



Plant Breeding Tools

USER'S MANUAL



Plant Breeding Tools

Version 1.4

June 2014

A NOTE TO THE READER:

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

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

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1. Introduction

Plant Breeding Tools (PBTools) is a software that has been developed to assist plant breeders in the design of experiments and analysis of data. It has an easy-to-navigate graphical user interface that does not require users to have programming skills to perform data manipulation and analysis. It uses R functions that were specifically written for the development of this software and those that are available in the following R packages: ade4, agricolae, dae, DiGGER, doBy, fields, fitdstrplus, gdata, gplots, gtools, Hmisc, leaps, lme4, lmerTest, MASS, multcomp, mvtnorm, numDeriv, pastecs, permute, plotrix, plyr, qtl, R.methodsS3, R.oo, rJava, spam, stringr and vegan.

Featured Modules

PBTools provides the following modules:

- Data management in spreadsheet view
- Randomization for commonly used experimental designs in plant breeding
- Single-environment analysis
- Multiple-environment analysis
- QTL analysis
- Selection index
- Commonly used mating designs
- Generation mean analysis

New Features in PBTools 1.4

In the latest version of PBTools, augmented RCB and augmented Latin Square designs are now available in one-stage multi-environment analysis module.

About the Manual

This manual provides step-by-step instructions on how to perform certain tasks that are of interest to users. Tasks are discussed using sample datasets that are included when PBTools is installed. In most tasks, dialog boxes are displayed and the user has to specify required fields and additional options as desired. Descriptions and limitations of these fields and options are also provided. Screen images are also included for additional references.

This manual is written using the following format:

- Menu items, names of dialogs and form controls appear in **bold** letters
- Filenames, folder names, variables names and directories are *italicized*
- Menu items appear in the form **Project | New Project**, which means “choose **New Project** from the **Project** menu”

Citing the Software

The suggested citation of PBTools in publications is as follows:

PBTools, version 1.4. 2014. Biometrics and Breeding Informatics, PBGB Division, International Rice Research Institute, Los Baños, Laguna.

2. Getting Started

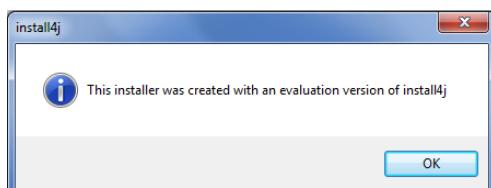
Installation

The installer of PBTools 1.4 and its required R packages can be downloaded from bbi.irri.org. To download the installers, click the links labeled as *PBTools 1.4* and *R-Packages1.5* at the right-hand side of the page.

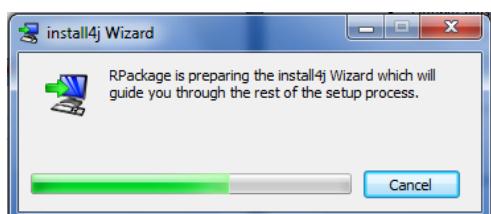
The screenshot shows the IRRI Biometrics and Breeding Informatics website. The main navigation bar includes Home, About Us (which is selected), Products, Trainings, Research, and Contact Us. The 'About Us' section contains information about the BBI group's research support, consultation, and training services. The 'Products Download' sidebar on the right lists various software tools and their download links. A red box highlights the 'Plant Breeding Tools' section, which includes links for PBTools 1.X and Installation Procedure. Another red box highlights the 'STAR and PBTools required R Packages' section, which includes links for R-Packages1.5 and Installation Procedure. Below these are links for FieldLabV2-9.apk and Interact with us on social media platforms like facebook, twitter, and scribd.

The steps to install the required R packages are as follows:

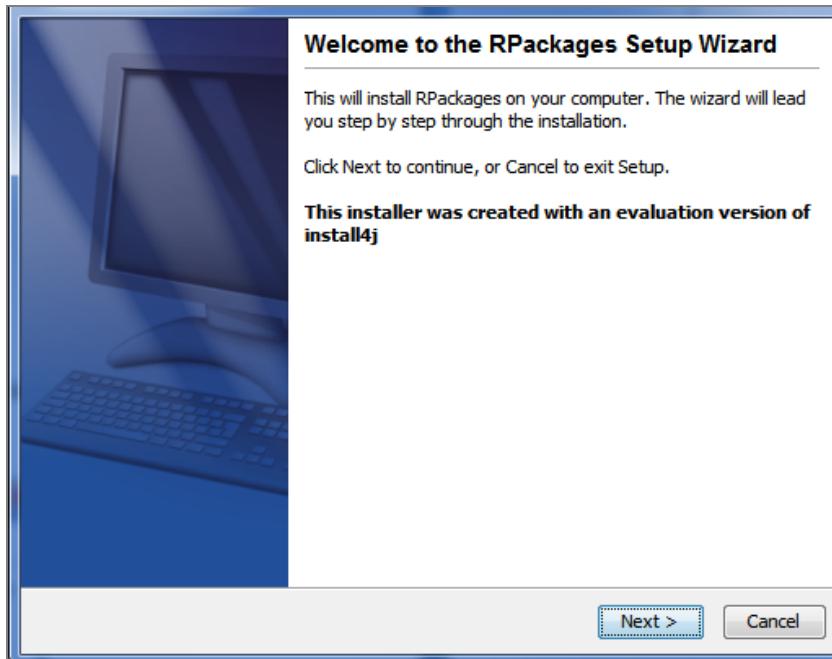
- Double-click the installer icon to launch the setup. A dialog as shown below is displayed. Click **OK**.



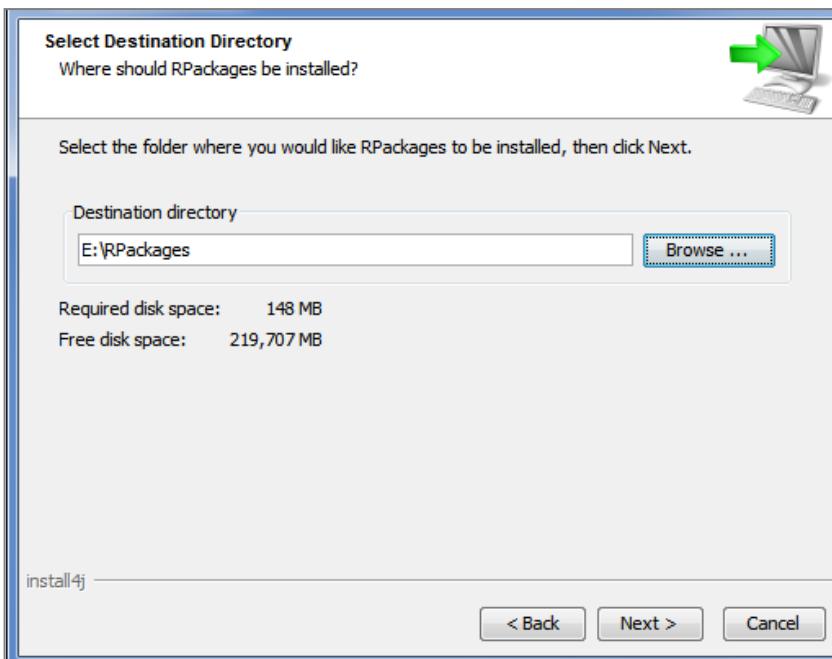
- The next step is the preparation of the wizard. A dialog with progress bar is displayed. Wait until the preparation is completed.



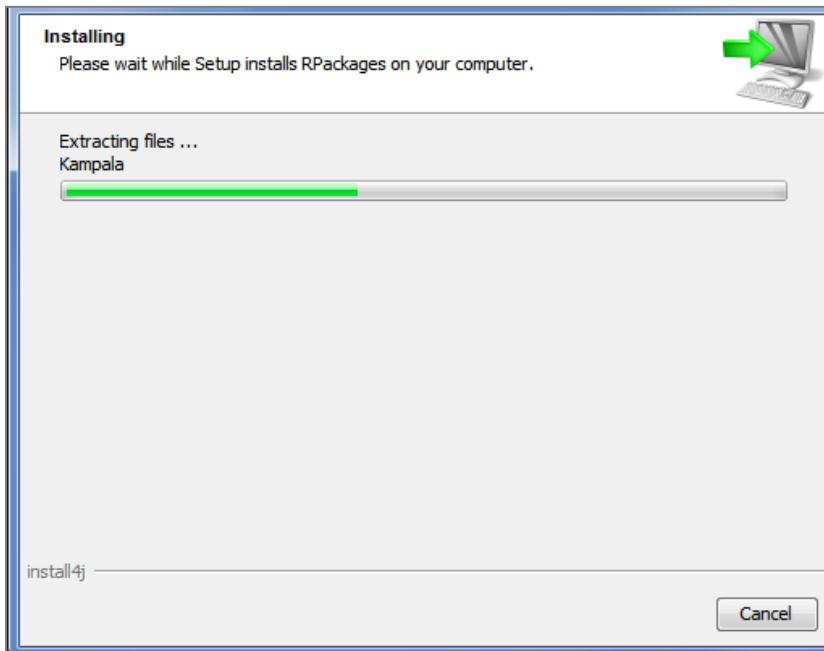
- When installing R Packages for the first time, the **Welcome** dialog as shown below is displayed. Click **Next**.



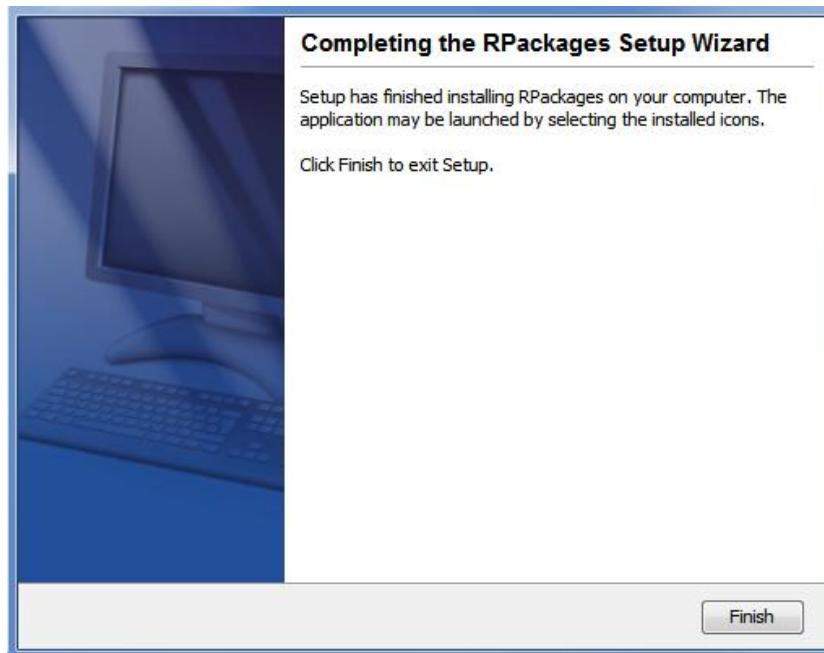
- Select the destination folder, preferably **not in C:\Program Files** as problems were encountered when RPKages is installed in this location. Click **Next**.



- Wait until the installation is completed.

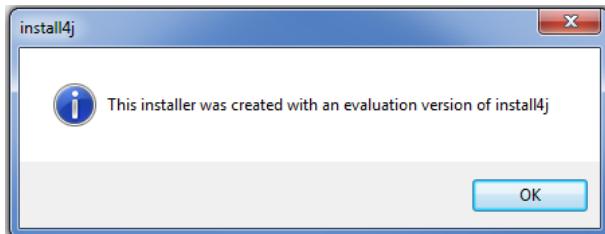


- Click **Finish** to exit Setup.

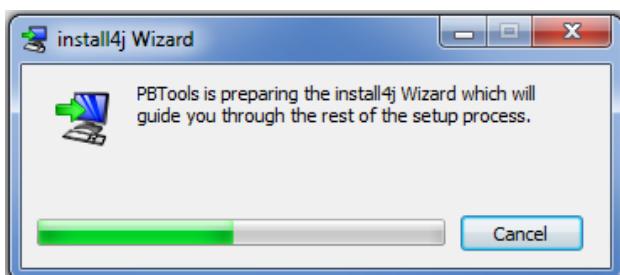


The steps to install PBTools are as follows:

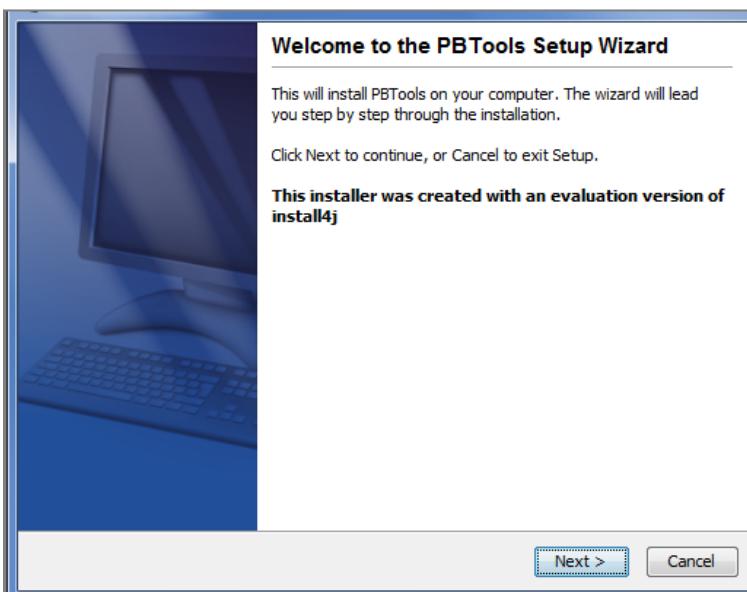
- Double-click the installer icon  to launch the setup. A dialog as shown below is displayed. Click **OK**.



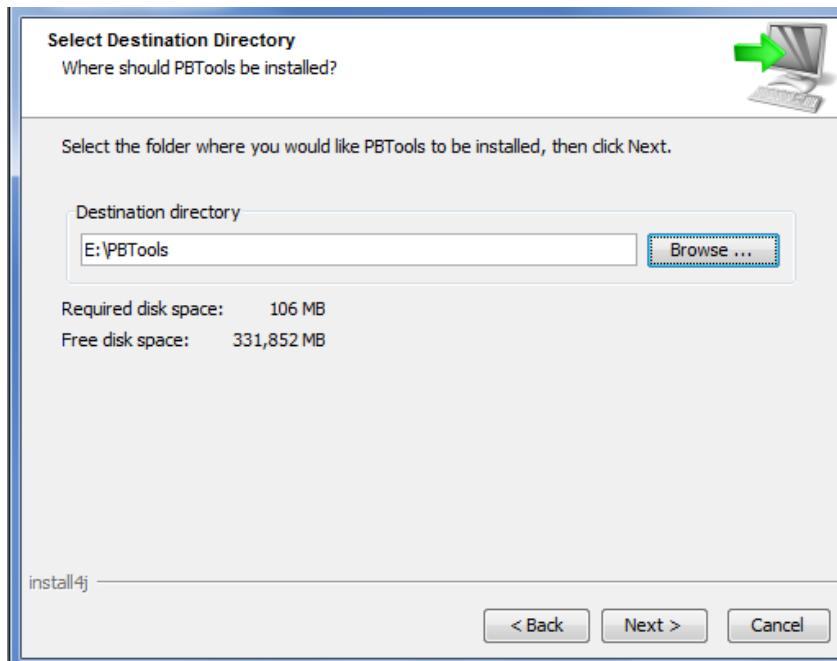
- The next step is the preparation of the wizard. A dialog with progress bar is displayed. Wait until the preparation is completed.



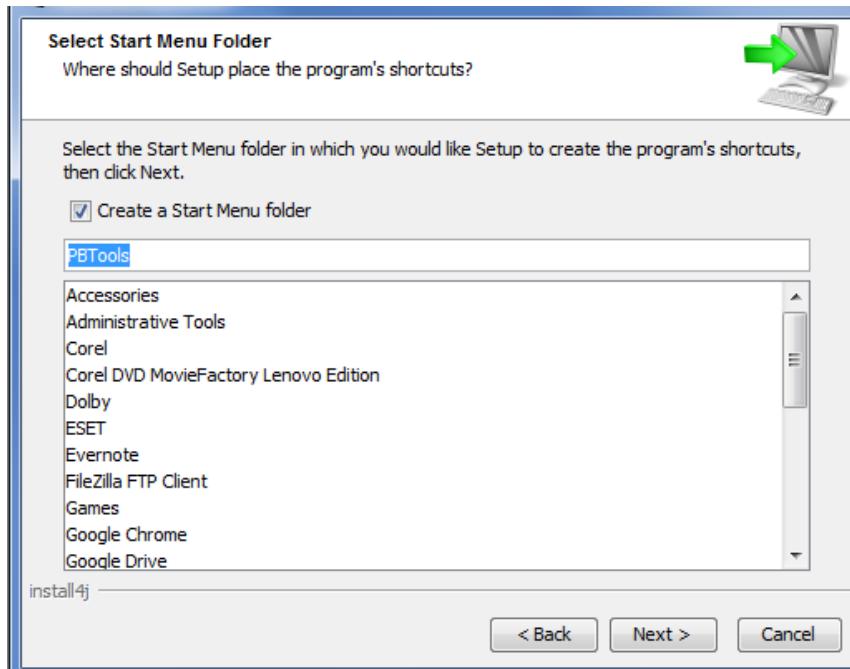
- When installing PBTools for the first time, the **Welcome** dialog as shown below is displayed. Click **Next**.



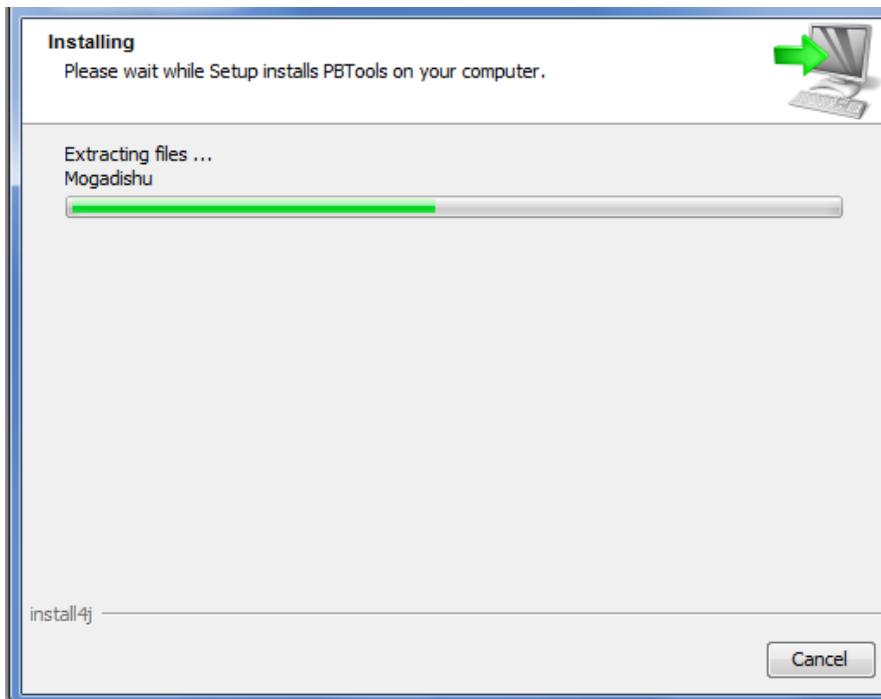
- Select the destination folder, preferably **not in C:\Program Files** as problems were encountered when PBTools is installed in this location. Click **Next**.



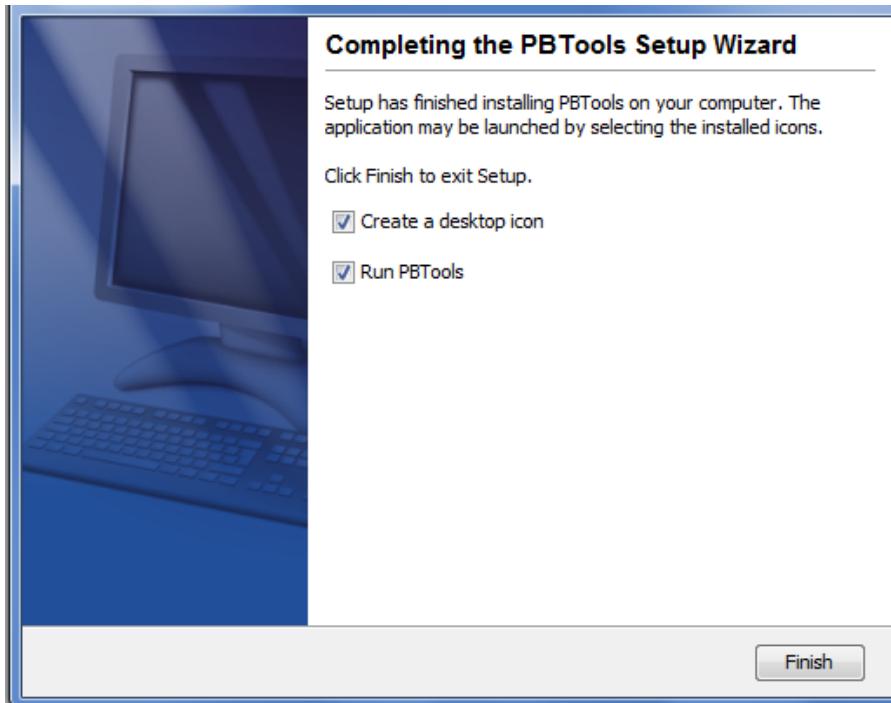
- Select which start menu folder you want to place the PBTools icons in and click **Next**.



- Wait until the installation is completed.



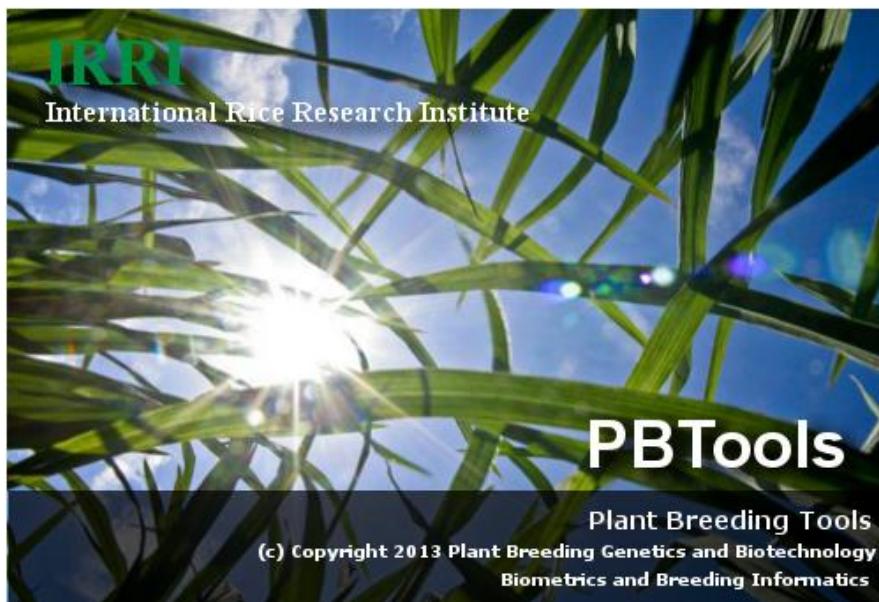
- Finally, specify if you want to create a desktop icon and run PBTools. Click **Finish**.



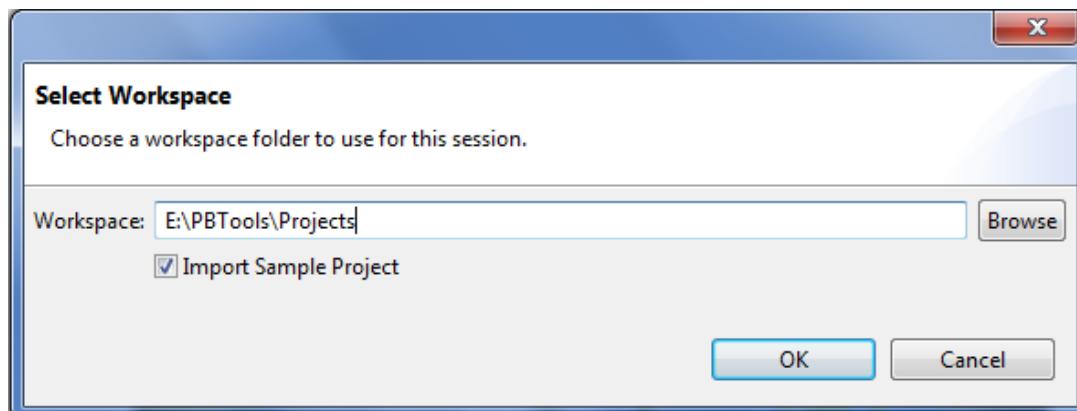
Launching PBTools

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

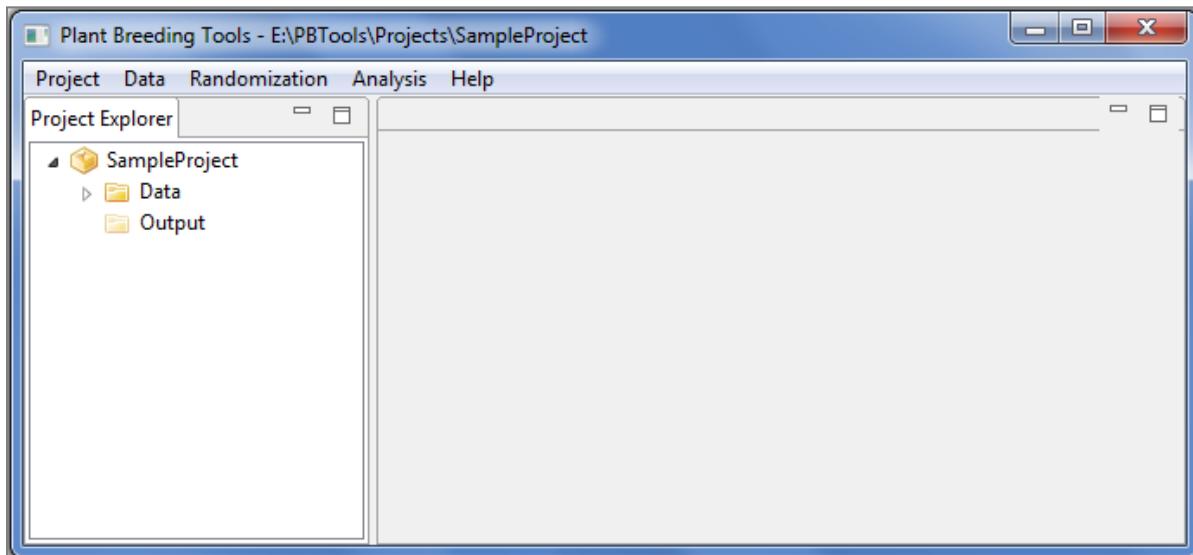
Upon launching, the splash image as shown below will appear.



When PBTools 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.

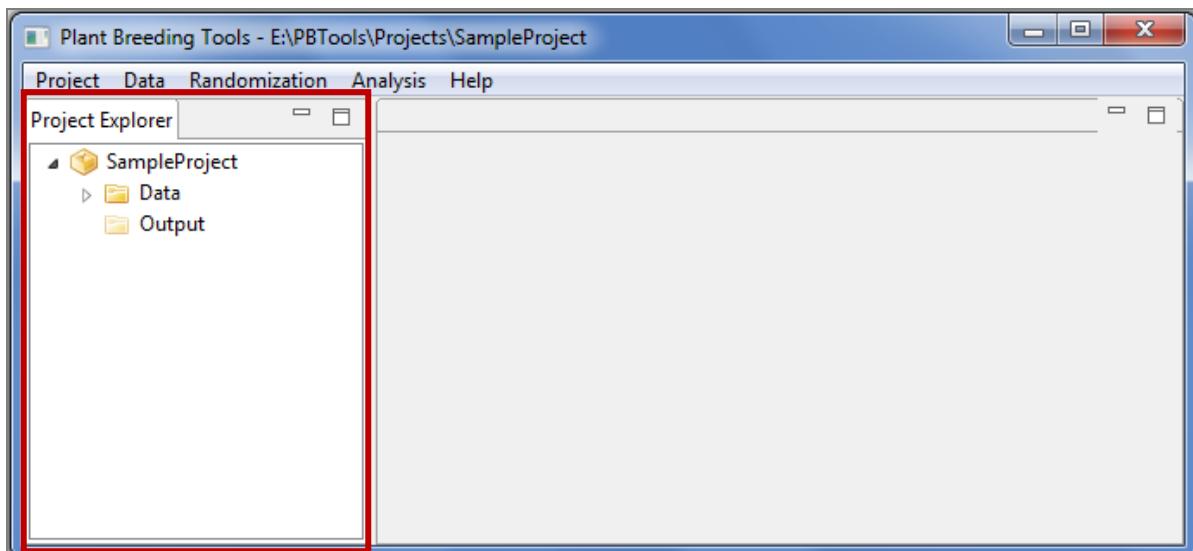


The main window will appear.



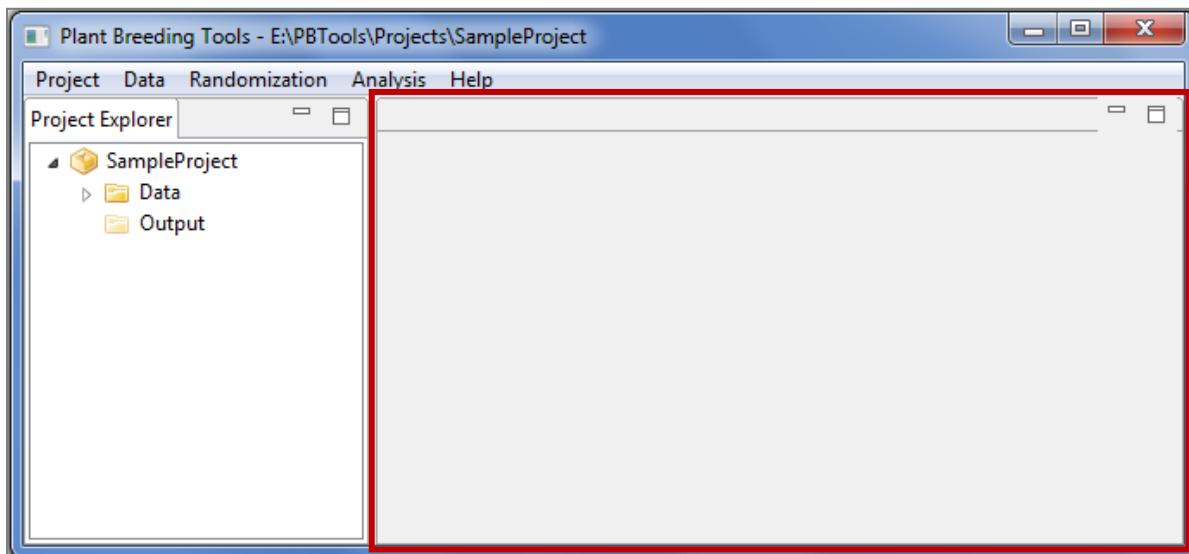
Project Explorer Panel

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 PBTools session. When the 'Import Sample Project' option is selected in the **Select Workspace** dialog, a default project named *SampleProject* is displayed with *Data* folder and *Output* folder inside it. The *Data* folder contains 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.



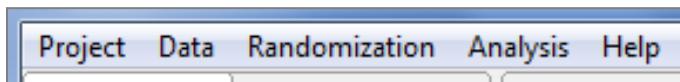
Editor Panel

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

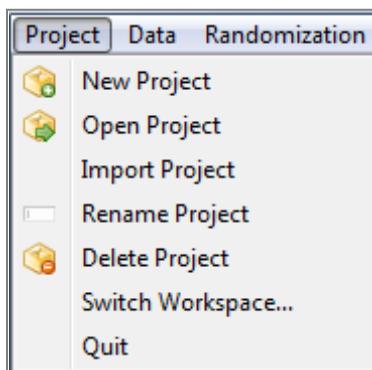


Menu Bar

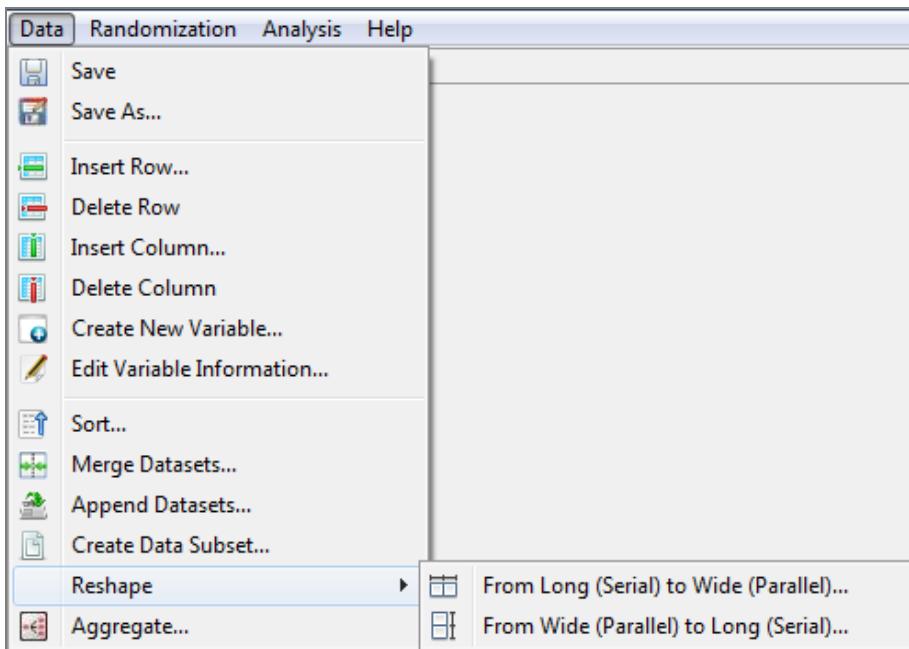
PBTools has five items in the menu bar as shown below:



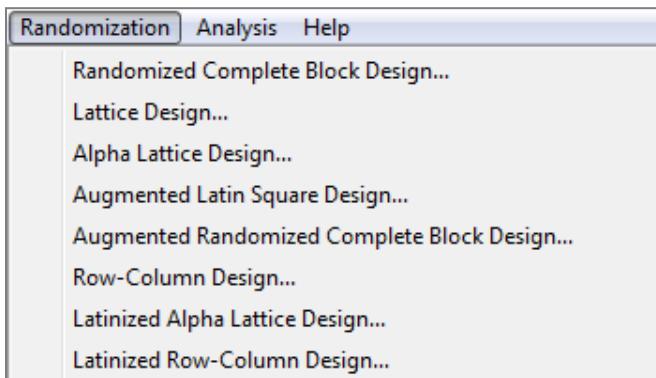
Project Menu contains functions for creating and managing projects. This menu can also be used to quit or terminate PBTools session. It contains the following submenu items:



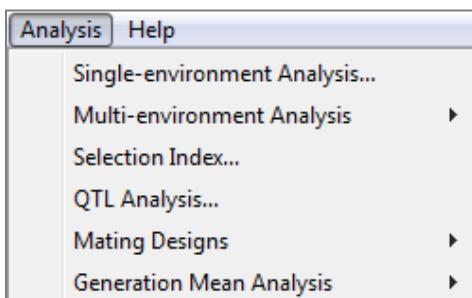
Data Menu contains functions for reading, managing and manipulating datasets. Items under this menu can be used only when a data in CSV format is displayed in the active tab of the editor panel. It contains the following submenu items:



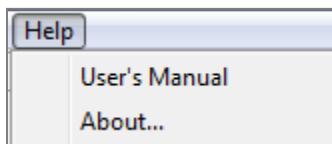
Randomization Menu contains functions for generating random assignment of factor levels for commonly used experimental designs in plant breeding. It contains the following submenu items:



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

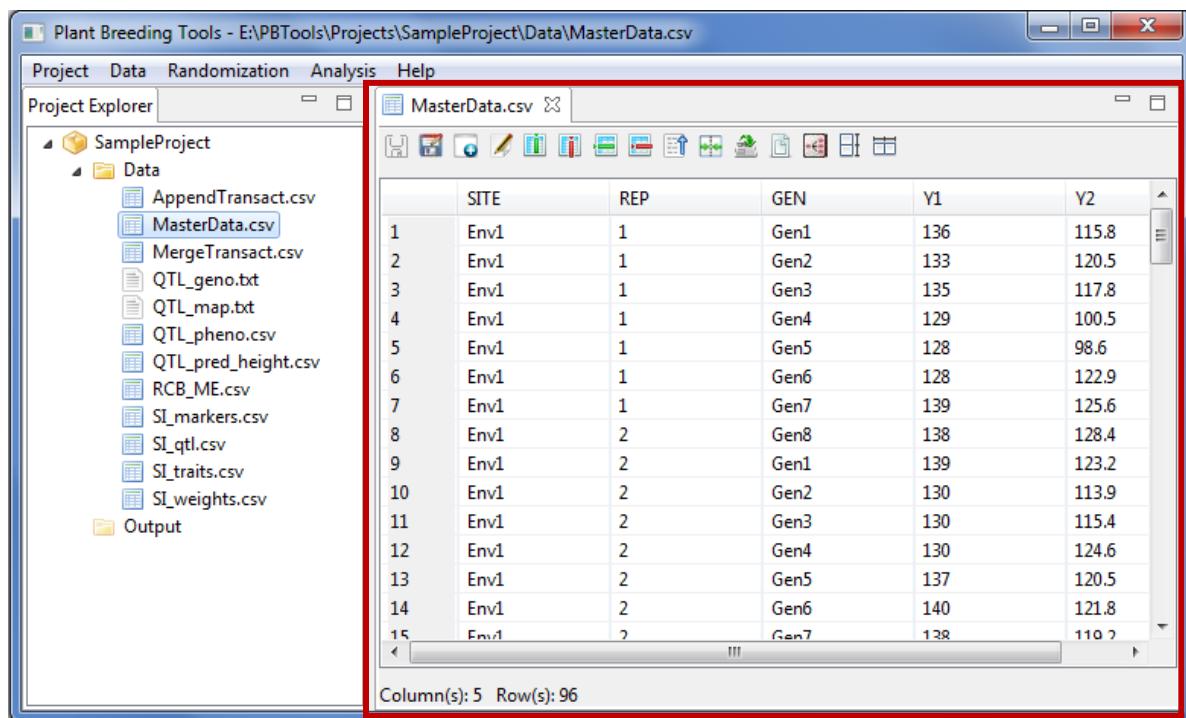


Help Menu is used to access PBTools user's manual and some information about the software.



Data Viewer

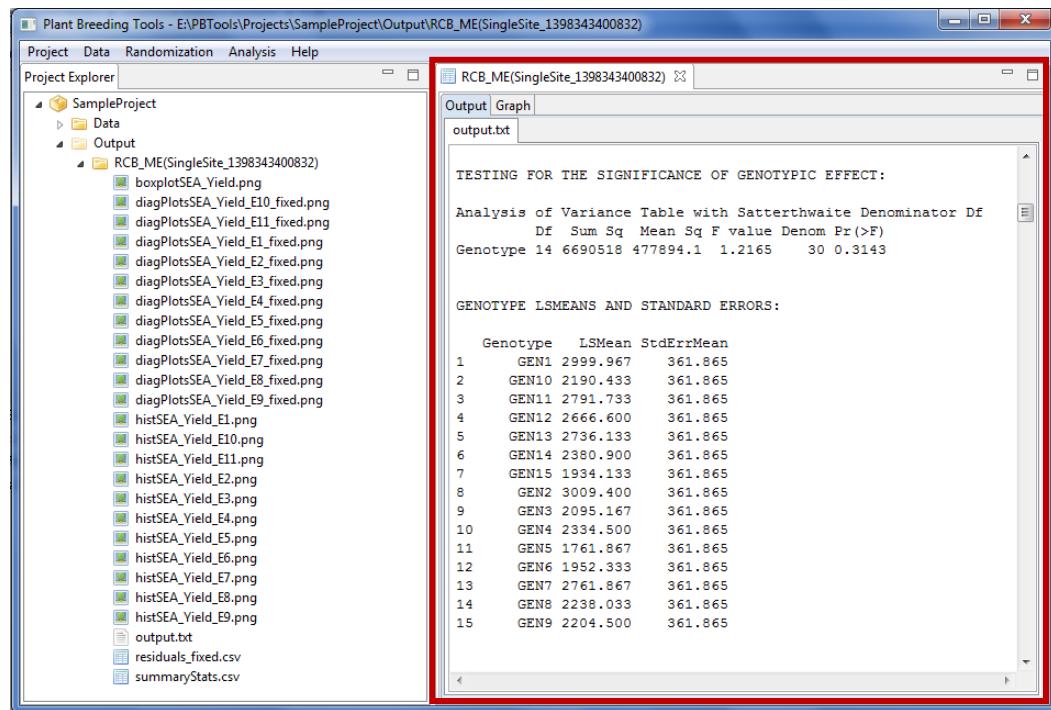
Data Viewer is displayed in the editor panel when a CSV file is double-clicked from the Project Explorer tree. It is used for viewing data file in spreadsheet format, editing data values and performing data manipulation. Several Data Viewers can be opened simultaneously inside the Editor Panel but only one is considered to be the active tab. Each Data Viewer contains toolbars which can be used for managing the data. The toolbars have the same functionalities as the options under the **Data** menu.



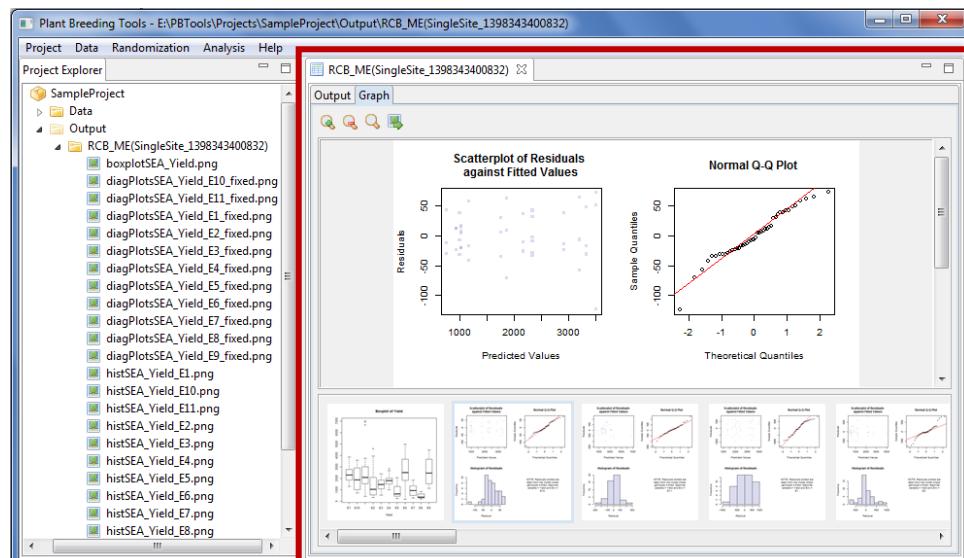
The name of the tab indicates the name of the dataset. When an asterisk appears in the tab name ***MasterData.csv**, it indicates that there has been modification made in the data. If data manipulation or analysis is performed on the data on the active tab, PBTools captures all information in the active tab (even unsaved modifications) and submit it for manipulation or analysis. If a Data Viewer with unsaved changes is closed, the user will be prompted to save the changes.

Results Viewer

The Results Viewer 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 Results Viewer may have an *Output* page and/or *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.

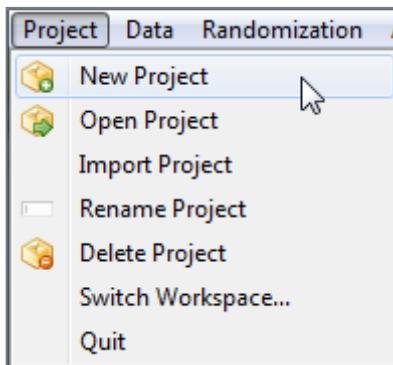


3. Project and File Management

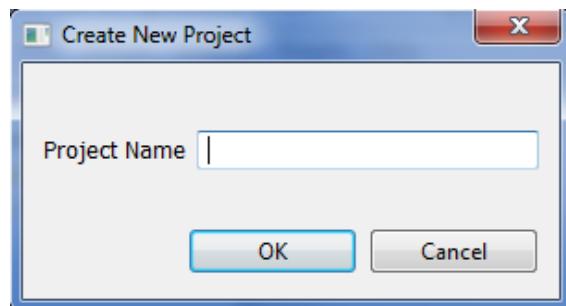
Creating New Project

The user can create several projects in PBTools. However, only one project can be considered as the active project and is visible in the Project Explorer. The steps for creating new project are listed below.

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



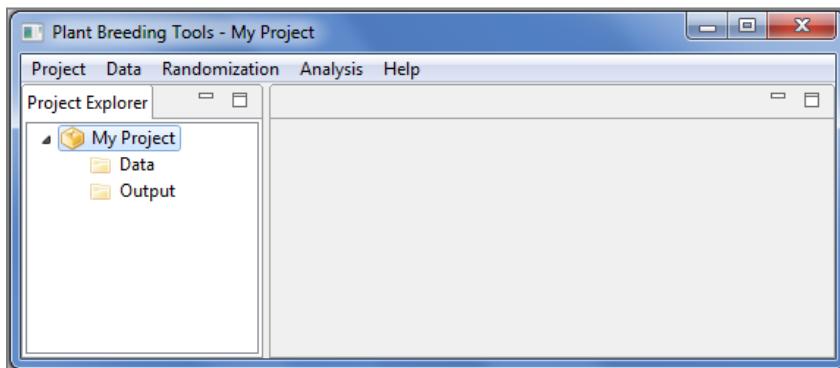
- The **Create New Project** dialog box will appear. In the **Project Name** field, specify a name of the new project.



In naming a project, the following rules apply:

- The name must start with a letter. The remaining characters can be a letter, digit, 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 *My Project*. Click **OK**.
- The new project named *My Project*, 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.

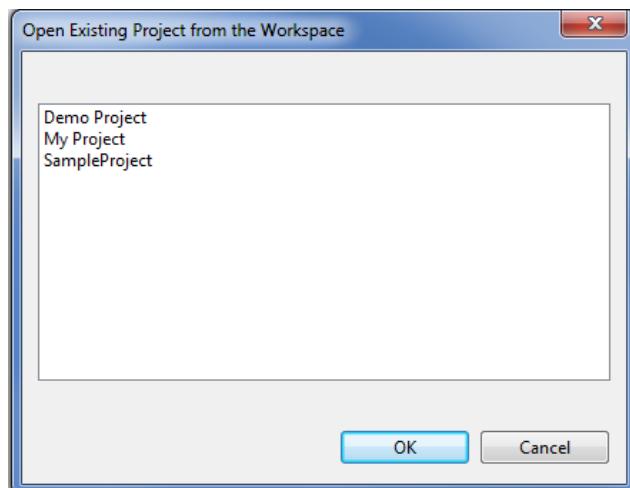


- NOTE: As part of the example, create another project named *Demo Project*.

Opening Existing Project

The steps for opening existing project 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.

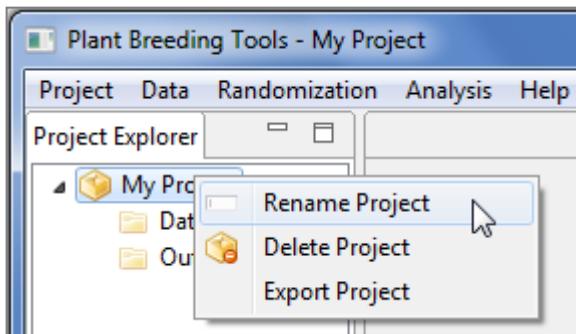


- For the example, select the project named *My Project*. Click **OK**. *My Project* should now be the active project in the Project Explorer.

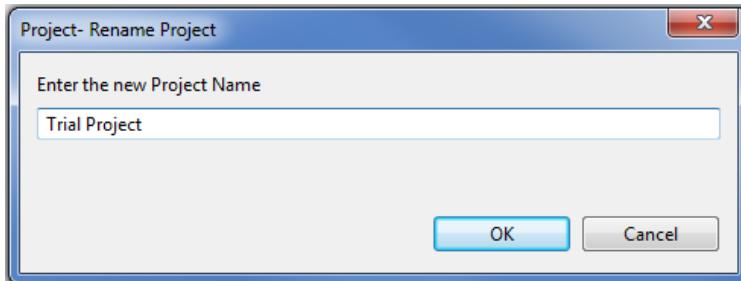
Renaming Project

The steps for renaming the active project are listed below.

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



- Enter a new project name, say *Trial Project*. Click **OK**.

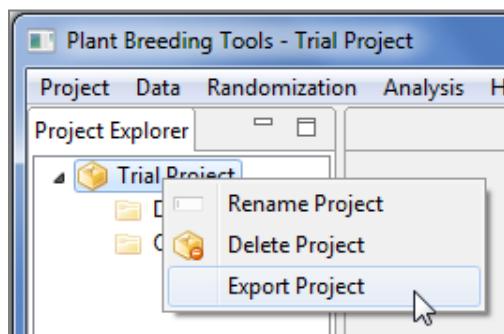


- The project should be displayed in the Project Explorer with the new name.

