

PLANT BREEDING TOOLS (PBTOOLS)¹

TUTORIAL

¹ working name

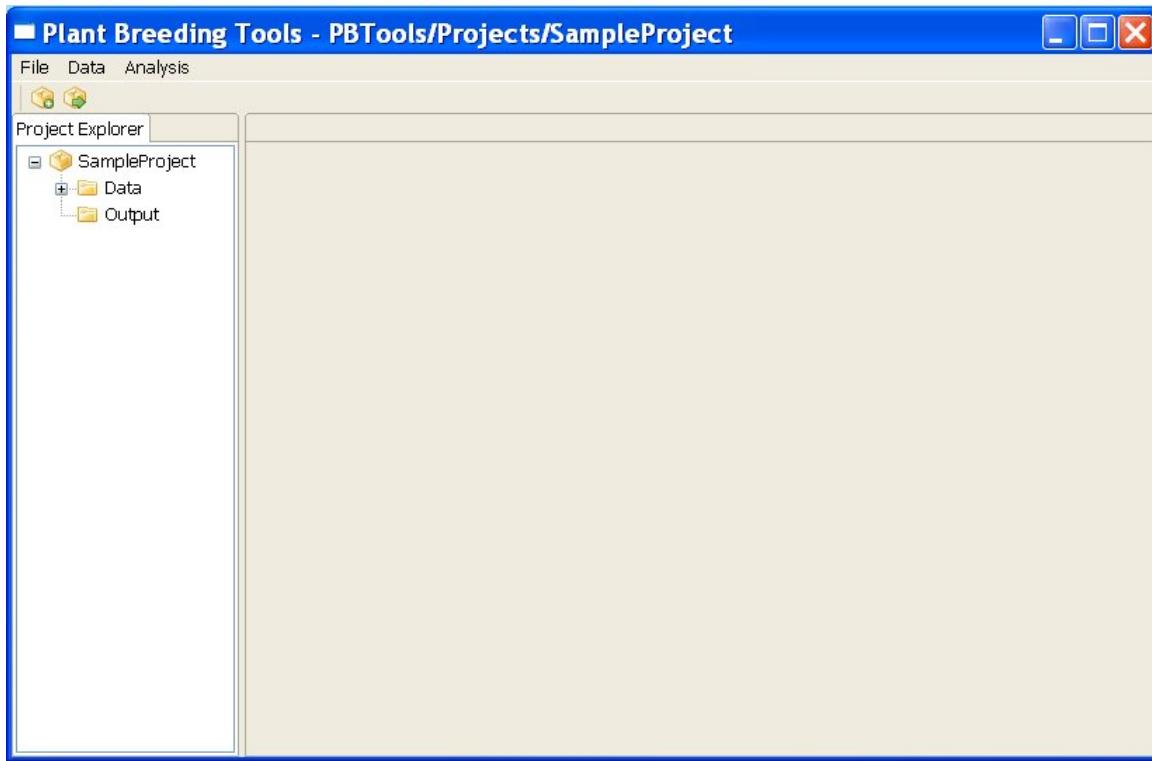
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1. INTRODUCTION

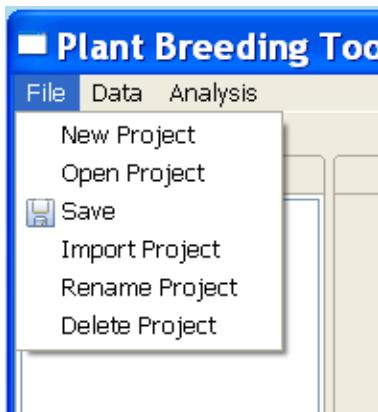
Upon launching the *PBTools*, the main window will appear.



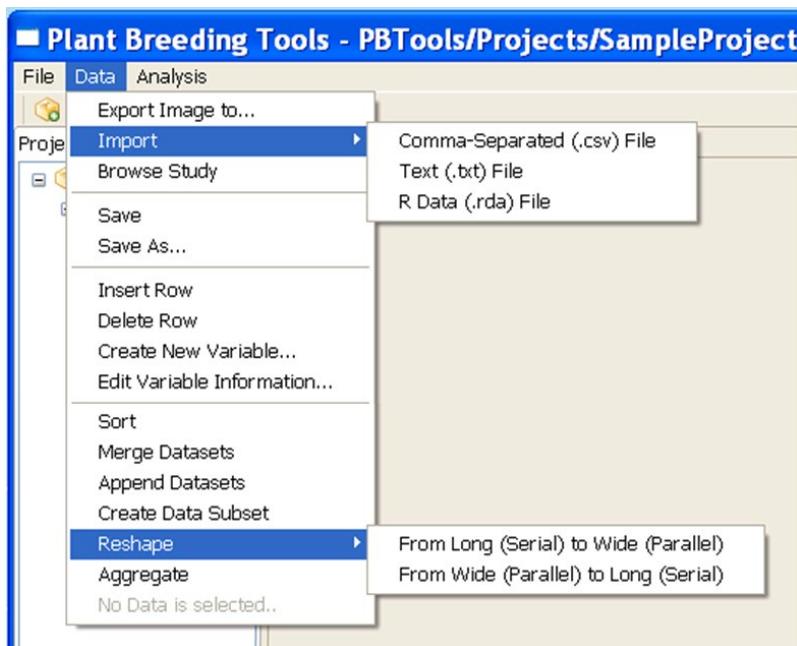
Project Explorer can be seen at the right-hand side of the main window. For first-time users, a default project named *SampleProject* is available with *Data* folder and *Output* folder inside it. The *Data* folder contains sample datasets that will be used in this tutorial. The *Output* folder, on the other hand, will contain all output files that will be created when an analysis is performed.

The software has three menu items: **File**, **Data**, and **Analysis**.

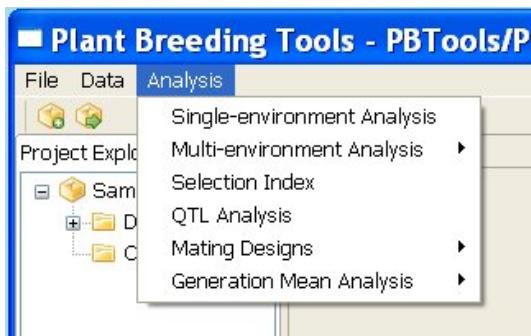
The **File** menu has several sub-items as shown below:



The **Data** menu has several sub-items as shown below:



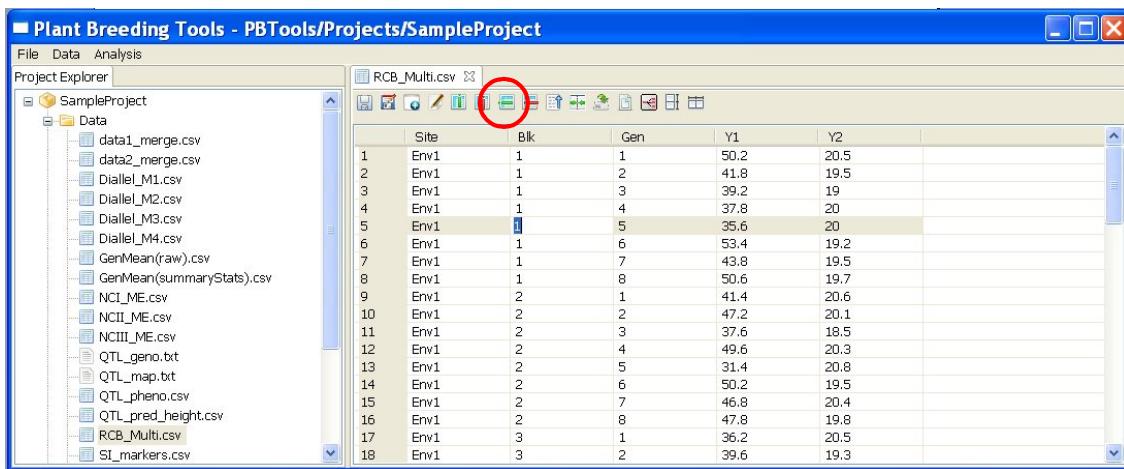
The **Analysis** menu has several sub-items as shown below:



