates the **Output** page of the **Result Viewer** tab.

Sample text output as displayed in the **Output** page.

```
DISTRIBUTION FITTING
METHOD: maximum likelihood estimation
```

VARIABLE: PLHT

DISTRIBUTION: Normal

Fitting of the distribution 'norm' by maximum likelihood

Parameters:

	estimate	Std. Error
mean	128.47756	1.2203140
sd	15.24172	0.8628923

Goodness-of-fit

	Statistic	Decision
Cramer-von Mises	0.5887	NULL
Anderson-Darling	2.9911	NULL
Kolmogorov-Smirnov	0.1364	rejected

DISTRIBUTION: Gamma

Fitting of the distribution 'gamma' by maximum likelihood

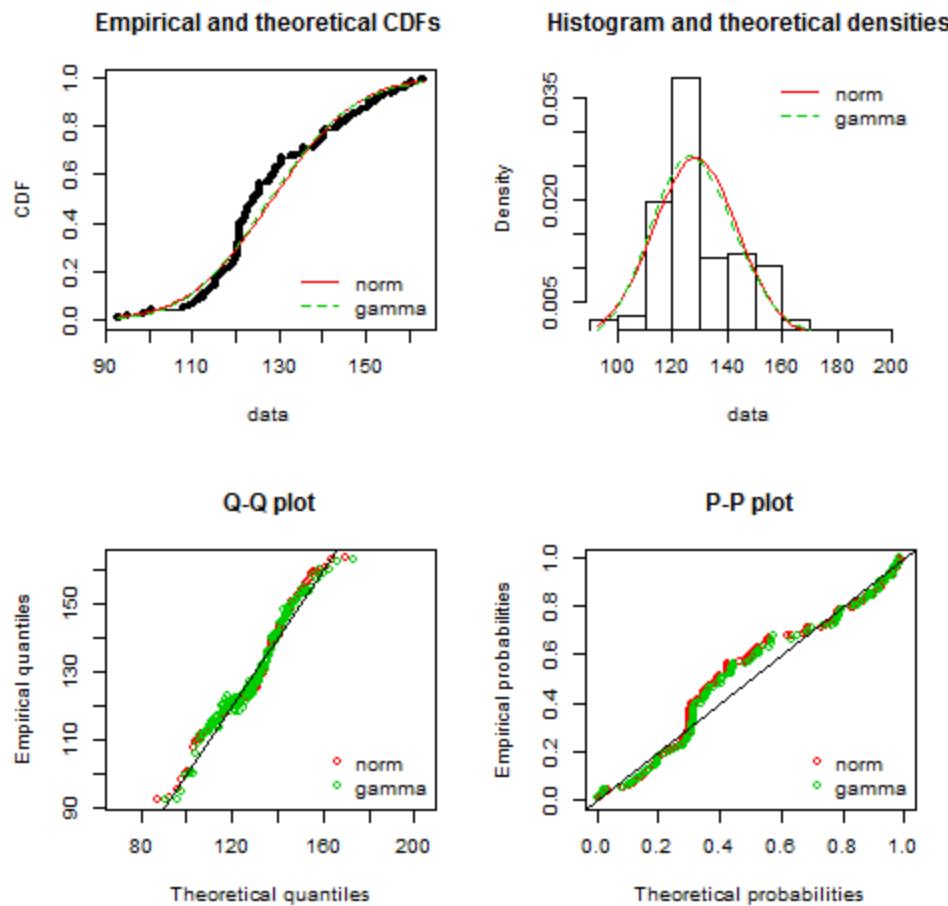
Parameters:

	estimate	Std. Error
shape	71.8758920	8.11707165
rate	0.5594382	0.06339853

Goodness-of-fit

	Statistic	Decision
Cramer-von Mises	0.4672	rejected
Anderson-Darling	2.4234	rejected
Kolmogorov-Smirnov	0.1219	rejected

Sample graphical output as displayed in the **Graph** page.



t-Test

One Sample t-test

The One Sample *t*-test procedure determine whether the mean of one variable differ from the hypothesized value. It assumes that the samples are randomly taken from the population of interest and that the observations are obtained from a normal distribution.

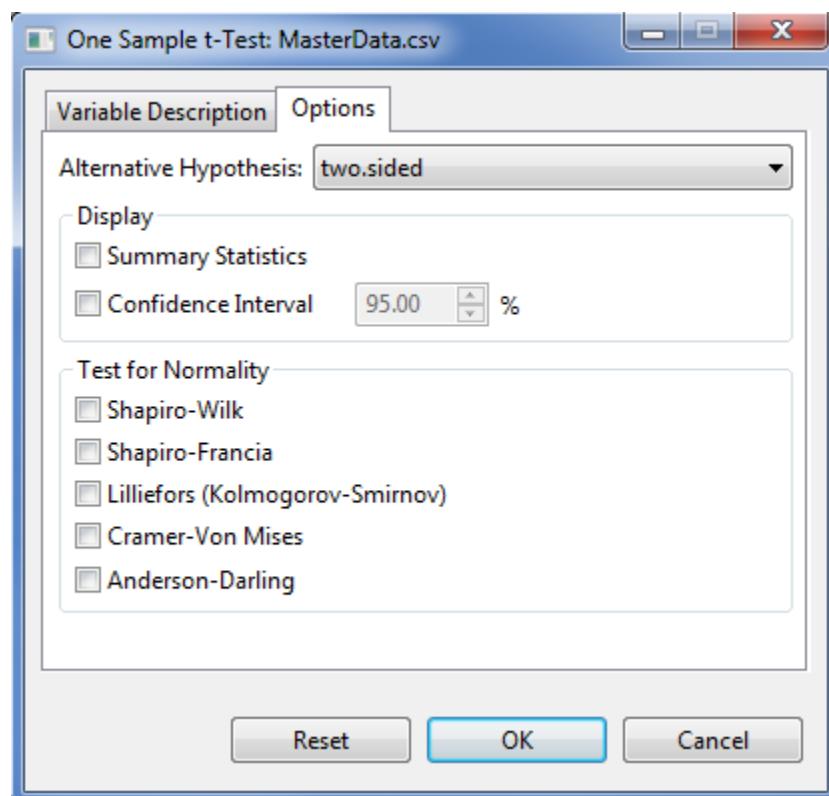
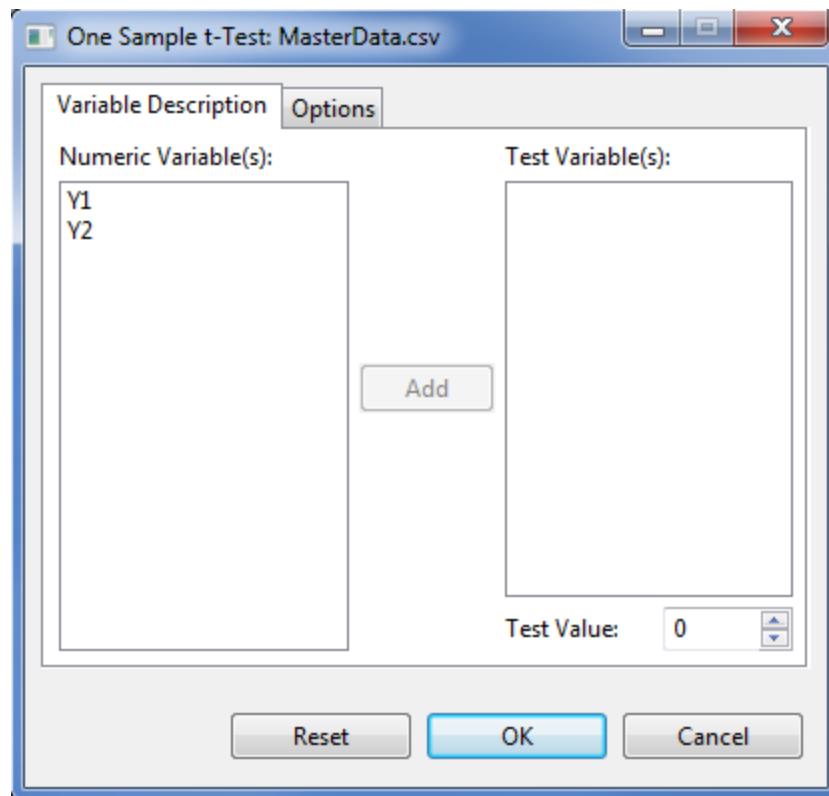
The steps to perform the one sample t-test are listed below:

- On the **Project Explorer** panel, double-click the file to be used for the analysis to open it and view it in the Data Viewer tab.

For the example, using the project named *MyProject*, import the data *MasterData.csv* from the *Data* folder of the project named *SampleProject*. To import data from the *SampleProject*, see *Importing Data from Other Project* section of this user's manual.

Opening the data for the first time, *REP* field is regarded by STAR as numerical variable. To change its type, choose the variable *REP* and click on the **Set to Factor** button.

- Click **Analyze | t-Test | One Sample....** The **One Sample** dialog box will appear.



- Specify the required field and appropriate options for the analysis.

Variable Description Tab

Test Variable(s)

At least one entry should be specified for the analysis to proceed. Entries should come from the **Numeric Variable(s)** dialog box.

Test Value

This field is required and will only accept one entry at a time. The default value is 0. User can change the value by typing a value inside the spin box or by pressing the up-arrow key to increment the value, down-arrow key, otherwise.

Options Tab

Alternative Hypothesis

User can select a one-tailed or two-tailed test. The default alternative hypothesis used is that for the two-sided test.

Summary Statistics

If this option is selected, a summary table with number of observations, minimum, maximum, mean and standard deviation will be displayed.

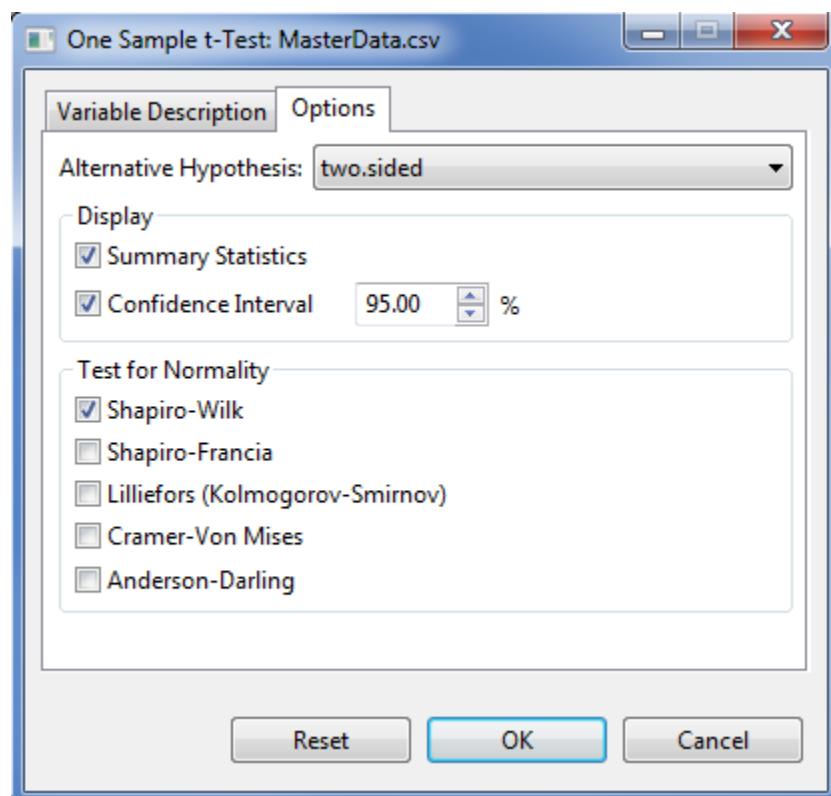
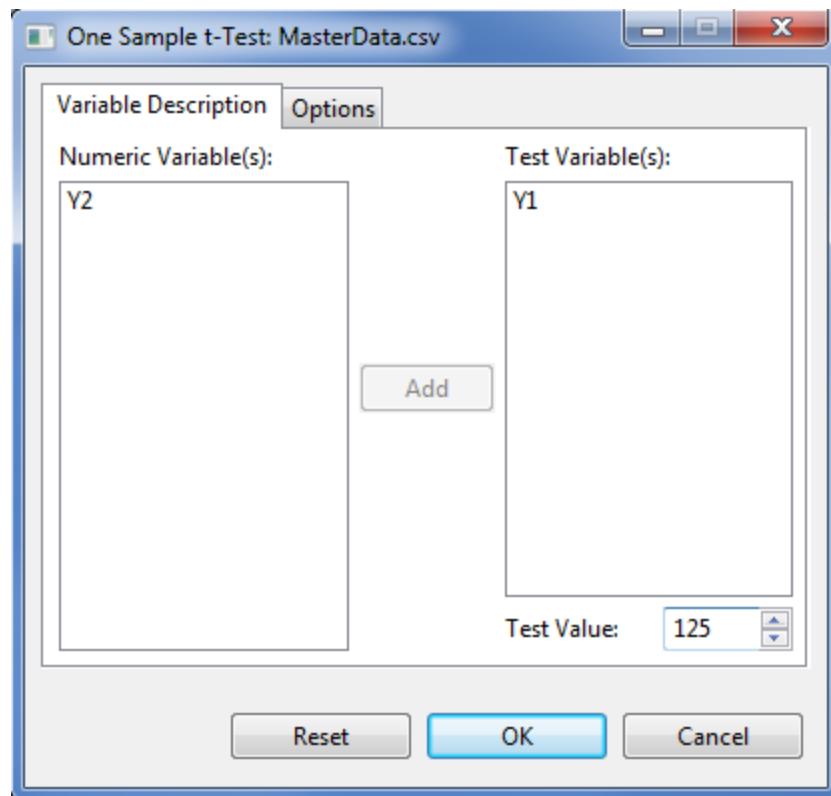
Confidence Interval

If this option is selected, a confidence interval of the mean will be displayed. If this is selected, by default, a 95% confidence interval is displayed.

Test for Normality

If at least one option is selected, if display the test for normality test for each level of the **Grouping Variable**. There are five available tests for normality procedure.

For the example, suppose we want to determine whether the mean of Y1 is significantly different from 125. The completed **Variable Description** tab and **Option** tab should appear as shown below:



- Click the **OK** button to perform the test. The **One Sample t-Test** dialog box will be minimized and STAR activates the **Output** page of the **Result Viewer** tab.

Sample output as displayed in the **Output** page.

```
Test for Normality
-----
Variable   Method          Statistics      Prob
-----
Y1        Shapiro-Wilk      0.6908    0.0000
-----

Descriptive Statistics
-----
Variable     N   Lower CI*       Mean   Upper CI*     StdDev   SE_Mean
-----
Y1         96   127.18    130.43    133.68    16.05    1.64
-----
* At 95% Confidence Level.

One Sample t-Test, h0: mean = 125
-----
Variable   DF   t Value   Pr > |t|
-----
Y1         95   3.31    0.0013
-----
```

Paired Sample t-tests

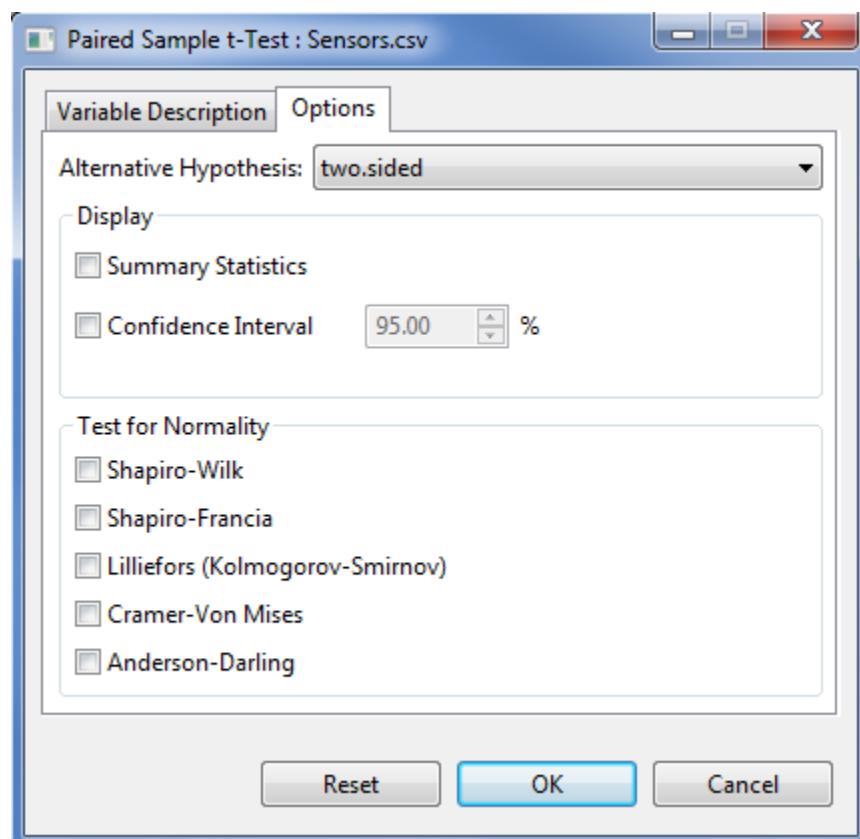
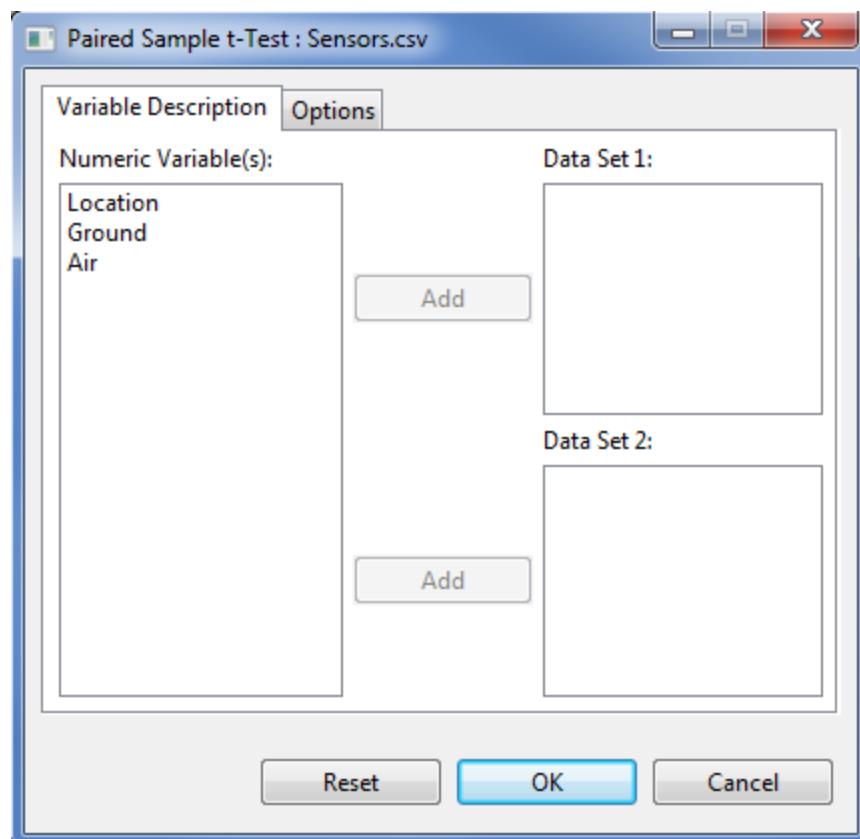
The paired sample *t*-test is used to compares the means of paired or related samples. It assumes that the samples are randomly taken from the population of interest and the population of differences is normally distributed.

The steps to perform paired *t*-test are listed below:

- On the **Project Explorer** panel, double-click the file to be used for the analysis to open it and view it in the Data Viewer tab.

For the example, using the project named *My Project*, import the data *Sensors* from the package. To import data from the package, see *Importing Data from the Package* section of this user's manual.

- Click **Analyze | t-Tests | Paired Samples...** from the main window. The **Paired Samples t-Test** dialog box will appear.



- Specify the required field and appropriate options for the analysis.

Variable Description Tab

Data Set 1

This field needs at least one entry for the analysis to proceed and must have the same number of entry as **Data Set 2**.

Data Set 2

This field needs at least one entry for the analysis to proceed and must have the same number of entry as **Data Set 1**.

Options Tab

Alternative Hypothesis

User can select a one-tailed or two-tailed test. The default alternative hypothesis used is that for the two-sided test.

Summary Statistics

If this option is selected, a summary table with number of observations, minimum, maximum, mean and standard deviation will be displayed.

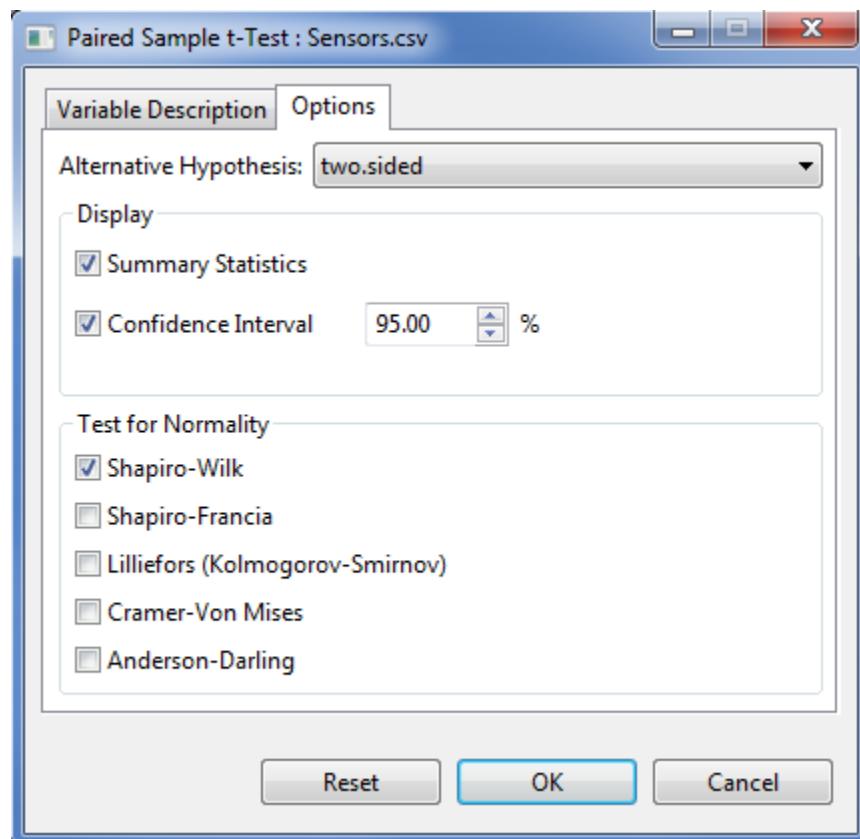
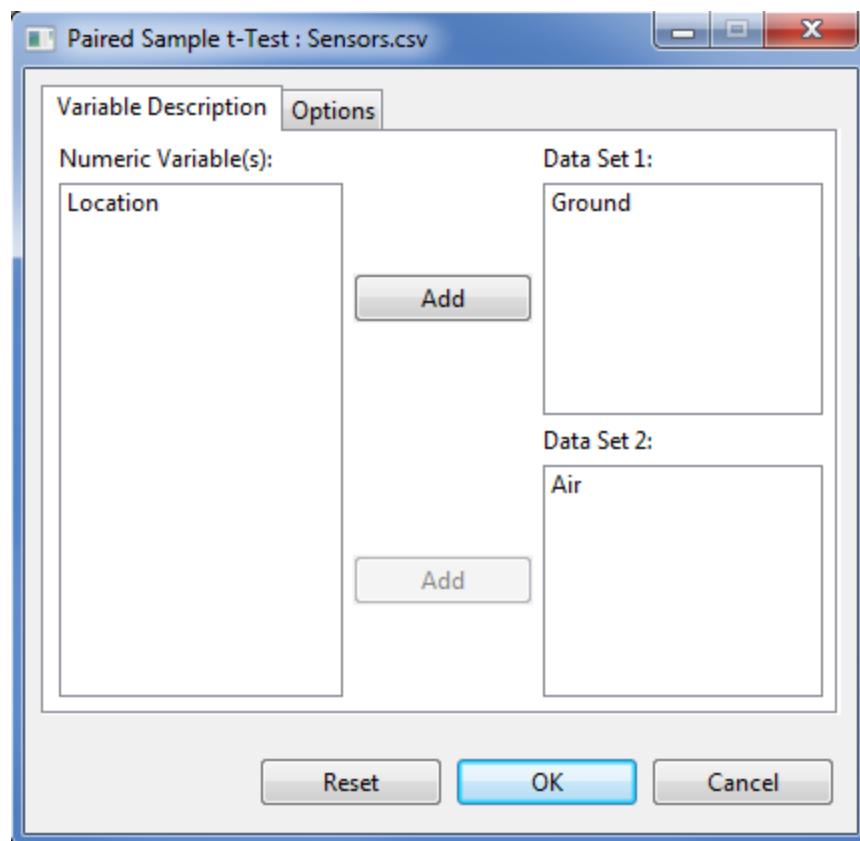
Confidence Interval

If this option is selected, a confidence interval of the mean will be displayed. If this is selected, by default, a 95% confidence interval is displayed.

Test for Normality

If at least one option is selected, if display the test for normality test for the difference between each pair of variables. There are five available tests for normality procedure.

For the example, the completed **Variable Description** tab and **Options** tab should appear as shown below:



- Click the **OK** button to perform the analysis. The **Paired Sample t-Test** dialog box will be minimized and STAR activates the **Output** page of the **Result Viewer** tab.

Sample output of the analysis as shown in the Output page is displayed below:

```
Test for Normality
-----
Difference      Method          Statistics     Prob
-----
Ground - Air   Shapiro-Wilk      0.9403    0.5562
-----

Descriptive Statistics
-----
Difference      N   Lower CI*    Mean   Upper CI*   StdDev   SE_Mean
-----
Ground - Air   10    -2.10    -1.55    -0.9987   0.7706   0.2437
-----
* At 95% Confidence Level.

Paired Sample t-Test, h0: mean = 0
-----
Difference      DF   t Value   Pr > |t|
-----
Ground - Air   9    -6.36    0.0001
-----
```

Independent Sample *t*-tests

The independent sample *t*-test is used to determine whether the means between two groups or populations are equal. It assumes that (i) the samples are drawn independently from each population; (ii) the samples from each population are randomly taken; and (iii) the observations from each population are obtained from a normal distribution.

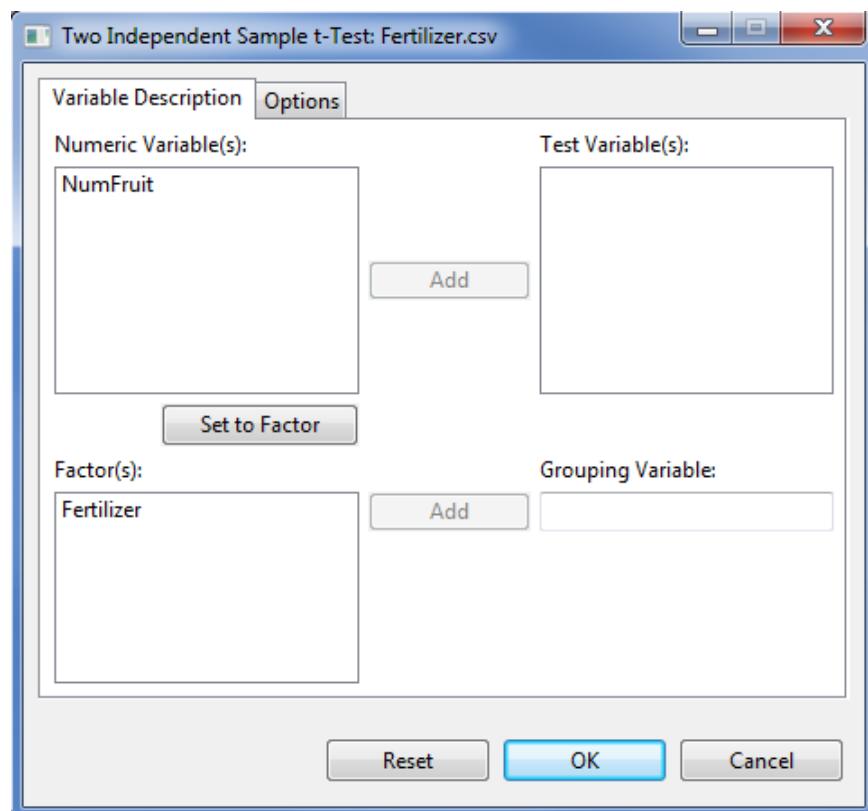
Default output of the *t*-test for two independent samples in STAR includes the test for equality of variances. Depending on the result of the equality of variances, pooled *t*-test or a *t*-test with satterwaite adjustment is computed.

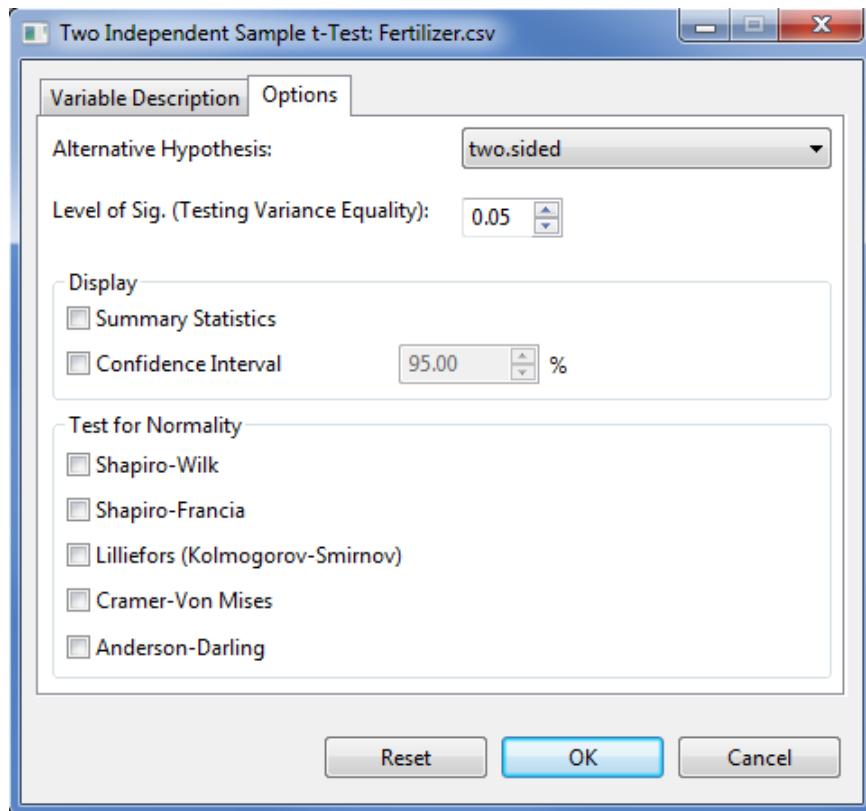
The steps to perform *t*-Test for two independent samples are listed below:

- On the **Project Explorer**, double-click the file to be used for the analysis to open and view it in the Data Viewer.

For the example, using the project named *My Project*, import the data *Fertilizer* from package. To import that data from package, see *Importing from Package* section of this user's manual.

- Click **Analyze | t-test | Independent Sample...** from the main window. The **Two Independent Sample t-Test** dialog box will appear.





- Specify the required field and appropriate options for the analysis.

Variable Description Tab

Test Variable(s)

This field need at least one entry for the analysis to proceed and should come from the **Numeric Variable(s)** list box.

Grouping Variable

This field accepts one entry at a time and needs an entry for the analysis to proceed. The entry must come from the **Factor(s)** list box. The entry should have only two levels.

Options Tab

Alternative Hypothesis

User can select a one-tailed or two-tailed test. The default alternative hypothesis used is that for the two-sided test.

Level of Significance

This will be used to determine if the two groups have equal variance. Its default value is 0.05. The user can change this value by specifying a numeric value from zero to 1.

Summary Statistics

If this option is selected, a summary table with number of observations, minimum, maximum, mean and standard deviation will be displayed.

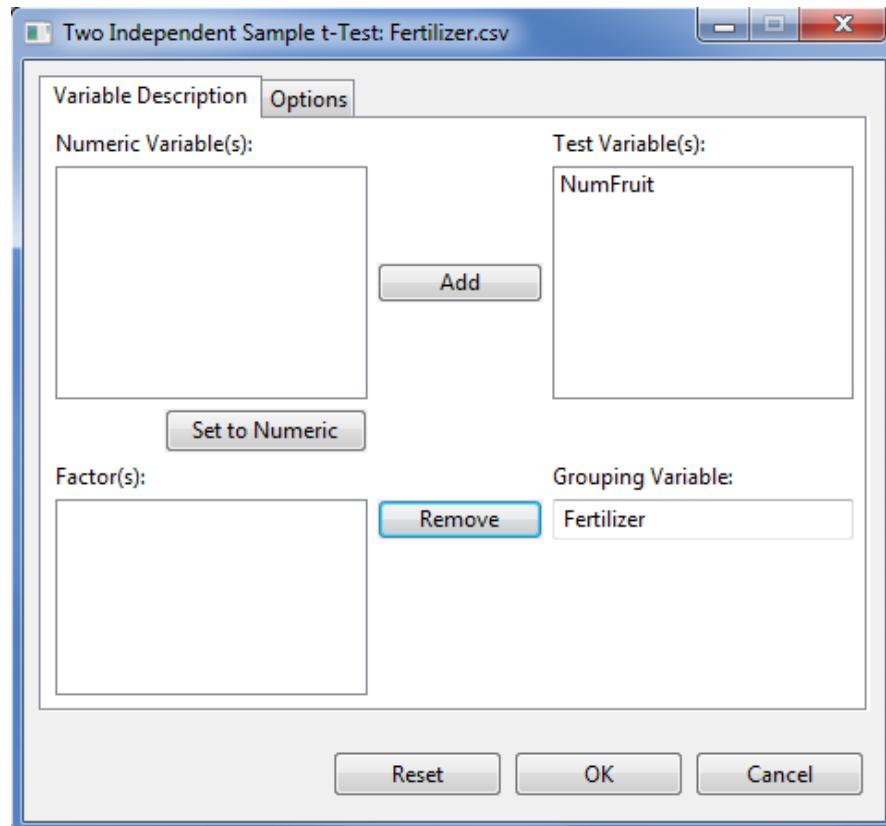
Confidence Interval

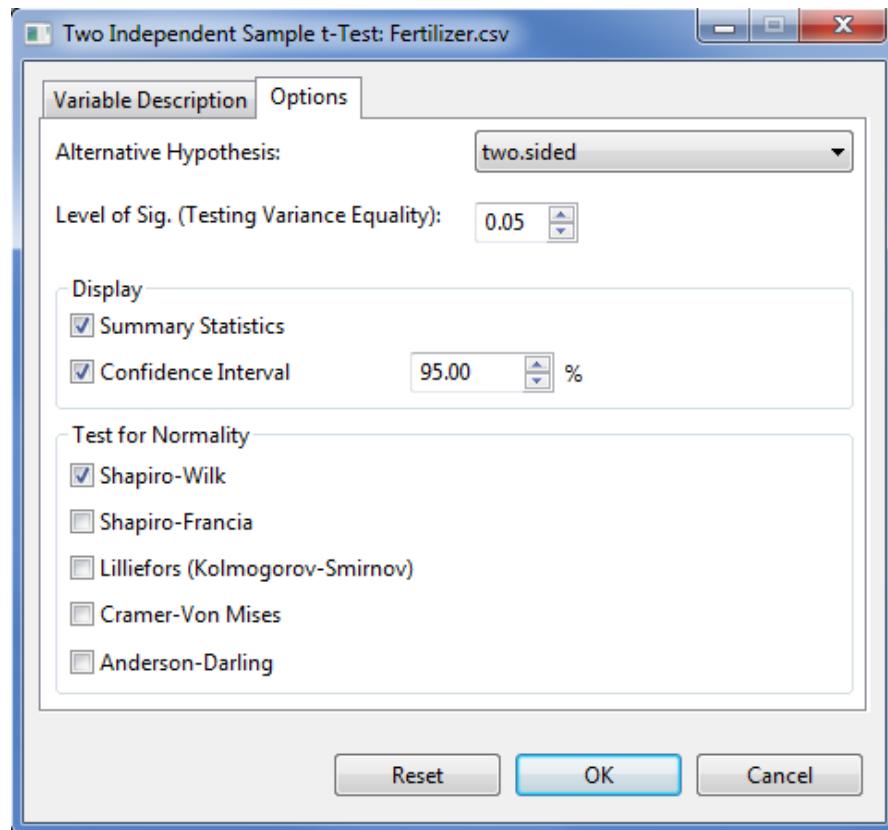
If this option is selected, a confidence interval of the mean will be displayed. If this is selected, by default, a 95% confidence interval is displayed.

Test for Normality

If at least one option is selected, it displays the test for normality test for each level of the **Grouping Variable**. There are five available tests for normality procedure.

For the example, suppose we want to test the hypothesis that the mean number of fruits from trees sprayed by the two fertilizers are the same. The completed **Variable Description** tab and **Option** tab should appear as shown below:





- Click the **OK** button to perform the analysis. The **Two Independent Sample t-test** dialog box will be minimized and STAR actives the **Output** page of the **Result Viewer** tab.

Sample output of the analysis as shown in the Output page is displayed below.

Test for Normality					
Grp	Level	Variable	Method	Statistics	Prob
<hr/>					
Fertilizer	A	NumFruit	Shapiro-Wilk	0.9726	0.8950
Fertilizer	B	NumFruit	Shapiro-Wilk	0.9198	0.1916
<hr/>					

Descriptive Statistics

Variable	Fertilizer	N	Lower CI*	Mean	Upper CI*	StdDev	SE_Mean
NumFruit	A	15	21.51	23.13	24.75	2.92	0.76
NumFruit	B	15	19.25	20.87	22.49	3.54	0.91
NumFruit	Diff(A-B)		-0.16	2.27	4.70	3.25	1.19

* At 95% Confidence Level.

Homogeneity of Variances

Variable	Method	Num DF	Den DF	F Value	Pr > F
NumFruit	Folded F	14	14	1.47	0.4820

Two Independent Sample t-Test, h0: mean diff = 0

Variable	Method*	Variances	DF	t Value	Pr > t
NumFruit	Pooled	Equal	28	1.91	0.0663

* At 0.05 level of significance.

Chi-Square Test

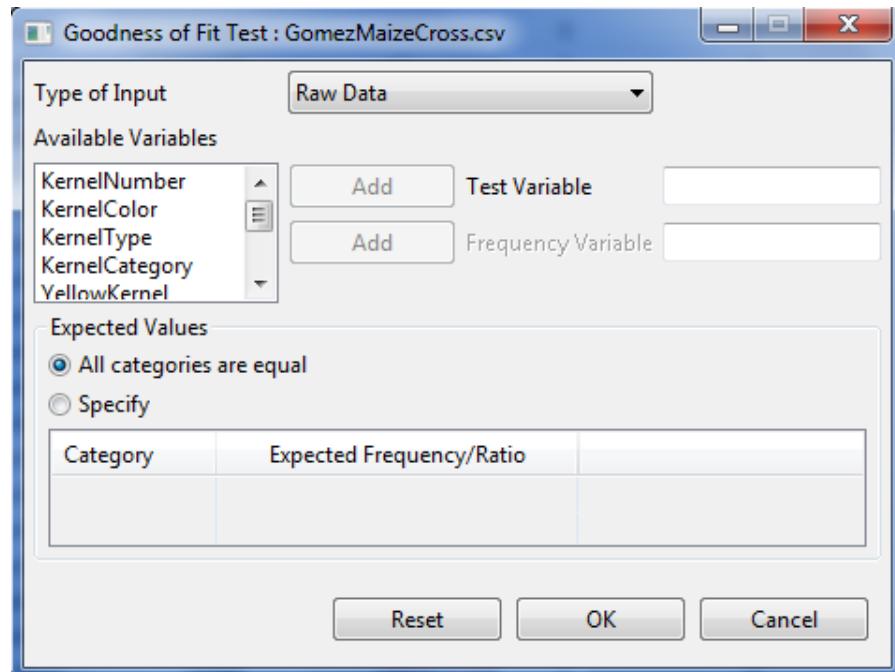
Goodness of fit Test

The steps to perform chi-square goodness of fit test are listed below:

- On the **Project Explorer**, double-click the file to be used for the analysis to open and view it in the Data Viewer tab.

For the example, using the project named *MyProject*, import the data *GomezMaizeCross* from the package. To import the data from the package, see *Importing from Package* section of this user's manual.

- Click **Analyze | Chi-Square | Goodness of Fit...** from the main window. The **Goodness of Fit Test** dialog box will appear as shown below:



- Specify the required field and appropriate options for the analysis.

Type of Input

There are two options available, *Raw Data* (default option) and *Summary Data*.

Test Variable

This variable is required.

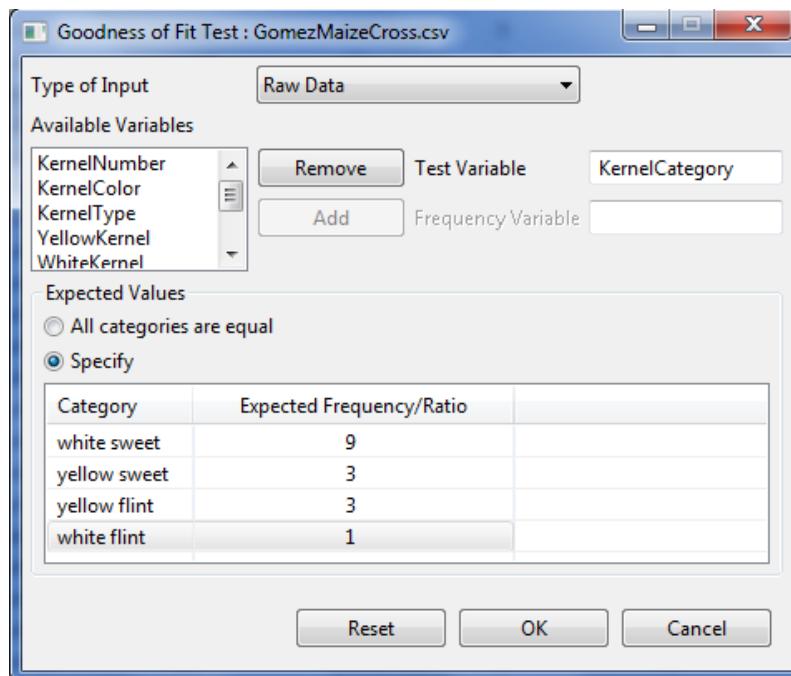
Frequency Variable

If the *Summary Data* is chosen as type of input, this variable is required.

Expected Values

There are two options available, *All categories are equal* (default option) and *specify*. If *specify* option is selected, table will be enable wherein user need to indicate the expected frequency/ratio for each of the unique categories of the test variable. The default and minimum expected frequency/ratio for each category is 1.

For the example, the completed dialog box should appear as shown below:



- Click **OK** button to perform the analysis. The **Goodness of Fit Test** dialog box will be minimized and STAR activates the **Output** page of the **Result Viewer** tab.

Sample text output is shown below.

Frequency Table:

KernelCategory	Obs	Freq	Exp Freq
white flint	112	50	
white sweet	34	150	
yellow flint	496	450	
yellow sweet	158	150	

Chi-Square Goodness of Fit Test

Chi-Square	171.7156
DF	3
Pr > Chi-Square	0.0000

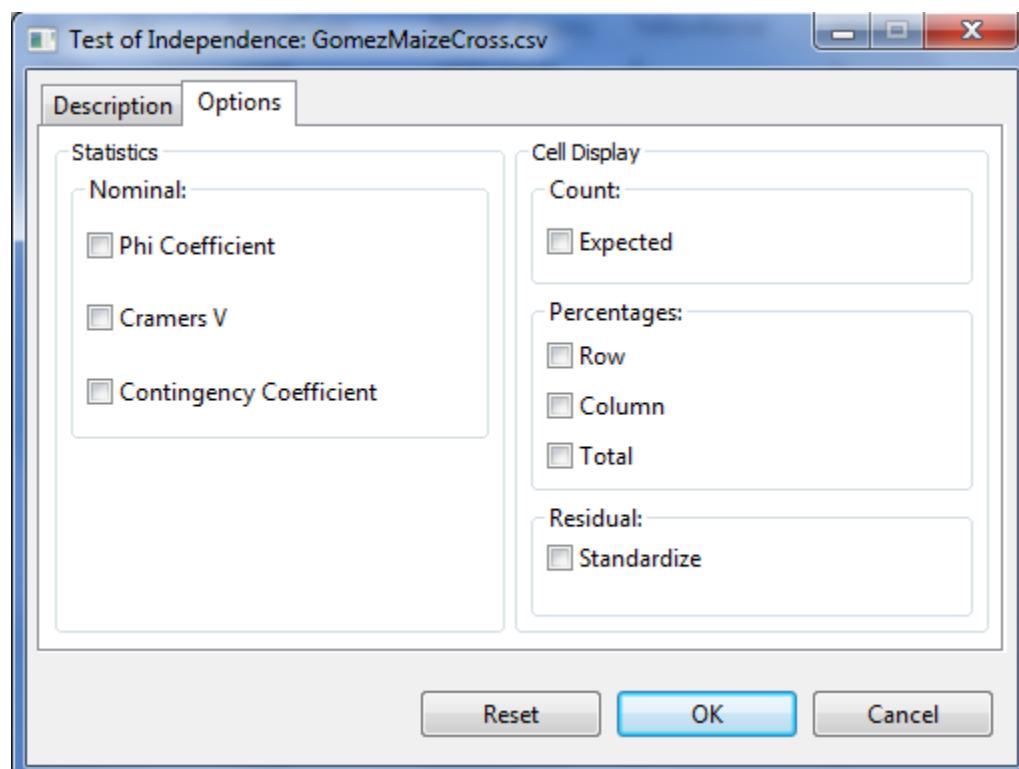
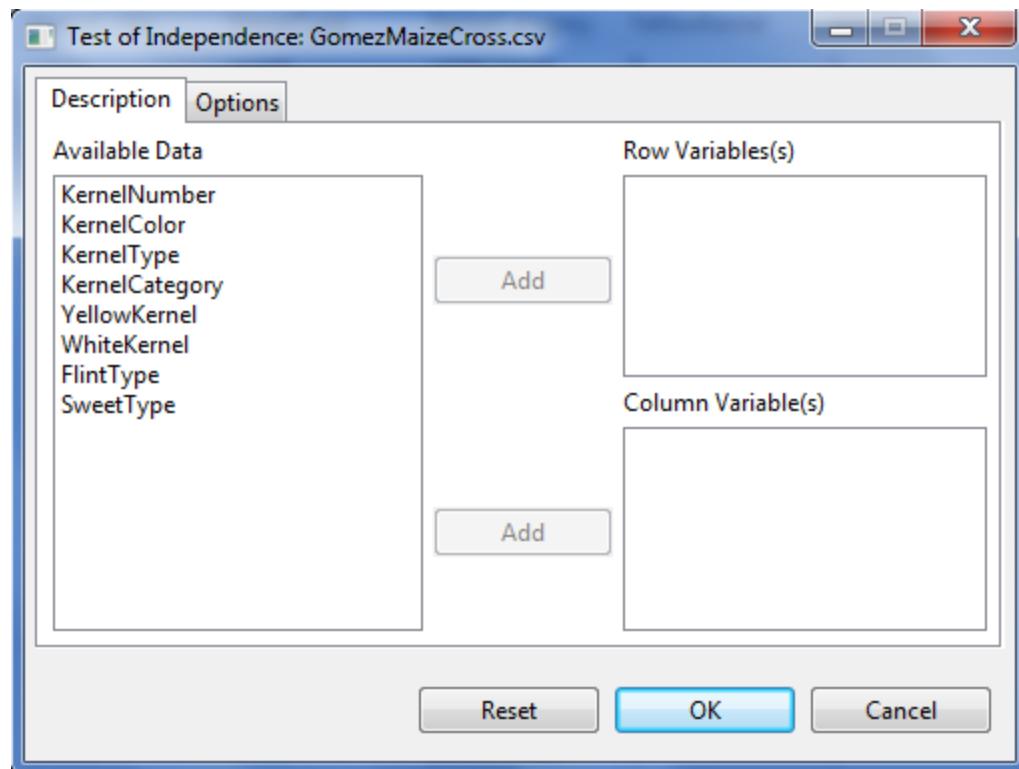
Test of Independence

The steps to perform Chi-Square test of independence are listed below:

- On the **Project Explorer**, double-click the file to be used for the analysis to open and view it in the Data Viewer tab.