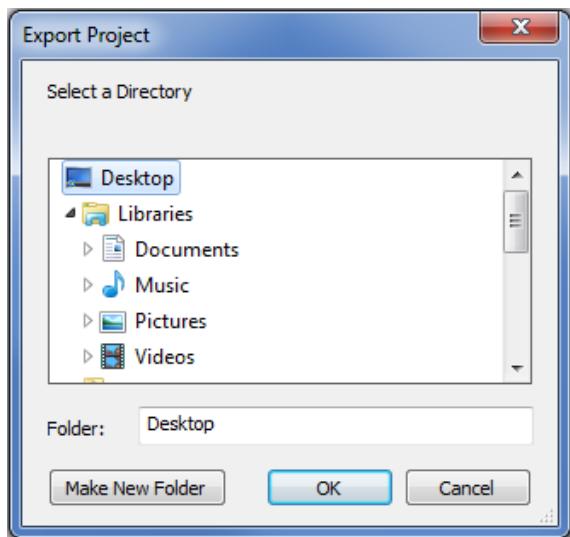
Exporting Project

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 *Trial Project* then select **Export Project**.



- Select the directory where the active project will be saved. For the example, choose **Desktop**. Click **OK**.

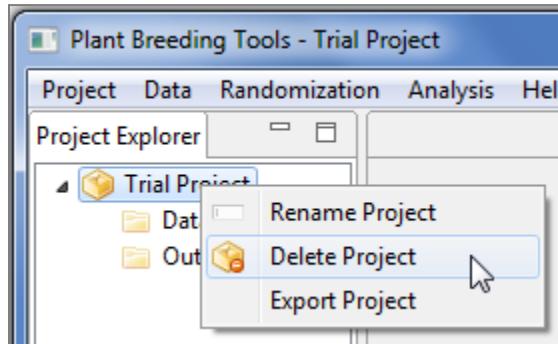


- A *Trial Project* folder is now on the desktop.

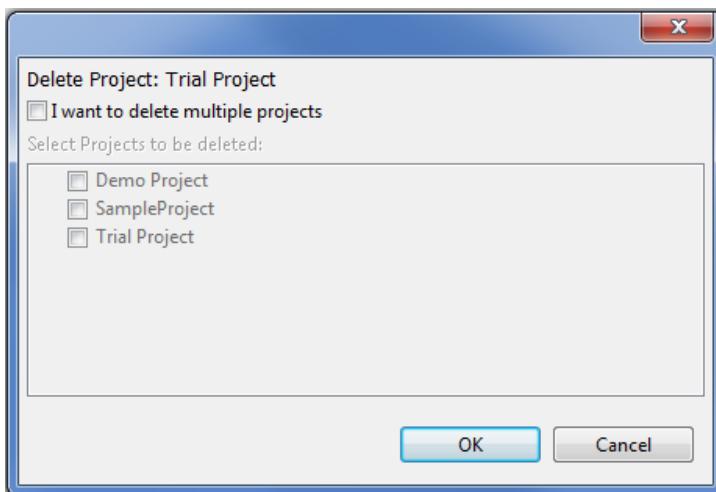
Deleting Project

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

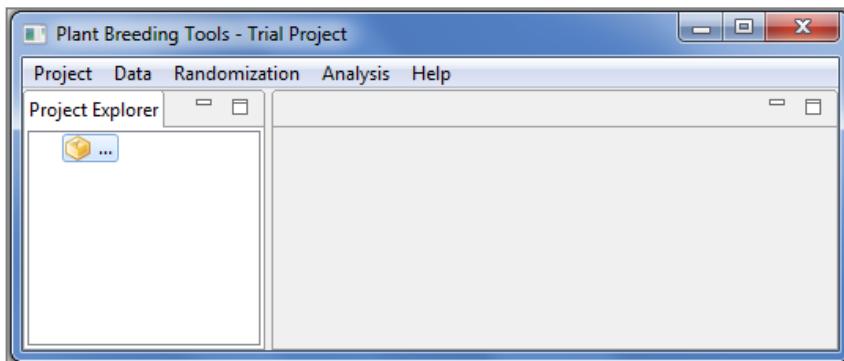
- Right-click on the active project, say *Trial Project* then select **Delete Project** or select **Project | Delete Project** from the main menu.



- Another dialog will be displayed. If the user wants to delete multiple projects, click on the check box labeled 'I want to delete multiple projects' then select from the list the projects to be deleted. For the example, delete only *Trial Project* by clicking **OK**.



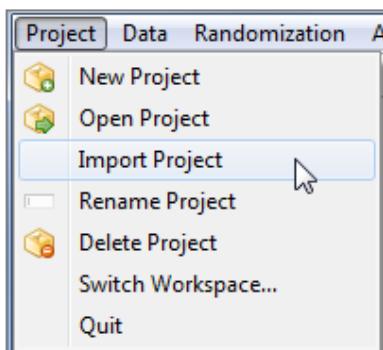
- Since *Trial Project* is now deleted from the PBTools workspace, there is no active project displayed in the Project Explorer as shown below.



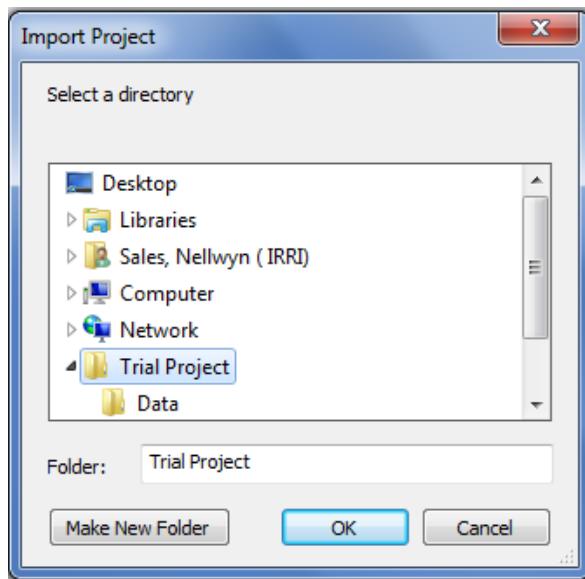
Importing Project

Projects, as long as it is a valid PBTools project, can be saved inside the PBTools 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 *Trial Project* folder on the desktop. Click **OK**.



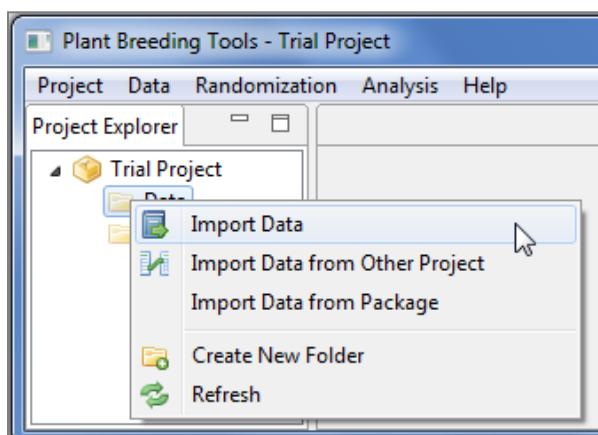
- *Trial Project* is now the active project in the Project Explorer.

Importing Data from External Source

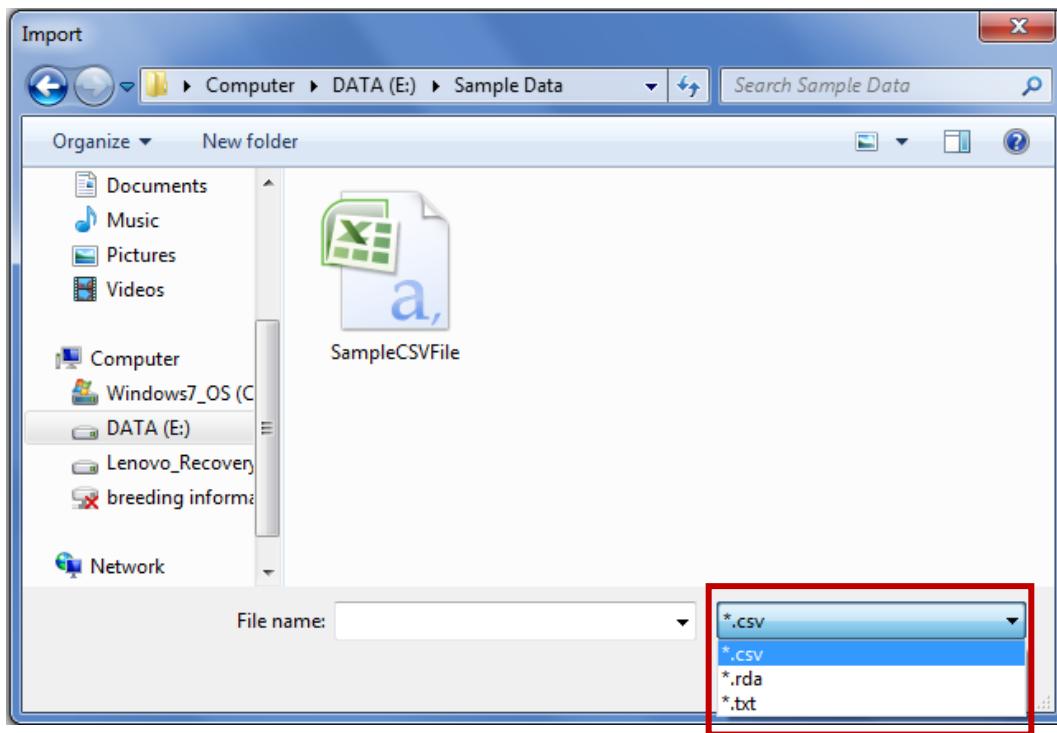
There are three file formats that PBTools accepts to import from external source namely: R datasets; text files with tab, space, comma and semi-colon delimiter; and comma separated value files.

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 *Trial Project*. Choose **Import Data**.

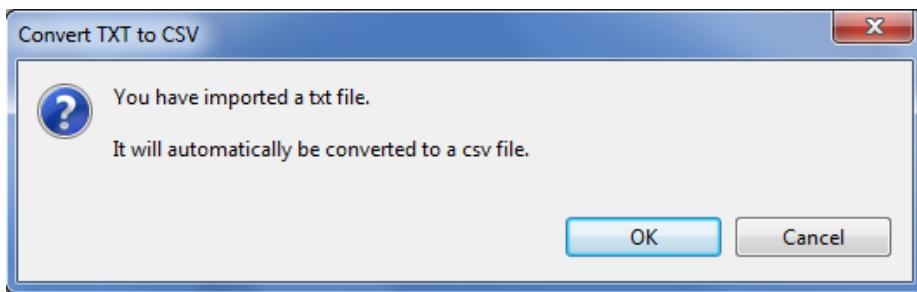


- The Import dialog box will appear. Choose the appropriate file type to be imported in the File of Types drop-down box. The default file type is ***.csv**. Go to the directory where the file to be imported is located. Select the file or type the file name on the **File name** text box.

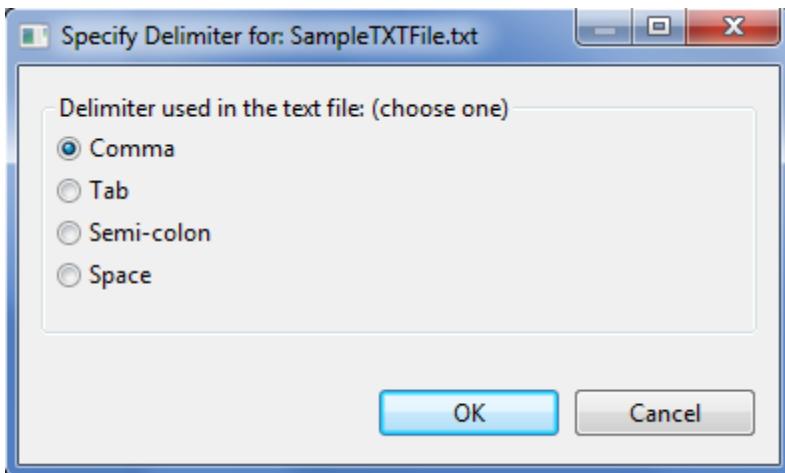


- Click the **Open** button.

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



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 **OK**.

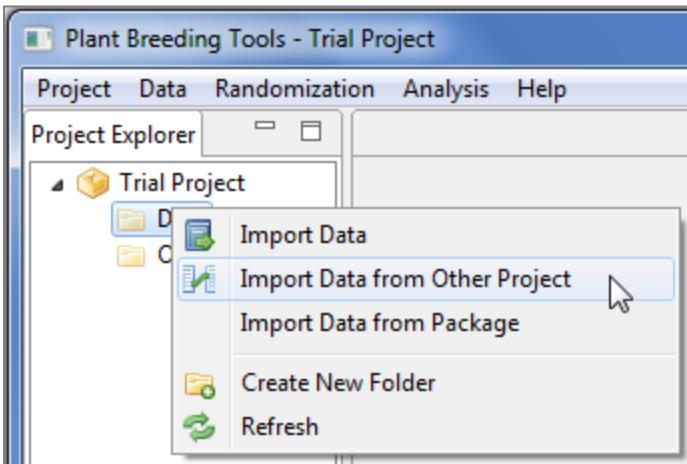


- The newly imported data will now be displayed inside the *Data* folder of the active project in the Project Explorer. To view the data in a spreadsheet format, double-click the icon of the data file.

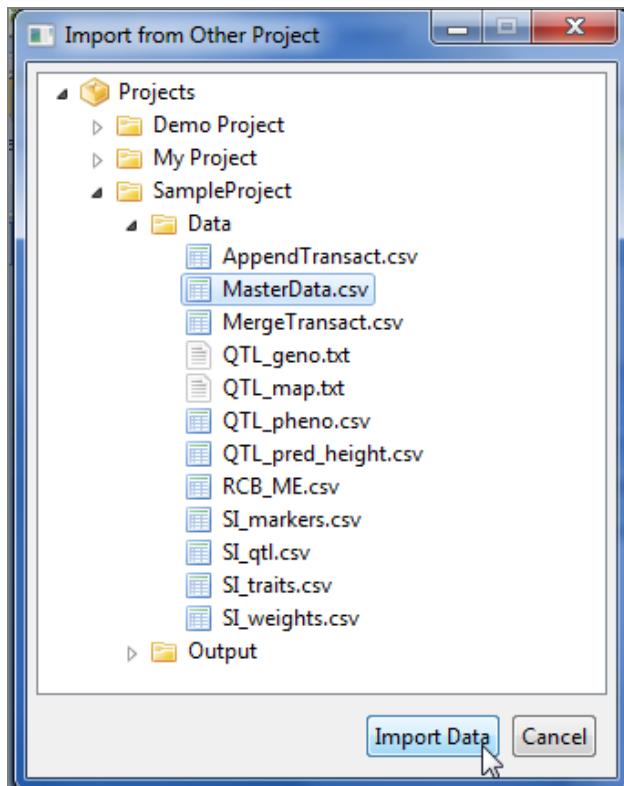
Importing Data from Other Project

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 *Trial Project*. Choose **Import Data from Other Project**.



- The **Import from Other Project** dialog box will appear. This dialog box contains all existing PBTools projects in the workspace. The user can 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.

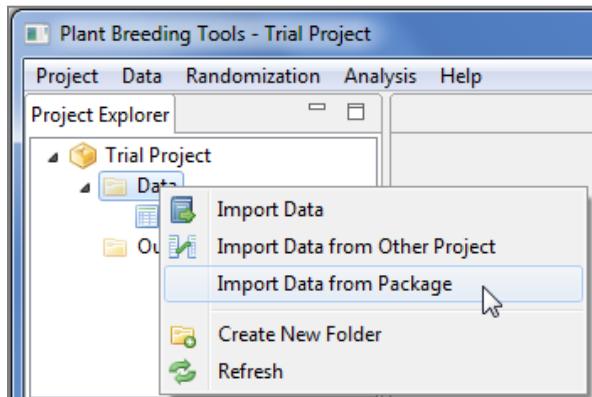


- Click the **Import Data** button. The newly imported data will now be displayed inside the *Data* folder of the active project in the Project Explorer. To view the data in a spreadsheet format, double-click the icon of the data file.

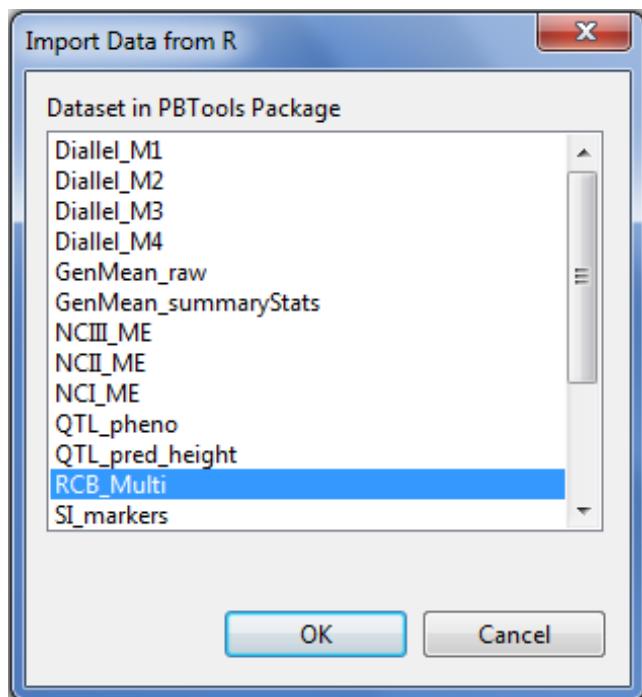
Importing Data from Package

Datasets in the R package named *PBTools* can be imported. The steps are listed below:

- On the **Project Explorer** panel, right-click the *Data* folder of the project named *Trial Project*. Choose **Import Data from Package**.



- The **Import Data from R** dialog box will appear. Choose one dataset to be imported. Only one data set can be imported at a time. For the example, choose *RCB_Multi*.



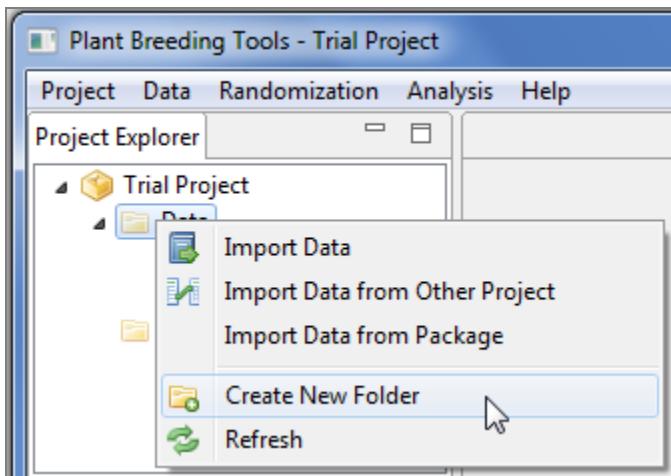
- Click **OK**. A dialog will appear confirming the data is successfully imported. The newly imported data will now be displayed inside the *Data* folder of the active project in the Project Explorer. To view the data in a spreadsheet format, double- click the icon of the data file.

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. For the example, right-click the *Data* folder of the project named *Trial Project*. Choose **Create New Folder**.

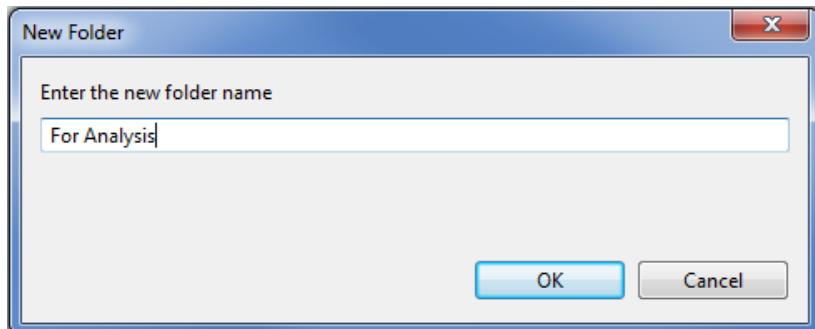


- The **New Folder** dialog box will appear. In the **Enter the new folder name** field, user can specify the name for the new folder. If the sub folder will be created within the *Data* folder, the default folder name is *Data*. If the sub folder will be created within the *Output* folder, the default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

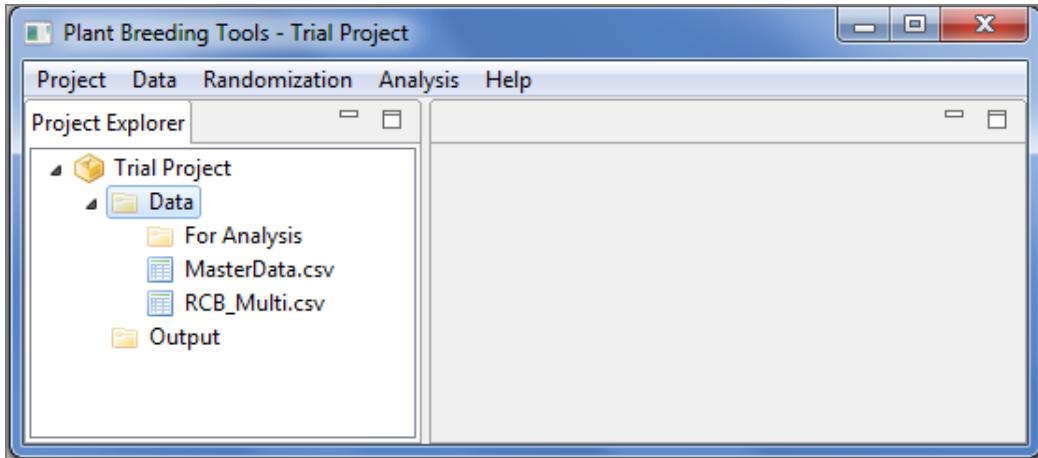
In naming a folder, the following rules apply:

- 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 *For Analysis* as the new folder name.



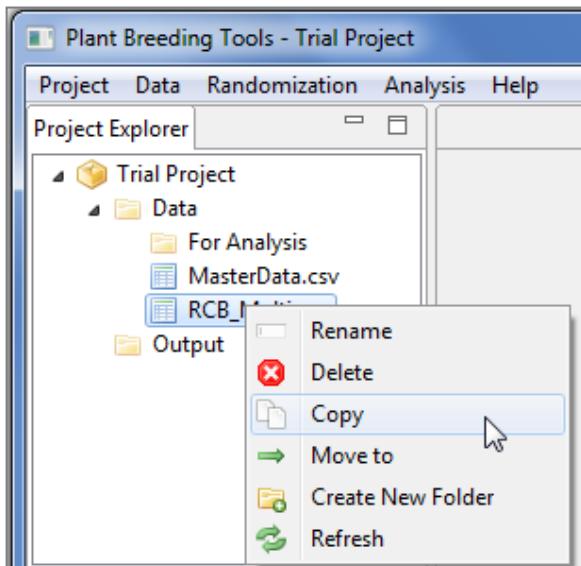
- A new sub-folder inside *Data* folder is now created and can be seen in the Project Explorer.



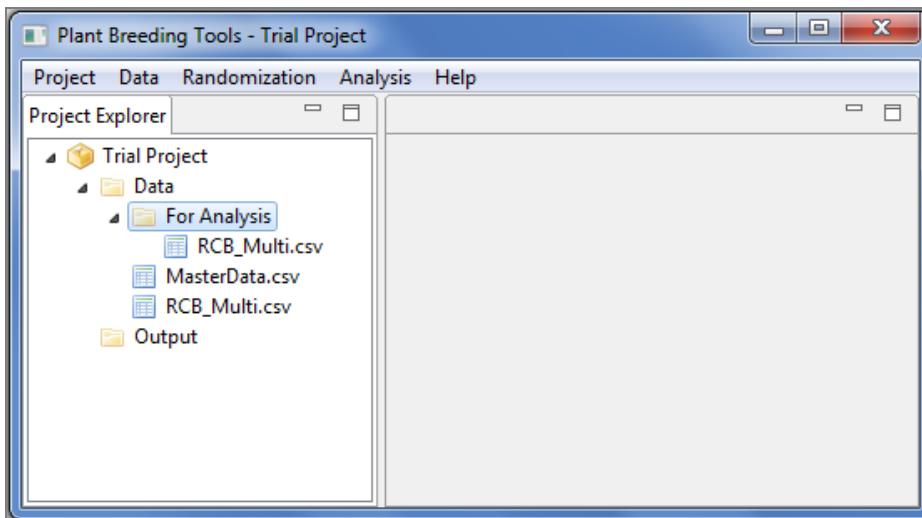
Copying File / Folder

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. For the example, right-click *RCB_Multi.csv* inside the *Data* folder of the project named *Trial Project*. Choose **Copy**.



- Go to the desired destination folder, which can be within or outside PBTools workspace, then right-click then choose **Paste**. For the example, right-click on the *For Analysis* folder then choose **Paste**.
- The file is now copied inside the destination folder.

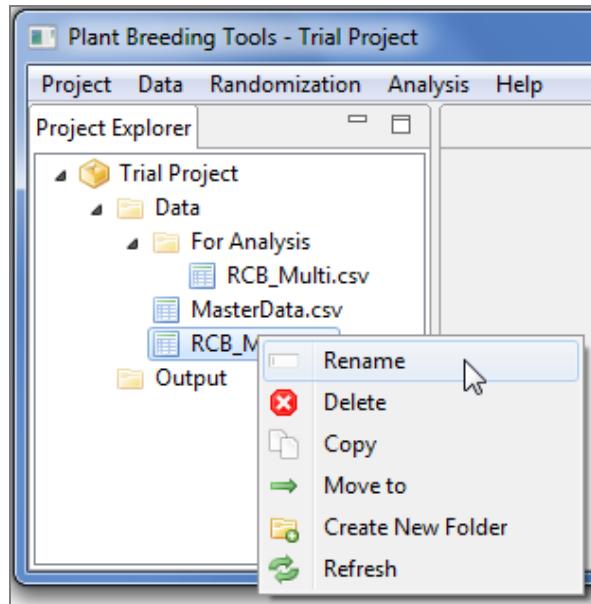


These steps also apply when copying sub-folders within the *Data* and *Output* folders.

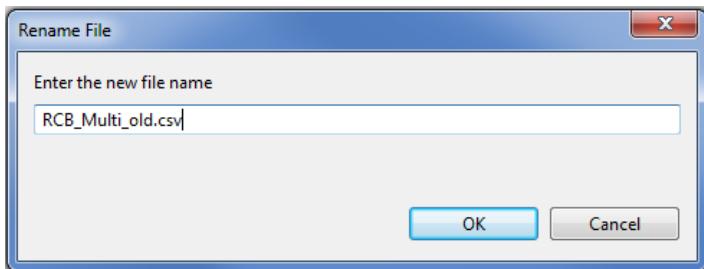
Renaming File / Folder

The steps to rename files are listed below:

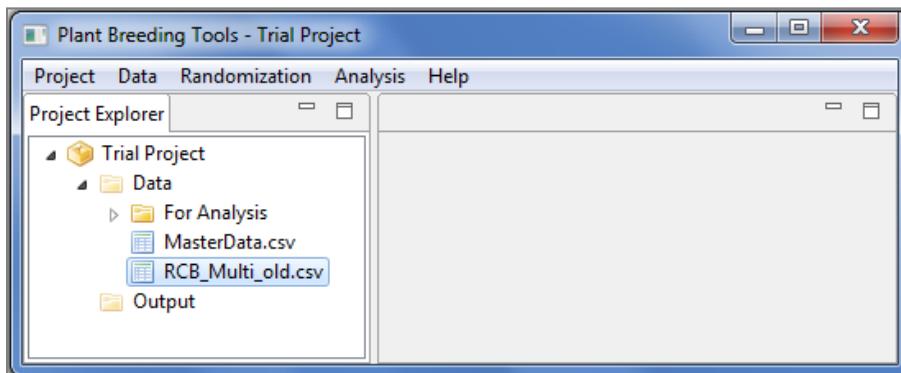
- On the **Project Explorer** panel, right-click the file you want to rename. For the example, right-click *RCB_Multi.csv* inside the *Data* folder of the project named *Trial Project*. Choose **Rename**.



- The **Rename File** dialog box will appear. In the **Enter the new file name** field, user can specify the new filename. For the example, set the new filename to *RCB_Multi_old.csv*.



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

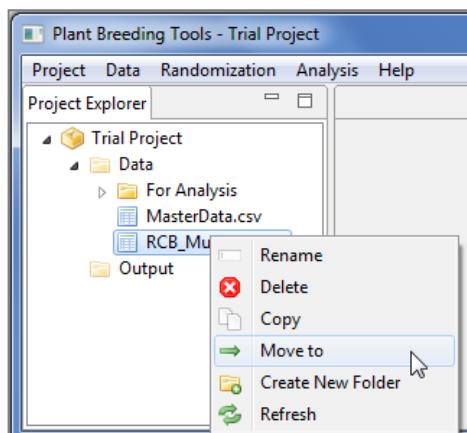


These steps also apply when renaming sub-folders within the *Data* and *Output* folders. Note that the *Data* and *Output* folders are required folders for a PBTools project so it cannot be renamed.

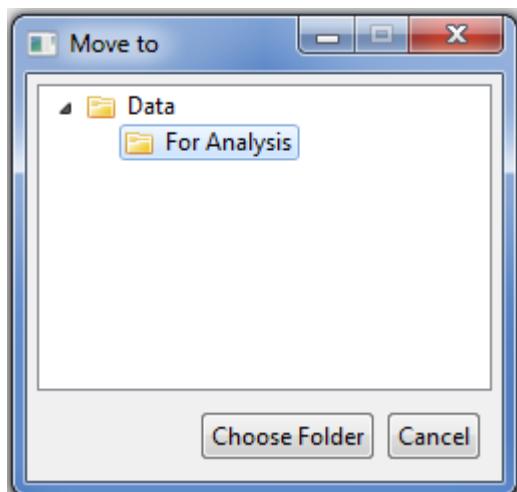
Moving File / Folder

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

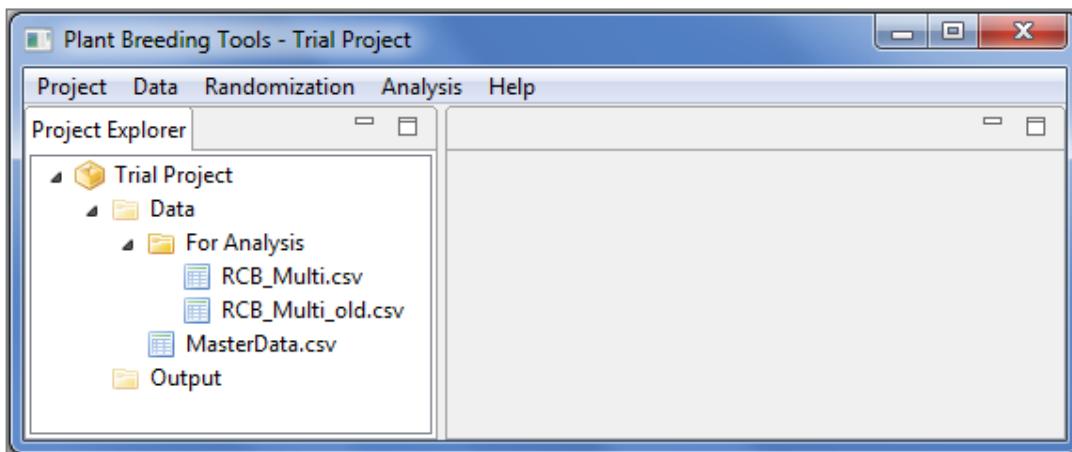
- On the **Project Explorer** panel, right-click the file you want to rename. For the example, right-click *RCB_Multi_old.csv* inside the *Data* folder of the project named *Trial Project*. Choose **Move to**.



- The **Move to** dialog box will appear. Select the destination folder. For the example, choose the *For Analysis* folder inside the *Data* folder.



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

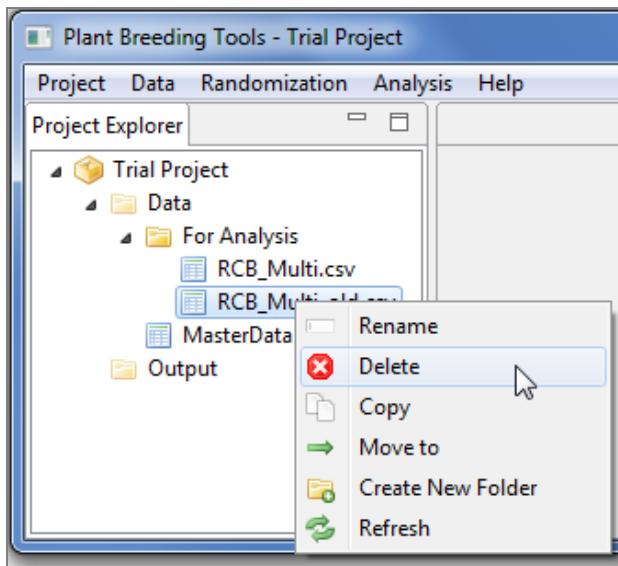


These steps also apply when moving sub-folders within the *Data* and *Output* folders.

Deleting File / Folder

The steps to delete data files are listed below:

- On the **Project Explorer** panel, right-click the file you want to delete. For the example, right-click *RCB_Multi_old.csv* inside *For Analysis* folder in the *Data* folder of the project named *Trial Project*. Choose **Delete**.



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



- Click **Yes** to delete.

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

4. Data Handling and Manipulation

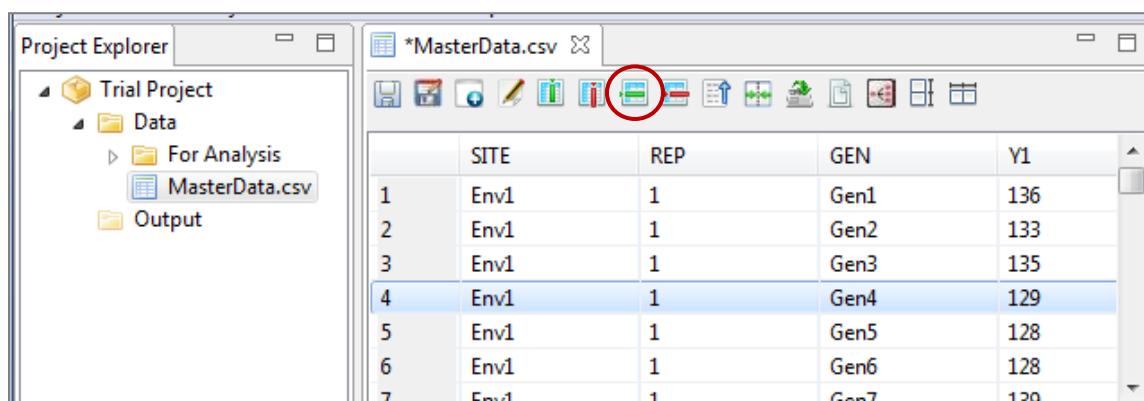
Representing Missing Value(s)

In PBTools, missing values can be represented by using any of the following: NA, space, period or blank. Using other symbol, say asterisk (*), to represent missing values will affect how PBTools identifies the attributes of the columns of the dataset. A column with numeric values but contains asterisks will be classified as a factor column. This misclassification may cause problems later when the data is subjected to manipulation or analysis.

Inserting Row(s)

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

- On the Project Explorer, locate the *MasterData.csv* from the *Data* folder of the project named *Trial Project*. Double-click the file to view it in the Data Viewer.
- Select any row(s) or any cell in the row(s) where the user wants to insert new row(s) 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 or click the Insert Row icon  in the **Data Viewer** toolbar.



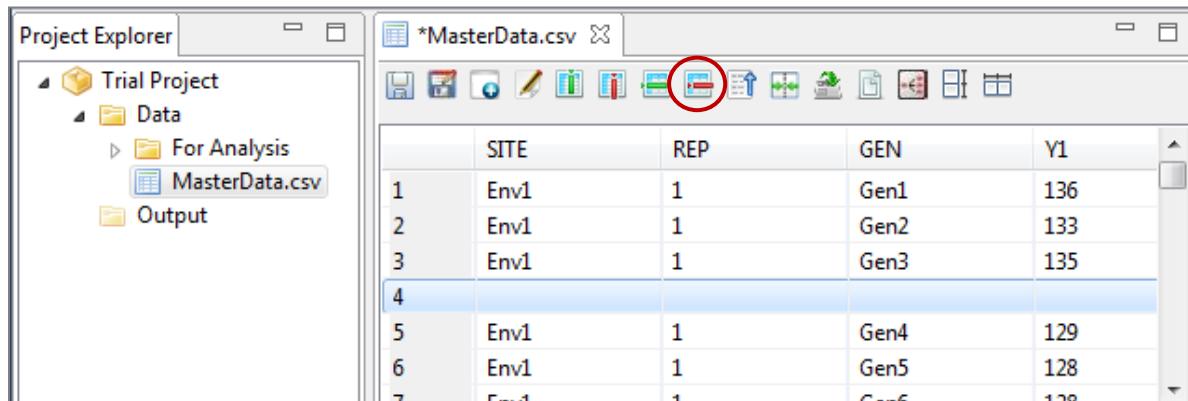
- The data now contains the newly inserted row.

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.

Deleting Row(s)

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

- For the example, use the modified and unsaved *MasterData.csv* from the previous section that is displayed in the Data Viewer.
- Select any row(s) or any cell in the row(s) that the user wants to delete. 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 or click the Delete Row icon  in the Data Viewer tool bar.

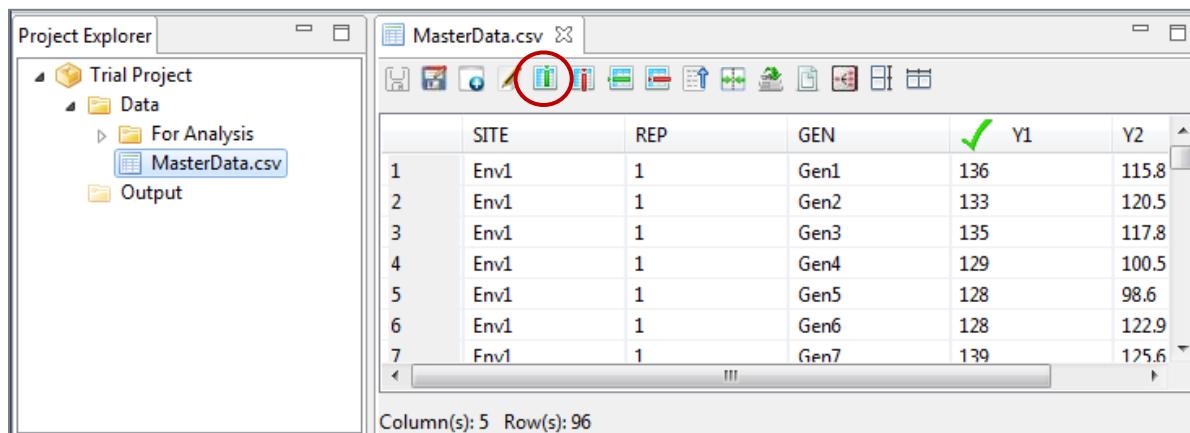


- The Delete Row dialog box will appear. Confirm that row deletion is desired by clicking **Yes**.
- The changes made should be reflected in the Data Viewer.
- For the example, close the modified *MasterData.csv* and do not save the changes.

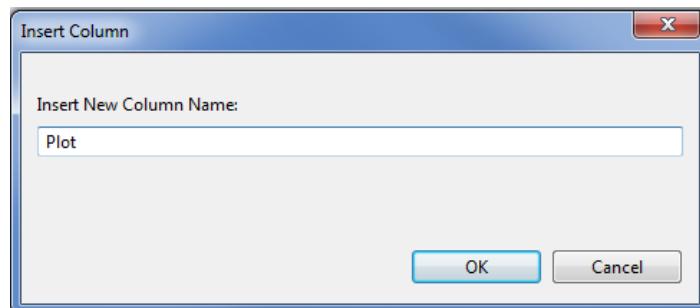
Inserting Column

The steps to insert column are listed below:

- On the Project Explorer, locate the *MasterData.csv* from the *Data* folder of the project named *Trial Project*. Double-click the file to view it in the Data Viewer.
- Select a column where the user wants a new column to 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 or click the Insert Column icon  in the Data Viewer tool bar.



- The **Insert Column** dialog box will appear. In the **Insert New Column Name** field, user can specify the name of the new column. The default name is *NewColumn*. For the example, type *Plot*.



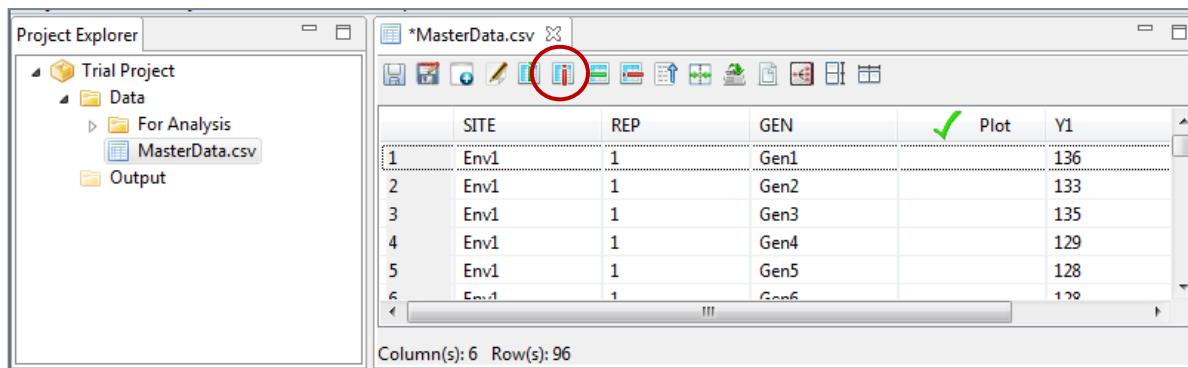
In naming a column, the following rules apply:

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

Deleting Column(s)

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

- For the example, use the modified and unsaved *MasterData.csv* from the previous section that is displayed in the Data Viewer.
 - 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 menu bar or click on the Insert Column icon  in the Data Viewer tool bar.



- A dialog box will appear. To confirm the deletion of the column is desired, click **Yes**.

If the user wants to delete other column(s), select the check box labeled "I want to delete multiple columns" then select the column(s) on the text box that will appear.

- The changes made should be reflected in the Data Viewer. For the example, close the modified *MasterData.csv* and do not save the changes.

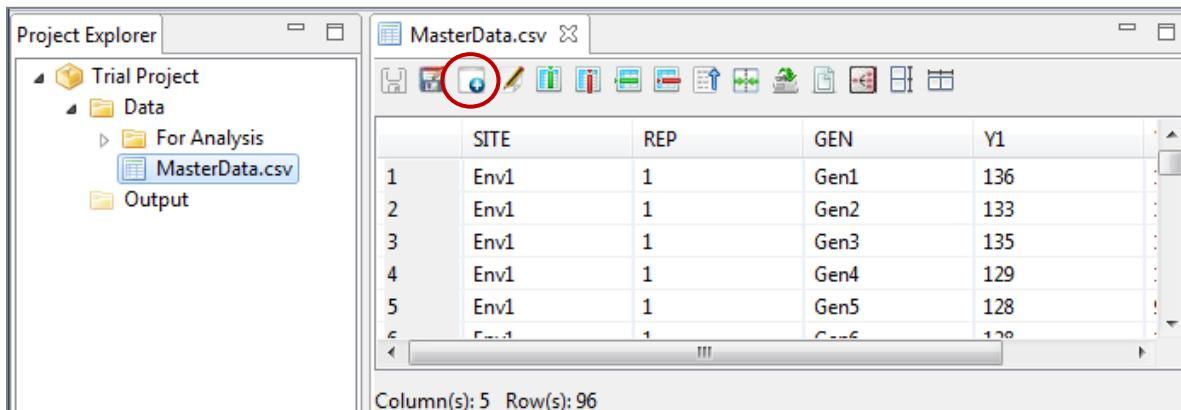
Creating a New Variable

The user can create new variables in the active data set by transforming existing variables or collapsing the values of two or more existing variables.

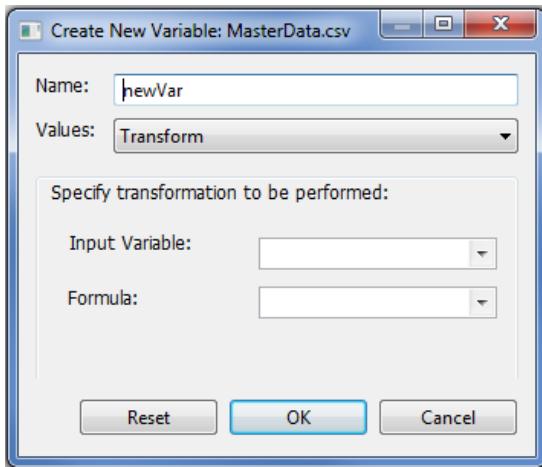
For transformations, there are six available functions, namely: logarithm, natural logarithm, square root, power, exponential and standardized. For logarithm, natural logarithm, square root and power transformation, the variables to be transformed should not contain negative values. For logarithm and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

The steps to create new variables are listed below:

- On the Project Explorer, locate the *MasterData.csv* from the *Data* folder of the project named *Trial Project*. Double-click the file to view it in the Data Viewer.
- Click **Data | Create New Variable...** from the menu bar 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.
- The name must be different from the existing column names in the data.
- The 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*.

If transformation option is selected, the user needs to specify the following:

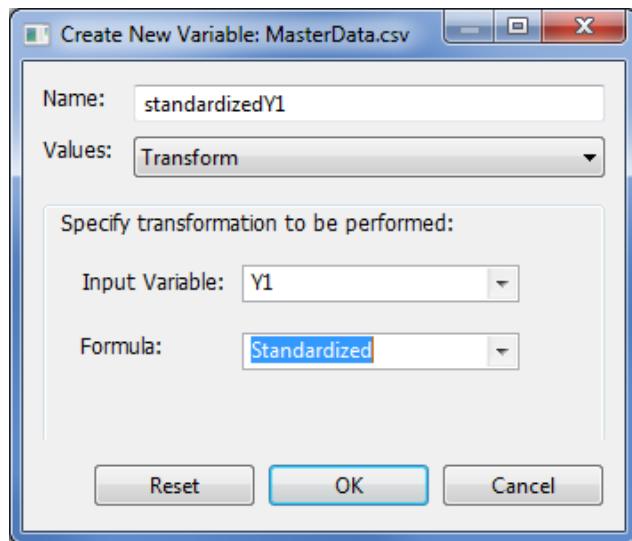
Input Variable

This 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. Select one variable where the transformation will be performed.

Formula

This pertains to the formula that will be used in the transformation. The available options are logarithm, natural logarithm, square root, power, exponential and standardized.

For the example, suppose we want to create a new variable named *standardizedY1* by standardizing the values of Y1. The completed dialog box should appear as shown below:

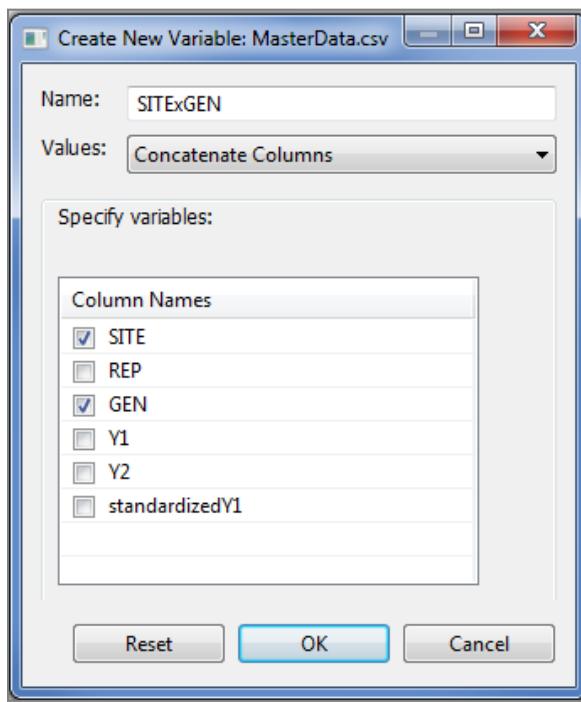


If concatenation of columns is selected, a table containing all the columns of the active data will appear at the lower part of the dialog box. The user needs to specify the columns to concatenate by ticking at least two column names.

- Click **OK**.
- The changes are saved to the original dataset and the file is displayed in the Data Viewer.

The Data Viewer window shows the 'MasterData.csv' file. The Project Explorer on the left shows a 'Trial Project' with 'Data' and 'Output' folders, and a 'MasterData.csv' file under 'For Analysis'. The Data Viewer window displays four columns: EN, Y1, Y2, and standardizedY1. The data rows are: en1 (136, 115.8, 0.34725590982...), en2 (133, 120.5, 0.16032188734...), en3 (135, 117.8, 0.28494456899...), en4 (129, 100.5, -0.0889234759...), en5 (128, 98.6, -0.1512348168...), en6 (128, 122.9, -0.1512348168...), en7 (139, 125.6, 0.53418993231...), and en8 (138, 128.4, 0.47187859148...). The status bar at the bottom indicates 'Column(s): 6 Row(s): 96'.