2. DATA MANIPULATION

2.1. Inserting Row(s)

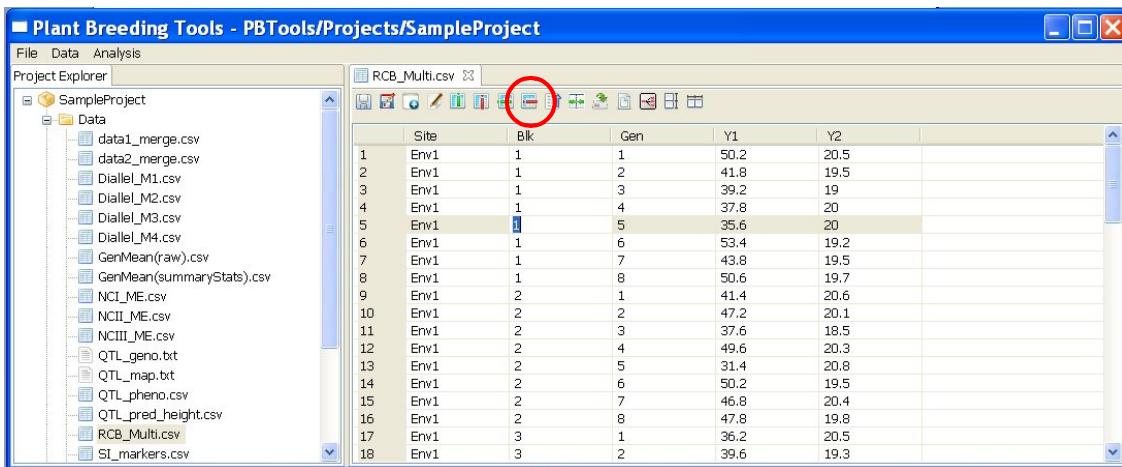
- On the Project Explorer, locate the *RCB_Multi.csv* file from the *Data* folder of the project named *SampleProject*. Double-click the file to view it in the Data Viewer.
- Select any row(s) or any cell in the row(s) where the user wants to insert new row(s) above it. To select several cells/rows, 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.
- Choose **Data > Insert Row** or click on the Insert Row icon in the Data Viewer tool bar.



- 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.

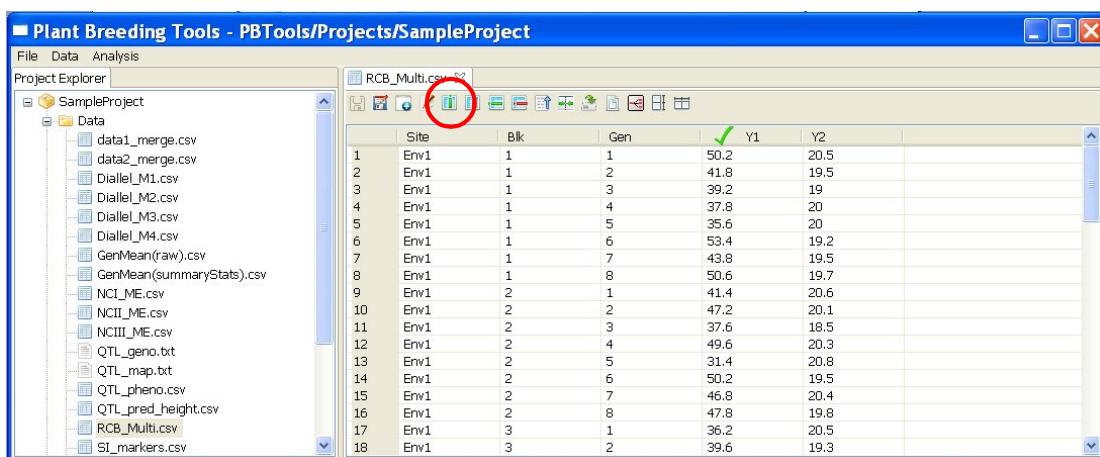
2.2. Deleting Row(s)

- On the Project Explorer, locate the *RCB_Multi.csv* file from the *Data* folder of the project named *SampleProject*. Double-click the file to view it 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.
- Choose **Data > Delete Row** or click on the Delete Row icon in the Data Viewer tool bar.



2.3. Inserting Column(s)

- On the Project Explorer, locate the *RCB_Multi.csv* file from the *Data* folder of the project named *SampleProject*. 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.
- Click on the Insert Column icon in the Data Viewer tool bar.



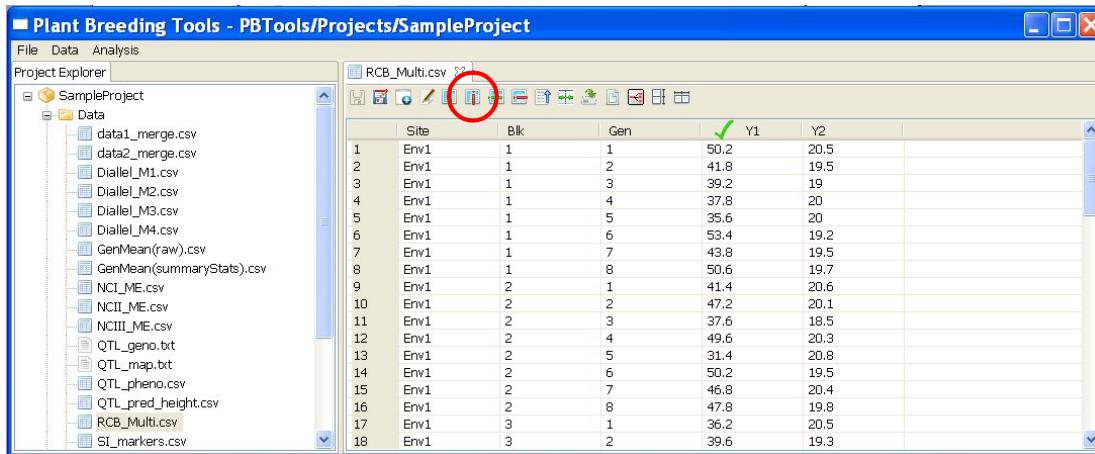
- The user will be asked to specify the name of the new column, say, *Plot*.



- Click OK.

2.4. Deleting Column(s)

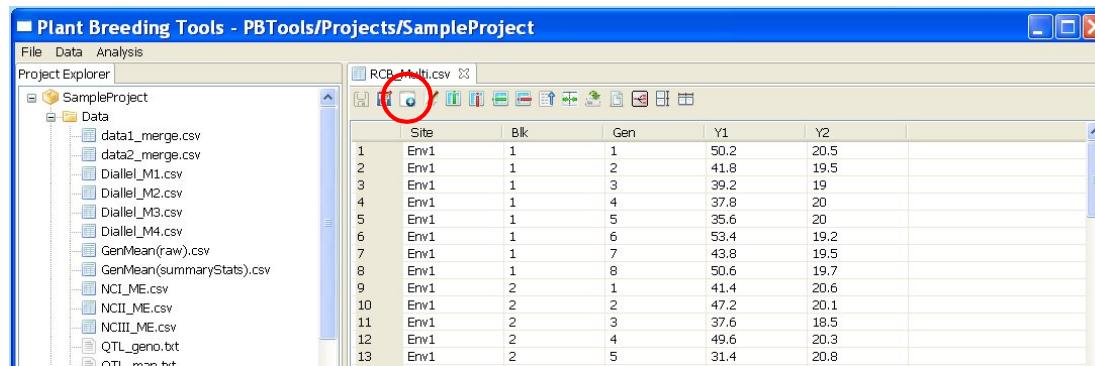
- On the Project Explorer, locate the *RCB_Multi.csv* file from the *Data* folder of the project named *SampleProject*. Double-click the file to view it in the Data Viewer.
- Select the column or the first column to be deleted by clicking on the column name. A check icon will appear on the column header.
- Click on the Insert Column icon in the Data Viewer tool bar.



- 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.
- Click OK.

2.5. Creating a New Variable

- On the Project Explorer, locate the *RCB_Multi.csv* file from the *Data* folder of the project named *SampleProject*. Double-click the file to view it in the Data Viewer.
- Choose **Data > Create New Variable** or click on the Create New Variable icon in the Data Viewer tool bar.



- Specify the required fields and appropriate options.

Name

This is the name of the new variable to be created.

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.