For the example, using the project named *MyProject*, import the data *GomezMaizeCross* from the package. To import the data the package, see *Importing from Package* section of this user's manual.

- Click **Analyze | Chi-Square | Test of Independence...** from the main window. The **Test of Independence** dialog box will appear as shown below:



- Specify the required field and appropriate options for the analysis.

Description Tab

Row Variable(s)

At least one entry is need for the analysis to proceed.

Column Variable(s)

At least one entry is need for the analysis to proceed.

Options Tab

Phi Coefficient

If this option is selected, the phi coefficient will be displayed.

Cramer's V

If this option is selected, the cramer's v coefficient will be displayed.

Contingency Coefficient

If this option is selected, the contingency coefficient will be displayed.

Expected Count

If this option is selected, the expected frequency will be displayed.

Row Percentages

If this option is selected, the row percentage will be displayed.

Column Percentages

If this option is selected, the column percentage will be displayed.

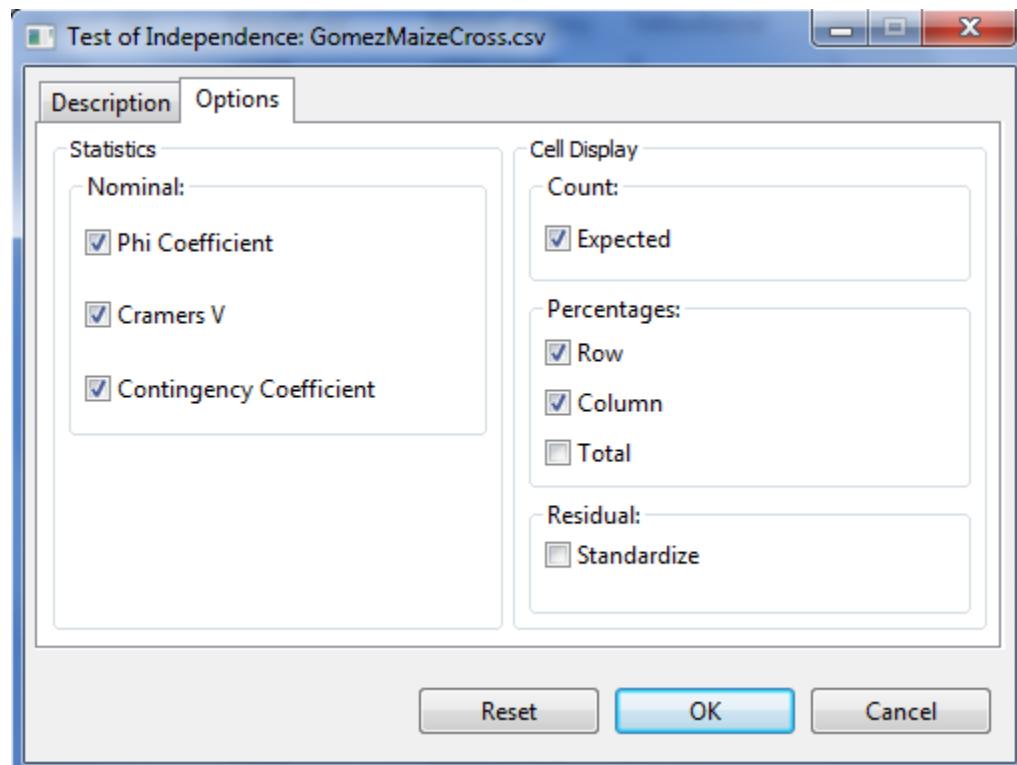
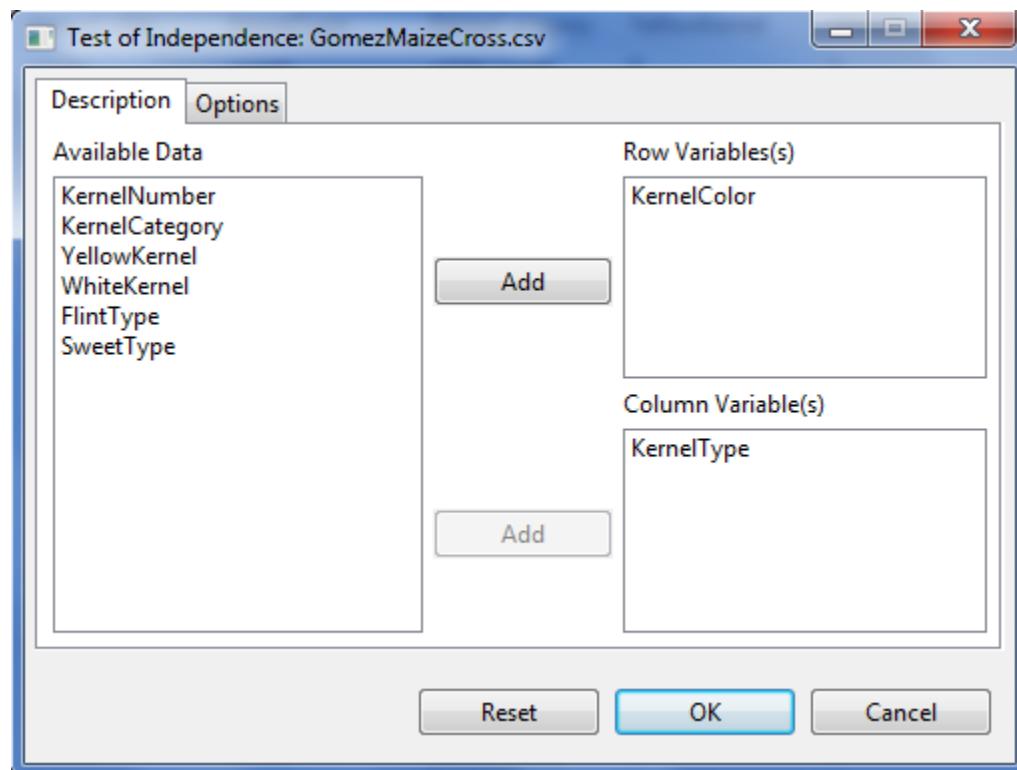
Total Percentages

If this option is selected, the total percentage will be displayed.

Standardize Residual

If this option is selected, the standardize residual will be displayed.

For the example, the completed dialog box is shown below:



- Click the **OK** button to perform the analysis. The **Test of Independent** dialog box will be minimized and STAR actives the **Output** page of the **Result Viewer** tab.

Sample text output as displayed in the **Output** page is shown below:

Table of KernelColor by KernelType

		KernelType		
		flint	sweet	Total
white	Obs Freq	112	34	146
	Expected Freq	110.9600	35.0400	146.0000
	% within KernelColor	76.7123	23.2877	100.0000
	% within KernelType	18.4211	17.7083	
	% of Total	14.0000	4.2500	18.2500
yellow	Obs Freq	496	158	654
	Expected Freq	497.0400	156.9600	654.0000
	% within KernelColor	75.8410	24.1590	100.0000
	% within KernelType	81.5789	82.2917	
	% of Total	62.0000	19.7500	81.7500
Total	Obs Freq	608	192	800
	Expected Freq	608.0000	192.0000	800.0000
	% within KernelType	100.0000	100.0000	
	% of Total	76.0000	24.0000	100.0000

Statistics for Table KernelColor by KernelType

Statistics	DF	Value	Prob
Pearson Chi-Square	1	0.0134	0.9079
Likelihood Ratio Chi-Square	1	0.0499	0.8232
Phi Coefficient		0.0482	
Contingency Coefficient		0.0482	
Cramer's V		0.0482	
Fisher's Exact Test		0.9147	

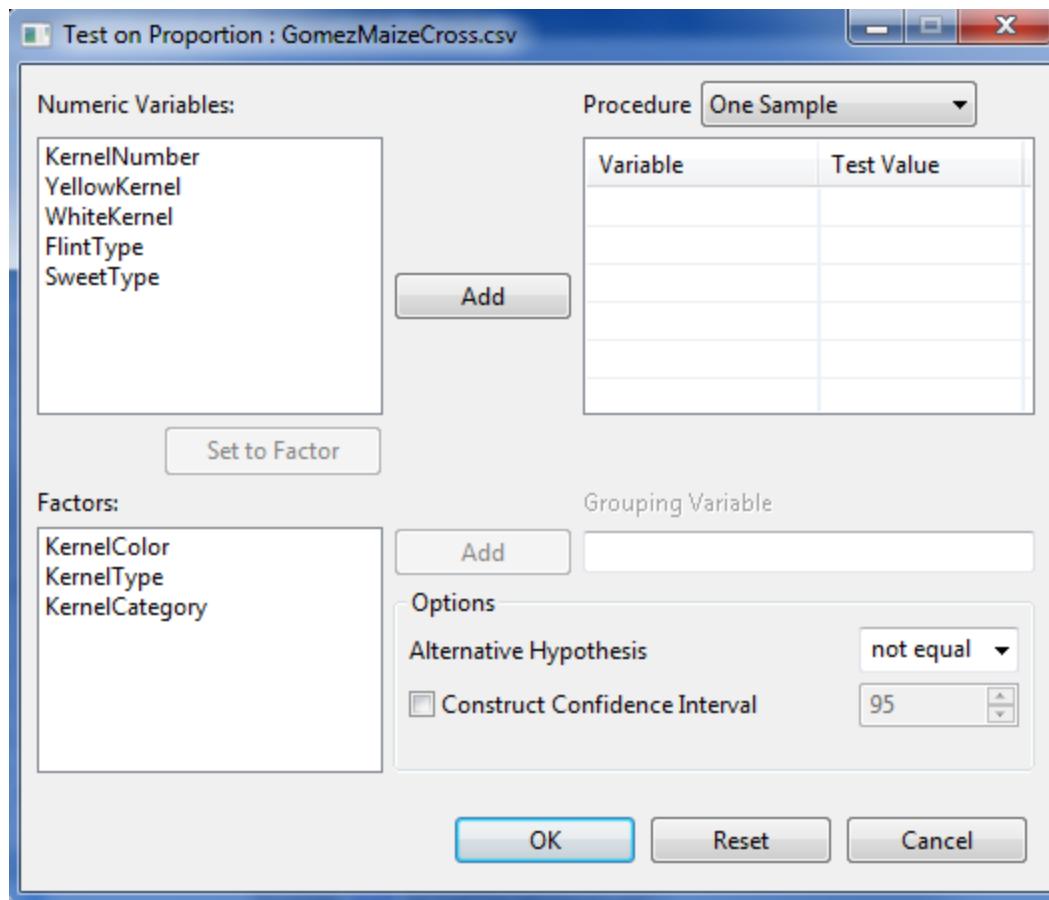
Test on Proportion

The steps to perform test on proportion are listed below:

- On the **Project Explorer**, double-click the file to be used for the analysis to open and view it in the Data Viewer tab.

For the example, using the project named *MyProject*, import the data *GomezMaizeCross* from the package. To import the data, see *Importing from Package* section of this user's manual.

- Click **Analyze | Test on Proportion ...** from the main window. The **Test on Proportion** dialog box will appear as shown below:



- Specify the required field and appropriate options for the analysis.

Procedure

There are three available procedures available: *One Sample* (default value), *Two Related Samples* and *Independent Sample*.

Variable

At least one entry is need for the analysis to proceed. Entries for this list box should come from the **Numeric Variable** list box.

Test Value

For every variable entered in the table, a default test value is specified. User can change the value by typing a value inside the spin box or by pressing the up-arrow key to increment the value, down-arrow key, otherwise. Valid value is between 0 to 1.

Grouping Variable

This field is required and visible if the procedure is *Independent Samples* is chosen. Entries for this list box should come from the **Factors** list box.

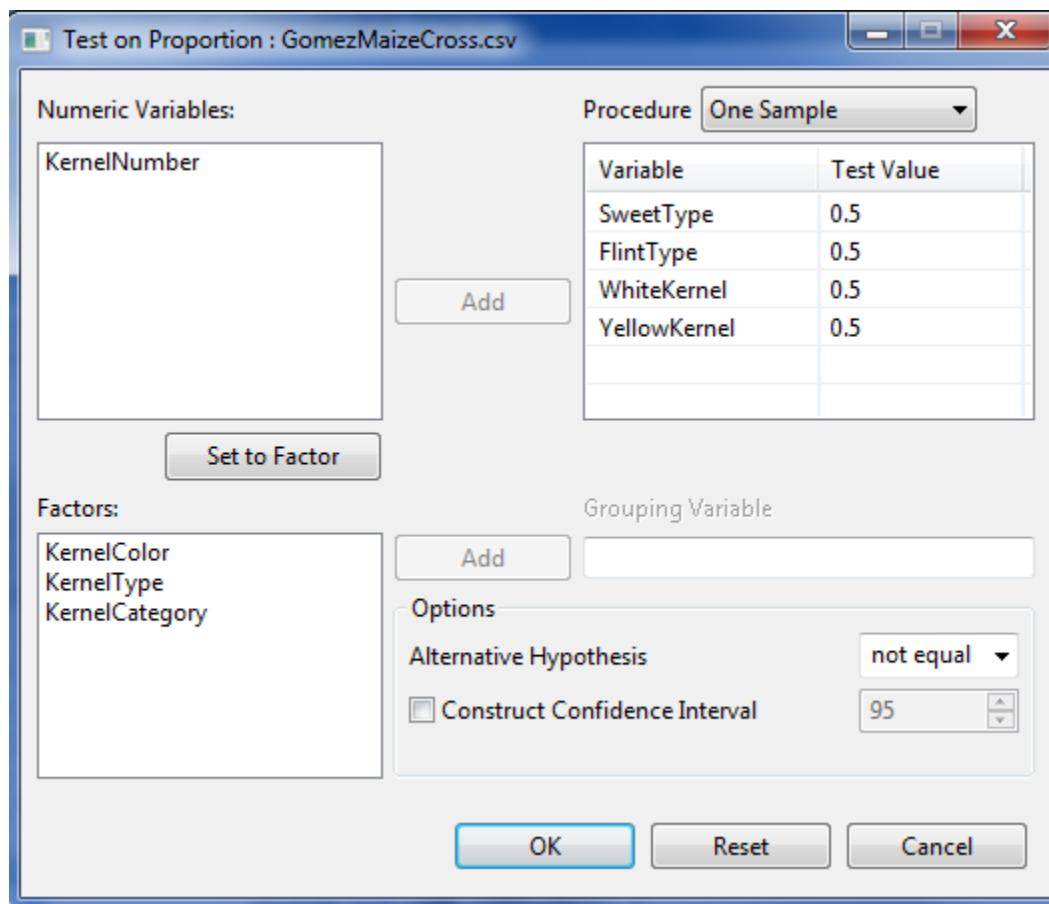
Alternative hypothesis

There are three available options: *less*, *greater* and *not equal* (default value).

Construct Confidence Interval

This option is available only if the procedure chosen is either *One Sample* or *Independent Sample*. If this option is selected, a confidence interval will be constructed.

For the example, the completed dialog box is illustrated below:



- Click the **OK** button to perform the analysis. The **Test on Proportion** dialog box will be minimized and STAR actives the **Output** page of the **Result Viewer** tab.

Sample output of the analysis as displayed in the Output page is shown below.

Summary

Variable	Num Success	Num Trial	Proportion
SweetType	192	800	0.2400
FlintType	608	800	0.7600
WhiteKernel	146	800	0.1825
YellowKernel	654	800	0.8175

Test on One Proportion

Variable	Procedure	TestValue	Statistics	Prob
SweetType	Chi-Square	0.5000	216.32	0.0000
SweetType	Exact Binomial	0.5000	192.00	0.0000
SweetType	Approx Z	0.5000	-14.71	0.0000
FlintType	Chi-Square	0.5000	216.32	0.0000
FlintType	Exact Binomial	0.5000	608.00	0.0000
FlintType	Approx Z	0.5000	14.71	0.0000
WhiteKernel	Chi-Square	0.5000	322.58	0.0000
WhiteKernel	Exact Binomial	0.5000	146.00	0.0000
WhiteKernel	Approx Z	0.5000	-17.96	0.0000
YellowKernel	Chi-Square	0.5000	322.58	0.0000
YellowKernel	Exact Binomial	0.5000	654.00	0.0000
YellowKernel	Approx Z	0.5000	17.96	0.0000

* alternative hypothesis = 'two.sided'

Analysis of Variance

The Analysis of Variance is a statistical technique which partitions the total variation into explained variation and unexplained variation.

The **Analysis of Variance submenu** can be used to perform analysis of variance for data from experimental designs with single error (e.g., RCB) and with 2 or more errors (e.g., Split Plot).

The Analysis of Variance in STAR uses fixed model and can be used for balanced data set. For data set with less than 10% missing observations, STAR can still perform the analysis of variance by first estimating the missing observations.

Treatment means or means of the treatment combination will be displayed depending on the result of the analysis of variance. If the analysis is performed on single factor and the treatment effect is not significant, the table of means is displayed. If the analysis is performed on multi-factor experiment and the highest interaction is not significant, the mean of the treatment combination are displayed.

Depending on the results of the analysis of variance, pairwise comparison means will be automatically generated for all effects that are significant using one applicable pairwise comparison procedure. If the factor being compared has at most 5 levels, the default pairwise comparison procedure used in STAR is the Least Significant Difference (LSD) test; otherwise the Honestly Significant Difference (HSD) or Tukey's test is used. Aside from LSD and HSD, Duncan's Multiple Range test, Student Newmann-Keul's test and Scheffe's test maybe also be requested.

Boxplot of the response variable and two diagnostic plots are automatically displayed in the *Graph* page of the **Result Viewer** tab. The *Residuals vs. Fitted* is for assessing the distribution of the residuals. An ideal plot should reveal that the points are distributed around 0. The residuals should not be affected by the size of the fitted values. Problematic data may result to a plot wherein the points increase as the fitted values increase, thus forming a “funnel-shaped” distribution. This will indicate a violation of the

homogeneity of variances requirement for analysis of variance. The *Normal Q-Q* plot is used for assessing normality. The points should lie about the line.

Contrast analysis maybe requested in this menu. There are three available contrast analyses that maybe request for each factor, namely: compare with control, orthogonal polynomial contrast and user specified contrast.

Completely Randomized Design

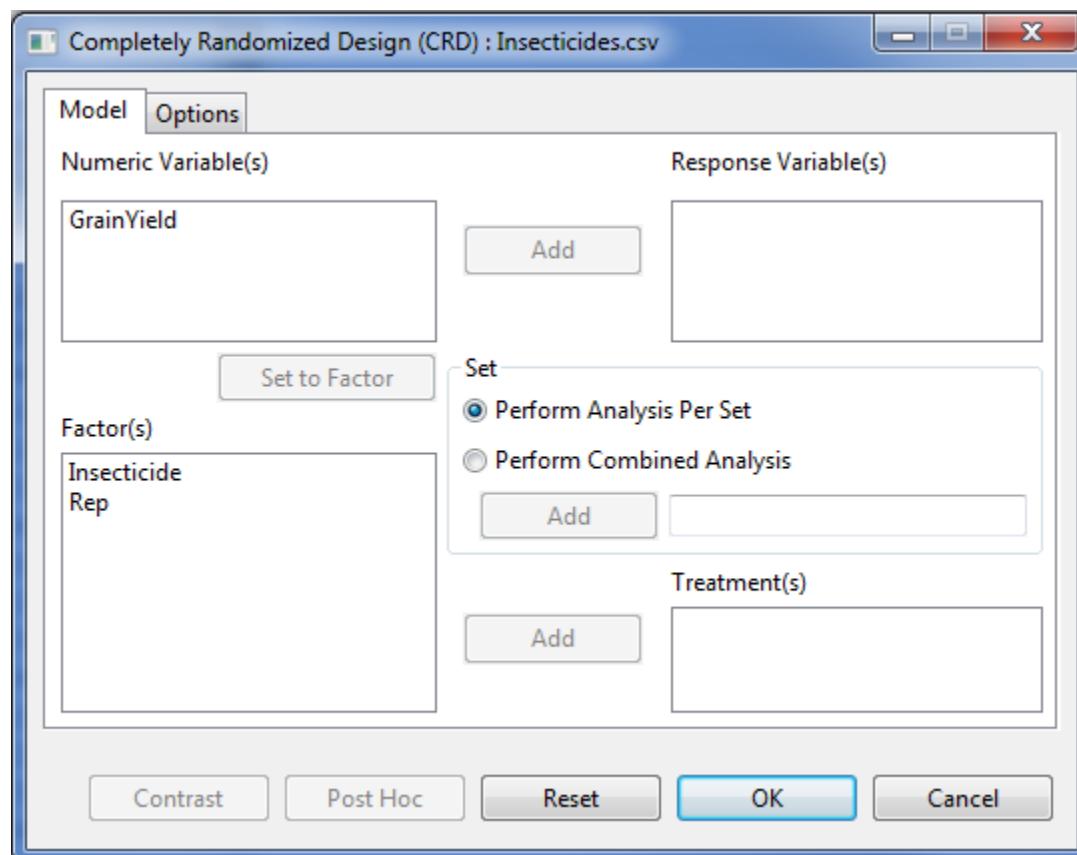
This submenu can be used to perform analysis of variance for single or multi factor experiment.

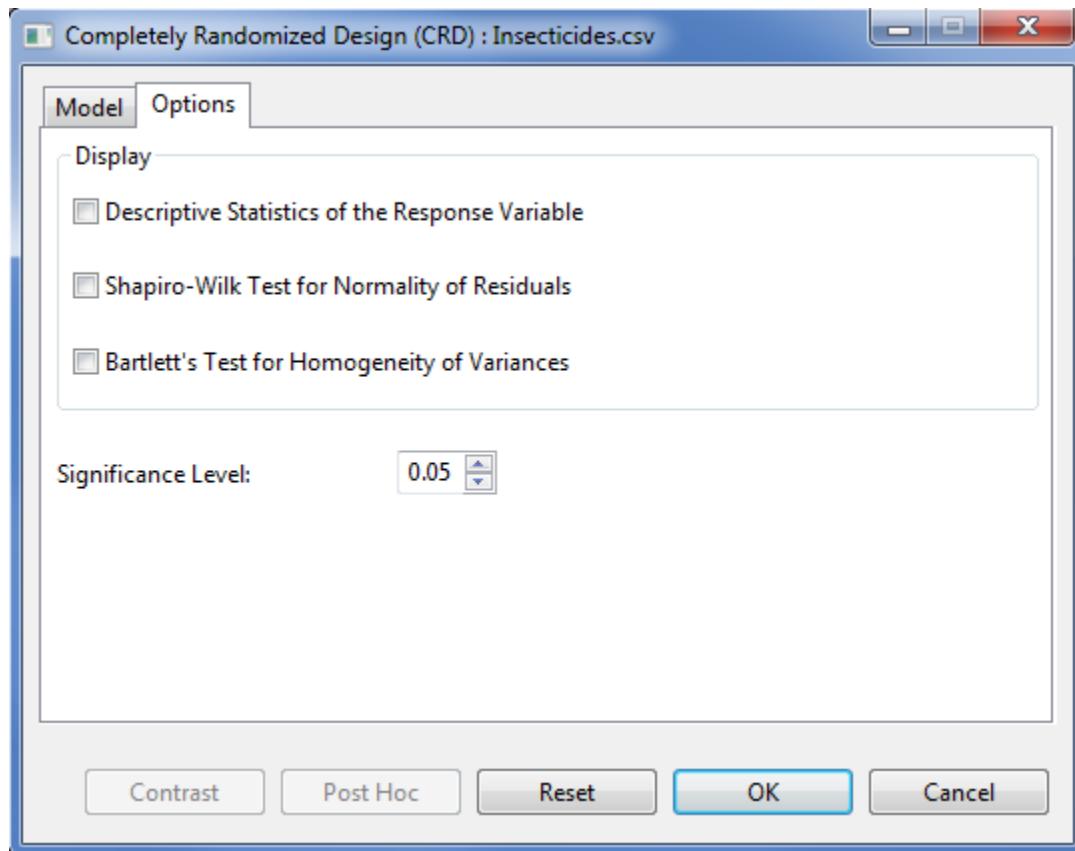
The steps to perform the analysis are listed below:

- On the **Project Explorer**, double-click the file to be used for the analysis to open and view it in the Data Viewer.

For the example, using the project named *MyProject*, import the data *Insecticides* from package. To import the data from the package, see *Importing from Package* section of this user's manual.

- Click **Analyze | Analysis of Variance | Completely Randomized Design...** from the main window. The **Completely Randomized Design** dialog box will appear as below:





- Specify the required field and appropriate options for the analysis.

Model Tab

Response Variable(s)

For the analysis to proceed, at least one item should be entered in the list box. Only items from the **Numeric Variable(s)** can be added in this dialog box.

Set

There are two options available, *perform analysis per set* (default) and *perform combined analysis*. If default option is selected and a **Set** variable is specified, STAR will perform analysis for each level of the **Set** variable. If the default option is selected and no **Set** variable is specified, STAR will perform the analysis as if the entire data came from only one set variable. If *perform combined analysis* is selected, a **Set** variable with at least two levels must be specified. The item should come from the **Factor(s)** list box.

Factor(s)

At least one item should be added in this list box and should come from the **Factor(s)** list box.

Options Tab

Descriptive Statistics of the Response Variable

If this option is selected, a summary table with number of non-missing observations, minimum, maximum, mean and standard deviation of the response variable will be displayed.

Shapiro-Wilk Test for Normality of Residuals

If this option is selected, test for normality of residuals using Shapiro-Wilk will be displayed, if the number of observation is between 3 and 5000.

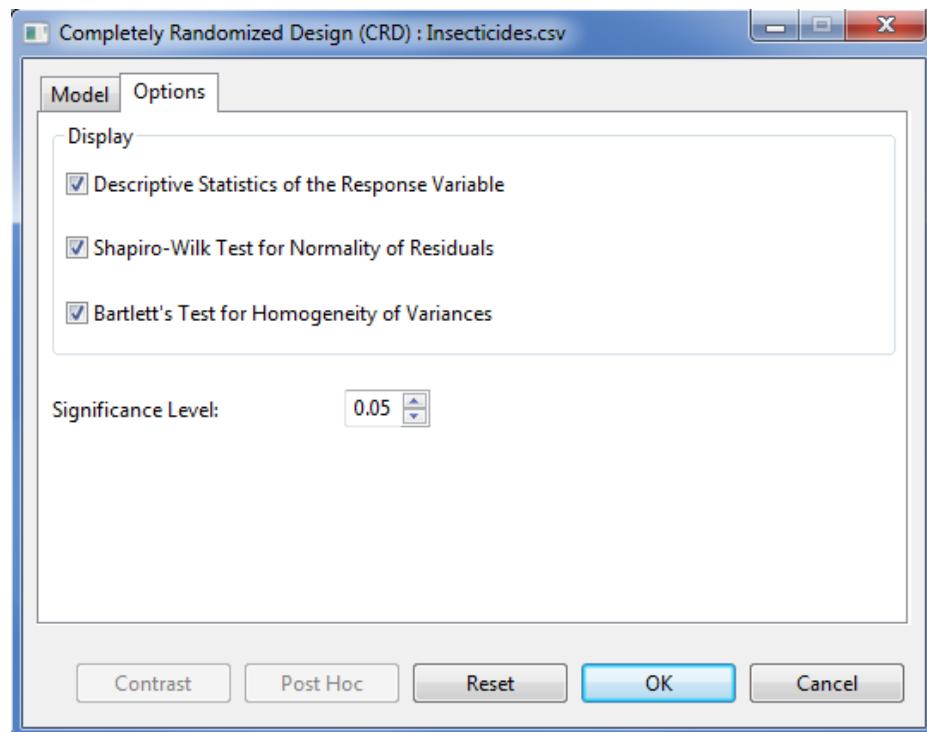
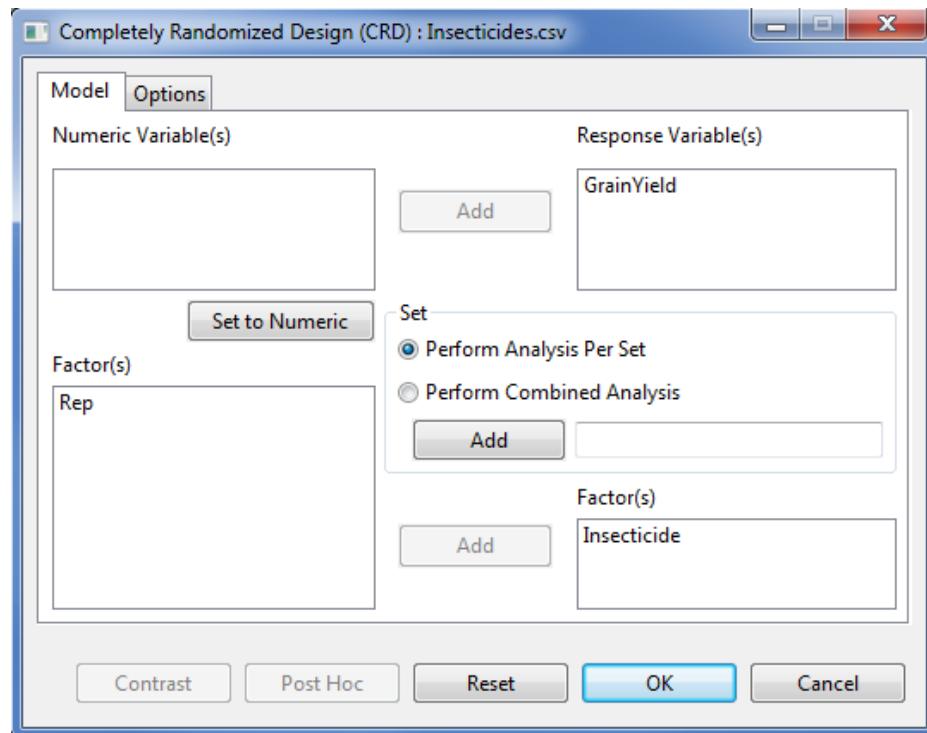
Bartlett's Test for Homogeneity of Variances

This option is visible if *perform analysis per set* is selected. If this option is selected, test for homogeneity of variances using Bartlett's Test will be displayed.

Significance Level

This will be used to determine if the treatment effects and interaction effects are significant in the Analysis of Variance. This is also the level of significance to be used when pairwise mean comparison is performed. Its default value is 0.05. The user can change this value by specifying a numeric value from 0 to 1.

For the example, the completed **Model** tab and **Option** tab should appear as shown below:



- Click **OK** button to perform the analysis. The **Completely Randomized Design** dialog box will be minimized and STAR activates the **Output** page of the **Result Viewer** tab.

Sample text output is shown below.

```
Analysis of Variance
Completely Randomized Design
=====
ANALYSIS FOR RESPONSE VARIABLE: GrainYield
=====

Summary Information
-----
FACTOR      NO. OF LEVELS   LEVELS
-----
Insecticide    7           Azodin, Control, ..., Dol-Mix (2kg)
-----
Number of Observations Read and Used: 28

Descriptive Statistics
-----
Variable     N_Obs     Min     Max      Mean     StdDev
-----
GrainYield    28       1077    3366    2039.64   529.76
-----

Test for Homogeneity of Variances
-----
Method      DF   Statistics     Prob
-----
bartlett    6      5.56    0.4744
-----

Test for Normality
-----
Variable      Method      Statistics     Prob
-----
GrainYield_resid  Shapiro-Wilk    0.9857    0.9587
-----

ANOVA TABLE
Response Variable: GrainYield
-----
Source        DF   Sum of Square   Mean Square   F Value   Pr > F
-----
Insecticide    6      5587174.9286   931195.8214   9.83    0.0000
Error         21     1990237.5000   94773.2143
Total         27     7577412.4286
-----

Summary Statistics
-----
CV(%)  GrainYield Mean
-----
15.09    2039.64
-----
```

```

Standard Errors
-----
Effects      StdErr
-----
Insecticide   217.68
-----
Pairwise Mean Comparison of Insecticide

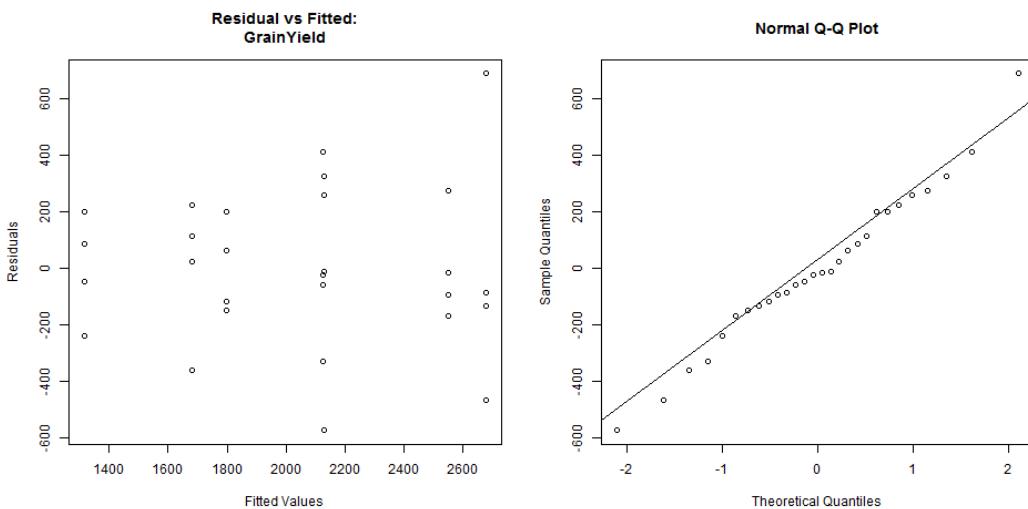
Tukeys's Honest Significant Difference (HSD) Test

Alpha          0.05
Error Degrees of Freedom    21
Error Mean Square     94773.2143
Critical Value       4.5973
Test Statistics      707.6456

Summary of the Result:
-----
Insecticide      means      N group
-----
Azodin          2128.00    4 ab
Control         1316.00    4 c
DDT + phi-BHC  2551.75    4 a
Dimercon-Boom  1796.00    4 bc
Dimercon-Knap  1681.00    4 bc
Dol-Mix (1kg)  2126.75    4 ab
Dol-Mix (2kg)  2678.00    4 a
-----
Means with the same letter are not significantly different.

```

Sample graphical output displayed in the **Graph** page.



Additional Options

If there are still modifications to be made, the following option buttons may be used:

- **Post Hoc**

Use this option if other pairwise comparison procedures, other than what was presented in the **Output** page, are desired. There are five pairwise mean comparison procedure available, namely: Least Significant Difference Test, Duncan Multiple Range Test, Tukey's Honest Significant Test, Student Newmann-Keul's Test and the Scheffe's Test. This button will be disabled if *F*-tests conducted using ANOVA yielded results that are not significant. Use of this button will be discussed in Pairwise Comparison section on this module.

- **Contrast**

This button will be enabled if there is at least one factor that has more than two levels. Use of this button will be discussed in Partitioning Sum of Squares section of this module.

Randomized Complete Block Design

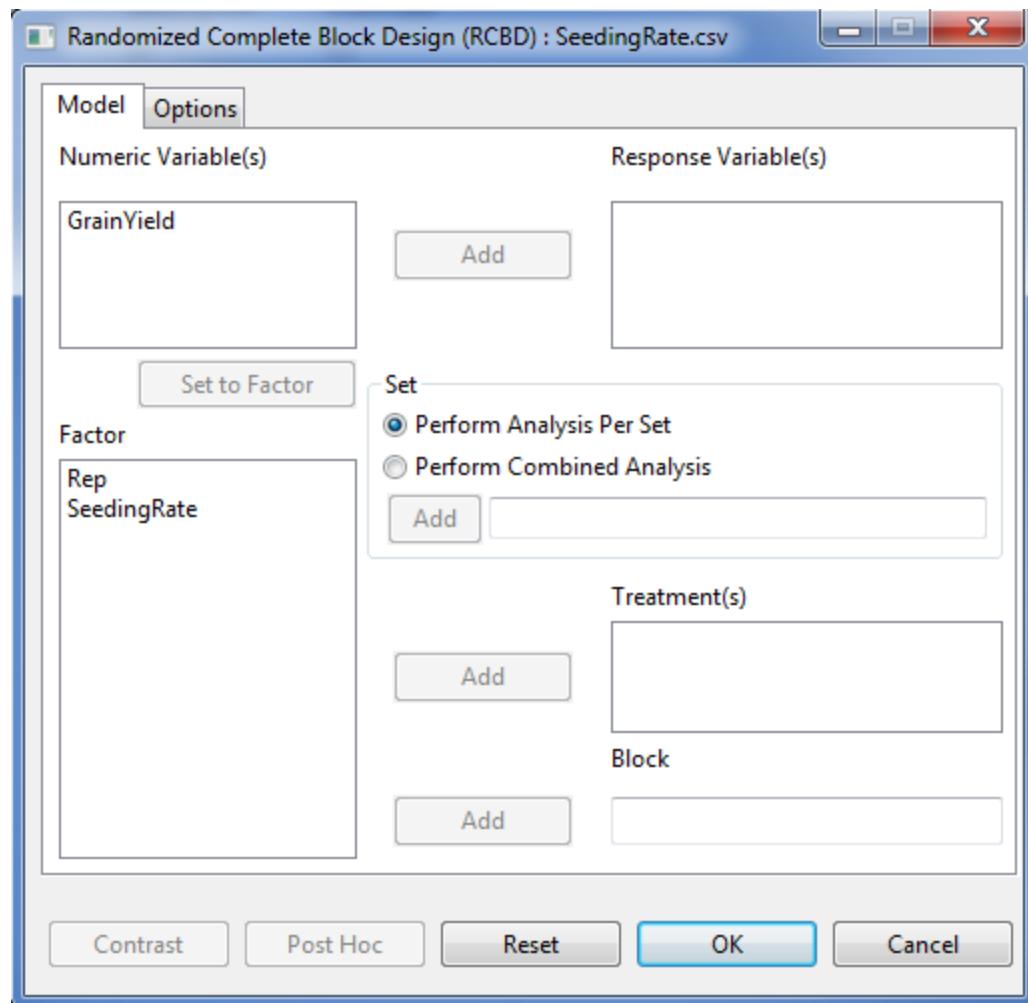
This submenu can be used to perform analysis of variance for single or multi factor experiment.

The steps to perform the analysis are listed below:

- On the **Project Explorer**, double-click the file to be used for the analysis to open and view it in the Data Viewer.

For the example, using the project named *MyProject*, import the data *SeedingRate* from package. To import that data, see *Importing from Project* section of this user's manual.

- From the main window of STAR click **Analyze | Analysis of Variance | Randomized Complete Block Design....** The **Randomized Complete Block Design** dialog box will appear.



- Specify the required field and appropriate options for the analysis.

Model Tab

Response Variable(s)

For the analysis to proceed, at least one item should be entered in the list box. Only Items from the **Numeric Variable(s)** can be added in this dialog box.

Set

There are two options available, *perform analysis per set* (default option) and *perform combined analysis*. If default option is selected and a **Set** variable is specified, STAR will perform analysis for each level of the **Set** variable. If the default option is selected and the **Set** variable is not specified, STAR will perform the analysis as if the entire data came from only one site. If **perform combined analysis is selected**, a Set variable must be specified.

Factor(s)

At least one item should be added in this list box and should come from the **Factor(s)** list box.

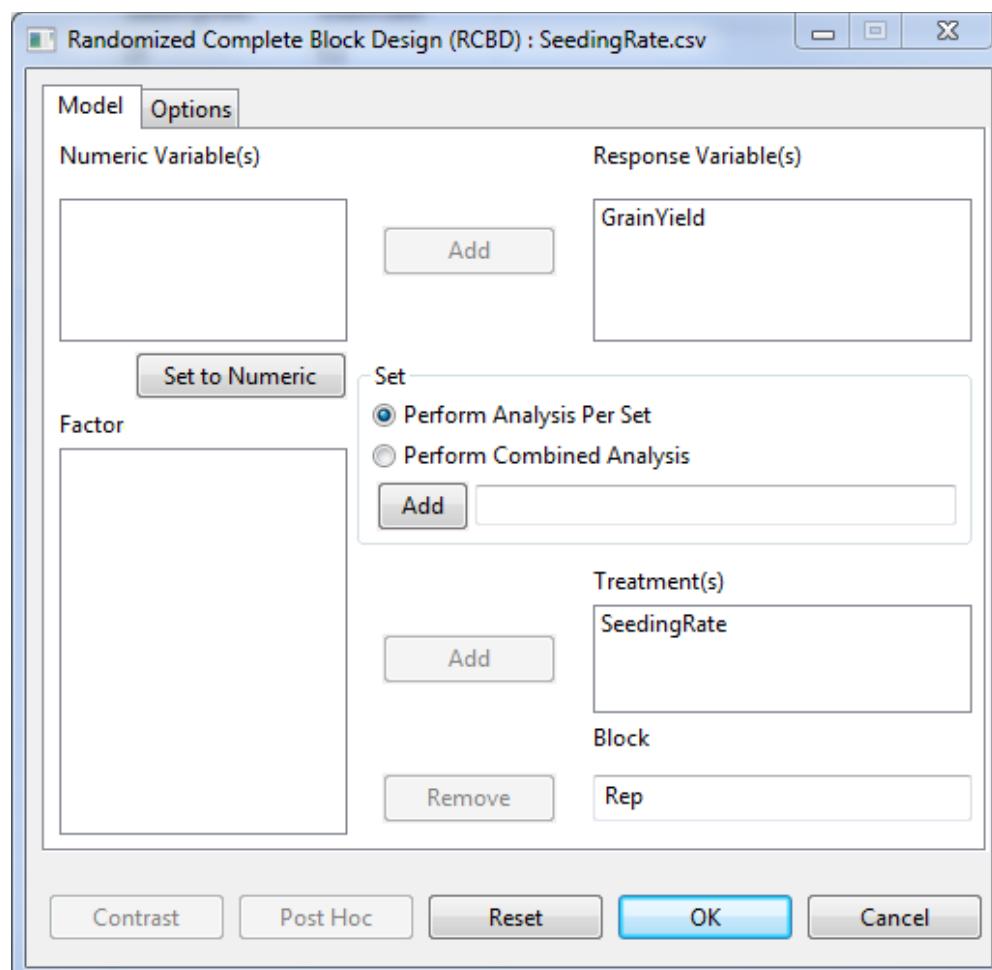
Block

Only one item can be added in this field and should come from the **Factor(s)** list box.

Options Tab

This tab lets the user identify additional output to be displayed and set the level of significance to be used. To know more about the options in detail, see the discussion under *Analysis of Variance > Completely Randomized Design > Options tab* of this user's manual.

For the example, the completed **Model** tab should appear as illustrated below:



- Click **OK** button to perform the analysis. The **Randomized Complete Block Design (RCBD)** dialog box will be minimized and STAR activates the **Output Viewer** tab and the **Graph Viewer** tab.