Suppose the user also wants to create a new variable named *SITExGEN* by concatenating the values of *SITE* and *GEN*, click on the Create New Variable icon. The completed dialog box should appear as shown below:



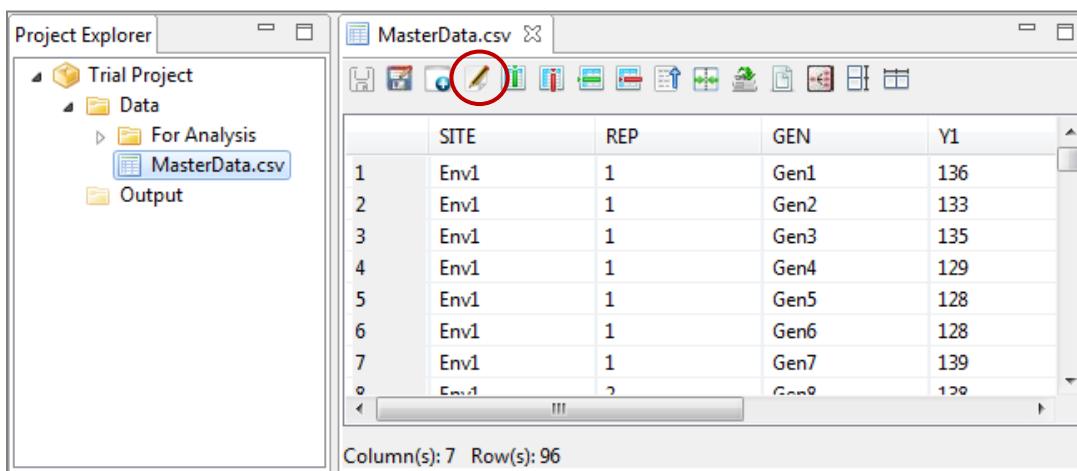
- Click the **OK**. The changes are saved to the original dataset and the file is displayed in the Data Viewer.

The screenshot shows the software interface with two main windows. On the left is the "Project Explorer" window, which displays a "Trial Project" with a "Data" folder containing "For Analysis" and "MasterData.csv", and an "Output" folder. On the right is the "MasterData.csv" Data Viewer window, showing a table with columns: 1, Y2, standardizedY1, and SITExGEN. The data rows show values for Y2 and standardizedY1, and concatenated values for SITExGEN (e.g., Env1_Gen1, Env1_Gen2, etc.). Below the table, it says "Column(s): 7 Row(s): 96".

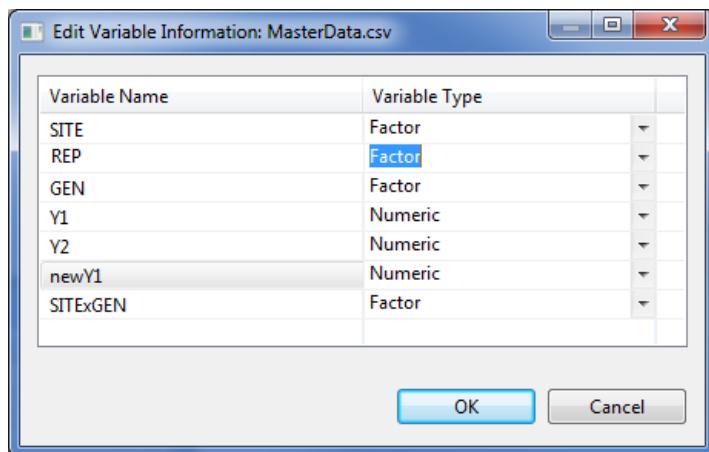
Editing Variable Information

The steps to edit the variable information are listed below:

- On the Project Explorer, locate the *MasterData.csv* from the *Data* folder of the project named *Trial Project*. Double-click the file to view it in the Data Viewer.
- Click **Data | Edit Variable Information** from the menu bar or click 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 listed and classified as either a factor or numeric variable. The user can modify the name and type of any variable in the dataset.
- For the example, change the variable type of *REP* from Numeric to Factor and rename *standardizedY1* to *newY1*. The complete dialog box should appear as shown below:

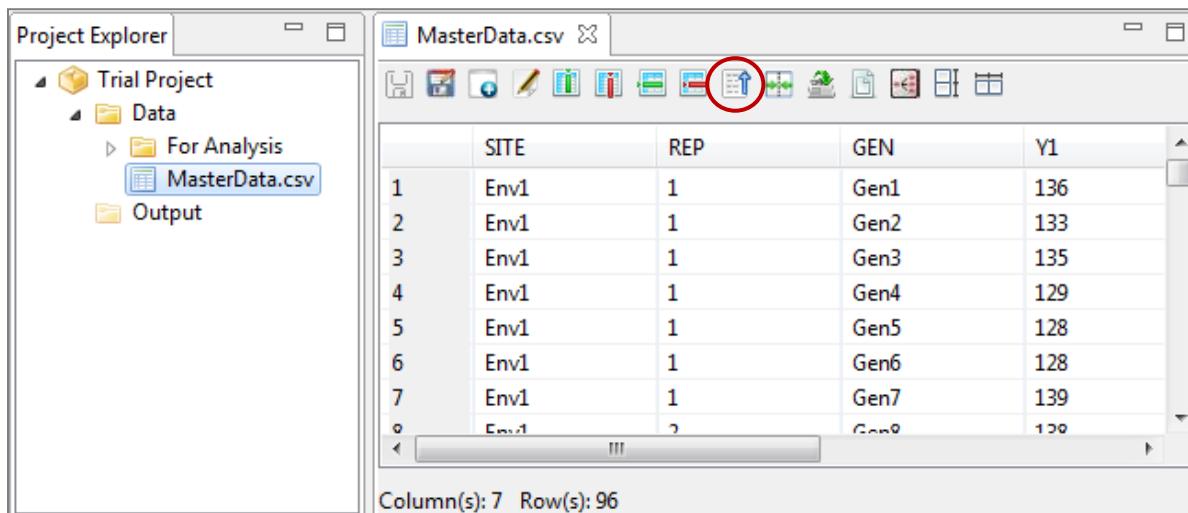


- Click **OK**.
- A message dialog box will appear prompting that changes have been saved. Click **OK**.
- The changes made should be reflected in the Data Viewer. For the example, close the modified *MasterData.csv* and do not save the changes.

Sorting data

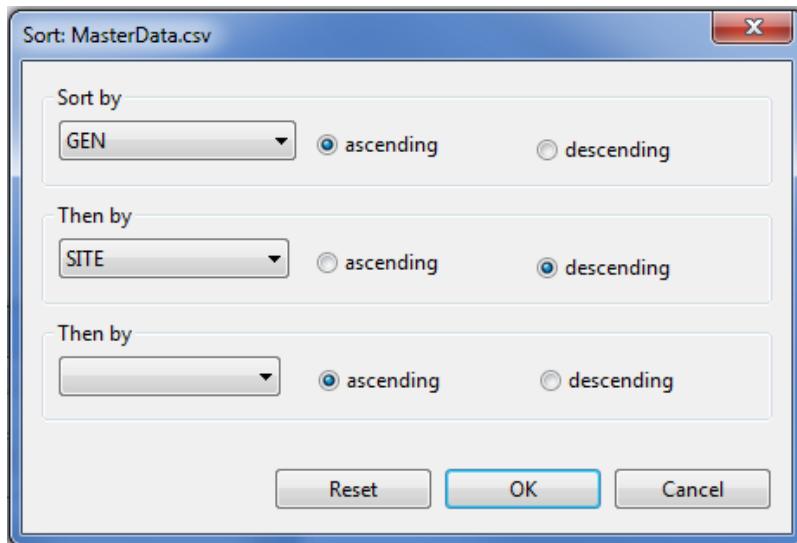
Re-arranging or sorting the rows or cases of the data file is often useful and sometimes necessary for certain types of analysis. The steps to re-arrange the rows based on the value of one or more sorting variables are listed below:

- On the Project Explorer, locate the *MasterData.csv* from the *Data* folder of the project named *Trial Project*. Double-click the file to view it in the Data Viewer. The data file is arranged by *SITE*, *REP* then by *GEN*.
- Choose **Data | Sort...** from the menu bar or click the Sort icon  in the Data Viewer tool bar.



- The **Sort** dialog box will appear.
- The user can 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 rows of the data based on ascending order of the variable *GEN* then by descending order of the variable *SITE*. The completed dialog box should appear as illustrated below:



- Click the **OK**. The sorted data is created and saved in the parent folder of the active data and displayed in the Data Viewer.

The screenshot shows the software interface. On the left is the "Project Explorer" panel, which displays a "Trial Project" with a "Data" folder containing "MasterData.csv" and "MasterData_sorted.csv". "MasterData_sorted.csv" is highlighted with a red box. On the right is the "Data Viewer" panel, which shows a table with columns: SITE, REP, GEN, Y1, and Y2. The data is as follows:

	SITE	REP	GEN	Y1	Y2
1	Env3	1	Gen1	143	112.
2	Env3	2	Gen1	134	115.
3	Env3	3	Gen1	113	154.
4	Env3	4	Gen1	121	163.
5	Env2	1	Gen1	136	143.
6	Env2	2	Gen1	144	130.
7	Env2	3	Gen1	130	119.
8	Env2	4	Gen1	143	146

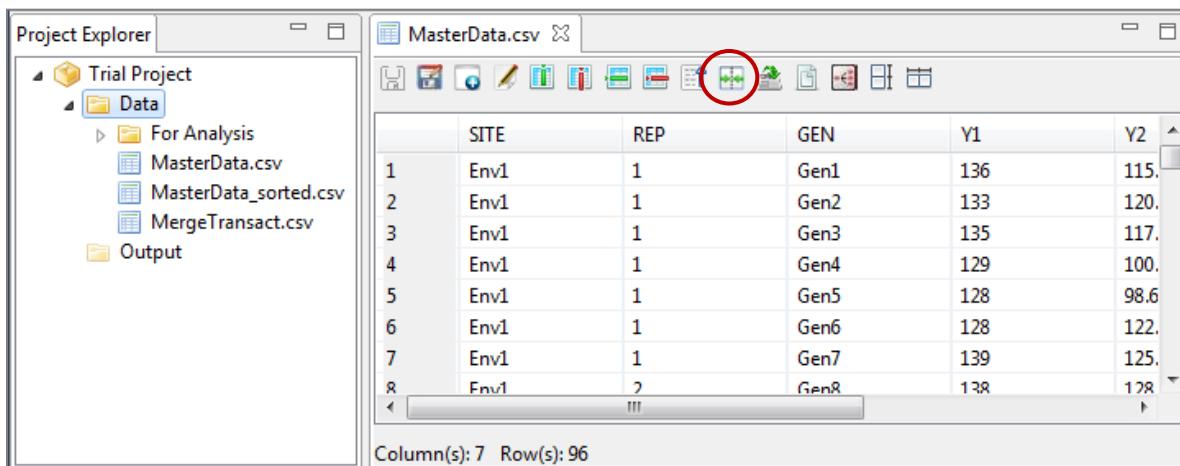
At the bottom of the Data Viewer, it says "Column(s): 7 Row(s): 96".

Merging datasets

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

The steps to merge datasets are listed below:

- For the example, two datasets will be used. The first one is the *MasterData.csv* from the *Data* folder of the project named *Trial Project*. The second one is the file named *MergeTransact.csv* which should be imported from the project named *SampleProject*. Double-click the file *MasterData.csv* to open it and view it in the Data Viewer.
- 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(s). Only *.txt* and *.csv* data file format can be selected as the transaction file.

Text File Delimiter

If the transaction file selected is a text file, the delimiter 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.

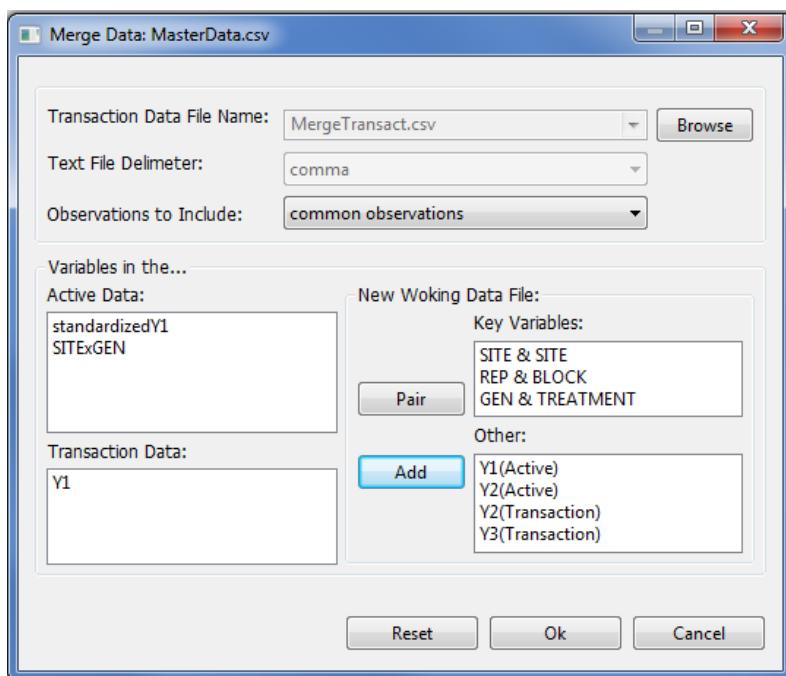
Key Variables

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 paired variables have different names, the 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. 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 illustrated below:

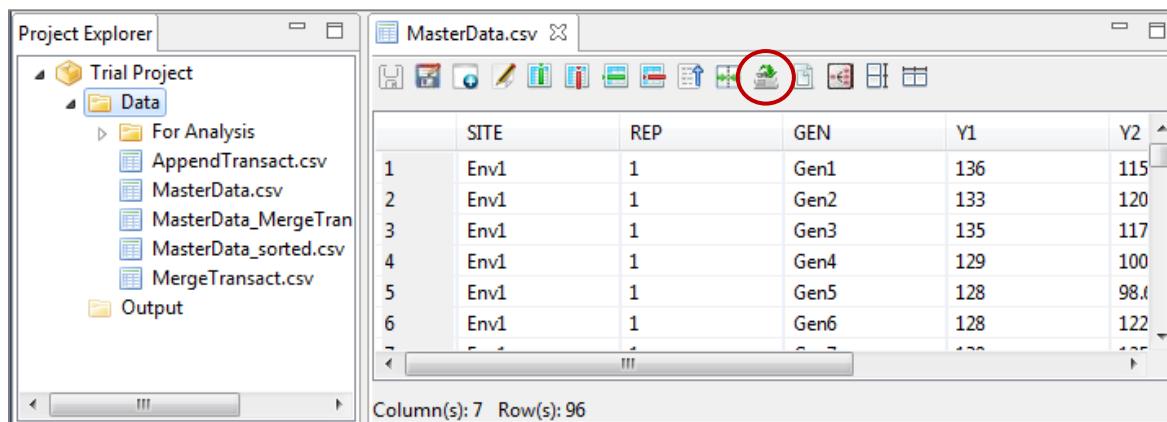


- Click **OK**. The merged data is saved in the parent folder of the active data and displayed in the Data Viewer tab. The default filename of the merged data set follows the format <activeDataFilename>_<TransactionDataFilename>_merge.csv.

Appending Datasets

This feature can be used to combine two data files with the same variables but different cases. The steps to merge datasets are listed below:

- For the example, two datasets will be used. The first one is the *MasterData.csv* from the *Data* folder of the project named *Trial Project*. The second one is the file named *AppendTransact.csv* which should be imported from the project named *SampleProject*. Double-click the file *MasterData.csv* to open it and view it in the Data Viewer.
- 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(s). Only .txt and .csv data file format can be selected as the transaction file.

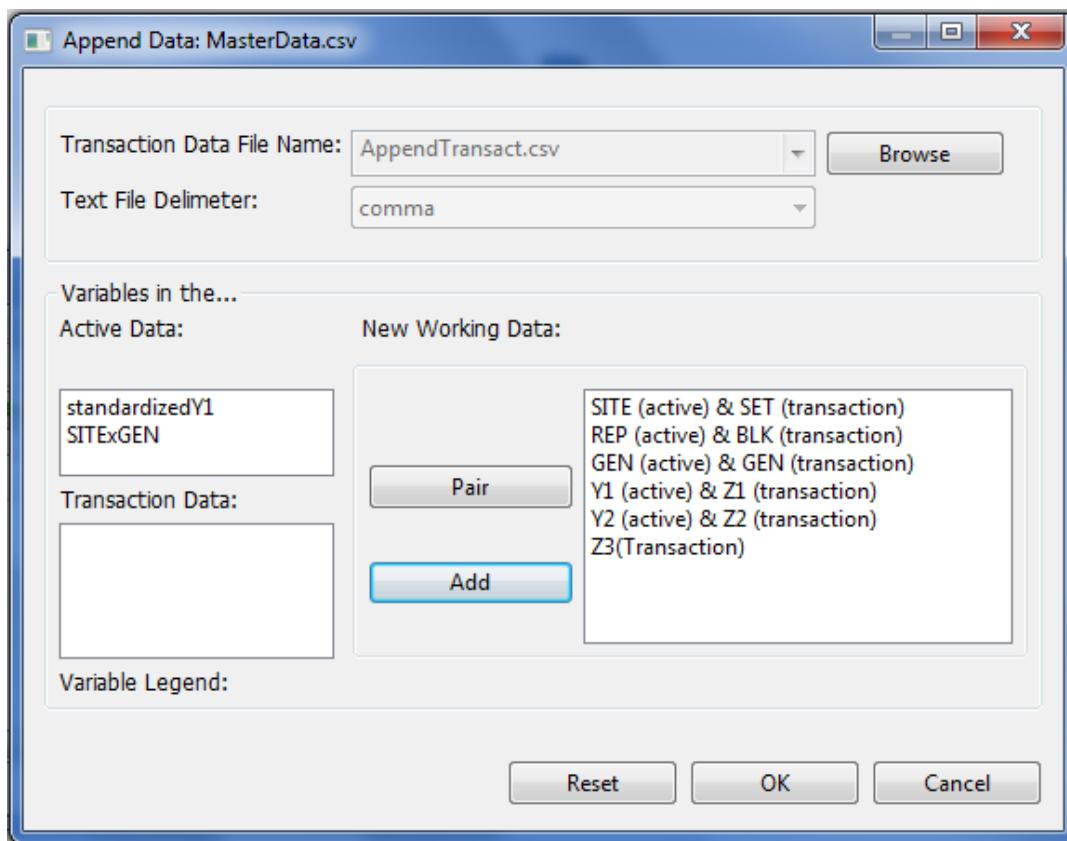
Text File Delimiter

If the transaction file selected is a text file, the delimiter should be specified. Four delimiters 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 file. 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:

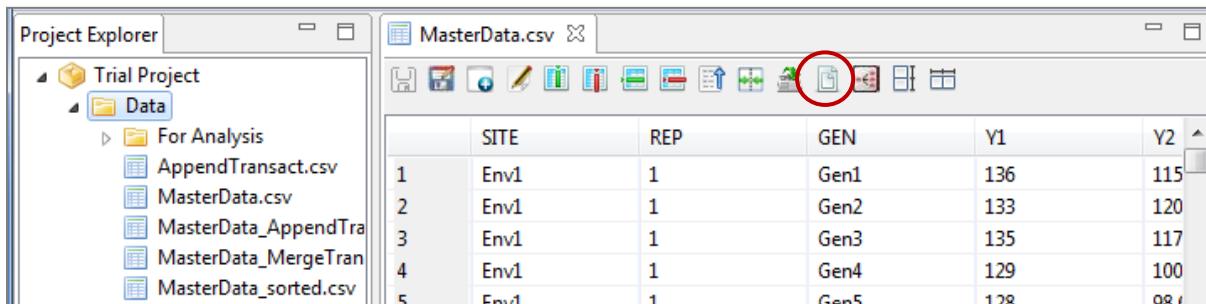


- Click **OK**. The generated file is saved in the parent folder of the active data and displayed in the Data Viewer tab. It will contain an additional column named Source which indicates where the data came from. The default filename of the appended data set follows the format *<activeDataFilename>_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

Creating Data Subset

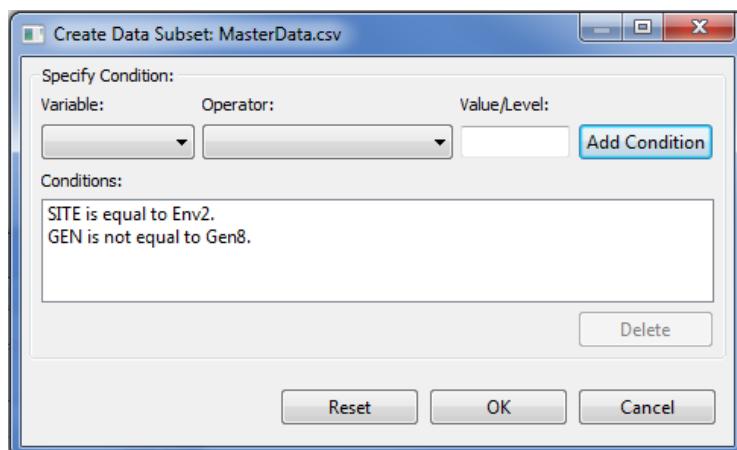
The steps in creating a subset of a data are listed below:

- On the Project Explorer, locate the *MasterData.csv* from the *Data* folder of the project named *Trial Project*. Double-click the file to view it in the Data Viewer.
- 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.
- For the example, suppose the user wants to select only the observations from *Env2* except those belonging to *Gen8*. This can be done by selecting variable *Site*, operator *equals (==)*, typing *Env2* under Value/Level and clicking the **Add Condition** button. Do the same for the condition “*GEN not equal to Gen8*”.

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



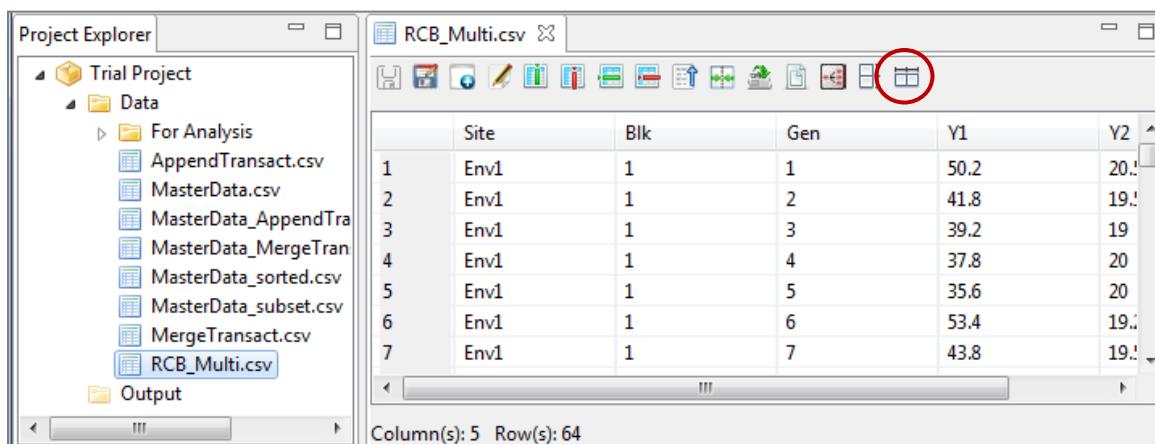
- Click **OK**. The new data is saved in the *Data* folder and displayed in the Data Viewer.

Reshaping Data From Long (Serial) to Wide (Parallel)

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:

- Import *RCB_Multi* file from PBTools package. Double-click the file to view it in the Data Viewer.
- Click **Data | Reshape | Long (Serial) to Wide (Parallel)** ... from the menu bar or click on the Reshape to Wide icon  in the Data Viewer tool bar.



- The **Reshape Data (Long to Wide)** dialog box will appear.
- Specify the required fields and appropriate options.

Variable(s) to Reshape

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

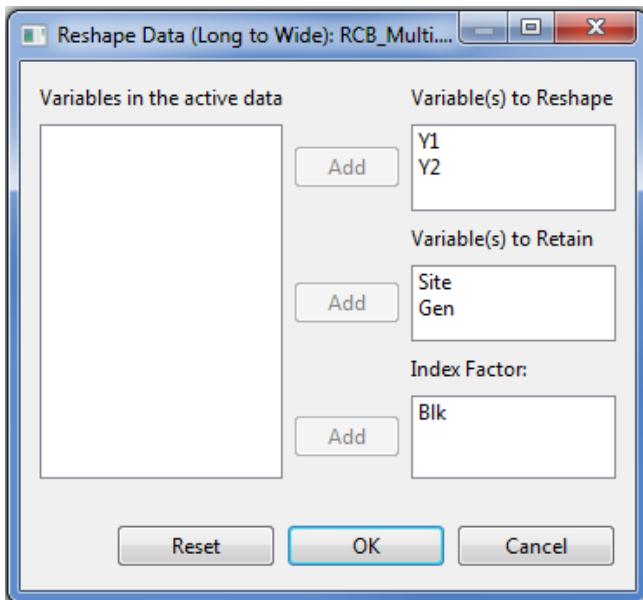
Variable(s) to Retain

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 dialog box should appear as illustrated below:



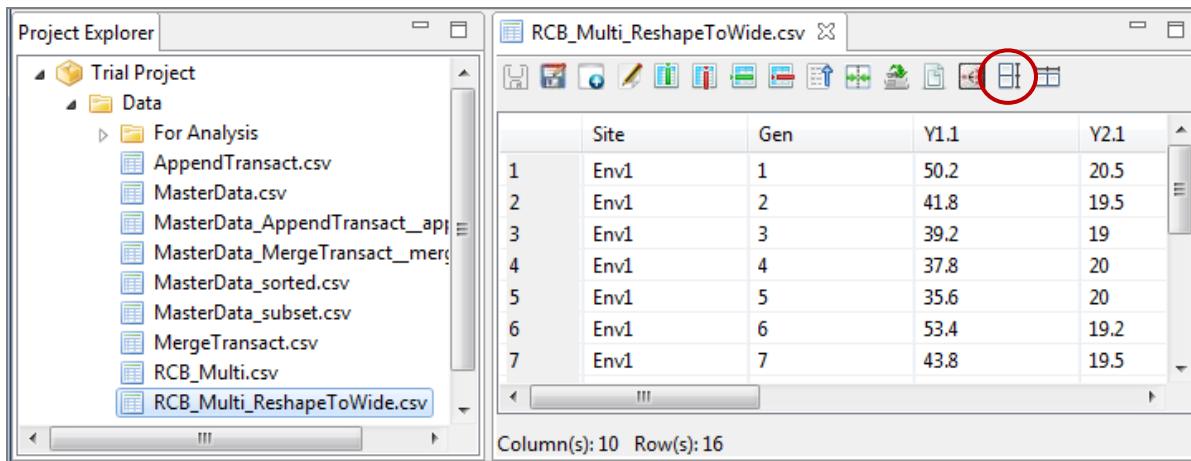
- Click **OK**. The restructured data set is saved in the parent folder of the active data and displayed in the Data Viewer tab. The default filename of the restructured data set follows the format <activeDataFilename>_ReshapeToWide.csv.

Reshaping Data From Wide (Parallel) to Long (Serial)

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, locate the *RCB_Multi_ReshapeToWide.csv* file (the generated file from the previous section) from the *Data* folder of the project named *Trial Project*. Double-click the file to view it in the Data Viewer.
- Click **Data | Reshape | From Wide (Parallel) to Long (Serial) ...** from the menu bar 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.

Variables to 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 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.

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.

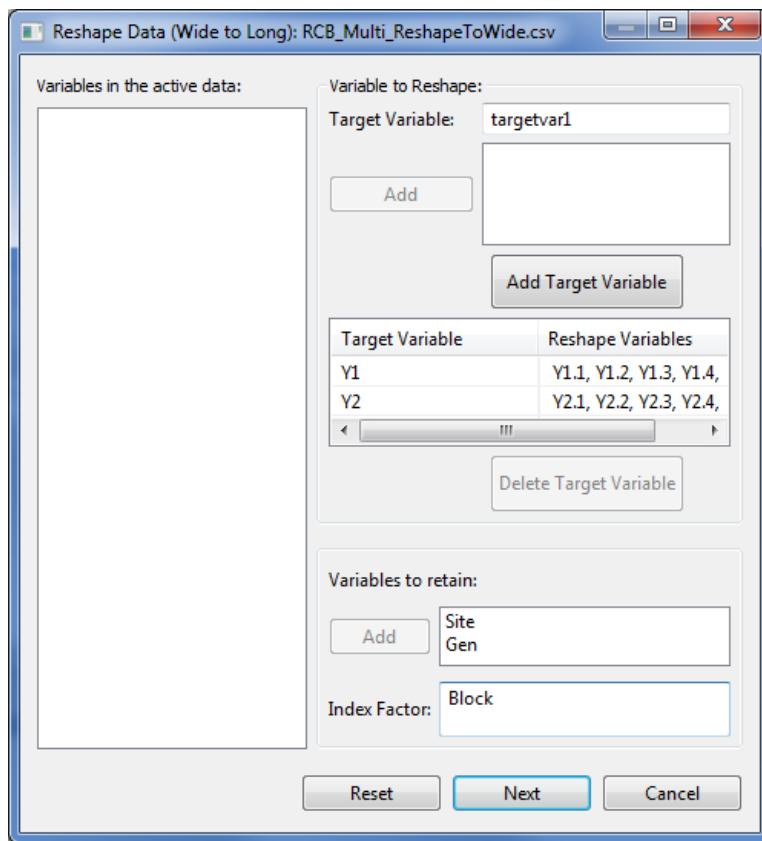
Variables to Retain

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

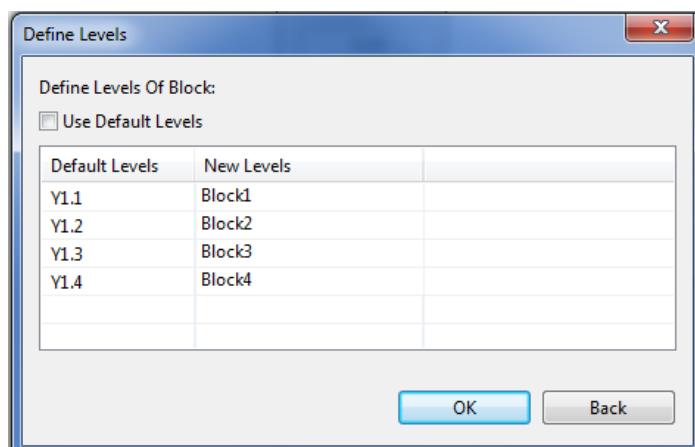
Index Factor

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

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



- Click the **Next** button to proceed.
- The **Define Levels** dialog box will appear. To specify the levels of the Index Factor that will be created, the user can use the default values or type the desired levels in the column labeled 'New Levels'. For now, PBTools only accepts non-numeric values for the levels.



- 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.

Aggregating Data

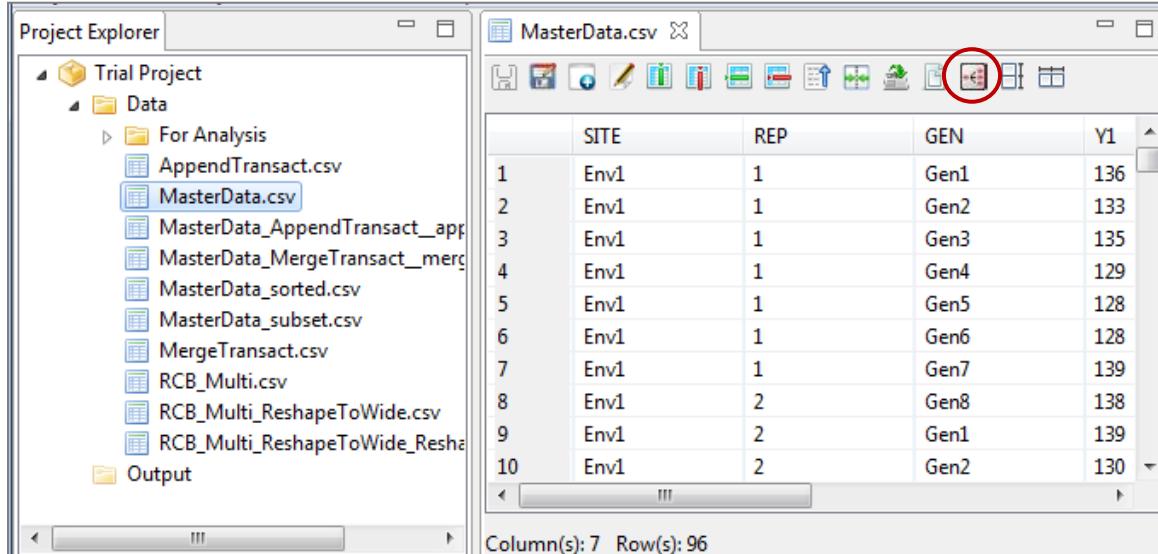
This feature aggregates group of observations into single observation and creates a new, aggregated data file or creates new columns in the active data file that contain the aggregated data. Observations are aggregated based on the value of one or more grouping variables.

The steps for aggregating the data are listed below:

- On the Project Explorer, locate the *MasterData.csv* from the *Data* folder of the project named *Trial Project*. Double-click the file to open it and view it in the Data Viewer.

Opening the data for the first-time, *REP* field is regarded by PBTools 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.



- The **Aggregate Data** dialog box will appear.

- 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.

Grouping Factor(s)

Specify this if the user wants to summarize the values per level of a grouping factor.

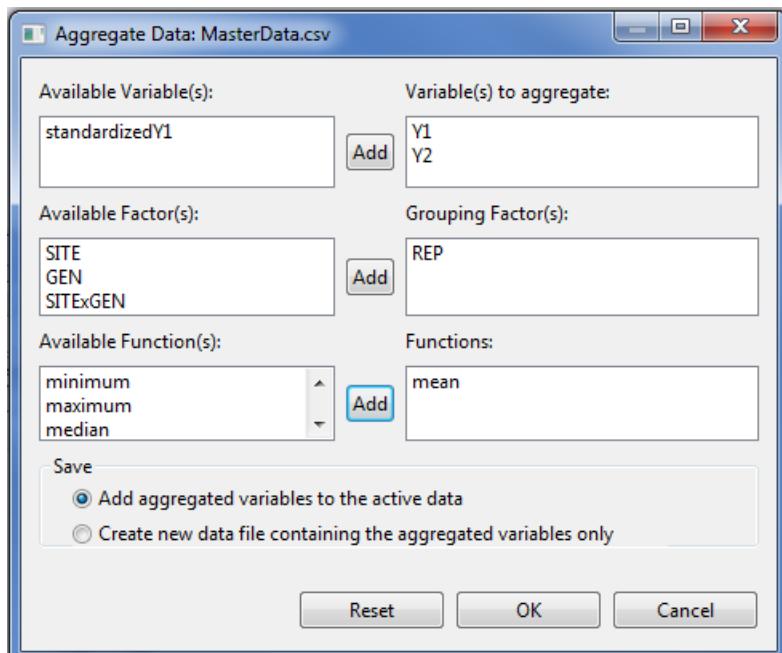
Functions

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 option) 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 illustrated 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 >*.

	ndardizedY1	SITEExGEN	Mean.Y1	Mean.Y2
4725590982...	Env1_Gen1	137.142857142...	118.795238095...	
6032188734...	Env1_Gen2	137.142857142...	118.795238095...	
8494456899...	Env1_Gen3	137.142857142...	118.795238095...	
0889234759...	Env1_Gen4	137.142857142...	118.795238095...	
1512348168...	Env1_Gen5	137.142857142...	118.795238095...	
1512348168...	Env1_Gen6	137.142857142...	118.795238095...	
3418993231...	Env1_Gen7	137.142857142...	118.795238095...	
2112395479...	Env2_Gen2	137.142857142...	118.795238095...	
4574663645...	Env2_Gen3	137.142857142...	118.795238095...	
8494456899...	Env2_Gen4	137.142857142...	118.795238095...	

Column(s): 9 Row(s): 96

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 aggregated data follows the format *<Function>.<Variable name to aggregate>* and the default filename of the aggregated data set follows the format *<activeDataFilename>_aggregate.csv*.

	REP	Mean.Y1	Mean.Y2
1	1	137.142857142...	118.795238095...
2	2	133.296296296...	122.770370370...
3	3	121.375	126.45
4	4	130.375	129.475

Column(s): 3 Row(s): 4

5. Randomization for Some Experimental Designs

The **Randomization** menu allows user to generate randomization of treatments 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>*.

Randomized Complete Block Design

The steps to generate randomization for Randomized Complete Block design are listed below:

- Click **Randomization | 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 Table

Name

This column contains the default name for each factor which can be changed. In specifying the factor name, the following rules apply:

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

Factor ID

This column contains 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

The column contains 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 (down-arrow) key of the spin box to increase (decrease) the value. The default and minimum value of the levels is equal to 2 while the maximum value of the levels is 500.

Number of Blocks

Specify in this field the number of blocks to be generated. The default and minimum value is equal to 2.

Number of Rows per Block

Specify in this field the number of rows per block. The default and minimum value is equal to 1.

Number of Field Rows

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

Number of Trial

Specify in this field the number of trials to be generated. The default and minimum value is equal to 1.

Field Book Filename

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

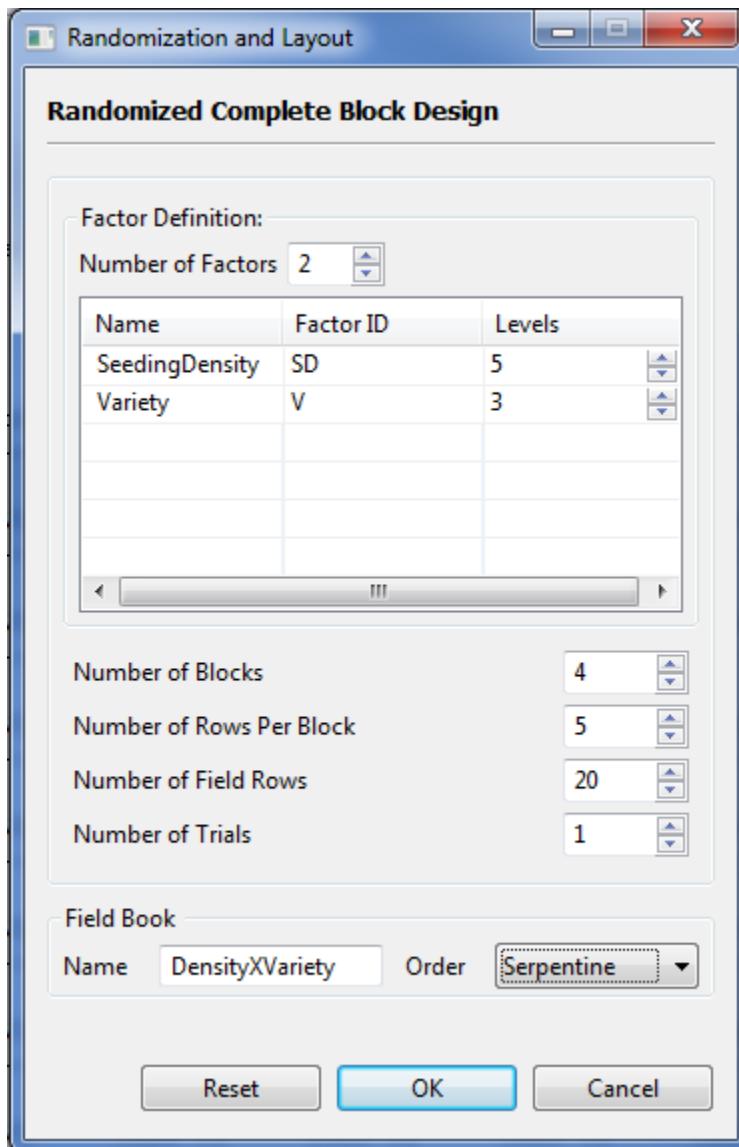
Field Book Order

Specify in this field 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 and layout for an experiment whose aim is to compare the effects of five seeding densities on the grain yield of three rice varieties. The experiment will be conducted in randomized complete block design with four blocks in one trial. The planned field layout is shown below:

	Field Column 1	Field Column 2	Field Column 3
Field Row 1			
Field Row 2			
Field Row 3			
Field Row 4			
Field Row 5			
Field Row 6			
Field Row 7			
Field Row 8			
Field Row 9			
Field Row 10			
Field Row 11			
Field Row 12			
Field Row 13			
Field Row 14			
Field Row 15			
Field Row 16			
Field Row 17			
Field Row 18			
Field Row 19			
Field Row 20			

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 PBTools 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

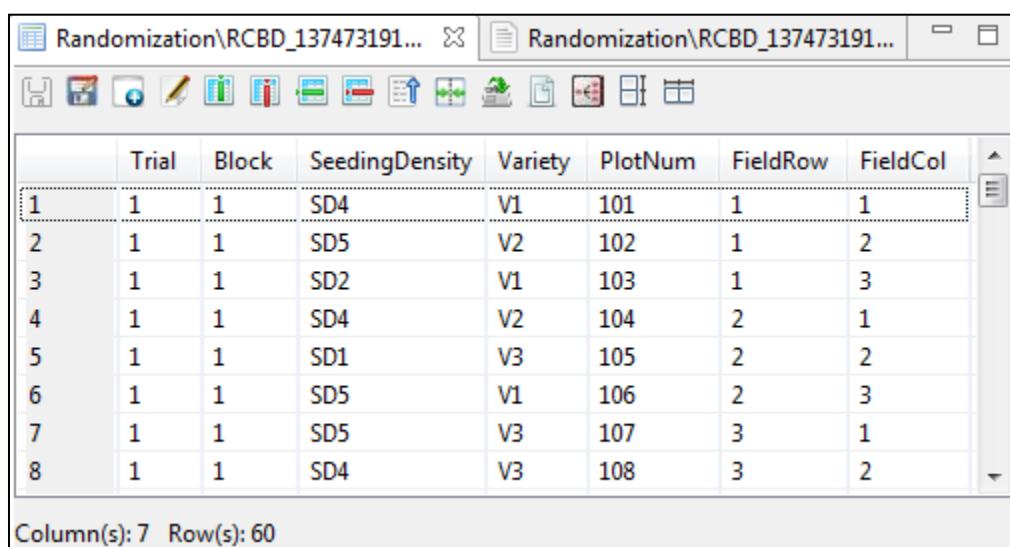
Trial = 1

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



The screenshot shows a software interface for data management. At the top, there are two tabs labeled "Randomization\RCBD_137473191...". Below the tabs is a toolbar with various icons for file operations like Open, Save, Print, and Edit. The main area is a data viewer displaying a CSV file. The data is organized into columns: Trial, Block, SeedingDensity, Variety, PlotNum, FieldRow, and FieldCol. The first row is a header, and the subsequent rows contain data entries. At the bottom of the data viewer, it displays "Column(s): 7 Row(s): 60".

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

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

Lattice Design

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

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

Number of Treatments

Specify in this field 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

Specify in this field the number of replicates to be generated. The default value and minimum value is equal to 2. If the \sqrt{trmt} is odd, the maximum number of replicates is $\sqrt{trmt} + 1$. If the \sqrt{trmt} is equal to 4, the maximum number of replicates is 5. If the \sqrt{trmt} is even and not equal to 4, the maximum number of replicates is 3.

Number of Field Rows

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

Number of Trial

Specify in this field the number of trials to be generated. The default value and minimum value is equal to 1.

Field Book Filename

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

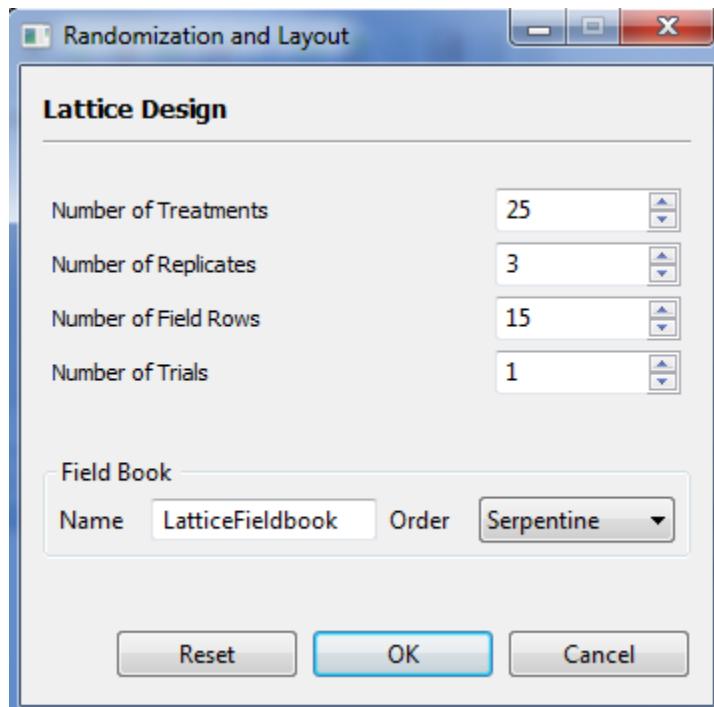
Field Book Order

Specify in this field 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 planned field layout is shown below:

	Field Column 1	Field Column 2	Field Column 3	Field Column 4	Field Column 5
Field Row 1					
Field Row 2					
Field Row 3					
Field Row 4					
Field Row 5					
Field Row 6					
Field Row 7					
Field Row 8					
Field Row 9					
Field Row 10					
Field Row 11					
Field Row 12					
Field Row 13					
Field Row 14					
Field Row 15					

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 PBTools 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

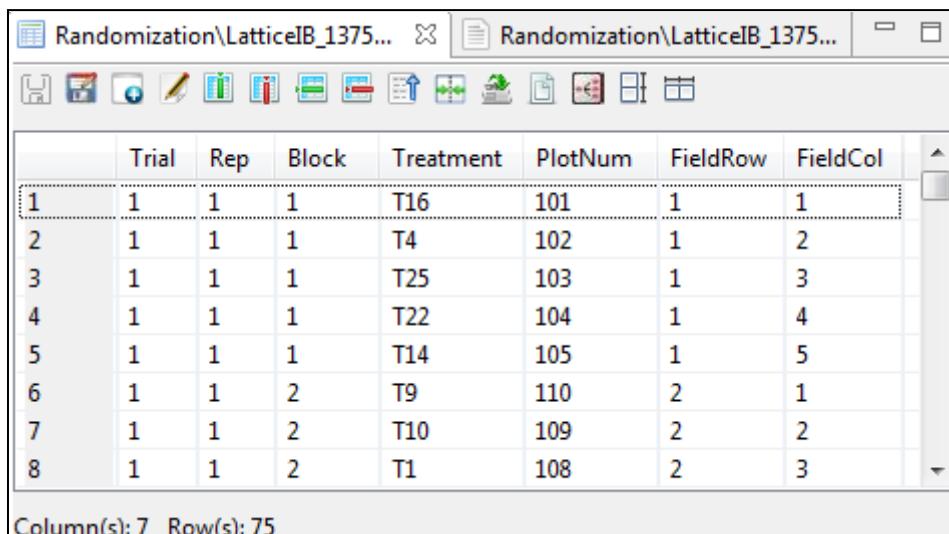
Layout for Lattice Design

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	1	T16	101	1	1
2	1	1	1	T4	102	1	2
3	1	1	1	T25	103	1	3
4	1	1	1	T22	104	1	4
5	1	1	1	T14	105	1	5
6	1	1	2	T9	110	2	1
7	1	1	2	T10	109	2	2
8	1	1	2	T1	108	2	3

Column(s): 7 Row(s): 75

Alpha Lattice Design

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

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

Number of Treatments

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

Number of Replicates

Specify in this field the number of replicates to be generated per trial. The default and minimum value is 2.

Number of Plots per Block

Specify in this field the number of plots per block or the block size. The default value is 3 and the minimum is 2.

Number of Blocks per Replicate

PBTools automatically computes this value.

Number of Rows in Each Block

Specify in this field the number of rows per block. The default value is 3, minimum is 1 and the maximum is equal to the block size. If Latinized alpha lattice design is chosen, this field is not needed.

Number of Rows in Each Replicate

Specify in this field the number of rows per replicate. The default value is 3, minimum is equal to the number of rows per block and the maximum is equal to the number of treatments. If Latinized alpha lattice design is chosen, this field is not needed.

Number of Field Rows

Specify in this field the total number of rows in the field layout for each trial. The default value is 3, minimum is equal to the number of rows per replicate and the maximum is equal to the product of the number of rows per replicate and the number of replicates.

Number of Trial

Specify in this field the number of trials to be generated. The default value and minimum value is equal to 1.