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

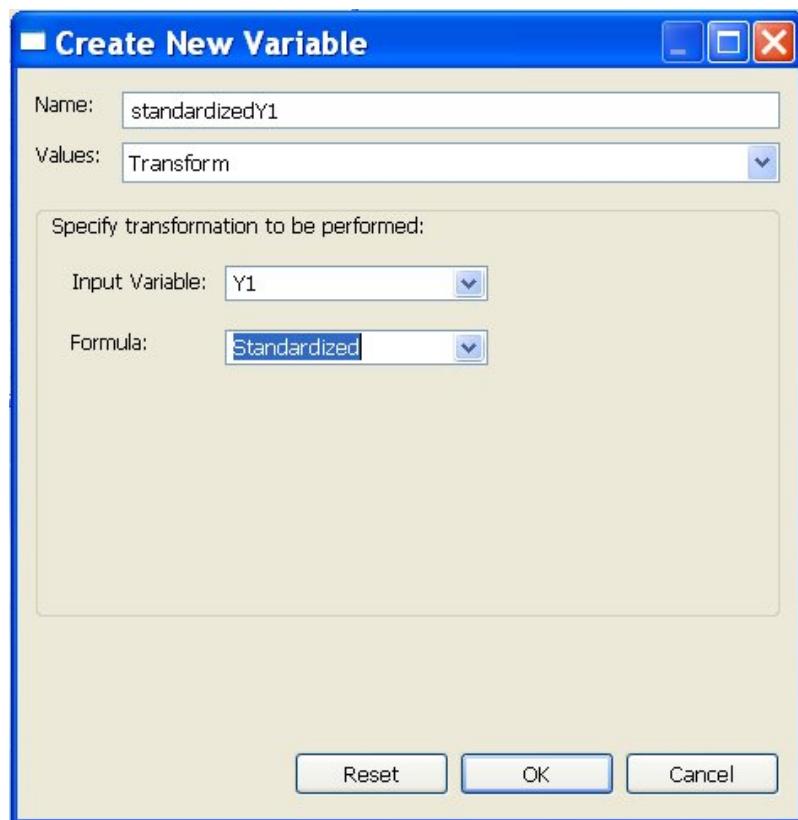
Input Variable

This is variable where the transformation will be performed.

Formula

Transformation options available are logarithm, natural logarithm, square root, power, exponential and standardized.

For the example, select the options as shown below:

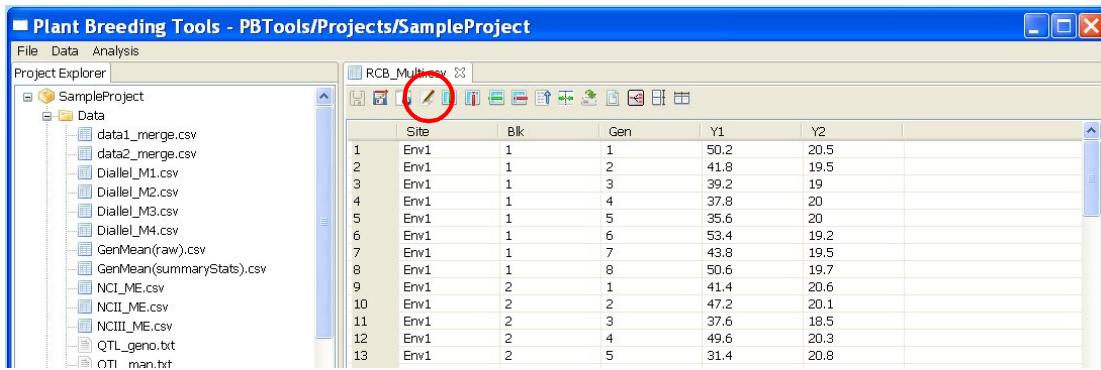


If concatenation of columns is selected, the user needs to specify the columns to concatenate.

- Click OK.

2.6. Edit Variable Information

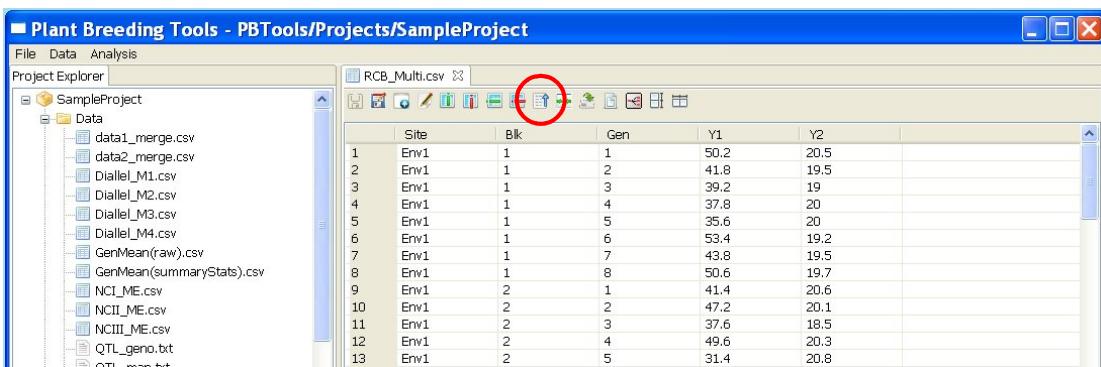
- On the Project Explorer, locate the *RCB_Multi.csv* file from the *Data* folder of the project named *SampleProject*. Double-click the file to view it in the Data Viewer.
- Choose **Data > Edit Variable Information** or click on the Edit Variable Information icon in the Data Viewer tool bar.



- The user can modify the variable type of the variables in the data set.
- Click OK.

2.7. Sorting data

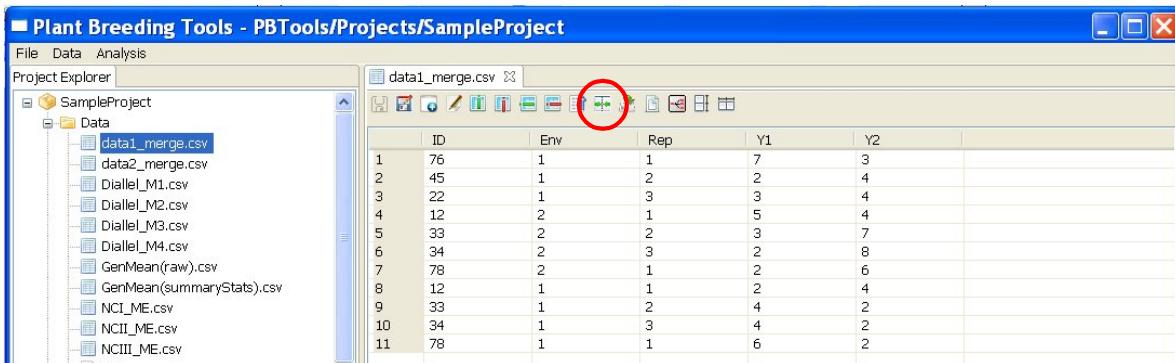
- On the Project Explorer, locate the *RCB_Multi.csv* file from the *Data* folder of the project named *SampleProject*. Double-click the file to view it in the Data Viewer.
- Choose **Data > Sort** or click on the Sort icon in the Data Viewer tool bar.



- The user can specify up to three variables as the basis for sorting and the order of sorting.
- Click OK. The sorted data is saved in the *Data* folder and displayed in the Data Viewer.

2.8. Merging datasets

- On the Project Explorer, locate the *data1_merge.csv* file from the *Data* folder of the project named *SampleProject*. Double-click the file to view it in the Data Viewer.
- Choose **Data > Merge Datasets** or click on the Merge Datasets icon in the Data Viewer tool bar.



- Specify the required fields and appropriate options.

Transaction File Name

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 *data2_merge.csv* file from the drop-down combo box.

Text File Delimiter

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

Observations to Include

The options available are to include common observations, all observations in the active data, all observations in the transaction data and all observations.