Sample text output of the analysis displayed in the Output Viewer tab is shown below:

```
Analysis of Variance
Randomized Complete Block Design

=====
ANALYSIS FOR RESPONSE VARIABLE: GrainYield
=====

Summary Information
-----
FACTOR      NO. OF LEVELS   LEVELS
-----
SeedingRate  6            25, 50, ..., 150
Rep          4            1, 2, 3, 4
-----
Number of Observations Read and Used: 24

Descriptive Statistics
-----
Variable     N_Obs    Min    Max    Mean    StdDev
-----
GrainYield   24      2.80    6      4.65    0.7735
-----

Test for Homogeneity of Variances
-----
Method      DF   Statistics     Prob
-----
bartlett    5      4.76    0.4462
-----

Test for Normality
-----
Variable       Method       Statistics     Prob
-----
GrainYield_resid  Shapiro-Wilk    0.9346    0.1235
-----
```

ANOVA TABLE

Response Variable: GrainYield

Source	DF	Sum of Square	Mean Square	F Value	Pr > F
Rep	3	1.7667	0.5889	4.87	0.0147
SeedingRate	5	10.1800	2.0360	16.84	0.0000
Error	15	1.8133	0.1209		
Total	23	13.7600			

Summary Statistics

CV (%)	GrainYield	Mean
7.48		4.65

Standard Errors

Effects	StdErr
Rep	0.2007
SeedingRate	0.2459

Pairwise Mean Comparison of SeedingRate

Tukey's Honest Significant Difference (HSD) Test

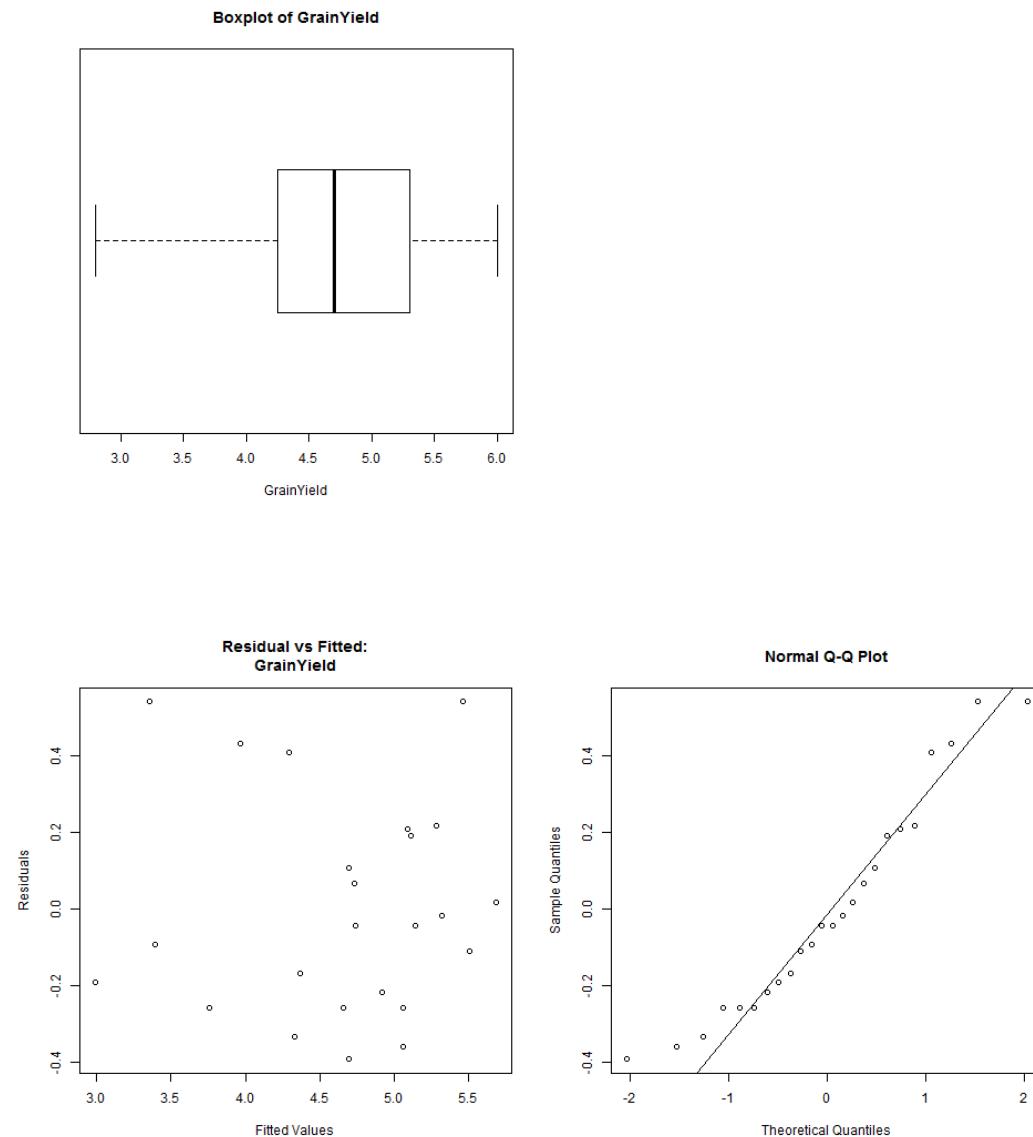
Alpha	0.05
Error Degrees of Freedom	15
Error Mean Square	0.1209
Critical Value	4.5947
Test Statistics	0.7988

Summary of the Result:

SeedingRate	means	N	group
25	5.12	4	ab
50	5.08	4	ab
75	5.30	4	a
100	4.35	4	b
125	4.67	4	ab
150	3.38	4	c

Means with the same letter are not significantly different.

Sample graphical output of the analysis displayed in the Graph Viewer tab is shown below:



Modifications can still be made on the analysis submitted. To know more about the modification that can be made, see the discussion under *Analysis of Variance > Completely Randomized Design > Additional Options* of this user's manual.

Latin Square Design

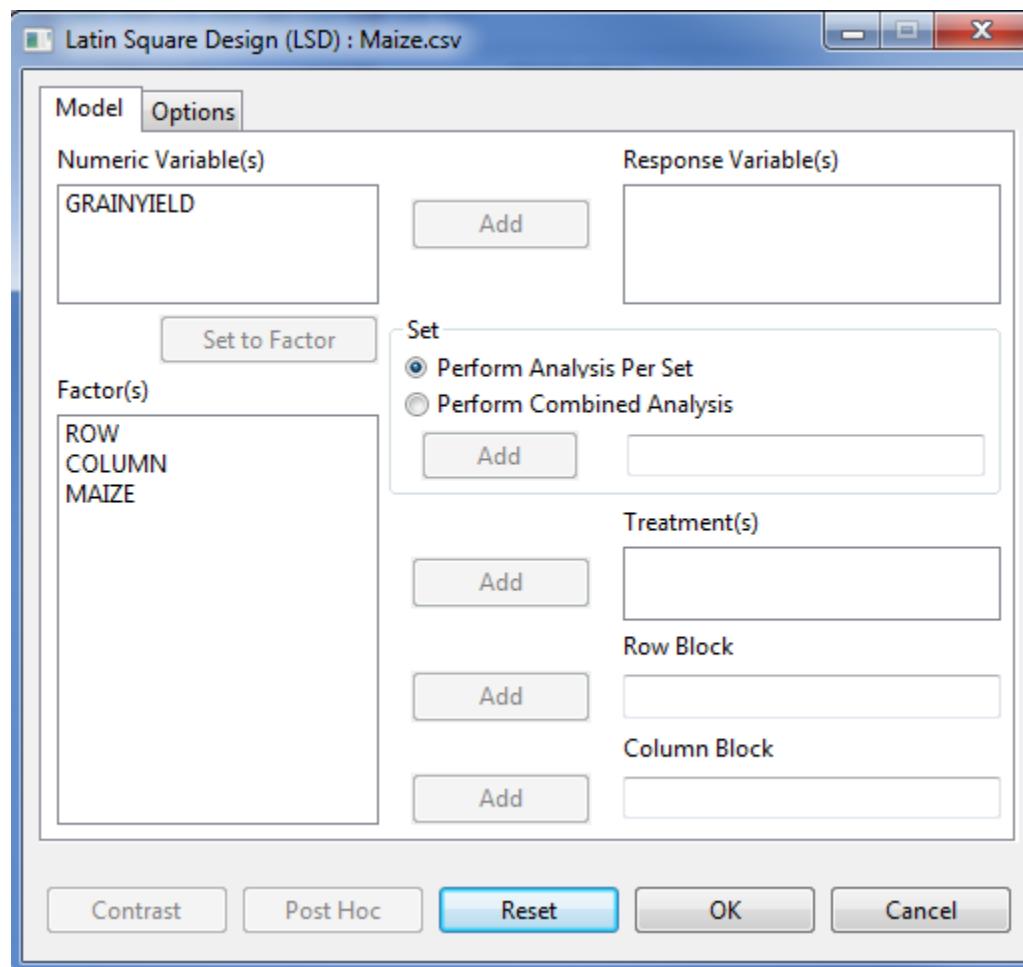
This submenu can be used to perform analysis of variance for single or multi factor experiment.

The steps to perform the analysis are listed below:

- On the **Project Explorer**, double-click the file to be used for the analysis to open and view it in the Data Viewer.

For the example, using the project named *MyProject*, import the data *Maize* from package. To import that data, see *Importing from Package* section of this user's manual.

- From the main window of STAR click **Analyze | Analysis of Variance | Latin Square Design....** The **Latin Square Design** dialog box will appear.



- Specify the required field and appropriate options for the analysis.

Model Tab

Response Variable(s)

For the analysis to proceed, at least one item should be entered in the list box. Only Items from the **Numeric Variable(s)** can be added in this dialog box.

Set

There are two options available, *perform analysis per set* (default option) and *perform combined analysis*. If default option is selected and a **Set** variable is specified, STAR will perform analysis for each level of the **Set** variable. If the default option is selected and the **Set** variable is not specified, STAR will perform the analysis as if the entire data came from only one site. If **perform combined analysis is selected**, a Set variable must be specified.

Factor(s)

At least one item should be added in this list box and should come from the **Factor(s)** list box.

Row Block

Only one item can be added in this field and should come from the **Factor(s)** list box.

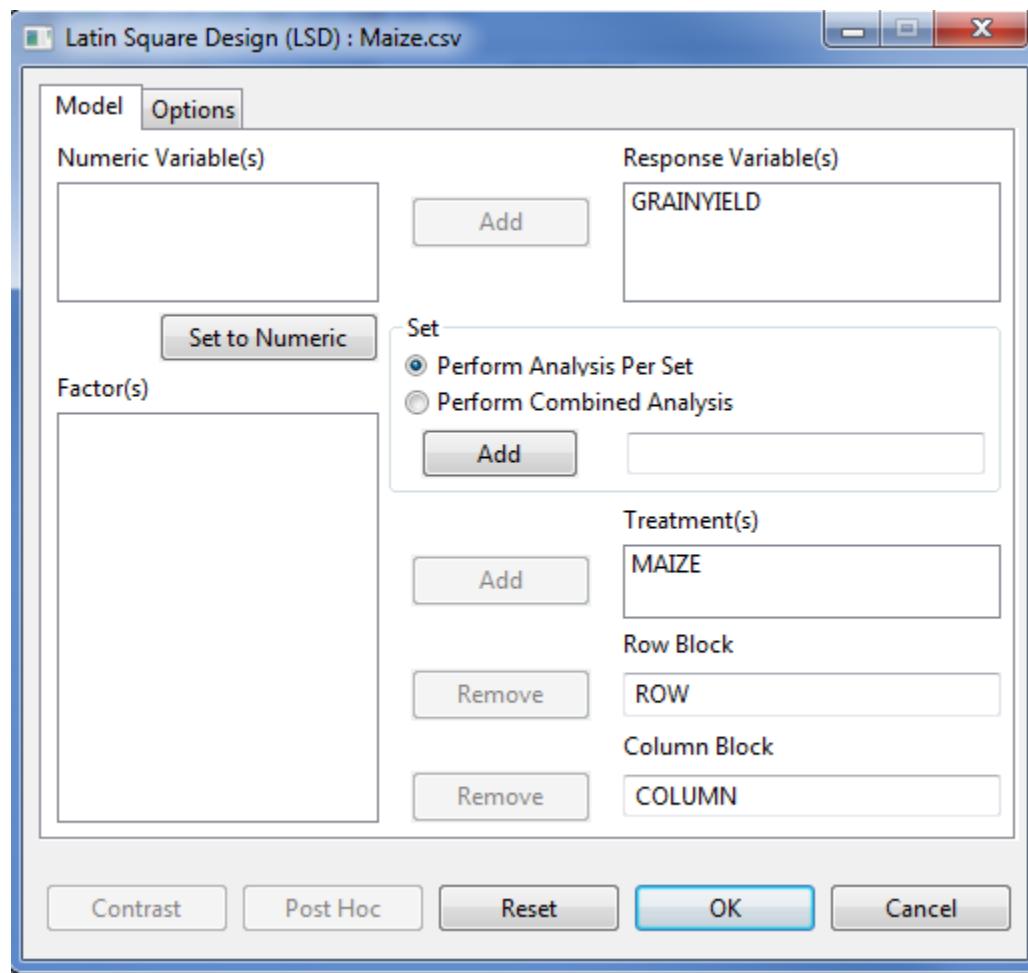
Column Block

Only one item can be added in this field and should come from the **Factor(s)** list box.

Options Tab

This tab lets the user identify additional output to be displayed and set the level of significance to be used. To know more about the options in detail, see the discussion under *Analysis of Variance > Completely Randomized Design > Options tab* of this user's manual.

For the example, the completed **Model** tab should appear as illustrated below:



- Click **OK** button to perform the analysis. The **Latin Square Design** dialog box will be minimized and STAR activates the **Output Viewer** tab and the **Graph Viewer** tab.

Sample text output of the analysis displayed in the Output Viewer tab is shown below:

```
Analysis of Variance
Latin Square Design
=====
ANALYSIS FOR RESPONSE VARIABLE: GRAINYIELD
=====
Summary Information
-----
FACTOR    NO. OF LEVELS   LEVELS
-----
MAIZE      4              A, B, C, D
```

```
ROW      4          1, 2, 3, 4
COLUMN   4          1, 2, 3, 4
-----
Number of Observations Read and Used: 16

Descriptive Statistics
-----
Variable    N_Obs     Min     Max     Mean    StdDev
-----
GRAINYIELD    16  0.6600  1.67    1.34    0.3070
-----

Test for Homogeneity of Variances
-----
Method      DF  Statistics     Prob
-----
bartlett    3      3.81    0.2825
-----

Test for Normality
-----
Variable        Method       Statistics     Prob
-----
GRAINYIELD_resid  Shapiro-Wilk    0.9250  0.2026
-----

ANOVA TABLE
Response Variable: GRAINYIELD
-----
Source      DF  Sum of Square  Mean Square   F Value   Pr > F
-----
ROW         3      0.0302      0.0101      0.47    0.7170
COLUMN      3      0.8273      0.2758     12.77    0.0051
MAIZE        3      0.4268      0.1423      6.59    0.0251
Error        6      0.1296      0.0216
Total        15     1.4139
-----

Summary Statistics
-----
CV(%)  GRAINYIELD Mean
-----
11.01      1.34
-----

Standard Errors
-----
Effects    StdErr
-----
ROW        0.1039
COLUMN    0.1039
MAIZE      0.1039
-----

Pairwise Mean Comparison of MAIZE
```

Least Significant Difference (LSD) Test

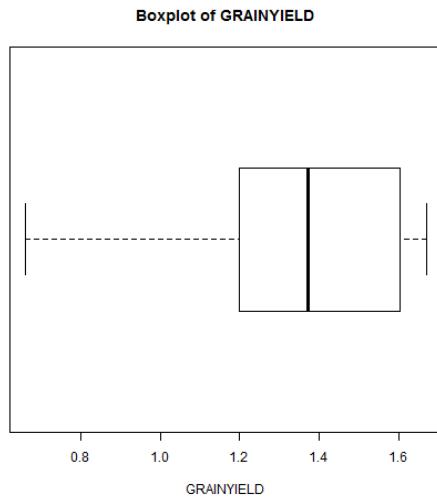
Alpha	0.05
Error Degrees of Freedom	6
Error Mean Square	0.0216
Critical Value	2.4469
Test Statistics	0.2543

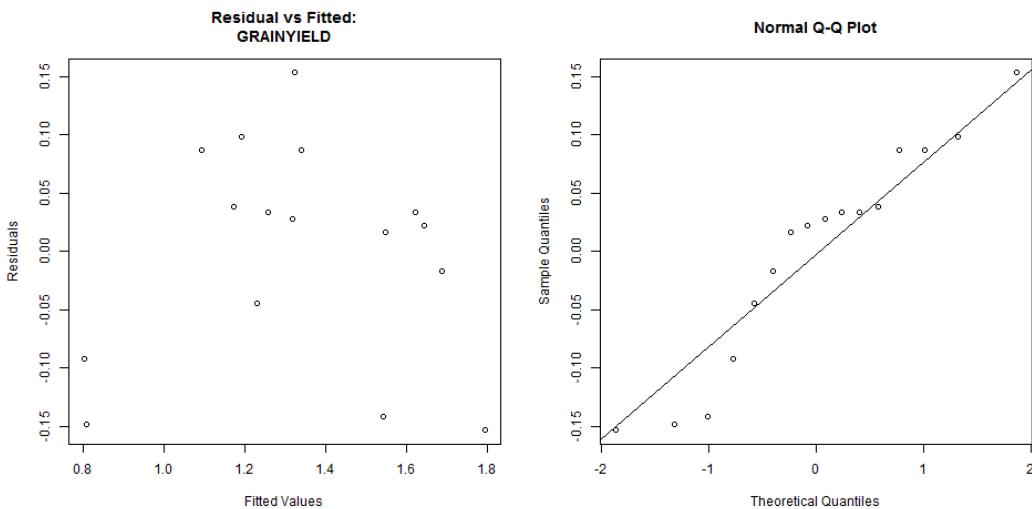
Summary of the Result:

MAIZE	means	N	group
A	1.46	4	a
B	1.47	4	a
C	1.07	4	b
D	1.34	4	a

Means with the same letter are not significantly different.

Sample graphical output of the analysis displayed in the Graph Viewer tab is shown below:





Modifications can still be made on the analysis submitted. To know more about the modification that can be made, see the discussion under *Analysis of Variance > Completely Randomized Design > Additional Options* of this user's manual.

Split Plot Design

This analysis can be performed for experiments where the main plot is arranged in completely randomized, randomized complete block or Latin square design.

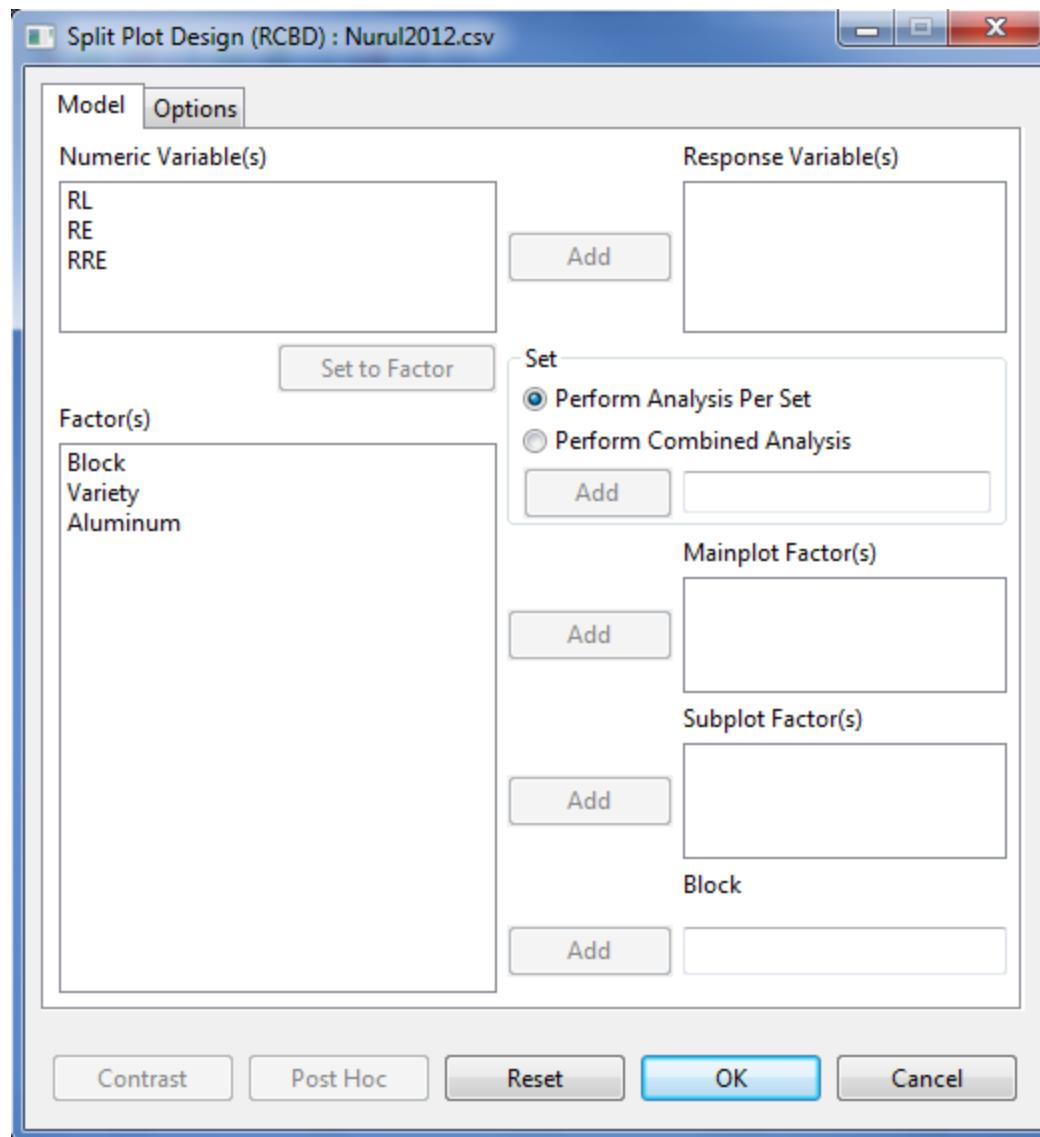
The steps to perform the Analysis of Variance using Split Plot Design are listed below:

- On the **Project Explorer**, double-click the file to be used for the analysis to open and view it in the Data Viewer.

For the example, using the project named *My Project*, import the data *Nurul2012* from the package. To import the data from the package, see *Importing from Package* section of this user's manual.

- From the main window of STAR click **Analyze | Analysis of Variance | Split Plot Design**. Choose the appropriate design for the main plot. The **Split Plot Design** dialog box will appear.

For the example, click **Analyze | Analysis of Variance | Split Plot Design | Randomized Complete Block Design ...** from the main window.



- Specify the required field and appropriate options for the analysis.

Model Tab

Response Variable(s)

For the analysis to proceed, at least one item should be entered in the list box. Only items from the **Numeric Variable(s)** can be added in this dialog box.

Set

There are two options available, *perform analysis per set* (default) and *perform combined analysis*. If default option is selected and a **Set** variable is specified, STAR will perform analysis for each level of the **Set** variable. If the default option is selected and no **Set** variable is specified, STAR will perform the analysis as if the

entire data came from only one set variable. If *perform combined analysis* is selected, a **Set** variable with at least two levels must be specified. The item should come from the **Factor(s)** list box.

Mainplot Factor(s)

At least one item should be added in this list box and should come from the **Factor(s)** list box.

Subplot Factor(s)

At least one item should be added in this list box and should come from the **Factor(s)** list box.

Replicate

Applicable only if completely randomized design is chosen. Only one item can be added in this field and should come from the **Factor(s)** list box.

Block

Applicable only if randomized complete block design is chosen. Only one item can be added in this field and should come from the **Factor(s)** list box.

Row Block

Applicable only if Latin square design is chosen. Only one item can be added in this field and should come from the **Factor(s)** list box.

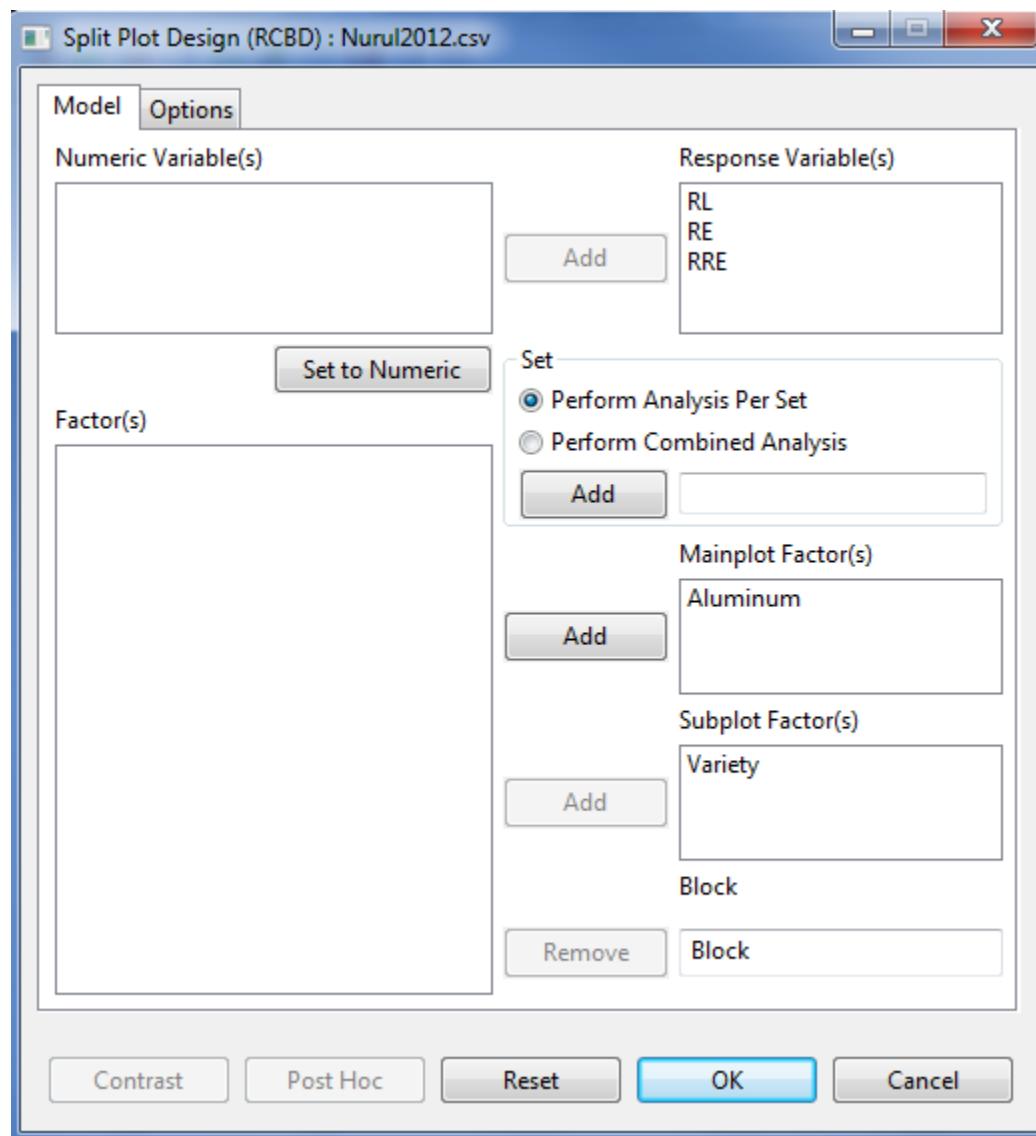
Column Block

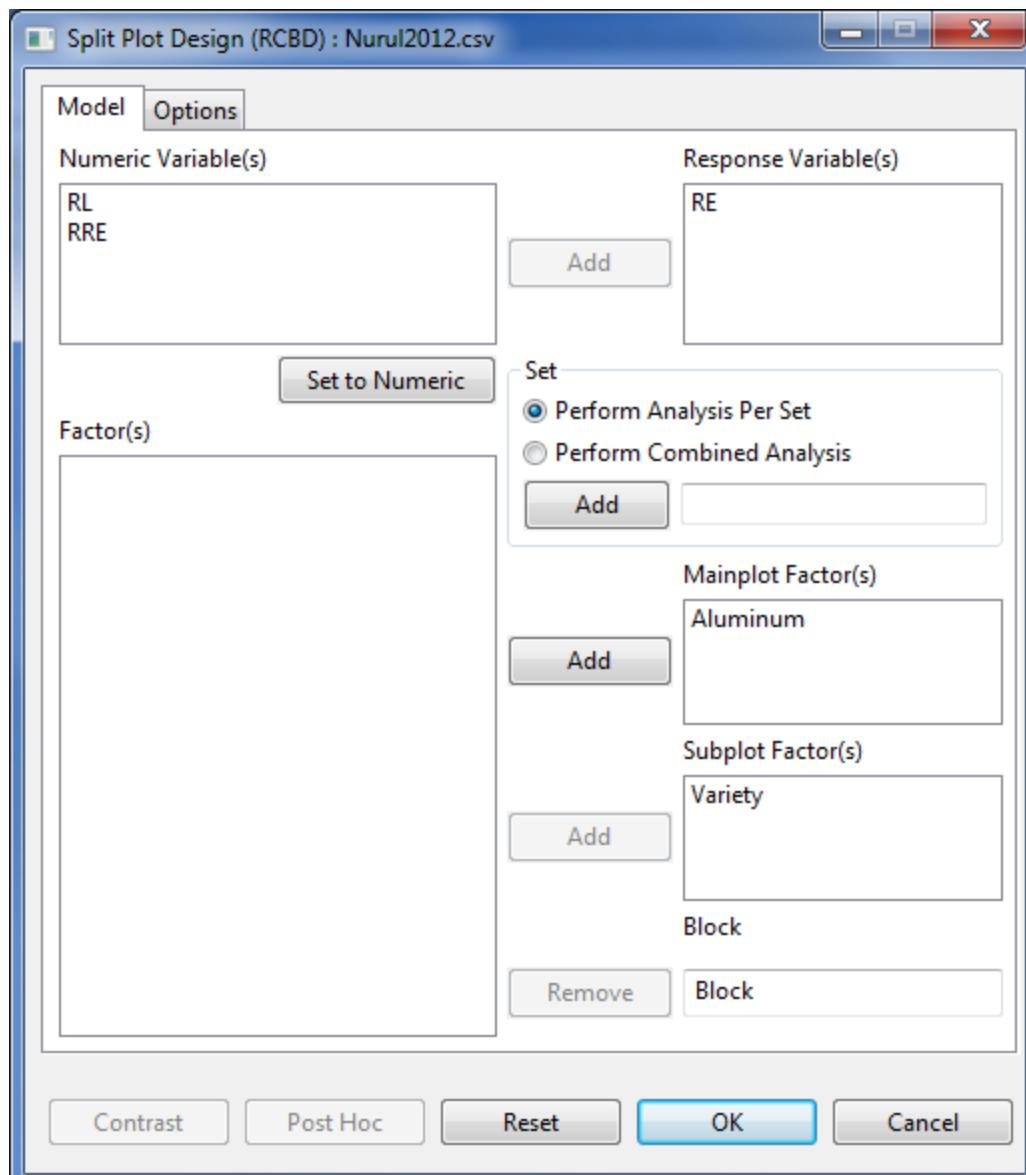
Applicable only if Latin square design is chosen. Only one item can be added in this field and should come from the **Factor(s)** list box.

Options Tab

This tab lets the user identify additional output to be displayed and set the level of significance to be used. To know more about the options in detail, see the discussion under *Analysis of Variance > Completely Randomized Design > Options tab* of this user's manual.

For the example, the completed **Model** tab should appear as illustrated:





- Click **OK** button to perform the analysis. The **Split Plot Design** dialog box will be minimized and STAR activates the **Output Viewer** tab and the **Graph Viewer** tab.

Sample text output of the analysis displayed in the Output Viewer tab is shown below:

```
Analysis of Variance
Split Plot in Randomized Complete Block Design
=====
ANALYSIS FOR RESPONSE VARIABLE: RE
=====

Summary Information
-----
FACTOR      NO. OF LEVELS   LEVELS
-----
Aluminum    4              0, 540, 750, 1300
Variety     8              Azucena112854, Azucena47125, ..., Pokalli
Block       2              I, II
-----
Number of Observations Read and Used: 64

Descriptive Statistics
-----
Variable   N_Obs      Min      Max      Mean     StdDev
-----
RE         64        13.62    107.62   55.93    23.38
-----
Test for Homogeneity of Variances
-----
Method      DF   Statistics      Prob
-----
bartlett   31        28.15    0.6136
-----
Test for Normality
-----
Variable   Method          Statistics      Prob
-----
RE_resid   Shapiro-Wilk    0.9926    0.9675
-----
ANOVA TABLE
Response Variable: RE
-----
Source        DF   Sum of Square   Mean Square   F Value   Pr > F
-----
Block         1      647.2572     647.2572     177.11    0.0009
Aluminum     3      11826.5606    3942.1869    1078.68    0.0000
Error(a)     3      10.9639      3.6546
Variety      7      17768.2497    2538.3214     64.04    0.0000
Aluminum:Variety 21      3085.8037    146.9430      3.71    0.0007
Error(b)     28      1109.9079     39.6396
Total        63      34448.7430
-----
```

Summary Statistics

CV(a) %	CV(b) %	RE Mean
3.42	11.26	55.93

Comparison of Aluminum at each level of Variety

Least Significant Difference (LSD) Test

Alpha	0.05
Error Degrees of Freedom	28
Error Mean Square	35.1415
Critical Value	2.0462
Test Statistic	12.1297

Summary:

Aluminum	N	Variety = Azucena112854 group	...
0	2	65.1400 a	...
540	2	54.9500 ab	...
750	2	44.6000 b	...
1300	2	23.0750 c	...

Means with the same letter are not significantly different

Comparison of Variety at each level of Aluminum

Tukeys's Honest Significant Difference (HSD) Test

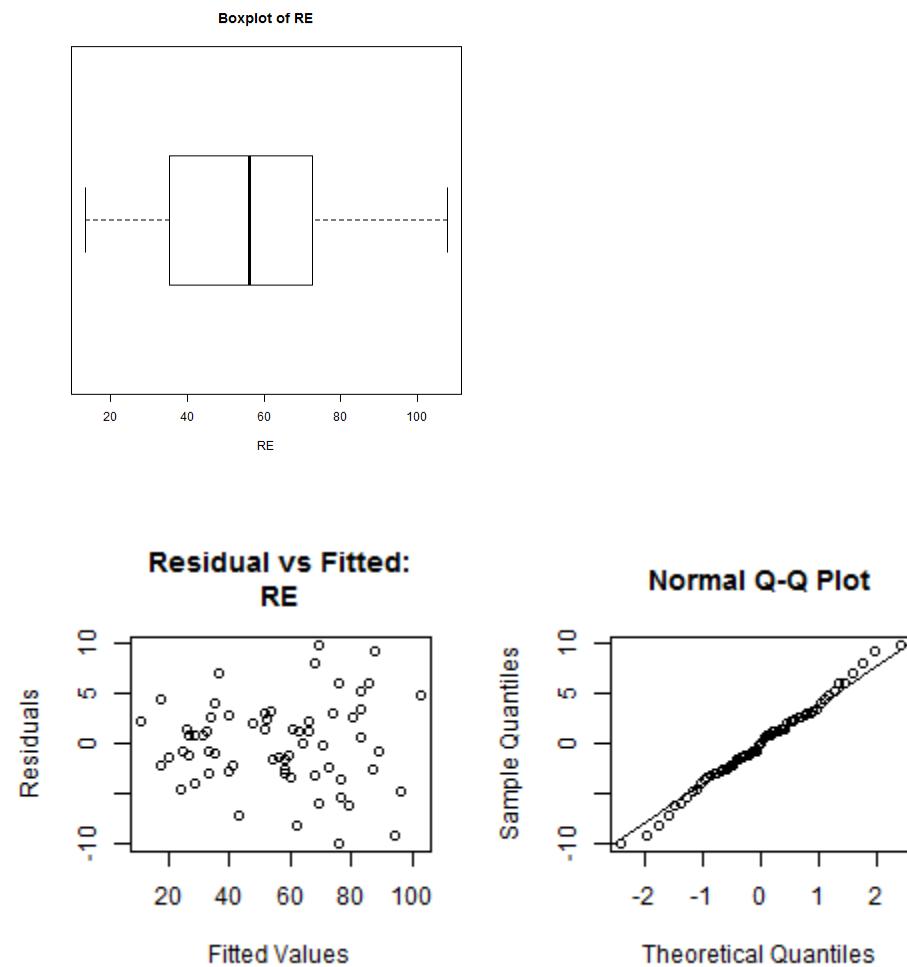
Alpha	0.05
Error Degrees of Freedom	28
Error Mean Square	39.6396
Critical Value	4.6248
Test Statistic	20.5893

Summary:

Variety	N	Aluminum = 0 group	Aluminum = 540 group	...
Azucena112854	2	65.1400 bc	54.9500 bc	...
Azucena47125	2	79.6300 ab	82.3350 a	...
Azucena52992	2	99.3100 a	86.0500 a	...
Chadungda	2	54.8650 c	36.9400 c	...
IR20	2	32.0500 d	40.0300 c	...
IR64	2	56.9600 c	70.9350 ab	...
IR74	2	67.3950 bc	83.8500 a	...
Pokalli	2	91.1000 a	79.6000 a	...

Means with the same letter are not significantly different

Sample graphical output of the analysis displayed in the Graph Viewer tab is shown below:



Modifications can still be made on the analysis submitted. To know more about the modification that can be made, see the discussion under *Analysis of Variance > Completely Randomized Design > Additional Options* of this user's manual.

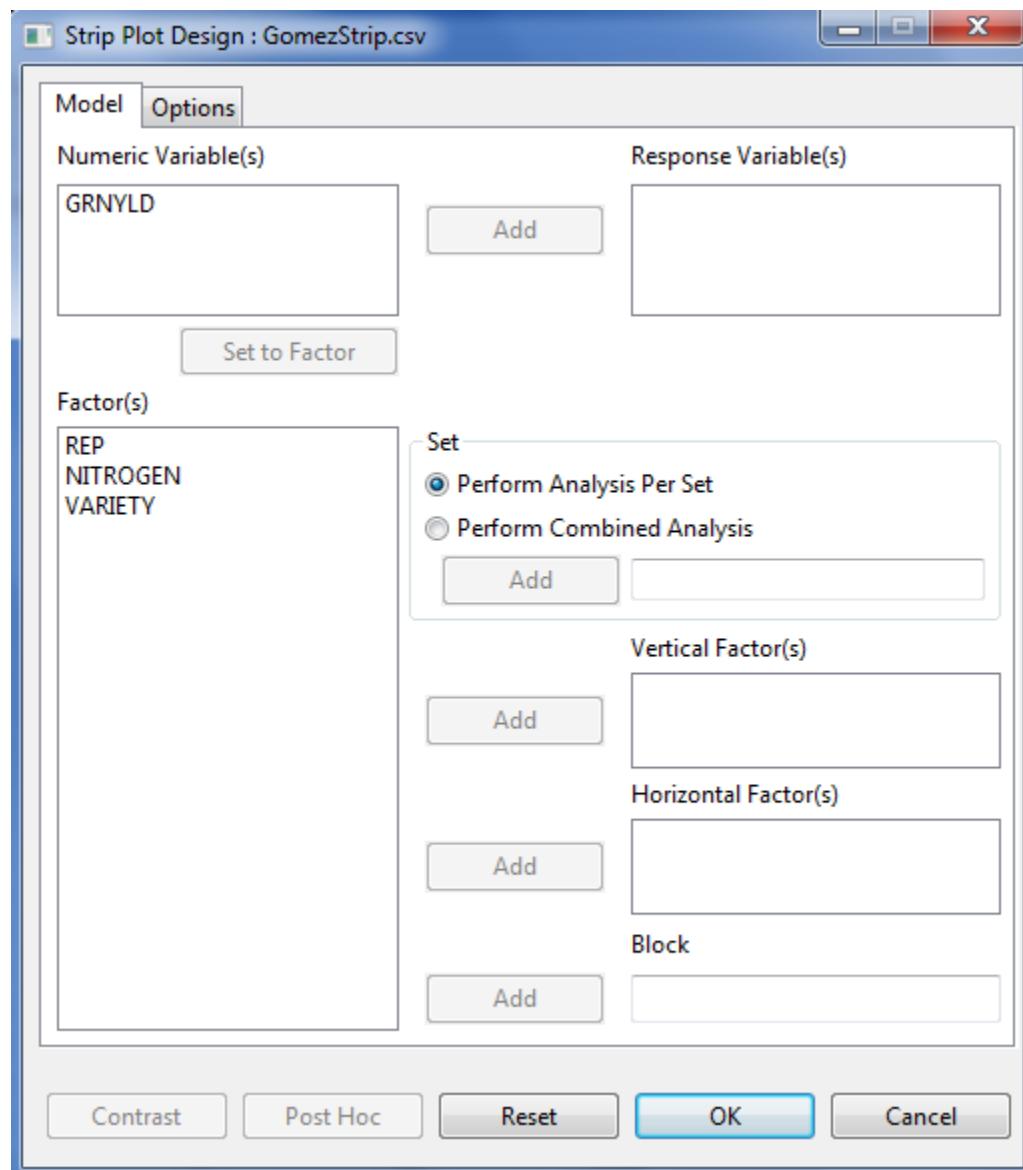
Strip Plot Design

The steps to perform the Analysis of Variance in Strip Plot Design are listed below:

- On the **Project Explorer**, double-click the file to be used for the analysis to open and view it in the Data Viewer tab.

For the example, using the project named *MyProject*, import the data *GomezStrip* from package. To import the data from the package, see *Importing from Package* section of this user's manual.

- From the main window of STAR click **Analyze | Analysis of Variance | Strip Plot Design**. The **Strip Plot** dialog box will appear.



- Specify the required field and appropriate options for the analysis.

Model Tab

Response Variable(s)

For the analysis to proceed, at least one item should be entered in the list box. Only Items from the **Numeric Variable(s)** can be added in this dialog box.

Set

There are two options available, *perform analysis per set* (default option) and *perform combined analysis*. If default option is selected and a **Set** variable is specified, STAR will perform analysis for each level of the **Set** variable. If the default option is selected and the **Set** variable is not specified, STAR will perform the analysis as if the entire data came from only one site. If **perform combined analysis is selected**, a Set variable must be specified.

Vertical Factor(s)

At least one item should be added in this list box and should come from the **Factor(s)** list box.

Horizontal Factor(s)

At least one item should be added in this list box and should come from the **Factor(s)** list box.

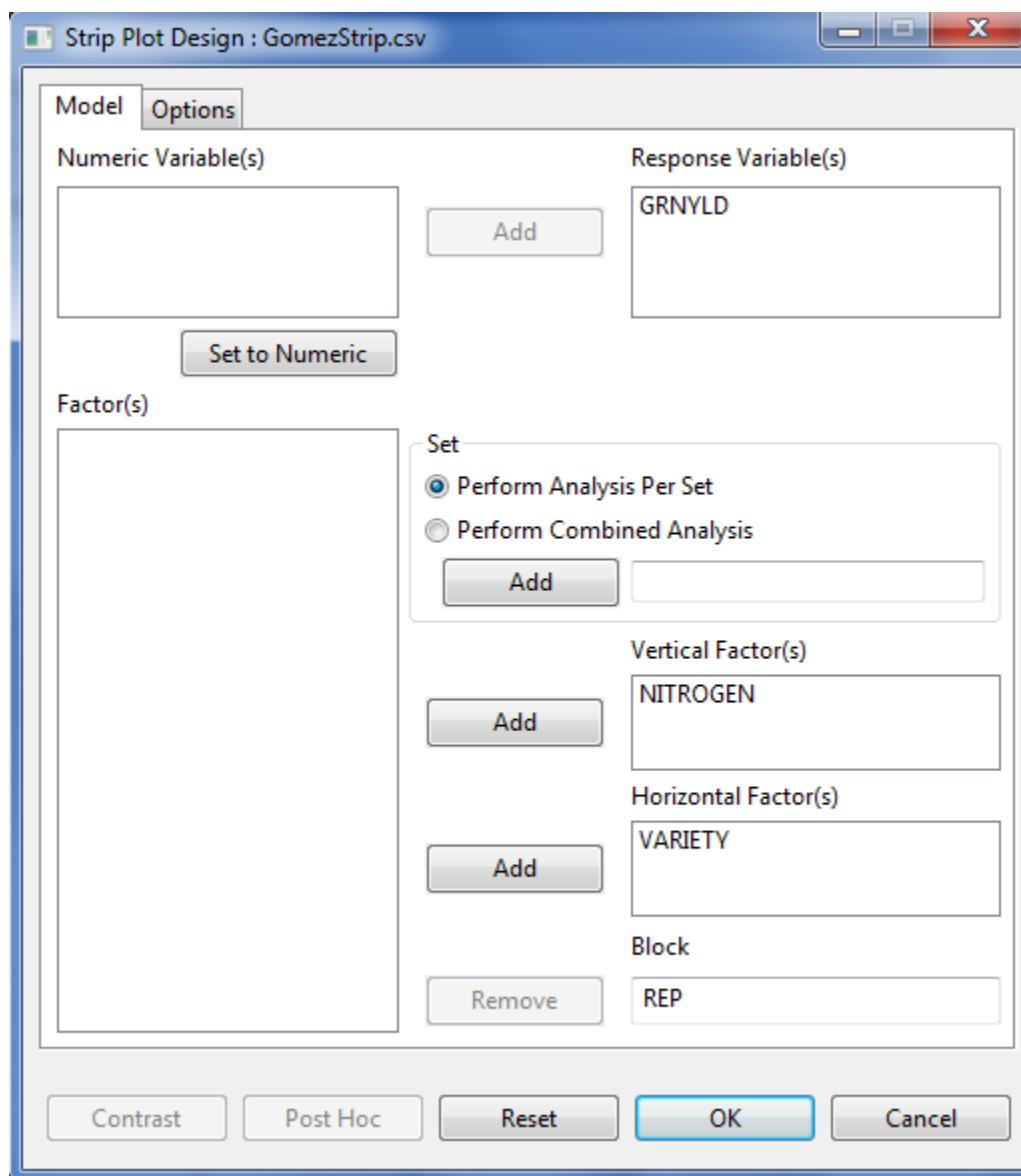
Block

Only one item can be added in this field and should come from the **Factor(s)** list box.

Options Tab

This tab lets the user identify additional output to be displayed and set the level of significance to be used. To know more about the options in detail, see the discussion under *Analysis of Variance > Completely Randomized Design > Options tab* of this user's manual.

For the example, the completed **Model** Specification tab should appear as illustrated below:



- Click **OK** button to perform the analysis. The **Strip Plot Design** dialog box will be minimized and STAR activates the **Output Viewer** tab and the **Graph Viewer** tab.

Sample text output of the analysis displayed in the Output Viewer tab is shown below:

```
Analysis of Variance
Strip Plot Design
=====
ANALYSIS FOR RESPONSE VARIABLE: GRNYLD
=====

Summary Information
-----
FACTOR      NO. OF LEVELS   LEVELS
-----
NITROGEN    3              0, 60, 120
VARIETY     6              V1, V2, ..., V6
REP         3              1, 2, 3
-----
Number of Observations Read and Used: 54

Descriptive Statistics
-----
Variable   N_Obs   Min     Max      Mean     StdDev
-----
GRNYLD     54     1556   8611   5289.94   1775.12
-----

Test for Homogeneity of Variances
-----
Method      DF   Statistics     Prob
-----
bartlett    17     21.30   0.2130
-----

Test for Normality
-----
Variable      Method       Statistics     Prob
-----
GRNYLD_resid Shapiro-Wilk     0.9732   0.2665
-----

ANOVA TABLE
Response Variable: GRNYLD
-----
Source        DF   Sum of Square   Mean Square   F Value   Pr > F
-----
REP          2    9220962.3333   4610481.1667   6.20     0.0595
NITROGEN     2    50676061.4444   25338030.7222   34.07    0.0031
Error(a)      4    2974907.8889   743726.9722
VARIETY      5    57100201.2778   11420040.2556   7.65     0.0034
Error(b)      10   14922619.2222   1492261.9222
NITROGEN:VARIETY 10   23877979.4444   2387797.9444   5.80     0.0004
```

Error(c)	20	8232917.2222	411645.8611
Total	53	167005648.8333	

Summary Statistics

CV(a) %	CV(b) %	CV(c) %	GRNYLD	Mean
16.30	23.09	12.13		5289.94

Comparison of NITROGEN at each level of VARIETY

Least Significant Difference (LSD) Test

Alpha	0.05
Error Degrees of Freedom	22
Error Mean Square	466992.7130
Critical Value	2.0716
Test Statistic	1155.8848

Summary:

NITROGEN	N	VARIETY = V1 group	VARIETY = V2 group	VARIETY = V3 group
0	3	3571.6667 c	4934.3333 b	4249.6667 c ...
60	3	5132.0000 b	6713.6667 a	6122.3333 b ...
120	3	7548.0000 a	7211.3333 a	7868.3333 a ...