Field Book Filename

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

Field Book Order

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

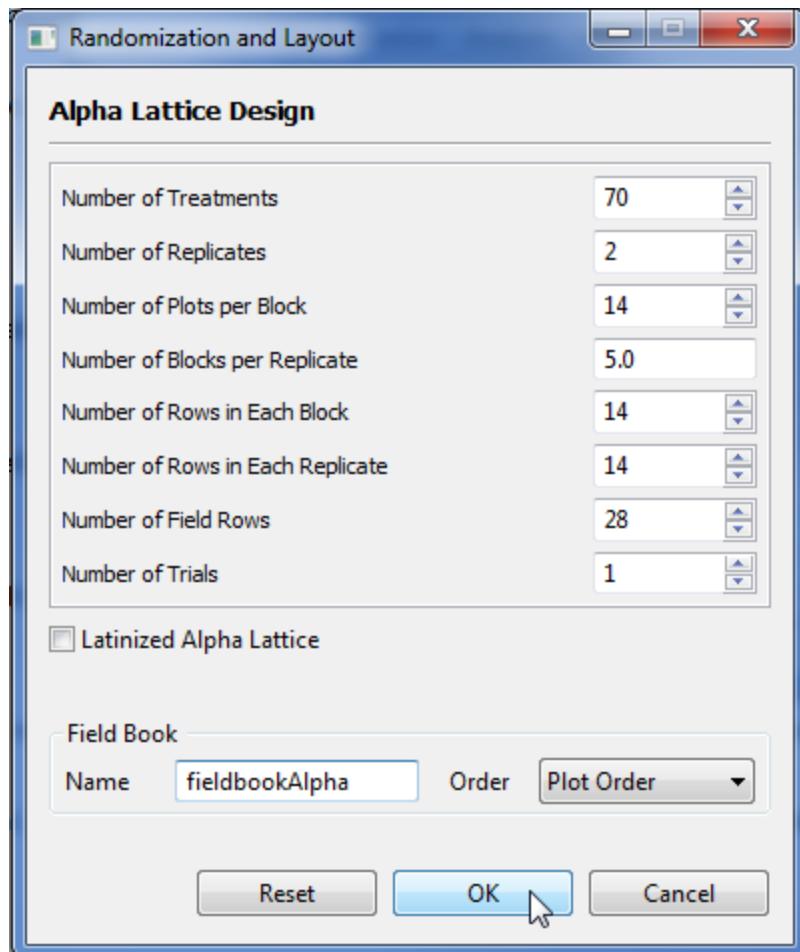
For this example, suppose we want to generate a randomization and layout for an experiment that will be conducted using Alpha Lattice design with 70 entries grouped into 14 with two replicates. The planned field layout is shown below:

	Block 1	Block 2	Block 3	Block 4	Block 5
Field Row 1					
Field Row 2					
⋮	⋮	⋮	⋮	⋮	⋮
Field Row 14					
Field Row 15					
Field Row 16					
⋮	⋮	⋮	⋮	⋮	⋮
Field Row 28					

Replicate 1

Replicate 2

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 PBTools 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 = 70
Number of Replicates = 2
Number of Plots per Block = 14
Number of Blocks per Replicate = 5

Number of Field Rows = 28
Number of Field Columns = 5

Layout for Alpha Lattice Design:

Trial = 1

	FieldCol1	FieldCol2	FieldCol3	FieldCol4	FieldCol5
FieldRow1	101	102	103	104	105
FieldRow2	T27	T41	T26	T3	T30
FieldRow3	106	107	108	109	110
FieldRow4	T16	T14	T31	T56	T46
FieldRow5	111	112	113	114	115
FieldRow6	T15	T23	T45	T13	T28
FieldRow7	116	117	118	119	120
FieldRow8	T34	T54	T39	T62	T70
FieldRow9	121	122	123	124	125
FieldRow10	T29	T60	T7	T40	T36
FieldRow11	126	127	128	129	130
FieldRow12	T22	T6	T69	T32	T55
FieldRow13	131	132	133	134	135
FieldRow14	T21	T43	T47	T51	T25
FieldRow15	136	137	138	139	140
FieldRow16	T44	T5	T66	T24	T17
FieldRow17	141	142	143	144	145
FieldRow18	T18	T58	T64	T53	T65
FieldRow19	146	147	148	149	150
FieldRow20	T50	T48	T35	T8	T4
FieldRow21	151	152	153	154	155
FieldRow22	T38	T1	T2	T63	T10

FieldRow12	156	157	158	159	160
	T59	T33	T42	T67	T37
FieldRow13	161	162	163	164	165
	T57	T52	T49	T9	T12
FieldRow14	166	167	168	169	170
	T11	T19	T20	T61	T68
FieldRow15	201	202	203	204	205
	T68	T4	T67	T60	T49
FieldRow16	206	207	208	209	210
	T53	T57	T28	T31	T19
FieldRow17	211	212	213	214	215
	T48	T20	T62	T65	T63
FieldRow18	216	217	218	219	220
	T39	T12	T14	T2	T59
FieldRow19	221	222	223	224	225
	T33	T25	T38	T22	T9
FieldRow20	226	227	228	229	230
	T61	T69	T24	T37	T1
FieldRow21	231	232	233	234	235
	T17	T64	T21	T52	T32
FieldRow22	236	237	238	239	240
	T47	T8	T55	T44	T56
FieldRow23	241	242	243	244	245
	T35	T16	T13	T54	T26
FieldRow24	246	247	248	249	250
	T10	T3	T58	T15	T42
FieldRow25	251	252	253	254	255
	T23	T70	T29	T66	T18
FieldRow26	256	257	258	259	260
	T5	T51	T11	T41	T7
FieldRow27	261	262	263	264	265
	T46	T27	T6	T36	T34
FieldRow28	266	267	268	269	270
	T40	T45	T30	T50	T43

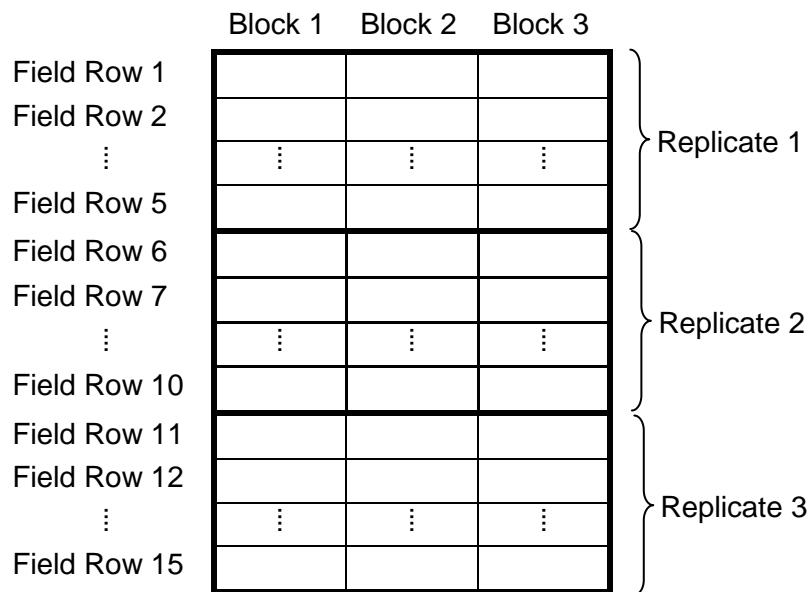
**Note: Cells contain plot numbers on top, treatments/entries below

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

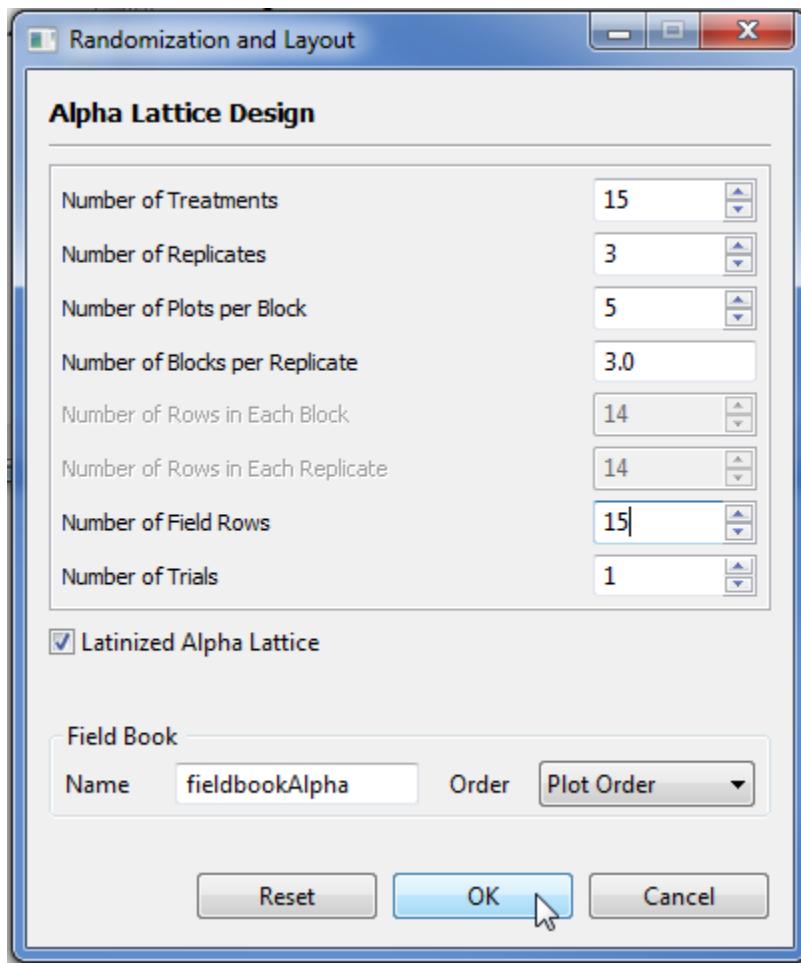
	Trial	Rep	Block	Treatment	PlotNum	FieldRow	FieldCol
1	1	1	1	T27	101	1	1
2	1	1	2	T41	102	1	2
3	1	1	3	T26	103	1	3
4	1	1	4	T3	104	1	4
5	1	1	5	T30	105	1	5
6	1	1	1	T16	106	2	1
7	1	1	2	T14	107	2	2
8	1	1	3	T31	108	2	3
9	1	1	4	T56	109	2	4
10	1	1	5	T46	110	2	5

Column(s): 7 Row(s): 140

Suppose we want to generate a randomization and layout for an experiment that will be conducted using Latinized Alpha Lattice design with 15 entries grouped into 5 with three replicates. The planned field layout is shown below:



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 PBTools 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  
Latinized Alpha Lattice Design  
  
DESIGN PARAMETERS:  
Number of Trials = 1  
Number of Treatments = 15  
Number of Replicates = 3  
Number of Plots per Block = 5  
Number of Blocks per Replicate = 3  
Number of Field Rows = 15
```

Layout for Latinized Alpha Lattice Design:

Trial = 1

	FieldCol1	FieldCol2	FieldCol3
FieldRow1	101	102	103
	T2	T4	T15
FieldRow2	104	105	106
	T10	T14	T1
FieldRow3	107	108	109
	T13	T9	T6
FieldRow4	110	111	112
	T8	T3	T7
FieldRow5	113	114	115
	T11	T5	T12
FieldRow6	201	202	203
	T15	T7	T9
FieldRow7	204	205	206
	T6	T2	T5
FieldRow8	207	208	209
	T3	T11	T10
FieldRow9	210	211	212
	T4	T1	T8
FieldRow10	213	214	215
	T12	T13	T14
FieldRow11	301	302	303
	T9	T8	T2
FieldRow12	304	305	306
	T1	T12	T3
FieldRow13	307	308	309
	T5	T15	T13
FieldRow14	310	311	312
	T7	T10	T4
FieldRow15	313	314	315
	T14	T6	T11

**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	T2	101	1	1
2	1	1	2	T4	102	1	2
3	1	1	3	T15	103	1	3
4	1	1	1	T10	104	2	1
5	1	1	2	T14	105	2	2
6	1	1	3	T1	106	2	3
7	1	1	1	T13	107	3	1
8	1	1	2	T9	108	3	2
9	1	1	3	T6	109	3	3
10	1	1	1	T8	110	4	1

Column(s): 7 Row(s): 45

Augmented Design in Randomized Complete Block

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

- Click **Randomization | Augmented 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

Specify in this field 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

Specify in this field the number of blocks to be generated. The default and minimum value is 2.

Number of Unreplicated Treatments

Specify in this field 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

Specify in this field the number of rows in the field layout. It should be greater than or equal to the number of blocks. The default and minimum value is equal to 2.

Number of Trials

Specify in this field the number of trials to be generated. The default and minimum value is 1.

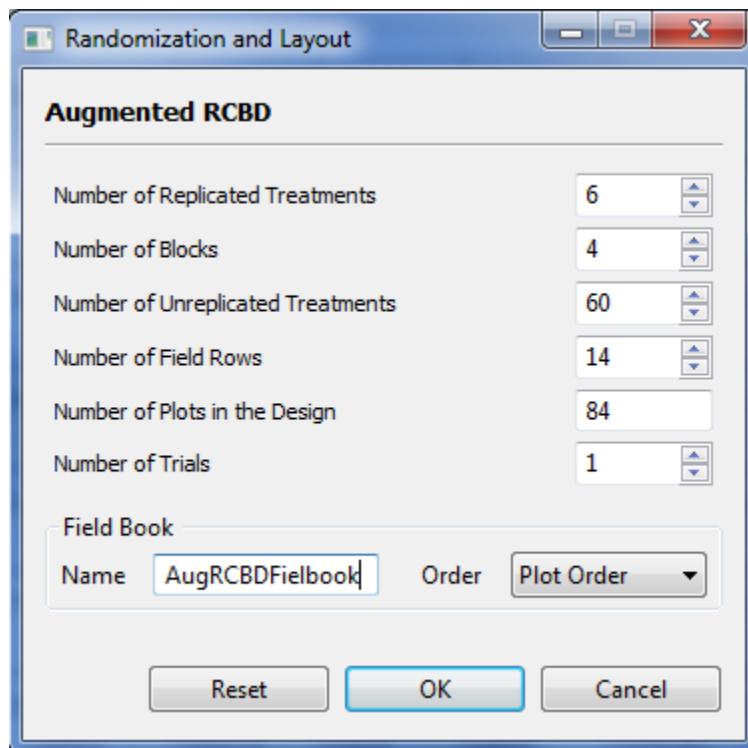
Field Book Filename

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

Field Book Order

Specify in this field 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 PBTools 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

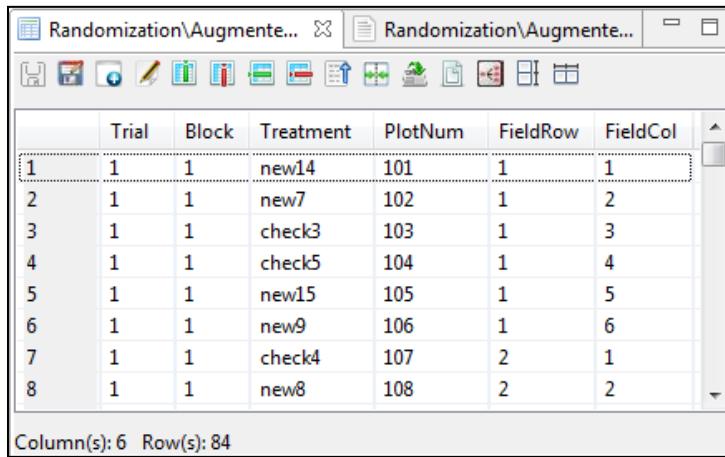
Layout for Augmented Randomized Complete Block Design

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 displays a table with 8 rows and 6 columns. The columns are labeled: Trial, Block, Treatment, PlotNum, FieldRow, and FieldCol. The data entries are as follows:

	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

Column(s): 6 Row(s): 84

Augmented Design in Latin Square

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

- Click **Randomization | Augmented 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

Specify in this field 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

Specify in this field 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

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

Number of Trials

Specify in this field the number of trials to be generated. The default and minimum value is 1.

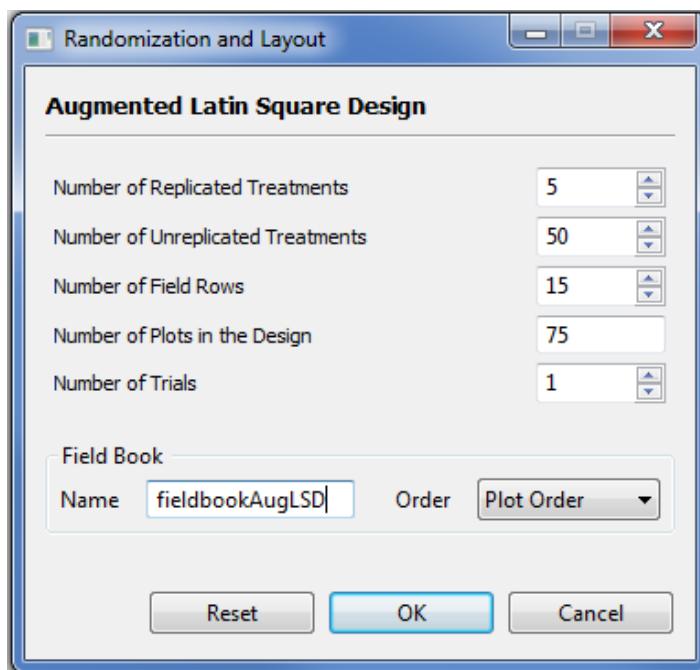
Field Book Filename

This field is required and it specifies the filename 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 PBTools 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

```

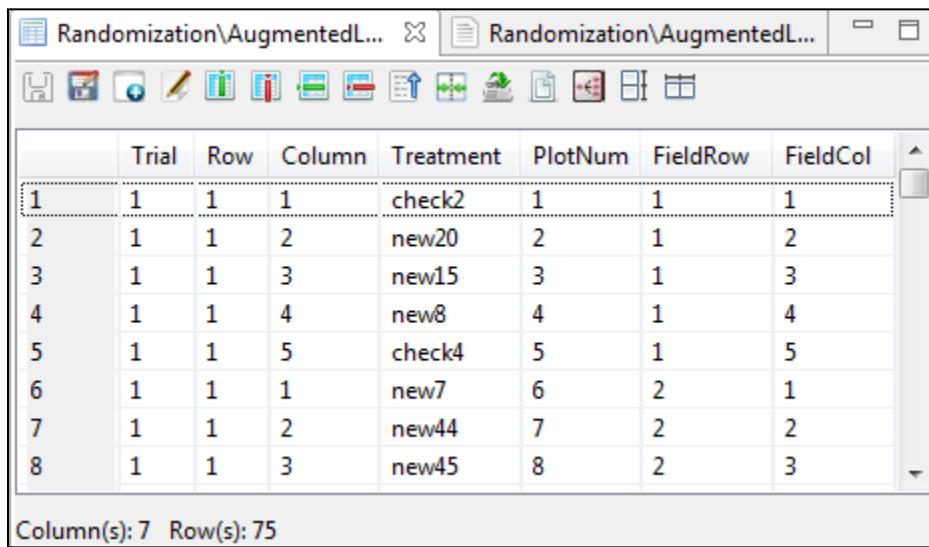
Layout for Augmented Latin Square Design

Trial = 1

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

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

Column(s): 7 Row(s): 75

Row-Column Design

The steps to generate randomization for row-column design are listed below:

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

Number of Treatments

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

Number of Replicates

Specify in this field the number of replicates to be generated. The default and minimum value is 2.

Number of Rows in Each Replicate

Specify in this field the number of rows per replicate. The default value is 3 and the minimum is 2.

Number of Field Rows

Specify in this field the number of rows in the field layout. It should be greater than or equal to the number of rows in each replicate. The default value is 3. If the user chooses

Latinized Row-Column design, this should be equal to the number of rows in each replicate or equal to the number of treatments or equal to the product of the number of replicates and the number of rows in each replicate.

Number of Trials

Specify in this field the number of trials to be generated. The default and minimum value is 1.

Latinized Row-Column Option

Check this option if the user wants Latinized Row-Column design.

Field Book Filename

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

Field Book Order

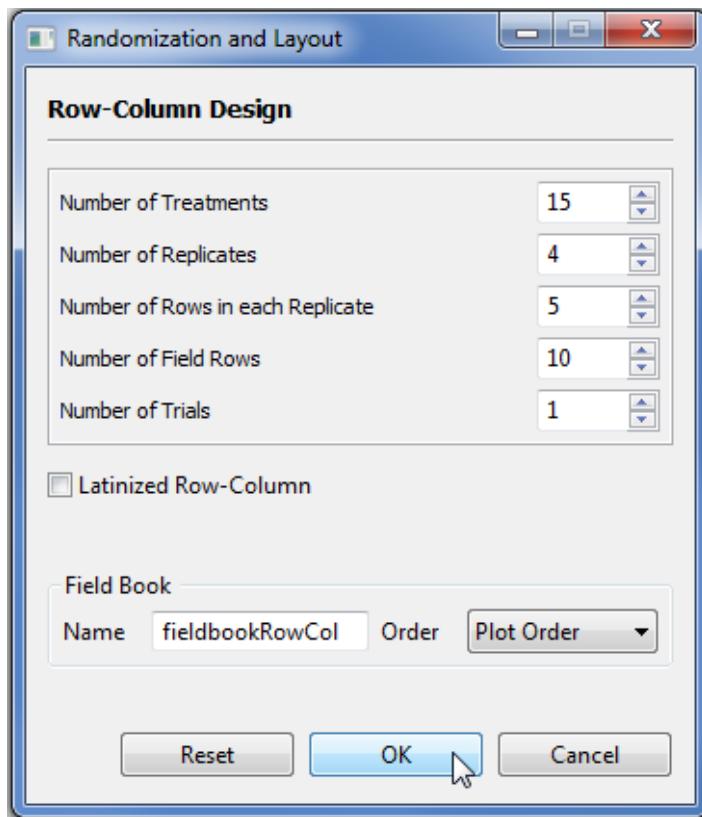
Specify in this field how the plot number will be arranged. There are two options available: *Plot Order* (default value) and *Serpentine*.

For this example, suppose we want to generate a randomization for an experiment which will be conducted using row-column design with 15 treatments in 5 rows, 3 columns and four replicates. The planned field layout is shown below:

	Column 1	Column 2	Column 3	Column 4	Column 5	Column 6
Field Row 1						
Field Row 2						
Field Row 3						
Field Row 4						
Field Row 5						
Field Row 6						
Field Row 7						
Field Row 8						
Field Row 9						
Field Row 10						

NOTE: - represents one replicate

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 PBTools 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:  
Incomplete Block Design  
Row-Column Design  
  
DESIGN PARAMETERS:  
Number of Trials = 1  
Number of Treatments = 15  
Number of Replicates = 4  
Number of Rows per Replicate = 5  
Number of Columns per Replicate = 3  
Number of Field Rows = 10  
Number of Field Columns = 6
```

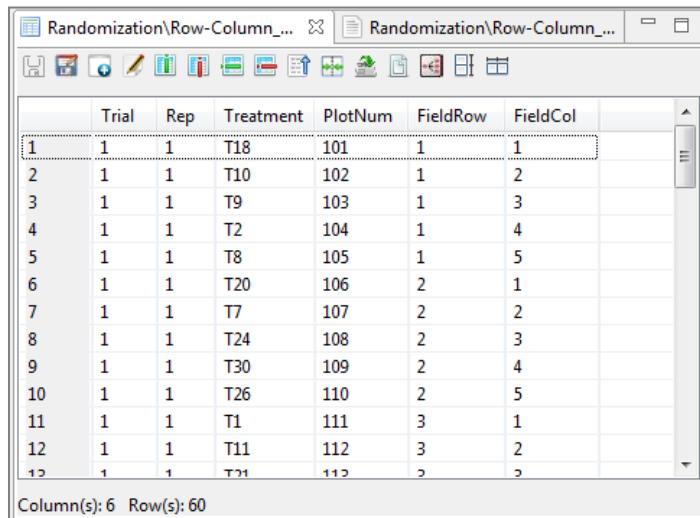
Layout for Row-Column Design:

Trial = 1

	FieldCol1	FieldCol2	FieldCol3	FieldCol4	FieldCol5	FieldCol6
FieldRow1	101 T11	102 T3	103 T9	301 T12	302 T14	303 T10
FieldRow2	104 T14	105 T12	106 T6	304 T9	305 T8	306 T15
FieldRow3	107 T15	108 T2	109 T5	307 T4	308 T6	309 T11
FieldRow4	110 T1	111 T10	112 T4	310 T13	311 T7	312 T2
FieldRow5	113 T13	114 T8	115 T7	313 T5	314 T3	315 T1
FieldRow6	201 T8	202 T4	203 T11	401 T7	402 T1	403 T5
FieldRow7	204 T10	205 T7	206 T12	404 T13	405 T11	406 T8
FieldRow8	207 T5	208 T15	209 T13	407 T6	408 T10	409 T12
FieldRow9	210 T3	211 T6	212 T2	410 T14	411 T9	412 T15
FieldRow10	213 T9	214 T1	215 T14	413 T4	414 T2	415 T3

**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 Data Viewer window with two tabs open, both titled "Randomization\Row-Column ...". The left tab displays a header row with columns: Trial, Rep, Treatment, PlotNum, FieldRow, and FieldCol. Below the header, there are 12 rows of data. The right tab is currently inactive.

	Trial	Rep	Treatment	PlotNum	FieldRow	FieldCol
1	1	1	T18	101	1	1
2	1	1	T10	102	1	2
3	1	1	T9	103	1	3
4	1	1	T2	104	1	4
5	1	1	T8	105	1	5
6	1	1	T20	106	2	1
7	1	1	T7	107	2	2
8	1	1	T24	108	2	3
9	1	1	T30	109	2	4
10	1	1	T26	110	2	5
11	1	1	T1	111	3	1
12	1	1	T11	112	3	2
13	1	1	T21	113	3	3

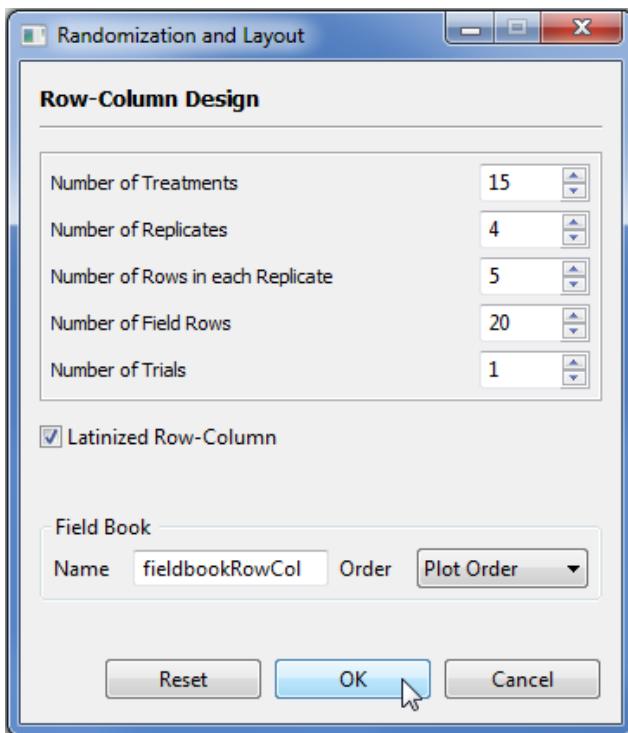
Column(s): 6 Row(s): 60

Suppose we want to generate a randomization for the same experiment (15 treatments in 5 rows, 3 columns and four replicates) but this time in Latinized row-column design. The planned field layout is shown below:

	Column 1	Column 2	Column 3
Field Row 1			
Field Row 2			
Field Row 3			
Field Row 4			
Field Row 5			
Field Row 6			
Field Row 7			
Field Row 8			
Field Row 9			
Field Row 10			
Field Row 11			
Field Row 12			
Field Row 13			
Field Row 14			
Field Row 15			
Field Row 16			
Field Row 17			
Field Row 18			
Field Row 19			
Field Row 20			

NOTE: - represents one replicate

- 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 PBTools 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:
Incomplete Block Design
Latinized Row-Column Design

DESIGN PARAMETERS:
Number of Trials = 1
Number of Treatments = 15
Number of Replicates = 4
Number of Rows per Replicate = 5
Number of Field Rows = 20

Layout for Latinized Row-Column Design:

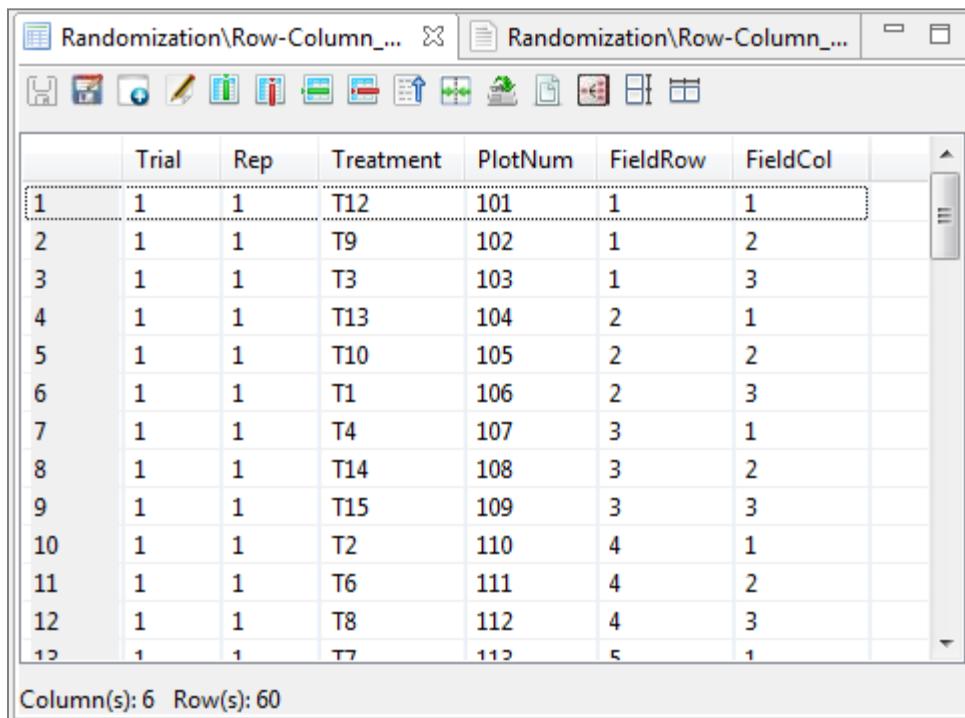
Trial = 1

	FieldCol1	FieldCol2	FieldCol3
FieldRow1	101	102	103
	T12	T9	T3

FieldRow2	104 105 106		
	T13 T10 T1		
+-----+-----+-----+			
FieldRow3	107 108 109		
	T4 T14 T15		
+-----+-----+-----+			
FieldRow4	110 111 112		
	T2 T6 T8		
+-----+-----+-----+			
FieldRow5	113 114 115		
	T7 T11 T5		
+-----+-----+-----+			
FieldRow6	201 202 203		
	T6 T5 T7		
+-----+-----+-----+			
FieldRow7	204 205 206		
	T15 T2 T9		
+-----+-----+-----+			
FieldRow8	207 208 209		
	T4 T3 T10		
+-----+-----+-----+			
FieldRow9	210 211 212		
	T1 T14 T12		
+-----+-----+-----+			
FieldRow10	213 214 215		
	T11 T13 T8		
+-----+-----+-----+			
FieldRow11	301 302 303		
	T14 T8 T11		
+-----+-----+-----+			
FieldRow12	304 305 306		
	T5 T1 T13		
+-----+-----+-----+			
FieldRow13	307 308 309		
	T9 T4 T6		
+-----+-----+-----+			
FieldRow14	310 311 312		
	T3 T12 T15		
+-----+-----+-----+			
FieldRow15	313 314 315		
	T7 T10 T2		
+-----+-----+-----+			
FieldRow16	401 402 403		
	T8 T7 T12		
+-----+-----+-----+			
FieldRow17	404 405 406		
	T10 T15 T5		
+-----+-----+-----+			
FieldRow18	407 408 409		
	T2 T13 T14		
+-----+-----+-----+			
FieldRow19	410 411 412		
	T11 T9 T4		
+-----+-----+-----+			
FieldRow20	413 414 415		
	T3 T1 T6		
+-----+-----+-----+			

**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\Row-Column_...". The window contains a data grid with the following structure:

	Trial	Rep	Treatment	PlotNum	FieldRow	FieldCol
1	1	1	T12	101	1	1
2	1	1	T9	102	1	2
3	1	1	T3	103	1	3
4	1	1	T13	104	2	1
5	1	1	T10	105	2	2
6	1	1	T1	106	2	3
7	1	1	T4	107	3	1
8	1	1	T14	108	3	2
9	1	1	T15	109	3	3
10	1	1	T2	110	4	1
11	1	1	T6	111	4	2
12	1	1	T8	112	4	3
13	1	1	T7	113	5	1

Below the grid, the status bar displays "Column(s): 6 Row(s): 60".

6. Phenotypic Analysis

Single environment analysis

The steps to perform Single-environment Analysis are listed below:

- Create a new PBTools project named *Analysis*.
- Import *RCB_Multi* file from PBTools package. Double-click the file to view it in the Data Viewer. The file contains data for an experiment conducted using Randomized Complete Block (RCB) design for two response variables, *Y1* and *Y2*. The environment variable *Site* has two levels (*Env1* and *Env2*), the blocking variable *Blk* has four levels (1, 2, 3, and 4) and the genotype variable *Gen* has eight levels (1, 2, ..., 8).

The screenshot shows the PBTools software interface. On the left is the 'Project Explorer' window, which displays a project named 'Analysis' containing a 'Data' folder with a file named 'RCB_Multi.csv'. To the right is the 'Data Viewer' window, which is currently displaying the 'RCB_Multi.csv' file. The Data Viewer has a toolbar with various icons at the top and a large table below. The table has columns labeled 'Site', 'Blk', 'Gen', 'Y1', and 'Y2'. The first six rows of the table are shown, with data points corresponding to Site Env1, Blk 1, Gen 1 through 6, and Y1 values ranging from 35.6 to 53.4, and Y2 values ranging from 19 to 20.5. At the bottom of the Data Viewer window, it says 'Column(s): 5 Row(s): 64'.

	Site	Blk	Gen	Y1	Y2
1	Env1	1	1	50.2	20.5
2	Env1	1	2	41.8	19.5
3	Env1	1	3	39.2	19
4	Env1	1	4	37.8	20
5	Env1	1	5	35.6	20
6	Env1	1	6	53.4	19.2

- Choose **Analysis | Single-environment Analysis...** from the menu bar.
- *Blk* and *Gen* fields are already defined in PBTools package as factors. In some cases wherein the data is not imported from package and is opened for the first time, columns with numeric values will be classified by PBTools as numeric variables. To set these as factors, choose these variables and click the **Set to Factor** button.
- Specify the required fields and appropriate options for the analysis.

Model Specifications Tab

Type of Design

There are seven available experimental designs, namely: Randomized Complete Block Design (RCB), Augmented RCB, Augmented Latin Square, Alpha-Lattice, Row-Column, Latinized Alpha-Lattice and Latinized Row-Column. For the example, select RCB.

Response Variables(s)

This is a required field. This list may contain one or more numeric variables. The analysis will be done per response variable.

Environment

If this field is specified, the analysis will be done per environment level. Otherwise, the data will be treated as if it came from one environment.

Genotype

This is a required field.

'Genotype as Fixed' Option

Select this if genotype is considered as a fixed factor.

'Genotype as Random' Option

Select this if genotype is considered as a random factor.

Block

This field is required if the design is RCB, Augmented RCB, Alpha-Lattice or Latinized Alpha-Lattice.

Replicate

This field is required if the design is Augmented Latin Square, Alpha-Lattice, Latinized Alpha-Lattice, Row-Column or Latinized Row-Column.

Row

This field is required if the design is Augmented Latin Square, Row-Column or Latinized Row-Column.

Column

This field is required if the design is Augmented Latin Square, Row-Column or Latinized Row-Column.

Options Tab

Perform pairwise mean comparisons: Compare with control(s)

If this is selected, the user should specify the control level(s) to be compared with the rest of the genotype levels. This can be done by selecting the level(s) of genotype that are considered as control(s) then click the **Add** button.

Perform pairwise mean comparisons: Perform all comparisons

This option is not recommended when the number of genotype levels is very large. For now, PBTools only executes this option if the number of genotype levels is at most fifteen.

Exclude controls in the estimation of genotypic variance

If this is selected and the design is RCB, Alpha-Lattice or Row-Column, the user should specify the control level(s) to exclude. This can be done by selecting the level(s) of genotype that are considered as control(s) then click the **Add** button.

If this is selected and the design is Augmented RCB or Augmented Latin Square, PBTools will automatically identify the replicated genotypes and set these as controls.

Estimate genotypic and phenotypic correlations

This option is enabled if two or more response variables are specified in the Model Specifications tab.

Display Descriptive Statistics

If selected, a summary table with number of missing observations, mean and standard deviation will be displayed.

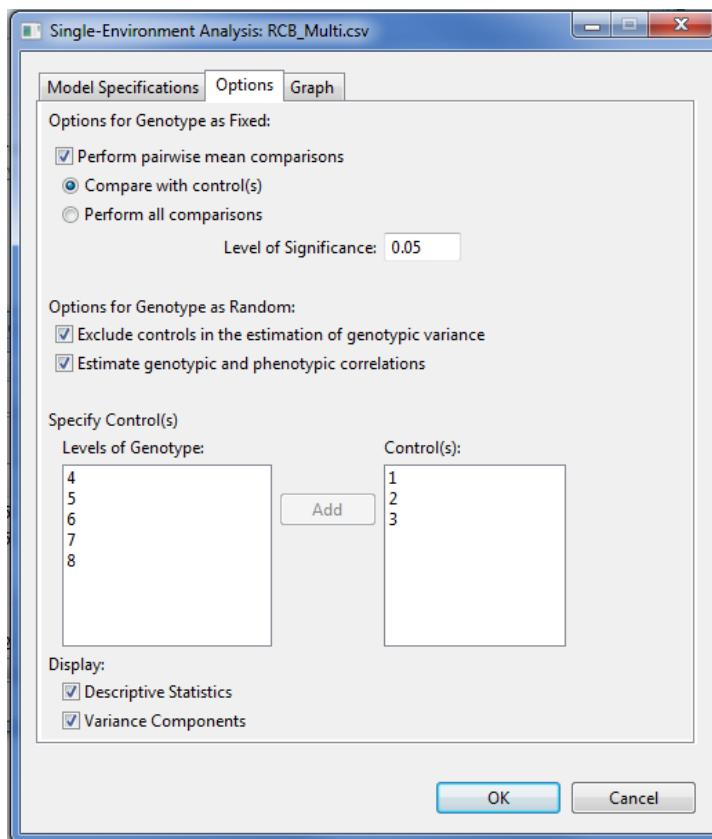
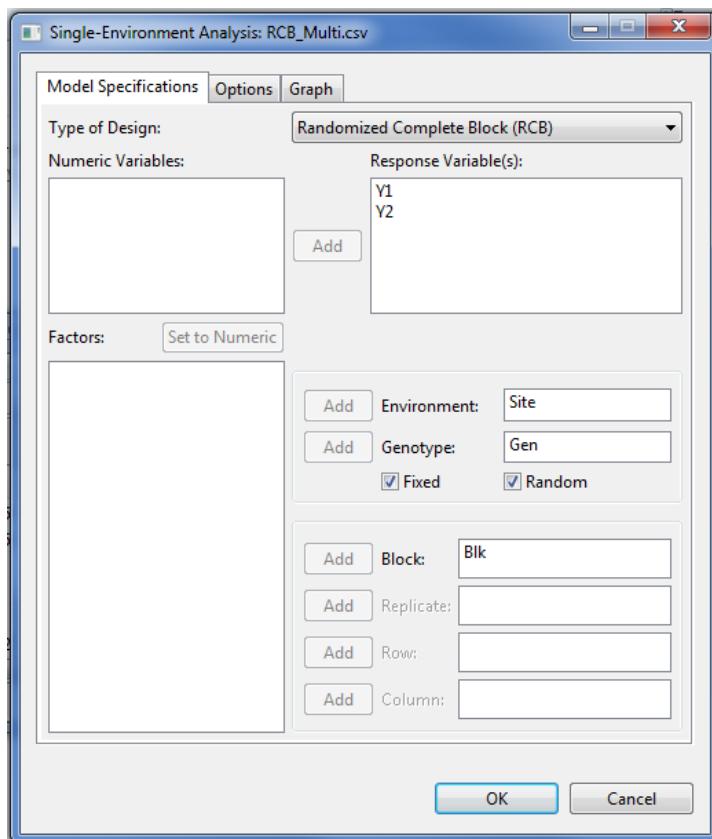
Display Variance Components

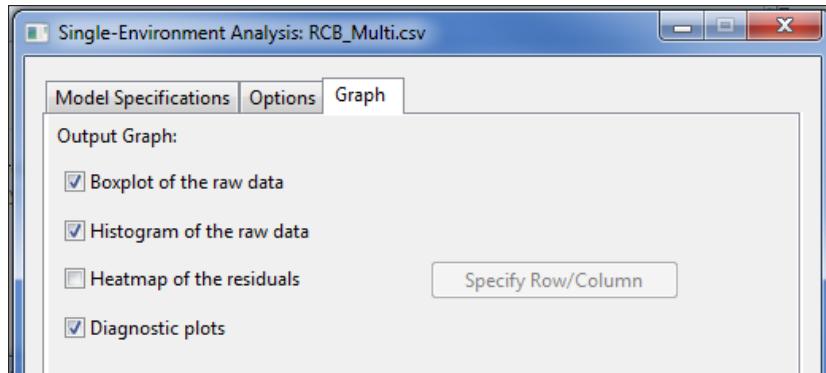
If selected, a table with the variance estimates of the some model components will be displayed.

Graph Tab

Graphs like boxplot, histogram, heatmap and diagnostic plots can be generated as part of the output of the analysis. If heatmap option is selected, field row and field column variables should be specified. These columns must be numeric and each observation should have a corresponding unique row-column label.

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





- Click **OK**. Processing the analysis may take a while.
- Sample output of the analysis (only results from *response variable* = *Y1* and *Site* = *Env1*) is shown below:

```
DATA FILE: E:/PBTools/Projects/Analysis/Data/RCB_Multi.csv
```

```
SINGLE-ENVIRONMENT ANALYSIS
```

```
DESIGN: Randomized Complete Block (RCB)
```

```
=====
GENOTYPE AS: Fixed
=====
```

```
-----
RESPONSE VARIABLE: Y1
-----
```

```
DESCRIPTIVE STATISTICS:
```

Variable	Site	N_NonMissObs	Mean	StdDev
1	Y1 Env1	32	42.49063	6.739166
2	Y1 Env2	32	42.99063	5.741213