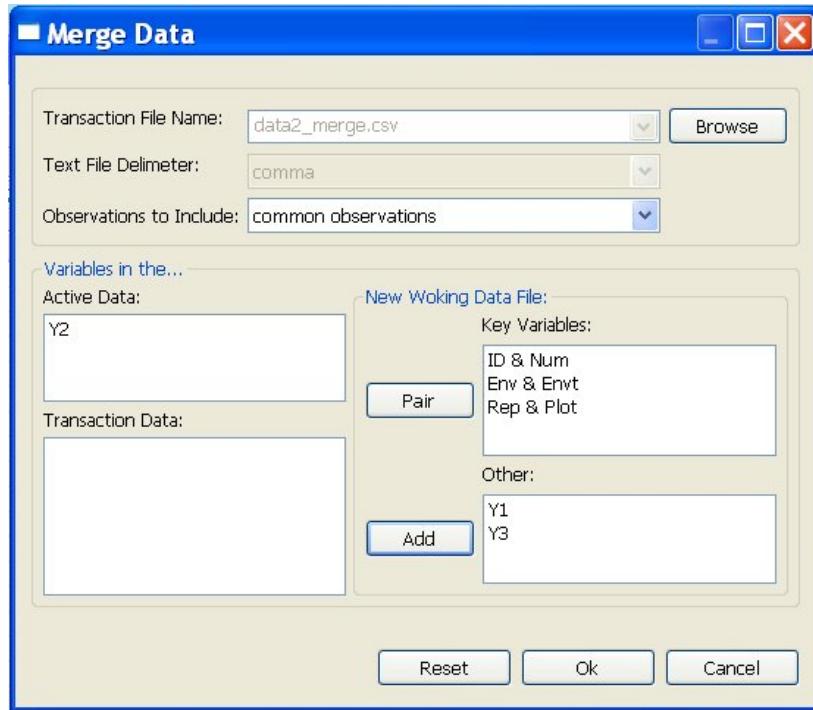
Key Variables

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.

Other

These are the other variables the user wants to include in the merged data set.

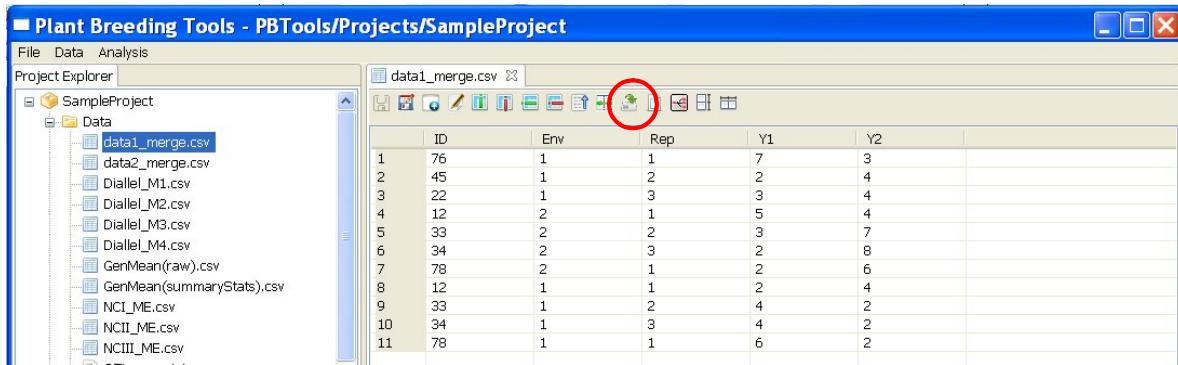
For the *example*, the completed dialog box should appear as illustrated below:



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

2.9. Append Datasets

- On the Project Explorer, locate the *data1_merge.csv* file from the *Data* folder of the project named *SampleProject*. Double-click the file to view it in the Data Viewer.
- Choose **Data > Append Datasets** or click on the Append Datasets icon in the Data Viewer tool bar.



- Specify the required fields and appropriate options.

Transaction File Name

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 *data2_merge.csv* file from the drop-down combo box.

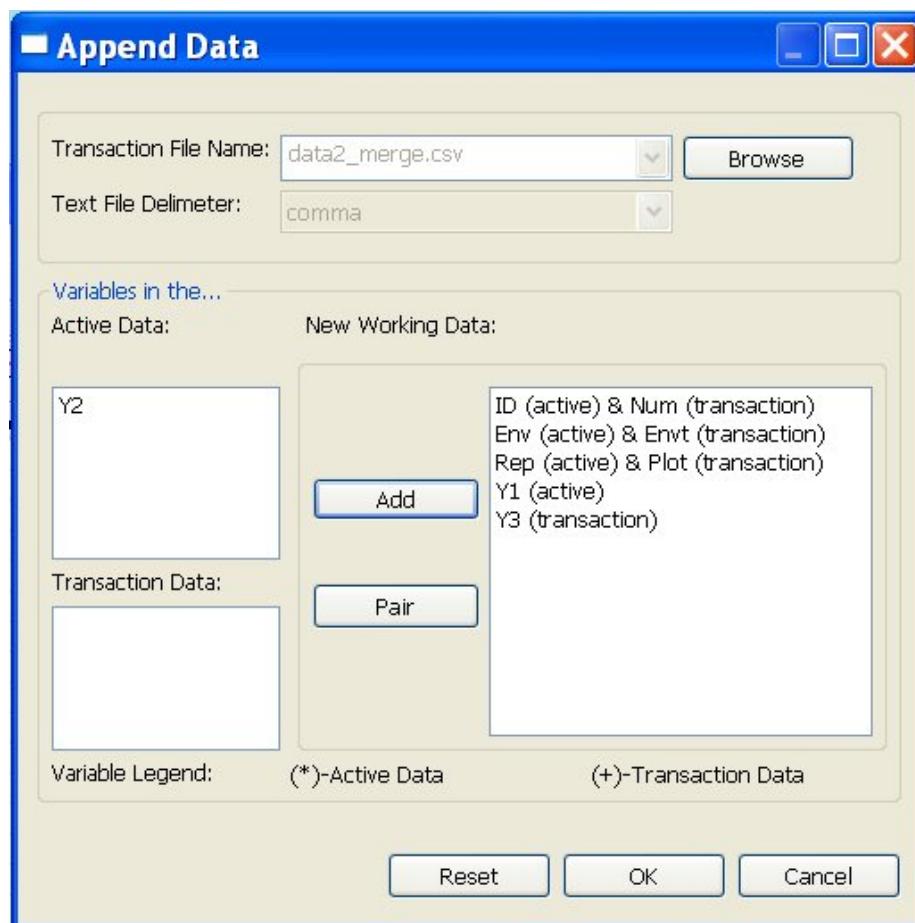
Text File Delimeter

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

New Working Data

This is the list of variables or paired variables that will be included in the new data set. Variables can be paired by clicking one variable in the active data and clicking one variable in the transaction data then clicking the **Pair** button. Other variables can be added to this list by clicking the variable then clicking the **Add** button.

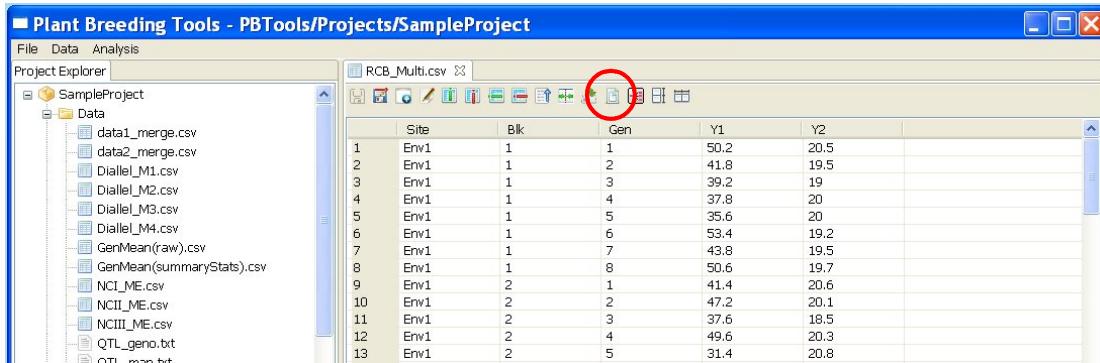
For the *example*, the completed dialog box should appear as illustrated below:



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

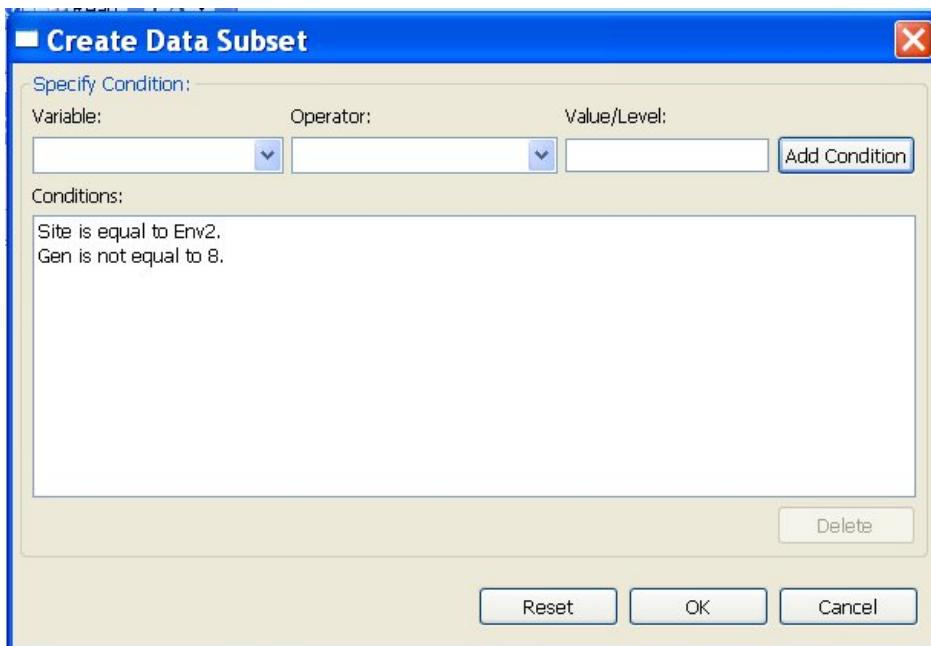
2.10. Creating Data Subset

- On the Project Explorer, locate the *RCB_Multi.csv* file from the *Data* folder of the project named *SampleProject*. 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 tool bar.



- Suppose the user wants to select only the observations from *Env2*. 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 8”.

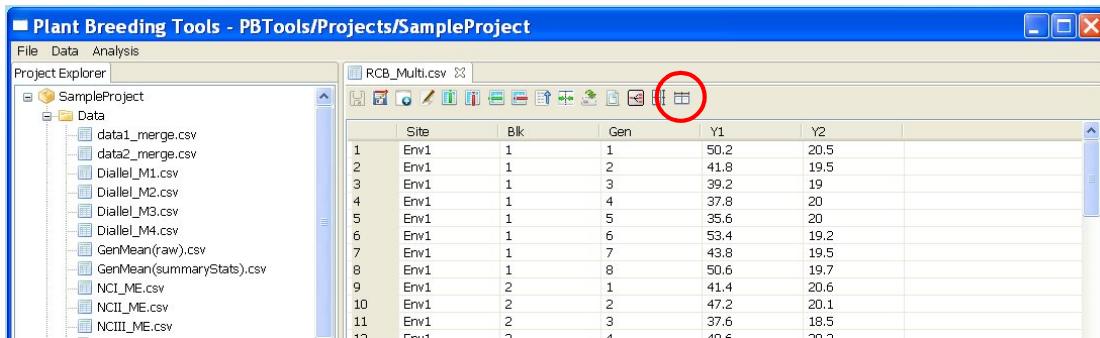
For the *example*, the completed dialog box should appear as illustrated below:



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

2.11. Reshaping Data From Long to Wide

- On the Project Explorer, locate the *RCB_Multi.csv* file from the *Data* folder of the project named *SampleProject*. Double-click the file to view it in the Data Viewer.
- Choose **Data > Reshape > From Long (Serial) to Wide (Parallel)** or click on the Reshape to Wide icon in the Data Viewer tool bar.



- Specify the required fields and appropriate options.

Variable(s) to Reshape

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

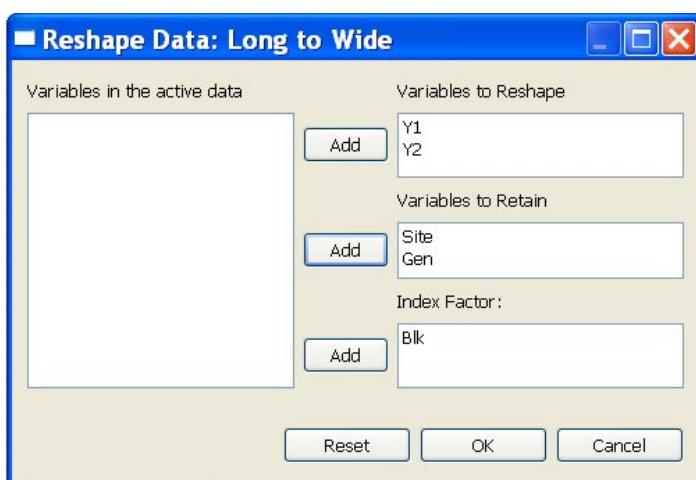
Variables to Retain

These are the variables that will still be included in the new data set

Index Factor

This is the basis for splitting-up the values of the variable(s) to reshape.

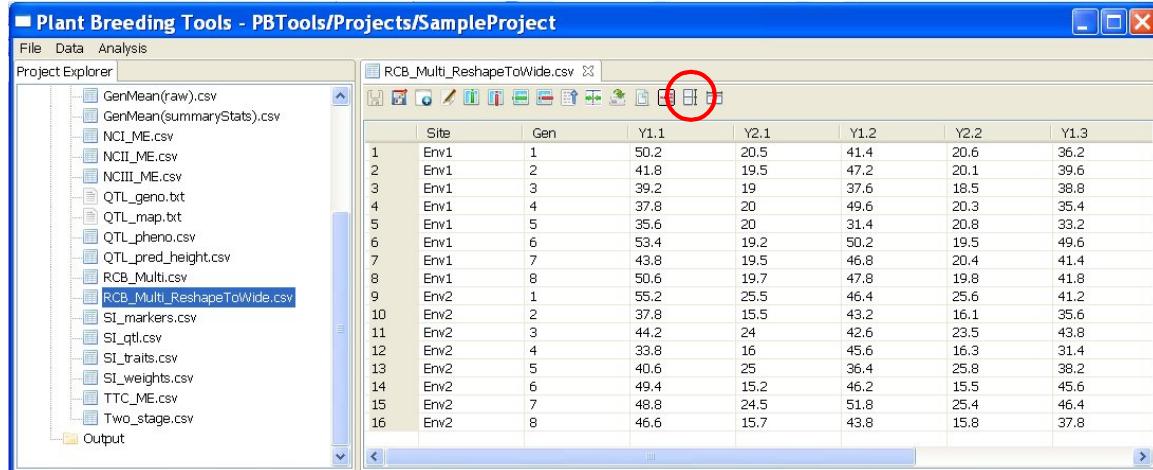
For the *example*, the completed dialog box should appear as illustrated below:



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

2.12. Reshaping Data From Wide to Long

- On the Project Explorer, locate the *RCB_Multi_ReshapeToWide.csv* file (the generated file from section 2.11) from the *Data* folder of the project named *SampleProject*. Double-click the file to view it in the Data Viewer.
- Choose **Data > Reshape > From Wide (Parallel) to Long (Serial)** or click on the Reshape to Long icon in the Data Viewer tool bar.



- 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. Then click the **Add Target Variable**.

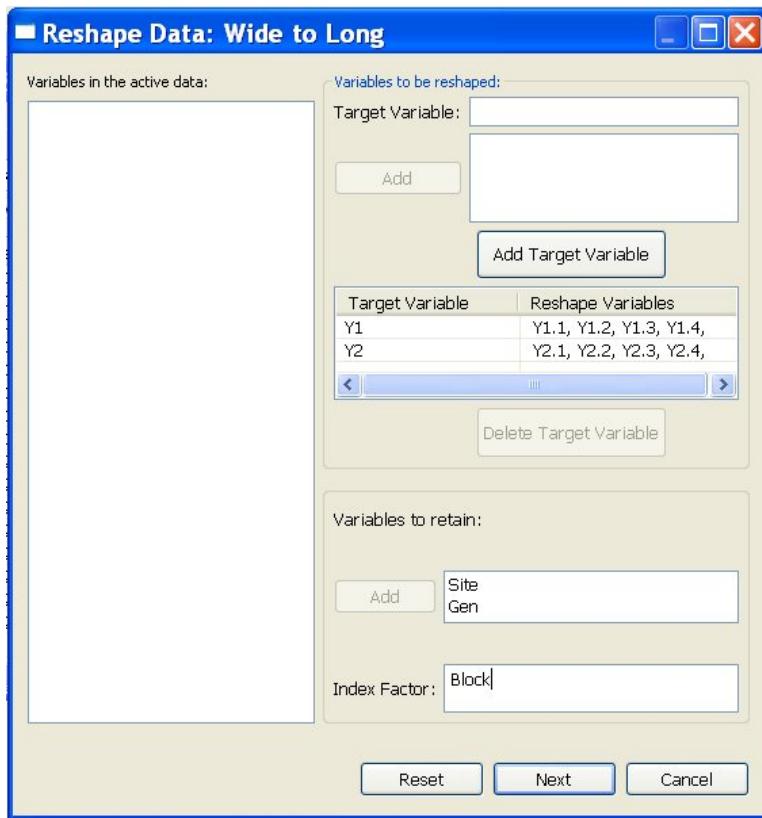
Variables to Retain

These are the variables that will still be included in the new data set.