Means with the same letter are not significantly different

Comparison of VARIETY at each level of NITROGEN

Tukey's Honest Significant Difference (HSD) Test

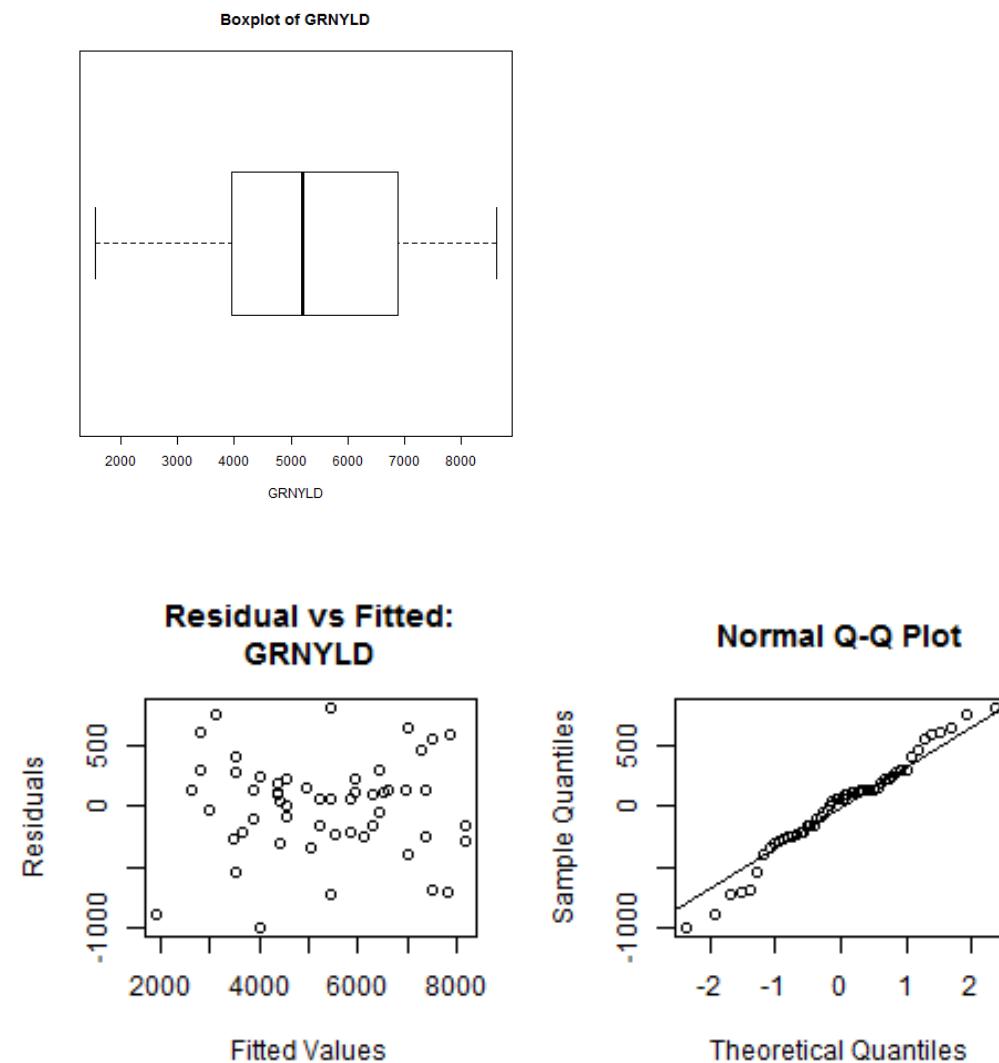
Alpha	0.05
Error Degrees of Freedom	10
Error Mean Square	1492261.9222
Critical Value	4.9120
Test Statistic	3464.3491

Summary:

VARIETY	N	NITROGEN = 0 group	NITROGEN = 60 group	NITROGEN = 120 group
V1	3	3571.6667 a	5132.0000 a	7548.0000 a
V2	3	4934.3333 a	6713.6667 a	7211.3333 a
V3	3	4249.6667 a	6122.3333 a	7868.3333 a
V4	3	4059.0000 a	5553.6667 a	7094.3333 a
V5	3	4101.6667 a	5633.3333 a	6012.0000 a
V6	3	3207.3333 a	3714.3333 a	2492.0000 b

Means with the same letter are not significantly different

Sample graphical output of the analysis displayed in the Graph Viewer tab is shown below:



Modifications can still be made on the analysis submitted. To know more about the modification that can be made, see the discussion under *Analysis of Variance > Completely Randomized Design > Additional Options* of this user's manual.

Split-Split Plot Design

This analysis can be performed for experiments where the main plot is arranged in completely randomized, randomized complete block or Latin square design.

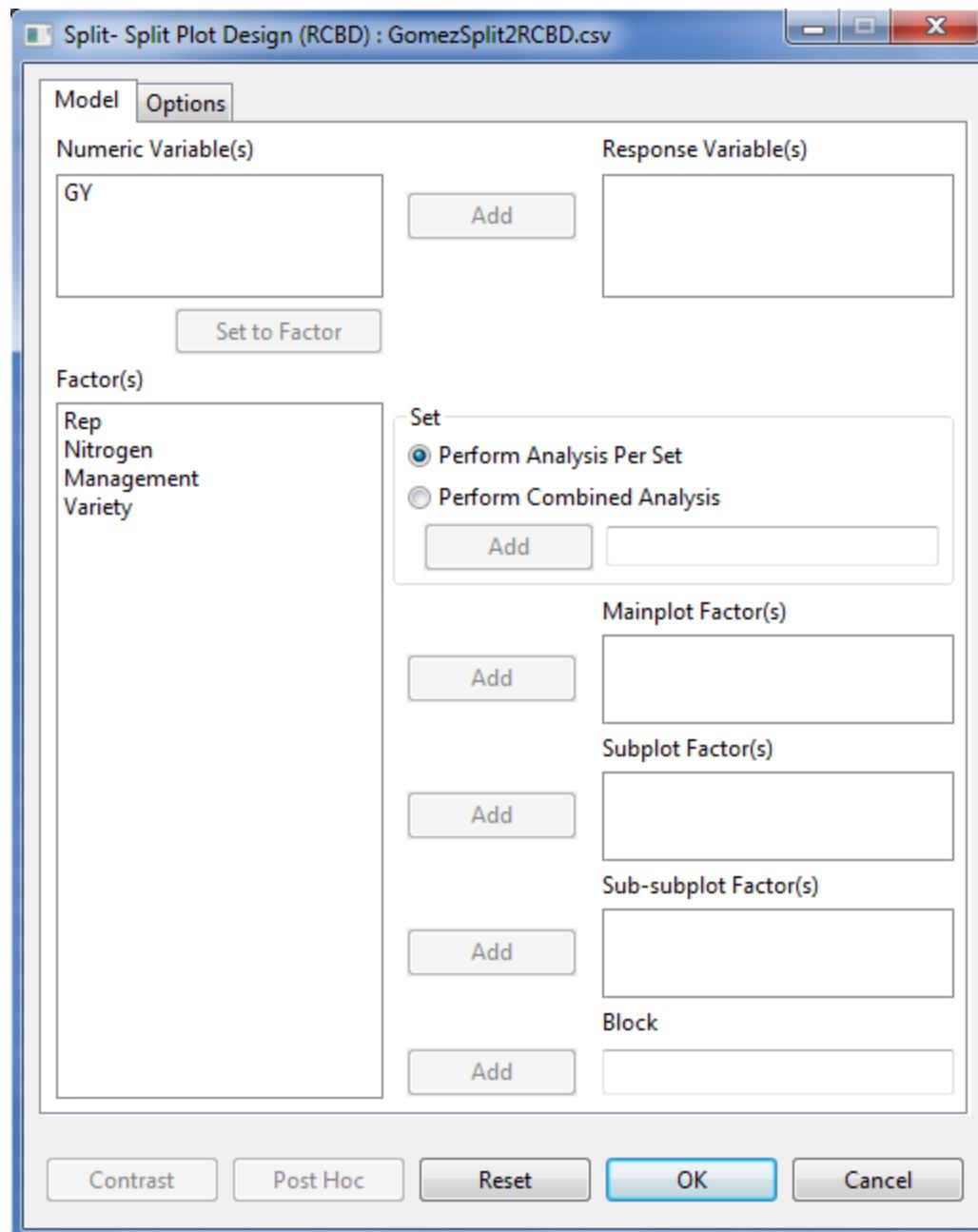
The steps to perform the Analysis of Variance using Split-Split Plot Design are listed below:

- On the **Project Explorer**, double-click the file to be used for the analysis to open and view it in the Data Viewer tab.

For the example, using the project named *MyProject*, import the data *GomezSplit2RCBD* from the package. To import the data from the package, see *Importing from Package* section of this user's manual.

- From the main window of STAR click **Analyze | Analysis of Variance | Split-Split Plot Design**. Choose the appropriate design for the mainplot. The **Split-Split Plot Design** dialog box will appear.

For the example, choose **Analyze | Analysis of Variance | Split-Split Plot Design | Randomized Complete Block Design ...** from the main window.



- Specify the required field and appropriate options for the analysis.

Model Tab

Response Variable(s)

For the analysis to proceed, at least one item should be entered in the list box. Only Items from the **Numeric Variable(s)** can be added in this dialog box.

Set

There are two options available, *perform analysis per set* (default) and *perform combined analysis*. If default option is selected and a **Set** variable is specified, STAR will perform analysis for each level of the **Set** variable. If the default option is selected and no **Set** variable is specified, STAR will perform the analysis as if the entire data came from only one set variable. If *perform combined analysis* is selected, a **Set** variable with at least two levels must be specified. The item should come from the **Factor(s)** list box.

Mainplot Factor(s)

At least one item should be added in this list box and should come from the **Factor(s)** list box.

Subplot Factor(s)

At least one item should be added in this list box and should come from the **Factor(s)** list box.

Sub-subplot Factor(s)

At least one item should be added in this list box and should come from the **Factor(s)** list box.

Replicate

Applicable only if completely randomized design is chosen. Only one item can be added in this field and should come from the **Factor(s)** list box.

Block

Applicable only if randomized complete block design is chosen. Only one item can be added in this field and should come from the **Factor(s)** list box.

Row Block

Applicable only if Latin square design is chosen. Only one item can be added in this field and should come from the **Factor(s)** list box.

Column Block

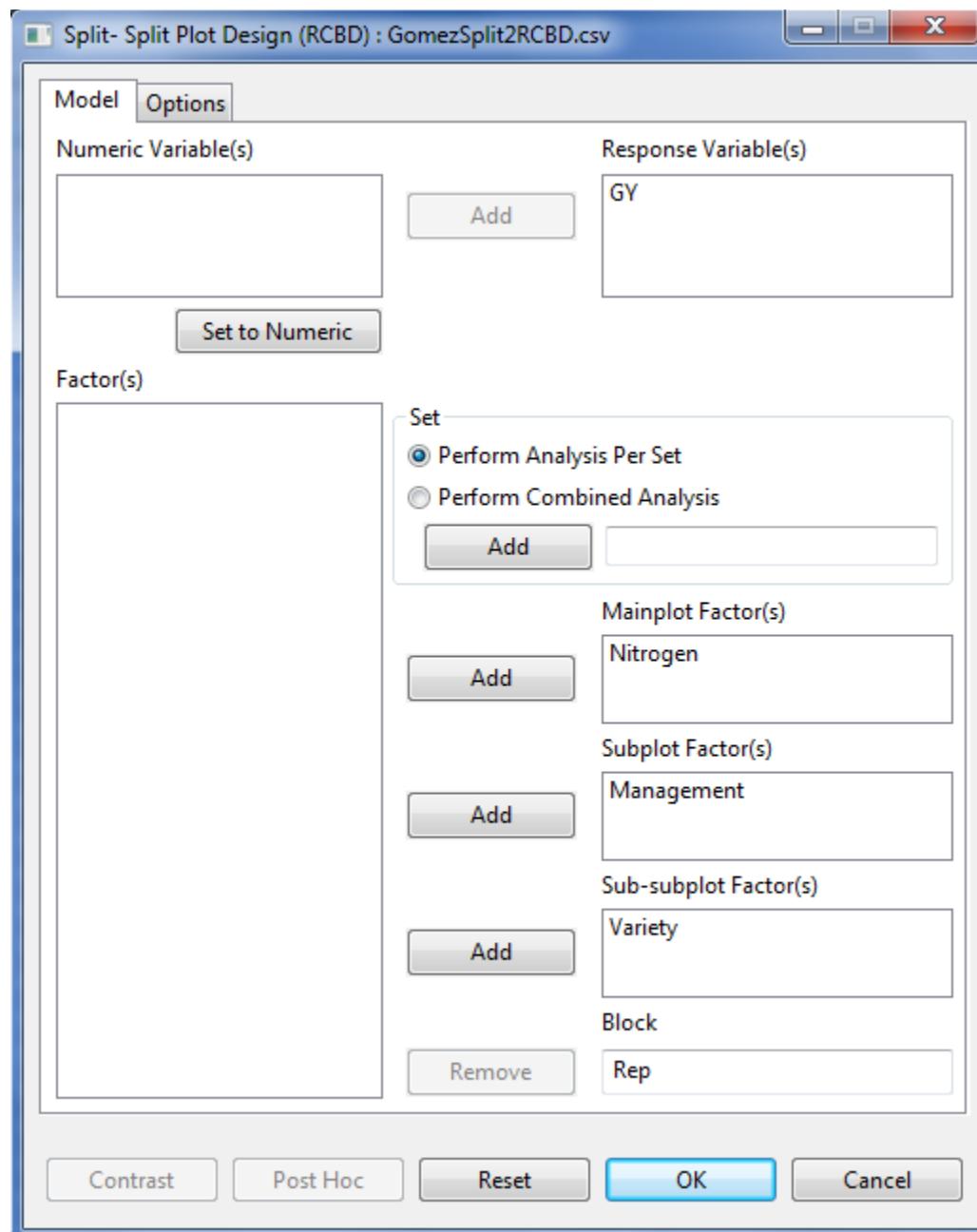
Applicable only if Latin square design is chosen. Only one item can be added in this field and should come from the **Factor(s)** list box.

Options Tab

This tab lets the user identify additional output to be displayed and set the level of significance to be used. To know more about the options in detail, see the discussion

under *Analysis of Variance > Completely Randomized Design > Options tab* of this user's manual.

For the example, the completed **Model** tab should appear as illustrated:



- Click **OK** button to perform the analysis. The **Split-Split Plot Design** dialog box will be minimized and STAR activates the **Output** page of the **Result Viewer** tab.

Sample text output displayed in the Output page is shown below:

Analysis of Variance
Split-Split Plot in Randomized Complete Block Design

=====

ANALYSIS FOR RESPONSE VARIABLE: GY

=====

Summary Information

FACTOR	NO. OF LEVELS	LEVELS
Nitrogen	5	N1, N2, N3, N4, N5
Management	3	M1, M2, M3
Variety	3	V1, V2, V3
Rep	3	1, 2, 3

Number of Observations Read and Used: 135

Descriptive Statistics

Variable	N_Obs	Min	Max	Mean	StdDev
GY	135	3.13	10.36	6.55	1.67

Test for Homogeneity of Variances

Method	DF	Statistics	Prob
bartlett	44	44.66	0.4440

Test for Normality

Variable	Method	Statistics	Prob
GY_resid	Shapiro-Wilk	0.9951	0.9279

ANOVA TABLE

Response Variable: GY

Source	DF	Sum of Square	Mean Square	F Value	Pr > F
Rep	2	0.7320	0.3660	0.66	0.5439
Nitrogen	4	61.6408	15.4102	27.70	0.0001
Error(a)	8	4.4514	0.5564		
Management	2	42.9361	21.4681	82.00	0.0000
Nitrogen:Management	8	1.1030	0.1379	0.53	0.8226
Error(b)	20	5.2363	0.2618		
Variety	2	206.0132	103.0066	207.87	0.0000
Nitrogen:Variety	8	14.1445	1.7681	3.57	0.0019
Management:Variety	4	3.8518	0.9629	1.94	0.1149
Nitrogen:Management:Variety	16	3.6992	0.2312	0.47	0.9538
Error(c)	60	29.7325	0.4955		

Total	134	373.5407
-------	-----	----------

Summary Statistics

CV(a) %	CV(b) %	CV(c) %	GY Mean
11.38	7.81	10.74	6.55

Table of Means

		Nitrogen	N1	N2	N3	N4	N5
Management Variety	M1	V1	3.897000	4.232000	5.226000	4.650333	4.061667
		V2	5.346000	5.921667	5.979667	6.252000	6.775667
		V3	5.378333	6.781333	7.933333	7.452667	8.618000
	M2	V1	4.317333	4.576333	5.732333	5.447333	5.200000
		V2	4.711667	5.815000	6.500000	7.004000	7.084333
		V3	6.496000	7.816667	8.567333	8.624667	9.399333
	M3	V1	5.325000	5.482667	6.546333	6.236333	5.971667
		V2	5.431000	6.312000	7.286000	7.517667	8.005333
		V3	7.560000	9.045333	9.190667	9.251333	9.989333

Comparison of Nitrogen at each level of Variety

Least Significant Difference (LSD) Test

Alpha	0.05
Error Degrees of Freedom	43
Error Mean Square	0.5158
Critical Value	2.0160
Test Statistic	0.6826

Summary:

Nitrogen	N	Variety = V1 group	Variety = V2 group	Variety = V3 group
N1	9	4.5131 c	5.1629 d	6.4781 d
N2	9	4.7637 bc	6.0162 c	7.8811 c
N3	9	5.8349 a	6.5886 bc	8.5638 b
N4	9	5.4447 ab	6.9246 ab	8.4429 bc
N5	9	5.0778 bc	7.2884 a	9.3356 a

Means with the same letter are not significantly different

Comparison of Variety at each level of Nitrogen

Least Significant Difference (LSD) Test

Alpha	0.05
Error Degrees of Freedom	60
Error Mean Square	0.4955
Critical Value	2.0003
Test Statistic	0.6638

Summary:

Variety	N	Nitrogen = N1 group	Nitrogen = N2 group	Nitrogen = N3 group	...
V1	9	4.5131 b	4.7637 c	5.8349 c	...
V2	9	5.1629 b	6.0162 b	6.5886 b	...
V3	9	6.4781 a	7.8811 a	8.5638 a	...

Means with the same letter are not significantly different

Pairwise Mean Comparison of Management

Least Significant Difference (LSD) Test

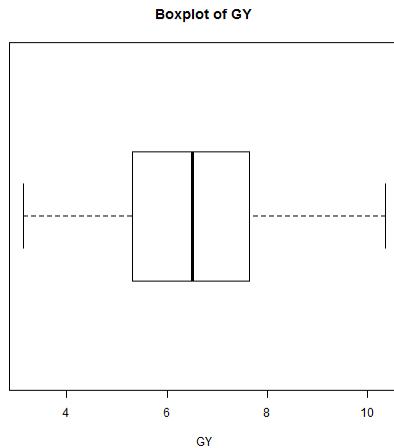
Alpha	0.05
Error Degrees of Freedom	20
Error Mean Square	0.2618
Critical Value	2.0860
Test Statistics	0.2250

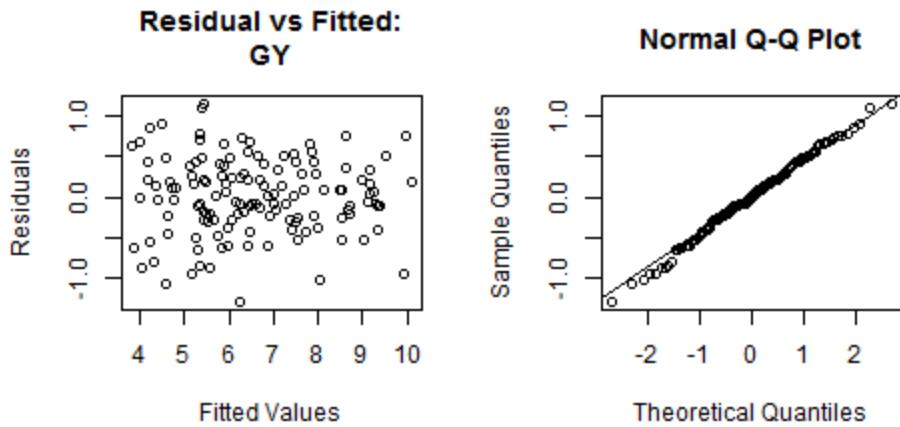
Summary of the Result:

Management	means	N group
M1	5.90	45 c
M2	6.49	45 b
M3	7.28	45 a

Means with the same letter are not significantly different.

Sample graphical output of the analysis displayed in the Graph Viewer tab is shown below:





Modifications can still be made on the analysis submitted. To know more about the modification that can be made, see the discussion under *Analysis of Variance > Completely Randomized Design > Additional Options* of this user's manual.

Strip-Split Plot Design

The steps to perform the Analysis of Variance in Strip-Split Plot Design are listed below:

- On the **Project Explorer**, double-click the file to be used for the analysis to open and view it in the Data Viewer.
- From the main window of STAR click **Analyze | Analysis of Variance | Strip-Split Plot Design**. The **Strip-Split Plot** dialog box will appear.
- Specify the required field and appropriate options for the analysis.

Model Tab

Response Variable(s)

For the analysis to proceed, at least one item should be entered in the list box. Only Items from the **Numeric Variable(s)** can be added in this dialog box.

Set

There are two options available, *perform analysis per set* (default option) and *perform combined analysis*. If default option is selected and a **Set** variable is specified, STAR will perform analysis for each level of the **Set** variable. If the default option is selected and the **Set** variable is not specified, STAR will perform the

analysis as if the entire data came from only one site. If **perform combined analysis is selected**, a Set variable must be specified.

Vertical Factor(s)

At least one item should be added in this list box and should come from the **Factor(s)** list box.

Horizontal Factor(s)

At least one item should be added in this list box and should come from the **Factor(s)** list box.

Subplot Factor(s)

At least one item should be added in this list box and should come from the **Factor(s)** list box.

Block

Only one item can be added in this field and should come from the Factor(s) list box.

Options Tab

This tab lets the user identify additional output to be displayed and set the level of significance to be used. To know more about the options in detail, see the discussion under *Analysis of Variance > Completely Randomized Design > Options tab* of this user's manual.

- Click **OK** button to perform the analysis. The **Strip-Split Plot Design** dialog box will be minimized and STAR activates the **Output** page of the **Result Viewer** tab.

Modifications can still be made on the analysis submitted. To know more about the modification that can be made, see the discussion under *Analysis of Variance > Completely Randomized Design > Additional Options* of this user's manual.

Split-Split-Split Plot Design

This analysis can be performed for experiments where the main plot is arranged in completely randomized, randomized complete block or Latin square design.

The steps to perform the Analysis of Variance using Split-Split-Split Plot Design are listed below:

- On the **Project Explorer**, double-click the file to be used for the analysis to open and view it in the Data Viewer.
- From the main window of STAR click **Analyze | Analysis of Variance | Split-Split-Split Plot Design**. Choose the appropriate design for the mainplot. The **Split-Split-Split Plot Design** dialog box will appear.
- Specify the required field and appropriate options for the analysis.

Model Tab

Response Variable(s)

For the analysis to proceed, at least one item should be entered in the list box. Only Items from the **Numeric Variable(s)** can be added in this dialog box.

Set

There are two options available, *perform analysis per set* (default option) and *perform combined analysis*. If default option is selected and a **Set** variable is specified, STAR will perform analysis for each level of the **Set** variable. If the default option is selected and the **Set** variable is not specified, STAR will perform the analysis as if the entire data came from only one site. If **perform combined analysis is selected**, a Set variable must be specified.

Mainplot Factor(s)

At least one item should be added in this list box and should come from the **Factor(s)** list box.

Subplot Factor(s)

At least one item should be added in this list box and should come from the **Factor(s)** list box.

Sub-subplot Factor(s)

At least one item should be added in this list box and should come from the **Factor(s)** list box.

Sub-sub-subPlot Factor(s)

At least one item should be added in this list box and should come from the **Factor(s)** list box.

Replicate

Applicable only if completely randomized design is chosen. Only one item can be added in this field and should come from the **Factor(s)** list box.

Block

Applicable only if randomized complete block design is chosen. Only one item can be added in this field and should come from the **Factor(s)** list box.

Row Block

Applicable only if Latin square design is chosen. Only one item can be added in this field and should come from the **Factor(s)** list box.

Column Block

Applicable only if Latin square design is chosen. Only one item can be added in this field and should come from the **Factor(s)** list box.

Options Tab

This tab lets the user identify additional output to be displayed and set the level of significance to be used. To know more about the options in detail, see the discussion under *Analysis of Variance > Completely Randomized Design > Options tab* of this user's manual.

- Click **OK** button to perform the analysis. The **Split-Split-Split Plot Design (RCBD)** dialog box will be minimized and STAR activates the **Output** page of the **Result Viewer** tab.

Modifications can still be made on the analysis submitted. To know more about the modification that can be made, see the discussion under *Analysis of Variance > Completely Randomized Design > Additional Options* of this user's manual.

Strip-Split-Split Plot Design

The steps to perform the Analysis of Variance in Strip-Split-Split Plot Design are listed below:

- On the **Project Explorer**, double-click the file to be used for the analysis to open and view it in the Data Viewer.
- From the main window of STAR click **Analyze | Analysis of Variance | Strip-Split-Split Plot Design**. The **Strip-Split-Split Plot** dialog box will appear.
- Specify the required field and appropriate options for the analysis.

Model Tab

Response Variable(s)

For the analysis to proceed, at least one item should be entered in the list box. Only Items from the **Numeric Variable(s)** can be added in this dialog box.

Set

There are two options available, *perform analysis per set* (default option) and *perform combined analysis*. If default option is selected and a **Set** variable is specified, STAR will perform analysis for each level of the **Set** variable. If the default option is selected and the **Set** variable is not specified, STAR will perform the analysis as if the entire data came from only one site. If **perform combined analysis is selected**, a Set variable must be specified.

Vertical Factor(s)

At least one item should be added in this list box and should come from the **Factor(s)** list box.

Horizontal Factor(s)

At least one item should be added in this list box and should come from the **Factor(s)** list box.

Subplot Factor(s)

At least one item should be added in this list box and should come from the **Factor(s)** list box.

Sub-subplot Factor(s)

At least one item should be added in this list box and should come from the **Factor(s)** list box.

Block

Only one item can be added in this field and should come from the Factor(s) list box.

Options Tab

This tab lets the user identify additional output to be displayed and set the level of significance to be used. To know more about the options in detail, see the discussion under *Analysis of Variance > Completely Randomized Design > Options tab* of this user's manual.

- Click **OK** button to perform the analysis. The **Strip-Split-Split Plot Design** dialog box will be minimized and STAR activates the **Output** page of the **Result Viewer** tab.

Modifications can still be made on the analysis submitted. To know more about the modification that can be made, see the discussion under *Analysis of Variance > Completely Randomized Design > Additional Options* of this user's manual.

Pairwise Mean Comparison

The **Post Hoc** option is used to request for other pairwise comparison procedures. This button will be enabled if there is at least one effect that is significant.

The steps to request for other pairwise mean comparison are listed below:

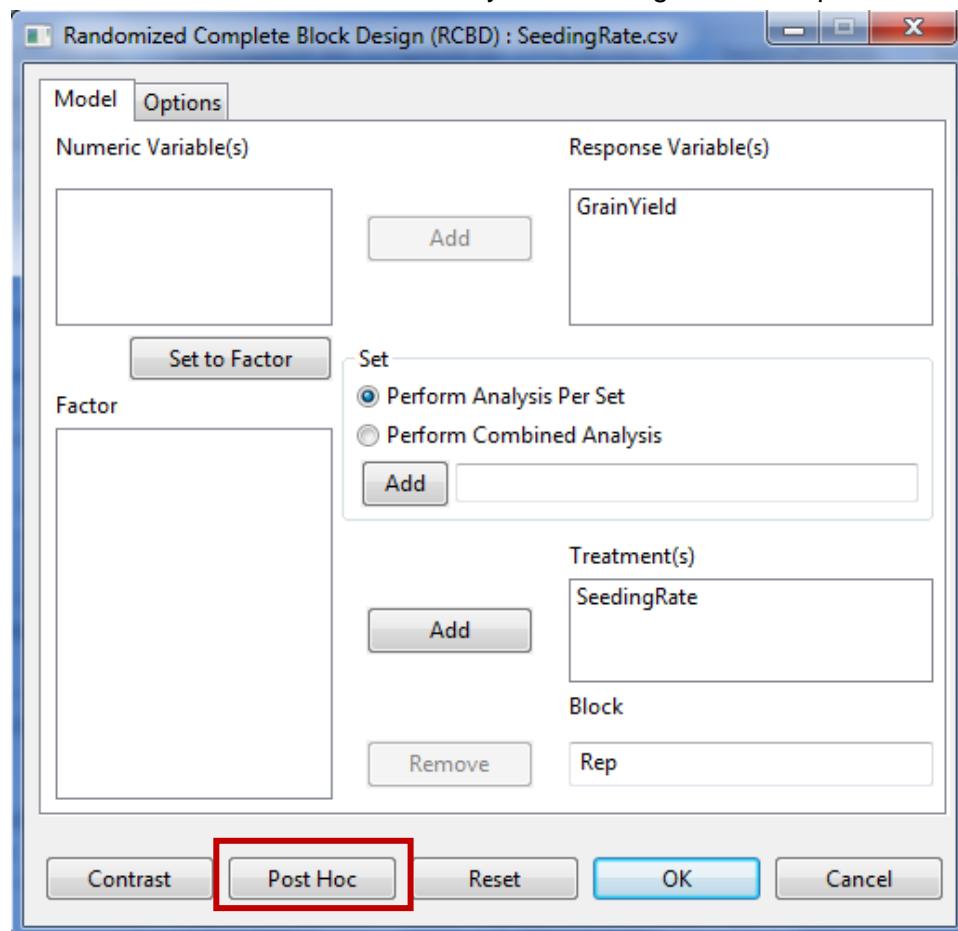
- On the **Project Explorer**, double-click the file to be used for the analysis to open and view it in the Data Viewer tab.

For the example, using the project named *MyProject*, import the data *SeedingRate* from STAR package. To import the data from the package, see *Importing from Package* section of this user's manual.

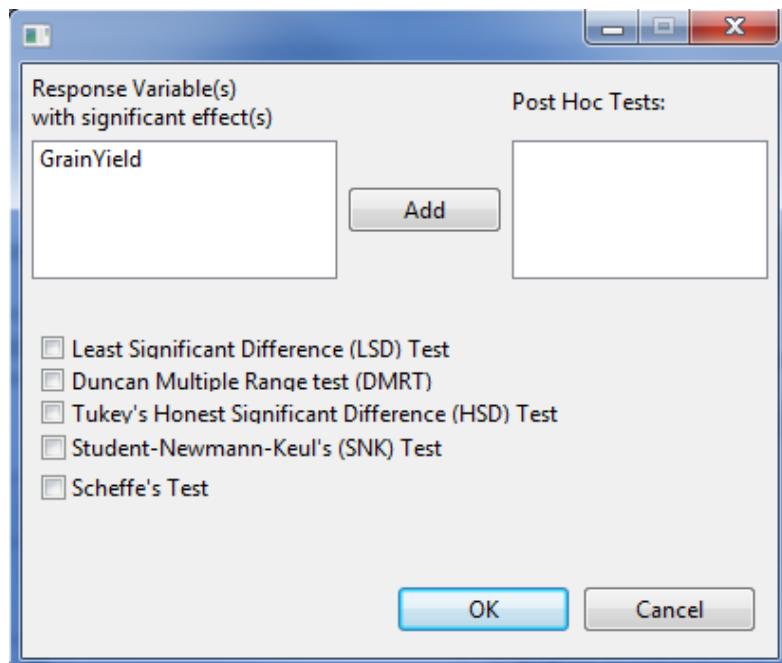
- Perform the Analysis of Variance.

For the example, follow the discussion in **Randomized Complete Block Design** of this module with *SeedingRate* as Factor and *Rep* as Block.

- After performing the Analysis of Variance, the **Post hoc** button will be enabled if there is at least one effect in the analysis that is significant at specified level.



- Click the **Post Hoc** button. A dialog box will appear.



- Specify the required field and appropriate options for the analysis.

Response Variable(s)

This list box displays all response variables with at least one significant effect. User need to select one item from this list and transfer to the **Post Hoc Test** list box to proceed with the analysis

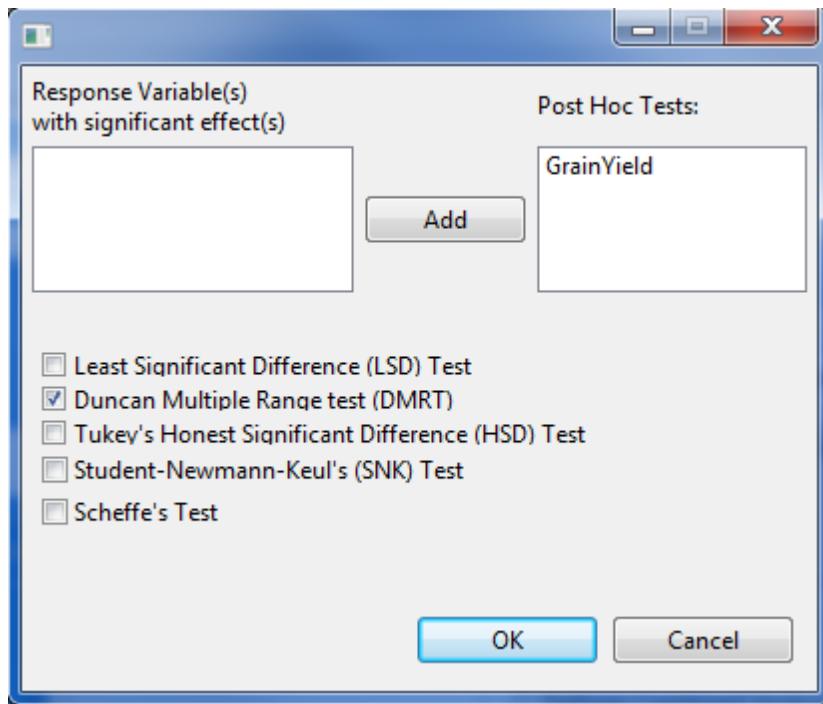
Post Hoc Tests

This list box should contain at least one item that will come from the **Response Variable(s)** list box. STAR will perform the additional pairwise comparison procedure for all effects of the response variable(s) selected.

Pairwise Comparison Procedure

At least one of the checkbox should be ticked for the analysis to proceed.

For the example, the completed dialog should appear as illustrated below:



- Click the **OK** button to perform the pairwise mean comparison. The **Pairwise Comparison** dialog box will be closed. The *PairwiseOutput.txt* is created in the parent folder within the *Output* folder and STAR activates the **Result Viewer** tab.

Sample content of the *PairwiseOutput.txt* displayed in the **Result Viewer** tab is shown below:

Response Variable: GrainYield

Pairwise Mean Comparison of SeedingRate

Duncan's Multiple Range Test (DMRT)

Alpha	0.05
Error Degrees of Freedom	15
Error Mean Square	0.1209

Number of Means	2	3	4	5	6
-----------------	---	---	---	---	---

Tabular Value	3.01	3.16	3.25	3.31	3.36
Test Statistics	0.52	0.55	0.57	0.58	0.58

Summary of the Result:

```
SeedingRate   means   N group
-----
100          4.35   4   c
125          4.67   4   bc
150          3.38   4   d
25           5.12   4   ab
50           5.08   4   ab
75           5.30   4   a
```

Means with the same letter are not significantly different.

- After performing the pairwise comparison test, user can click the **OK** button to embed the requested pairwise mean comparison procedure with the Analysis of Variance output.

Sample content of the text file when user click the **OK** button after performing the pairwise comparison.

```
Analysis of Variance
Randomized Complete Block Design
```

```
=====
ANALYSIS FOR RESPONSE VARIABLE: GrainYield
=====
```

```
Summary Information
-----
```

```
FACTOR      NO. OF LEVELS  LEVELS
-----
SeedingRate  6            25, 50, ..., 150
Rep          4            1, 2, 3, 4
-----
```

```
Number of Observations Read and Used: 24
```

```
ANOVA TABLE
```

```
Response Variable: GrainYield
```

```
Source       DF  Sum of Square  Mean Square  F Value  Pr > F
-----
Rep          3    1.7667        0.5889      4.87    0.0147
SeedingRate  5    10.1800       2.0360     16.84    0.0000
Error         15   1.8133        0.1209
Total         23   13.7600
-----
```

Summary Statistics

CV (%)	GrainYield Mean
7.48	4.65

Standard Errors

Effects	StdErr
Rep	0.2007
SeedingRate	0.2459

Pairwise Mean Comparison of SeedingRate

Duncan's Multiple Range Test (DMRT)

Alpha	0.05
Error Degrees of Freedom	15
Error Mean Square	0.1209

Number of Means	2	3	4	5	6
-----------------	---	---	---	---	---

Tabular Value	3.0143	3.1598	3.2502	3.3118	3.3560
Test Statistics	0.5240	0.5493	0.5650	0.5757	0.5834

Summary of the Result:

SeedingRate	means	N	group
25	5.12	4	ab
50	5.08	4	ab
75	5.30	4	a
100	4.35	4	c
125	4.67	4	bc
150	3.38	4	d

Means with the same letter are not significantly different.

Partitioning Sum of Squares

The **Contrast** option is used in partitioning sum of squares that decompose the variability of the response(s) into various components to have a better view of the nature of variability. There are different selections in partitioning sum of squares such as, “Compare with Control”, “User Specified Contrast (Group Comparison)” and “Orthogonal Polynomial Contrast”.

Group Comparison

The steps to perform the Group Comparison are listed below:

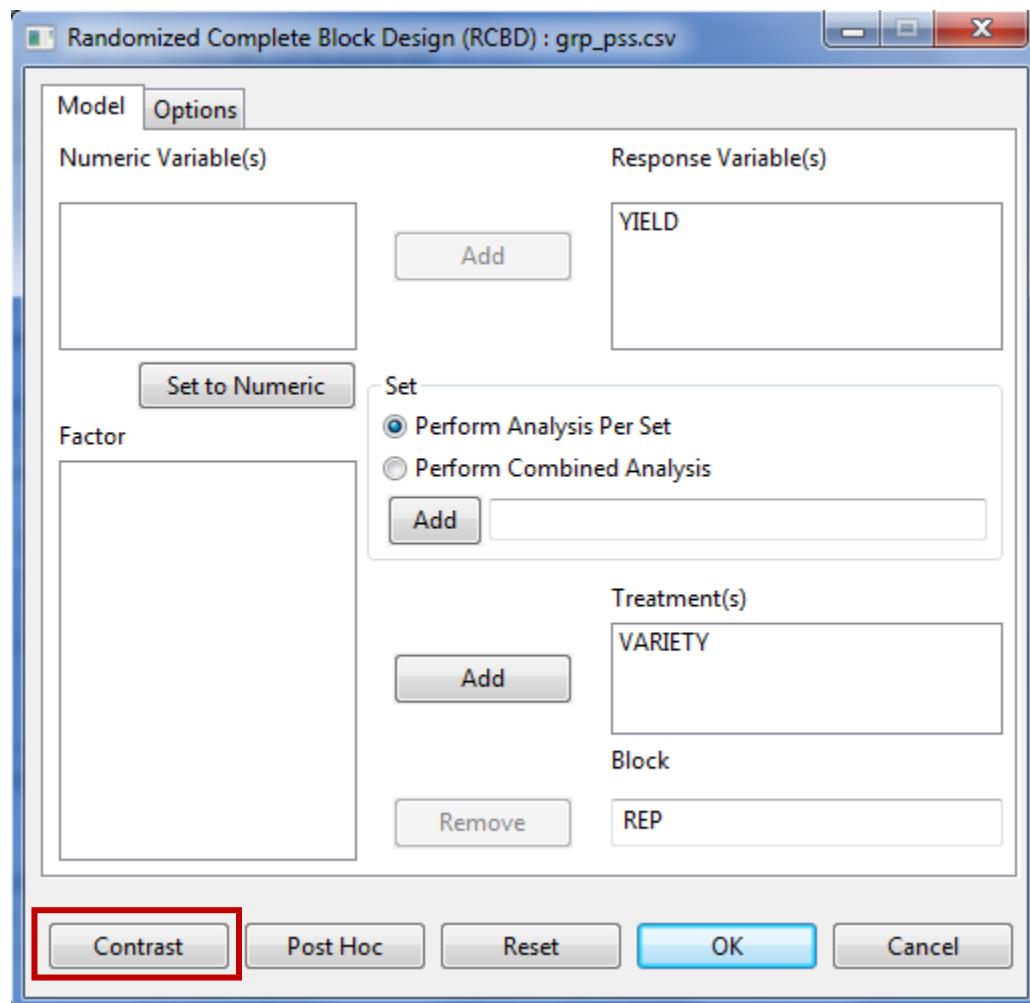
- On the **Project Explorer**, double-click the file to use for the analysis to open and view it in the Data Viewer tab.

For the example, using the project named *MyProject*, import the data *grp_pss* from STAR package. To import the data from the package, see *Importing from Package* section of this user's manual.

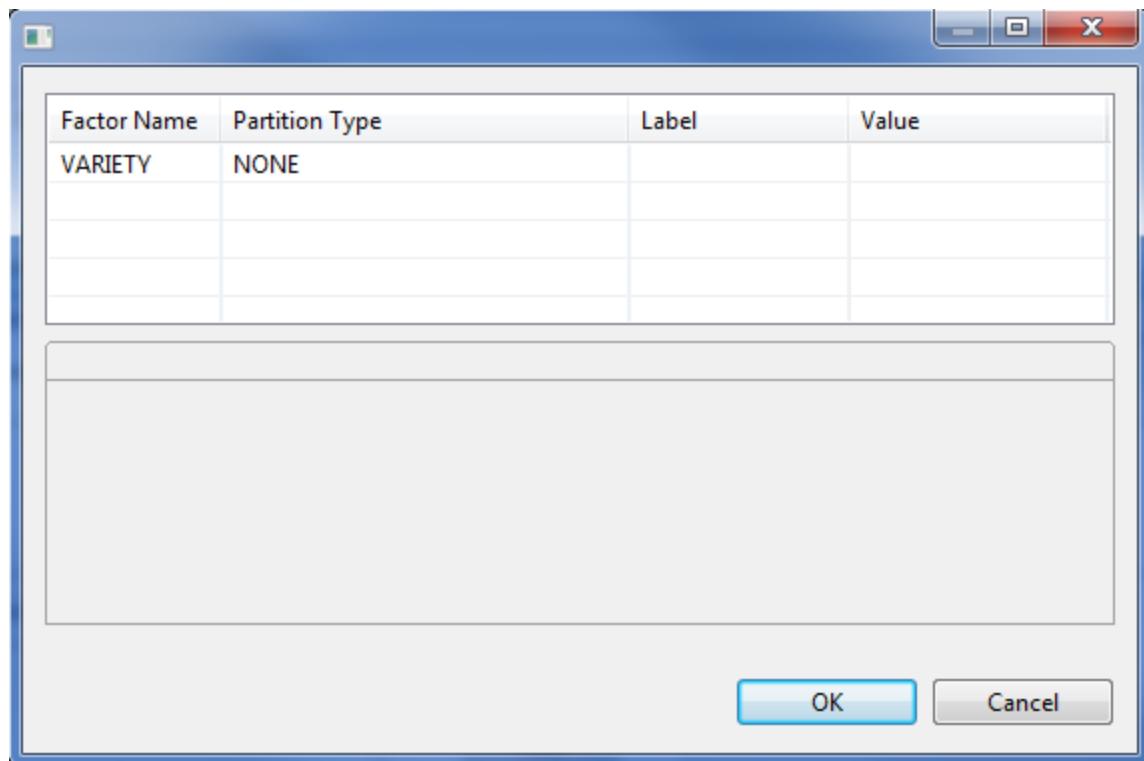
- Perform the Analysis of Variance.

For the example, follow the discussion in **Randomized Complete Block Design** of this module with *VARIETY* as Factor and *REP* as Block.

- After performing the Analysis of Variance, the **Contrast** button will be enabled if there is at least one factor in the analysis with more than two levels.



- Click the **Contrast** button. A dialog box will appear.



- Specify the required field and appropriate options for the analysis.

Factor Name column

All factors included in the analysis with more than two levels will be displayed in this column.

Partition Type column

Specify the type of partitioning to be performed by clicking the drop-down menu. If the levels of the factor are quantitative, the 3 choices are available, otherwise; only the choices *Compare with Control* and *User-Specified Contrast* will be available for that factor.

Value column

If *Compare with Control* is chosen, this column specifies which level of the factor is considered as control level. By default, the first level of the factor is considered the control. To change the control level, click the drop-down box to display the different levels of the factor.