```
-----
ANALYSIS FOR: Site = Env1
-----
```

```
DATA SUMMARY:
```

```
Number of observations read: 32
Number of observations used: 32
```

Factors	Number of Levels	Levels
Gen	8	1 2 3 ... 8
Blk	4	1 2 3 4

VARIANCE COMPONENTS TABLE:

	Groups	Variance	Std.Dev.
1	Blk	2.857857	1.690520
2	Residual	13.563289	3.682837

TESTING FOR THE SIGNIFICANCE OF GENOTYPIC EFFECT:

Analysis of Variance Table with Satterthwaite Denominator Df
Df Sum Sq Mean Sq F value Denom Pr(>F)
Gen 7 1013.8 144.8285 10.678 20.9994 0.0000

GENOTYPE LSMEANS AND STANDARD ERRORS:

	Gen	LSMean	StdErrMean
1	1	41.900	2.026107
2	2	43.800	2.026107
3	3	37.300	2.026107
4	4	41.150	2.026107
5	5	32.500	2.026107
6	6	52.625	2.026107
7	7	43.900	2.026107
8	8	46.750	2.026107

STANDARD ERROR OF THE DIFFERENCE (SED) :

	Estimate
Minimum	2.6042
Average	2.6042
Maximum	2.6042

SIGNIFICANT PAIRWISE COMPARISONS (IF ANY) :

Compared with control(s)

	Trmt[i]	Trmt[j]	Difference	Lower	Upper
1	5	1	-9.400	-16.206616	-2.593384
2	6	1	10.725	3.918384	17.531616
3	5	2	-11.300	-18.104529	-4.495471
4	6	2	8.825	2.020471	15.629529
5	6	3	15.325	8.520974	22.129026
6	8	3	9.450	2.645974	16.254026

=====
GENOTYPE AS: Random
=====

RESPONSE VARIABLE: Y1

DESCRIPTIVE STATISTICS:

	Variable	Site	N_NonMissObs	Mean	StdDev
1	Y1	Env1	32	42.49063	6.739166
2	Y1	Env2	32	42.99063	5.741213

ANALYSIS FOR: Site = Env1

DATA SUMMARY:

Number of observations read: 32
Number of observations used: 32

Factors	Number of Levels	Levels
Gen	8	1 2 3 ... 8
Blk	4	1 2 3 4

VARIANCE COMPONENTS TABLE:

	Groups	Variance	Std.Dev.
1	Test:Check	51.720292	7.191682
2	Blk	2.857874	1.690525
3	Residual	13.563282	3.682836

TESTING FOR THE SIGNIFICANCE OF GENOTYPIC EFFECT USING -2 LOGLIKELIHOOD RATIO TEST:

Formula for Model1: Y1 ~ 1 + Check + (1|Blk) + (1|Test:Check)
Formula for Model2: Y1 ~ 1 + Check + (1|Blk)

AIC	BIC	logLik	Chisq	Df	Pr(>Chisq)
Model2	205.5525	214.3469	-96.77626		
Model1	187.7383	197.9985	-86.86916	19.8142	1 0.0000

TESTING FOR THE SIGNIFICANCE OF CHECK EFFECT:

Analysis of Variance Table with Satterthwaite Denominator Df
Df Sum Sq Mean Sq F value Denom Pr(>F)
Check 3 8.1229 2.7076 0.1996 3.9998 0.8917

PREDICTED MEANS:

Gen	Means
1	4 41.28751
2	5 33.16972
3	6 52.05649
4	7 43.86831
5	8 46.54296

CHECK/CONTROL LSMEANS:

Gen	LSMean	StdErrMean
1	1 41.9	7.471644
2	2 43.8	7.471644
3	3 37.3	7.471644

HERITABILITY:

0.94

=====

GENOTYPIC CORRELATIONS:

Site = Env1

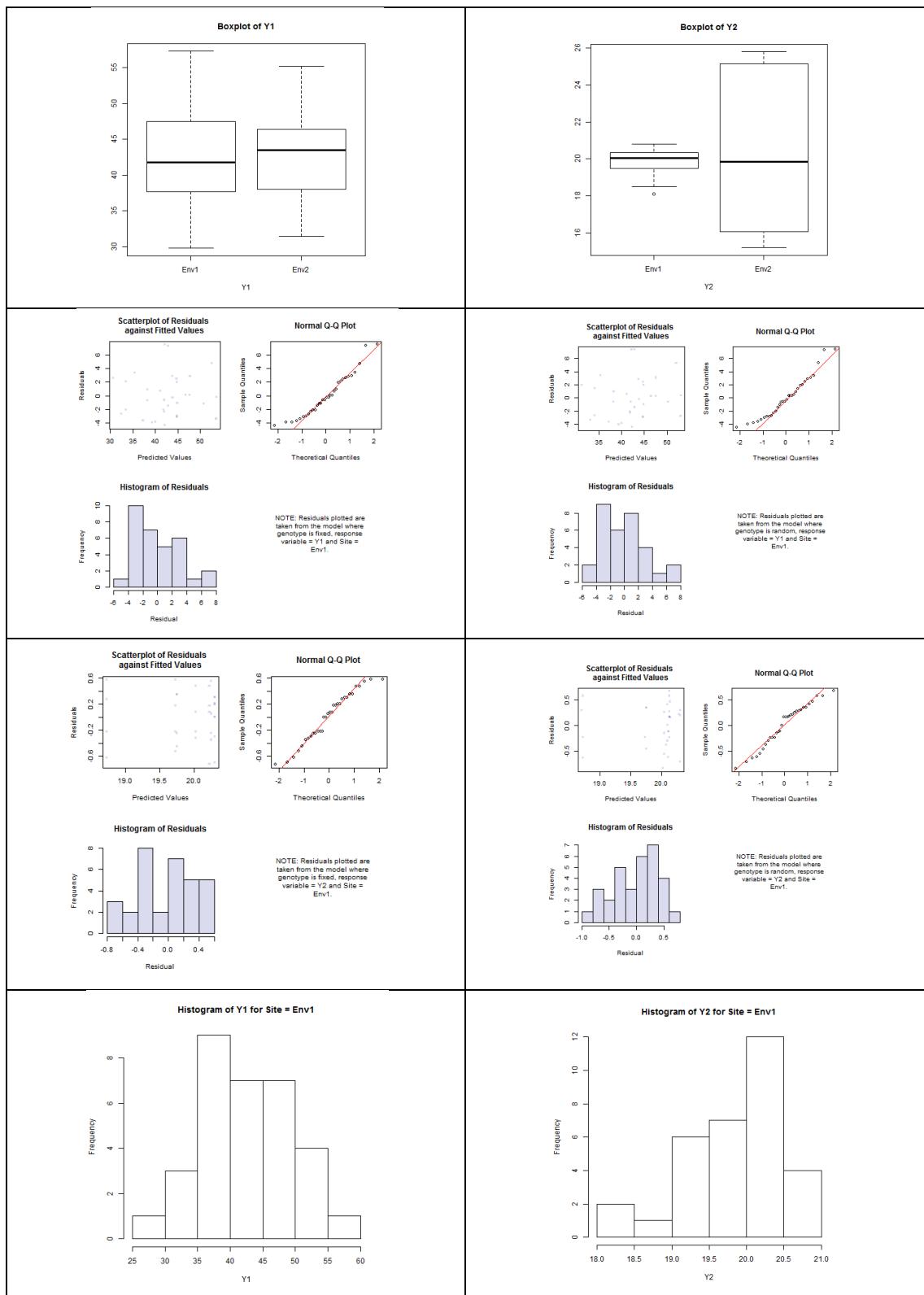
Y1	Y2
Y1	-1.0000
Y2	-1.0000

PHENOTYPIC CORRELATIONS:

Site = Env1

Y1	Y2
Y1	-0.8154
Y2	-0.8154

- Generated graphs can be viewed by clicking the Graph Tab of the displayed analysis folder. Sample generated graphs are shown below:



Multi-environment analysis

One-Stage Analysis

The steps to perform Multi-environment Analysis using the raw data are listed below:

- Import *RCB_ME.csv* from the project named *SampleProject*. Double-click the file to view it in the Data Viewer. The file contains data for an experiment conducted using Randomized Complete Block (RCB) design for response variable *Yield*. The environment variable *Env* has eleven levels (*E1, E2, ..., E11*), the blocking variable *Block* has three levels (1, 2 and 3) and the genotype variable *Genotype* has fifteen levels (GEN1, GEN2, ..., GEN15).
- Choose **Analysis | Multi-environment Analysis | One-Stage Analysis...** from the menu bar.
- Opening the data for the first time, *Block* is regarded by R as a numerical variable. To set this as factor, choose this variable and click on the **Set to Factor** button.
- Specify the required fields and appropriate options for the analysis.

Model Specifications Tab

Type of Design

There are three available experimental designs, namely: Randomized Complete Block Design (RCB), Augmented RCB, Augmented Latin Square, Alpha-Lattice, Row-Column, Latinized Alpha-Lattice and Latinized Row-Column. For the example, select RCB.

Response Variables(s)

This is a required field. This list may contain one or more numeric variables. The analysis will be done per response variable.

Environment

This is a required field.

Genotype

This is a required field.

'Genotype as Fixed' Option

Select this if genotype is considered as a fixed factor.

'Genotype as Random' Option

Select this if genotype is considered as a random factor.

Block

This field is required if the design is RCB, Augmented RCB or Alpha-Lattice.

Replicate

This field is required if the design is Augmented Latin Square, Alpha-Lattice or Row-Column.

Row

This field is required if the design is Augmented Latin Square or Row-Column.

Column

This field is required if the design is Augmented Latin Square or Row-Column.

Options Tab

Perform pairwise mean comparisons: Compare with control(s)

If this is selected, the user should specify the control level(s) to be compared with the rest of the genotype levels. This can be done by selecting the level(s) of genotype that are considered as control(s) then click the **Add** button.

Perform pairwise mean comparisons: Perform all comparisons

This option is not recommended when the number of genotype levels is very large. For now, PBTools only executes this option if the number of genotype levels is at most fifteen.

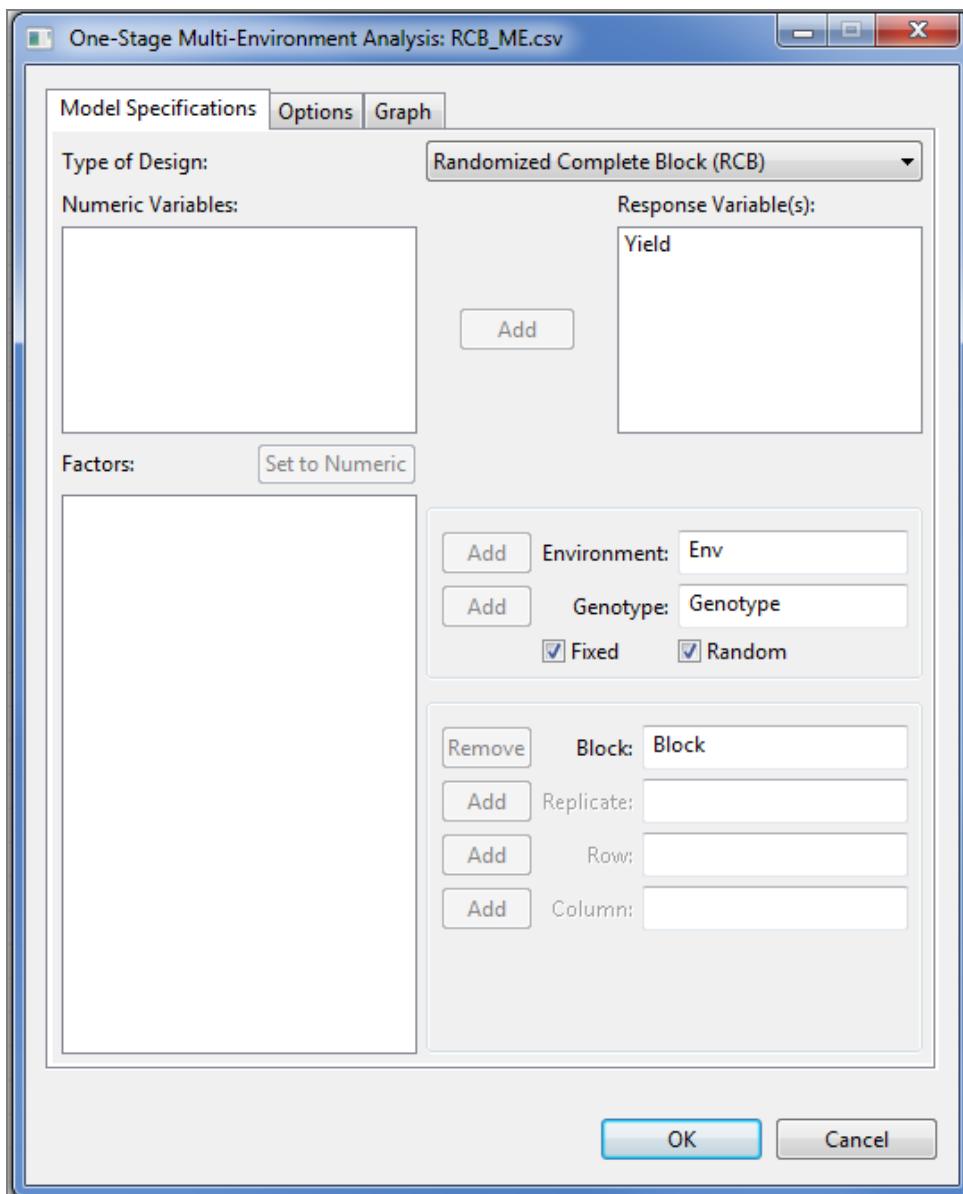
Display

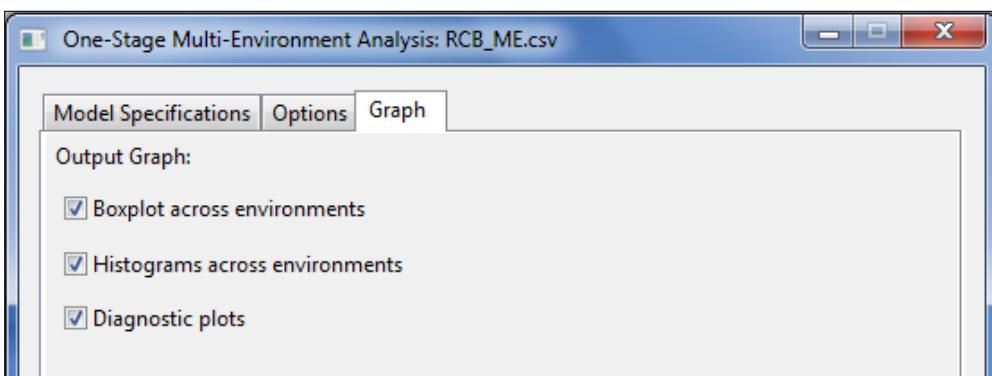
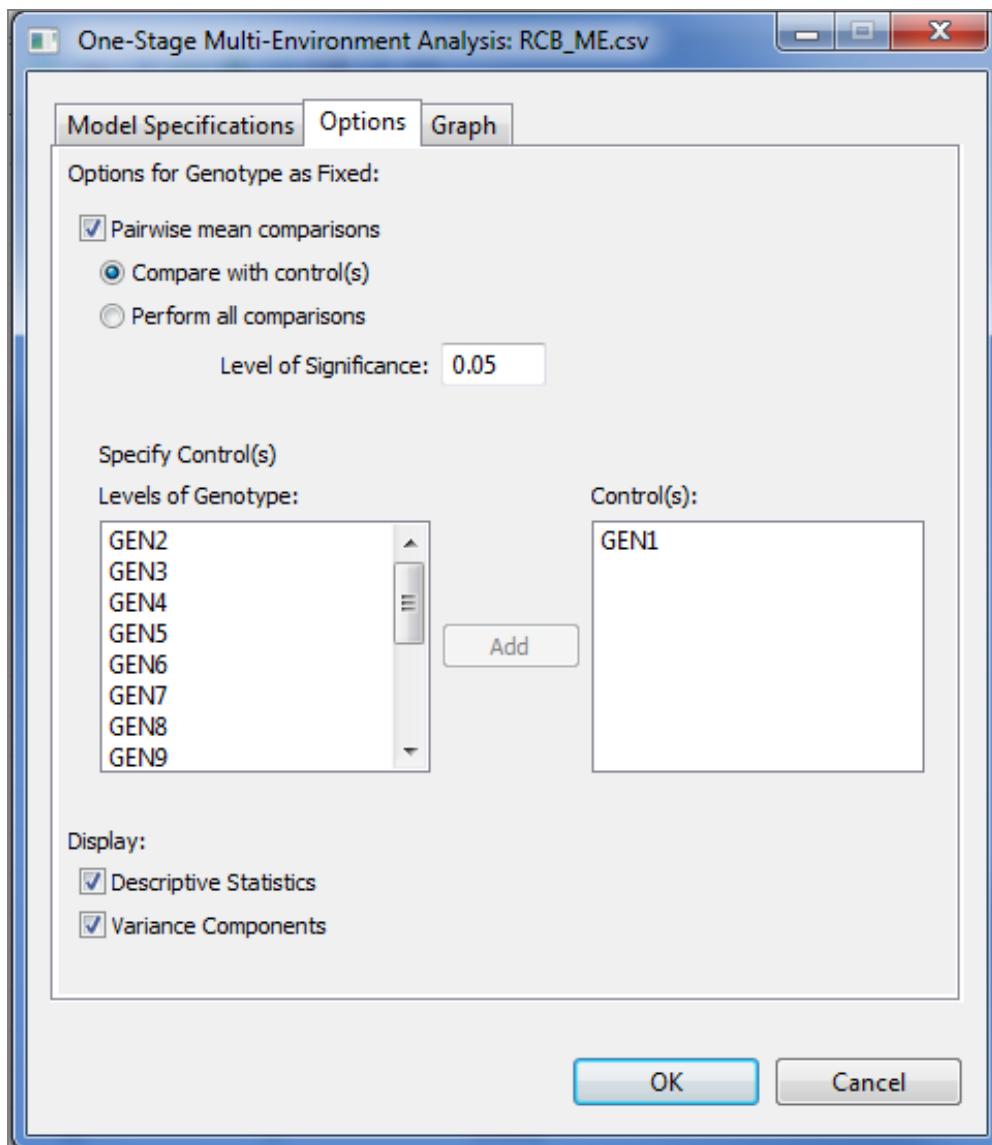
The user has the options to display descriptive statistics and variance components.

Graph Tab

Graphs like boxplot, histogram and diagnostic plots can be generated as part of the output of the analysis.

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





- Click **OK**.

- Sample output of the analysis is shown below:

```
DATA FILE: E:/PBTools/Projects/Analysis/Data/RCB_ME.csv
```

```
MULTI-ENVIRONMENT ANALYSIS (ONE-STAGE)
```

```
DESIGN: Randomized Complete Block (RCB)
```

```
=====
```

```
GENOTYPE AS: Fixed
```

```
=====
```

```
-----  
RESPONSE VARIABLE: Yield  
-----
```

```
DATA SUMMARY:
```

```
Number of observations read: 495
```

```
Number of observations used: 495
```

Factors	Number of Levels	Levels
Env	11	E1 E10 E11 ... E9
Genotype	15	GEN1 GEN10 GEN11 ... GEN9
Block	3	1 2 3

```
DESCRIPTIVE STATISTICS:
```

Variable	N	NonMissObs	Mean	StdDev
1 Yield	495	1718.596	1117.791	

```
VARIANCE COMPONENTS TABLE:
```

	Groups	Variance	Std.Dev.
1	Genotype:Env	664747.696	815.32061
2	Block:Env	6497.161	80.60497
3	Env	530979.863	728.68365
4	Residual	94709.288	307.74874

```
TESTING FOR THE SIGNIFICANCE OF GENOTYPIC EFFECT:
```

Analysis of Variance Table with Satterthwaite Denominator Df					
	Df	Sum Sq	Mean Sq	F value	Denom Pr(>F)
Genotype	14	1386210	99015	1.0455	139.9947 0.4127

TESTING FOR THE SIGNIFICANCE OF ENVIRONMENT EFFECT USING -2 LOGLIKELIHOOD RATIO TEST:

Formula for Model1: Yield ~ 1 + Genotype + (1|Env) + (1|Block:Env) + (1|Genotype:Env)

Formula for Model2: Yield ~ 1 + Genotype + (1|Block:Env) + (1|Genotype:Env)

	AIC	BIC	logLik	Chisq	Df	Pr(>Chisq)
Model2	7513.743	7589.425	-3738.871			
Model1	7457.593	7537.480	-3709.797	58.1496	1	0.0000

TESTING FOR THE SIGNIFICANCE OF GENOTYPE X ENVIRONMENT EFFECT USING -2 LOGLIKELIHOOD RATIO TEST:

Formula for Model1: Yield ~ 1 + Genotype + (1|Env) + (1|Block:Env) + (1|Genotype:Env)

Formula for Model2: Yield ~ 1 + Genotype + (1|Env) + (1|Block:Env)

	AIC	BIC	logLik	Chisq	Df	Pr(>Chisq)
Model2	7942.529	8018.211	-3953.264			
Model1	7457.593	7537.480	-3709.797	486.9356	1	0.0000

GENOTYPE X ENVIRONMENT MEANS:

	Genotype	E1	E5	E4	E11	...	E8
1	GEN1	2958.164	352.6978	1294.798	2072.8784	...	299.9992
2	GEN10	2199.114	1012.1162	1856.555	2351.7368	...	717.7737
3	GEN11	2777.579	1125.8198	1359.307	3161.8980	...	302.4992
4	GEN12	2663.602	954.9771	1964.795	3042.9571	...	358.8341
5	GEN13	2726.812	1655.7099	2150.647	3539.0740	...	581.7587
6	GEN14	2397.222	1256.6844	1706.243	6681.1756	...	694.8774
7	GEN15	1955.552	1785.8101	2090.610	1542.3468	...	309.5644
8	GEN2	2981.912	1391.8241	1311.927	1558.7381	...	314.3661
9	GEN3	2099.569	280.0127	1609.770	519.7356	...	534.5689
10	GEN4	2325.432	426.4795	2225.294	1778.8608	...	698.1242
11	GEN5	1764.656	484.0382	1470.849	2145.3480	...	313.7380
12	GEN6	1962.796	368.6027	2626.068	1677.6422	...	722.2527
13	GEN7	2731.895	496.6144	1934.025	2424.5930	...	521.3835
14	GEN8	2247.593	858.3659	2006.610	2280.9466	...	244.3071
15	GEN9	2192.044	542.0348	1291.421	1071.0839	...	274.4865

GENOTYPE LSMEANS AND STANDARD ERRORS:

	Genotype	LSMean	StdErrMean
1	GEN1	1500.965	334.2864
2	GEN10	1804.918	334.2864
3	GEN11	1902.555	334.2864
4	GEN12	2023.497	334.2864

5	GEN13	1953.552	334.2864
6	GEN14	2163.924	334.2864
7	GEN15	1829.575	334.2864
8	GEN2	1826.130	334.2864
9	GEN3	1615.296	334.2864
10	GEN4	1557.518	334.2864
11	GEN5	1246.419	334.2864
12	GEN6	1606.112	334.2864
13	GEN7	1523.806	334.2864
14	GEN8	1871.903	334.2864
15	GEN9	1352.776	334.2864

SUMMARY OF THE DATA:

	Estimate
Minimum	355.8134
Average	355.8134
Maximum	355.8134

SIGNIFICANT PAIRWISE COMPARISONS (IF ANY):
Compared with control(s)

(No significant pairwise comparisons.)

=====
GENOTYPE AS: Random
=====

RESPONSE VARIABLE: Yield

DATA SUMMARY:

Number of observations read: 495
Number of observations used: 495

Factors	Number of Levels	Levels
Env	11	E1 E10 E11 ... E9
Genotype	15	GEN1 GEN10 GEN11 ... GEN9
Block	3	1 2 3

DESCRIPTIVE STATISTICS:

Variable	N_NonMissObs	Mean	StdDev
Yield	495	1718.596	1117.791

VARIANCE COMPONENTS TABLE:

	Groups	Variance	Std.Dev.
1	Genotype:Env	664747.522	815.32050
2	Block:Env	6497.219	80.60533
3	Genotype	2876.978	53.63747
4	Env	530984.967	728.68715
5	Residual	94709.311	307.74878

TESTING FOR THE SIGNIFICANCE OF GENOTYPIC EFFECT USING -2 LOGLIKELIHOOD RATIO TEST:

Formula for Model1: Yield ~ 1 + (1|Genotype) + (1|Env) + (1|Block:Env) + (1|Genotype:Env)
Formula for Model2: Yield ~ 1 + (1|Env) + (1|Block:Env) + (1|Genotype:Env)

AIC	BIC	logLik	Chisq	Df	Pr(>Chisq)
Model2	7627.446	7648.469	-3808.723		
Model1	7629.433	7654.661	-3808.717	0.0127	1 0.9102

TESTING FOR THE SIGNIFICANCE OF ENVIRONMENT EFFECT USING -2 LOGLIKELIHOOD RATIO TEST:

Formula for Model1: Yield ~ 1 + (1|Genotype) + (1|Env) + (1|Block:Env) + (1|Genotype:Env)
Formula for Model2: Yield ~ 1 + (1|Genotype) + (1|Block:Env) + (1|Genotype:Env)

AIC	BIC	logLik	Chisq	Df	Pr(>Chisq)
Model2	7686.930	7707.953	-3838.465		
Model1	7629.433	7654.661	-3808.717	59.4969	1 0.0000

TESTING FOR THE SIGNIFICANCE OF GENOTYPE X ENVIRONMENT EFFECT USING -2 LOGLIKELIHOOD RATIO TEST:

Formula for Model1: Yield ~ 1 + (1|Genotype) + (1|Env) + (1|Block:Env) + (1|Genotype:Env)
Formula for Model2: Yield ~ 1 + (1|Genotype) + (1|Env) + (1|Block:Env)

AIC	BIC	logLik	Chisq	Df	Pr(>Chisq)
Model2	8114.369	8135.392	-4052.184		
Model1	7629.433	7654.661	-3808.717	486.9356	1 0.0000

GENOTYPE X ENVIRONMENT MEANS:

	Genotype	E1	E5	E4	E11	...	E8
1	GEN1	2967.628	362.1033	1304.239	2082.3420	...	309.3893
2	GEN10	2195.396	1008.3402	1852.814	2348.0189	...	713.9822
3	GEN11	2769.627	1117.8096	1351.332	3153.9459	...	294.4734
4	GEN12	2650.405	941.7219	1951.575	3029.7600	...	345.5635
5	GEN13	2716.648	1645.4881	2140.460	3528.9102	...	571.5213
6	GEN14	2377.935	1237.3393	1686.933	6661.8885	...	675.5168
7	GEN15	1950.765	1780.9648	2085.800	1537.5596	...	304.7036
8	GEN2	2977.274	1387.1282	1307.267	1554.1003	...	309.6547
9	GEN3	2104.075	284.4601	1614.252	524.2411	...	539.0008
10	GEN4	2332.444	433.4326	2232.282	1785.8719	...	705.0617
11	GEN5	1785.159	504.4827	1491.329	2165.8505	...	334.1670
12	GEN6	1967.700	373.4483	2630.949	1682.5460	...	727.0829
13	GEN7	2740.368	505.0294	1942.476	2433.0661	...	529.7830
14	GEN8	2240.970	851.6849	1999.964	2274.3237	...	237.6107
15	GEN9	2207.934	557.8670	1307.289	1086.9741	...	290.3031

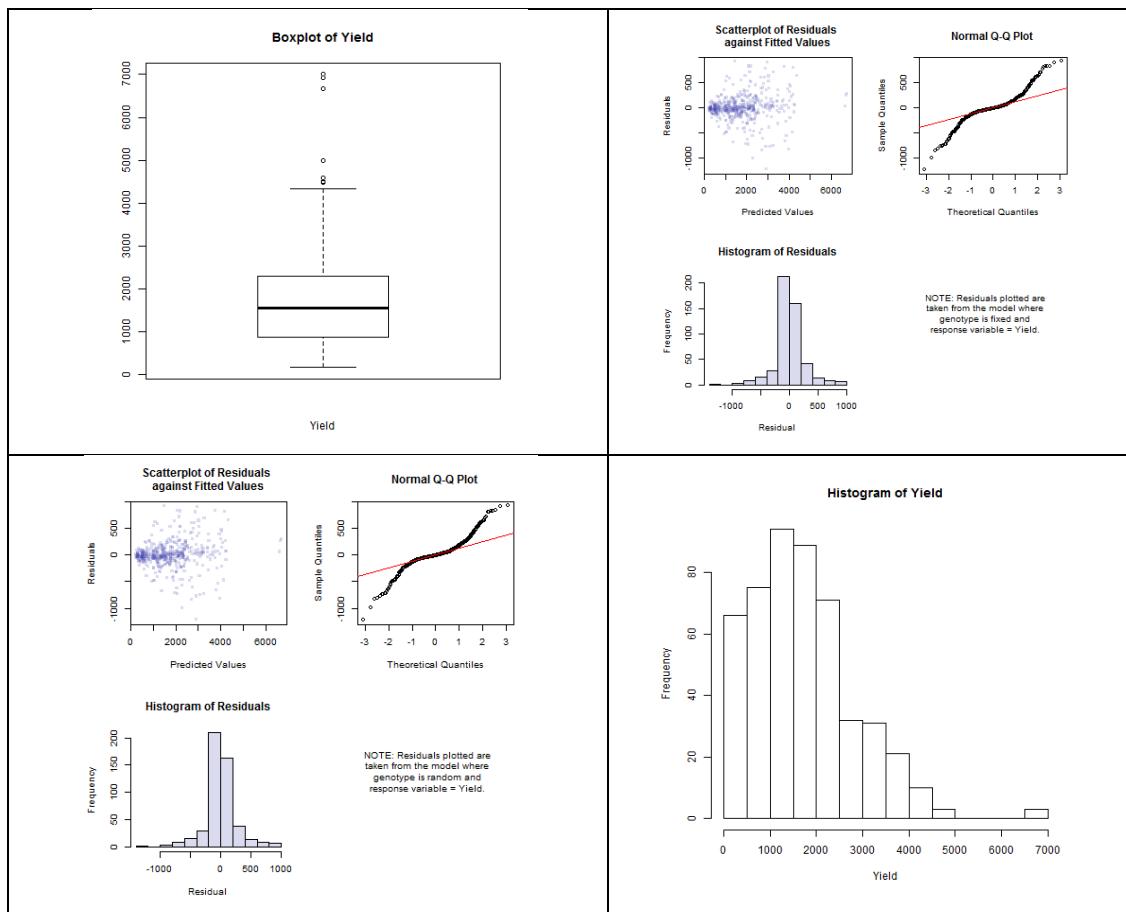
PREDICTED GENOTYPE MEANS:

	Genotype	Mean
1	GEN1	1709.135
2	GEN10	1722.349
3	GEN11	1726.594
4	GEN12	1731.851
5	GEN13	1728.811
6	GEN14	1737.956
7	GEN15	1723.421
8	GEN2	1723.271
9	GEN3	1714.106
10	GEN4	1711.594
11	GEN5	1698.069
12	GEN6	1713.706
13	GEN7	1710.128
14	GEN8	1725.261
15	GEN9	1702.693

HERITABILITY:

0.05

- Generated graphs can be viewed by clicking the Graph Tab of the displayed analysis folder. Sample generated graphs are shown below:



Two-Stage Analysis

The steps to perform Multi-environment Analysis using the summary of data from single-environment analysis as input are listed below:

- Import *Two_stage* file from PBTools package. Double-click the file to view it in the Data Viewer. The file contains four columns (variables) for yield: *Yield_Mean*, *Yield_StdErrMean*, *Yield_sigma2*, *Yield_No.rep* and the *Env* and *Genotype* factors, with 10 and 15 levels, respectively.
- Choose **Analysis | Multi-environment Analysis | Two-Stage Analysis...** from the menu bar.
- Specify the required fields and appropriate options for the analysis.

Model Specifications Tab

Weight Option

The user has the option to either apply no weights or use the reciprocal of the variance of the mean as weights.

Response Variables

This is a required field which contains the column name corresponding to the mean of a trait.

Standard Error

If the selected weight option is the reciprocal of the variance of the mean ($1/(sem^2)$), this field should be specified to proceed to the entire process of the analysis.

Residual Variance

This field should be specified to proceed to the entire process of the analysis.

Number of Replicates

This field should be specified to proceed to the entire process of the analysis.

For each trait, the user has to specify the response variable, its standard error (if required), residual variance and number of replicates. To indicate that this set of variables corresponds to one trait, click the **Add to Table** button. The variables corresponding to one trait will be displayed in a row of the summary table. Do the same for the rest of the traits.

Environment

This is a required field.

Genotype

This is a required field.

'Genotype as Fixed' Option

Select this if genotype is considered as a fixed factor

'Genotype as Random' Option

Select this if genotype is considered as a random factor

If genotype is considered as a fixed factor and PBTools detects that in the summary table a row has missing standard error or residual variance or number of replicates, a dialog box will appear prompting the user that only AMMI and stability analysis can be done.

Options Tab

Perform pairwise mean comparisons: Compare with control(s)

If this is selected, the user should specify the control level(s) to be compared with the rest of the genotype levels. This can be done by selecting the level(s) of genotype that are considered as control(s) then click the **Add** button.

Perform pairwise mean comparisons: Perform all comparisons

This option is not recommended when the number of genotype levels is very large. For now, PBTools only executes this option if the number of genotype levels is at most fifteen.

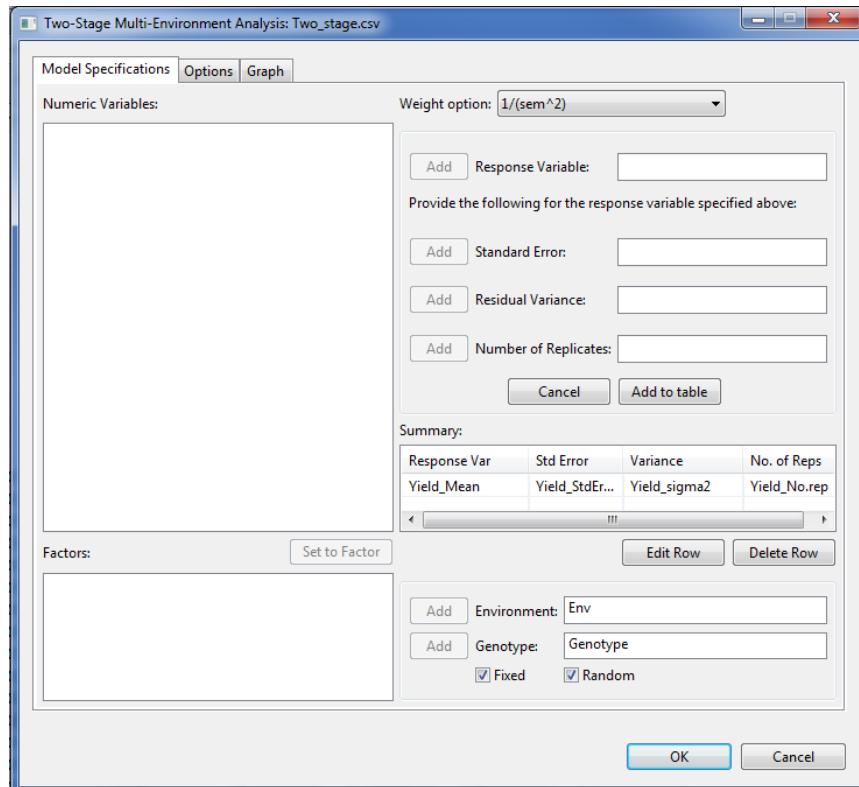
Display

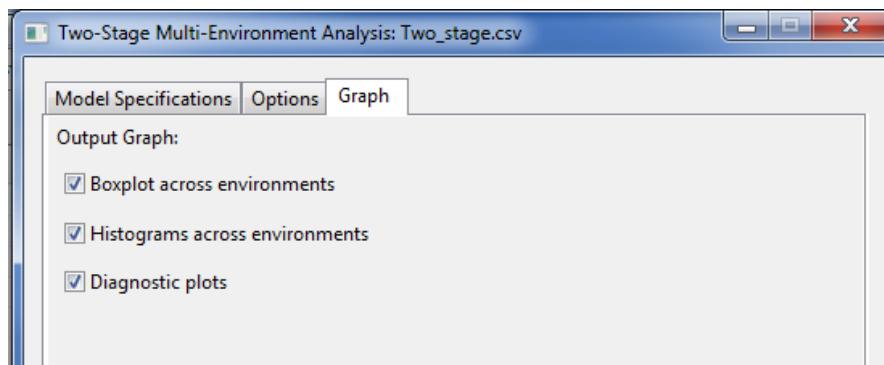
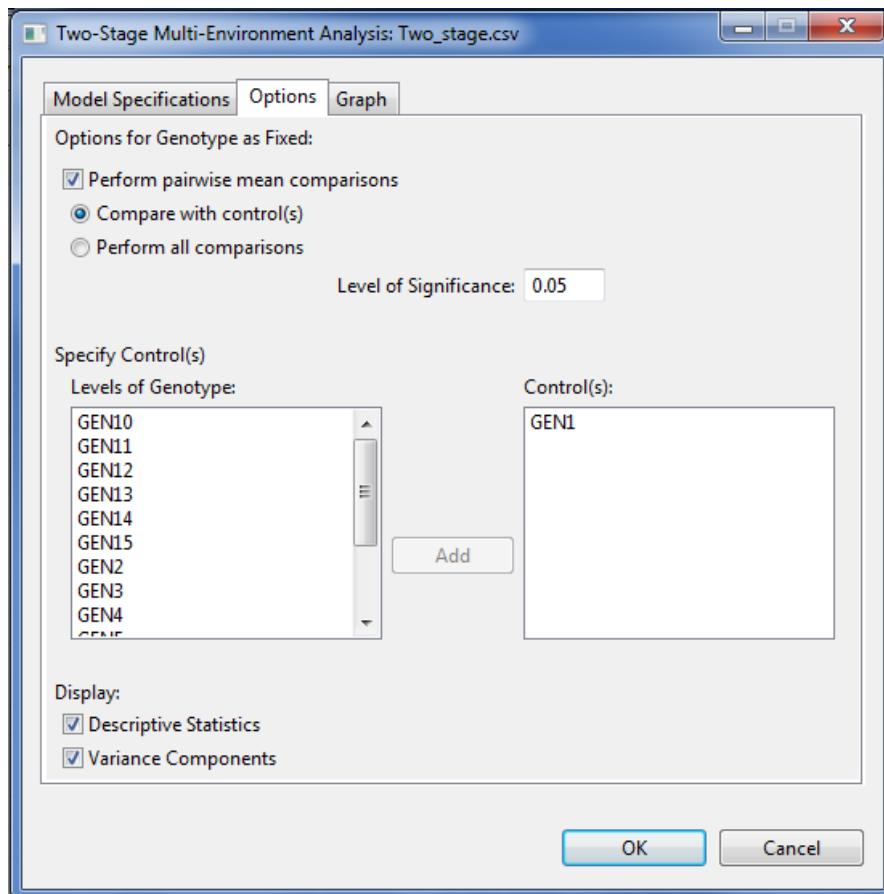
The user has the options to display descriptive statistics and variance.

Graph Tab

Graphs like boxplot, histogram and diagnostic plots can be generated as part of the output of the analysis.

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





- Click **OK**.

- Sample output of the analysis is shown below:

```
DATA FILE: E:/PBTools/Projects/Analysis/Data/Two_stage.csv
```

```
MULTI-ENVIRONMENT ANALYSIS (TWO-STAGE)
```

```
WEIGHT OPTION: 1/(sem^2)
```

```
=====
```

```
GENOTYPE AS: Fixed
```

```
=====
```

```
-----
```

```
RESPONSE VARIABLE: Yield_Mean
```

```
-----
```

```
DATA SUMMARY:
```

```
Number of observations read: 150
```

```
Number of observations used: 150
```

Factors	Number of Levels	Levels
Genotype	15	GEN1 GEN10 GEN11 ... GEN9
Env	10	E1 E10 E2 ... E9

```
DESCRIPTIVE STATISTICS:
```

Variable	N_NonMissObs	Mean	StdDev
Yield_Mean	150	1629.058	1054.553

```
VARIANCE COMPONENTS TABLE:
```

Groups	Variance	Std.Dev.
1 Env	1536420379.9	39197.1986
2 Residual	404328.3	635.8681

```
TESTING FOR THE SIGNIFICANCE OF GENOTYPIC EFFECT:
```

```
Analysis of Variance Table with Satterthwaite Denominator Df
```

Df	Sum Sq	Mean Sq	F value	Denom	Pr(>F)
Genotype	14	10504543	750324.5	1.1602	126 0.3140