Index Factor

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

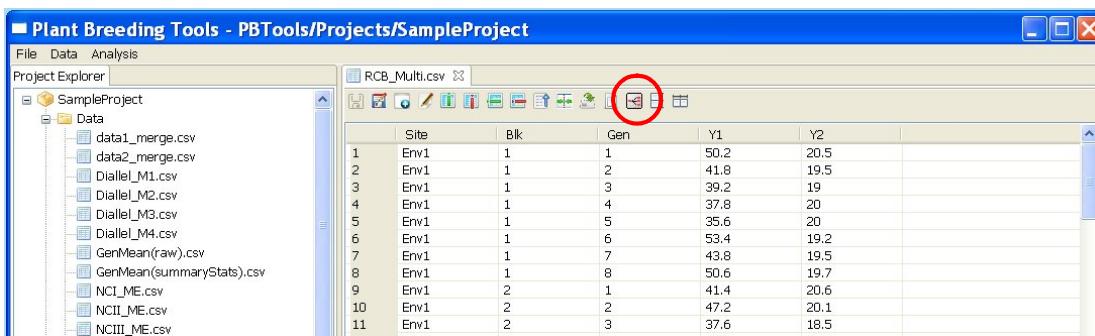
For the *example*, the completed dialog box should appear as illustrated below:



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

2.13. Aggregating Data

- On the Project Explorer, locate the *RCB_Multi.csv* file from the *Data* folder of the project named *SampleProject*. Double-click the file to view it in the Data Viewer.
- Choose **Data > Aggregate** or click on the Aggregate Data icon in the Data Viewer tool bar.



- Specify the required fields and appropriate options.

Variable(s) to Aggregate

This is the list of variables whose values will be summarized using the selected functions.

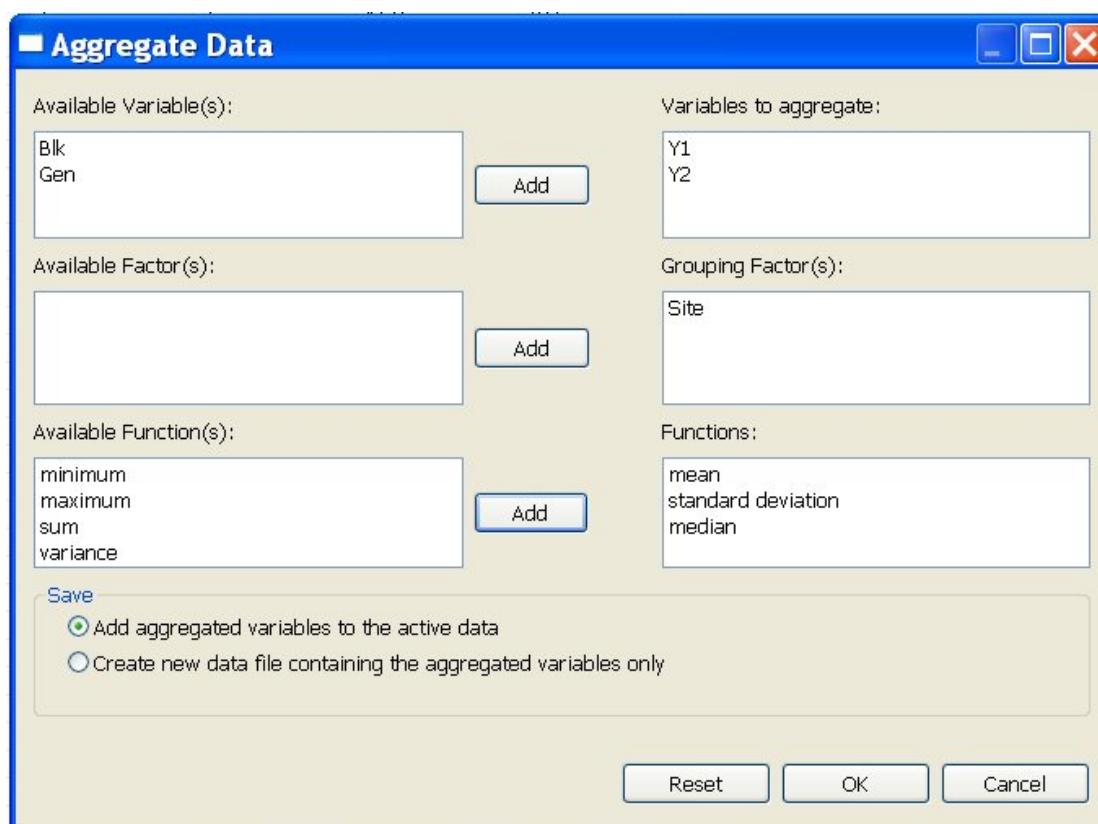
Grouping Factor(s)

Specify this grouping factor, 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.

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



- Click OK. The active data is saved with the additional columns and displayed in the Data Viewer.

3. PHENOTYPIC ANALYSIS

3.1. Single environment analysis

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

- On the Project Explorer, locate the *RCB_Multi.csv* file from the *Data* folder of 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 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).

	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
7	Env1	1	7	43.8	19.5
8	Env1	1	8	50.6	19.7
9	Env1	2	1	41.4	20.6
10	Env1	2	2	47.2	20.1
11	Env1	2	3	37.6	18.5
12	Env1	2	4	49.6	20.3
13	Env1	2	5	31.4	20.8
14	Env1	2	6	50.2	19.5

- Choose **Analysis > Single-environment Analysis**.
- Opening the data for the first time, *Blk* and *Gen* fields are regarded by R as numerical variables, they need to be changed as factors. Choose these 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 five available experimental designs, Randomized Complete Block Design (RCB), Augmented RCB, Augmented Latin Square, Alpha-Lattice and Row-Column. For the example, select RCB.

'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.

Exclude controls in the estimation of genotypic variance

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.

Estimate genotypic and phenotypic correlations

This option is enabled if there are two or more response variables 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.