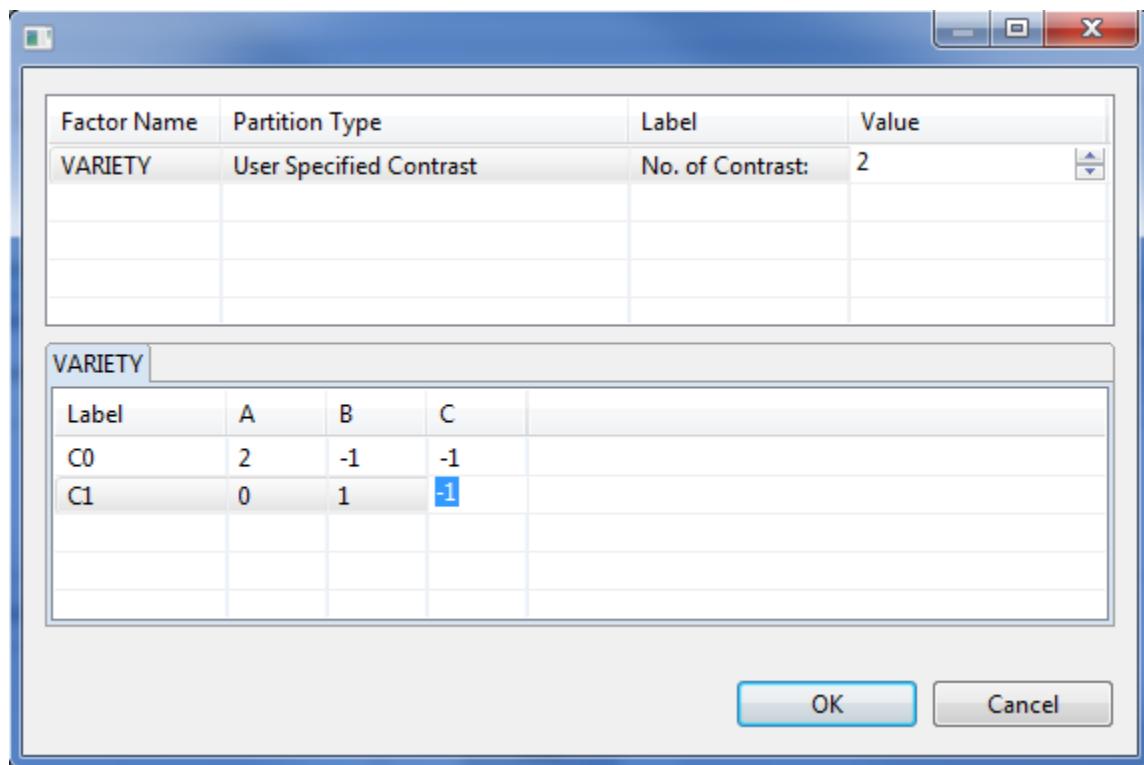
If *User Specified Contrast* or *Orthogonal Polynomial Contrast* is chosen, this column specifies the number of contrast that will be used for the analysis. The default value is 1 while the maximum number is equal to the treatment degrees of freedom.

If **User Specified Contrast** is selected, a tab with the factor name as label will be displayed at the lower part of the **Contrast Analysis** dialog box to specify the coefficients for each contrast. The sum of each contrast should be equal to zero. If there are 2 or more contrasts, the sum of the cross product of each pair wise contrast should be equal to zero.

For the example, suppose we want to determine the following:

- i. If the mean of the traditional variety (A) is significantly different from the new varieties (B and C).
- ii. If the mean of the new varieties (B and C) are significantly different.

The completed dialog box should appear as shown below:



- Click the **OK** button to perform Group Comparison. The **Contrast Analysis** dialog box will be closed. The *ContrastAnalysisOutput.txt* is created in the parent folder within the *Output* folder and STAR actives the **Result Viewer** tab.

Sample content of the *ContrastAnalysisOutput.txt* displayed in the **Result Viewer** tab is shown below:

Result of Contrast Analysis

ANOVA TABLE

Response Variable: YIELD

Source	DF	Sum of Square	Mean Square	F Value	Pr > F
REP	3	0.5867	0.1956	2.20	0.1889
VARIETY	2	1.0400	0.5200	5.85	0.0390
VARIETY: C0	1	0.9600	0.9600	10.80	0.0167
VARIETY: C1	1	0.0800	0.0800	0.90	0.3794
Error	6	0.5333	0.0889		
Total	11	2.1600			

Trend Comparison

This procedure is applicable and available if the levels of the factor are quantitative. The steps to perform the Group Comparison are listed below:

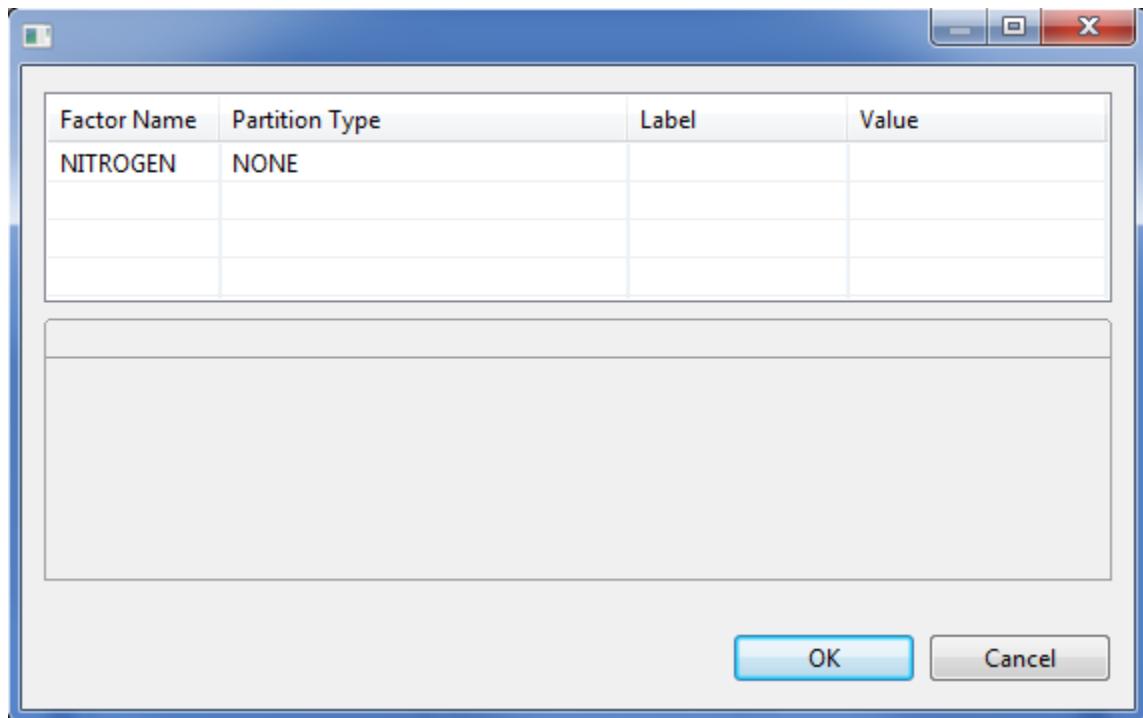
- On the **Project Explorer**, double-click the file to be used for the analysis to open and view it in the Data Viewer tab.

For the example, using the project named *MyProject*, import the data *OP_pss* from STAR package. To import the data from the package, see *Importing from Package* section of this user's manual.

- Perform the Analysis of Variance.

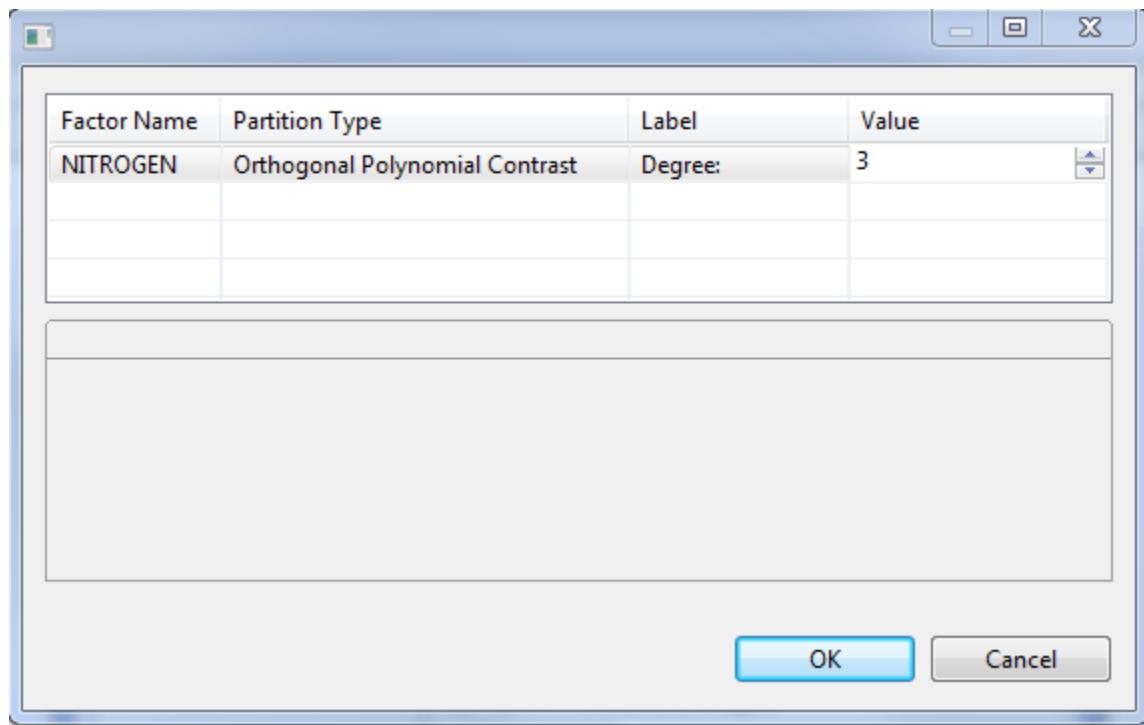
For the example, follow the discussion in **Randomized Complete Block Design** of this module with *NITROGEN* as Factor and *REP* as Block.

- After performing the Analysis of Variance, the **Contrast** button will be enabled if there is at least one factor in the analysis with more than two levels.
- Click the **Contrast** button. A dialog box will appear.



- Specify the required field and appropriate options for the analysis. To know more about the options in detail, see the discussion under *Analysis of Variance > Partitioning Sum of Squares > Group Comparison* of this user's manual.

For the example, suppose we want to know the highest degree of relationship between the yield response and Nitrogen Rate. The completed dialog box should appear as illustrated below:



- Click the **OK** button to perform Group Comparison. The **Contrast Analysis** dialog box will be closed. The *ContrastAnalysisOutput.txt* is created in the parent folder within the *Output* folder and STAR actives the **Result Viewer** tab.

Sample text output of the analysis displayed in the Output Viewer tab is shown below:

ANOVA TABLE
Response Variable: YIELD

Source	DF	Sum of Square	Mean Square	F Value	Pr > F
REP	2	0.4067	0.2033	0.65	0.5557
NITROGEN	3	11.0225	3.6742	11.73	0.0064
NITROGEN: 1	1	10.6562	10.6562	34.01	0.0011
NITROGEN: 2	1	0.1913	0.1913	0.61	0.4643
NITROGEN: 3	1	0.1750	0.1750	0.56	0.4831
Error	6	1.8800	0.3133		
Total	11	13.3092			

Incomplete Block Design

The Incomplete Block submenu can be used to perform analysis for mixed model for the following design: Balanced Incomplete Block, Augmented Randomized Complete Block, Augmented Latin Square, Alpha Lattice and Row-Column design with treatment considered as fixed and the other effects as random.

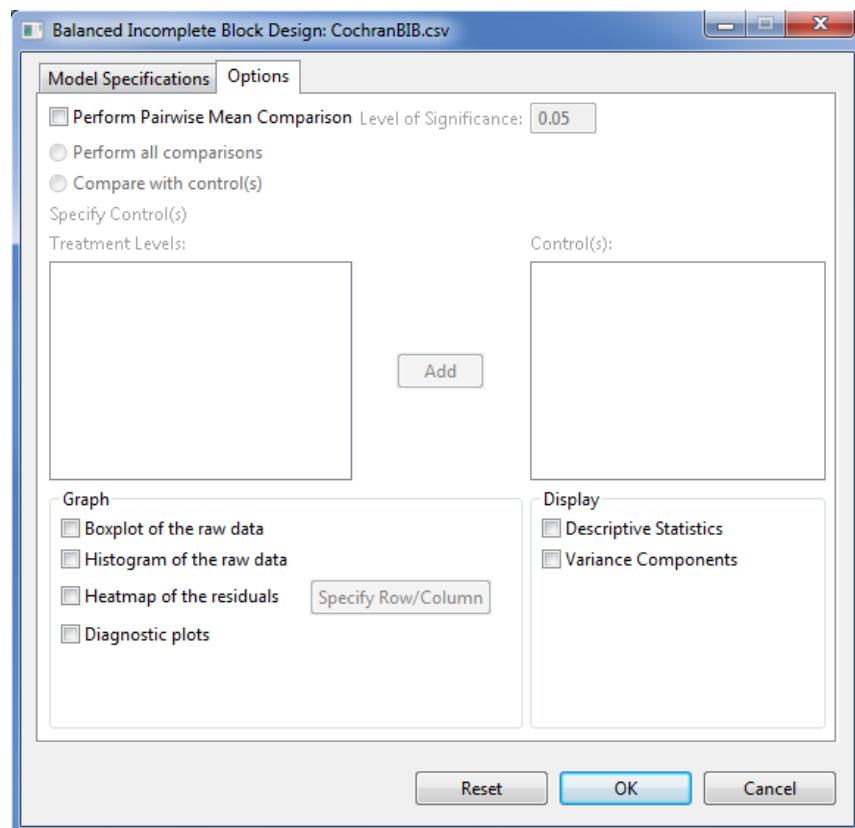
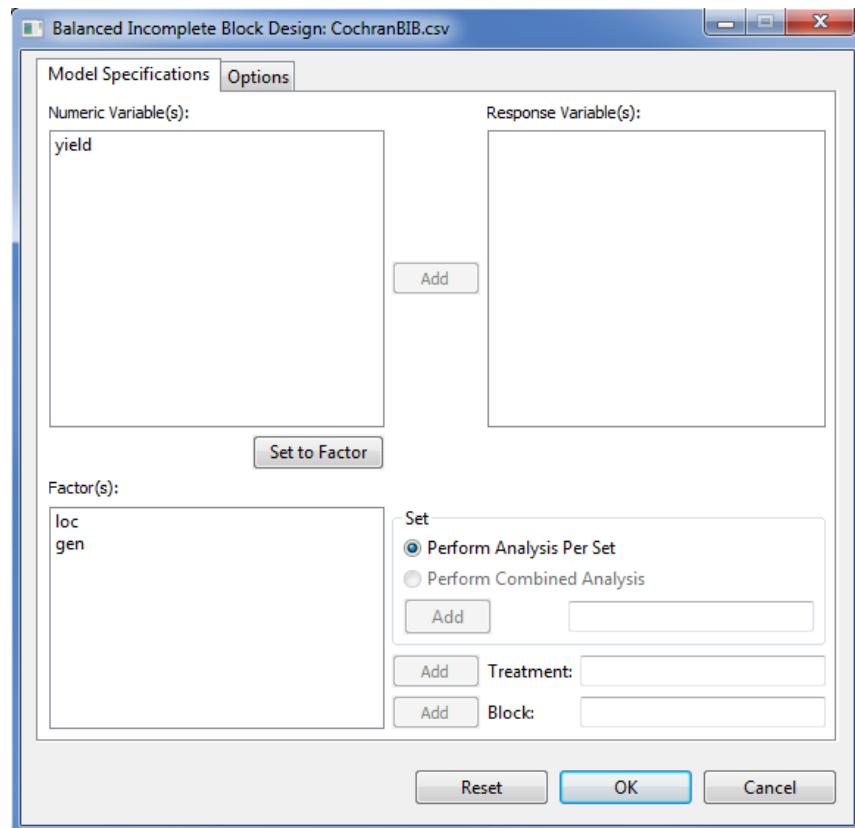
Balanced Incomplete Block Design

The steps to perform analysis for balanced incomplete block design are listed below:

- On the **Project Explorer**, double-click the file to be used for the analysis to open and view it in the Data Viewer.

For the example, using the project named *MyProject*, import the data *CochranBIB* from the package. To import the data from the package, see *Importing from Package* section of this user's manual.

- Choose **Analyze | Incomplete Block | Balanced Incomplete Block Design...** from the main window. The **Balanced Incomplete Block Design** dialog box will appear.



- Specify the required fields and appropriate options for the analysis.

Model Specifications Tab

Response Variable(s)

For the analysis to proceed, at least one item should be entered in the list box. The items to be entered should come from the **Numeric Variable(s)** list box.

Set

There are two options available, *perform analysis per set* (default) and *perform combined analysis*. If default option is selected and a **Set** variable is specified, STAR will perform analysis for each level of the **Set** variable. If the default option is selected and no **Set** variable is specified, STAR will perform the analysis as if the entire data came from only one set variable. If *perform combined analysis* is selected, a **Set** variable with at least two levels must be specified. Only one item can be added in this entry box and should come from the **Factor(s)** list box.

Treatment

This field is required. Only one item can be added in this entry box and should come from the **Factor(s)** list box.

Block

This field is required. Only one item can be added in this entry box and should come from the **Factor(s)** list box.

Options Tab

Perform pairwise mean comparisons

If this option is selected, user can either choose *Perform all comparisons* or *Compare with control(s)*. The option *Perform all comparisons* is not recommended when the number of treatment levels is very large. For now, STAR executes this option if the treatment levels is at most fifteen. If the treatment has more than 15 levels, user can only choose the option *Compare with control(s)*. If the option *Compare with control(s)* was selected, the user should specify the control levels to be compared with the rest of the treatment levels. This can be done by selecting the level(s) of the treatment that are considered as the control(s) then click the **Add** button.

Level of Significance

This will be enabled if *Perform pairwise mean comparison* is selected. This will be the level of significance to be used when pairwise mean comparison is performed. Its default value is 0.05.

Display Descriptive Statistics

If selected, a summary table with number of missing observations, mean and standard deviation will be displayed.

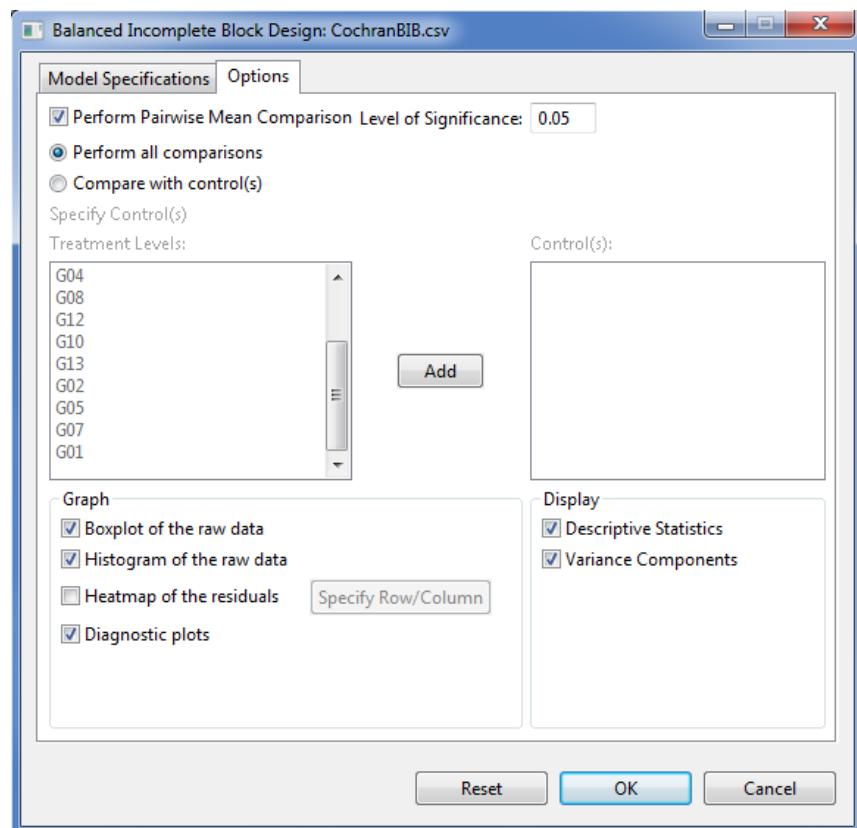
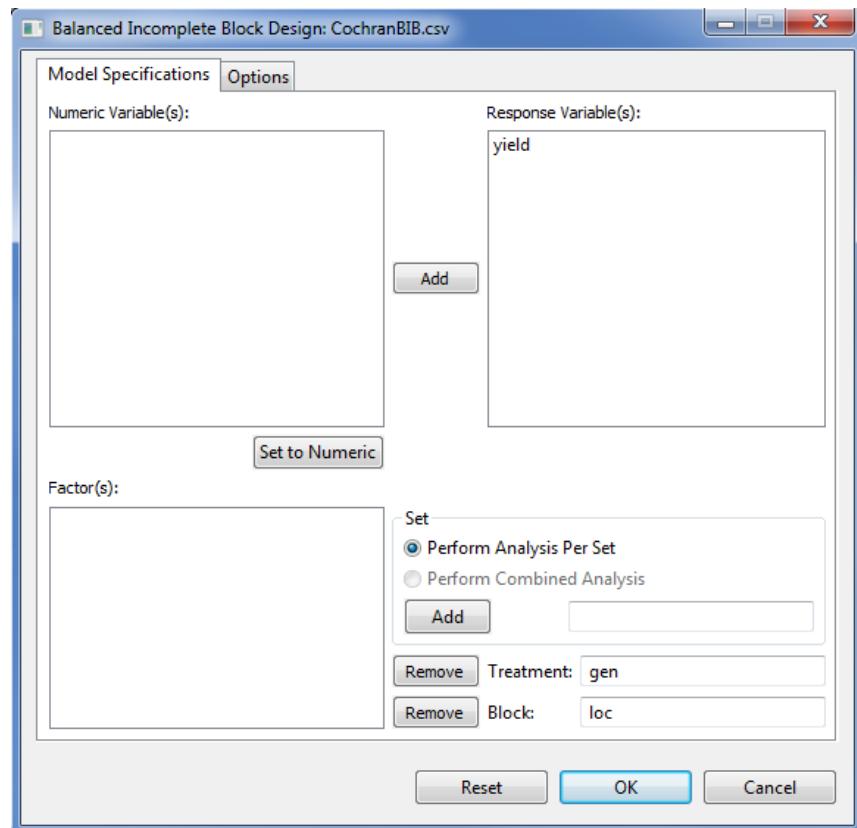
Display Variance Components

If selected, a table with the variance estimates of the some model components will be displayed.

Graph

Graphs like boxplot, histogram, heatmap and diagnostic plots can be generated as part of the output of the analysis. If heatmap is selected, user needs to specify a row and a column variable.

For the example, the completed **Model Specification** tab and **Options** tab should appear as illustrated:



- Click **OK** button to perform the analysis. The **Augmented RCB** dialog box will be minimized and STAR activates the **Output** page of the **Result Viewer** tab.

Sample text output of the analysis is shown below:

DESIGN: Balanced Incomplete Block Design (BIBD)

=====

ANALYSIS FOR RESPONSE VARIABLE: yield

=====

Descriptive Statistics

Variable	N	NonMissObs	Mean	StdDev
yield		52	29.78	5.52

Summary Information

FACTOR	NO. OF LEVELS	LEVELS
loc	13	B01, B02, ..., B13
gen	13	G01, G02, ..., G13

Number of Observations Read and Used: 52

Estimates of Variance Components

Groups	Variance	StdDev
loc	6.0527	2.4602
Residual	19.9340	4.4647

Testing for the Significance of Genotypic Effect

Models:

model2: yield ~ 1 + (1|loc)
model1: yield ~ 1 + gen + (1|loc)

Source	Df	AIC	BIC	logLik	Chisq	Chi Df	Pr(>Chisq)
model2	3	326.1376	331.9913	-160.0688			
model1	15	328.4084	357.6770	-149.2042	21.73	12	0.0407

Source	Df	Sum Sq	Mean Sq	F value	Prob
gen	12	400.63	33.39	1.67	0.0407

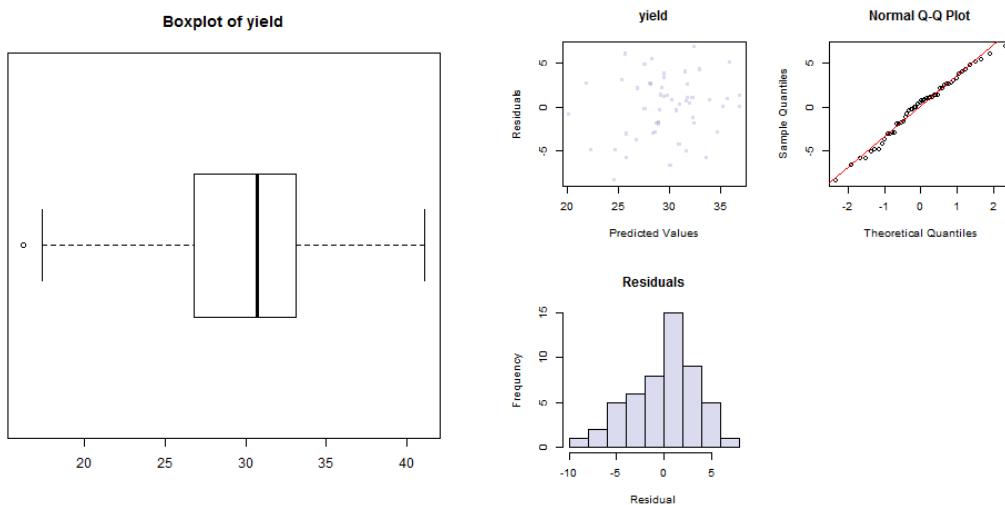
gen LSMeans and Standard Error

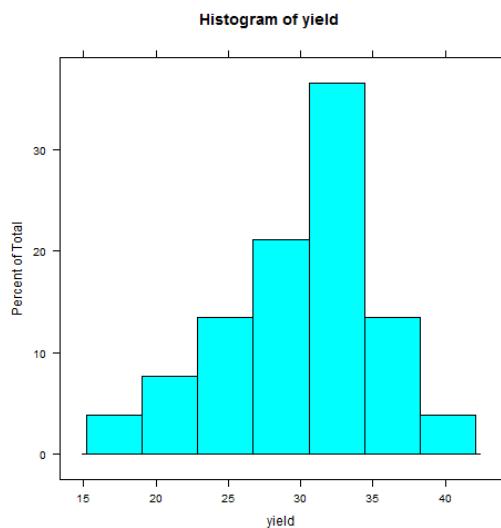
gen	LSMean	StdErrMean
<hr/>		
G01	34.17	2.44
G02	29.04	2.44
G03	30.11	2.44
G04	28.08	2.44
G05	30.34	2.44
G06	27.59	2.44
G07	30.76	2.44
G08	32.75	2.44
G09	28.56	2.44
G10	28.10	2.44
G11	23.47	2.44
G12	28.99	2.44
G13	35.18	2.44
<hr/>		

List of gen pairs that are significantly different using Tukey at alpha = 0.05

gen[i]	gen[j]	Estimate	lwr	upr
<hr/>				
G13	G11	11.71	0.6738	22.74
<hr/>				

Sample graphical output of the analysis is shown below:





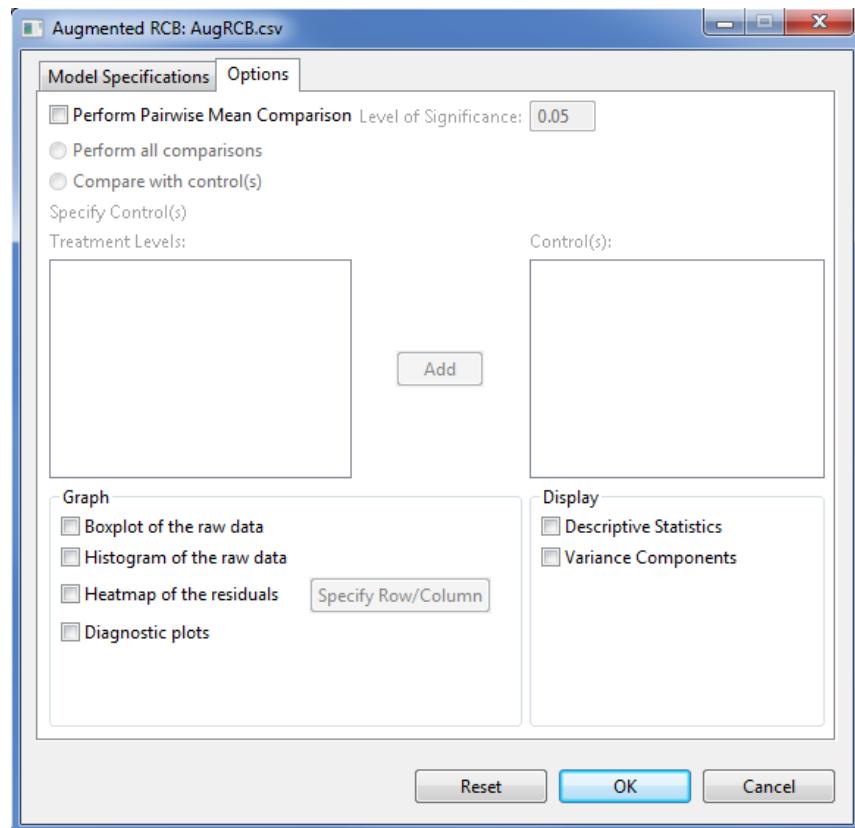
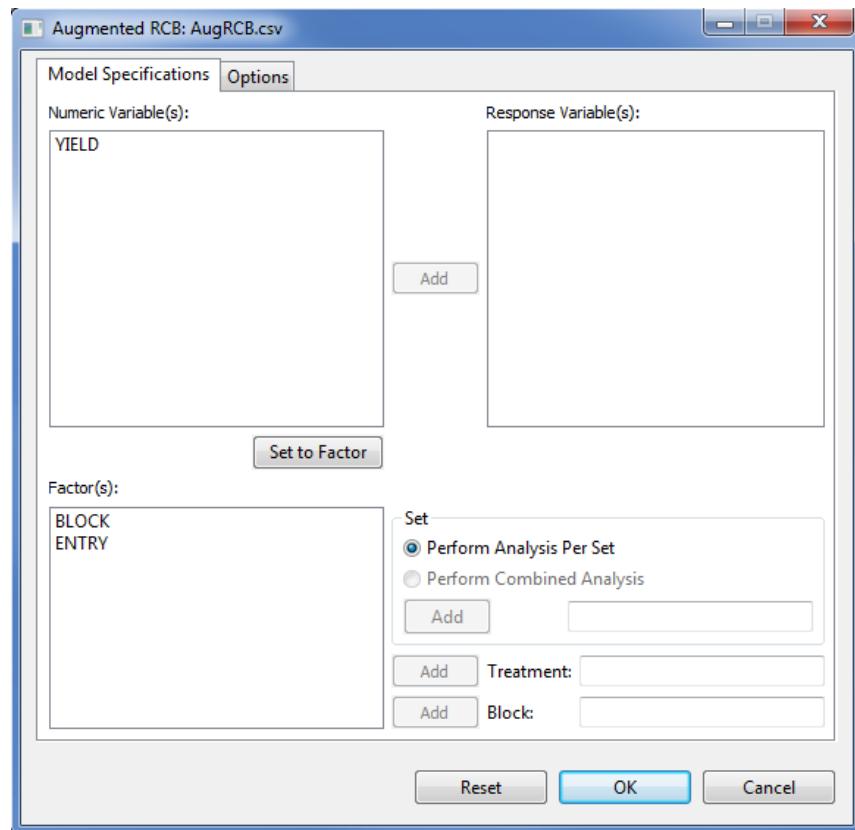
Augmented Randomized Complete Block Design

The steps to perform analysis for augmented in randomized complete block design are listed below:

- On the **Project Explorer**, double-click the file to be used for the analysis to open and view it in the Data Viewer.

For the example, using the project named *My Project*, import the data *AugRCB* from the package. To import the data from the package, see *Importing from Package* section of this user manual.

- Choose **Analyze | Incomplete Block | Augmented RCB...** from the main window. The **Augmented RCB** dialog box will appear.



- Specify the required fields and appropriate options for the analysis.

Model Specifications Tab

Response Variable(s)

For the analysis to proceed, at least one item should be entered in the list box. The items to be entered should come from the **Numeric Variable(s)** list box.

Set

There are two options available, *perform analysis per set* (default) and *perform combined analysis*. If default option is selected and a **Set** variable is specified, STAR will perform analysis for each level of the **Set** variable. If the default option is selected and no **Set** variable is specified, STAR will perform the analysis as if the entire data came from only one set variable. If *perform combined analysis* is selected, a **Set** variable with at least two levels must be specified. Only one item can be added in this entry box and should come from the **Factor(s)** list box.

Treatment

This field is required. Only one item can be added in this entry box and should come from the **Factor(s)** list box.

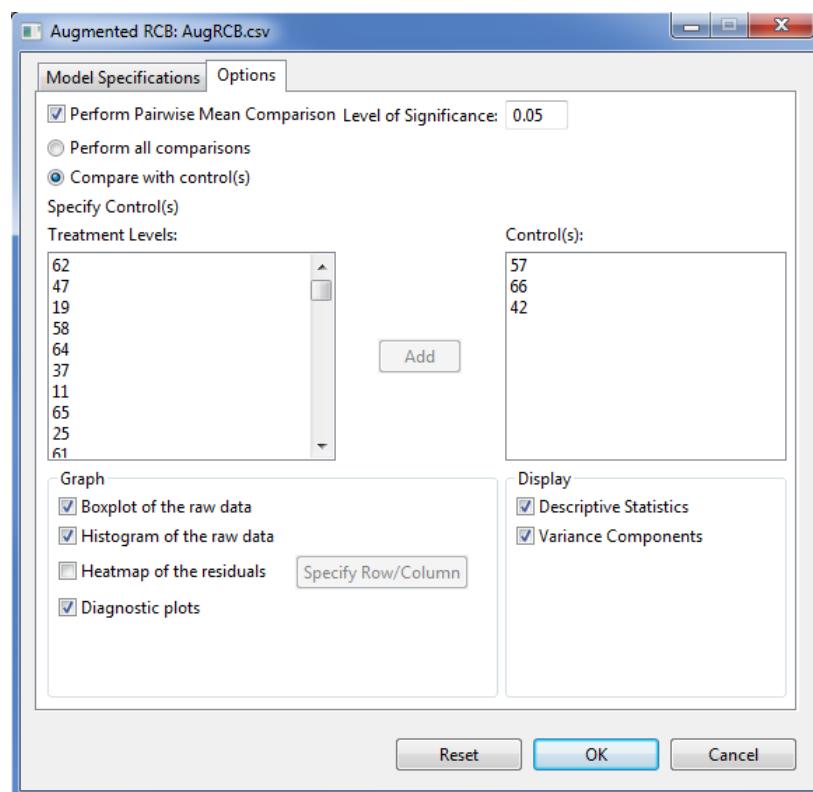
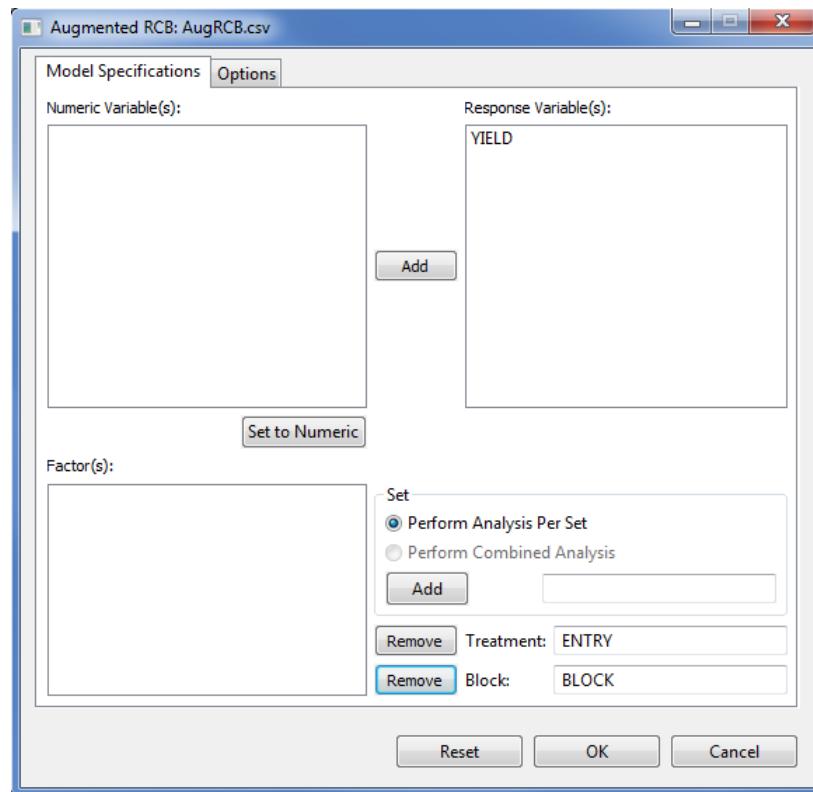
Block

This field is required. Only one item can be added in this entry box and should come from the **Factor(s)** list box.

Options Tab

This tab lets the user identify additional output to be displayed and set the level of significance to be used. To know more about the options in detail, see the discussion under *Incomplete Block Design > Balanced Incomplete Block > Options tab* of this user's manual.

For the example, the completed **Model Specification** tab and **Options** tab should appear as illustrated:



- Click **OK** button to perform the analysis. The **Augmented RCB** dialog box will be minimized and STAR activates the **Output** page of the **Result Viewer** tab.

Sample text output of the analysis is shown below:

DESIGN: Augmented Randomized Complete Block (ARCB)

=====

ANALYSIS FOR RESPONSE VARIABLE: YIELD

=====

Descriptive Statistics

Variable	N_NonMissObs	Mean	StdDev
YIELD	84	4.33	1.38

Summary Information

FACTOR	NO. OF LEVELS	LEVELS
BLOCK	4	1, 2, 3, 4
ENTRY	66	1, 2, ..., 66

Number of Observations Read and Used: 84

Estimates of Variance Components

Groups	Variance	StdDev
BLOCK	0.0000	0.0000
Residual	0.8766	0.9362

Testing for the Significance of Genotypic Effect

Models:

model2: YIELD ~ 1 + (1|BLOCK)
model1: YIELD ~ 1 + ENTRY + (1|BLOCK)

Source	Df	AIC	BIC	logLik	Chisq	Chi Df	Pr(>Chisq)
model2	3	296.3952	303.6877	-145.1976			
model1	68	233.7532	399.0488	-48.8766	192.64	65	0.0000

Source	Df	Sum Sq	Mean Sq	F value	Prob
ENTRY	65	141.50	2.18	2.48	0.0000

ENTRY LSMeans and Standard Error

ENTRY	LSMean	StdErrMean
-------	--------	------------

1	6.35	0.9362
2	6.50	0.9362
3	3.95	0.9362
4	5.60	0.9362
5	2.00	0.9362
6	3.50	0.9362
7	4.55	0.9362
8	3.90	0.9362
9	4.20	0.9362
10	1.05	0.9362
11	3.75	0.9362
12	3.80	0.9362
13	4.40	0.9362
14	2.60	0.9362
15	3.40	0.9362
16	8.25	0.9362
17	4.25	0.9362
18	4.35	0.9362
19	5.90	0.9362
20	4.40	0.9362
21	1.80	0.9362
22	3.45	0.9362
23	5.50	0.9362
24	5.40	0.9362
25	4.80	0.9362
26	4.70	0.9362
27	4.90	0.9362
28	3.75	0.9362
29	6.20	0.9362
30	4.50	0.9362
31	2.40	0.9362
32	4.00	0.9362
33	3.90	0.9362
34	6.60	0.9362
35	5.30	0.9362
36	3.90	0.9362
37	5.15	0.9362
38	3.70	0.9362
39	5.30	0.9362
40	7.00	0.9362
41	4.70	0.9362
42	3.40	0.9362
43	1.50	0.9362
44	4.05	0.9362
45	5.55	0.9362
46	5.60	0.9362
47	3.85	0.9362
48	3.40	0.9362
49	3.40	0.9362
50	4.90	0.9362
51	3.20	0.9362
52	2.00	0.9362
53	3.00	0.9362
54	4.05	0.9362
55	2.20	0.9362
56	3.05	0.9362
57	6.50	0.9362
58	7.00	0.9362
59	4.40	0.9362
60	7.50	0.9362
61	3.74	0.4681
62	4.34	0.4681

63	3.51	0.4681
64	4.55	0.4681
65	5.10	0.4681
66	4.17	0.4681

List of ENTRY pairs that are significantly different using Dunnett at alpha = 0.05

Compare with control = 57

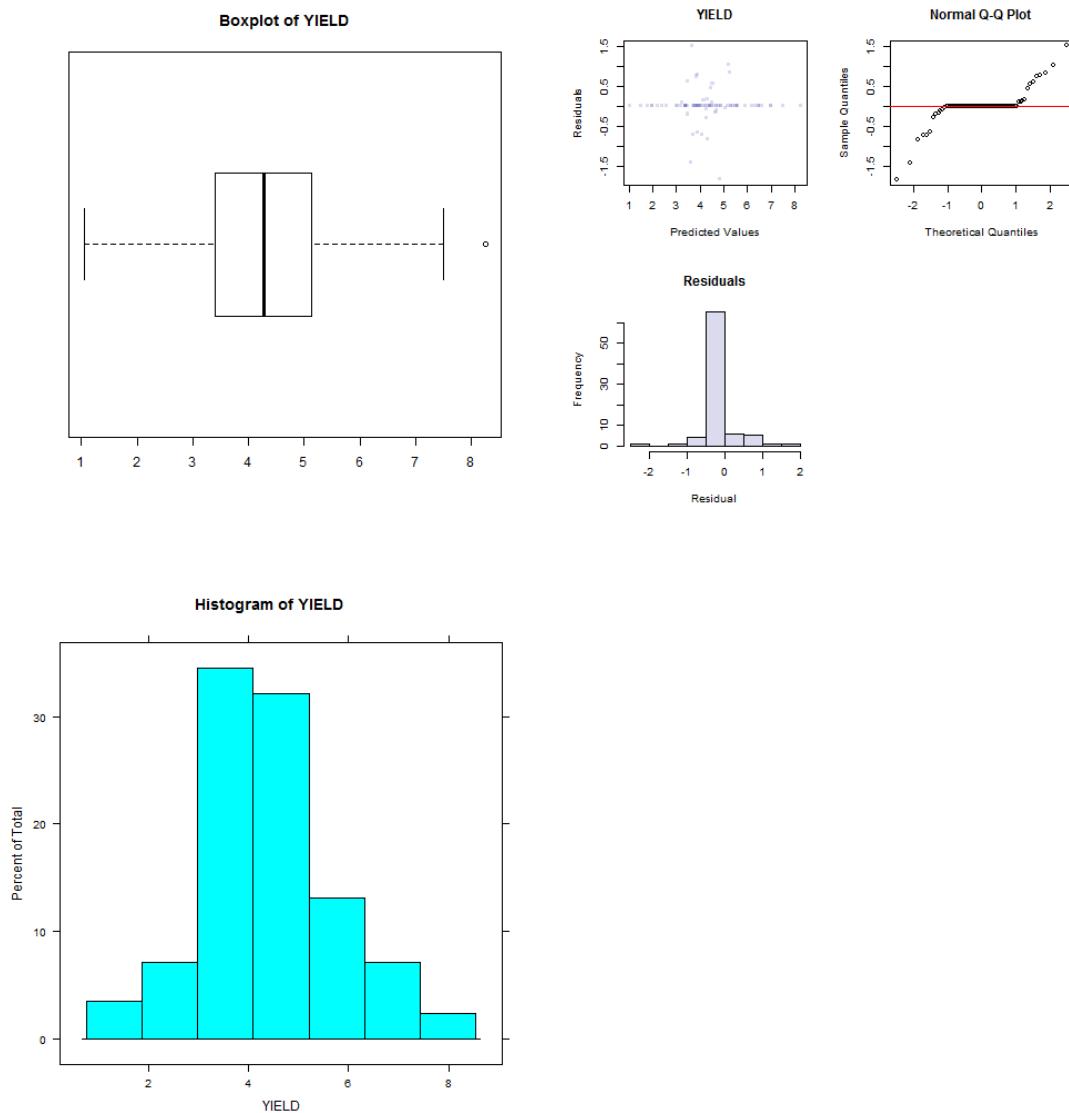
ENTRY	Control	Estimate	lwr	upr
5	57	-4.50	-8.71	-0.29
10	57	-5.45	-9.66	-1.24
21	57	-4.70	-8.91	-0.49
43	57	-5.00	-9.21	-0.79
52	57	-4.50	-8.71	-0.29
55	57	-4.30	-8.51	-0.09

Compare with control = 66

ENTRY	Control	Estimate	lwr	upr
16	66	4.08	0.5904	7.56

```
Compare with control = 42
-----
ENTRY Control Estimate lwr upr
-----
16      42       4.85  0.6388 9.06
-----
```

Sample graphical output of the analysis is shown below:



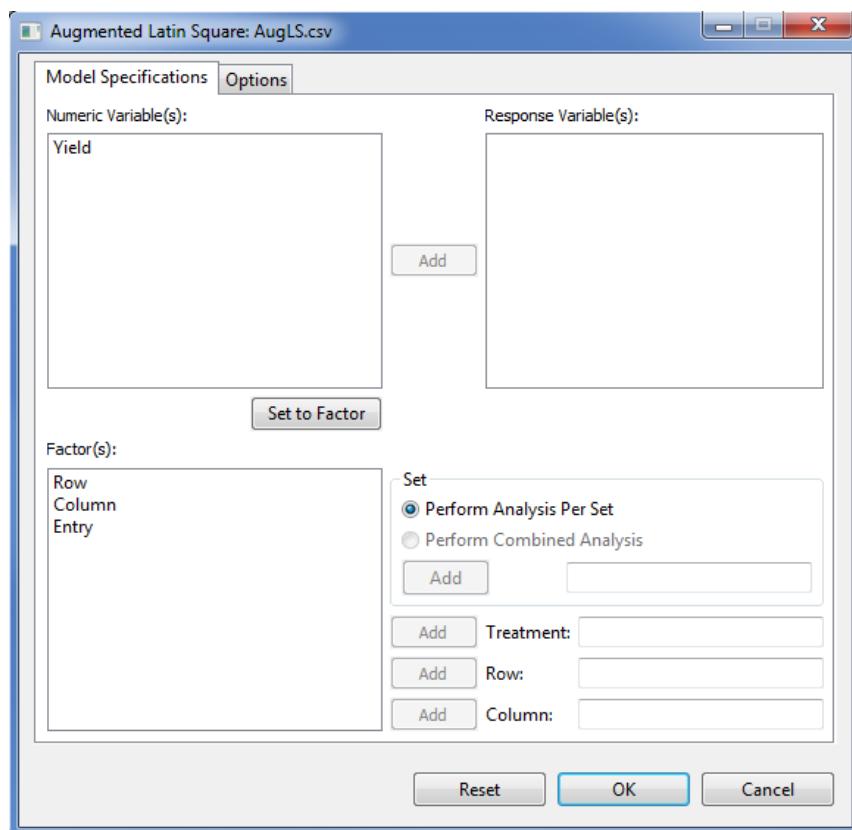
Augmented Latin Square Design

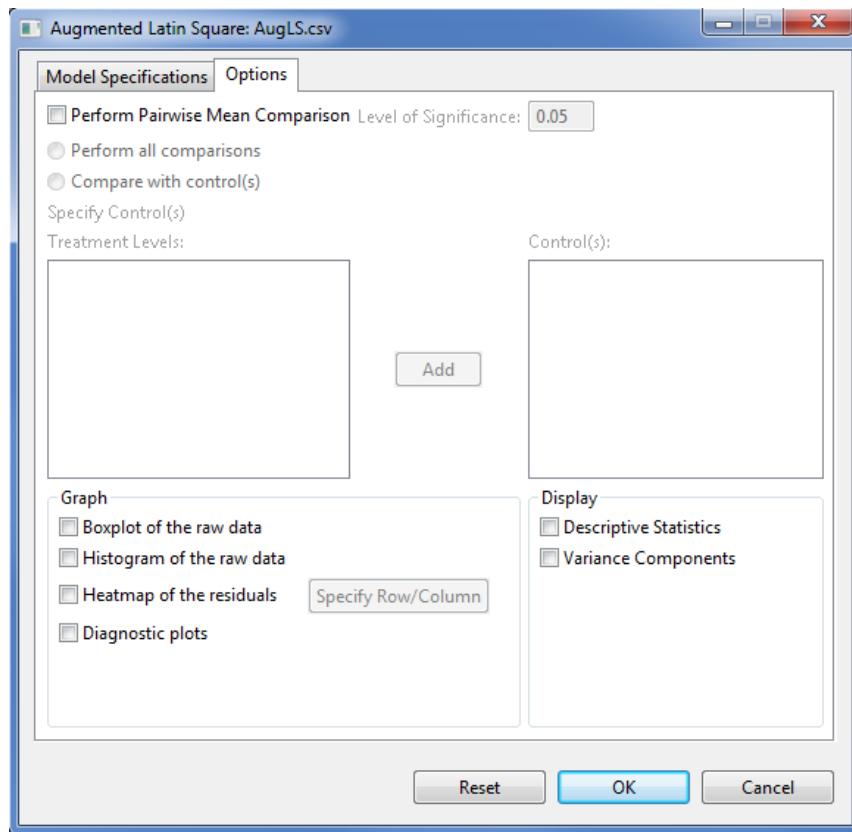
The steps to perform analysis for Incomplete Block Design are listed below:

- On the **Project Explorer**, double-click the file to be used for the analysis to open and view it in the Data Viewer.