```
GENOTYPE LSMEANS AND STANDARD ERRORS:
```

Genotype	LSMean	StdErrMean
1 GEN1	909.7275	18597.93
2 GEN10	2388.7966	18597.93
3 GEN11	1521.2375	18597.93
4 GEN12	2108.5082	18597.93
5 GEN13	2095.4355	18597.93
6 GEN14	1777.4761	18597.93

7	GEN15	1979.3168	18597.93
8	GEN2	1552.8571	18597.93
9	GEN3	1073.8184	18597.93
10	GEN4	1592.7507	18597.93
11	GEN5	918.8396	18597.93
12	GEN6	1179.8754	18597.93
13	GEN7	1118.9574	18597.93
14	GEN8	1572.1282	18597.93
15	GEN9	817.5437	18597.93

STANDARD ERROR OF THE DIFFERENCE (SED):

	Estimate
Minimum	16828.4000
Average	16828.4000
Maximum	16828.4000

SIGNIFICANT PAIRWISE COMPARISONS (IF ANY):

Compared with control(s)

(No significant pairwise comparisons.)

=====

GENOTYPE AS: Random

=====

RESPONSE VARIABLE: Yield_Mean

DATA SUMMARY:

Number of observations read: 150

Number of observations used: 150

Factors	Number of Levels	Levels
Genotype	15	GEN1 GEN10 GEN11 ... GEN9
Env	10	E1 E10 E2 ... E9

DESCRIPTIVE STATISTICS:

Variable	N_NonMissObs	Mean	StdDev
1 Yield_Mean	150	1629.058	1054.553

VARIANCE COMPONENTS TABLE:

	Groups	Variance	Std.Dev.
1	Genotype	713658226.5	26714.3824
2	Env	1536420294.8	39197.1975
3	Residual	404328.3	635.8681

TESTING FOR THE SIGNIFICANCE OF GENOTYPIC EFFECT USING -2 LOGLIKELIHOOD RATIO TEST:

Formula for Model1: Yield_Mean ~ 1 + (1|Genotype) + (1|Env)
Formula for Model2: Yield_Mean ~ 1 + (1|Env)

	AIC	BIC	logLik	Chisq	Df	Pr(>Chisq)
Model2	1206.641	1215.673	-600.3206			
Model1	1176.498	1188.540	-584.2490	32.1432	1	0.0000

TESTING FOR THE SIGNIFICANCE OF ENVIRONMENT EFFECT USING -2 LOGLIKELIHOOD RATIO TEST:

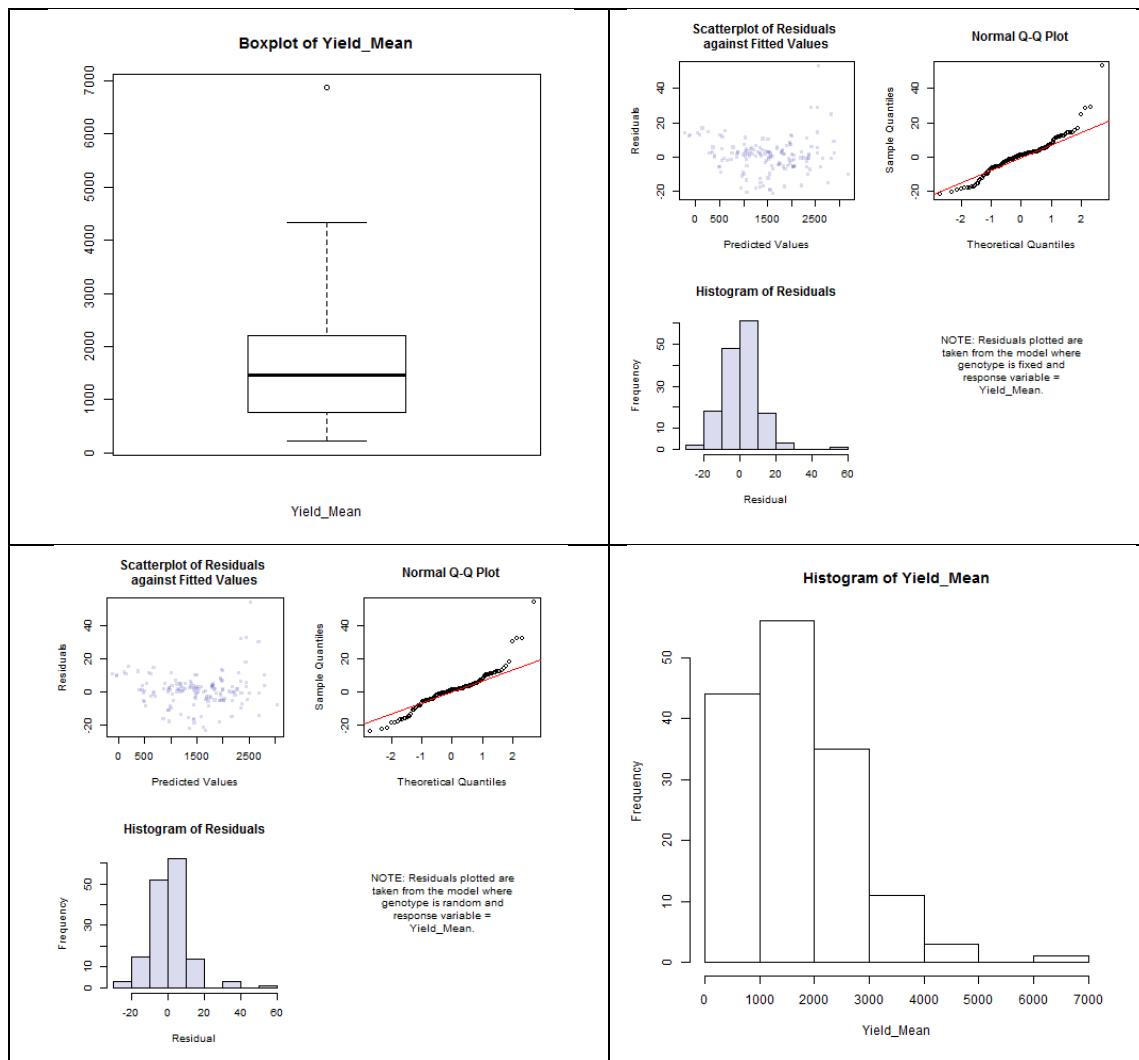
Formula for Model1: Yield_Mean ~ 1 + (1|Genotype) + (1|Env)
Formula for Model2: Yield_Mean ~ 1 + (1|Genotype)

	AIC	BIC	logLik	Chisq	Df	Pr(>Chisq)
Model2	1271.648	1280.68	-632.8242			
Model1	1176.498	1188.54	-584.2490	97.1504	1	0.0000

PREDICTED GENOTYPE MEANS:

	Genotype	Mean
1	GEN1	1008.6335
2	GEN10	2242.8254
3	GEN11	1518.9009
4	GEN12	2008.9421
5	GEN13	1998.0337
6	GEN14	1732.7162
7	GEN15	1901.1398
8	GEN2	1545.2855
9	GEN3	1145.5572
10	GEN4	1578.5742
11	GEN5	1016.2370
12	GEN6	1234.0552
13	GEN7	1183.2229
14	GEN8	1561.3660
15	GEN9	931.7118

- Generated graphs can be viewed by clicking the Graph Tab of the displayed analysis folder. Sample generated graphs are shown below:



GxE Analysis

Stability Models

The steps to perform stability analysis using the summary of data from single-environment analysis as input are listed below:

- Import *Two_stage* file from PBTools package. Double-click the file to view it in the Data Viewer. The file contains four columns (variables) for yield: *Yield_Mean*, *Yield_StdErrMean*, *Yield_sigma2*, *Yield_No.rep* and the *Env* and *Genotype* factors, with 10 and 15 levels, respectively.
- Choose **Analysis | Multi-environment Analysis | GxE Analysis | Stability Models...** from the menu bar.
- Specify the required fields and appropriate options for the analysis.

Model Specifications Tab

Response Variables

This is a required field which contains the column name corresponding to the mean of a trait.

Environment

This is a required field. PBTools requires that the number of environment levels is at least five to perform the analysis.

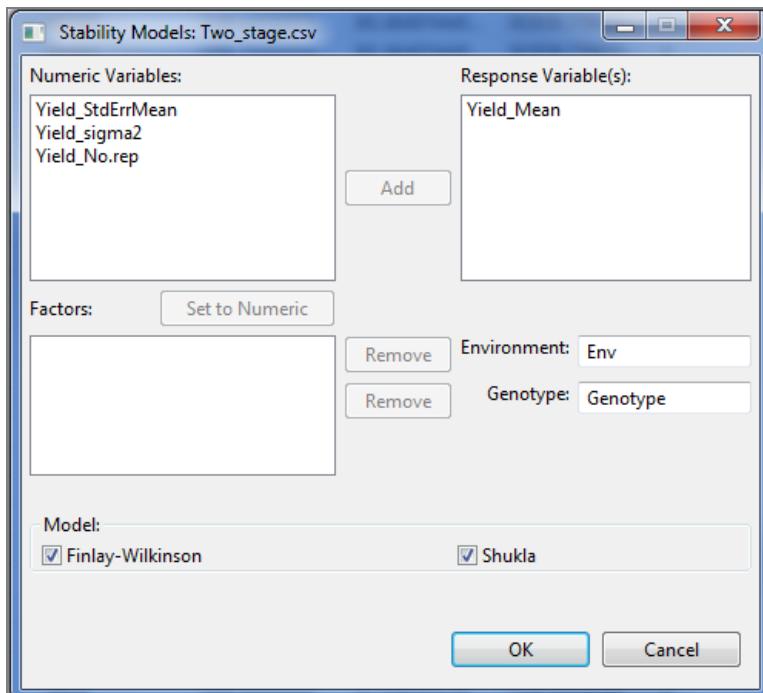
Genotype

This is a required field.

Model

The user has to specify the stability model to be used. The available models are Finlay-Wilkinson and Shukla.

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



- Click **OK**.
- Sample output of the analysis is shown below:

STABILITY ANALYSIS

RESPONSE VARIABLE: Yield_Mean

MODEL: FINLAY-WILKINSON

	Slope	SE	t.value	Prob	MSReg	MSDev
GEN1	0.9959142	0.2131061	4.6733257	0.0015956208	4873724.0	223156.1
GEN10	0.8484889	0.2784564	3.0471163	0.0158905007	3537605.8	381005.6
GEN11	1.6656718	0.2693899	6.1831271	0.0002642465	13633140.2	356598.5
GEN12	1.6542959	0.2703369	6.1193868	0.0002833593	13447559.3	359110.1
GEN13	1.2874242	0.2567362	5.0145802	0.0010338390	8144424.4	323885.3
GEN14	1.6300465	0.6835077	2.3848253	0.0442114578	13056206.8	2295640.6
GEN15	1.1784947	0.4083819	2.8857661	0.0203308103	6824522.9	819502.1
GEN2	1.2331710	0.3151059	3.9135133	0.0044589293	7472461.1	487899.1
GEN3	0.5118599	0.3610126	1.4178452	0.1939889247	1287417.1	640415.2
GEN4	0.2911745	0.3470663	0.8389593	0.4258490364	416604.4	591891.4
GEN5	0.6689718	0.1451654	4.6083411	0.0017364237	2199038.0	103548.4
GEN6	0.5243238	0.2717067	1.9297422	0.0897563679	1350878.4	362758.6
GEN7	0.7307594	0.2697616	2.7089079	0.0267031998	2624012.4	357583.4
GEN8	0.9286961	0.4162939	2.2308664	0.0562209397	4238033.0	851563.8
GEN9	0.8507071	0.2896187	2.9373351	0.0187860797	3556126.5	412164.1

MODEL: SHUKLA

	lower	est.	upper
GEN1	199.20782	382.9876	736.314
GEN10	159.53690	694.5456	3023.712
GEN11	225.37755	955.7149	4052.715
GEN12	228.97306	972.1788	4127.698
GEN13	172.46276	741.8346	3190.941
GEN14	368.07146	1564.2532	6647.861
GEN15	243.28824	1055.8627	4582.408
GEN2	197.85128	844.6951	3606.293
GEN3	178.11266	793.6803	3536.685
GEN4	159.50509	731.1260	3351.274
GEN5	41.00058	245.7681	1473.198
GEN6	112.10707	527.8490	2485.344
GEN7	91.33933	435.5675	2077.080
GEN8	195.09817	879.5450	3965.180
GEN9	144.81779	638.4840	2814.998

Multiplicative Models

The steps to perform AMMI and GGE analyses using the summary of data from single-environment analysis as input are listed below:

- Import *Two_stage* file from PBTools package. Double-click the file to view it in the Data Viewer. The file contains four columns (variables) for yield: *Yield_Mean*, *Yield_StdErrMean*, *Yield_sigma2*, *Yield_No.rep* and the *Env* and *Genotype* factors, with 10 and 15 levels, respectively.
- Choose **Analysis | Multi-environment Analysis | GxE Analysis | Multiplicative Models...** from the menu bar.
- Specify the required fields and appropriate options for the analysis.

Model Specifications Tab

Response Variables

This is a required field which contains the column name corresponding to the mean of a trait.

Residual Variance

If a column corresponding to residual variances is available, specify it in this field.

Number of Replicates

If a column corresponding to number of replicates is available, specify it in this field.

To indicate that a set of response variable, residual variance and number of replicates corresponds to one trait, click the **Add to Table** button. The variables corresponding to one trait will be displayed in a row of the summary table. Do the same for the rest of the traits.

Environment

This is a required field.

Genotype

This is a required field.

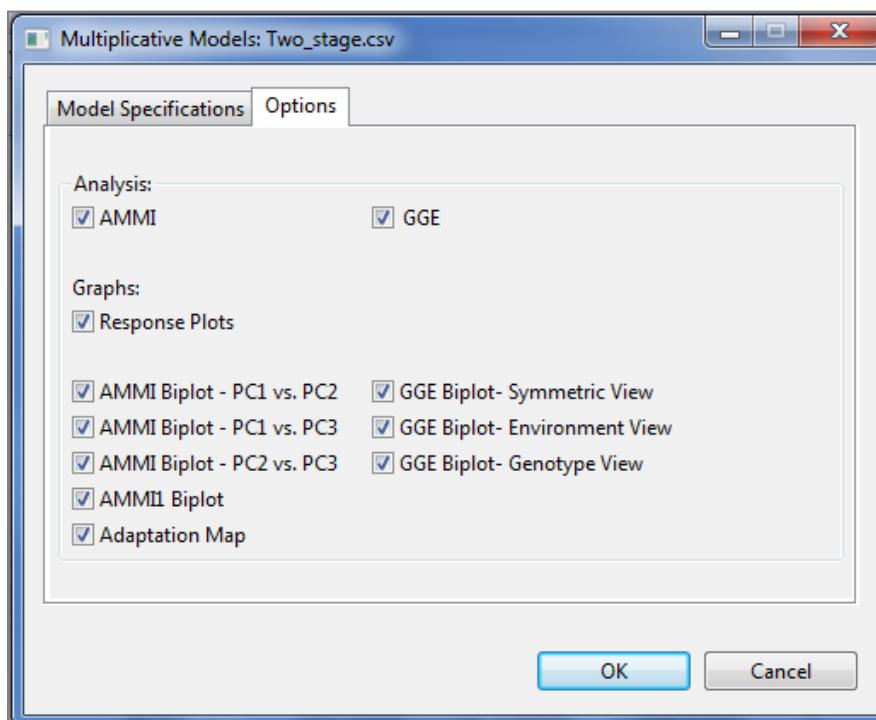
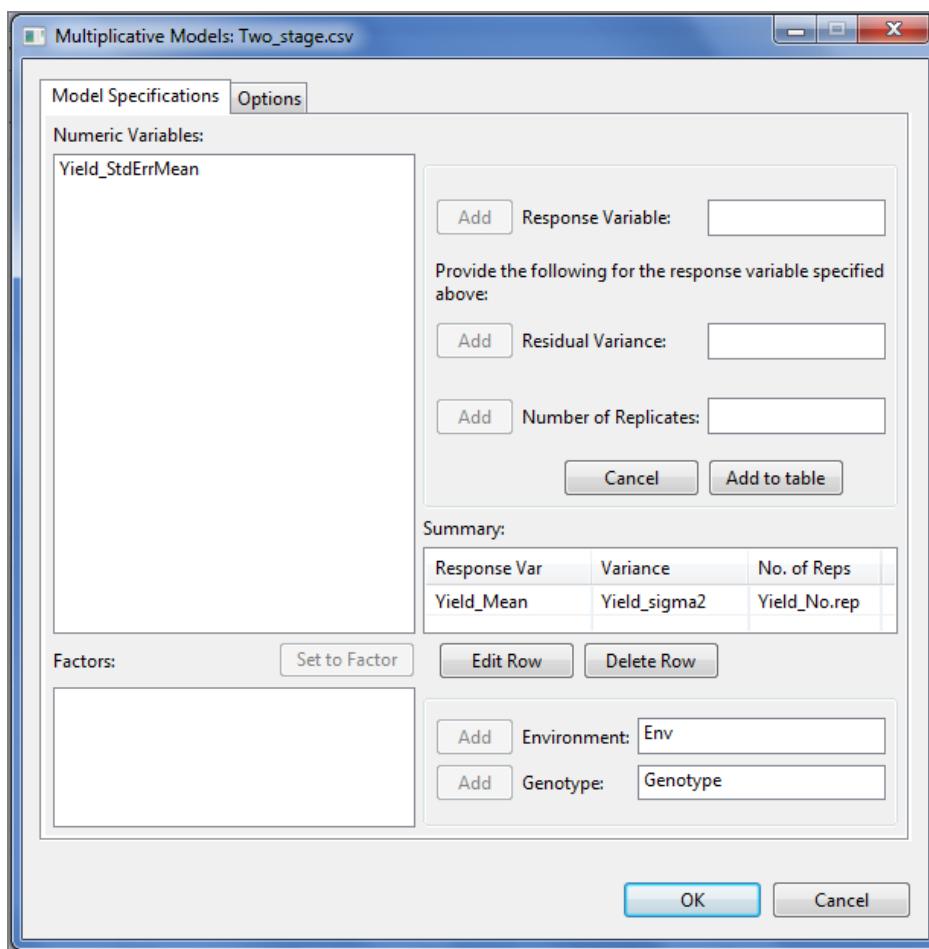
If PBTools detects that in the summary table a row has missing residual variance or number of replicates, a dialog box will appear prompting the user to specify the numerical value of MSE and number of replicates.

Options Tab

The user has to specify the multiplicative model to be used. The available models are AMMI and GGE. If AMMI analysis is selected, the user can request for graphs such as response plot, AMMI biplots (PC1 vs. PC2, PC1 vs. PC3, PC2 vs. PC3), AMMI1 biplot and adaptation map. If GGE analysis is selected, PBTools can present the GGE biplot in three views, namely, symmetric, environment and genotype.

Note: If the levels of the environment and genotype factors are coded using more than four characters, PBTools will automatically recode the levels of environment and genotype to E1, E2, etc. and G1, G2, etc, respectively. If recoding of the levels was done, the coding used will be reflected in the text output and all the requested graphs.

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



- Click **OK**.
- Sample output of the analysis is shown below:

MULTIPLICATIVE MODELS

RESPONSE VARIABLE: Yield_Mean

AMMI ANALYSIS:

	percent	acum	Df	Sum.Sq	Mean.Sq	F.value	Pr.F
PC1	45.7	45.7	22	111669055.7	5075866.17	51.22	0.0000
PC2	28.5	74.2	20	69670255.6	3483512.78	35.15	0.0000
PC3	11.8	86.0	18	28835650.3	1601980.57	16.16	0.0000
PC4	8.0	94.0	16	19596895.3	1224805.96	12.36	0.0000
PC5	2.8	96.8	14	6918224.5	494158.89	4.99	0.0000
PC6	1.4	98.2	12	3458554.3	288212.85	2.91	0.0008
PC7	1.1	99.3	10	2773777.9	277377.79	2.80	0.0025
PC8	0.5	99.8	8	1267436.4	158429.55	1.60	0.1245
PC9	0.1	99.9	6	275967.4	45994.57	0.46	0.8376
PC10	0.0	99.9	4	0.0	0.00	0.00	1.0000

GGE ANALYSIS:

	percent	acum	Df	Sum.Sq	Mean.Sq	F.value	Pr.F
PC1	46.2	46.2	22	127504474.60	5795657.94	58.48	0.0000
PC2	25.4	71.6	20	70051541.68	3502577.08	35.34	0.0000
PC3	11.3	82.9	18	31082789.22	1726821.62	17.42	0.0000
PC4	10.3	93.2	16	28316136.22	1769758.51	17.86	0.0000
PC5	2.6	95.8	14	7262841.82	518774.42	5.23	0.0000
PC6	1.6	97.4	12	4374564.38	364547.03	3.68	0.0000
PC7	1.2	98.6	10	3295838.89	329583.89	3.33	0.0004
PC8	1.0	99.6	8	2765865.54	345733.19	3.49	0.0007
PC9	0.5	100.1	6	1261950.34	210325.06	2.12	0.0512
PC10	0.0	100.1	4	63443.89	15860.97	0.16	0.9583

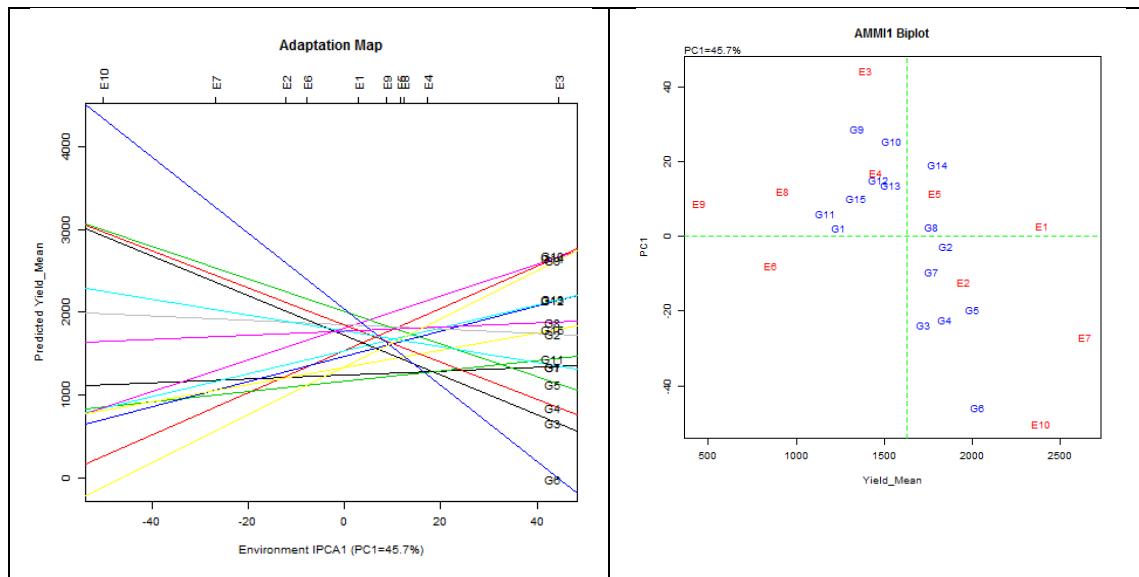
CODES USED IN GRAPHS:

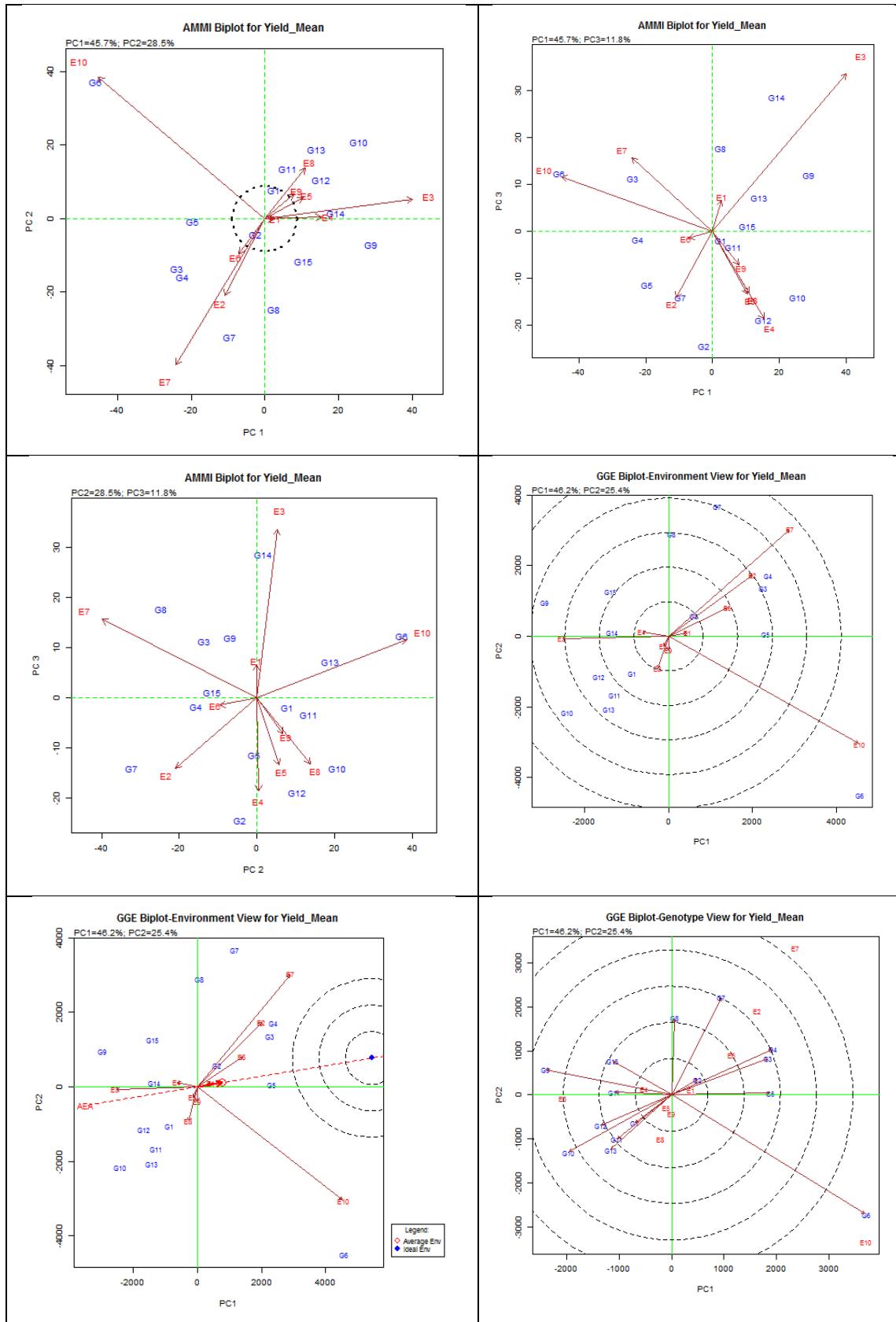
	Genotype	Code
1	GEN1	G1
2	GEN10	G2
3	GEN11	G3
4	GEN12	G4
5	GEN13	G5

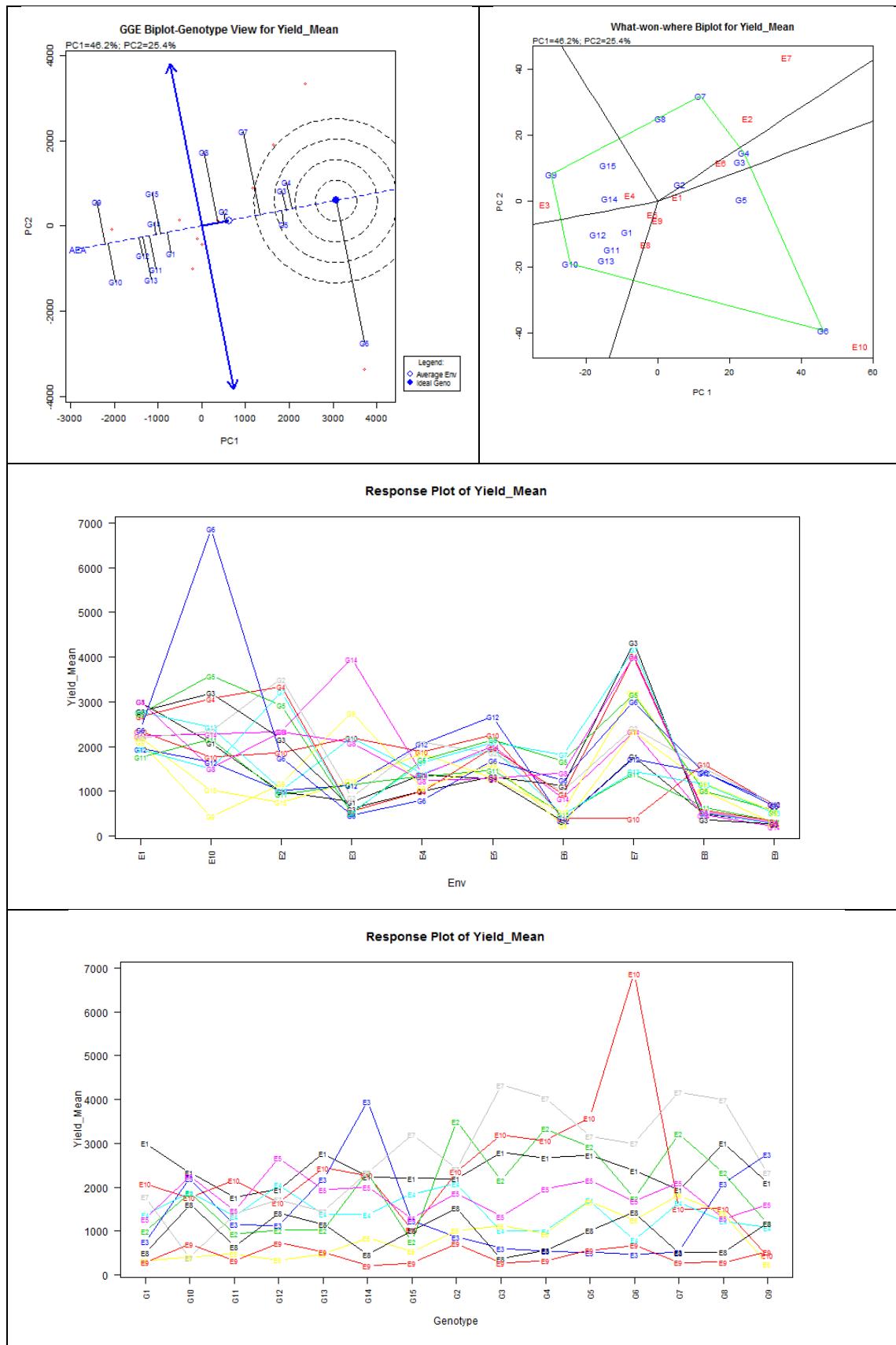
6	GEN14	G6
7	GEN15	G7
8	GEN2	G8
9	GEN3	G9
10	GEN4	G10
11	GEN5	G11
12	GEN6	G12
13	GEN7	G13
14	GEN8	G14
15	GEN9	G15

	Environment Code	
1	E1	E1
2	E10	E2
3	E2	E3
4	E3	E4
5	E4	E5
6	E5	E6
7	E6	E7
8	E7	E8
9	E8	E9
10	E9	E10

- Generated graphs can be viewed by clicking the Graph Tab of the displayed analysis folder. Sample generated graphs are shown below:







7. QTL Analysis

In this module, the QTL analysis is done per environment level only.

Predicted Means as Input

The steps to perform QTL Analysis using predicted means as input are listed below:

- Open the project named *SampleProject*. Double-click the *QTL_pred_height.csv* file to view it in the Data Viewer.
- Choose **Analysis | QTL Analysis...** from the menu bar.
- Specify the required fields and appropriate options for the analysis.

Data Input Tab

Phenotypic Data Used

The *Estimated Means* button is selected if the values in the phenotypic data displayed in the Data Viewer are estimated means. If the values in the phenotypic data are raw data, select the *Raw* button.

Genotypic data file

Specify this file by selecting from the project *Data* folder using the drop-down combo box or by locating it using the **Browse** button. For the example, select *QTL_genotype.txt* file from the drop-down combo box.

Genetic map file

Specify this file by selecting from the project *Data* folder using the drop-down combo box or by locating it using the **Browse** button. For the example, select *QTL_map.txt* file from the drop-down combo box.

Model Specifications Tab

- Opening the data for the first time, *env* field is regarded by R as numerical variable. To set this as factors, choose this variable and click on the **Set to Factor** button.

Response Variable(s)

This is a required field. This list may contain one or more numeric variables. The analysis will be done per response variable.

Genotype

This is a required field.

Environment

Specifying the environment factor is optional.

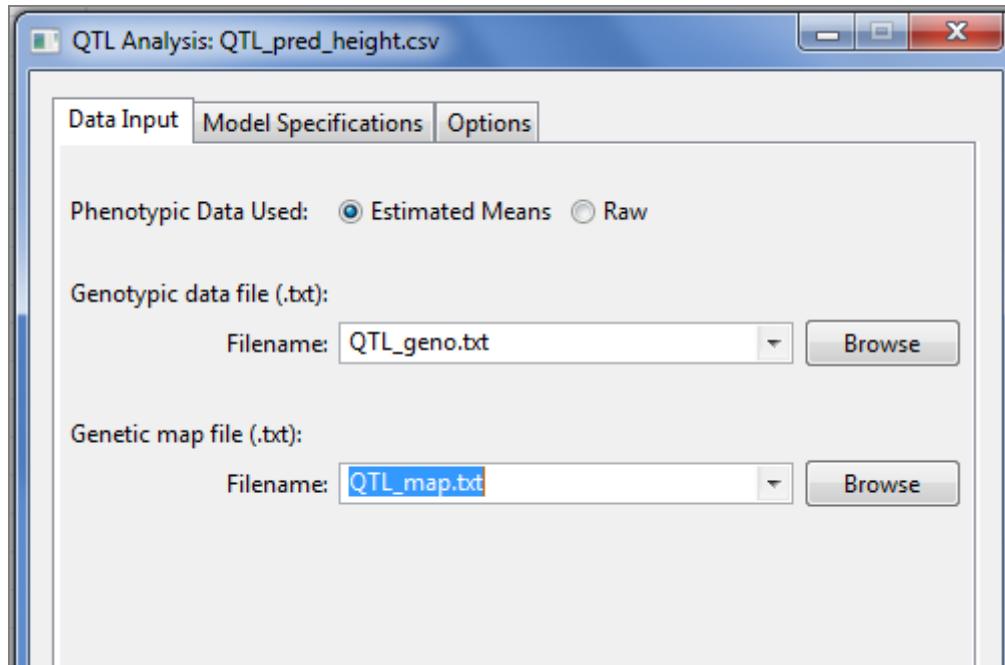
Environment Level(s)

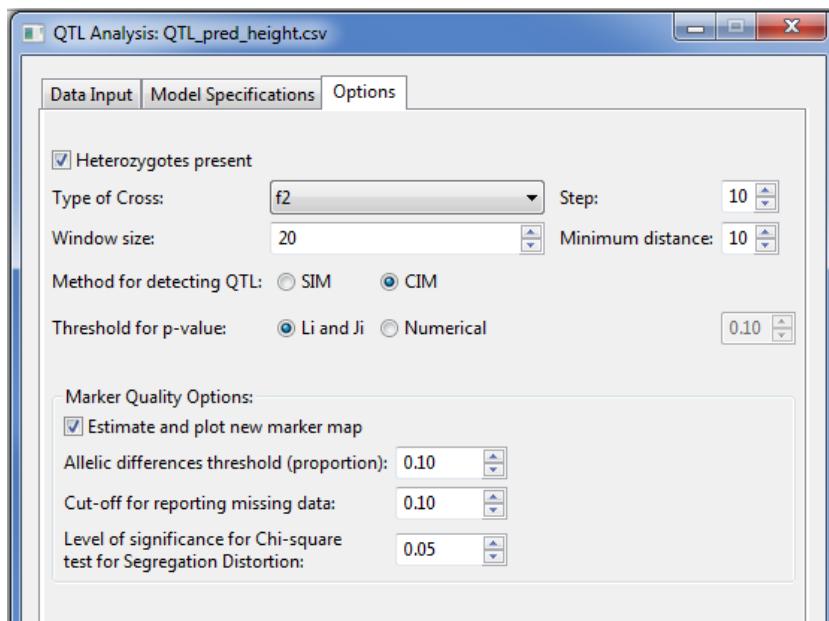
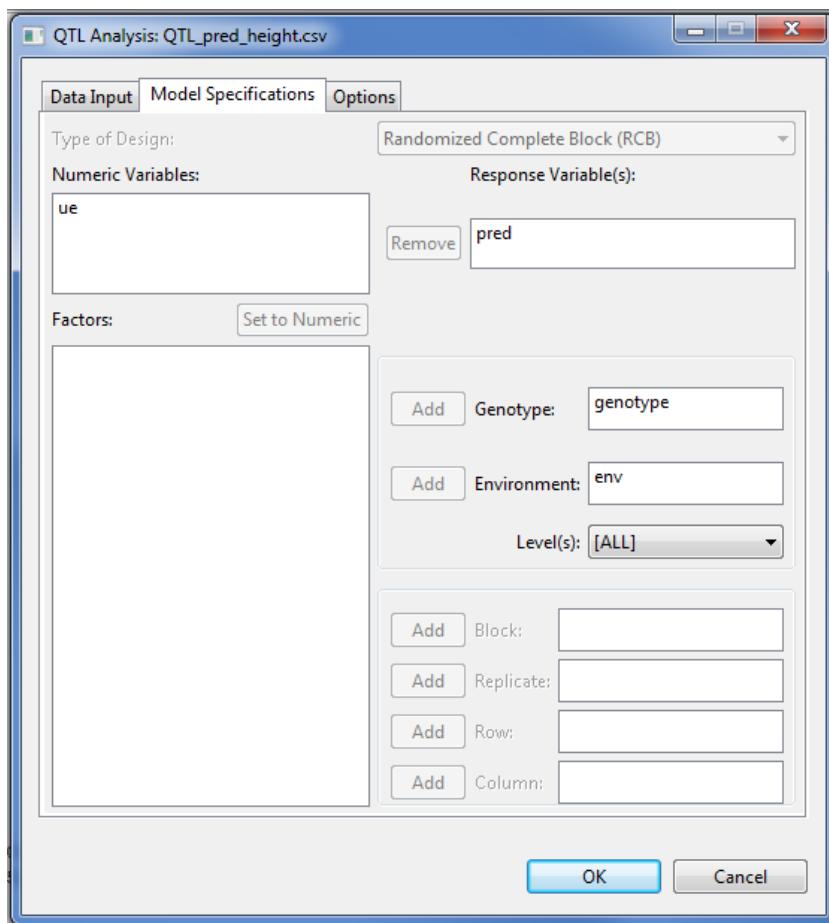
If the environment factor is specified, the user has the option to perform the analysis for each of the environment levels by selecting “[ALL]”. To perform the analysis on a specific environment level, select environment level of interest in the combo box.

Options Tab

- Examine and change, if desired, the default options set.

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





- Click **OK**.

- Sample output of the analysis is shown below:

DATA FILE: E:/PBTools/Projects/SampleProject/Data/QTL_pred_height.csv

QTL ANALYSIS

Method: CIM

TRAIT: pred

ENVIRONMENT: 1

LOD of All Markers (partial results are shown below)

QTL RESULT (ALL):

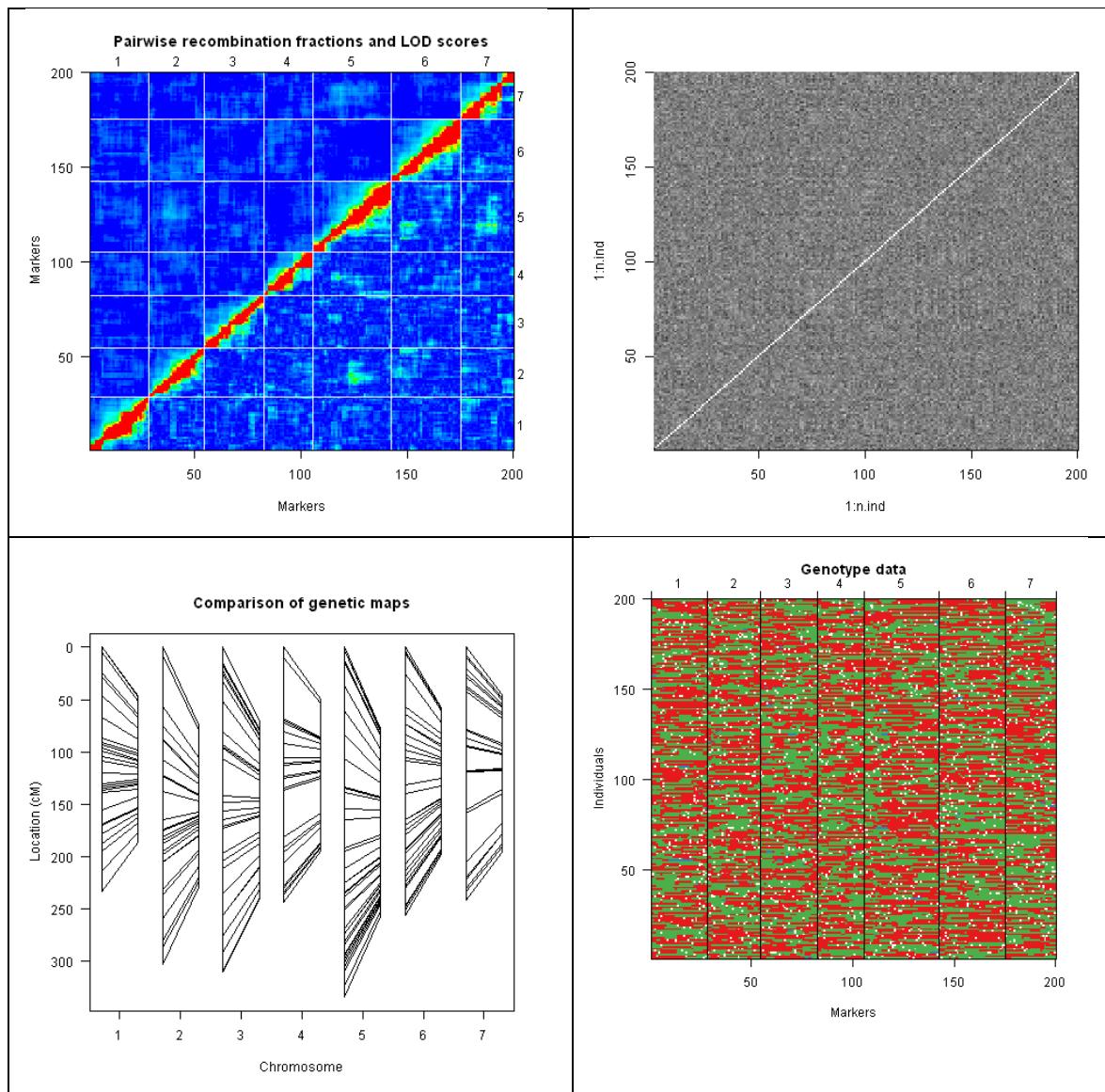
	marker	Chr	Pos	LOD
1	M_0001	1	0	1.174800566
2	M_0002	1	1	1.203821631
3	M_0006	1	5	1.668347468
4	1_loc10	1	10	1.188279464
5	M_0018	1	17	0.402935738
6	1_loc20	1	20	0.225377662
7	M_0022	1	21	0.167893203
8	1_loc30	1	30	0.027011398
9	M_0032	1	31	0.010962483
10	1_loc40	1	40	0.354145428
11	M_0042	1	41	7.571604389
12	1_loc50	1	50	10.147830671
13	M_0053	1	52	9.607553808
14	M_0056	1	55	7.779334005
15	M_0058	1	57	7.203216436
16	1_loc60	1	60	0.115636404
17	M_0062	1	61	0.121921684
18	M_0063	1	62	0.204758238
19	M_0066	1	65	0.205360985
20	M_0069	1	68	0.638024571
21	1_loc70	1	70	0.520645664
22	M_0076	1	75	0.153868813
23	M_0081	1	80	0.245741558
24	M_0083	1	82	1.527724377
25	M_0085	1	84	1.944514227
26	M_0086	1	85	2.453003945
27	M_0090	1	89	2.255778133
28	1_loc90	1	90	2.461440368
29	M_0097	1	96	2.747008898
30	1_loc100	1	100	0.592397083
31	M_0108	1	107	0.296877445
32	M_0109	1	108	0.227384432

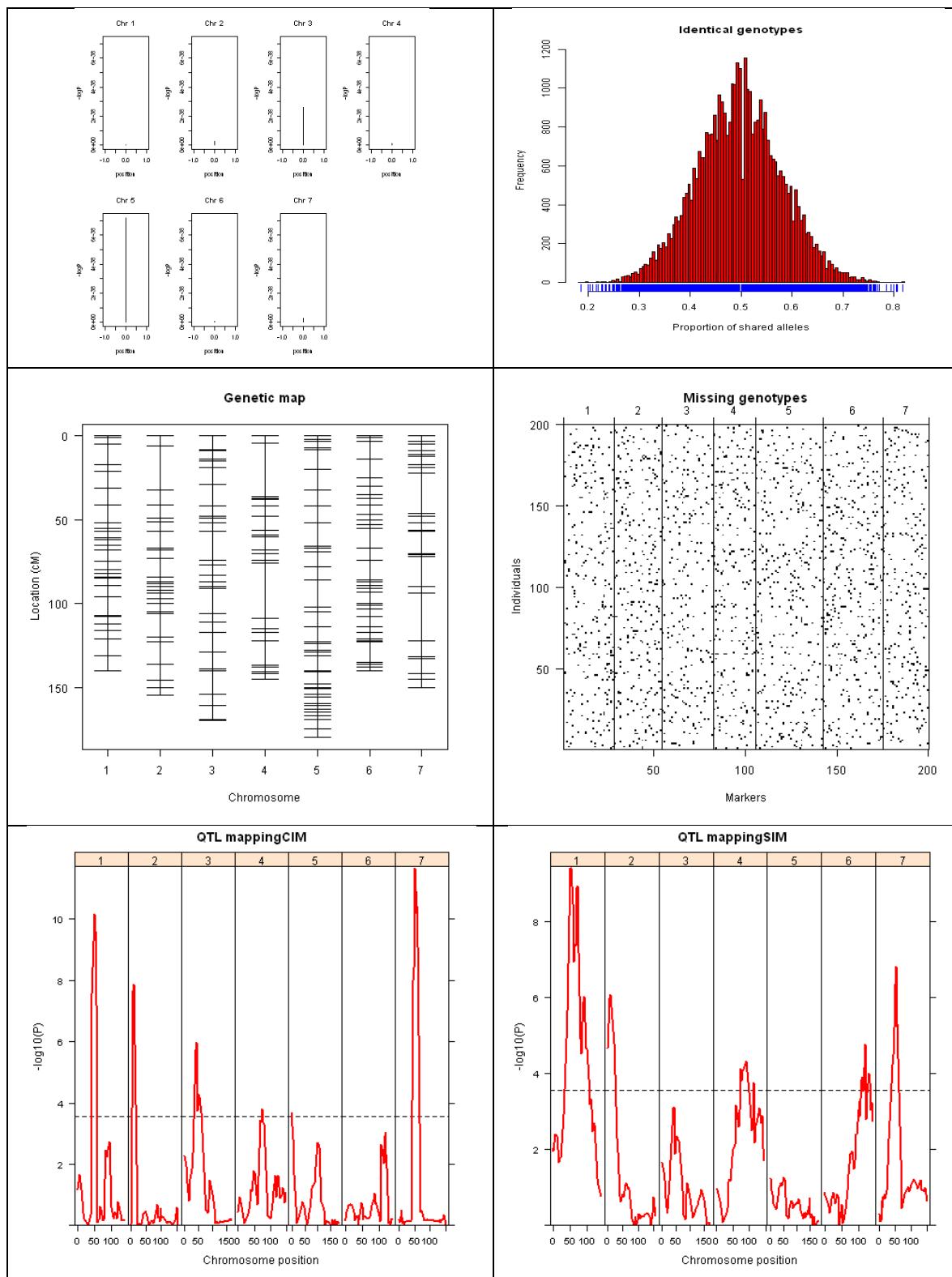
Characteristics of the Selected Markers

QTL RESULT (SELECTED) :

	marker	Chr	Pos	LOD	m.eff	Rsq
1	1_loc50	1	50	10.147831	8.550234	0.01500826
2	2_loc10	2	10	7.869992	-7.398572	0.05434154
3	M_0340	3	42	5.963655	-4.560166	0.06830667
4	M_0543	4	74	3.793779	5.271883	0.09855792
5	M_0617	5	2	3.673243	-2.450220	0.15389838
6	M_0989	7	52	11.673238	7.733852	0.17982716

- Generated graphs can be viewed by clicking the Graph Tab of the displayed analysis folder. Sample generated graphs are shown below:





Raw Data as Input

The steps to perform QTL Analysis using raw data as input are listed below:

- Open the project named *SampleProject*. Double-click the *QTL_pheno.csv* file to view it in the Data Viewer.
- Choose **Analysis | QTL Analysis...** from the menu bar.
- Specify the required fields and appropriate options for the analysis.

Data Input Tab

Phenotypic Data Used

The *Predicted* button is selected if the values in the phenotypic data displayed in the Data Viewer are predicted means. If the values in the phenotypic data are raw data, select the *Raw* button.

Genotypic data file

Specify this file by selecting from the project *Data* folder using the drop-down combo box or by locating it using the **Browse** button. For the example, select *QTL_geno.txt* file from the drop-down combo box.

Genetic map file

Specify this file by selecting from the project *Data* folder using the drop-down combo box or by locating it using the **Browse** button. For the example, select *QTL_map.txt* file from the drop-down combo box.

Model Specifications Tab

- Opening the data for the first time, *ENV* and *REP* fields are regarded by R as numerical variables. To set these as factors, choose these variable and click on the **Set to Factor** button.

Type of Design

There are five available experimental designs, namely: Randomized Complete Block Design (RCB), Augmented RCB, Augmented Latin Square, Alpha-Lattice and Row-Column. For the example, select RCB.

Response Variable(s)

This is a required field. This list may contain one or more numeric variables. The analysis will be done per response variable.

Genotype

This is a required field.

Environment

Specifying the environment factor is optional.

Environment Level(s)

If the environment factor is specified, the user has the option to perform the analysis for each of the environment levels by selecting “[ALL]”. To perform the analysis on a specific environment level, select environment level of interest in the combo box.

Block

This field is required if the design is RCB, Augmented RCB or Alpha-Lattice.

Replicate

This field is required if the design is Augmented Latin Square, Alpha-Lattice or Row-Column.

Row

This field is required if the design is Augmented Latin Square or Row-Column.

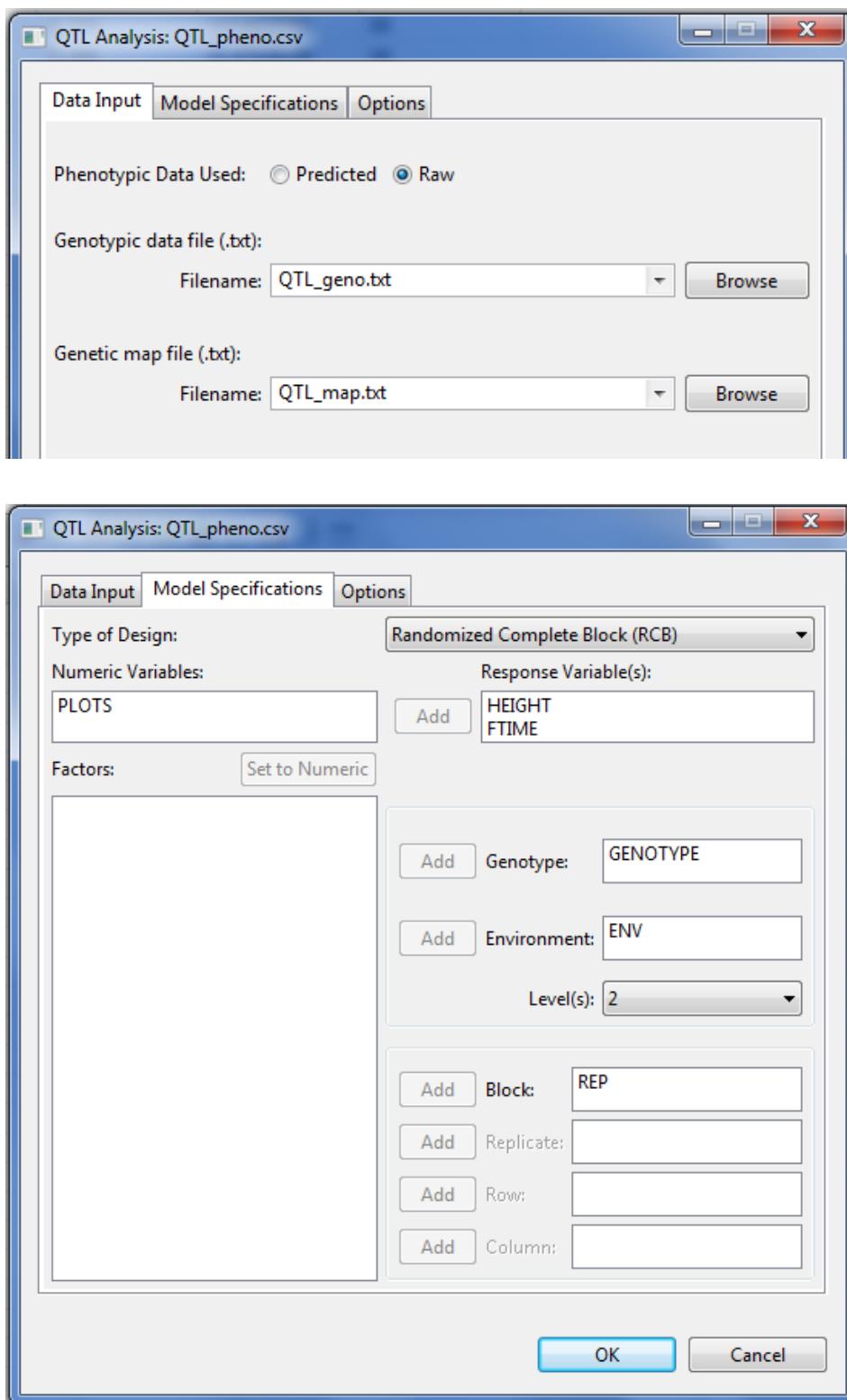
Column

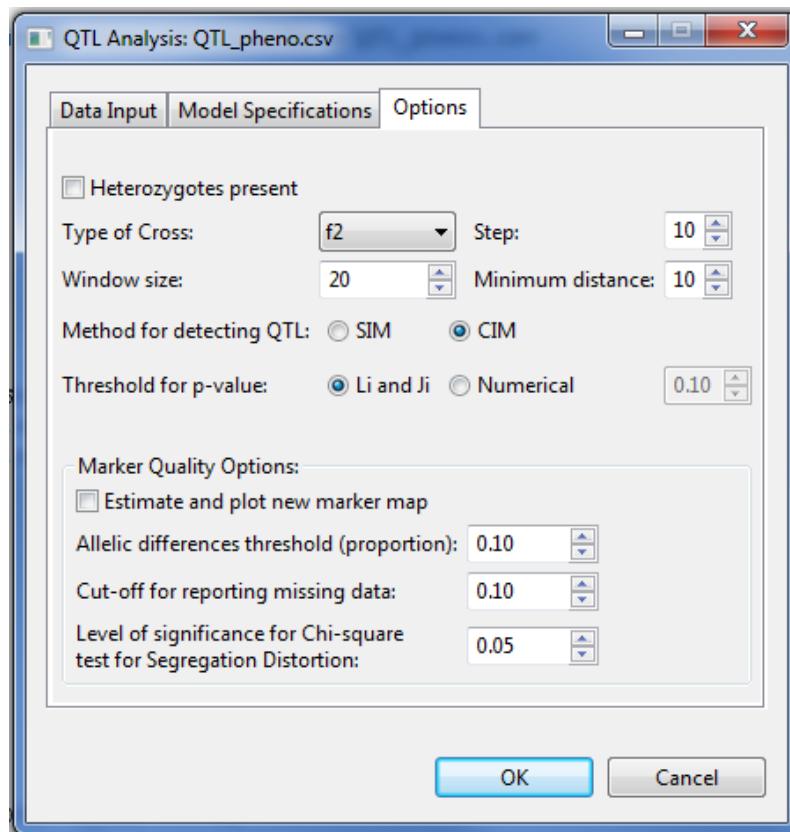
This field is required if the design is Augmented Latin Square or Row-Column.

Options Tab

- Examine and change, if desired, the default options set.

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





- Click **OK**.
- Sample output of the analysis (only results from *response variable = HEIGHT*) is shown below:

DATA FILE: E:/PBTools/Projects/SampleProject/Data/QTL_pheno.csv

SINGLE-ENVIRONMENT ANALYSIS

DESIGN: Randomized Complete Block (RCB)

RESPONSE VARIABLE: HEIGHT

Descriptive Statistics:

Variable	ENV	N_NonMissObs	Mean	StdDev
1	HEIGHT	2	86.69455	31.62887

```
-----  
ANALYSIS FOR: ENV = 2  
-----
```

Trial Summary:

Number of observations read: 606
Number of observations used: 606

Factors	Number of Levels	Levels
GENOTYPE	202	G_001 G_002 G_003 ... P2
REP	3	1 2 3

Estimates of the Variance Components

Variance Components Table:

Groups	Variance	Std.Dev.
1 REP	611.3356	24.72520
2 Residual	302.7346	17.39927

Test for Significance of Genotypic Effect

Testing for the Significance of Genotypic Effect:

Models:

model2: HEIGHT ~ 1 + (1|REP)
model1: HEIGHT ~ 1 + GENOTYPE + (1|REP)

Df	AIC	BIC	logLik	Chisq	Chi Df	Pr(>Chisq)
model2	3	5610.1	5623.3	-2802.1		
model1	204	5362.1	6261.1	-2477.0	650.03	201 < 2.2e-16

Df	Sum Sq	Mean Sq	F value	p-value
GENOTYPE	201	235948.7	1173.874	3.877569 0.0000

Genotype Means and Standard Errors

Genotype means and standard errors:

GENOTYPE	Mean	StdErrMean
1 G_001	104.09469	17.45067
2 G_002	67.11523	17.45067
3 G_003	129.68455	17.45067
4 G_004	114.59435	17.45067
5 G_005	108.58281	17.45067
.		
.		
.		
202 P2	75.78512	17.45067

QTL ANALYSIS

Method: CIM

TRAIT: HEIGHT

ENVIRONMENT: 2

LOD of All Markers (partial results are shown below)

QTL RESULT (ALL) :

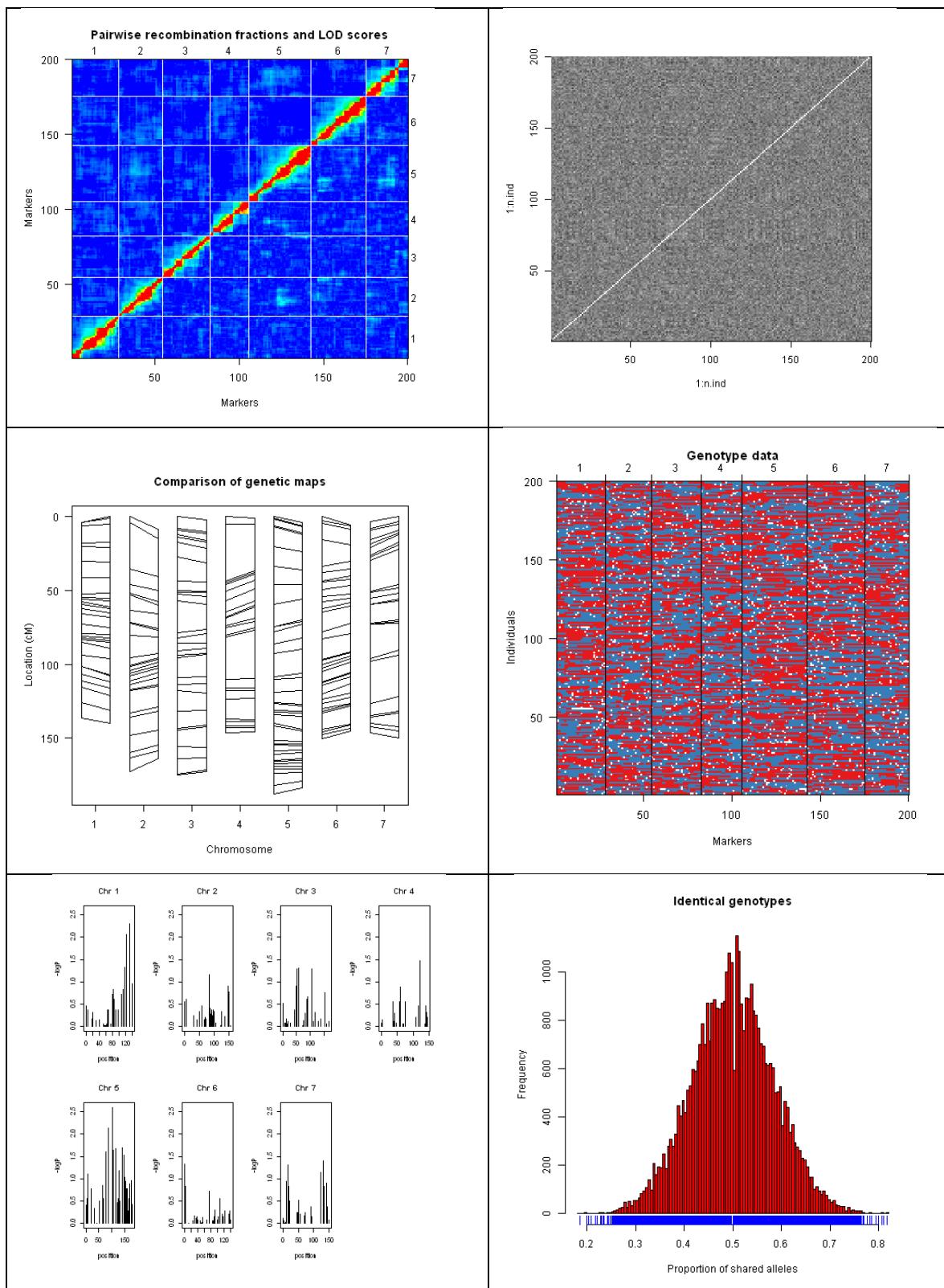
	marker	Chr	Pos	LOD
1	M_0001	1	0	9.661112e-01
2	M_0002	1	1	1.016853e+00
3	M_0006	1	5	9.769430e-01
4	1_loc10	1	10	6.512969e-01
5	M_0018	1	17	1.608477e-01
.				
.				
.				
284	M_1087	7	150	1.331439e-01

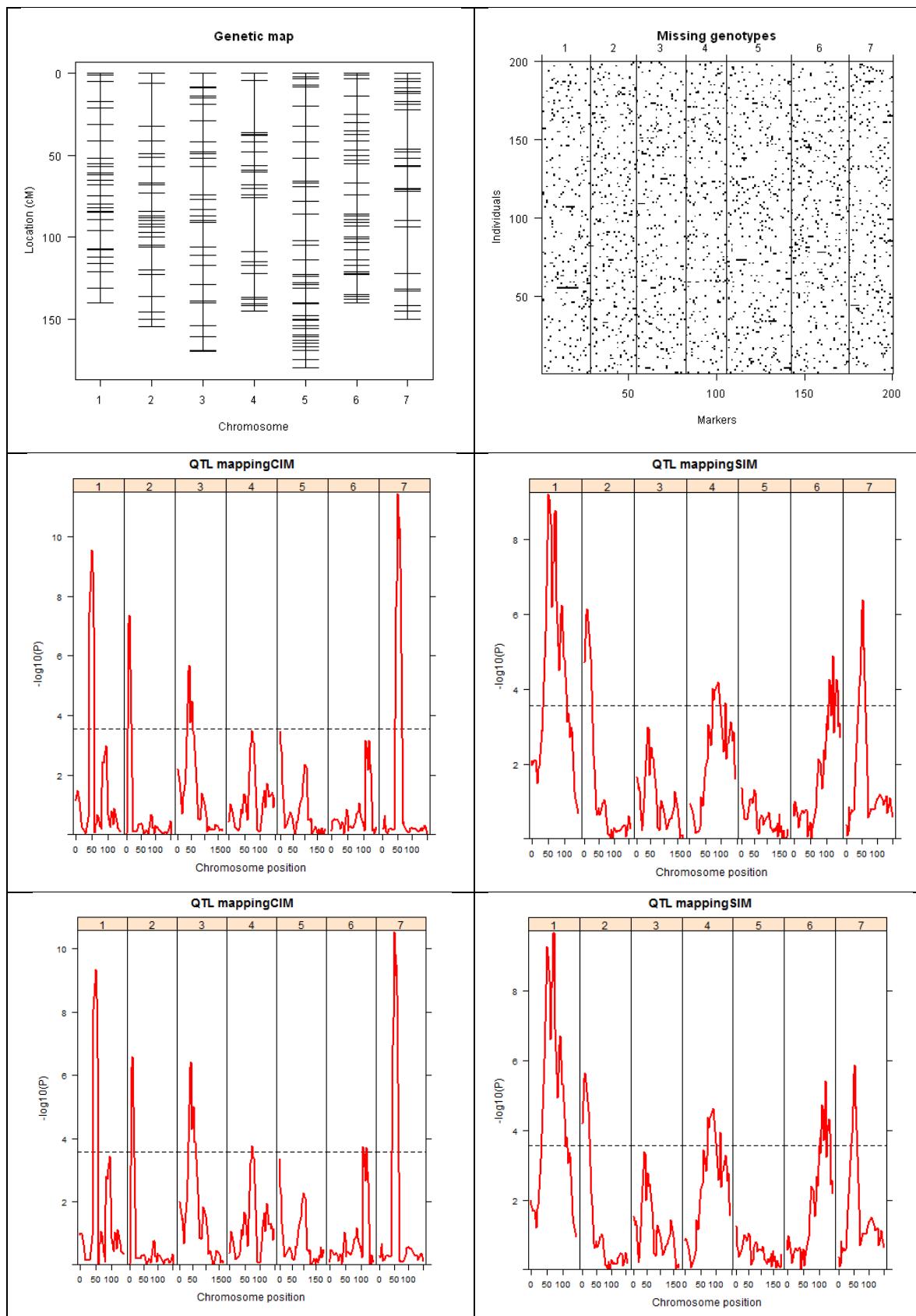
Characteristics of the Selected Markers

QTL RESULT (SELECTED) :

	marker	Chr	Pos	LOD	m.eff	Rsq
1	1_loc50	1	50	9.350702	8.328936	0.03822631
2	2_loc10	2	10	6.579351	-6.526687	0.05935303
3	M_0340	3	42	6.414814	-4.899655	0.07238491
4	M_0543	4	74	3.766788	5.009470	0.08592566
5	M_0904	6	108	3.753643	3.984999	0.13875675
6	M_0989	7	52	10.544196	7.416265	0.17716468

- Generated graphs can be viewed by clicking the Graph Tab of the displayed analysis folder. Sample generated graphs are shown below:





8. Selection Index

The steps to perform Selection Index Analysis are listed below:

- Open the project named *SampleProject*. Double-click the *SI_traits.csv* file to view it in the Data Viewer. The file contains the *REP*, *Block*, and *ENTRY* columns and several traits (*MFL1*, *FFL1*, *EHT1*, *PHT1*, *GY1*, ...).
- Choose **Analysis | Selection Index...** from the menu bar.
- Specify the required fields and appropriate options for the analysis.

Selection Index

Choose one selection index from among the four under *Phenotypic selection indices* and two under *Molecular selection indices*. Note that the molecular selection indices require a markers and QTL file to be specified, in addition to the weights file. For the example, click on the Lande and Thompson Selection Index and leave Variance-Covariance Matrix as basis for selection index and Lattice as design.

Weights file

Specify this file by selecting from the project *Data* folder using the drop-down combo box or by locating it using the **Browse** button. For the example, select *SI_weights.csv* file from the drop-down combo box.

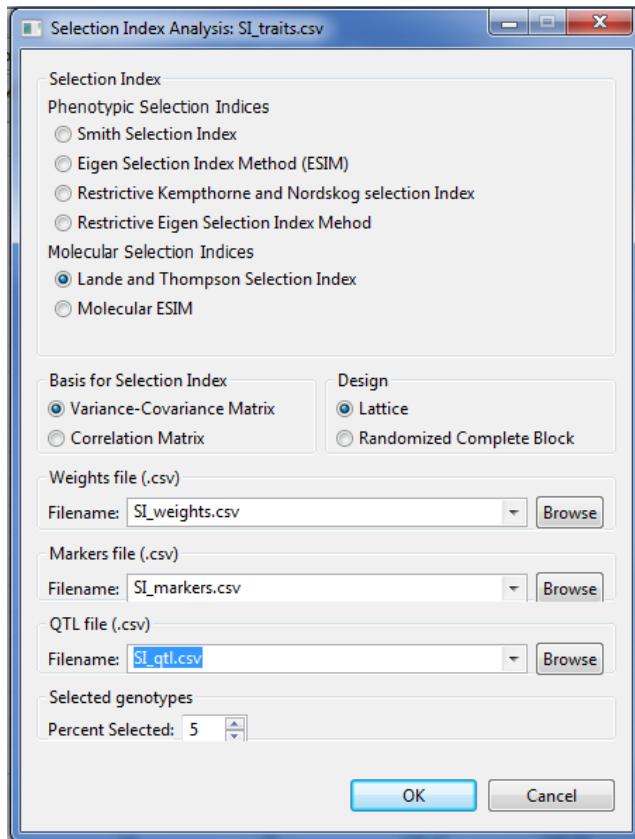
Markers file and QTL file

If needed, specify these by selecting them from the project *Data* folder using the respective drop-down combo box or by locating them using the **Browse** buttons. For the example, select *SI_markers.csv* and *SI_qtl.csv* files from the drop-down combo box.

Percent Selected Genotypes

If desired, change the value of the percentage using the spin box. The default value is 5%.

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



- Click **OK**.
- Sample output of the analysis is shown below:

```
DATA FILE: E:/PBTools/Projects/SampleProject/Data/SI_traits.csv
```

```
Lande and Thompson Selection Index
```

```
DESIGN: Lattice
```

Genetic and Phenotypic Correlation Matrices

GENETIC CORRELATION MATRIX

	MFL1	FFL1	EHT1	PHT1	GY1	MFL.2	FFL2	EHT2	PHT2	GY2
MFL1	1.00	0.88	0.19	-0.33	-0.62	0.96	0.88	0.23	-0.25	-0.36
FFL1	0.88	1.00	0.18	-0.20	-0.77	0.83	0.68	0.15	-0.28	-0.41
EHT1	0.19	0.18	1.00	0.75	-0.03	0.18	0.04	1.09	0.96	0.13
PHT1	-0.33	-0.20	0.75	1.00	0.32	-0.23	-0.28	0.75	1.09	0.28
GY1	-0.62	-0.77	-0.03	0.32	1.00	-0.59	-0.70	0.09	0.40	0.98
MFL.2	0.96	0.83	0.18	-0.23	-0.59	1.00	0.91	0.31	-0.23	-0.52
FFL2	0.88	0.68	0.04	-0.28	-0.70	0.91	1.00	0.27	-0.23	-0.61
EHT2	0.23	0.15	1.09	0.75	0.09	0.31	0.27	1.00	0.77	-0.08

PHT2	-0.25	-0.28	0.96	1.09	0.40	-0.23	-0.23	0.77	1.00	0.20
GY2	-0.36	-0.41	0.13	0.28	0.98	-0.52	-0.61	-0.08	0.20	1.00

PHENOTYPIC CORRELATION MATRIX

MFL1	FFL1	EHT1	PHT1	GY1	MFL.2	FFL2	EHT2	PHT2	GY2	
MFL1	1.00	0.71	0.01	-0.37	-0.47	0.63	0.56	0.10	-0.17	-0.29
FFL1	0.71	1.00	0.04	-0.26	-0.48	0.54	0.51	0.03	-0.20	-0.31
EHT1	0.01	0.04	1.00	0.80	0.07	0.13	0.06	0.71	0.51	0.06
PHT1	-0.37	-0.26	0.80	1.00	0.32	-0.14	-0.15	0.49	0.53	0.17
GY1	-0.47	-0.48	0.07	0.32	1.00	-0.35	-0.39	0.04	0.15	0.44
MFL.2	0.63	0.54	0.13	-0.14	-0.35	1.00	0.72	0.05	-0.31	-0.40
FFL2	0.56	0.51	0.06	-0.15	-0.39	0.72	1.00	0.05	-0.21	-0.45
EHT2	0.10	0.03	0.71	0.49	0.04	0.05	0.05	1.00	0.81	0.15
PHT2	-0.17	-0.20	0.51	0.53	0.15	-0.31	-0.21	0.81	1.00	0.34
GY2	-0.29	-0.31	0.06	0.17	0.44	-0.40	-0.45	0.15	0.34	1.00

Molecular Covariance Matrix

MOLECULAR COVARIANCE MATRIX

MFL1	FFL1	EHT1	PHT1	GY1	MFL.2	FFL2	EHT2	PHT2	GY2	
MFL1	1.00	0.33	0.69	0.63	0.11	0.43	-0.23	0.48	0.79	0.37
FFL1	0.33	1.00	0.46	0.37	0.02	0.24	0.22	0.16	0.23	-0.12
EHT1	0.69	0.46	1.00	0.48	0.23	0.51	-0.41	0.58	0.41	0.13
PHT1	0.63	0.37	0.48	1.00	-0.21	0.47	0.25	0.48	0.50	-0.10
GY1	0.11	0.02	0.23	-0.21	1.00	-0.04	-0.34	-0.01	0.27	-0.18
MFL.2	0.43	0.24	0.51	0.47	-0.04	1.00	0.15	0.73	0.31	0.04
FFL2	-0.23	0.22	-0.41	0.25	-0.34	0.15	1.00	-0.14	-0.04	-0.16
EHT2	0.48	0.16	0.58	0.48	-0.01	0.73	-0.14	1.00	0.32	0.01
PHT2	0.79	0.23	0.41	0.50	0.27	0.31	-0.04	0.32	1.00	-0.02
GY2	0.37	-0.12	0.13	-0.10	-0.18	0.04	-0.16	0.01	-0.02	1.00

Covariance, Variances and Correlation of Selection Index and Breeding Value

COVARIANCE BETWEEN SELECTION INDEX AND BREEDING VALUE: 3.205508

VARIANCE OF THE SELECTION INDEX: 1.50582

VARIANCE OF THE BREEDING VALUE: 6.145354

CORRELATION BETWEEN SELECTION INDEX AND BREEDING VALUE: 0.9999

Characteristics of the Selected Individuals

VALUES OF THE TRAITS, SELECTION INDEX, MEANS, GAINS FOR THE 5% SELECTED INDIVIDUALS

MFL1	FFL1	EHT1	PHT1	GY1	MFL.2	FFL2
------	------	------	------	-----	-------	------

Entry 240	102.01	102.12	80.53	140.12	0.00	100.70	100.74
Entry 2	104.88	104.42	100.22	148.82	28.72	99.60	100.36
Entry 21	101.23	100.75	93.45	163.42	34.45	100.23	98.34
Entry 132	104.69	104.71	75.75	126.00	44.00	97.88	100.35
Entry 167	106.75	105.49	81.67	132.64	0.83	106.21	108.25
Entry 179	104.39	101.50	76.00	126.03	23.78	100.74	99.34
Entry 220	105.34	104.37	78.75	137.92	97.16	99.84	98.31
Entry 174	103.13	102.54	96.84	146.33	47.44	96.59	99.25
Entry 165	104.61	103.66	90.75	150.25	79.00	99.32	103.80
Entry 161	103.12	99.05	85.75	148.50	82.50	101.46	103.00
Entry 87	101.53	100.88	103.66	156.84	68.33	102.34	99.20
Mean of Selected Individuals	103.79	102.68	87.58	143.35	46.02	100.44	100.99
Mean of all Individuals	102.01	102.12	80.53	140.12	75.99	100.70	100.74
Selection Differential	1.78	0.56	7.04	3.23	-29.97	-0.26	0.26
Expected Genetic Gain for 5%	1.57	1.64	1.52	1.19	-1.13	1.95	1.37

	EHT2	PHT2	GY2	LT	index
Entry 240	78.47	133.44	0.00	2.88	
Entry 2	106.75	161.75	140.00	2.59	
Entry 21	89.69	156.81	1.50	2.34	
Entry 132	76.09	127.28	33.39	2.24	
Entry 167	75.00	113.64	0.00	2.14	
Entry 179	74.31	124.14	9.24	2.14	
Entry 220	87.00	143.50	129.50	1.94	
Entry 174	94.93	149.59	18.61	1.83	
Entry 165	96.25	160.25	41.00	1.80	
Entry 161	76.50	125.69	12.75	1.74	
Entry 87	91.95	140.56	35.00	1.70	
Mean of Selected Individuals	86.08	139.69	38.27	NA	
Mean of all Individuals	78.47	133.44	51.70	NA	
Selection Differential	7.61	6.26	-13.43	NA	
Expected Genetic Gain for 5%	1.73	1.08	-1.02	NA	

Values of the Traits and Selection Index for All Individuals (partial results are shown below)

VALUES OF THE TRAITS AND THE SELECTION INDEX FOR ALL INDIVIDUALS

	MFL1	FFL1	EHT1	PHT1	GY1	MFL.2	FFL2	EHT2	PHT2	GY2
Entry 1	102.21	100.25	71.45	123.75	42.45	99.29	98.95	68.51	117.47	16.87
Entry 2	104.88	104.42	100.22	148.82	28.72	99.60	100.36	106.75	161.75	140.00
Entry 3	98.97	100.44	80.17	154.36	77.78	97.93	96.82	66.75	133.75	116.00
Entry 4	102.73	103.32	78.16	137.57	488.89	100.89	100.92	85.76	145.25	52.78
Entry 5	94.09	96.60	80.94	152.67	225.25	95.00	96.10	72.94	130.42	63.89
Entry 6	99.90	101.92	94.04	153.39	121.00	100.75	100.09	93.06	149.92	66.00
.										
.										
.										

9. Mating Designs

North Carolina I (NCI)

In this design, n_1 male parents are chosen and each male is crossed to a different set of n_2 females. This design follows the hierarchical or nested design in Statistics. The progenies of all the crosses are tested for the traits of interest using the chosen experimental design.

The steps to perform such analysis are listed below:

- Import *NCI_ME* file from package. Double-click the file to view it in the Data Viewer. The example file contains data for an experiment conducted for crosses derived from a NCI mating design with four inbred males and 11 inbred females per male using Randomized Complete Block (RCB) field design with two blocks (1 and 2) in two environments (*A* and *B*) and one trait, *Y*.
- Choose **Analysis | Mating Designs | North Carolina I...** from the menu bar.
- Opening the data for the first time, *Block*, *Male* and *Female* fields are regarded by R as numerical variables. To set these as factors, choose these variables and click on the **Set to Factor** button.
- Specify the required fields and appropriate options for the analysis.

Type of Design

There are four available experimental designs, namely: Completely Randomized Design (CRD), Randomized Complete Block Design (RCB), Alpha-Lattice and Row-Column Design.

'Inbred' Option

This is selected if the parental lines are inbreds.

'Crossed' Option

This is selected if the parental lines are from random-mating population (outcrossing species).

Data Input

The input data for the analysis may be plot-means or observations of individual plants (*not yet implemented*).

Response Variable(s)

This is a required field. This list may contain one or more numeric variables.

'Perform Analysis Per Site' Option

If this option is selected and the Environment factor is specified, the analysis will be performed for each level of the Environment factor.

If this option is selected but the Environment factor is **not** specified, PBTools will perform the analysis as if the entire data came from only one site.

'Perform Multiple Environment Analysis' Option

If this option is selected, the *Environment* factor must be specified.

Environment

This is a required field if the 'Perform Multiple Environment Analysis' option is selected. Moreover, the number of its levels must be at least two.

Female

This is a required field.

Male

This is a required field.

Block

This is a required field if the selected experimental design is Randomized Complete Block or Alpha-Lattice.

Replicate

This is a required field if the selected experimental design is Completely Randomized Design, Alpha-Lattice or Row-Column.

Row

This is a required field if the selected experimental design is Row-Column.

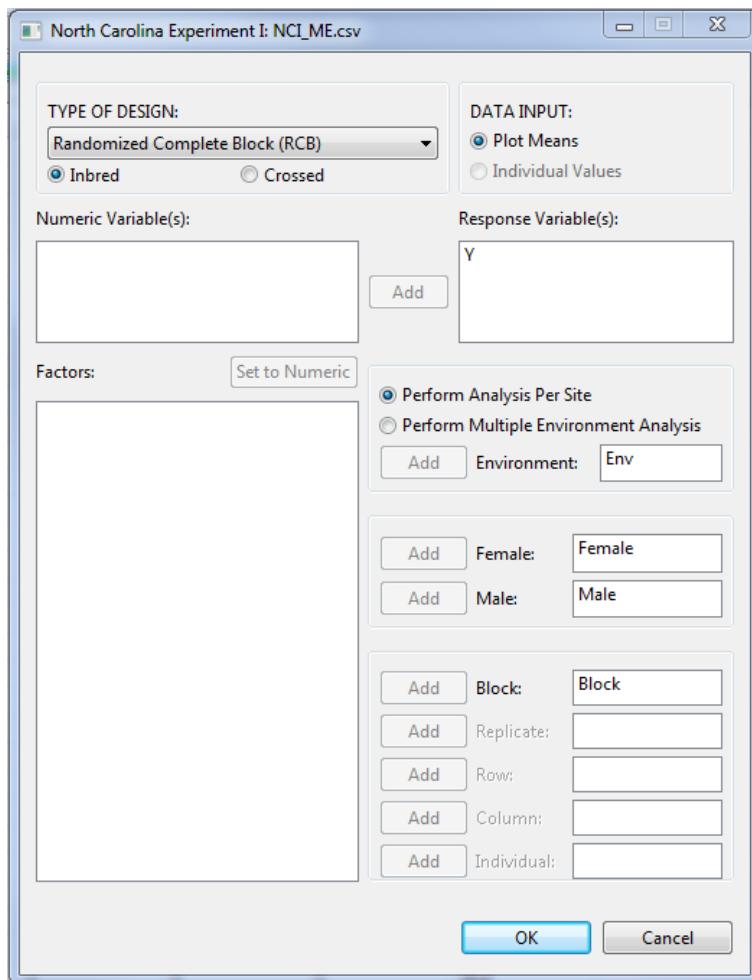
Column

This is a required field if the selected experimental design is Row-Column.

Individual

This is a required field if the selected data input is Individual Values.

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



- Click **OK**.
- Sample output of the analysis (only results from *Env = A*) is shown below:

```
DATA FILE: E:/PBTools/Projects/SampleProject/Data/NCI_ME.csv
```

```
DESIGN: NORTH CAROLINA EXPERIMENT I IN RCB (INBRED)
```

```
-----  
RESPONSE VARIABLE: Y  
-----
```

ANALYSIS FOR: Env = A

DATA SUMMARY:

Factors	No of Levels	Levels
Env	1	A
Male	4	1 2 3 4
Female	11	1 10 11 ... 9
Block	2	1 2

Number of observations read: 88
Number of observations used: 88

Analysis of Variance Table

ANOVA TABLE FOR THE EXPERIMENT:

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Block	1	15.9801	15.9801	2.17	0.1483
Male	3	479.9476	159.9825	21.70	0.0000
Male:Female	40	1161.6870	29.0422	3.94	0.0000
Residuals	43	317.0749	7.3738		

REMARK: Raw dataset is balanced.

Estimated Variance Components of Random Effects

LINEAR MIXED MODEL FIT BY RESTRICTED MAXIMUM LIKELIHOOD:

Formula: Y ~ 1 + (1|Block) + (1|Male/Female)

AIC	BIC	logLik	deviance	REMLdev
500.0305	512.4172	-245.0152	492.5127	490.0305

Random Effects:

Groups	Variance	Std. Deviation
Female:Male	10.8342	3.2915
Male	5.9518	2.4396
Block	0.1956	0.4423
Residual	7.3738	2.7155

Genetic Variance Components

ESTIMATES OF GENETIC VARIANCE COMPONENTS:

	Estimate
VA	11.903600
VD	4.882400
h2-narrow sense	0.492703
H2-broad sense	0.694791
Dominance Ratio	0.905717

North Carolina II (NCII)

In this design, n_1 male parents and n_2 female parents are chosen. Each male is crossed to every female. This design follows the factorial design in Statistics. The progenies of all the crosses are tested for the traits of interest using the chosen experimental design.

The steps to perform such analysis are listed below:

- Import *NCII_ME* file from the package. Double-click the file to view it in the Data Viewer. The example file contains data for an experiment conducted for crosses derived from a NCII mating design with eight inbred males and eight inbred females using Randomized Complete Block (RCB) field design with three blocks (1, 2 and 3) in two environments (A and B) and one trait, Y.
- Choose **Analysis | Mating Designs | North Carolina II...** from the menu bar.
- Opening the data for the first time, *Block*, *Male* and *Female* fields in the data file are regarded by R as numerical variables. To set these as factors, choose these variables and click on the **Set to Factor** button.
- Specify the required fields and appropriate options for the analysis.

Type of Design

There are four available experimental designs, namely: Completely Randomized Design (CRD), Randomized Complete Block Design (RCB), Alpha-Lattice and Row-Column Design.

'Inbred' Option

This is selected if the parental lines are inbreds.

'Crossed' Option

This is selected if the parental lines are from random-mating population (outcrossing species).

Data Input

The input data for the analysis may be plot-means or observations of individual plants (*not yet implemented*).

Response Variable(s)

This is a required field. This list may contain one or more numeric variables.

'Perform Analysis Per Site' Option

If this option is selected and the Environment factor is specified, the analysis will be performed for each level of the Environment factor.

If this option is selected but the Environment factor is **not** specified, PBTools will perform the analysis as if the entire data came from only one site.

'Perform Multiple Environment Analysis' Option

If this option is selected, the *Environment* factor must be specified.

Environment

This is a required field if the 'Perform Multiple Environment Analysis' option is selected. Moreover, the number of its levels must be at least two.

Female

This is a required field.

Male

This is a required field.

Block

This is a required field if the selected experimental design is Randomized Complete Block or Alpha-Lattice.

Replicate

This is a required field if the selected experimental design is Completely Randomized Design, Alpha-Lattice or Row-Column.

Row

This is a required field if the selected experimental design is Row-Column.

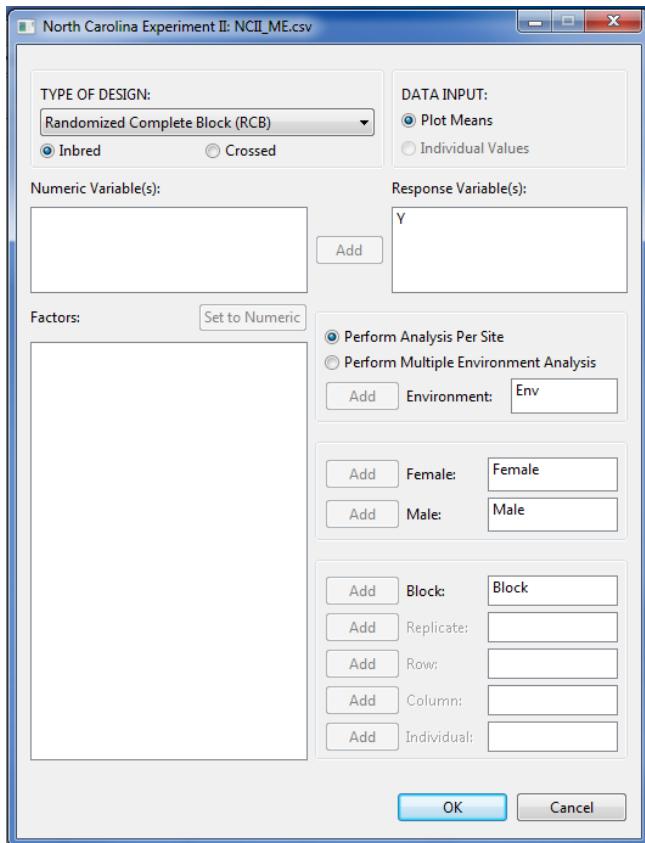
Column

This is a required field if the selected experimental design is Row-Column.

Individual

This is a required field if the selected data input is Individual Values.

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



- Click **OK**.
- Sample output of the analysis (only results from Env = A) is shown below:

```
DATA FILE: E:/PBTools/Projects/SampleProject/Data/NCII_ME.csv
```

```
DESIGN: NORTH CAROLINA EXPERIMENT II IN RCB (INBRED)
```

```
-----  
RESPONSE VARIABLE: Y  
-----  
-----
```

```
ANALYSIS FOR: Env = A  
-----
```

DATA SUMMARY:

Factors	No of Levels	Levels
Env	1	A
Female	8	1 2 3 ... 8
Male	8	10 11 12 ... 9
Block	3	1 2 3

Number of observations read: 192

Number of observations used: 192

Analysis of Variance Table

ANOVA TABLE FOR THE EXPERIMENT:

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Block	2	22.3531	11.1766	1.14	0.3220
Male	7	1112.6490	158.9498	16.26	0.0000
Female	7	735.2669	105.0381	10.75	0.0000
Male:Female	49	823.1469	16.7989	1.72	0.0086
Residuals	126	1231.4730	9.7736		

REMARK: Raw dataset is balanced.

Estimated Variance Components of Random Effects

LINEAR MIXED MODEL FIT BY RESTRICTED MAXIMUM LIKELIHOOD:

Formula: $Y \sim 1 + (1|Block) + (1|Male) + (1|Female) + (1|Male:Female)$

AIC BIC logLik deviance REMLdev
1057.665 1077.21 -522.8323 1047.758 1045.665

Random Effects:

Groups	Variance	Std. Deviation
Male:Female	2.3418	1.5303
Female	3.6767	1.9175
Male	5.9229	2.4337
Block	0.0219	0.1481
Residual	9.7736	3.1263

Genetic Variance Components

ESTIMATES OF GENETIC VARIANCE COMPONENTS:

	Estimate
VA	9.599670
VD	2.341800
Narrow sense heritability(plot-mean based)	0.442075
Broad sense heritability(plot-mean based)	0.549917
Dominance Ratio	0.698492

- Suppose the user opted to perform Multiple Environment Analysis, sample output of the analysis is shown below:

```
DATA FILE: E:/PBTools/Projects/SampleProject/Data/NCII_ME.csv
```

```
MULTIPLE ENVIRONMENT ANALYSIS
```

```
DESIGN: NORTH CAROLINA EXPERIMENT II IN RCB (INBRED)
```

```
-----  
RESPONSE VARIABLE: Y  
-----
```

```
DATA SUMMARY:
```

Factors	No of Levels	Levels
Env	2	A B
Female	8	1 2 3 ... 8
Male	8	10 11 12 ... 9
Block	3	1 2 3

```
Number of observations read: 384
```

```
Number of observations used: 384
```

ANOVA Table

```
ANOVA TABLE:
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Env	1	8.7665	8.7665	0.38	0.5724
Env:Block	4	93.0194	23.2549	2.21	0.0682
Male	7	840.6569	120.0938	11.43	0.0000
Female	7	821.7501	117.3929	11.17	0.0000
Male:Female	49	1233.6320	25.1762	2.40	0.0000
Env:Male	7	493.0000	70.4286	6.70	0.0000
Env:Female	7	215.9051	30.8436	2.93	0.0057
Env:Male:Female	49	974.2153	19.8819	1.89	0.0009
Residuals	252	2648.7840	10.5110		

```
-----  
REMARK: Raw dataset is balanced.
```

Estimated Variance Components of Random Effects

```
LINEAR MIXED MODEL FIT BY RESTRICTED MAXIMUM LIKELIHOOD:
```

```
Formula: Y ~ 1 + (1|Env) + (1|Env:Block) + (1|Male) + (1|Female) +  
(1|Male:Female) + (1|Env:Male) + (1|Env:Female) + (1|Env:Male:Female)
```

AIC	BIC	logLik	deviance	REMLdev
2147.079	2186.586	-1063.54	2128.376	2127.079

Random Effects:

Groups	Variance	Std. Deviation
Env:Male:Female	3.1506	1.7750
Male:Female	0.8681	0.9317
Env:Female	0.3985	0.6313
Env:Male	1.8441	1.3580
Female	1.7219	1.3122
Male	1.0554	1.0273
Env:Block	0.1792	0.4233
Env	0.0000	0.0000
Residual	10.5157	3.2428

Genetic Variance Components

ESTIMATES OF GENETIC VARIANCE COMPONENTS:

	Estimate
VA	2.777330
VAXE	2.242660
VD	0.868100
VDxE	3.150620
h2-narrow sense	0.142031
H2-broad sense	0.186425
Dominance Ratio	0.790653

North Carolina III (NCIII)

This design involves taking a number of F_2 individuals from a cross between two inbred lines (P_1 and P_2) and crossing each back to these same two lines. The two parental inbreds thus act as testers against which the F_2 are assessed.

The steps to perform such analysis using are listed below:

- Import *NCIII_ME* file from the package. Double-click the file to view it in the Data Viewer. The example file contains data for an experiment conducted for crosses derived from a NCIII mating design with 16 F_2 lines labeled as *Male* and two testers labeled as *Female* using Randomized Complete Block (RCB) field design with two blocks (1 and 2) in two environments (*A* and *B*) and one trait, *Y*.
- Choose **Analysis | Mating Designs | North Carolina III...** from the menu bar.
- Opening the data for the first time, *Block*, *Male* and *Female* fields are regarded by R as numerical variables. To set these as factors, choose these variables and click on the **Set to Factor** button.

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

Type of Design

There are four available experimental designs, namely: Completely Randomized Design (CRD), Randomized Complete Block Design (RCB), Alpha-Lattice and Row-Column Design.

Data Input

The input data for the analysis may be plot-means or observations of individual plants (*not yet implemented*).

Response Variable(s)

This is a required field. This list may contain one or more numeric variables.

'Perform Analysis Per Site' Option

If this option is selected and the Environment factor is specified, the analysis will be performed for each level of the Environment factor.

If this option is selected but the Environment factor is **not** specified, PBTools will perform the analysis as if the entire data came from only one site.

'Perform Multiple Environment Analysis' Option

If this option is selected, the *Environment* factor must be specified.

Environment

This is a required field if the 'Perform Multiple Environment Analysis' option is selected. Moreover, the number of its levels must be at least two.

Tester

This is a required field.

F2

This is a required field.

Block

This is a required field if the selected experimental design is Randomized Complete Block or Alpha-Lattice.

Replicate

This is a required field if the selected experimental design is Completely Randomized Design, Alpha-Lattice or Row-Column.

Row

This is a required field if the selected experimental design is Row-Column.

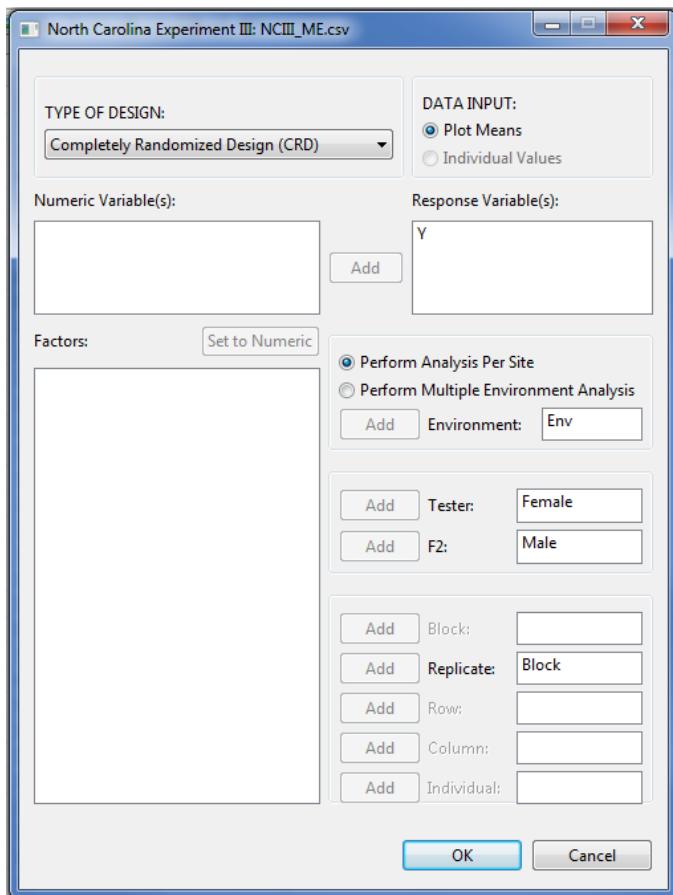
Column

This is a required field if the selected experimental design is Row-Column.

Individual

This is a required field if the selected data input is Individual Values.

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



- Click **OK**.
- Sample output of the analysis (only results from *Env = A*) is shown below:

DATA FILE: E:/PBTools/Projects/SampleProject/Data/NCIII_ME.csv

DESIGN: NORTH CAROLINA EXPERIMENT III IN RCB

```
-----  
RESPONSE VARIABLE: Y  
-----  
-----  
ANALYSIS FOR: Env = A  
-----  
  
DATA SUMMARY:  
Factors No of Levels Levels  
Env 1 A  
Male 16 1 10 11 ... 9  
Female 2 1 2  
Block 2 1 2  
Number of observations read: 64  
Number of observations used: 64
```

Analysis of Variance Table

ANOVA TABLE FOR THE EXPERIMENT:

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Block	1	3.8025	3.8025	13.13	0.0010
Female	1	0.9025	0.9025	3.12	0.0874
Male	15	6.8294	0.4553	1.57	0.1400
Female:Male	15	5.1925	0.3462	1.20	0.3255
Residuals	31	8.9775	0.2896		

REMARK: Raw dataset is balanced.

Estimated Variance Components of Random Effects

LINEAR MIXED MODEL FIT BY RESTRICTED MAXIMUM LIKELIHOOD:

Formula: Y ~ 1 + Female + (1|Block) + (1|Male) + (1|Female:Male)

AIC	BIC	logLik	deviance	REMLdev
130.0835	143.0368	-59.04175	115.1131	118.0835

Random Effects:

Groups	Variance	Std. Deviation
Female:Male	0.0283	0.1682
Male	0.0273	0.1652
Block	0.1098	0.3313
Residual	0.2896	0.5381

Genetic Variance Components

ESTIMATES OF GENETIC VARIANCE COMPONENTS:

Estimate

VA	0.109124
VD	0.056570
h2-narrow sense	0.239680
H2-broad sense	0.363930
h2-family	0.158537
Dominance Ratio	1.018235

Triple Test Cross

This design involves taking a number of F_2 individuals from a cross between two inbred lines (P_1 and P_2) and crossing each back to these same two parental lines and F_1 . The two parental inbreds and F_1 thus act as testers against which the F_2 are assessed.

The steps to perform such analysis are listed below:

- Import *TTC_ME* file from package. Double-click the file to view it in the Data Viewer. The example file contains data for an experiment conducted for crosses derived from a Triple Test Cross design with 10 F_2 lines labeled as *Male* and three testers labeled as *Female* using Randomized Complete Block (RCB) field design with three blocks (1, 2 and 3) in two environments (*A* and *B*) and one trait, *Y*.
- Choose **Analysis | Mating Designs | Triple Test Cross | Triple Test Cross (no parents)**... from the menu bar.
- Opening the data for the first time, *Block*, *Male* fields are regarded by R as numerical variables, they need to be changed as factors. Choose these variables and click on the **Set to Factor** button.
- Specify the required fields and appropriate options for the analysis.

Type of Design

There are four available experimental designs, namely: Completely Randomized Design (CRD), Randomized Complete Block Design (RCB), Alpha-Lattice and Row-Column Design.

Data Input

The input data for the analysis may be plot-means or observations of individual plants (*not yet implemented*).

Response Variable(s)

This is a required field. This list may contain one or more numeric variables.

'Perform Analysis Per Site' Option

If this option is selected and the Environment factor is specified, the analysis will be performed for each level of the Environment factor.

If this option is selected but the Environment factor is **not** specified, PBTools will perform the analysis as if the entire data came from only one site.

'Perform Multiple Environment Analysis' Option

If this option is selected, the *Environment* factor must be specified.

Environment

This is a required field if the 'Perform Multiple Environment Analysis' option is selected. Moreover, the number of its levels must be at least two.

Tester

This is a required field.

Levels of Tester

Once the Tester factor is specified, its levels appear on the 'Levels of Tester' text box. The user should specify which among these levels correspond to P₁, P₂ and F₁.

P1

This is a required field. This corresponds to the level of the Tester factor that represents P₁.

P2

This is a required field. This corresponds to the level of the Tester factor that represents P₂.

F1

This is a required field. This corresponds to the level of the Tester factor that represents F₁.

F2

This is a required field.

Block

This is a required field if the selected experimental design is Randomized Complete Block or Alpha-Lattice.

Replicate

This is a required field if the selected experimental design is Completely Randomized Design, Alpha-Lattice or Row-Column.

Row

This is a required field if the selected experimental design is Row-Column.

Column

This is a required field if the selected experimental design is Row-Column.

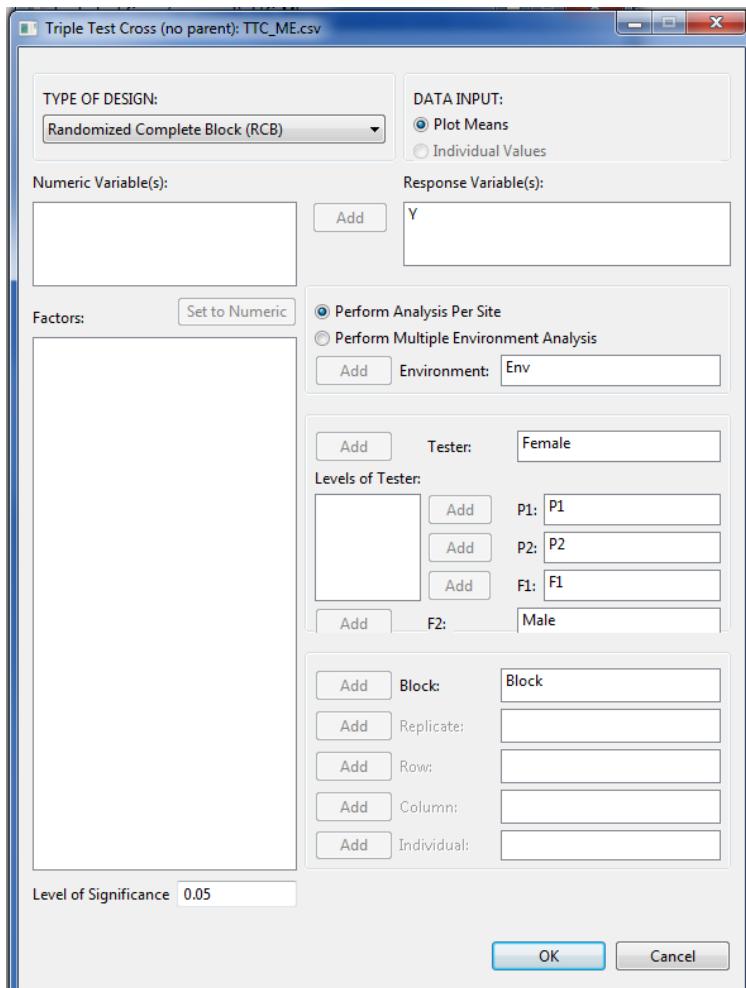
Individual

This is a required field if the selected data input is Individual Values.

Level of Significance

Its default value is 0.05. The user can change this value by specifying a numeric value from zero to 1.

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



- Click **OK**.

- Sample output of the analysis (only results from *Env = A*) is shown below:

Data Summary

```
DATA FILE: E:/PBTools/Projects/SampleProject/Data/TTC_ME.csv
```

```
DESIGN: TRIPLE TEST CROSS (NO PARENTS) IN RCB
```

```
-----  
RESPONSE VARIABLE: Y  
-----  
-----  
ANALYSIS FOR: Env = A  
-----
```

```
DATA SUMMARY:
```

Factors	No of Levels	Levels
Env	1	A
Block	3	1 2 3
Female	3	F1 P1 P2
Male	10	1 10 2 ... 9

```
Number of observations read: 90
```

```
Number of observations used: 90
```

Analysis of Variance Table

```
ANOVA TABLE FOR THE EXPERIMENT:
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Block	2	1.8842	0.9421	12.05	0.0000
Female	2	1.0709	0.5354	6.85	0.0021
Male	9	9.4432	1.0492	13.42	0.0000
Female:Male	18	1.9891	0.1105	1.41	0.1604
Residuals	58	4.5358	0.0782		

```
-----  
REMARK: Raw dataset is balanced.
```

Testing for the Differences Among Crosses

```
TESTING FOR THE SIGNIFICANCE OF CROSS EFFECT: (Crosses = Female:Male)
```

```
Model: Y ~ Crosses + (1|Block)
```

```
Analysis of Variance Table with Satterthwaite Denominator Df  
Df Sum Sq Mean Sq F value Denom Pr(>F)  
Crosses 29 12.5032 0.4311 5.5132 57.9793 0.0000
```

Testing for Epistasis

ANOVA FOR TESTING EPISTASIS:

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
AxA	1	0.0569	0.0569	0.78	0.3891
AxD and DxD	9	0.8142	0.0905	1.24	0.3328
Total	10	0.8711	0.0871	1.19	0.3572
Residuals	18	1.3149	0.0730		

REMARK: Raw dataset is balanced.

ANOVA TABLE:

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
s	9	9.4432	1.0492	16.25	0.0000
e(s)	18	1.1624	0.0646		
d	9	0.8227	0.0914	1.21	0.3476
e(d)	18	1.3553	0.0753		

REMARK: Raw dataset is balanced.

Genetic Variance Components and Heritability

ESTIMATES OF GENETIC VARIANCE COMPONENTS:

	Estimate	SE
VA	0.437630	0.039622
VD	0.005370	0.000232
VE	0.064580	
VP	0.507580	
Broad Sense Heritability	0.872768	0.004519
Narrow Sense Heritability	0.862188	0.005221
Dominance Ratio	0.156662	

Diallel Analysis (Griffing Method)

Method 1

In this design, all parents are crossed to make hybrids in all possible combinations. Parents and reciprocal crosses are involved along with F₁.

The steps to perform such analysis are listed below:

- Import *Diallel_M1* file from package. Double-click the file to view it in the Data Viewer. The example file contains data for an experiment conducted for crosses derived from full diallel design with seven parents using Randomized Complete Block (RCB) design with three blocks (1, 2 and 3) in two environments (*Normal* and *Saline*) and three traits, *Plant_height*, *Grain_yield* and *Th_grain_weight*.
- Choose **Analysis | Mating Designs | Diallel Analysis | Griffing Method I...** from the menu bar.
- Opening the data for the first time, *Block*, *P1* and *P2* fields are regarded by R as numerical variables. To set these as factors, choose these variables and click on the **Set to Factor** button.
- Specify the required fields and appropriate options for the analysis.

Type of Design

There are four available experimental designs, namely: Completely Randomized Design (CRD), Randomized Complete Block Design (RCB), Alpha-Lattice and Row-Column Design.

'Cross' Option

This is selected if the parental lines are from random-mating population (outcrossing species).

'Self' Option

This is selected if the parental lines are inbreds.

Data Input

The input data for the analysis may be plot-means or observations of individual plants (*not yet implemented*).

Response Variable(s)

This is a required field. This list may contain one or more numeric variables.

'Perform Analysis Per Site' Option

If this option is selected and the Environment factor is specified, the analysis will be performed for each level of the Environment factor.

If this option is selected but the Environment factor is **not** specified, PBTools will perform the analysis as if the entire data came from only one site.

'Perform Multiple Environment Analysis' Option

If this option is selected, the *Environment* factor must be specified.

Environment

This is a required field if the 'Perform Multiple Environment Analysis' option is selected. Moreover, the number of its levels must be at least two.

P1

This is a required field.

P2

This is a required field.

Block

This is a required field if the selected experimental design is Randomized Complete Block or Alpha-Lattice.

Replicate

This is a required field if the selected experimental design is Completely Randomized Design, Alpha-Lattice or Row-Column.

Row

This is a required field if the selected experimental design is Row-Column.

Column

This is a required field if the selected experimental design is Row-Column.

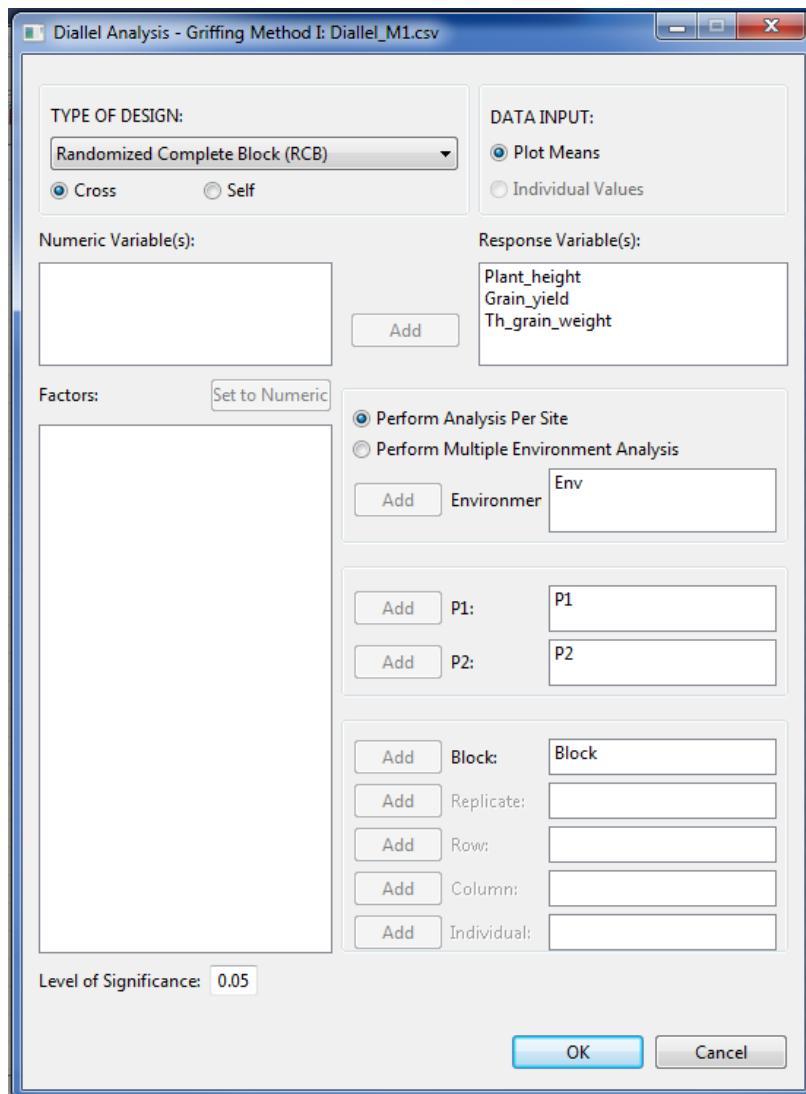
Individual

This is a required field if the selected data input is Individual Values.

Level of Significance

Its default value is 0.05. The user can change this value by specifying a numeric value from zero to 1.

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



- Click **OK**.
- Sample output of the analysis (only results from *response variable* = *Plant_height* and *Env* = *Normal*) is shown below:

DATA FILE: E:/PBTools/Projects/SampleProject/Data/Diallel_M1.csv

DIALLEL ANALYSIS: GRIFFING METHOD I IN RCB (CROSS)