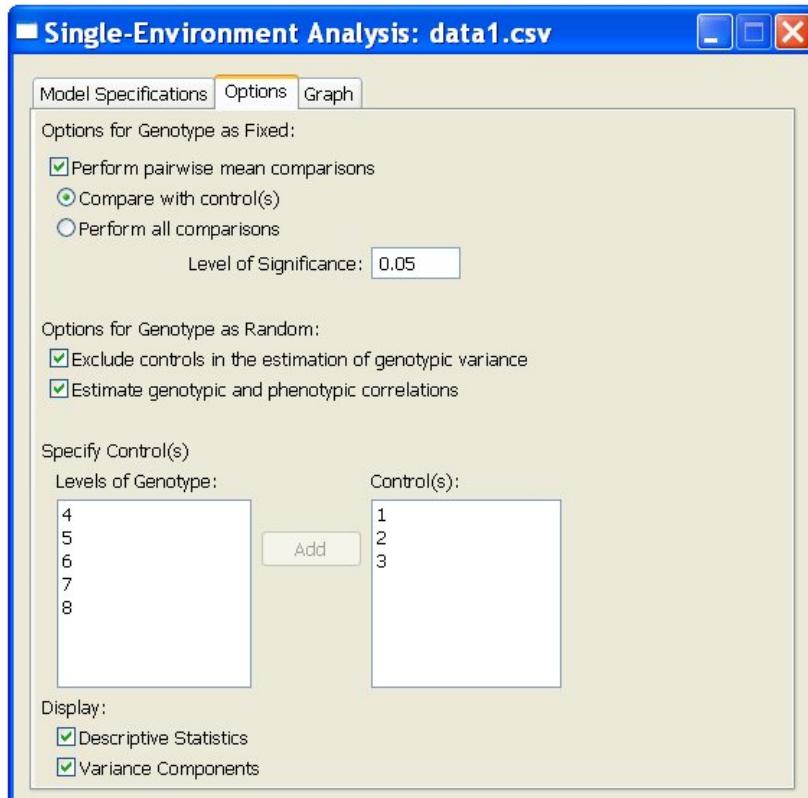
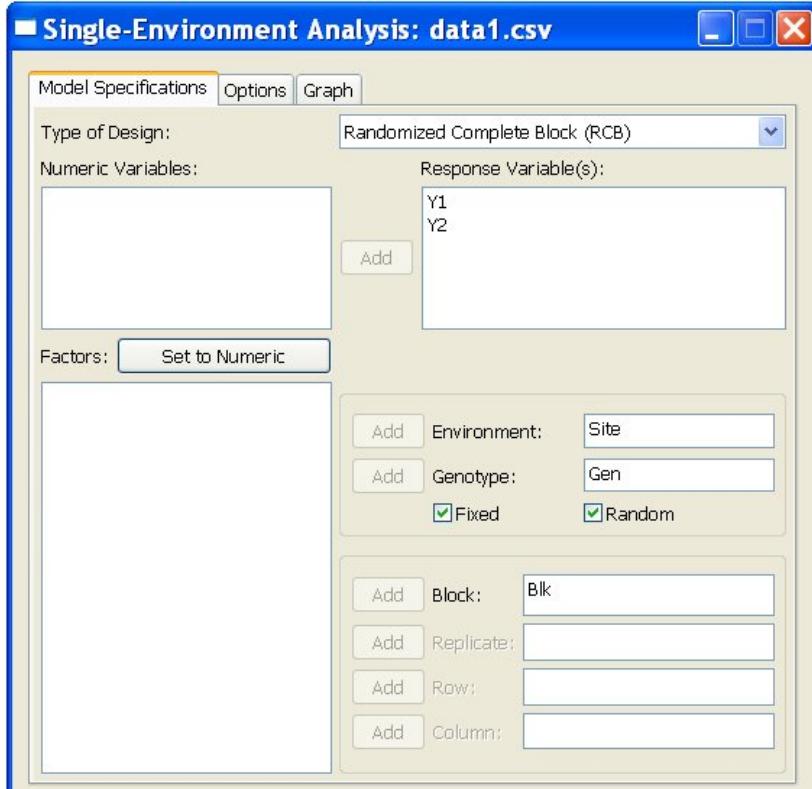
Display Variance Components

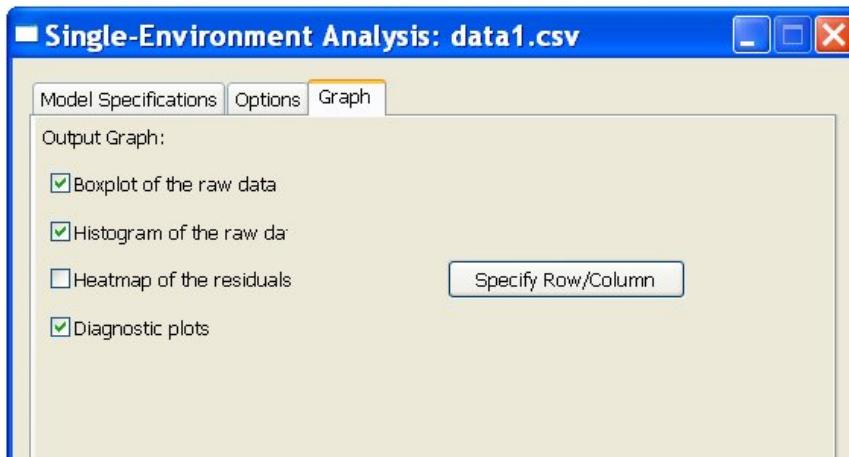
If selected, a table with the variance estimates of the some model components will be displayed.

Graph Tab

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

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





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

```
DATA FILE: C:/Documents and
Settings/NSales/workspace3/Star/Projects/SampleProject/Data/RCB_Multi.csv
```

```
SINGLE-ENVIRONMENT ANALYSIS
```

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

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

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

Descriptive Statistics

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
-----
```

Trial 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

Estimates of Variance Components

Variance Components Table:

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

Analysis of Variance Table

ANOVA Table:

Linear Mixed Model fit by Maximum likelihood ratio test
Environment Variable: Site = Env1
Response Variable: Y1

```
Df Sum Sq Mean Sq F value Chisq Chi Df Pr(>Chisq)
Gen 7 1013.8 144.83 10.678 42.910      7 3.471e-07 ***
---
Signif. codes: 0 '****' 0.001 '***' 0.01 '**' 0.05 '*' 0.1 '.' 1
```

Genotype Means and Standard Errors

Genotype means and standard errors:

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

Pairwise Mean Comparisons

Significant Pairwise Comparisons (if any):
Compared with control(s)