For the example, using the project named *My Project*, import the data *AugLS* from the package. To import the data from the package, see Importing from Package section of this user manual.

- Choose **Analyze | Incomplete Block | Augmented Latin Square...** from the main window. The **Augmented Latin Square** dialog box will appear.





- Specify the required fields and appropriate options for the analysis.

Model Specifications Tab

Response Variable(s)

For the analysis to proceed, at least one item should be entered in the list box. The items to be entered should come from the **Numeric Variable(s)** list box.

Set

There are two options available, *perform analysis per set* (default) and *perform combined analysis*. If default option is selected and a **Set** variable is specified, STAR will perform analysis for each level of the **Set** variable. If the default option is selected and no **Set** variable is specified, STAR will perform the analysis as if the entire data came from only one set variable. If *perform combined analysis* is selected, a **Set** variable with at least two levels must be specified. Only one item can be added in this entry box and should come from the **Factor(s)** list box.

Treatment

This field is required. Only one item can be added in this entry box and should come from the **Factor(s)** list box.

Row

This field is required. Only one item can be added in this entry box and should come from the **Factor(s)** list box.

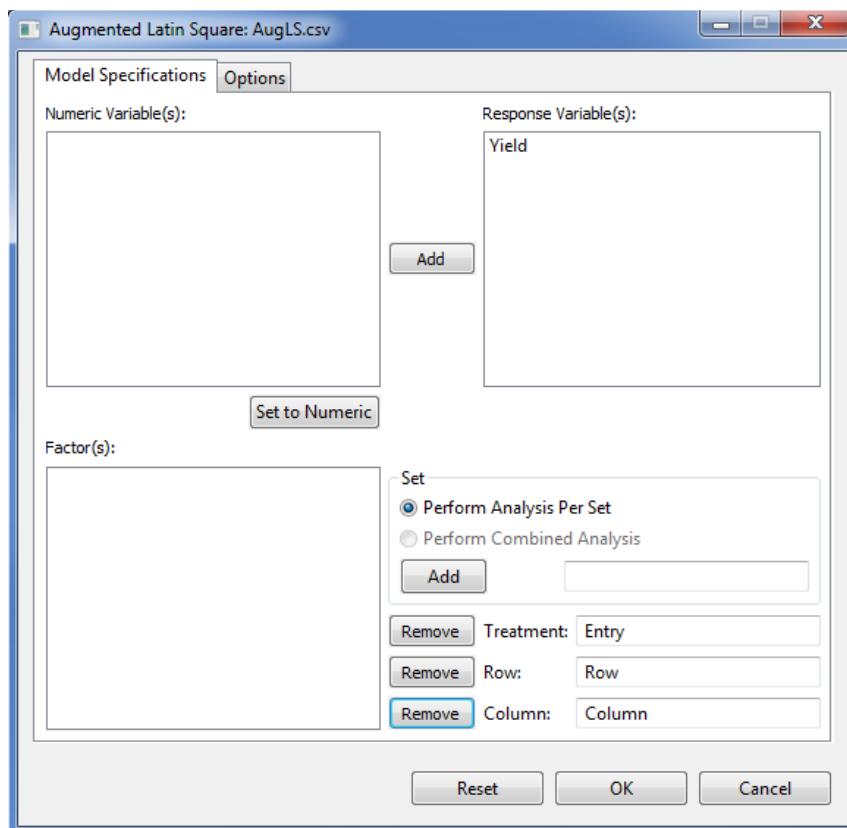
Column

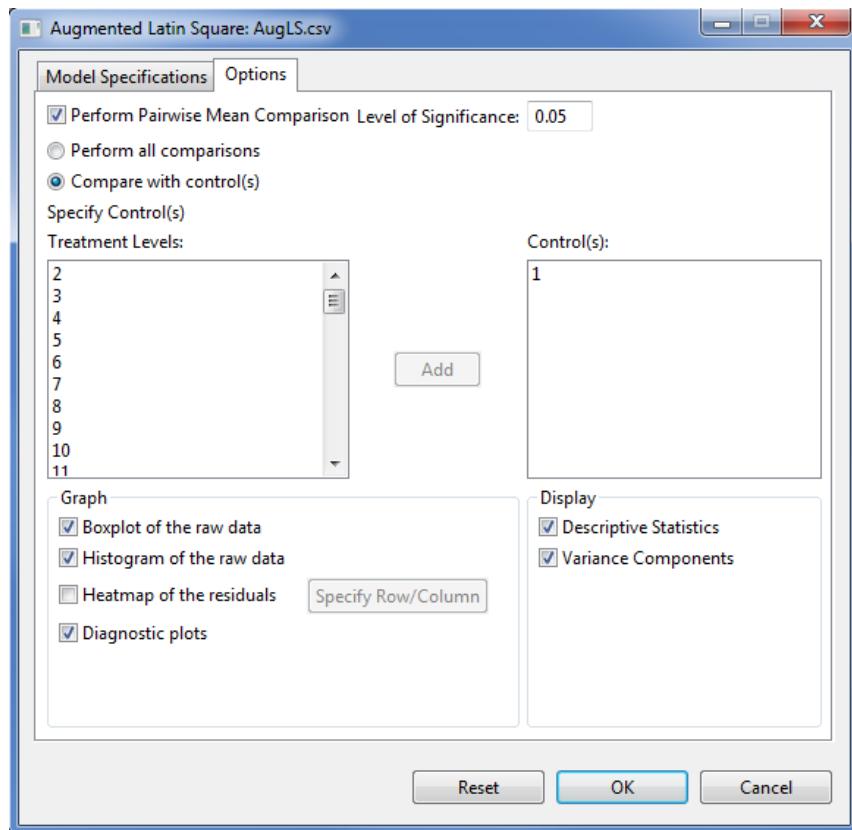
This field is required. Only one item can be added in this entry box and should come from the **Factor(s)** list box.

Options Tab

This tab lets the user identify additional output to be displayed and set the level of significance to be used. To know more about the options in detail, see the discussion under *Incomplete Block Design > Balanced Incomplete Block > Options tab* of this user's manual.

For the example, the completed **Model Specification** tab and **Options** tab should appear as illustrated:





- Click **OK** button to perform the analysis. The **Augmented Latin Square** dialog box will be minimized and STAR activates the **Output** page of the **Result Viewer** tab.

Sample text output of the analysis is shown below:

```

DESIGN: Augmented Latin Square
=====
ANALYSIS FOR RESPONSE VARIABLE: Yield
=====

Descriptive Statistics
-----
Variable   N_NonMissObs  Mean  StdDev
-----
Yield          75     4.78    1.91
-----

Summary Information
-----
FACTOR  NO. OF LEVELS  LEVELS
-----
Row      15           1, 10, ..., 9
Column    5           1, 2, 3, 4, 5
Entry     55           1, 2, ..., 55
-----
Number of Observations Read and Used: 75

```

Estimates of Variance Components

Groups	Variance	StdDev
Row	0.6662	0.8162
Column	0.2305	0.4801
Residual	1.8242	1.3506

Testing for the Significance of Genotypic Effect

Models:

model2: Yield ~ 1 + (1|Row) + (1|Column)
model1: Yield ~ 1 + Entry + (1|Row) + (1|Column)

Source	Df	AIC	BIC	logLik	Chisq	Chi Df	Pr(>Chisq)
model2	4	316.9567	326.2267	-154.4784			
model1	58	291.0435	425.4578	-87.5217	133.91	54	0.0000

Source	Df	Sum Sq	Mean Sq	F value	Prob
Entry	54	179.50	3.32	1.82	0.0000

Entry LSMeans and Standard Error

Entry LSMean StdErrMean

1	4.24	1.63
2	6.39	1.63
3	3.72	1.63
4	9.89	1.63
5	4.29	1.63
6	5.67	1.63
7	8.75	1.63
8	5.14	1.63
9	4.36	1.63
10	3.18	1.63
11	4.36	1.63
12	6.04	1.63
13	3.27	1.63
14	6.10	1.63
15	8.06	1.63
16	4.76	1.63
17	4.11	1.63
18	6.08	1.63
19	2.39	1.63
20	5.99	1.63
21	3.58	1.63
22	2.75	1.63
23	8.06	1.63
24	6.16	1.63
25	3.66	1.63
26	2.68	1.63
27	3.75	1.63
28	2.41	1.63

29	6.23	1.63
30	4.61	1.63
31	4.21	1.63
32	9.11	1.63
33	7.58	1.63
34	3.19	1.63
35	5.84	1.63
36	6.68	1.63
37	0.96	1.63
38	4.02	1.63
39	5.60	1.63
40	3.89	1.63
41	2.51	1.63
42	2.89	1.63
43	4.08	1.63
44	5.41	1.63
45	2.91	1.63
46	5.51	1.63
47	7.82	1.63
48	3.91	1.63
49	4.48	1.63
50	4.20	1.63
51	3.25	0.74
52	4.40	0.74
53	6.02	0.74
54	3.62	0.74
55	5.28	0.74

List of Entry pairs that are significantly different using Dunnett at alpha = 0.05

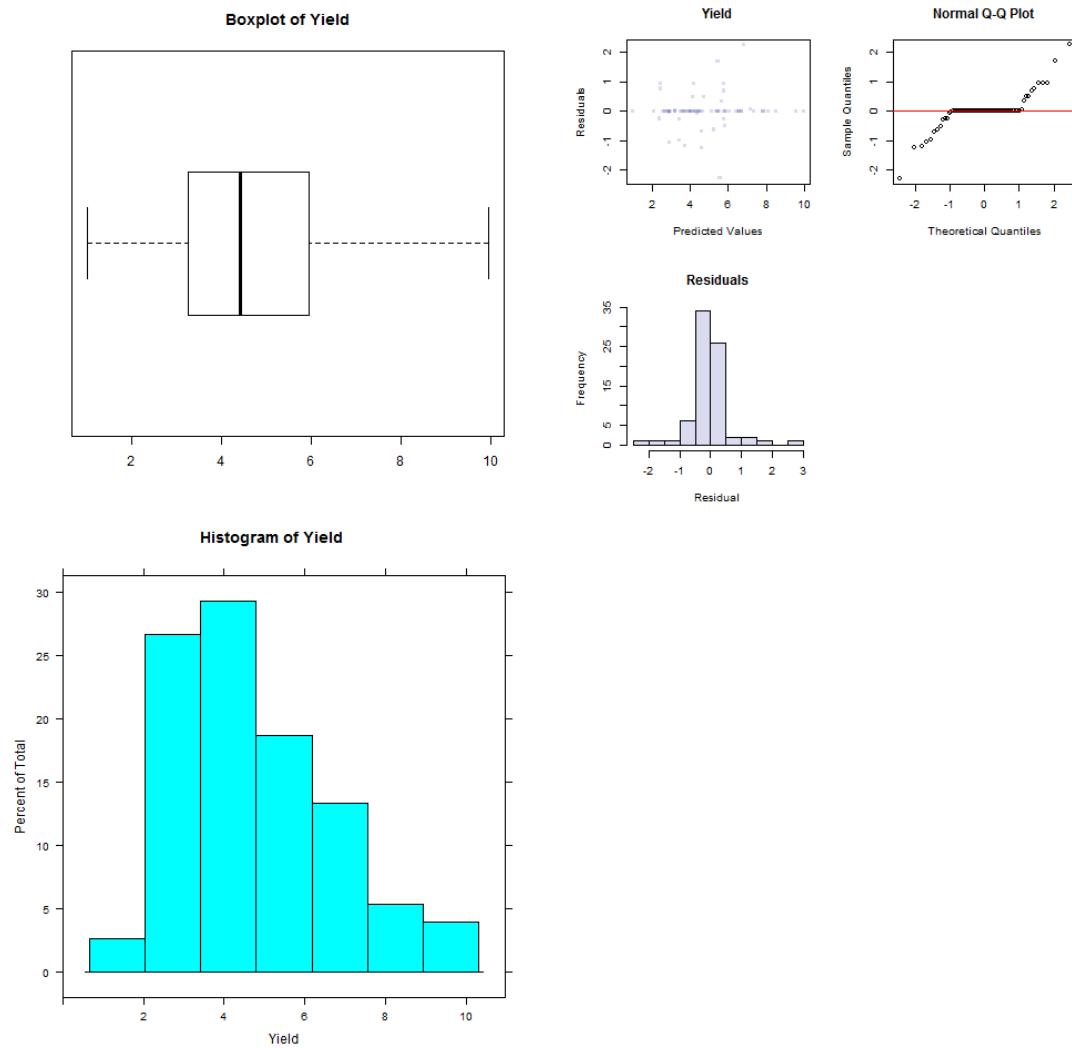
Compare with control = 51

Entry	Control	Estimate	lwr	upr
4	51	6.63	0.8524	12.41
32	51	5.85	0.0730	11.63

Compare with control = 54

Entry	Control	Estimate	lwr	upr
4	54	6.27	0.4892	12.05

Sample graphical output:



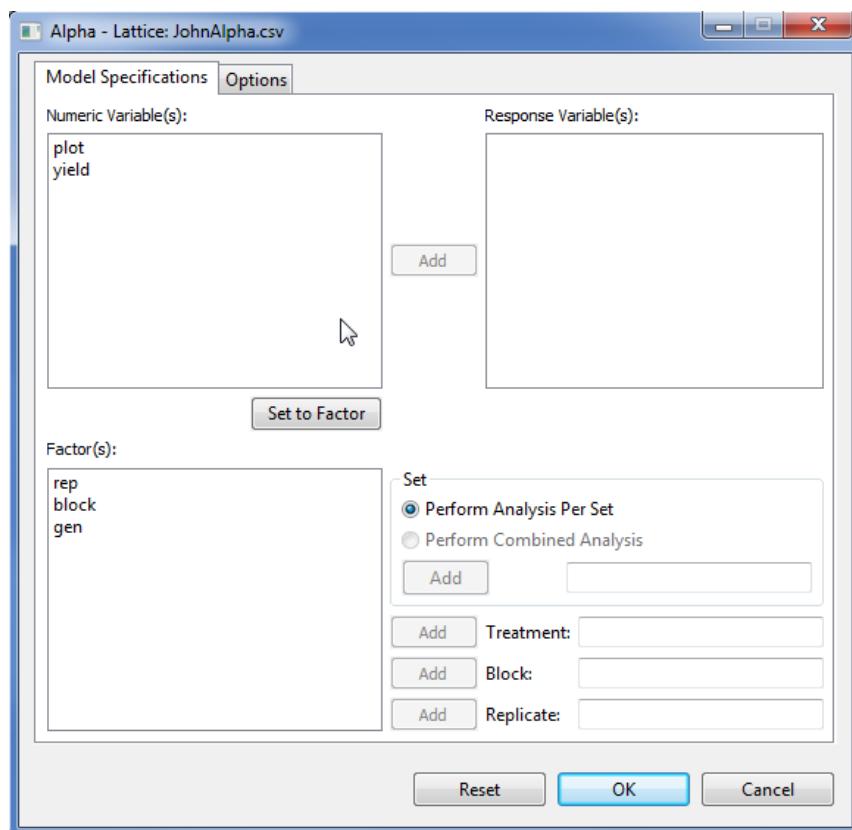
Alpha Lattice Design

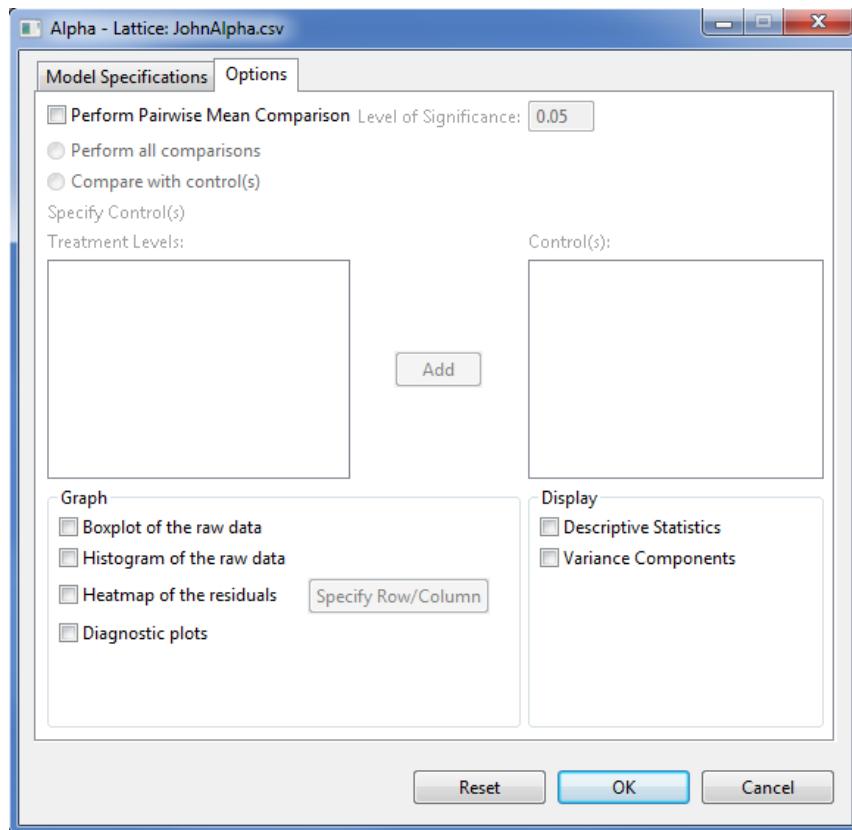
The steps to perform analysis for Incomplete Block Design are listed below:

- On the **Project Explorer**, double-click the file to be used for the analysis to open and view it in the Data Viewer.

For the example, using the project named *My Project*, import the data *JohnAlpha* from the package. To import the data from the package, see *Importing from Package* section of this user manual.

- Choose **Analyze | Incomplete Block | Augmented Latin Square...** from the main window. The **Alpha-Lattice** dialog box will appear.





- Specify the required fields and appropriate options for the analysis.

Model Specifications Tab

Response Variable(s)

For the analysis to proceed, at least one item should be entered in the list box. The items to be entered should come from the **Numeric Variable(s)** list box.

Set

There are two options available, *perform analysis per set* (default) and *perform combined analysis*. If default option is selected and a **Set** variable is specified, STAR will perform analysis for each level of the **Set** variable. If the default option is selected and no **Set** variable is specified, STAR will perform the analysis as if the entire data came from only one set variable. If *perform combined analysis* is selected, a **Set** variable with at least two levels must be specified. Only one item can be added in this entry box and should come from the **Factor(s)** list box.

Treatment

This field is required. Only one item can be added in this entry box and should come from the **Factor(s)** list box.

Block

This field is required. Only one item can be added in this entry box and should come from the **Factor(s)** list box.

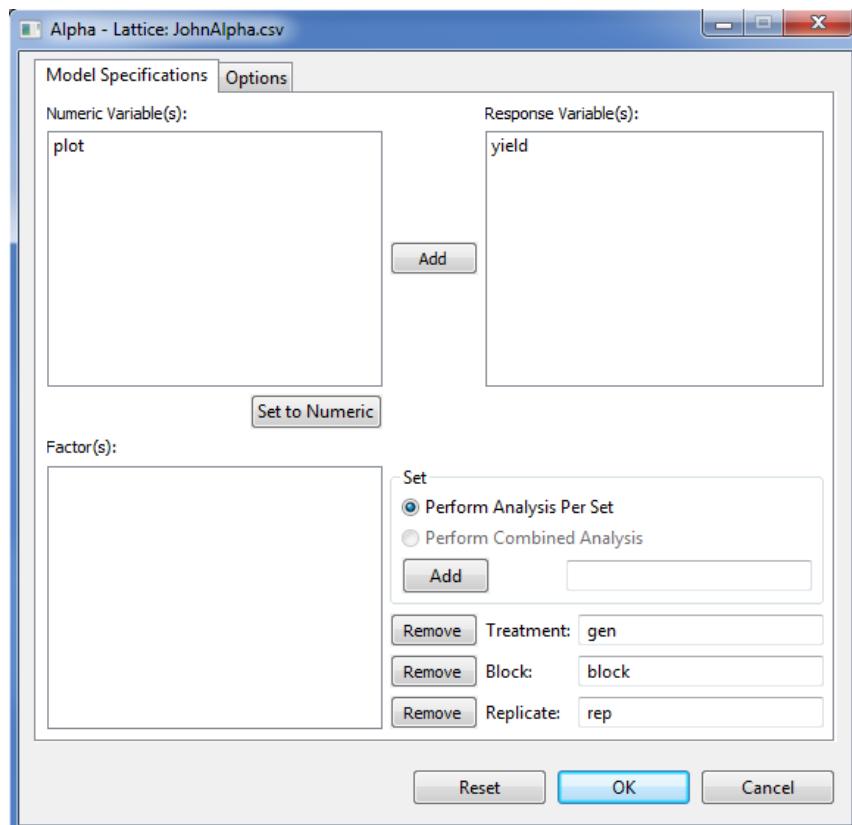
Replicate

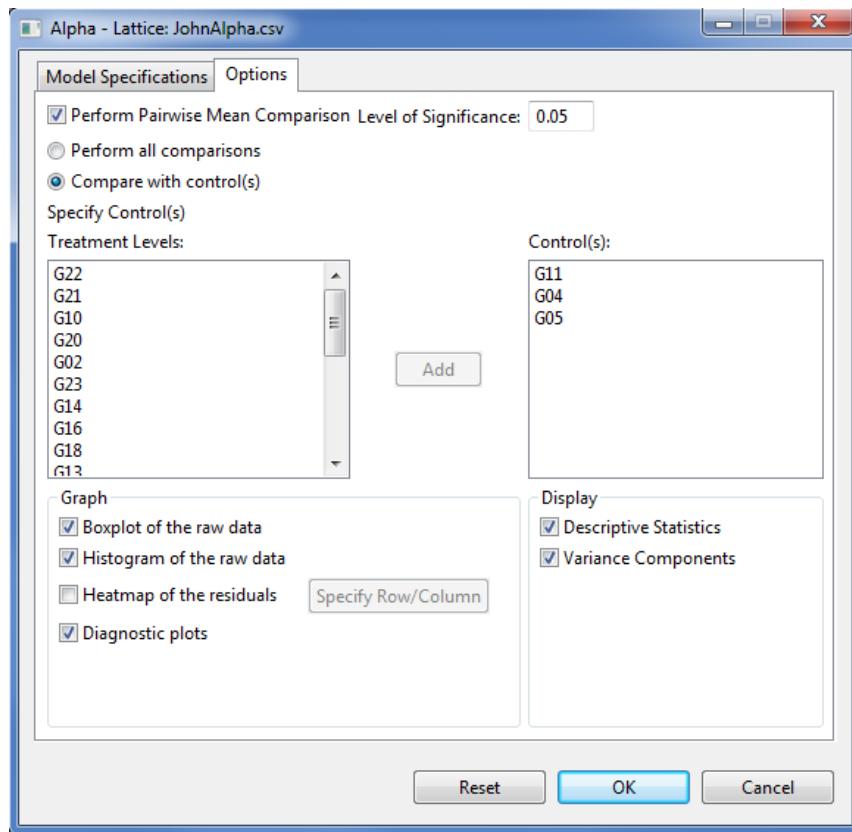
This field is required. Only one item can be added in this entry box and should come from the **Factor(s)** list box.

Options Tab

This tab lets the user identify additional output to be displayed and set the level of significance to be used. To know more about the options in detail, see the discussion under *Incomplete Block Design > Balanced Incomplete Block > Options tab* of this user's manual.

For the example, the completed **Model Specification** tab and **Options** tab should appear as illustrated:





- Click **OK** button to perform the analysis. The **Alpha Lattice** dialog box will be minimized and STAR activates the **Output** page of the **Result Viewer** tab.

Sample text output of the analysis is shown below:

```

DESIGN: Alpha Lattice
=====
ANALYSIS FOR RESPONSE VARIABLE: yield
=====

Descriptive Statistics
-----
Variable   N_NonMissObs  Mean  StdDev
-----
yield          72    4.48   0.6098
-----

Summary Information
-----
FACTOR  NO. OF LEVELS  LEVELS
-----
rep      3            R1, R2, R3
block    6            B1, B2, ..., B6
gen     24            G01, G02, ..., G24
-----
Number of Observations Read and Used: 72

```

Estimates of Variance Components

Groups	Variance	StdDev
block:rep	0.0619	0.2489
rep	0.1139	0.3376
Residual	0.0852	0.2919

Testing for the Significance of Genotypic Effect

Models:

model2: yield ~ 1 + (1|rep/block)
model1: yield ~ 1 + gen + (1|rep/block)

Source	Df	AIC	BIC	logLik	Chisq	Chi Df	Pr(>Chisq)
model2	4	125.9362	135.0428	-58.9681			
model1	27	81.7070	143.1770	-13.8535	90.23	23	0.0000

Source	Df	Sum Sq	Mean Sq	F value	Prob
gen	23	10.68	0.4643	5.45	0.0000

gen LSMeans and Standard Error

gen LSMean StdErrMean

G01	5.11	0.2761
G02	4.48	0.2761
G03	3.50	0.2761
G04	4.49	0.2761
G05	5.04	0.2760
G06	4.54	0.2760
G07	4.11	0.2761
G08	4.53	0.2761
G09	3.50	0.2760
G10	4.37	0.2761
G11	4.28	0.2761
G12	4.76	0.2761
G13	4.76	0.2760
G14	4.78	0.2760
G15	4.97	0.2760
G16	4.73	0.2761
G17	4.60	0.2760
G18	4.36	0.2761
G19	4.84	0.2760
G20	4.04	0.2760
G21	4.80	0.2760
G22	4.53	0.2760
G23	4.25	0.2760
G24	4.15	0.2761

List of gen pairs that are significantly different using Dunnett at alpha = 0.05

Compare with control = G11

gen	Control	Estimate	lwr	upr
G01	G11	0.8244	0.0671	1.58

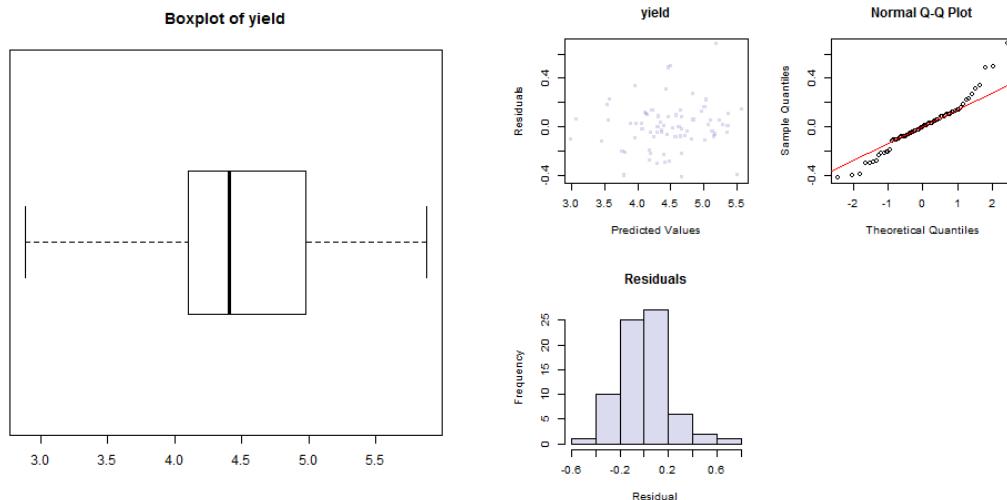
Compare with control = G04

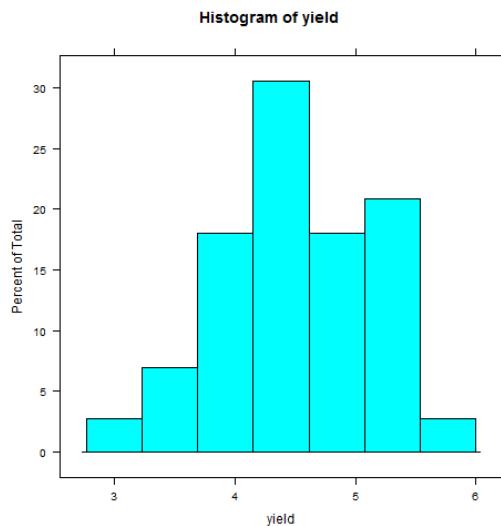
gen	Control	Estimate	lwr	upr
G03	G04	-0.9909	-1.78	-0.1993
G09	G04	-0.9879	-1.78	-0.1962

Compare with control = G05

gen	Control	Estimate	lwr	upr
G03	G05	-1.54	-2.30	-0.7760
G07	G05	-0.93	-1.69	-0.1665
G09	G05	-1.54	-2.30	-0.7734
G20	G05	-1.00	-1.75	-0.2403
G24	G05	-0.88	-1.67	-0.0919

Sample graphical output:





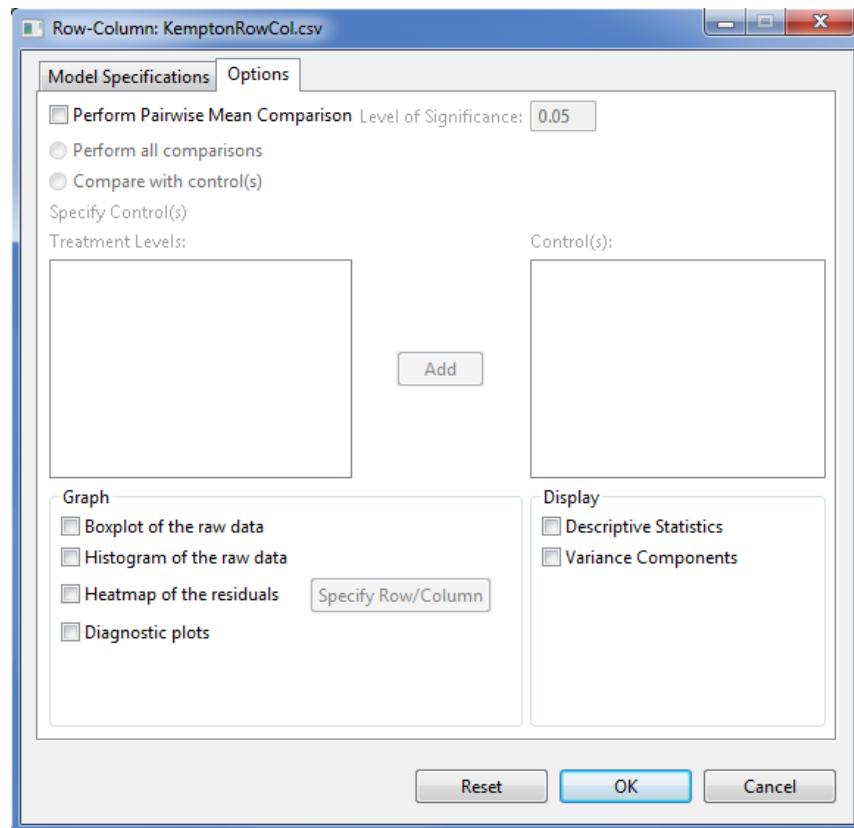
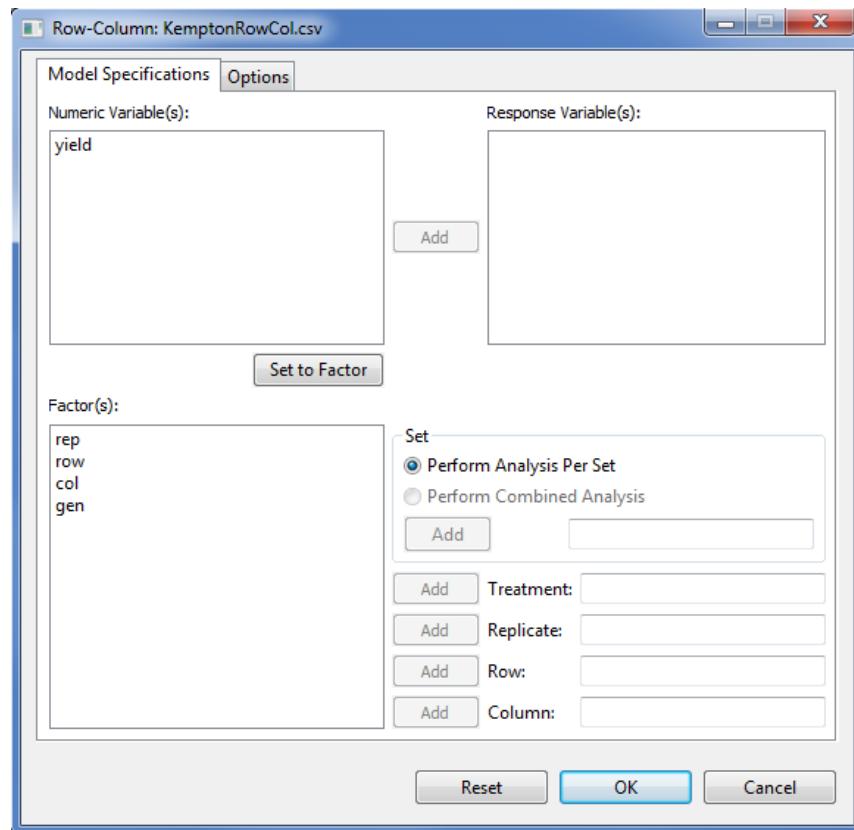
Row-Column Design

The steps to perform analysis for Incomplete Block Design are listed below:

- On the **Project Explorer**, double-click the file to be used for the analysis to open and view it in the Data Viewer.

For the example, using the project named *My Project*, import the data *KemptonRowCol* from the package. To import the data from the package, see Importing from Package section of this user manual.

- Choose **Analyze | Incomplete Block | Augmented Latin Square...** from the main window. The **Row-Column** dialog box will appear.



- Specify the required fields and appropriate options for the analysis.

Model Specifications Tab

Response Variable(s)

For the analysis to proceed, at least one item should be entered in the list box. The items to be entered should come from the **Numeric Variable(s)** list box.

Set

There are two options available, *perform analysis per set* (default) and *perform combined analysis*. If default option is selected and a **Set** variable is specified, STAR will perform analysis for each level of the **Set** variable. If the default option is selected and no **Set** variable is specified, STAR will perform the analysis as if the entire data came from only one set variable. If *perform combined analysis* is selected, a **Set** variable with at least two levels must be specified. Only one item can be added in this entry box and should come from the **Factor(s)** list box.

Treatment

This field is required. Only one item can be added in this entry box and should come from the **Factor(s)** list box.

Replicate

This field is required. Only one item can be added in this entry box and should come from the **Factor(s)** list box.

Row

This field is required. Only one item can be added in this entry box and should come from the **Factor(s)** list box.

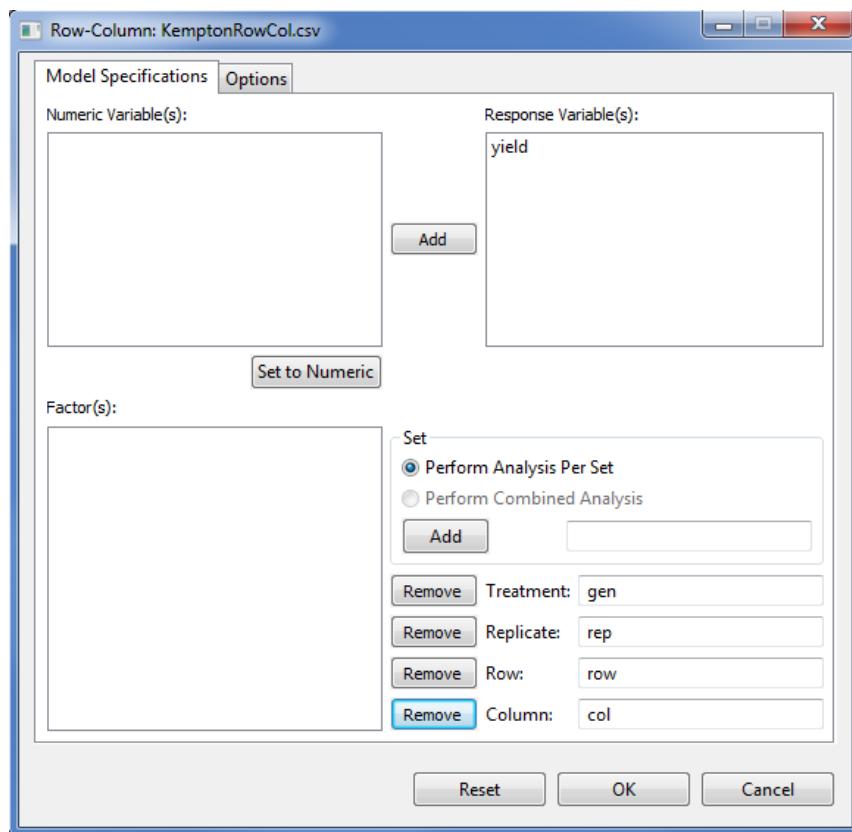
Column

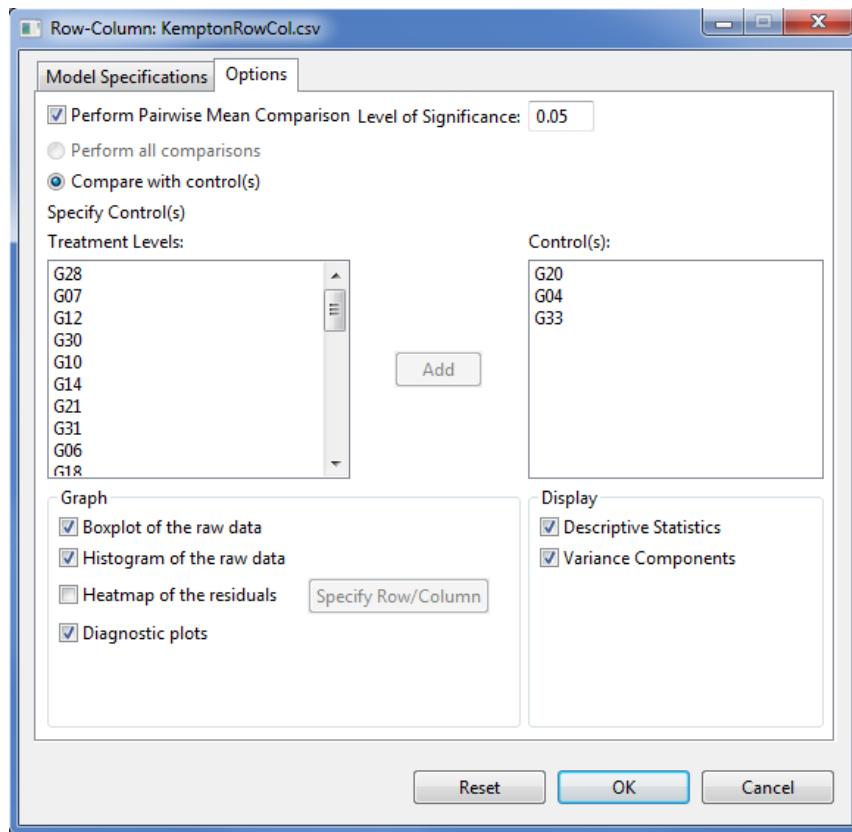
This field is required. Only one item can be added in this entry box and should come from the **Factor(s)** list box.

Options Tab

This tab lets the user identify additional output to be displayed and set the level of significance to be used. To know more about the options in detail, see the discussion under *Incomplete Block Design > Balanced Incomplete Block > Options tab* of this user's manual.

For the example, the completed **Model Specification** tab and **Options** tab should appear as illustrated:





- Click **OK** button to perform the analysis. The **Row-Column** dialog box will be minimized and STAR activates the **Output** page of the **Result Viewer** tab.