```
-----
RESPONSE VARIABLE: Plant_height
-----
ANALYSIS FOR: Env  =  Normal
-----
```

DATA SUMMARY:

Factors	No of Levels	Levels
Env	1	Normal
P1	7	1 2 3 4 5 6 7
P2	7	1 2 3 4 5 6 7
Block	3	1 2 3

Number of observations read: 147

Number of observations used: 147

Analysis of Variance Table

ANOVA TABLE FOR THE EXPERIMENT:

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Block	2	3026.5310	1513.2660	19.74	0.0000
P1	6	32496.7700	5416.1280	70.67	0.0000
P2	6	21855.2900	3642.5480	47.53	0.0000
P1:P2	36	22865.0000	635.1388	8.29	0.0000
Residuals	96	7357.5760	76.6414		

REMARK: Raw dataset is balanced.

Testing for the Differences among Crosses

TESTING FOR THE SIGNIFICANCE OF CROSS EFFECT: (Crosses = P1:P2)

Model: Plant_height ~ Crosses + (1|Block)

Analysis of Variance Table with Satterthwaite Denominator Df
Df Sum Sq Mean Sq F value Denom Pr(>F)
Crosses 48 77217.05 1608.689 20.9898 95.9989 0.0000

MATRIX OF MEANS:

	P2=1	P2=2	P2=3	P2=4	P2=5	P2=6	P2=7
P1=1	142.9000	148.3333	163.9000	152.9000	142.3667	160.6667	191.3333
P1=2	144.7667	129.6667	142.9000	143.9000	131.5667	143.5333	186.6667
P1=3	167.5667	149.0333	131.5667	163.5667	136.9000	166.4333	189.7667
P1=4	154.1000	156.1000	147.7667	159.3333	149.8000	164.8000	200.2333
P1=5	142.1000	133.8000	138.9000	149.6667	122.4333	138.9000	175.7667
P1=6	173.1000	146.2000	167.7667	184.3333	156.7667	146.1333	195.5667
P1=7	195.7667	194.5667	193.8000	213.4667	169.1000	218.0333	157.5333

REMARK: Raw dataset is balanced.

Combining Ability Analysis

ANALYSIS OF VARIANCE:

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
GCA	6	17675.6700	2945.9450	9.05	0.0000
SCA	21	6983.5130	332.5482	13.02	0.0000
Reciprocal	21	1079.8370	51.4208	2.01	0.0118
Error	96	2452.5120	25.5470		
<hr/>					

NOTE: MS* = 325.408666 Error used for GCA MS with df = 1920.5

GENERAL COMBINING ABILITY EFFECTS (diagonal), SPECIFIC COMBINING ABILITY EFFECTS (above diagonal) AND RECIPROCAL EFFECTS (below diagonal):

	P2=1	P2=2	P2=3	P2=4	P2=5	P2=6	P2=7
P1=1	-1.9718	-0.0997	11.1741	-8.7639	0.5980	3.9718	7.0122
P1=2	1.7833	-12.1146	1.5503	-2.1211	1.1908	-7.9020	14.2218
P1=3	-1.8333	-3.0667	-4.2051	-4.3639	-1.5020	6.4218	7.4789
P1=4	-0.6000	-6.1000	7.9000	3.4997	2.6265	6.1837	14.8408
P1=5	0.1333	-1.1167	-1.0000	0.0667	-17.1289	0.0789	1.0527
P1=6	-6.2167	-1.3333	-0.6667	-9.7667	-8.9333	4.1473	14.1432
P1=7	-2.2167	-3.9500	-2.0167	-6.6167	3.3333	-11.2333	27.7735

ESTIMATES OF VARIANCE COMPONENTS:

	Estimate	Std. Error
GCA	187.1811	121.6995
SCA	174.9193	58.5110
Reciprocal	12.9369	8.1458
Error	25.5470	3.6874

ESTIMATES OF GENETIC VARIANCE COMPONENTS:

	Estimate
VA	748.724542
VD	699.677221
h2-narrow sense	0.507972
H2-broad sense	0.982668
Dominance Ratio	1.367108

TABLE OF STANDARD ERRORS AND LSDs:

	Std. Error	LSD
Gi	1.2506	
Sii	4.3323	
Sij	3.1057	
Rij	3.5740	
Gi-Gj	1.9104	3.7921
Sii-Sjj	6.0412	11.9916

Sii-Sij	5.8882	11.6880
Sii-Sjk	5.2318	10.3851
Sij-Sik	4.6795	9.2887
Sij-Skl	4.2718	8.4794
Rij-Rkl	5.0544	10.0329

Method 2

If no reciprocal differences exist, there is no need to make reciprocal crosses. The parents and one set of F_1 's can be analyzed.

The steps to perform such analysis are listed below:

- Import *Diallel_M2* file from package. Double-click the file to view it in the Data Viewer. The example file contains data for an experiment conducted for crosses derived from partial diallel design (parents and one set of F_1 's) with seven parents using Randomized Complete Block (RCB) design with three blocks (1, 2 and 3) in two environments (*Normal* and *Saline*) and three traits, *Plant_height*, *Grain_yield* and *Th_grain_weight*.
- Choose **Analysis | Mating Designs | Diallel Analysis | Griffing Method II...** from menu bar.
- Opening the data for the first time, *Block*, *P1* and *P2* fields are regarded by R as numerical variables. To set these as factors, choose these variables and click on the **Set to Factor** button.
- Specify the required fields and appropriate options for the analysis.

Type of Design

There are four available experimental designs, namely: Completely Randomized Design (CRD), Randomized Complete Block Design (RCB), Alpha-Lattice and Row-Column Design.

'Cross' Option

This is selected if the parental lines are from random-mating population (outcrossing species).

'Self' Option

This is selected if the parental lines are inbreds.

Data Input

The input data for the analysis may be plot-means or observations of individual plants (*not yet implemented*).

Response Variable(s)

This is a required field. This list may contain one or more numeric variables.

'Perform Analysis Per Site' Option

If this option is selected and the Environment factor is specified, the analysis will be performed for each level of the Environment factor.

If this option is selected but the Environment factor is **not** specified, PBTools will perform the analysis as if the entire data came from only one site.

'Perform Multiple Environment Analysis' Option

If this option is selected, the *Environment* factor must be specified.

Environment

This is a required field if the 'Perform Multiple Environment Analysis' option is selected. Moreover, the number of its levels must be at least two.

P1

This is a required field.

P2

This is a required field.

Block

This is a required field if the selected experimental design is Randomized Complete Block or Alpha-Lattice.

Replicate

This is a required field if the selected experimental design is Completely Randomized Design, Alpha-Lattice or Row-Column.

Row

This is a required field if the selected experimental design is Row-Column.

Column

This is a required field if the selected experimental design is Row-Column.

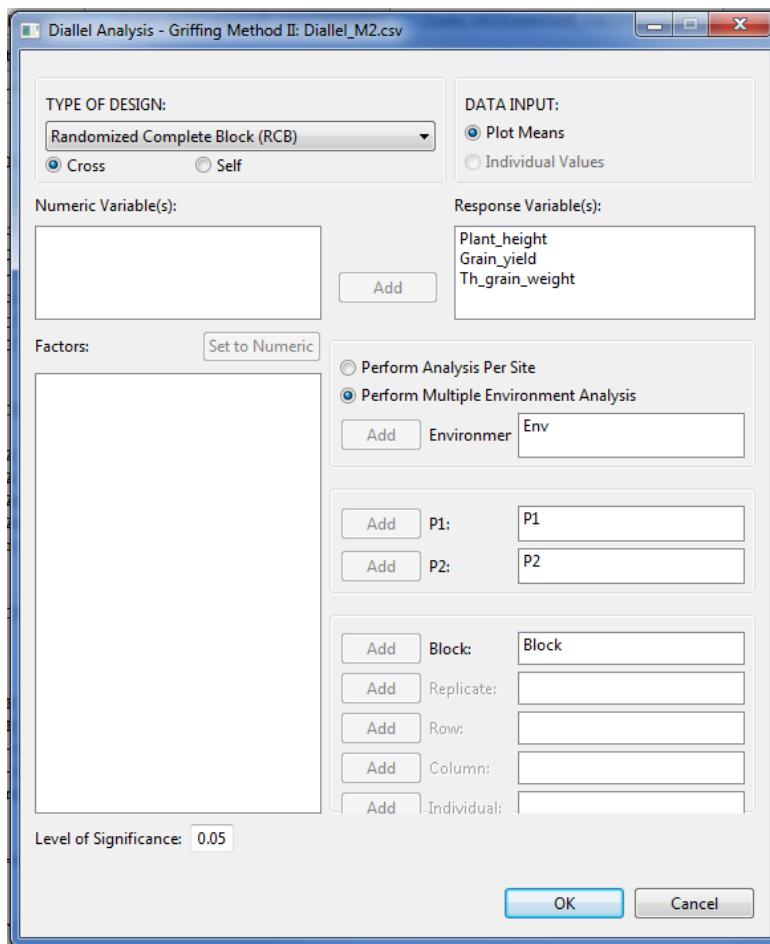
Individual

This is a required field if the selected data input is Individual Values.

Level of Significance

Its default value is 0.05. The user can change this value by specifying a numeric value from zero to 1.

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



- Click **OK**.
- Sample output of the analysis (only results from *response variable = Plant_height* and *Env = Normal*) is shown below:

DATA FILE: E:/PBTools/Projects/SampleProject/Data/Diallel_M2.csv

DIALLEL ANALYSIS: GRIFFING METHOD II IN RCB (CROSS)

RESPONSE VARIABLE: Plant_height

ANALYSIS FOR: Env = Normal

DATA SUMMARY:

Factors	No of Levels	Levels
P1	7	1 2 3 4 5 6 7
P2	7	1 2 3 4 5 6 7
Block	3	1 2 3
Env	1	Normal

Number of observations read: 84
Number of observations used: 84

ANOVA TABLE FOR THE EXPERIMENT:

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Block	2	852.4474	426.2237	9.65	0.0003
P1:P2	27	36854.8400	1364.9940	30.92	0.0000
Residuals	54	2383.9790	44.1478		

REMARK: Raw dataset is balanced.

Testing for the Differences among Crosses

TESTING FOR THE SIGNIFICANCE OF CROSS EFFECT: (Crosses = P1:P2)

Model: Plant_height ~ Crosses + (1|Block)

Analysis of Variance Table with Satterthwaite Denominator Df

Df	Sum Sq	Mean Sq	F value	Denom	Pr(>F)
Crosses	27	36854.84	1364.994	30.9188	53.9992 0.0000

MATRIX OF MEANS:

	1	2	3	4	5	6	7
1	142.9000	148.3333	163.9000	152.9000	142.3667	160.6667	191.3333
2		129.6667	142.9000	143.9000	131.5667	143.5333	186.6667
3			131.5667	163.5667	136.9000	166.4333	189.7667
4				159.3333	149.8000	164.8000	200.2333
5					122.4333	138.9000	175.7667
6						146.1333	195.5667
7							157.5333

REMARK: Raw dataset is balanced.

Combining Ability Analysis

ANALYSIS OF VARIANCE:

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
GCA	6	7784.3680	1297.3950	6.05	0.0008
SCA	21	4500.5790	214.3133	14.56	0.0000
Error	54	794.6640	14.7160		

GENERAL COMBINING ABILITY EFFECTS (diagonal), SPECIFIC COMBINING ABILITY EFFECTS (above diagonal) AND RECIPROCAL EFFECTS (below diagonal):

	1	2	3	4	5	6	7
1	-0.6608	3.1454	10.8935	-7.5806	1.1861	3.7083	13.0157
2		-10.5571	-0.2102	-6.6843	0.2824	-3.5287	18.2454
3			-2.7386	5.1639	-2.2028	11.5528	13.5269
4				4.7354	3.2231	2.4454	16.5194
5					-14.5646	-4.1546	11.3528
6						1.2132	15.3750
7							22.5725

ESTIMATES OF VARIANCE COMPONENTS:

	Estimate	Std. Error
GCA	120.3424	217.0737
SCA	199.5973	66.1426
Error	14.7160	2.8321

ESTIMATES OF GENETIC VARIANCE COMPONENTS:

	Estimate
VA	481.369471
VD	798.389175
h ² -narrow sense	0.371865
H ² -broad sense	0.988632
Dominance Ratio	1.821307

TABLE OF STANDARD ERRORS AND LSDs:

	Std. Error	LSD
Gi	1.1839	
Sii	2.9299	
Sij	3.4430	
Gi-Gj	1.8084	3.6256
Sii-Sjj	4.0437	8.1070
Sij-Sik	5.1149	10.2547
Sij-Skl	4.7845	9.5924

- Suppose the user opted to perform Multiple Environment Analysis, sample output of the analysis (only results from *response variable = Plant_height*) is shown below:

DATA FILE: E:/PBTools/Projects/SampleProject/Data/Diallel_M2.csv

MULTIPLE ENVIRONMENT ANALYSIS

DIALLEL ANALYSIS: GRIFFING METHOD II IN RCB (CROSS)

RESPONSE VARIABLE: Plant_height

DATA SUMMARY:

Factors	No of Levels	Levels
P1	7	1 2 3 4 5 6 7
P2	7	1 2 3 4 5 6 7
Env	2	Normal Saline
Block	3	1 2 3

Number of observations read: 168

Number of observations used: 168

Testing the Significance of Genotypic Differences

ANOVA TABLE: (Crosses = P1:P2)

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Env	1	17111.4300	17111.4300	28.18	0.0061
Block (Env)	4	2429.2920	607.3231	14.44	0.0000
Crosses	27	80041.5800	2964.5030	31.42	0.0000
Crosses x Env	27	2547.4580	94.3503	2.24	0.0018
Residuals	108	4543.8540	42.0727		

REMARK: Raw dataset is balanced.

Combining Ability Analysis

ANOVA TABLE:

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
GCA	6	54367.6700	9061.2780	51.14	0.0001
SCA	21	25673.9100	1222.5670	17.30	0.0000
GCAxE	6	1063.1420	177.1904	4.21	0.0008
SCAxE	21	1484.3160	70.6817	1.68	0.0451
Residuals	108	4543.8540	42.0727		

REMARK: Raw dataset is balanced.

MATRIX OF MEANS:

	1	2	3	4	5	6	7
1	131.0000	133.8333	153.5500	140.7333	128.9000	154.4333	182.2833
2		116.8333	130.5500	133.8500	122.7167	129.0500	175.9000
3			122.0000	154.5000	131.2167	153.2167	177.7833
4				137.3333	138.5667	155.7833	195.2333
5					111.8833	132.5667	166.3333
6						143.0167	188.6167
7							155.1000

REMARK: Raw dataset is balanced.

GENERAL COMBINING ABILITY EFFECTS, SPECIFIC COMBINING ABILITY EFFECTS (above diagonal):

	1	2	3	4	5	6	7
1		1.4884	11.7329	-6.4745	-1.7227	6.5181	12.5181
2			-0.5819	-2.6727	2.7792	-8.1801	16.8199
3				8.5051	1.8069	6.5144	9.2310
4					3.7662	3.6903	21.2903
5						-2.9412	8.9755
6							13.9662
7							
GCA	-1.6418	-12.3270	-2.8548	2.5360	-14.0492	3.2434	25.0934

TABLE OF STANDARD ERRORS AND LSDs:

	Std. Error	LSD
Gi	0.8172	
Sii	2.3767	
Sij	2.0225	
Gi-Gj	1.2483	2.4743
Sii-Sjj	2.7913	5.5328
Sij-Sik	3.5307	6.9985
Sij-Skl	3.3027	6.5465

ESTIMATES OF VARIANCE COMPONENTS:

	Estimate
GCA	143.1889
SCA	191.9809
GCAxE	3.9448
SCAxE	9.5363
Residuals	42.0727

ESTIMATES OF GENETIC VARIANCE COMPONENTS:

	Estimate
VA	572.755708
VAXE	15.779068
VD	767.923774
VDxE	38.145306
h2-narrow sense	0.398667
H2-broad sense	0.933181
Dominance Ratio	1.637530

Method 3

In this design, both F1's and reciprocal crosses are the only ones being considered.

The steps to perform such analysis are listed below:

- Import *Diallel_M3* file from package. Double-click the file to view it in the Data Viewer. The example file contains data for an experiment conducted for crosses derived from partial diallel design (F1's and reciprocal crosses) with seven parents using Randomized Complete Block (RCB) design with three blocks (1, 2 and 3) in two environments (*Normal* and *Saline*) and three traits, *Plant_height*, *Grain_yield* and *Th_grain_weight*.
- Choose **Analysis | Mating Designs | Diallel Analysis | Griffing Method III...** from the menu bar.
- Opening the data for the first time, *Block*, *P1* and *P2* fields are regarded by R as numerical variables, they need to be changed as factors. Choose these variables and click on the **Set to Factor** button.
- Specify the required fields and appropriate options for the analysis.

Type of Design

There are four available experimental designs, namely: Completely Randomized Design (CRD), Randomized Complete Block Design (RCB), Alpha-Lattice and Row-Column Design.

'Cross' Option

This is selected if the parental lines are from random-mating population (outcrossing species).

'Self' Option

This is selected if the parental lines are inbreds.

Data Input

The input data for the analysis may be plot-means or observations of individual plants (*not yet implemented*).

Response Variable(s)

This is a required field. This list may contain one or more numeric variables.

'Perform Analysis Per Site' Option

If this option is selected and the Environment factor is specified, the analysis will be performed for each level of the Environment factor.

If this option is selected but the Environment factor is **not** specified, PBTools will perform the analysis as if the entire data came from only one site.

'Perform Multiple Environment Analysis' Option

If this option is selected, the *Environment* factor must be specified.

Environment

This is a required field if the 'Perform Multiple Environment Analysis' option is selected. Moreover, the number of its levels must be at least two.

P1

This is a required field.

P2

This is a required field.

Block

This is a required field if the selected experimental design is Randomized Complete Block or Alpha-Lattice.

Replicate

This is a required field if the selected experimental design is Completely Randomized Design, Alpha-Lattice or Row-Column.

Row

This is a required field if the selected experimental design is Row-Column.

Column

This is a required field if the selected experimental design is Row-Column.

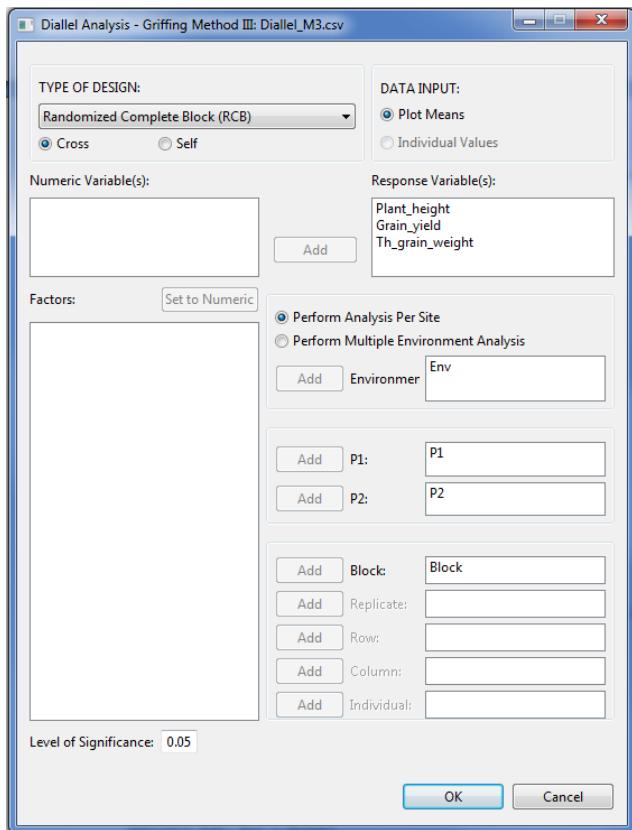
Individual

This is a required field if the selected data input is Individual Values.

Level of Significance

Its default value is 0.05. The user can change this value by specifying a numeric value from zero to 1.

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



- Click **OK**.
- Sample output of the analysis (only results from *response variable = Plant_height* and *Env = Normal*) is shown below:

DATA FILE: E:/PBTools/Projects/SampleProject/Data/Diallel_M3.csv

DIALLEL ANALYSIS: GRIFFING METHOD III IN RCB (CROSS)

RESPONSE VARIABLE: Plant_height

ANALYSIS FOR: Env = Normal

DATA SUMMARY:

Factors	No of Levels	Levels
Env	1	Normal
P1	7	1 2 3 4 5 6 7
P2	7	1 2 3 4 5 6 7
Block	3	1 2 3

Number of observations read: 126

Number of observations used: 126

ANOVA TABLE FOR THE EXPERIMENT:

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Block	2	3024.4780	1512.2390	18.44	0.0000
P1:P2	41	64423.4000	1571.3030	19.16	0.0000
Residuals	82	6723.2290	81.9906		

REMARK: Raw dataset is balanced.

Testing for the Differences among Crosses

TESTING FOR THE SIGNIFICANCE OF CROSS EFFECT: (Crosses = P1:P2)

Model: Plant_height ~ Crosses + (1|Block)

Analysis of Variance Table with Satterthwaite Denominator Df

Df	Sum Sq	Mean Sq	F value	Denom	Pr(>F)
Crosses	41	64423.4	1571.303	19.1644	81.9991 0.0000

MATRIX OF MEANS:

	P2=1	P2=2	P2=3	P2=4	P2=5	P2=6	P2=7
P1=1		148.3333	163.9000	152.9000	142.3667	160.6667	191.3333
P1=2	144.7667		142.9000	143.9000	131.5667	143.5333	186.6667
P1=3	167.5667	149.0333		163.5667	136.9000	166.4333	189.7667
P1=4	154.1000	156.1000	147.7667		149.8000	164.8000	200.2333
P1=5	142.1000	133.8000	138.9000	149.6667		138.9000	175.7667
P1=6	173.1000	146.2000	167.7667	184.3333	156.7667		195.5667
P1=7	195.7667	194.5667	193.8000	213.4667	169.1000	218.0333	

REMARK: Raw dataset is balanced.

Combining Ability Analysis

ANALYSIS OF VARIANCE:

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
GCA	6	19425.2300	3237.5380	46.76	0.0000
SCA	14	969.4004	69.2429	2.53	0.0047
Reciprocal	21	1079.8370	51.4208	1.88	0.0231
Error	82	2241.0870	27.3303		

GENERAL COMBINING ABILITY EFFECTS (diagonal), SPECIFIC COMBINING ABILITY EFFECTS (above diagonal) AND RECIPROCAL EFFECTS (below diagonal):

P2=1	P2=2	P2=3	P2=4	P2=5	P2=6	P2=7	
P1=1	-3.0671	0.2733	8.7633	-8.7033	1.5300	1.1333	-2.9967
P1=2	1.7833	-14.6205	0.5500	-0.6500	3.5333	-9.3300	5.6233
P1=3	-1.8333	-3.0667	-3.9271	-5.6767	-1.9433	2.2100	-3.9033
P1=4	-0.6000	-6.1000	7.9000	1.3062	4.6567	4.4433	5.9300
P1=5	0.1333	-1.1167	-1.0000	0.0667	-20.1938	-0.7900	-6.9867
P1=6	-6.2167	-1.3333	-0.6667	-9.7667	-8.9333	4.8529	2.3333
P1=7	-2.2167	-3.9500	-2.0167	-6.6167	3.3333	-11.2333	35.6495

ESTIMATES OF VARIANCE COMPONENTS:

	Estimate	Std. Error
GCA	316.8295	186.9377
SCA	20.9563	13.2586
Reciprocal	12.0452	8.2164
Error	27.3303	4.2683

ESTIMATES OF GENETIC VARIANCE COMPONENTS:

	Estimate
VA	1267.318169
VD	83.825111
h ² -narrow sense	0.919363
H ² -broad sense	0.980173
Dominance Ratio	0.363713

TABLE OF STANDARD ERRORS AND LSDs:

	Std. Error	LSD
Gi	1.5306	
Sii	3.0183	
Rij	3.6966	
Gi-Gj	2.3380	4.6510
Sij-Sik	4.6759	9.3019
Sij-Skl	4.0495	8.0557

Method 4

In this design, only one set of F1's are considered.

The steps to perform such analysis are listed below:

- Import *Diallel_M4* file from package. Double-click the file to view it in the Data Viewer. The example file contains data for an experiment conducted for crosses derived from partial diallel design (one set of F₁'s) with seven parents using Randomized Complete Block (RCB) design with three blocks (1, 2 and 3) in two environments (*Normal* and *Saline*) and three traits, *Plant_height*, *Grain_yield* and *Th_grain_weight*.
- Choose **Analysis | Mating Designs | Diallel Analysis | Griffing Method IV...** from the menu bar.

- Opening the data for the first time, *Block*, *P1* and *P2* fields are regarded by R as numerical variables, they need to be changed as factors. Choose these variables and click on the **Set to Factor** button.
- Specify the required fields and appropriate options for the analysis.

Type of Design

There are four available experimental designs, namely: Completely Randomized Design (CRD), Randomized Complete Block Design (RCB), Alpha-Lattice and Row-Column Design.

'Cross' Option

This is selected if the parental lines are from random-mating population (outcrossing species).

'Self' Option

This is selected if the parental lines are inbreds.

Data Input

The input data for the analysis may be plot-means or observations of individual plants (*not yet implemented*).

Response Variable(s)

This is a required field. This list may contain one or more numeric variables.

'Perform Analysis Per Site' Option

If this option is selected and the Environment factor is specified, the analysis will be performed for each level of the Environment factor.

If this option is selected but the Environment factor is **not** specified, PBTools will perform the analysis as if the entire data came from only one site.

'Perform Multiple Environment Analysis' Option

If this option is selected, the *Environment* factor must be specified.

Environment

This is a required field if the 'Perform Multiple Environment Analysis' option is selected. Moreover, the number of its levels must be at least two.

P1

This is a required field.

P2

This is a required field.

Block

This is a required field if the selected experimental design is Randomized Complete Block or Alpha-Lattice.

Replicate

This is a required field if the selected experimental design is Completely Randomized Design, Alpha-Lattice or Row-Column.

Row

This is a required field if the selected experimental design is Row-Column.

Column

This is a required field if the selected experimental design is Row-Column.

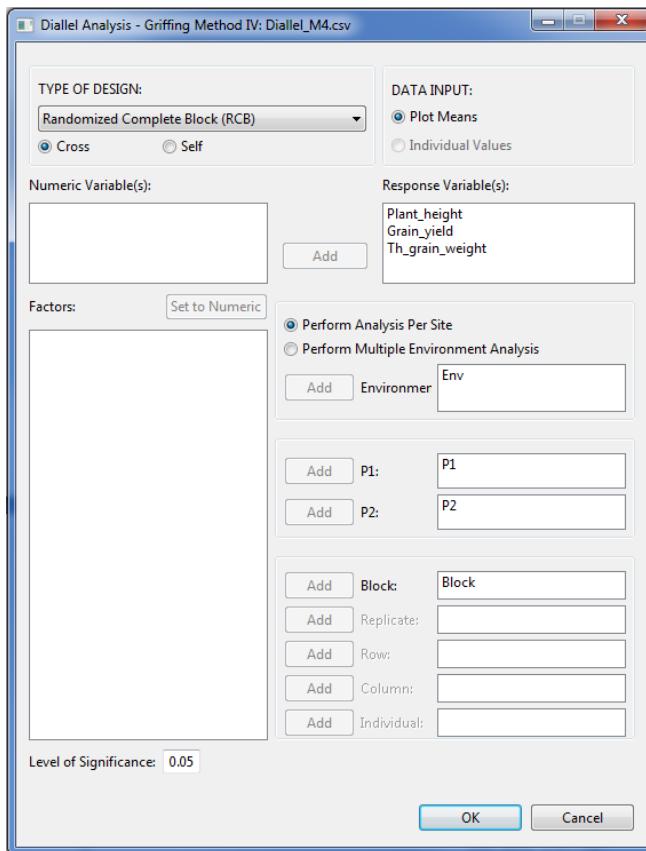
Individual

This is a required field if the selected data input is Individual Values.

Level of Significance

Its default value is 0.05. The user can change this value by specifying a numeric value from zero to 1.

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



- Click **OK**.
- Sample output of the analysis (only results from *response variable* = *Plant_height* and *Env* = *Normal*) is shown below:

DATA FILE: E:/PBTools/Projects/SampleProject/Data/Diallel_M4.csv

DIALLEL ANALYSIS: GRIFFING METHOD IV IN RCB (CROSS)

RESPONSE VARIABLE: Plant_height

ANALYSIS FOR: Env = Normal

DATA SUMMARY:

Factors	No of Levels	Levels
Env	1	Normal
P1	6	1 2 3 4 5 6
P2	6	2 3 4 5 6 7
Block	3	1 2 3

Number of observations read: 63
Number of observations used: 63

ANOVA TABLE FOR THE EXPERIMENT:

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Block	2	869.0552	434.5276	10.04	0.0003
P1:P2	20	26919.8900	1345.9950	31.10	0.0000
Residuals	40	1730.9710	43.2743		

REMARK: Raw dataset is balanced.

Testing for the Differences Among Crosses

TESTING FOR THE SIGNIFICANCE OF CROSS EFFECT: (Crosses = P1:P2)

Model: Plant_height ~ Crosses + (1|Block)

Analysis of Variance Table with Satterthwaite Denominator Df

	Df	Sum Sq	Mean Sq	F value	Denom	Pr(>F)
Crosses	20	26919.89	1345.995	31.1038	39.9994	0.0000

MATRIX OF MEANS:

	1	2	3	4	5	6	7
1	148.3333	163.9000	152.9000	142.3667	160.6667	191.3333	
2		142.9000	143.9000	131.5667	143.5333	186.6667	
3			163.5667	136.9000	166.4333	189.7667	
4				149.8000	164.8000	200.2333	
5					138.9000	175.7667	
6						195.5667	
7							

REMARK: Raw dataset is balanced.

Combining Ability Analysis

ANALYSIS OF VARIANCE:

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
GCA	6	8630.0020	1438.3340	58.66	0.0000
SCA	14	343.2947	24.5210	1.70	0.0945
Error	40	576.9867	14.4247		

GENERAL COMBINING ABILITY EFFECTS (diagonal), SPECIFIC COMBINING ABILITY EFFECTS (above diagonal) AND RECIPROCAL EFFECTS (below diagonal):

1	2	3	4	5	6	7	
1	-1.8029	3.0400	5.2933	-8.0533	1.3933	0.7733	-2.4467
2		-14.3229	-3.1867	-4.5333	3.1133	-3.8400	5.4067
3			-1.0095	1.8200	-4.8667	5.7467	-4.8067
4				1.3371	5.6867	1.7667	3.3133
5					-18.6429	-4.1533	-1.1733
6						0.2771	-0.2933
7							34.1638

ESTIMATES OF VARIANCE COMPONENTS:

	Estimate	Std. Error
GCA	282.7625	166.0948
SCA	10.0964	9.8133
Error	14.4247	0.8493

ESTIMATES OF GENETIC VARIANCE COMPONENTS:

	Estimate
VA	1131.050116
VD	40.385524
h2-narrow sense	0.953780
H2-broad sense	0.987836
Dominance Ratio	0.267231

TABLE OF STANDARD ERRORS AND LSDs:

	Std. Error	LSD
Gi	1.5725	
Sii	3.1010	
Gi-Gj	2.4021	4.8547
Sij-Sik	4.8041	9.7095
Sij-Skl	4.1605	8.4086

10. Generation Mean Analysis

In this analysis, *PBTools* uses the weighted regression approach. Two full models are fitted to the data. The first one is “mean = 0 + m + a + d + aa + ad” and the other one is “mean = 0 + m + a + d + aa + dd”. For each model, backward regression procedure is used to obtain the best model. Due to the number of parameters to be estimated in each full model, *PBTools* requires that there should be at least six generations available in the data set.

Raw Data as Input

The steps to perform such analysis are listed below:

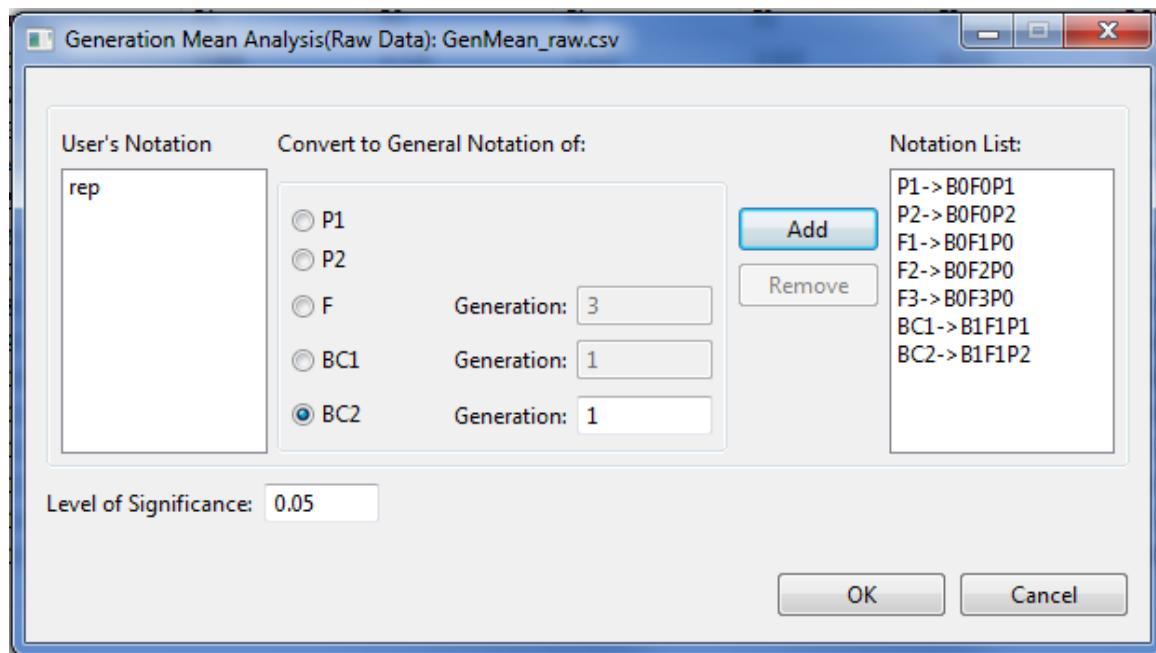
- Import *GenMean(raw)* file from package. Double-click the file to view it in the Data Viewer.
- Choose **Analysis | Generation Mean Analysis | Raw data as input...** from the menu bar.
- For each column that represents a generation, convert it to the general notation that *PBTools* recognizes by clicking one variable in the user's notation box, selecting the appropriate radio button that corresponds to its generation classification, specifying the generation number if necessary and clicking the **Add** button. A text indicating the conversion will be displayed in the Notation List.

For the example, do the following:

- select P1 column in the user's notation box, then classify it as P1 (the default selection) and click **Add** button
- select P2 column in the user's notation box, then classify it as P2 and click **Add** button
- select F1 column in the user's notation box, then classify it as F, specify the generation number as 1 and click **Add** button
- select F2 column in the user's notation box, then classify it as F, specify the generation number as 2 and click **Add** button
- select F3 column in the user's notation box, then classify it as F, specify the generation number as 3 and click **Add** button
- select BC1 column in the user's notation box, then classify it as BC1, specify the generation number as 1 and click **Add** button

- select BC2 column in the user's notation box, then classify it as BC2, specify the generation number as 1 and click **Add** button

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



- Click **OK**.
- Sample output of the analysis is shown below:

GENERATION MEAN ANALYSIS

DATA SUMMARY:

Generation	Mean	Std Dev	No of Obsn
P1	3.7030	0.2106	9
P2	4.6010	0.0956	9
F1	3.2317	0.1697	15
F2	3.5159	0.1263	15
F3	4.1406	0.1262	15
BC1	3.7756	0.1502	15
BC2	4.4830	0.3794	15

FULL MODEL: mean ~ 0 + m + a + d + aa + ad + dd

MODEL 1 :

Regression Model: mean ~ 0 + m + a + d + aa + ad + dd

Regression Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
m	4.3303	0.9640	4.4923	0.1394
a	-0.4130	0.4293	-0.9618	0.5124
d	-1.1949	3.5035	-0.3410	0.7908
aa	-0.1235	1.0144	-0.1218	0.9228
ad	0.6042	2.2432	0.2693	0.8325
dd	0.0726	2.7793	0.0261	0.9834

Residual Standard Error: 11.1775

Multiple R-square: 0.9982

Adjusted R-square: 0.9872

F-value: 91.0825

p-value: 0.0800

Observed and Predicted Values of Generation Means:

	Generation	Observed	Predicted
1	P1	3.703000	3.793826
2	P2	4.601000	4.619727
3	F1	3.231667	3.208086
4	F2	3.515867	3.751047
5	F3	4.140600	4.036147
6	BC1	3.775600	3.664735
7	BC2	4.483000	3.775585

Goodness-of-fit Test

Chi-square value: 124.9361

p-value: 5.255899e-29

MODEL 2 :

Regression Model: mean ~ 0 + m + a + d + aa + ad

Regression Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
m	4.3084	0.3351	12.8574	0.0060
a	-0.4138	0.3028	-1.3665	0.3051
d	-1.1058	0.5687	-1.9443	0.1913
aa	-0.1029	0.4499	-0.2287	0.8403
ad	0.5778	1.4172	0.4077	0.7230

Residual Standard Error: 7.9064

Multiple R-square: 0.9982

Adjusted R-square: 0.9936

F-value: 218.4485

p-value: 0.0046

Observed and Predicted Values of Generation Means:

		Generation	Observed	Predicted
1		P1	3.703000	3.791690
2		P2	4.601000	4.619287
3		F1	3.231667	3.202629
4		F2	3.515867	3.755507
5		F3	4.140600	4.031947
6		BC1	3.775600	3.667342
7		BC2	4.483000	3.792224

Goodness-of-fit Test

Chi-square value: 125.0215
p-value: 7.111018e-28

MODEL 3 :

Regression Model: mean ~ 0 + m + a + d + ad

Regression Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
m	4.2513	0.1850	22.9814	0.0002
a	-0.3836	0.2255	-1.7015	0.1874
d	-1.0222	0.3604	-2.8360	0.0659
ad	0.4871	1.1253	0.4328	0.6944

Residual Standard Error: 6.5394
Multiple R-square: 0.9981
Adjusted R-square: 0.9956
F-value: 399.1306
p-value: 0.0002

Observed and Predicted Values of Generation Means:

		Generation	Observed	Predicted
1		P1	3.703000	3.867672
2		P2	4.601000	4.634953
3		F1	3.231667	3.229141
4		F2	3.515867	3.740227
5		F3	4.140600	3.995770
6		BC1	3.775600	3.670172
7		BC2	4.483000	3.810281

Goodness-of-fit Test

Chi-square value: 128.2918
p-value: 1.26231e-27

MODEL 4 :

Regression Model: mean ~ 0 + m + a + d

Regression Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
m	4.2772	0.1563	27.3709	0.0000
a	-0.3389	0.1789	-1.8946	0.1311
d	-1.0359	0.3205	-3.2322	0.0319

Residual Standard Error: 5.8375
Multiple R-square: 0.998
Adjusted R-square: 0.9965
F-value: 667.778
p-value: 0.0000

Observed and Predicted Values of Generation Means:

	Generation	Observed	Predicted
1	P1	3.703000	3.938297
2	P2	4.601000	4.616091
3	F1	3.231667	3.241292
4	F2	3.515867	3.759243
5	F3	4.140600	4.018219
6	BC1	3.775600	3.589795
7	BC2	4.483000	3.928692

Goodness-of-fit Test

Chi-square value: 136.304
p-value: 1.74492e-28

MODEL 5 :

Regression Model: mean ~ 0 + m + d

Regression Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
m	4.4151	0.1704	25.9159	0.0000
d	-1.3037	0.3544	-3.6786	0.0143

Residual Standard Error: 7.1919
Multiple R-square: 0.9962
Adjusted R-square: 0.9947
F-value: 658.7258
p-value: 0.0000

Observed and Predicted Values of Generation Means:

	Generation	Observed	Predicted
1	P1	3.703000	4.415106
2	P2	4.601000	4.415106
3	F1	3.231667	3.111449
4	F2	3.515867	3.763277
5	F3	4.140600	4.089191
6	BC1	3.775600	3.763277

7 BC2 4.483000 3.763277

Goodness-of-fit Test
Chi-square value: 258.6178
p-value: 7.774878e-54

Summary Statistics as Input

The steps to perform such analysis using *PBTools* are listed below:

- Import *GenMean(summaryStats)* file from package. Double-click the file to view it in the Data Viewer.
- Choose **Analysis | Generation Mean Analysis | Summary statistics as input...** from the menu bar.
- Specify the required fields and appropriate options for the analysis.

No Computed Weights

This is selected if in the data set there is no column that corresponds to weights, hence, *PBTools* will automatically compute the weights needed for the analysis.

With Computed Weights

This is selected if in the data set there is a column that corresponds to weights.

Mean

This is the column that corresponds to the generation mean.

Weights

This is required if 'With Computed Weights' option is selected.

Standard Deviation

This is required if 'No Computed Weights' option is selected.

Number of Observations

This is required if 'No Computed Weights' option is selected.

Generation

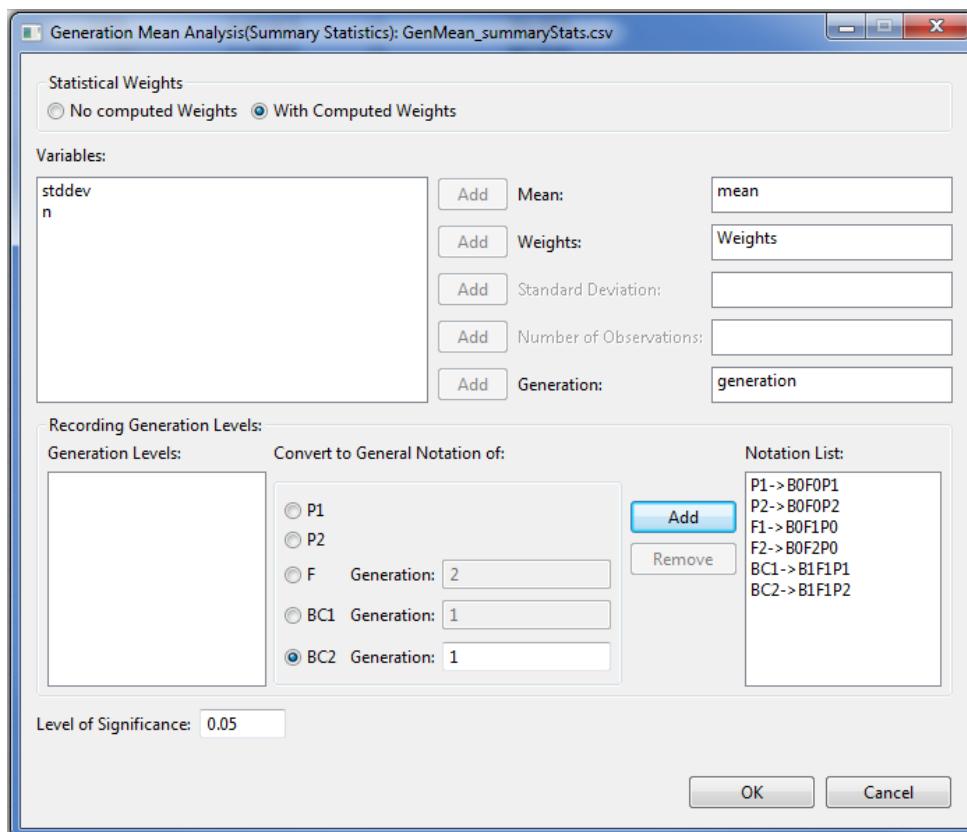
This is the column that corresponds to the generation classification.

- For each generation level, convert it to the general notation that PBTools recognizes by clicking one level in the user's notation box, selecting the appropriate radio button that corresponds to its generation classification, specifying the generation number if necessary and clicking the **Add** button. A text indicating the conversion will be displayed in the Notation List.

For the example, do the following:

- select P1 in the user's notation box, then classify it as P1 (the default selection) and click **Add** button
- select P2 in the user's notation box, then classify it as P2 and click **Add** button
- select F1 in the user's notation box, then classify it as F, specify the generation number as 1 and click **Add** button
- select F2 in the user's notation box, then classify it as F, specify the generation number as 2 and click **Add** button
- select BC1 column in the user's notation box, then classify it as BC1, specify the generation number as 1 and click **Add** button
- select BC2 column in the user's notation box, then classify it as BC2, specify the generation number as 1 and click **Add** button

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



- Click **OK**.
- Sample output of the analysis is shown below:

```
GENERATION MEAN ANALYSIS

-----
SET A FULL MODEL: mean ~ 0 + m + a + d + aa + ad
-----

SET A MODEL 1 :

Regression Model: mean ~ 0 + m + a + d + aa + ad

Regression Coefficients:
  Estimate Std. Error t value Pr(>|t|)
m     3.8952    0.7203  5.4076  0.1164
a     -0.4640   0.2816 -1.6481  0.3472
d     -0.5853   1.0100 -0.5795  0.6656
aa    0.2978    0.7773  0.3831  0.7671
ad    0.8323    1.5665  0.5313  0.6891

Residual Standard Error: 9.2487
Multiple R-square: 0.9984
Adjusted R-square: 0.9903
F-value: 123.755
p-value: 0.0681

Observed and Predicted Values of Generation Means:
  Generation Observed Predicted
  1          P1 3.676000 3.728934
  2          P2 4.634200 4.657033
  3          F1 3.231667 3.309876
  4          F2 3.515867 3.602534
  5          BC1 3.775600 3.653035
  6          BC2 4.483000 3.700929

Goodness-of-fit Test
Chi-square value: 85.53851
p-value: 2.272328e-20

-----
SET A MODEL 2 :

Regression Model: mean ~ 0 + m + a + d + ad

Regression Coefficients:
  Estimate Std. Error t value Pr(>|t|)
m     4.1527    0.1960 21.1824  0.0022
a     -0.4800   0.2109 -2.2767  0.1505
```

```
d   -0.9260      0.3628 -2.5525    0.1253  
ad   0.8271      1.1861  0.6973    0.5578
```

```
Residual Standard Error:    7.0034  
Multiple R-square:          0.9981  
Adjusted R-square:          0.9944  
F-value:                   269.7224  
p-value:                   0.0037
```

Observed and Predicted Values of Generation Means:

	Generation	Observed	Predicted
1	P1	3.676000	3.672681
2	P2	4.634200	4.632768
3	F1	3.231667	3.226763
4	F2	3.515867	3.689744
5	BC1	3.775600	3.656493
6	BC2	4.483000	3.722995

```
Goodness-of-fit Test  
Chi-square value:  98.09447  
p-value:          5.000995e-22
```

```
-----  
SET A MODEL 3 :
```

```
Regression Model: mean ~ 0 + m + a + d
```

Regression Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
m	4.1910	0.1713	24.4589	0.0001
a	-0.4197	0.1750	-2.3977	0.0961
d	-0.9292	0.3302	-2.8140	0.0671

```
Residual Standard Error:    6.3755  
Multiple R-square:          0.9977  
Adjusted R-square:          0.9954  
F-value:                   433.7527  
p-value:                   0.0002
```

Observed and Predicted Values of Generation Means:

	Generation	Observed	Predicted
1	P1	3.676000	3.771248
2	P2	4.634200	4.610674
3	F1	3.231667	3.261740
4	F2	3.515867	3.726351
5	BC1	3.775600	3.516494
6	BC2	4.483000	3.936207

```
Goodness-of-fit Test  
Chi-square value:  121.9421  
p-value:          2.945444e-26
```

SET A MODEL 4 :

Regression Model: mean ~ 0 + m + d

Regression Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
m	4.3104	0.2425	17.7778	0.0001
d	-1.1646	0.4663	-2.4975	0.0669

Residual Standard Error: 9.4291

Multiple R-square: 0.9933

Adjusted R-square: 0.9899

F-value: 296.1461

p-value: 0.0000

Observed and Predicted Values of Generation Means:

	Generation	Observed	Predicted
--	------------	----------	-----------

1	P1	3.676000	4.310434
2	P2	4.634200	4.310434
3	F1	3.231667	3.145865
4	F2	3.515867	3.728150
5	BC1	3.775600	3.728150
6	BC2	4.483000	3.728150

Goodness-of-fit Test

Chi-square value: 355.6286

p-value: 1.068149e-75

SET A MODEL 5 :

Regression Model: mean ~ 0 + m

Regression Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
m	3.8537	0.2278	16.9184	0

Residual Standard Error: 13.4921

Multiple R-square: 0.9828

Adjusted R-square: 0.9794

F-value: 286.2308

p-value: 0.0000

Observed and Predicted Values of Generation Means:

	Generation	Observed	Predicted
--	------------	----------	-----------

1	P1	3.676000	3.853678
2	P2	4.634200	3.853678
3	F1	3.231667	3.853678
4	F2	3.515867	3.853678

```
5      BC1 3.775600 3.853678
6      BC2 4.483000 3.853678
```

Goodness-of-fit Test
Chi-square value: 910.1826
p-value: 1.664558e-194

```
-----  
-----  
SET B FULL MODEL: mean ~ 0 + m + a + d + aa + dd  
-----
```

SET B MODEL 1 :

Regression Model: mean ~ 0 + m + a + d + aa + dd

Regression Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
m	2.0015	0.4243	4.7171	0.1330
a	-0.4967	0.0610	-8.1481	0.0777
d	4.8273	1.1225	4.3004	0.1455
aa	2.1466	0.4144	5.1796	0.1214
dd	-3.5971	0.7296	-4.9306	0.1274

Residual Standard Error: 2.0817
Multiple R-square: 0.9999
Adjusted R-square: 0.9995
F-value: 2446.4808
p-value: 0.0153

Observed and Predicted Values of Generation Means:

	Generation	Observed	Predicted
1	P1	3.676000	3.651347
2	P2	4.634200	4.644834
3	F1	3.231667	3.231667
4	F2	3.515867	3.515867
5	BC1	3.775600	3.804141
6	BC2	4.483000	4.300884

Goodness-of-fit Test
Chi-square value: 4.333597
p-value: 0.03736719

SET B MODEL 2 :

Regression Model: mean ~ 0 + m + a + aa + dd

Regression Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
--	----------	------------	---------	----------

m	3.7883	0.2687	14.0978	0.0050
a	-0.4175	0.1814	-2.3012	0.1480
aa	0.4303	0.3487	1.2341	0.3425
dd	-0.5247	0.4612	-1.1377	0.3732

Residual Standard Error: 6.4991
Multiple R-square: 0.9984
Adjusted R-square: 0.9952
F-value: 313.2789
p-value: 0.0032

Observed and Predicted Values of Generation Means:

	Generation	Observed	Predicted
1	P1	3.676000	3.801075
2	P2	4.634200	4.636054
3	F1	3.231667	3.263525
4	F2	3.515867	3.657078
5	BC1	3.775600	3.555909
6	BC2	4.483000	3.973399

Goodness-of-fit Test
Chi-square value: 84.47771
p-value: 4.527921e-19

SET B MODEL 3 :

Regression Model: mean ~ 0 + m + a + aa

Regression Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
m	3.5361	0.1593	22.2024	0.0002
a	-0.4025	0.1896	-2.1225	0.1239
aa	0.6958	0.2715	2.5628	0.0830

Residual Standard Error: 6.8106
Multiple R-square: 0.9974
Adjusted R-square: 0.9948
F-value: 379.9835
p-value: 0.0002

Observed and Predicted Values of Generation Means:

	Generation	Observed	Predicted
1	P1	3.676000	3.829457
2	P2	4.634200	4.634389
3	F1	3.231667	3.536143
4	F2	3.515867	3.536143
5	BC1	3.775600	3.508855
6	BC2	4.483000	3.911321

Goodness-of-fit Test
Chi-square value: 139.1521
p-value: 5.758125e-30

SET B MODEL 4 :

Regression Model: mean ~ 0 + m + aa

Regression Coefficients:
Estimate Std. Error t value Pr(>|t|)
m 3.4809 0.2152 16.1730 0.0001
aa 0.8898 0.3502 2.5413 0.0639

Residual Standard Error: 9.329
Multiple R-square: 0.9934
Adjusted R-square: 0.9902
F-value: 302.5775
p-value: 0.0000

Observed and Predicted Values of Generation Means:

	Generation	Observed	Predicted
1	P1	3.676000	4.370741
2	P2	4.634200	4.370741
3	F1	3.231667	3.480892
4	F2	3.515867	3.480892
5	BC1	3.775600	3.703354
6	BC2	4.483000	3.703354

Goodness-of-fit Test
Chi-square value: 348.1192
p-value: 4.467431e-74

SET B MODEL 5 :

Regression Model: mean ~ 0 + m

Regression Coefficients:
Estimate Std. Error t value Pr(>|t|)
m 3.8537 0.2278 16.9184 0

Residual Standard Error: 13.4921
Multiple R-square: 0.9828
Adjusted R-square: 0.9794
F-value: 286.2308
p-value: 0.0000

Observed and Predicted Values of Generation Means:

	Generation	Observed	Predicted
1	P1	3.676000	3.853678

2	P2	4.634200	3.853678
3	F1	3.231667	3.853678
4	F2	3.515867	3.853678
5	BC1	3.775600	3.853678
6	BC2	4.483000	3.853678

Goodness-of-fit Test

Chi-square value: 910.1826

p-value: 1.664558e-194