Sample text output of the analysis is shown below:

```

DESIGN: Row-Column
=====
ANALYSIS FOR RESPONSE VARIABLE: yield
=====

Descriptive Statistics
-----
Variable   N_NonMissObs  Mean  StdDev
-----
yield          68    4.39  0.9997
-----

Summary Information
-----
FACTOR  NO. OF LEVELS  LEVELS
-----
rep      2            R1, R2
row      5            1, 2, 3, 4, 5

```

```
col      7           1, 2, ..., 7
gen     35          G01, G02, ..., G35
-----
Number of Observations Read and Used: 68
```

Estimates of Variance Components

```
Groups      Variance   StdDev
-----
rep:col    0.1927    0.4389
rep:row    0.0639    0.2527
rep        0.7036    0.8388
Residual   0.0902    0.3003
-----
```

Testing for the Significance of Genotypic Effect

Models:

```
model2: yield ~ 1 + (1|rep) + (1|rep:row) + (1|rep:col)
model1: yield ~ 1 + gen + (1|rep) + (1|rep:row) + (1|rep:col)
```

```
Source      Df       AIC      BIC      logLik      Chisq      Chi Df  Pr(>Chisq)
-----
model2      5    160.7747  171.8723  -75.3874
model1     39    100.3049  186.8657  -11.1524   128.47      34      0.0000
-----
```

```
Source      Df  Sum Sq  Mean Sq  F value     Prob
-----
gen        34   15.02   0.4416     4.90   0.0000
-----
```

gen LSMeans and Standard Error

```
gen  LSMean  StdErrMean
-----
G01   4.81    0.6625
G02   3.92    0.6641
G03   5.10    0.6649
G04   3.52    0.6629
G05   4.40    0.6643
G06   5.41    0.6653
G07   5.09    0.6629
G08   4.60    0.6654
G09   4.35    0.6634
G10   4.33    0.6644
G11   4.93    0.6638
-----
```

G12	4.95	0.6676
G13	4.68	0.6653
G14	4.76	0.6631
G15	3.21	0.7270
G16	3.96	0.7254
G17	4.15	0.6655
G18	4.56	0.6646
G19	5.67	0.6650
G20	4.32	0.6623
G21	4.59	0.6627
G22	4.01	0.6647
G23	3.42	0.6628
G24	3.89	0.6623
G25	4.64	0.6647
G26	3.76	0.6666
G27	4.70	0.6651
G28	4.29	0.6646
G29	3.79	0.6638
G30	3.95	0.6630
G31	3.86	0.6643
G32	4.26	0.6638
G33	4.91	0.6653
G34	4.30	0.6623
G35	3.60	0.6644

List of gen pairs that are significantly different using Dunnett at alpha = 0.05

Compare with control = G20

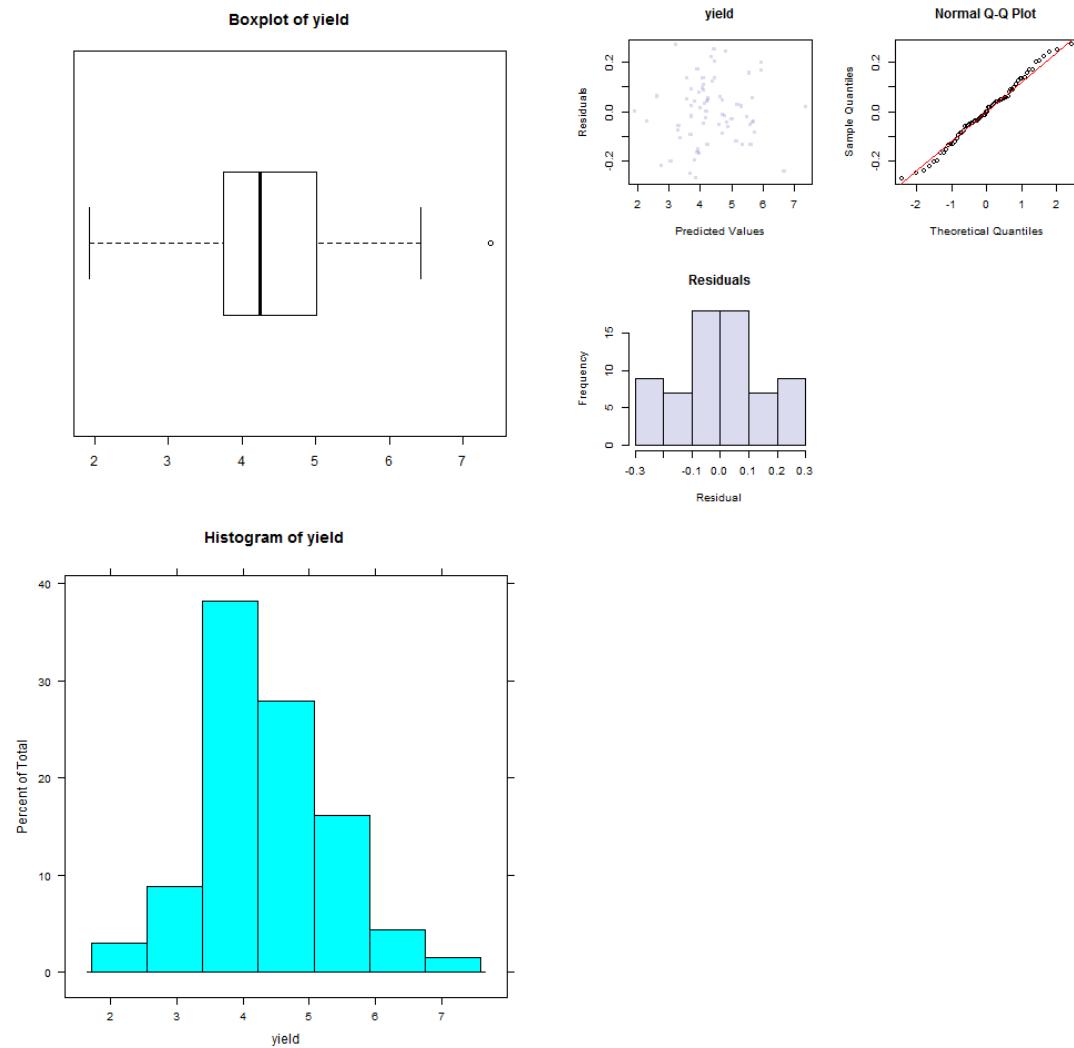
gen	Control	Estimate	lwr	upr
G19	G20	1.35	0.2005	2.50

Compare with control = G04

gen	Control	Estimate	lwr	upr
G01	G04	1.29	0.1485	2.44
G03	G04	1.58	0.4511	2.70
G06	G04	1.89	0.7015	3.08
G07	G04	1.56	0.4606	2.67
G11	G04	1.41	0.3262	2.49
G12	G04	1.43	0.3195	2.53
G13	G04	1.16	0.0313	2.29
G14	G04	1.24	0.1567	2.33
G19	G04	2.15	0.9890	3.31
G25	G04	1.12	0.0231	2.22

```
G27  G04          1.18  0.0044  2.35
G33  G04          1.39  0.2750  2.51
-----
Compare with control =  G33
-----
gen  Control      Estimate     lwr      upr
-----
G04  G33          -1.39  -2.51 -0.2784
G15  G33          -1.70  -3.23 -0.1696
G23  G33          -1.49  -2.67 -0.3130
G35  G33          -1.31  -2.52 -0.1095
-----
```

Sample graphical output:



Correlation Analysis

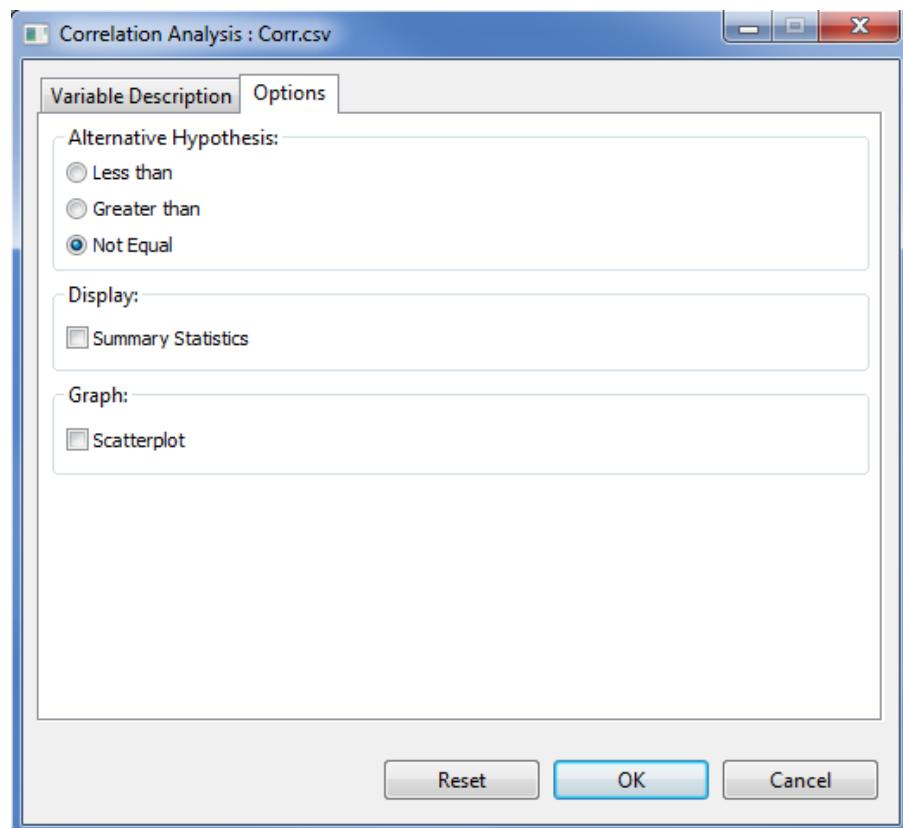
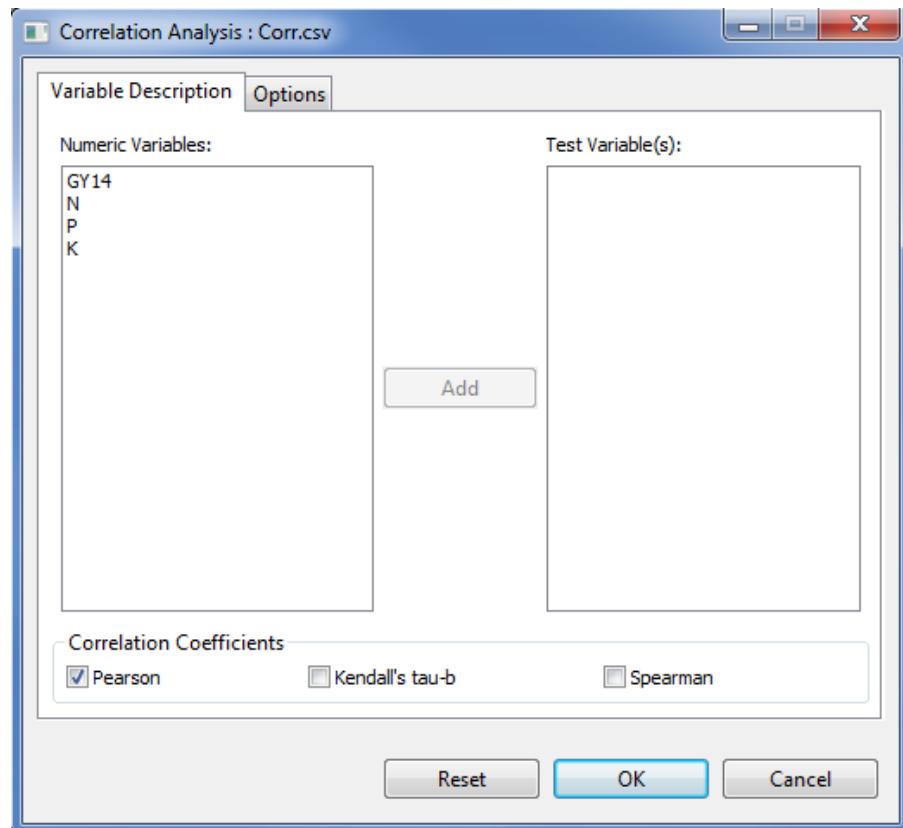
The **Correlation Analysis** is used to determine the strength of linear relationship between variables. The **Correlation Analysis** submenu performs bivariate correlation using the pearson's correlation coefficient, spearman's rho and kendall tau. By default, it uses the pearson's correlation coefficient.

The steps to perform Correlation Analysis are listed below:

- On the **Project Explorer**, double-click the file to be used for the analysis open and view it in the Data Viewer tab.

For the example, using the project named *MyProject*, import the data *Corr* from the package. To import the data from the package, see *Importing from Package* section of this user manual.

- Click **Analyze | Correlation...** from the main window. The **Correlation Analysis** dialog box will appear.



- Specify the required field and appropriate options for the analysis:

Variable Description Tab

Test Variable(s)

For the analysis to proceed, this list box should have at least two entries.

Correlation Coefficient

For the analysis to proceed, at least one method should be selected. By default, Pearson's correlation coefficient is chosen. For quantitative and normally distributed variables, choose the Pearson correlation coefficient. If the data are not normally distributed or ordinal level, choose Kendall's tau or Spearman, which measures the association between ranks. The correlation coefficient ranges from -1 to +1.

Option Tab

Alternative Hypothesis

User can select a one-tailed (less than or greater than) or two-tailed test (not equal). The default alternative hypothesis used is that for the two-sided test.

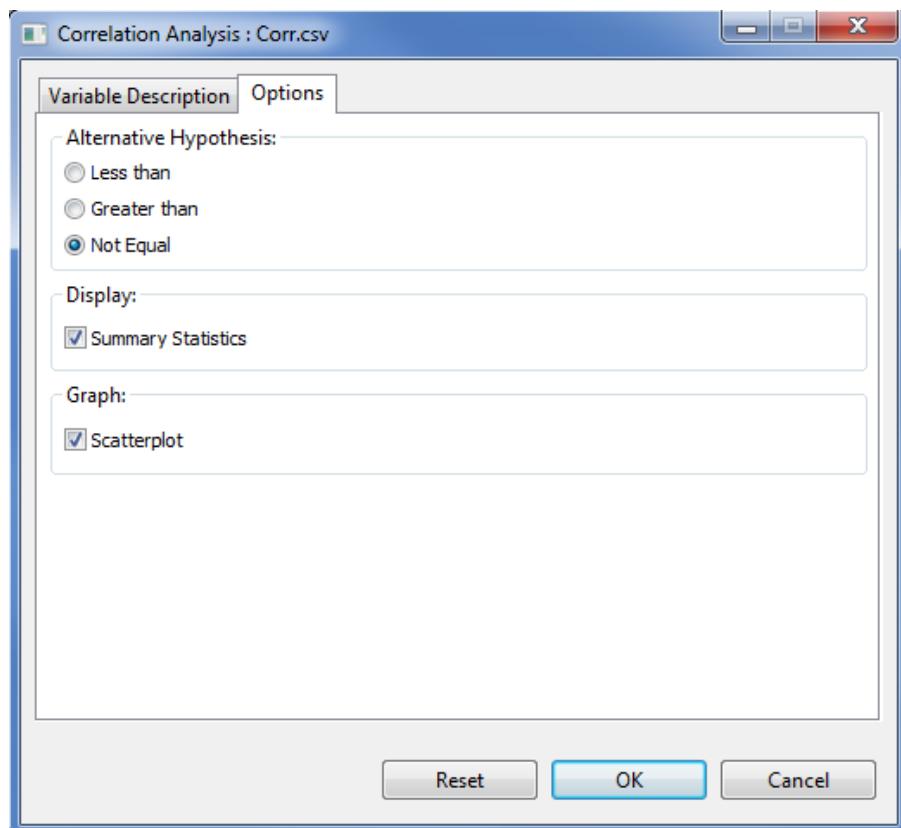
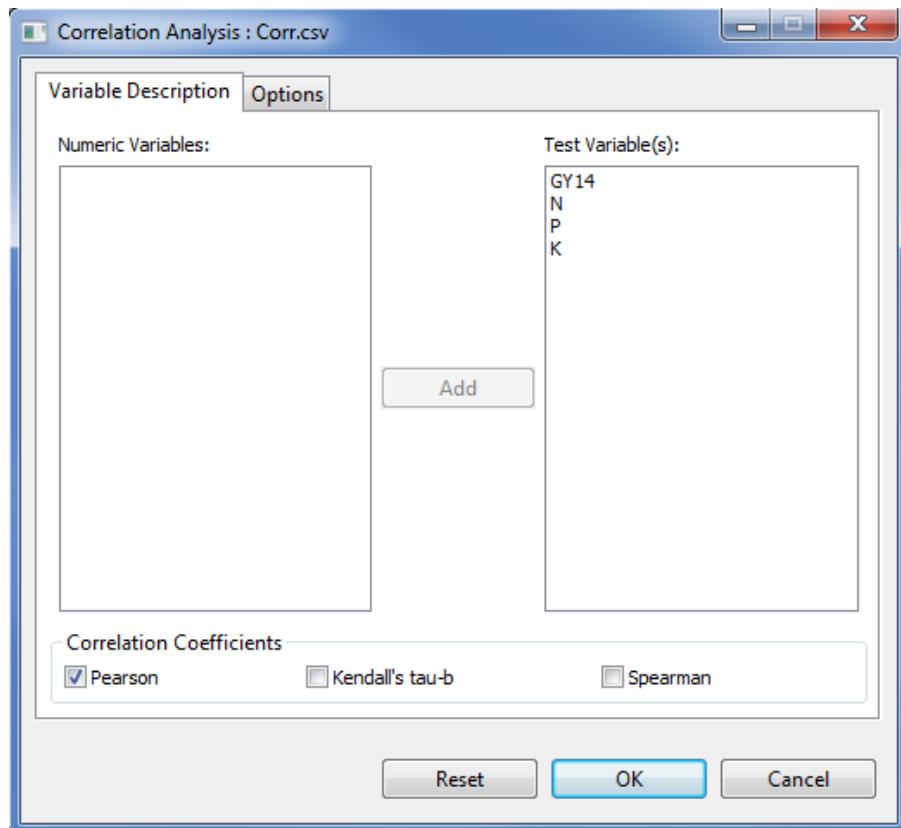
Display Summary Statistics

If this option is selected, a summary table with number of observations, minimum, maximum, mean and standard deviation will be displayed.

Scatterplot

If this option is selected, scatter plot for all pair of variables listed in the **Test Variable(s)** list box will be created.

For the example, the completed **Variable Description** tab and **Option** tab should appear as illustrated:



- Once all options have been specified, click the **OK** button. The **Correlation Analysis** dialog box will be minimized and STAR activates the **Result Viewer** tab which shows the results of the analysis.

Sample output of the Correlation Analysis using Pearson's product-moment correlation is shown below.

Result of Correlation Analysis

DESCRIPTIVE STATISTICS

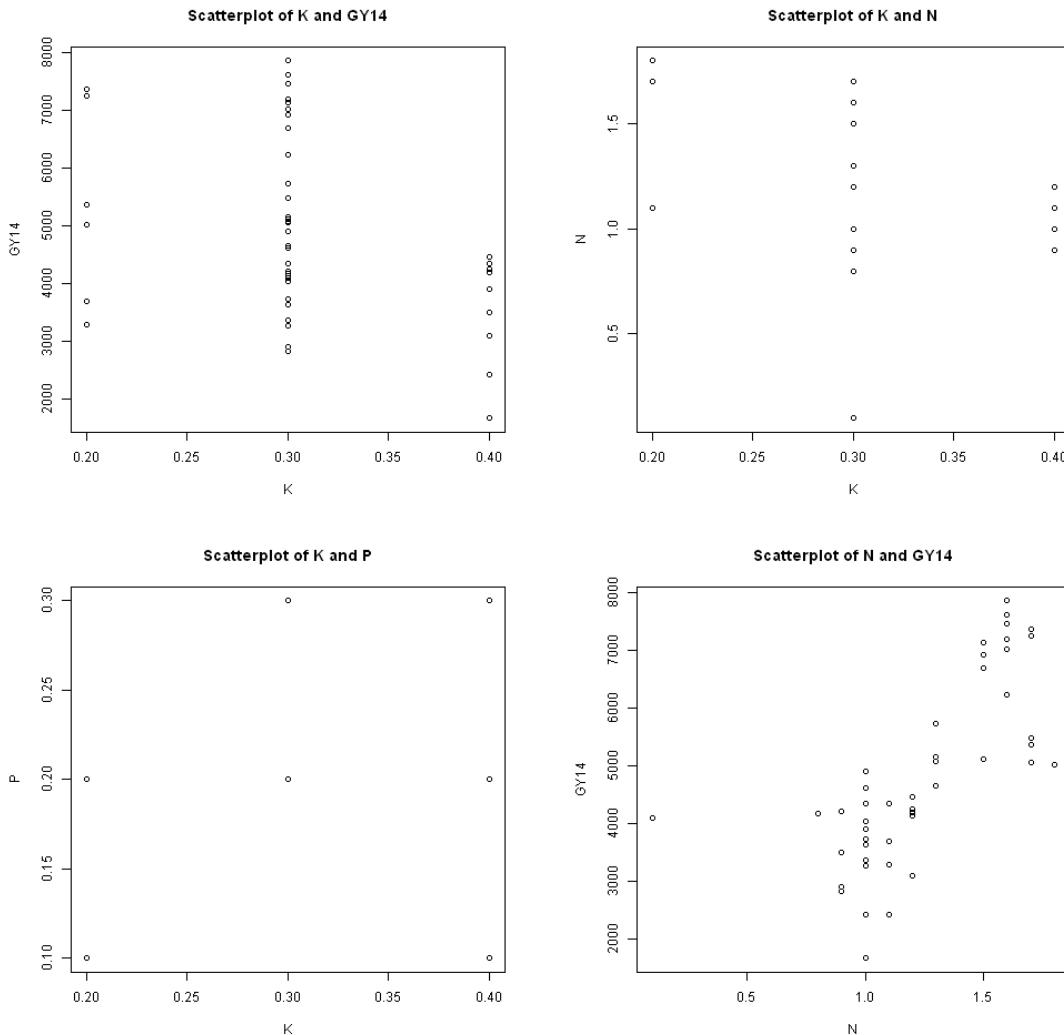
Variable	N_NonMissObs	Min	Max	Mean	StdDev
GY14	48	1678.00	7860.00	4788.67	1552.27
N	48	0.10	1.80	1.23	0.33
P	48	0.10	0.30	0.23	0.08
K	48	0.20	0.40	0.31	0.06

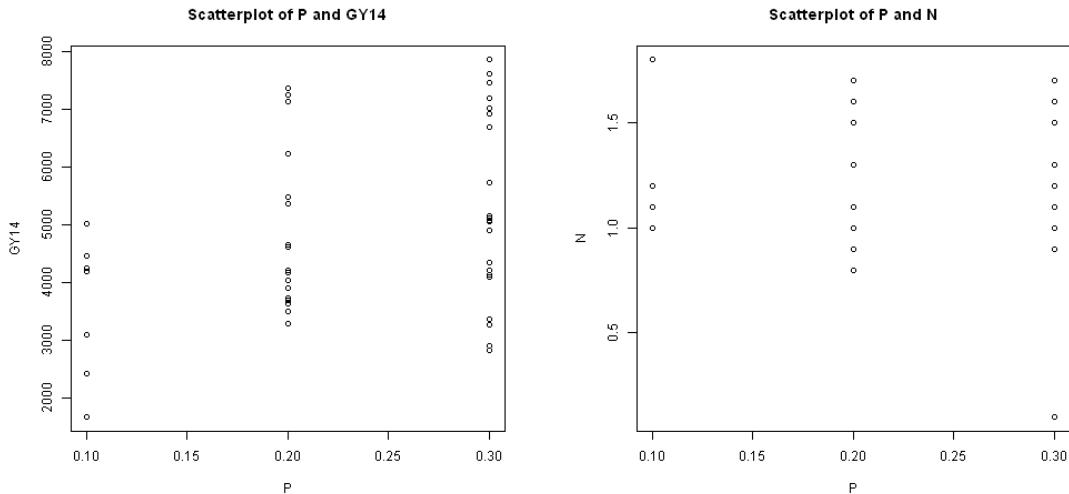
CORRELATION ANALYSIS

Pearson's product-moment correlation, Prob > |r|

		GY14	N	P	K
GY14	coef	1.00	0.72	0.38	-0.40
	p-value		0.0000	0.0080	0.0053
	n	48	48	48	48
N	coef	0.72	1.00	0.02	-0.34
	p-value	0.0000		0.8686	0.0180
	n	48	48	48	48
P	coef	0.38	0.02	1.00	-0.35
	p-value	0.0080	0.8686		0.0161
	n	48	48	48	48
K	coef	-0.40	-0.34	-0.35	1.00
	p-value	0.0053	0.0180	0.0161	
	n	48	48	48	48

If a scatter plot is requested, the graph can be viewed in the **Graph Viewer**. Sample generated graphs are shown below:





Linear Regression Analysis

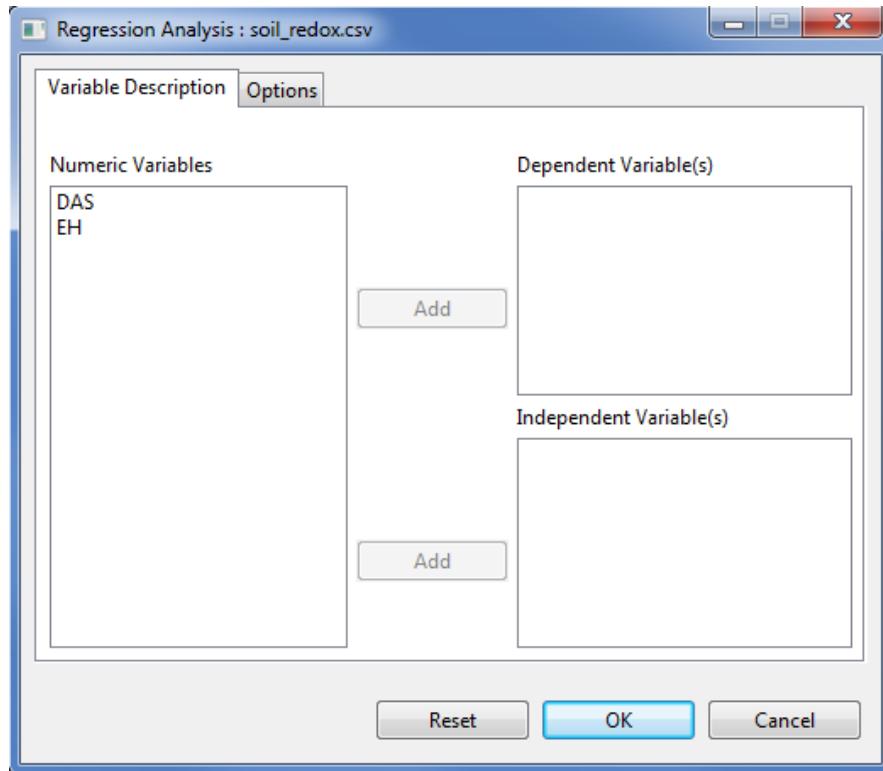
Regression Analysis is the statistical technique used to determine the strength of linear relationship between variables.

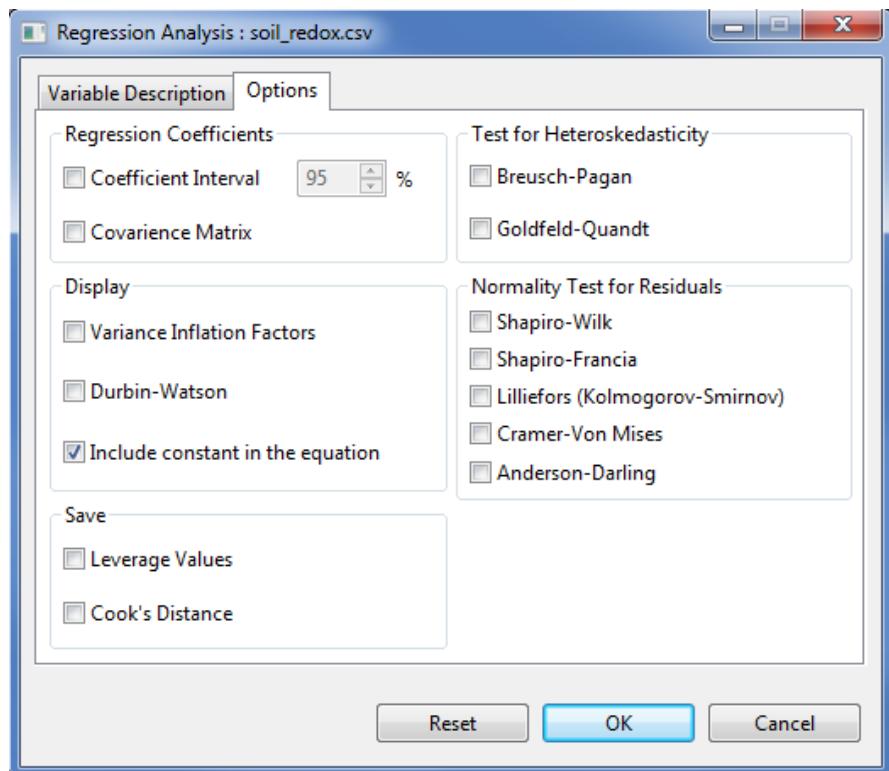
The steps to perform Linear Regression Analysis are listed below:

- On the **Project Explorer**, double-click the file to be used for the analysis to open and view it in the Data Viewer tab.

For the example, using the project named *My Project*, import the data *soil_redox* from the package. To import the data from the package, see *Importing from Package* section of this user manual.

- Click **Analyze | Regression ...** from the main window. The **Regression** dialog box will appear.





- Specify the required field and appropriate options for the analysis:

Variable Description Tab

Dependent Variable

For the analysis to proceed, this list box should have at least one entry.

Independent Variables

For the analysis to proceed, this list box should have at least one entry.

Option Tab

Regression Coefficients

User can choose to display the confidence interval and the covariance matrix. If at least one of this is selected, the result is embedded in the table of parameter estimates. For the confidence interval, the default value is 95%.

Test for Heteroskedasticity

There are two available procedures namely: Breusch-Pagan and Goldfeld-Quandt.

Normality Test

This option will perform normality test for the residuals. There are five procedures available, namely: Shapiro-Wilk, Shapiro-Francia, Lilliefors, Cramer-Von Mises and Anderson-Darling.

Variance Inflation Factors

If this is selected, it displays the variance inflation factors (VIF) which measures the Collinearity (or multicollinearity).

Durbin-Watson

If this is selected, it displays the Durbin-Watson test for serial correlation of the residuals.

Include constant in the equation

By default, the regression model includes a constant term in the equation. Deselecting this option forces regression through the origin, this is rarely done.

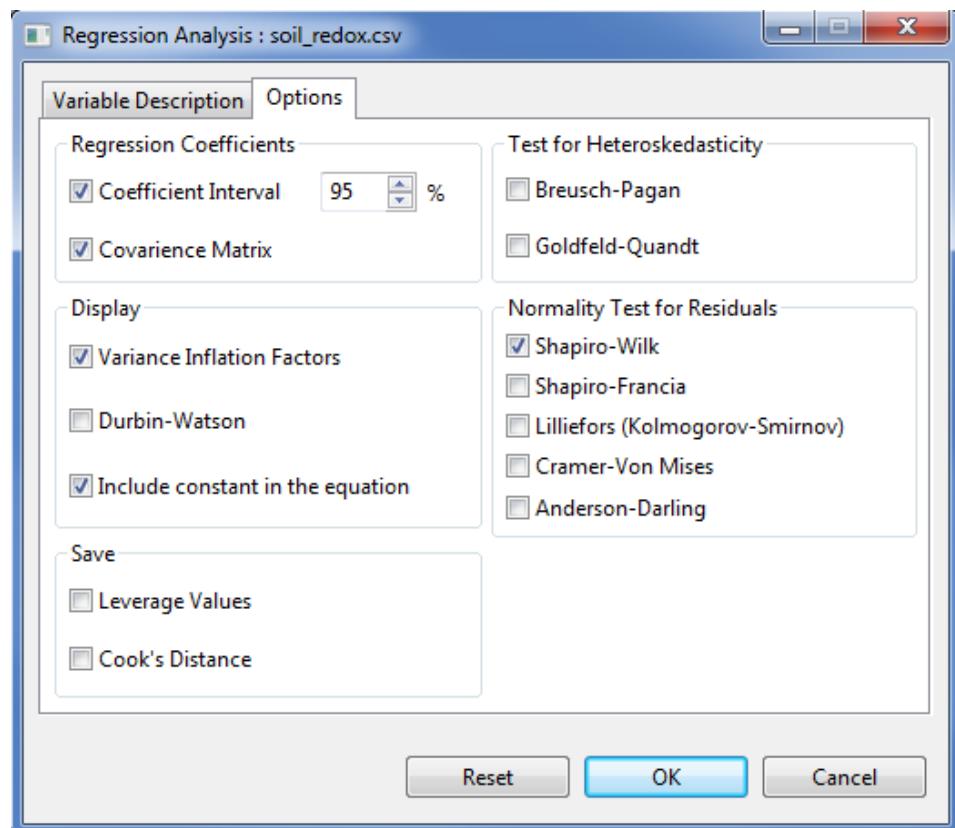
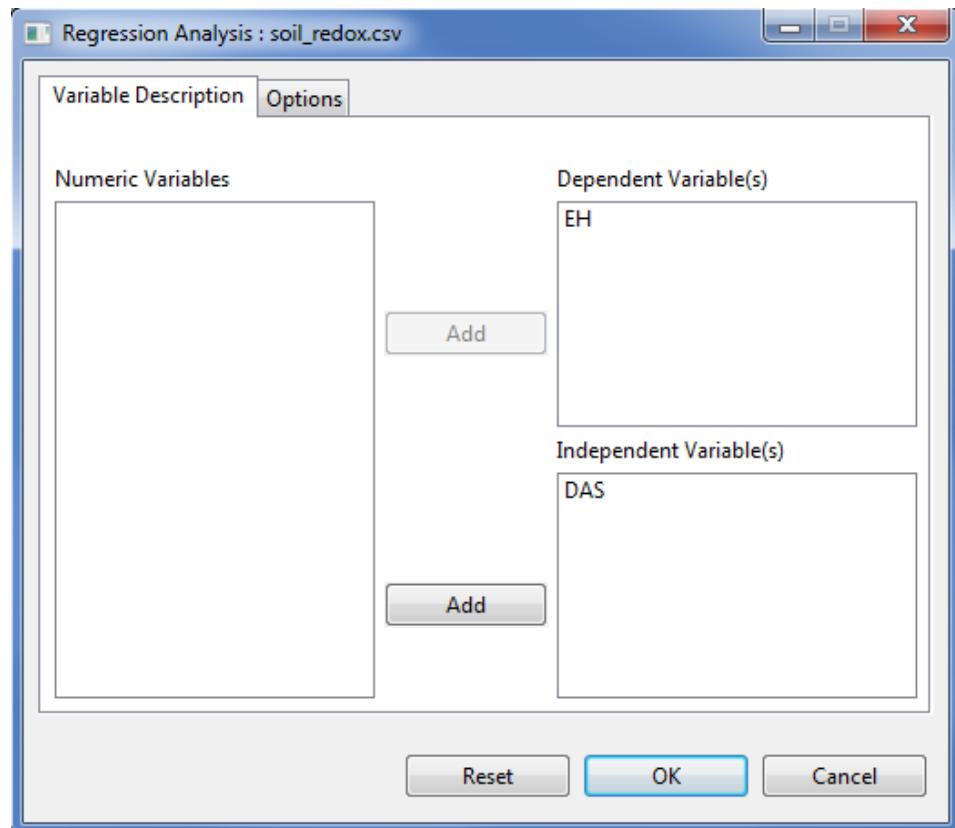
Cook's Distance

If this is selected, it will include the cook's distance in the data set.

Leverage Values

If this is selected, it will include the leverage values in the data set.

For the example, the completed **Variable Description** tab and **Option** tab should appear as illustrated below:



- Once all options have been specified, click the **OK** button. The **Regression Analysis** dialog box will be minimized and STAR activates the **Output** page of the **Result Viewer** tab.

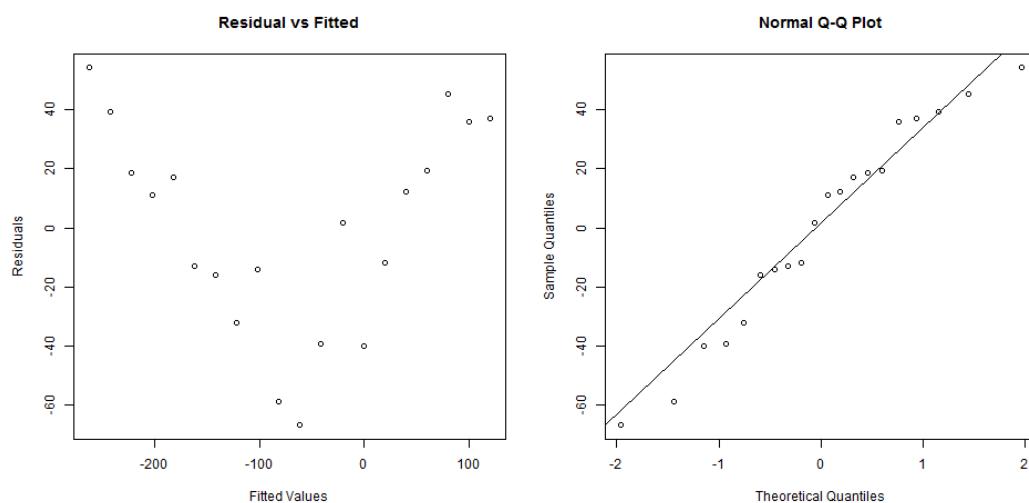
The Linear Regression Analysis procedure in STAR saves all text output in the filename *LinearRegOutput.txt*. By default, the text output includes the Analysis of Variance table, a table of model summary and the parameter estimates. The output starts with the descriptive statistics, if this option was specified in the **Options** tab Sample text output of the analysis as shown in the **Output** page:

```
Descriptive Statistics
-----
Variable      N_NonMissObs      Mean      StdDev      SE_Mean
-----
EH                  20     -71.36    124.17     27.76
DAS                 20      73.50     41.41      9.26
-----
LINEAR REGRESSION ANALYSIS
Model Fitted: EH ~ DAS

Analysis of Variance Table
-----
Source        DF   Sum of Square   Mean Square   F Value   Pr > F
-----
Model          1    269549.1605   269549.1605   207.43   0.0000
  DAS          1    269549.1605   269549.1605   207.43   0.0000
Error         18    23390.0748    1299.4486
Total         20    562488.3959
-----
Model Summary:
-----
Root MSE   EH Mean   Coeff Var   R-Square   Adj R-Sq
-----
      36.05    -71.36    -174.00     0.9202     0.9157
-----
Parameter Estimates:
-----
Variable      Estimate   Std. Error   t value   LL CI*   UL CI*   Pr(>|t|)
-----
Intercept     140.03      16.75      8.36    104.85   175.21   0.0000
DAS           -2.88       0.20     -14.40     -3.30    -2.46   0.0000
-----
* At 95% Confidence Interval

Test for Normality
-----
Variable      Method      Statistics   Prob
-----
residual    Shapiro-Wilk      0.9604   0.5521
-----
```

By default, a *png* file is created for each dependent variable used in the analysis. The file follows the filename format as: <dependent variable>*_DiagPlot.png*. Each *png* file contains two diagnostics plots. The *Residuals vs. Fitted* plot is for assessing the distribution of the residuals. An ideal plot should reveal that the points are distributed around 0. The residuals should not be affected by the size of the fitted values. Problematic data may result to a plot wherein the points increase as the fitted values increase, thus forming a “funnel-shaped” distribution. This will indicate a violation of the homogeneity of variances requirement for analysis of variance. The *Normal Q-Q* plot is used for assessing normality. The points should lie about the line. Sample generated graphs are shown below:



This procedure will also create the *LinearRegNewData.csv*. This file contains the original data with the residual and predicted values for each of the dependent variables used in the analysis. This file will also contain the *Leverage Values* and *Cooks's Distance*, if user chooses to save these values.

Nonparametric Tests

Nonparametric Tests procedure provides several tests that do not require assumptions about the shape of the underlying distribution.

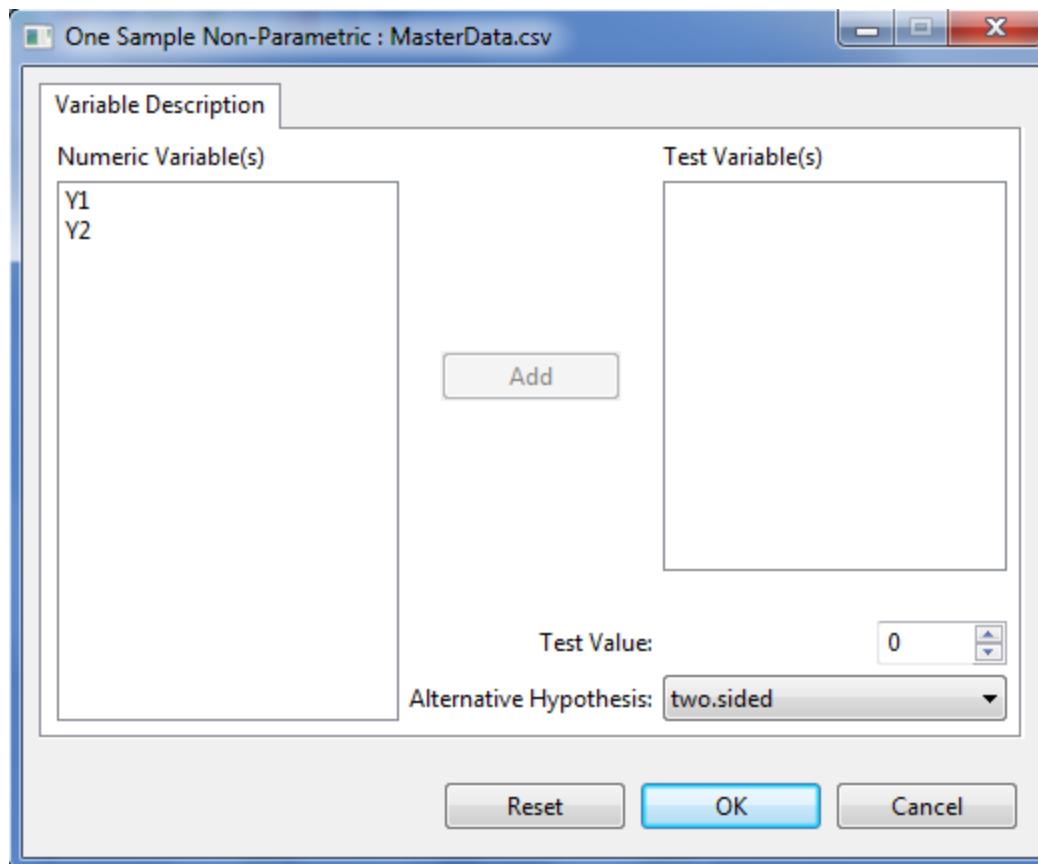
One Sample

The steps to perform one sample non-parametric test are listed below:

- On the **Project Explorer**, double-click the file to be used for the analysis to open and view it in the Data Viewer.

For the example, using the project named *MyProject*, import the data *MasterData* from the *Data* folder of the project named *SampleProject*. To import data from the *SampleProject*, see *Importing Data from Other Project* section of this user's manual.

- From the main window of STAR, click **Analyze | Non-Parametric Test | One Sample....** The **One Sample Non-Parametric** dialog box will appear.



- Specify the required field and appropriate options for the analysis.

Test Variable(s)

For the analysis to proceed, at least one item should be entered in the list box. Only items from the **Numeric Variable(s)** can be added in this dialog box.

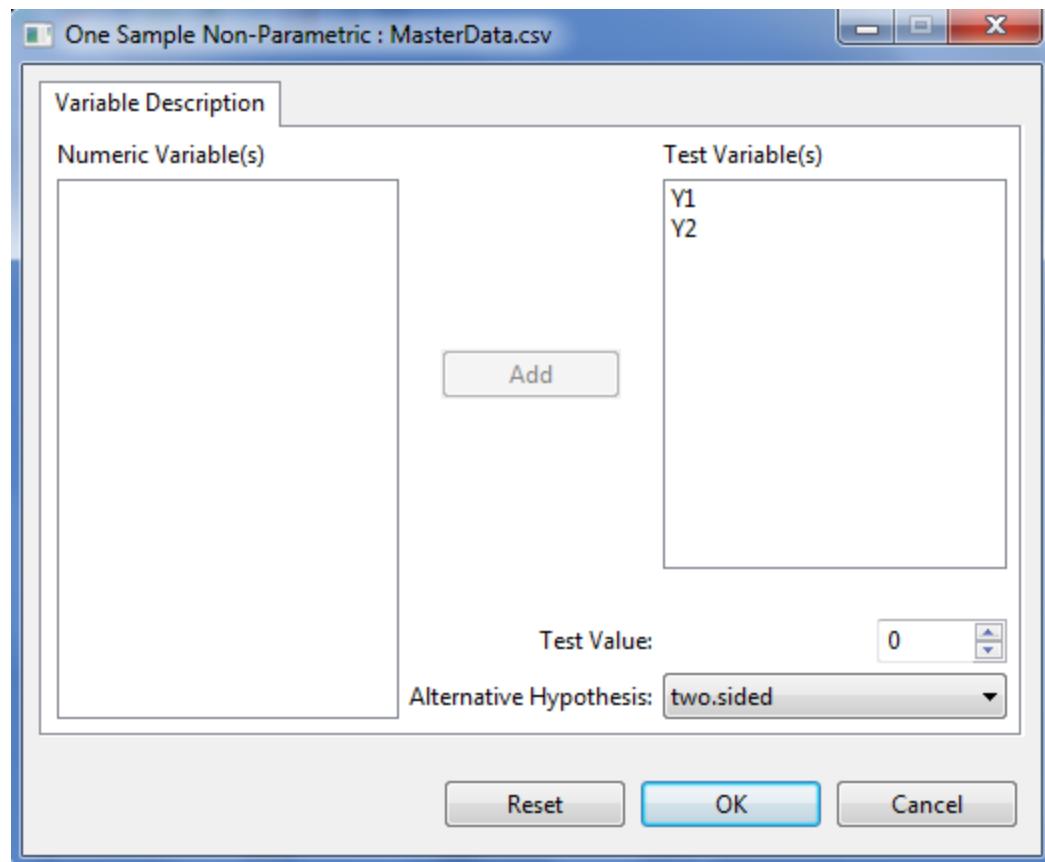
Test Value

This field is required and will only accept one entry at a time. The default value is 0. User can change the value by typing a value inside the spin box or by pressing the up-arrow key to increment the value, down-arrow key, otherwise.

Alternative Hypothesis

User can select a one-tailed or two-tailed test. The default alternative hypothesis used is that for the two-sided test.

For the example, the completed dialog box should appear as shown below:



- Click **OK** button to perform the analysis. The **One Sample Non-Parametric** dialog box will be minimized and STAR activates the **Output Viewer** tab of the **Result Viewer** tab.

Sample output is shown below:

```
Sigh Test: Md = 0
-----
Variable      Statistics   Prob > |V|    LL_CI *   Median   UL_CI *
-----
Y1            4656        0.0000    132.00    132.00    132.00
Y2            4656        0.0000    122.95    122.99    123.00
-----
* 95% Confidence Interval
```

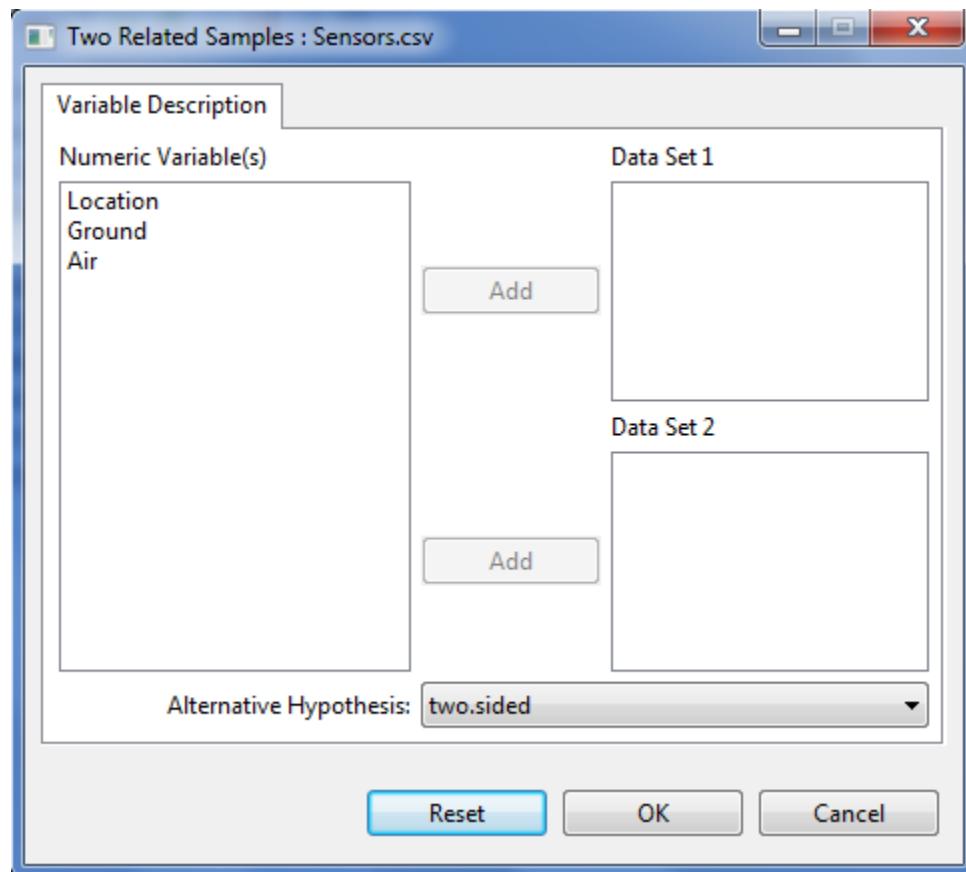
Two Related Samples

The steps to perform Kruskal Wallis test are listed below:

- On the **Project Explorer**, double-click the file to be used for the analysis to open and view it in the Data Viewer.

For the example, using the project named *MyProject*, import the data *Sensors* from package. To import the data from the package, see *Importing from Package* section of this user's manual.

- From the main window of STAR, click **Analyze | Non-Parametric Test | Two Related Samples....** The **Two Related Samples** dialog box will appear.



- Specify the required field and appropriate options for the analysis.

Data Set 1

This field needs at least one entry for the analysis to proceed and must have the same number of entry as **Data Set 2**.

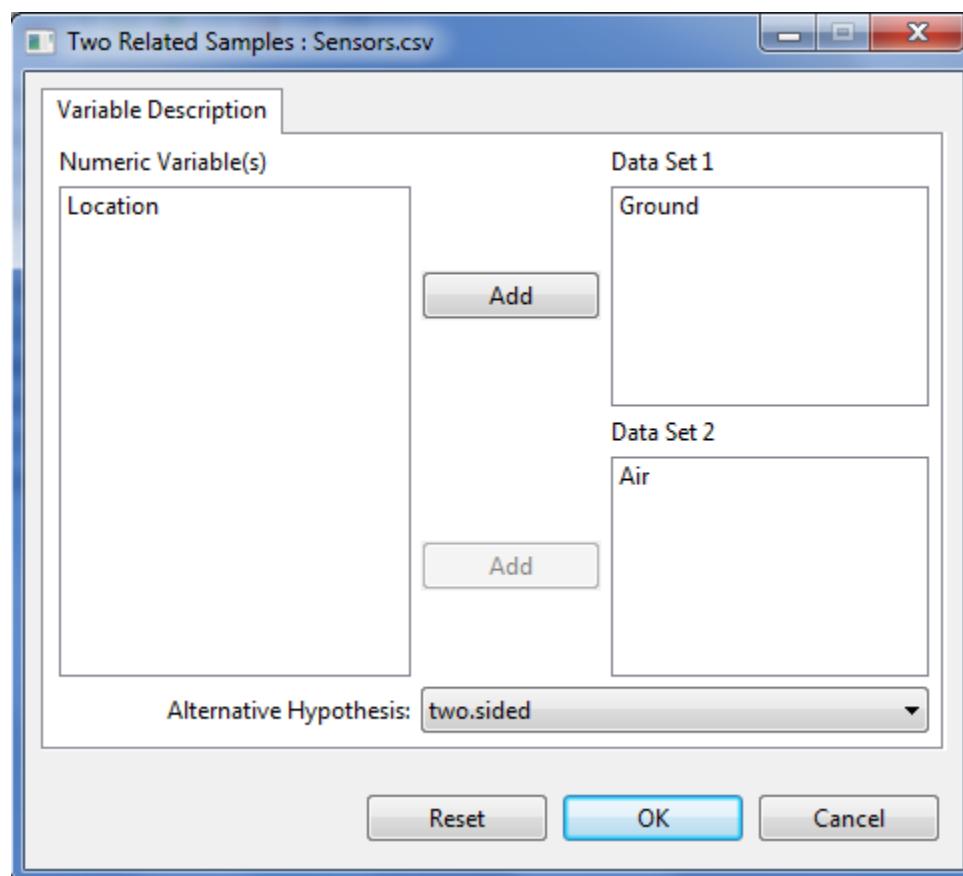
Data Set 2

This field needs at least one entry for the analysis to proceed and must have the same number of entry as **Data Set 1**.

Alternative Hypothesis

User can select a one-tailed or two-tailed test. The default alternative hypothesis used is that for the two-sided test.

For the example, the completed dialog box should appear as shown below:



- Click **OK** button to perform the analysis. The **Two Related Samples** dialog box will be minimized and STAR activates the **Output Viewer** tab of the **Result Viewer** tab.

Sample output is shown below:

```
Wilcoxon Signed Rank Test
-----
Variable      Statistics   Prob > |V|   Median
-----
Ground - Air      0.0000     0.0020    -1.60
-----
```

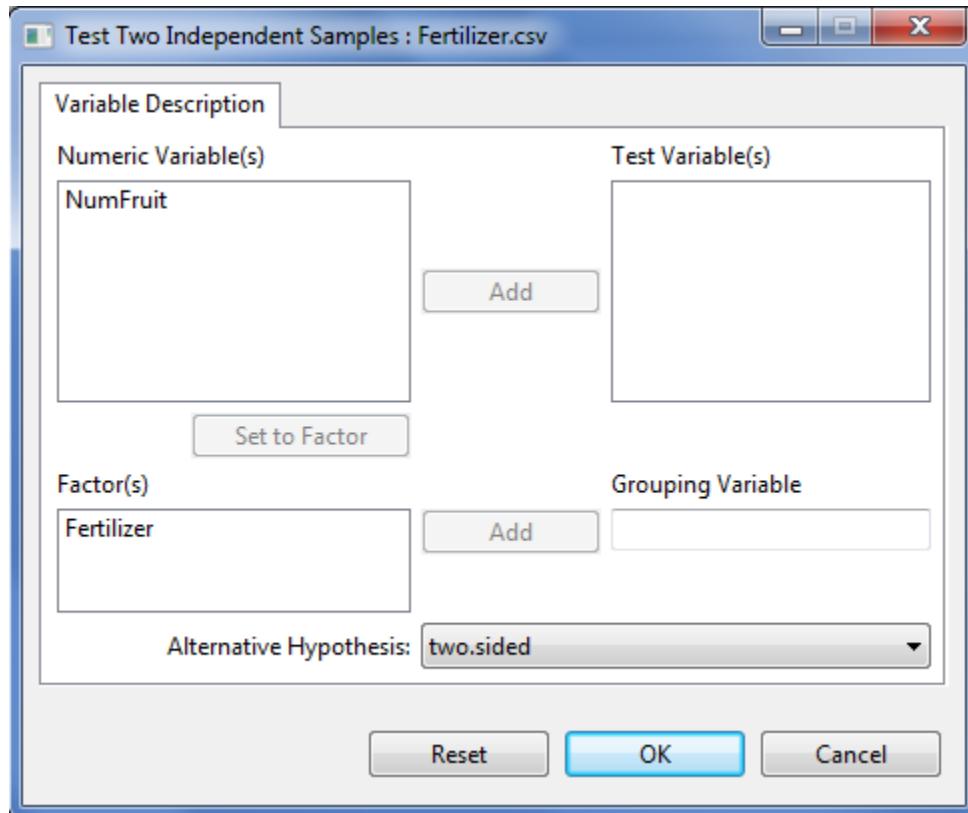
Two Independent Samples

The steps to perform Kruskal Wallis test are listed below:

- On the **Project Explorer**, double-click the file to be used for the analysis to open and view it in the Data Viewer.

For the example, using the project named *MyProject*, import the data *Fertilizer* from package. To import the data from the package, see *Importing from Package* section of this user's manual.

- From the main window of STAR, click **Analyze | Non-Parametric Test | Test for Two Independent Samples....** The **Test for Two Independent Samples** dialog box will appear.



- Specify the required field and appropriate options for the analysis.

Test Variable(s)

For the analysis to proceed, at least one item should be entered in the list box. Only items from the **Numeric Variable(s)** can be added in this dialog box.

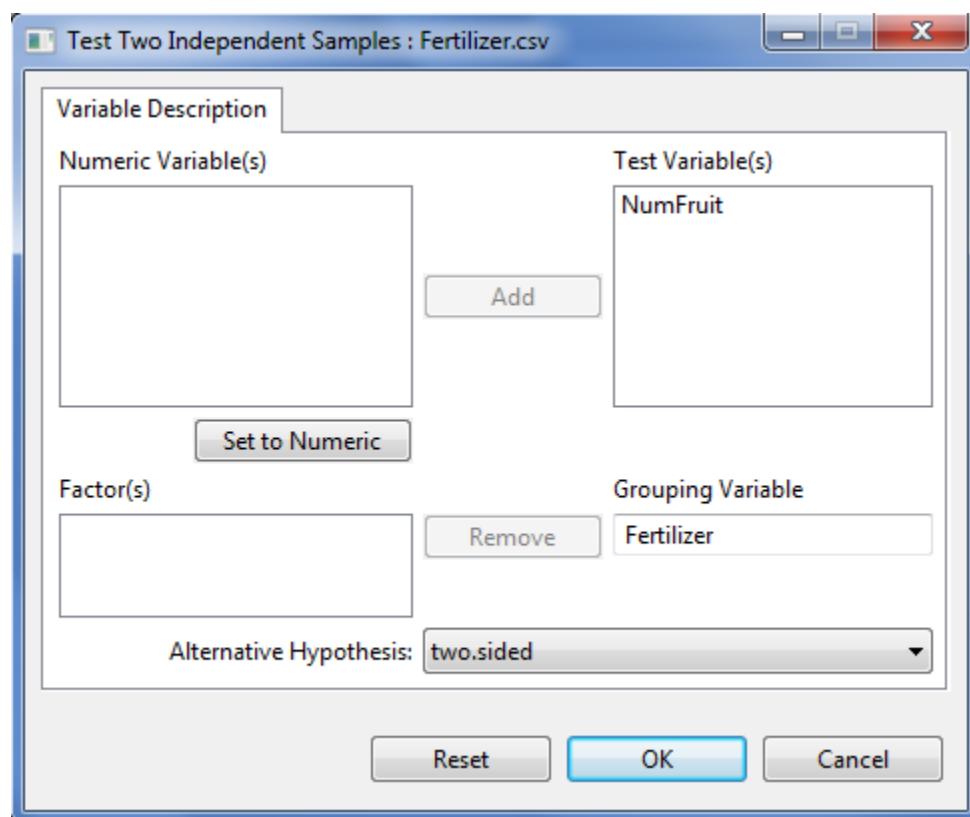
Grouping Variable

Only one item can be added in this field and should come from the **Factor(s)** list box.

Alternative Hypothesis

User can select a one-tailed or two-tailed test. The default alternative hypothesis used is that for the two-sided test.

For the example, the completed dialog box should appear as shown below:



- Click **OK** button to perform the analysis. The **Test for Two Independent Samples** dialog box will be minimized and STAR activates the **Output Viewer** tab of the **Result Viewer** tab.

Sample output is shown below:

```
Mann-Whitney (Wilcoxon Rank Sum) Test
```

```
-----  
Variable Statistics Prob > |W| LL_CI * Median UL_CI *  
-----
```

NumFruit	163	0.0371	0.0000	3.00	5.00

* 95% Confidence Interval					

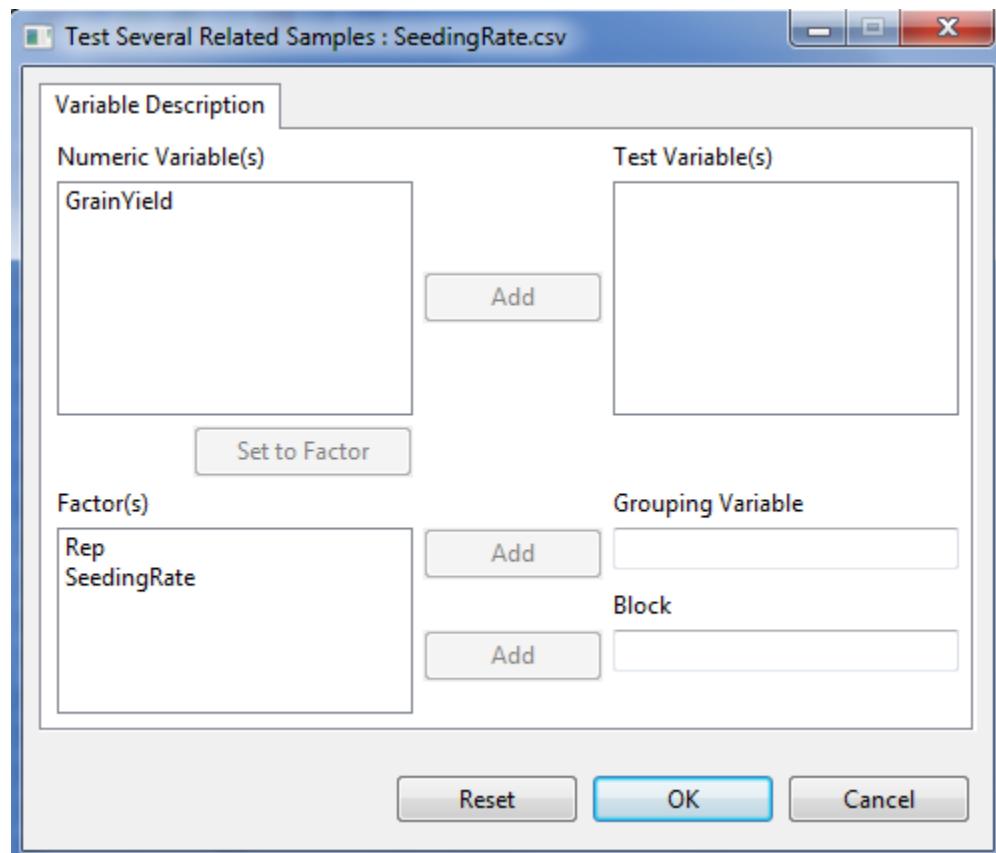
Test for Several Related Samples

The steps to perform Kruskal Wallis test are listed below:

- On the **Project Explorer**, double-click the file to be used for the analysis to open and view it in the Data Viewer.

For the example, using the project named *MyProject*, import the data *Insecticides* from package. To import the data from the package, see *Importing from Package* section of this user's manual.

- From the main window of STAR, click **Analyze | Non-Parametric Test | Test for Several Independent Samples....** The **Test for Several Independent Samples** dialog box will appear.



- Specify the required field and appropriate options for the analysis.

Test Variable(s)

For the analysis to proceed, at least one item should be entered in the list box. Only items from the **Numeric Variable(s)** can be added in this dialog box.

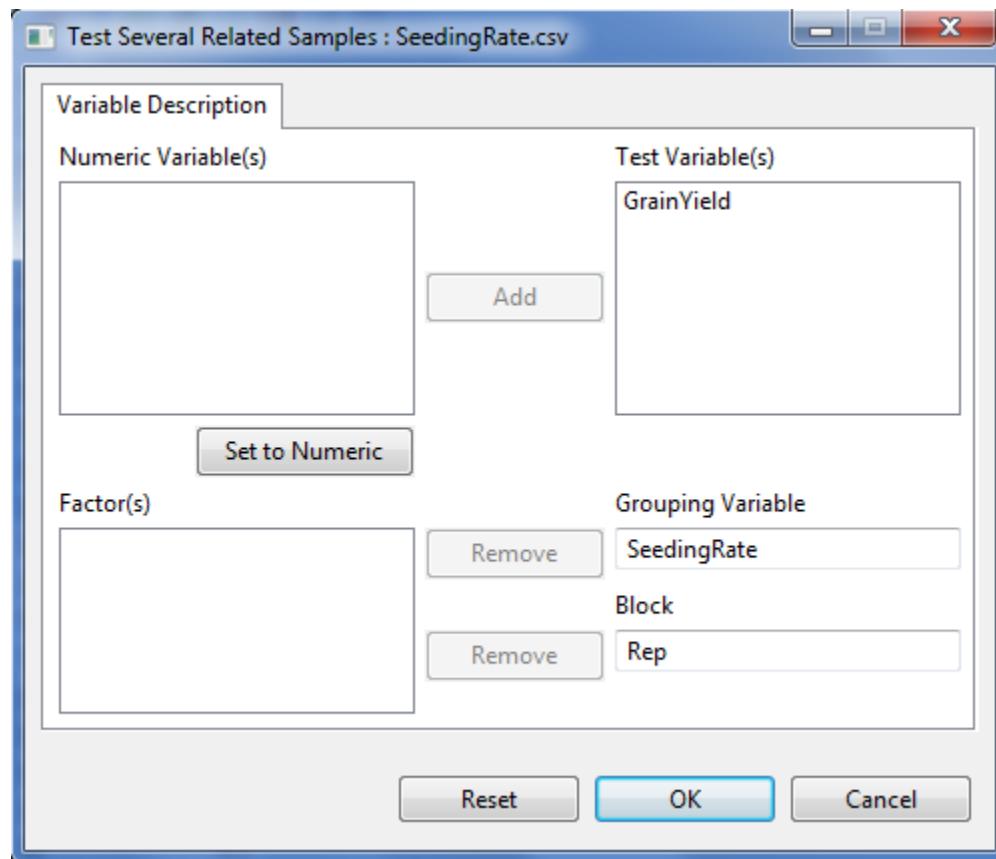
Grouping Variable

Only one item can be added in this field and should come from the **Factor(s)** list box.

Block

Only one item can be added in this field and should come from the **Factor(s)** list box.

For the example, the completed dialog box should appear as shown below:



- Click **OK** button to perform the analysis. The **Test for Several Independent Samples** dialog box will be minimized and STAR activates the **Output Viewer** tab of the **Result Viewer** tab.

Sample output is shown below:

```
Rank Sums for Variable GrainYield
Classified by SeedingRate
-----
SeedingRate      N   Sum of Ranks   Mean of Ranks
-----
25              4    20.50          5.12
50              4    20.30          5.08
75              4    21.20          5.30
100             4    17.40          4.35
125             4    18.70          4.67
150             4    13.50          3.38
-----
* Average scores are used for ties.

Friedman rank sum test
-----
Chi-Square        15.2985
DF                  5
Pr > Chi-Square     0.0092
-----
```

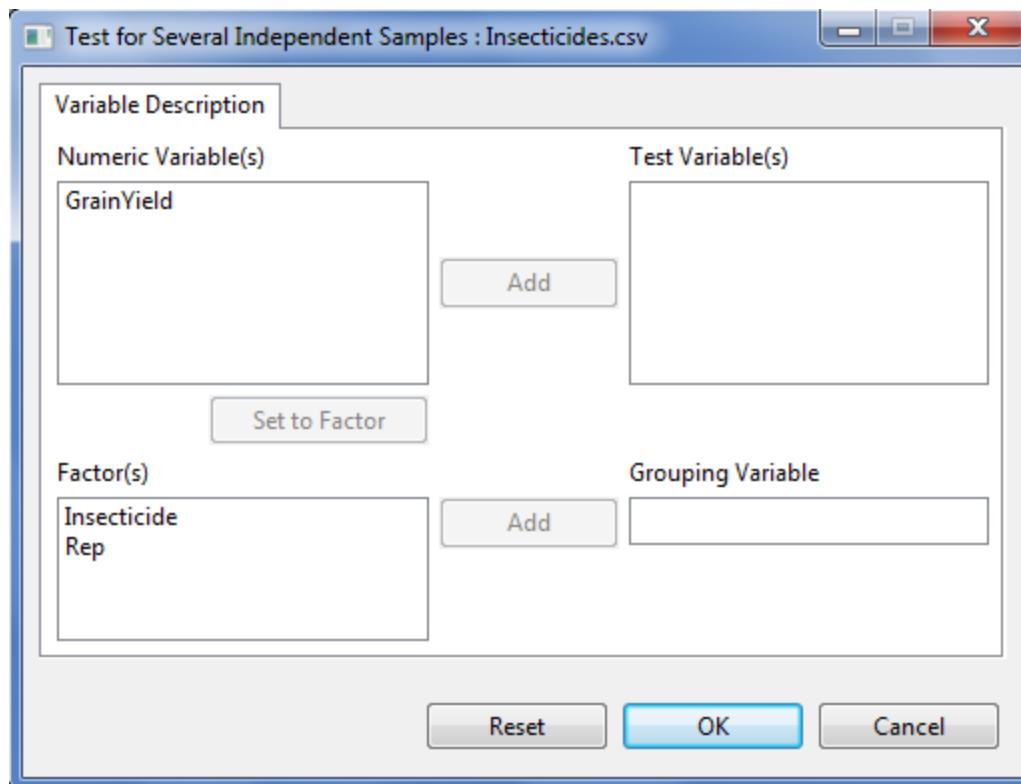
Test for Several Independent Samples

The steps to perform Kruskal Wallis test are listed below:

- On the **Project Explorer**, double-click the file to be used for the analysis to open and view it in the Data Viewer.

For the example, using the project named *MyProject*, import the data *Insecticides* from package. To import the data from the package, see *Importing from Package* section of this user's manual.

- From the main window of STAR, click **Analyze | Non-Parametric Test | Test for Several Independent Samples....** The **Test for Several Independent Samples** dialog box will appear.



- Specify the required field and appropriate options for the analysis.

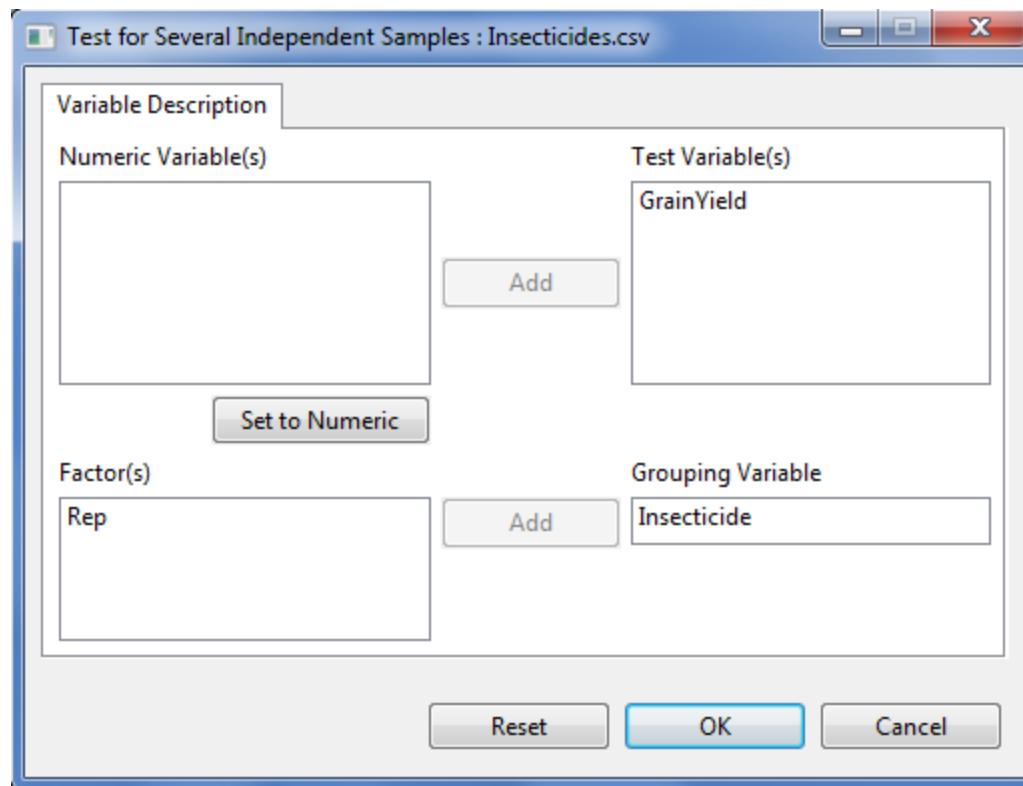
Test Variable(s)

For the analysis to proceed, at least one item should be entered in the list box. Only items from the **Numeric Variable(s)** can be added in this dialog box.

Grouping Variable

Only one item can be added in this field and should come from the **Factor(s)** list box.

For the example, the completed dialog box should appear as shown below:



- Click **OK** button to perform the analysis. The **Test for Several Independent Samples** dialog box will be minimized and STAR activates the **Output Viewer** tab of the **Result Viewer** tab.

Sample output is shown below:

Rank Sums for Variable YIELD Classified by Variable TREATMENT			
TREATMENT	N	Sum of Ranks	Mean of Ranks
Azodin	4	64	16.00
Control	4	12	3.00
DDT + phi-BHC	4	91	22.75
Dimercon-Boom	4	41	10.25
Dimercon-Knap	4	35	8.75
Dol-Mix (1kg)	4	66	16.50
Dol-Mix (2kg)	4	97	24.25

* Average scores are used for ties.

Kruskal-Wallis rank sum test

Chi-Square	20.8522
DF	6
Pr > Chi-Square	0.0020

Appendix

Data From STAR Package

AugLS

Description

Formats

This data contains the following columns:

Row	a factor with 15 levels (1 to 15) denoting the row
Column	a factor with 5 levels (1, 2, 3, 4, 5) denoting the column
Entry	a factor with 55 levels (1 to 55) denoting the treatment with levels 1 to 50 as the unreplicated entries and levels 51 to 55 as the replicated entries
Yield	a numeric vector of grain yield

Source

<c/o lei>

AugRCB

Description

Formats

This data contains the following columns:

BLOCK	a factor with 4 levels (1, 2, 3, 4) denoting the block
ENTRY	a factor with 55 levels (1, 2, ..., and 66) denoting the treatment with levels 1 to 60 as the unreplicated entries and levels 61 to 66 as the replicated entries
YIELD	a numeric vector of grain yield

Source

<c/o lei>

CochranBIB

Description

This file contains data of corn from an experiment conducted in 1943 in North Carolina Agricultural Experiment Station, United States Department of Agriculture which uses balanced incomplete block design. Each location or block has 4 genotypes. The blocks are planted at different location.

Formats

This data contains the following columns:

loc	a factor with 13 levels denoting the location or the blocking factor
gen	a factor with 13 levels denoting the genotype
yield	a numeric vector of grain yield (pounds per plot)

Source

Cochran, W.G. and Cox, G.M. (1957), Experimental Designs, 2nd ed., Wiley and Sons, New York, p. 448.

Corr

Description

The example file contains data from an experiment conducted to investigate the relationship between grain yield (*GY14*, in kg/ha), the grain's nitrogen (*N*), phosphorus

(P) and potassium (K) content in percent. The data were collected from 48 experimental plots with grains adjusted to 14% moisture content.

Formats

This data contains the following columns:

GY14	a numeric vector of grain yields in kg/ha adjusted to 14% moisture continent
N	a numeric vector of grain's nitrogen
P	a numeric vector of grain's phosphorus
K	a numeric vector of grain's potassium content in percent

Source

BEDDA Training

CropStatRCBDOverSite

Description

Formats

This data contains the following columns:

NTRT	a factor with 6 levels (1, 2, 3, 4, 5, 6) denoting the nitrogen
SITE	a factor with 3 levels (1, 2, 3) denoting the site
REP	a factor with 3 levels (1, 2, 3) denoting the block
YIELD	a numeric vector denoting the grain yield

Source

CropStat

Dule_AlphaGxE

Description

Formats

This data contains the following columns:

Env	a factor with 6 levels (A01WSCM, A03WS-0, A03WS-1, AWS01-D, UWS02-2, UWS02-8) denoting the environment
Rep	a factor with 3 levels (1, 2, 3) denoting the replication
Block	a factor with 5 levels (1, 2, 3, 4, 5) denoting the block
Plot	a numeric vector denoting the plot number
Geno	a factor with 40 levels (AUS196, AZUCENA, B6144F-MR-6-0-0, C22, CT13370-12-2-M, CT13377-4-2-M, CT13382-8-3-M, CT6510-24-1-2, CT6516-24-3-2, DINORADO, IR47686-30-3-2, IR55419-04, IR55423-01, IR60080-46A, IR65261-09-1-B, IR65907-116-1-B, IR66417-18-1-1-1, IR66421-062-1-1-2, IR66424-1-2-1-5, IR68702-072-1-4-B, IR70358-84-1-1, IR70360-38-1-B-1, IR71524-44-1-1, IR71525-19-1-1, IR72768-15-1-1, IRAT170, IRAT177, IRAT212, IRAT216, MARAVILHA, PALAWAN, PRIMAVERA, UPLRI-5, UPLRI-7, VANDANA, WAB181-18, WAB56-125, WAB638-1, WAB96-1-1, WAYRAREM)
FLOWER	a numeric vector
Duration	a numeric vector
PlantHt	a numeric vector
CropBF	a numeric vector
HI	a numeric vector
YLD	a numeric vector

Source

<c/o lei>

Fertilizer

Description

Formats

This data contains the following columns:

Fertilizer	a factor with two levels (A and B) denoting the fertilizer used
NumFruit	a numeric vector of number of fruits

Source

Gerua

Description

Formats

This data contains the following columns:

REP	a factor with three levels (1, 2 and 3) denoting the blocks
TPL	a factor with two levels (D and N) denoting the transplanting method; considered as the main plot factor
CULT	a factor with 26 levels denoting the cultivar; considered as the subplot factor
DFF	a numeric vector denoting the number of days after flowering
PLHT	a numeric vector denoting the plant height in cm
PNCLE	a numeric vector denoting the panicle number
GRNYLD	a numeric vector denoting the grain yield in kg/ha

Source

BEDDA Training

GomezMaizeCross

Description

"A plant breeder is studying a cross between a sweet maize inbred line with yellow kernels and a flint maize inbred line with white kernels. He would like to know whether the ratio of kernel type and color in the F2 population follows the normal di-hybrid ratio of 9:3:3:1. From the F1 plants produced by crossing the two inbred lines, he obtain F2 kernels and classifies them into four categories according to kernel color (yellow or white) and kernel type (flint or sweet) as follows: yellow flint, yellow sweet, white flint and white sweet." -- Gomez, Kwanchai A. and Arturo A. Gomez. (1984) *Statistical Procedures for Agricultural Research 2nd Edition*. John Wiley & Sons, Inc. Page 460.

Formats

This data contains the following columns:

KernelNumber	a numeric vector denoting the kernel id number
KernelColor	a factor with 2 levels (white and yellow) denoting the color of the kernel
KernelType	a factor with 2 levels (flint and sweet) denoting the kernel type
KernelCategory	a factor with 4 levels (white flint, white sweet, yellow flint, and yellow sweet) denoting the kernel type and color
YellowKernel	a numeric vector of values 0 and 1, with 1 denoting that the kernel is of color yellow
WhiteKernel	a numeric vector of values 0 and 1, with 1 denoting that the kernel is of color white
FlintType	a numeric vector of values 0 and 1, with 1 denoting that the kernel is of type flint
SweetType	a numeric vector of values 0 and 1, with 1 denoting that the kernel is of type sweet

Source

Gomez, Kwanchai A. and Arturo A. Gomez. (1984) *Statistical Procedures for Agricultural Research 2nd Edition*. John Wiley & Sons, Inc. Page 460.

GomezMaizeCrossSummary

Description

This data is a summary of *GomezMaizeCross*.

Formats

This data contains the following columns:

KernelCategory	a factor with 4 levels (white flint, white sweet, yellow flint, and yellow sweet) denoting the kernel type and color
Frequency	a numeric vector denoting the number of observation in that follows in that kernel category

Source

Gomez, Kwanchai A. and Arturo A. Gomez. (1984) *Statistical Procedures for Agricultural Research 2nd Edition*. John Wiley & Sons, Inc. Page 460.

GomezSplitRCBD

Description

Grain Yield of Data of Four Rice Varieties Grown in Six Levels of Nitrogen in a Split-Plot Design with three replications.

Formats

This data contains the following columns:

Rep	a factor with 3 levels (1 to 3) denoting the blocks
Nitrogen	main plot factor with 6 levels (0, 60, 90, 120, 150 and 180, in kg N/ha) denoting the Nitrogen Levels
Variety	subplot factor with 4 levels (C4-63, IR5, IR8 and Peta) denoting the Rice Variety
Yield	a numeric vector of grain yield in kg/ha

Source

Gomez, Kwanchai A. and Arturo A. Gomez. (1984) *Statistical Procedures for Agricultural Research 2nd Edition*. John Wiley & Sons, Inc. Page 102.

GomezSplit2RCBD

Description

Grain Yield of Three Rice Varieties Grown under Three Management Practices and Five Nitrogen Levels; in a split-split plot design in RCBD with three replications.

Formats

This data contains the following columns:

Rep	a factor with 3 levels (1 to 3) denoting the blocks
Nitrogen	main plot factor with 5 levels (N1, N2, N3, N4, and N5) denoting the Nitrogen Levels
	N1 0 kg N/ha
	N2 50 kg N/ha
	N3 80 kg N/ha
	N4 110 kg N/ha
	N5 140 kg N/ha
Management	subplot factor with 3 levels (M1, M2 and M3) denoting the Management Practices
	M1 Minimum
	M2 Optimum
	M3 Intensive
Variety	sub-subplot factor with 3 levels (V1, V2 and V3) denoting the Rice Variety
GY	a numeric vector of grain yield in t/ha

Source

Gomez, Kwanchai A. and Arturo A. Gomez. (1984) *Statistical Procedures for Agricultural Research 2nd Edition*. John Wiley & Sons, Inc. Page 143.

GomezStrip

Description

Grain Yield of Six Varieties of Rice, Broadcast Seeded and Grown with Three Nitrogen Rates in a Strip-plot Design with Three Replications

Formats

This data contains the following columns:

REP	a factor with 3 levels (1 to 3) denoting the blocks
NITROGEN	vertical factor with 3 levels (0, 60 and 120, kg N/ha) denoting the Nitrogen Levels
VARIETY	horizontal factor with 6 levels (V1, V2, V3, V4, V5 and V6) denoting the Rice Variety
	V1 IR8
	V2 IR127-80
	V3 IR305-4-12
	V4 IR400-2-5
	V5 IR665-58
	V6 Peta
GRNYLD	a numeric vector of grain yield in kg/ha

Source

Gomez, Kwanchai A. and Arturo A. Gomez. (1984) *Statistical Procedures for Agricultural Research 2nd Edition*. John Wiley & Sons, Inc. Page 110.

GomezStripSplit

Description

Grain yield of six rice varieties tested under two planting methods and three nitrogen rates in a Strip-Split plot Design with three replicates.

Formats

This data contains the following columns:

REP	a factor with 3 levels (1 to 3) denoting the blocks
NITROGEN	vertical factor with 3 levels (0, 60 and 120, kg N/ha) denoting the Nitrogen Levels
VARIETY	horizontal factor with 6 levels (V1, V2, V3, V4, V5 and V6) denoting the Rice Variety
	V1 IR8
	V2 IR127-80
	V3 IR305-4-12
	V4 IR400-2-5
	V5 IR665-58
	V6 Peta
PLANTING	subplot factor with two levels (Broadcast and Transplanted) denoting the planting methods
YIELD	a numeric vector of grain yield in kg/ha

Source

Gomez, Kwanchai A. and Arturo A. Gomez. (1984) *Statistical Procedures for Agricultural Research 2nd Edition*. John Wiley & Sons, Inc. Page 155.

GomezTenureStatus

Description

"An agricultural economist studying factors affecting the adoption of the newly introduced high-yielding rice varieties wishes to know if adoption is affected by the tenure status of farmers. With three distinct classes of tenure status (the first classification criterion) – owner operator, share-rent farmer, and fixed-rent farmer – and two classes of adoption status (the second classification criterion) – adopter and nonadopter – the resulting data form a 3 x 2 contingency table." -- Gomez, Kwanchai A. and Arturo A. Gomez. (1984) *Statistical Procedures for Agricultural Research 2nd Edition*. John Wiley & Sons, Inc. Page 462.

Formats

This data contains the following columns:

TenureStatus	a factor with 3 levels (fixed-rent, owner, and share-rent)
FarmerClassif	a factor with 2 levels (adopter and nonadopter)

Source

Gomez, Kwanchai A. and Arturo A. Gomez. (1984) *Statistical Procedures for Agricultural Research 2nd Edition*. John Wiley & Sons, Inc. Page 463.

GomezTwoCropSeasonRCB

Description

Grain yield of rice tested with five rates of nitrogen in two crop seasons.

Formats

This data contains the following columns:

Season	a factor with 2 levels (Dry and Wet) denoting the season
Rep	a factor with 3 levels (I, II and III) denoting the block
NitrogenRate	a factor with 5 levels (0, 60, 90, 120 and 150 kg/ha) denoting the Nitrogen Rate
GrainYield	a numeric vector of grain yield, t/ha

Source

Gomez, Kwanchai A. and Arturo A. Gomez. (1984) *Statistical Procedures for Agricultural Research 2nd Edition*. John Wiley & Sons, Inc. Page 318.

grp_pss

Description

Three (3) varieties, a traditional variety (A) and two new varieties B and C, were tested to determine if their yield means are equal. Analysis of variance showed that difference among the varieties exists. The researcher would like to know the nature of the differences among the groups.

Formats

This data contains the following columns:

VARIETY	a factor with three levels denoting the variety
REP	a factor with four levels (1 to 4) denoting block
YIELD	a numeric vector of grain yield

Source

<BEDDA TRAINING>

IASRICorrReg

Description

The data was collected through a pilot survey on Hybrid Jowar crop on yield and biometrical characters.

Formats

This data contains the following columns:

sampleNum	a numeric vector denoting the identification number of the sample
PP	a numeric vector denoting the average plant population
PH	a numeric vector denoting the average plant height
NGL	a numeric vector denoting the average number of green leaves
Yield	a numeric vector denoting the yield (kg/plot)

Source

Design Resources Server. *Indian Agricultural Statistics Research Institute (ICAR), New Delhi 110 012, India.* www.iasri.res.in/design (accessed lastly on December 20, 2012).

IASRILSD

Description

An experiment was conducted at Agricultural Research Station, Kopurgaon, Maharashtra on cotton during the year 1969 – 1970 using a Latin Square design to study

the effects of foliear application of urea in combination with insecticidal sprays on the cotton yield.

Formats

This data contains the following columns:

row	a factor with six levels (1 to 6) denoting the row
col	a factor with six levels (1 to 6) denoting the column
trt	a factor with six levels denoting the treatment
	T1 Control (No nitrogen and no insecticides)
	T2 100 kg N/ha as urea (half at final thinning and half at flowering as top dressing)
	T3 100 kg N/ha as urea (80 kg N/ha in 4 equal split does as spray and 20 kg N/ha at final thinning)
	T4 100 kg N/ha as CAN (half at final thinning and half at flowering as top dressing)
	T5 T2 + six insecticidal sprays
	T6 T4 + six insecticidal sprays
yield	a numeric vector denoting the yield in kg

Source

Design Resources Server. *Indian Agricultural Statistics Research Institute (ICAR), New Delhi 110 012, India.* www.iasri.res.in/design (accessed lastly on December 20, 2012).

IASRITomar

Description

An experiment was conducted to study compare the effect of natural pollination and hand pollination under open field conditions.

Formats

This data contains the following columns:

group	a factor with two levels (1 and 2) denoting the type of pollination used
-------	--

1	natural pollination
2	hand pollination
fs45	a numeric vector of number of fruit set for the period of 45 days
fw	a numeric vector of fruit weight in kilograms (kg)
syp	a numeric vector of seed yield per plant in grams
sl	a numeric vector of seedling length in cm

Source

Tomar, B.S. Descriptive Statistics: Design Resources Server. *Indian Agricultural Statistics Research Institute (ICAR)*, New Delhi 110 012, India. www.iasri.res.in/design (accessed lastly on December 20, 2012).

IASRITomar2

Description

An experiment was conducted to study compare the effect of hand pollination on hybrid of seed production in bottle gourd under open field and poly house conditions.

Formats

This data contains the following columns:

Group	a factor with two levels (2 and 3) denoting the type of conditions
	2 hand pollination in open field condition
	3 hand pollination in poly house condition
nmfp	a numeric vector of total number of male flowers per plant
fs45	a numeric vector of number of fruit set for the period of 45 days
fweight	a numeric vector of fruit weight in kilograms (kg)
flength	a numeric vector of fruit length in centimeter (cm)
syp	a numeric vector of seed yield per plant in grams
sl	a numeric vector of seedling length in centimeter

Source

Tomar, B.S. Descriptive Statistics: Design Resources Server. *Indian Agricultural Statistics Research Institute (ICAR)*, New Delhi 110 012, India. www.iasri.res.in/design (accessed lastly on December 20, 2012).

Inoculation

Description

An experiment was conducted on the effect of 6 times of inoculation of *S. linicola* on the oil content of Redwing Flaxseed. The experiment was conducted using an RCB design with 4 replications.

Formats

This data contains the following columns:

Rep	a factor with three levels (1, 2 and 3) denoting the blocks
InoculationTime	a factor with six levels (Seedling, Early Bloom, Full Bloom, Full Bloom (1/100), Ripening and Uninoculated) denoting the time of inoculation
OilContent	a numeric vector denoting the oil content

Source

Steel, R.G.D., J.H. Torrie, and D.A. Dickey. Principles and Procedures of Statistics: A Biometrical Approach.

Insecticides

Description

Grain yield of rice resulting from use of different foliar and granular insecticides for the control of brown planthoppers and stem borers from a Completely Randomized Design Experiment with Four Replicates and 7 treatments. The data contains 28 rows and 3 columns.

Formats

This data contains the following columns:

Treatment	a factor with 7 levels (Azodin, DDT + γ -BHC, Dimercon-Boom, Dimercon-Knap, Dol-Mix (1 kg), Dol-Mix (2 kg) and Control) denoting the Different Foliar and Granular Insecticides
Rep	a factor with 4 levels (1 to 4) denoting the replicates
GrainYield	a numeric vector of grain yield in kg/ha

Source

Gomez, Kwanchai A. and Arturo A. Gomez. (1984) *Statistical Procedures for Agricultural Research 2nd Edition*. John Wiley & Sons, Inc. Page 14.

KemptonRowCol

Description

Wheat yields of 35 genotypes, 2 reps, planted in a row-column design. Two plots are missing.

Formats

This data contains the following columns:

rep	a factor with 2 levels (R1 and R2) denoting the replicate
row	a factor with 5 levels (1 to 5) denoting the row
col	a factor with 7 levels (1 to 7) denoting the column
gen	a factor with 35 levels (G01, G02, G03, G04, G05, G06, G07, G08, G09, G10, G11, G12, G13, G14, G15, G16, G17, G18, G19, G20, G21, G22, G23, G24, G25, G26, G27, G28, G29, G30, G31, G32, G33, G34, G35)
yield	a numeric vector denoting the yield

Source

R A Kempton and P N Fox, Statistical Methods for Plant Variety Evaluation, Chapman and Hall, 1997.

R agricdat package.

Maize

Description

Grain yield of three promising maize hybrids and a check variety from an experiment using Latin Square design. The data contains 24 rows and 3 columns.

Formats

This data contains the following columns:

Maize	a factor with 4 levels denoting the Maize Hybrids (A, B, and D) and a Check Variety (C)
Row	a factor with 4 levels (1 to 4) denoting the row blocking factor
Column	a factor with 4 levels (1 to 4) denoting the column blocking factor
GrainYield	a numeric vector of grain yield in kg/ha

Source

Gomez, Kwanchai A. and Arturo A. Gomez. (1984) *Statistical Procedures for Agricultural Research 2nd Edition*. John Wiley & Sons, Inc. Page 33.

Nurul2012

Description

Formats

This data contains the following columns:

Block	a factor with levels I II
Variety	a factor with levels Azucena112854 Azucena47125 Azucena52992 Chadungda IR20 IR64 IR74 Pokalli
Aluminum	a factor with levels 0 540 750 1300
RL	a numeric vector
RE	a numeric vector
RRE	a numeric vector

Source

Gomez, Kwanchai A. and Arturo A. Gomez. (1984) *Statistical Procedures for Agricultural Research 2nd Edition*. John Wiley & Sons, Inc. Page 33.

OP_pss

Description

Grain yield of three promising maize hybrids and a check variety from an experiment using Latin Square design. The data contains 24 rows and 3 columns.

Formats

This data contains the following columns:

NITROGEN	a factor with levels 0 60 90 120
REP	a factor with levels 1 2 3
YIELD	a numeric vector

Source

Gomez, Kwanchai A. and Arturo A. Gomez. (1984) *Statistical Procedures for Agricultural Research 2nd Edition*. John Wiley & Sons, Inc. Page 33.

PGTYPIC

Description

Formats

This data contains the following columns:

Block	a factor with levels 1 2 3 4
Geno	a factor with levels 1 2 3 4 5 6 7 8
X1	a numeric vector
X2	a numeric vector
X3	a numeric vector

X4 a numeric vector

Source

SeedingRate

Description

A hypothetical data of grain yield in Randomized Complete Block Design.

Formats

This data contains the following columns:

Rep	a factor with levels 1 2 3 4
SeedingRate	a factor with levels 25 50 75 100 125 150
GrainYield	a numeric vector

Source

Sensors

Description

Formats

This data contains the following columns:

REP	a factor with three levels (1, 2 and B) denoting the blocks
GRNYLD	a numeric vector denoting the grain yield in kg/ha

Source

BEDDA Training

soil_redox

Description

The file contains the data of number of days after seeding (DAS) as independent variable and soil redox potential (EH) as dependent variable. Based on this data, simple linear regression analysis is to be conducted to assess how the days after seeding linearly affects soil redox potential, on the average.

Formats

This data contains the following columns:

DAS	a numeric vector denoting the number of days after seeding
EH	a numeric vector denoting the soil redox potential

Source

BEDDA Training

soil_var

Description

Formats

This data contains the following columns:

REP	a factor with three levels (1, 2 and B) denoting the blocks
GRNYLD	a numeric vector denoting the grain yield in kg/ha

Source

BEDDA Training

Survival

Description

Formats

This data contains the following columns:

REP	a factor with three levels (1, 2 and B) denoting the blocks
GRNYLD	a numeric vector denoting the grain yield in kg/ha

Source

BEDDA Training

tf_rcb

Description

Formats

This data contains the following columns:

REP	a factor with three levels (1, 2 and B) denoting the blocks
GRNYLD	a numeric vector denoting the grain yield in kg/ha

Source

BEDDA Training

upland

Description

Formats

This data contains the following columns:

Env	a factor with three levels (UDSO2-14, UDSO2-6 and UDSO2-6) denoting the environments
Rep	a factor with three levels (1, 2 and 3) denoting the replicate
Block	a factor with four levels (1, 2, 3 and 4) denoting the blocks
Plot	a numeric vector denoting the plots
Geno	a factor with 44 levels (1, 2 and B) denoting the genotypes
Yield	a numeric vector denoting the grain yield

Source

BEDDA Training

White_heads

Description

Formats

This data contains the following columns:

REP	a factor with three levels (1, 2 and B) denoting the blocks
GRNYLD	a numeric vector denoting the grain yield in kg/ha

Source

BEDDA Training

Year

Description

Formats

This data contains the following columns:

REP a factor with three levels (1, 2 and B) denoting the blocks

GRNYLD a numeric vector denoting the grain yield in kg/ha

Source

BEDDA Training

Yield94

Description

Formats

This data contains the following columns:

REP a factor with three levels (1, 2 and B) denoting the blocks

GRNYLD a numeric vector denoting the grain yield in kg/ha

Source

BEDDA Training

Description

Formats

This data contains the following columns:

REP a factor with three levels (1, 2 and B) denoting the blocks

GRNYLD a numeric vector denoting the grain yield in kg/ha

Source

BEDDA Training