```
Trmt[i] Trmt[j] Estimate      lwr      upr
1        4          1 -39.950 -48.01257 -31.88743
2        5          2 -48.600 -56.66257 -40.53743
3        6          3 -28.475 -36.53757 -20.41243
4        7          1 -37.200 -45.26257 -29.13743
5        8          2 -34.350 -42.41257 -26.28743
```

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

RESPONSE VARIABLE: Y1

Descriptive Statistics

Descriptive Statistics:

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

ANALYSIS FOR: Site = Env1

Trial Summary:

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

Factors	Number of Levels	Levels
Site	2	Env1 Env2
Gen	8	1 2 3 ... 8
Blk	4	1 2 3 4

Estimates of Variance Components

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

Genotype Predicted Means

Predicted means:

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

Estimate of Heritability

Heritability:

0.94

Test for the Significance of Genotypic Effect

Linear Mixed Model fit by Maximum likelihood ratio test
Environment Variable: Site = Env1
Response Variable: Y1

Chisq	Pr(>Chisq)
Gen	14.605 0.0001325 ***

Signif. codes:	0 '****' 0.001 '***' 0.01 '**' 0.05 '*' 0.1 '.' 1

Genotypic and Phenotypic Correlations

=====

Genotypic Correlations:

Site: Env1

Y1	Y2
Y1	-2.147807
Y2	-2.147807

Site: Env2

Y1	Y2
Y1	0.003393196
Y2	0.003393196

Phenotypic Correlations:

Site: Env1

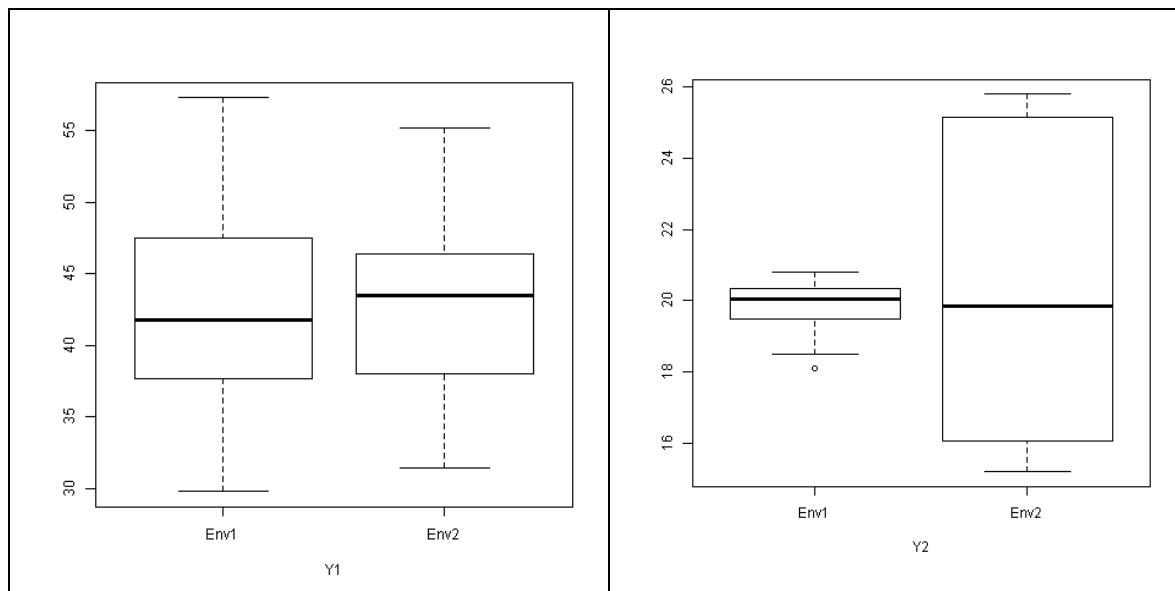
Y1	Y2
Y1	-0.815358
Y2	-0.815358

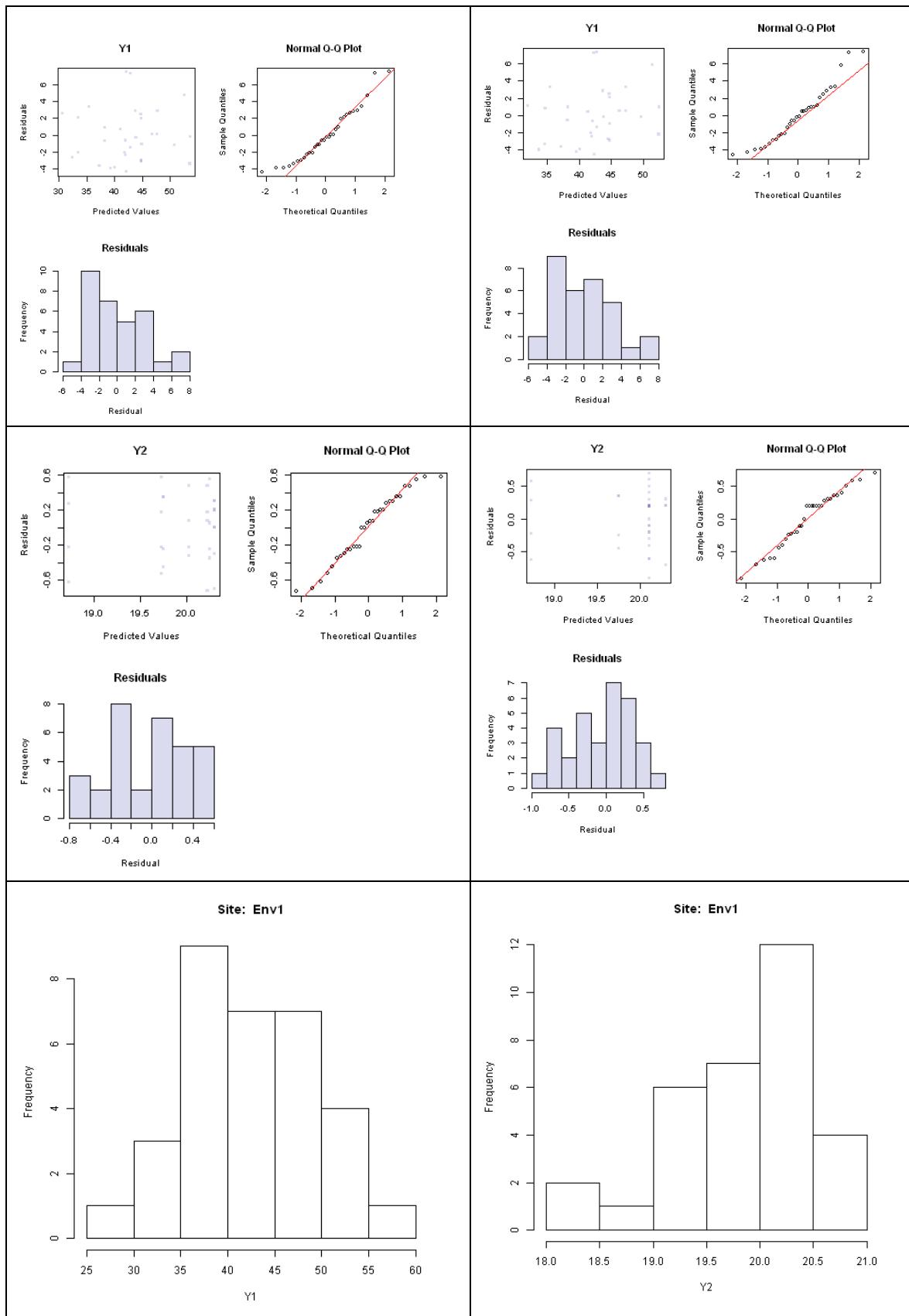
Site: Env2

Y1	Y2
Y1	0.004514488
Y2	0.004514488

=====

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





3.2. Multi-environment analysis

3.2.1. One-Stage Analysis

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

- On the Project Explorer, locate the *RCB_Multi.csv* file from the *Data* folder of 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 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).

	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
7	Env1	1	7	43.8	19.5
8	Env1	1	8	50.6	19.7
9	Env1	2	1	41.4	20.6
10	Env1	2	2	47.2	20.1
11	Env1	2	3	37.6	18.5
12	Env1	2	4	49.6	20.3
13	Env1	2	5	31.4	20.8
14	Env1	2	6	50.2	19.5

- Choose **Analysis > Multi-environment Analysis > One-Stage Analysis**
- Opening the data for the first time, *Blk* and *Gen* fields are regarded by R as numerical variables, they need to be changed as factors. Choose these 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, Randomized Complete Block Design (RCB), Alpha-Lattice and Row-Column. For the example, select RCB.

'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.

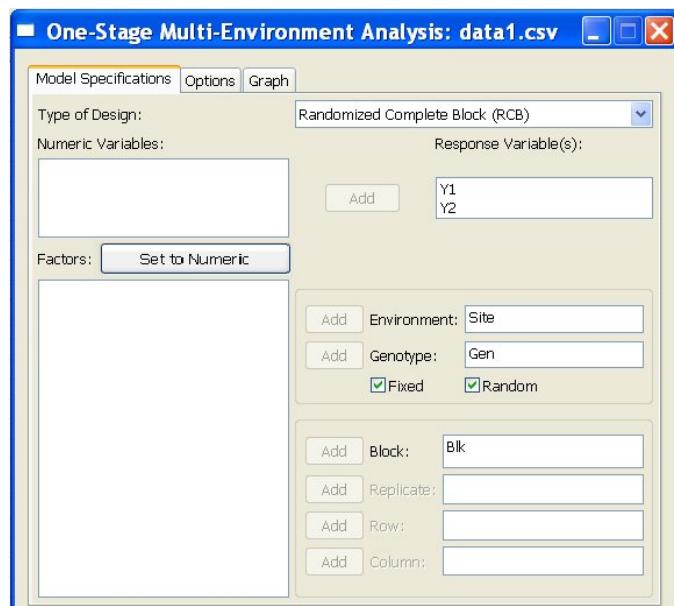
Perform pairwise mean comparisons: Perform all comparisons

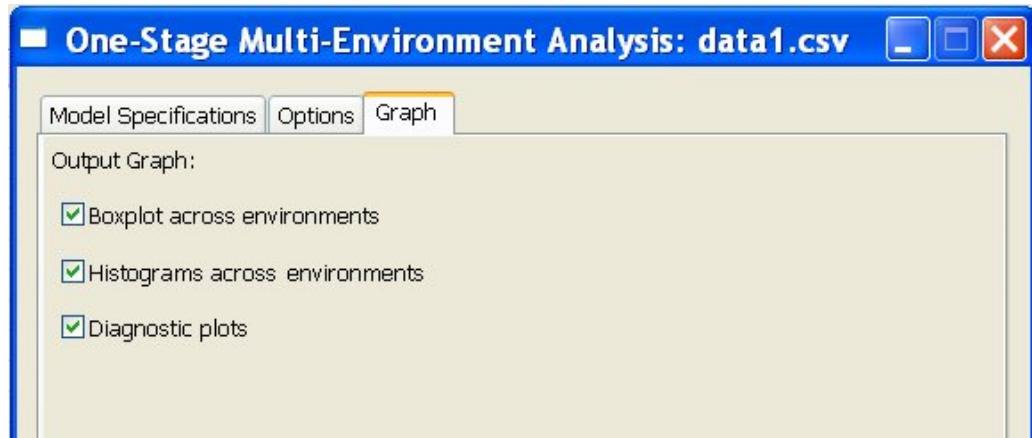
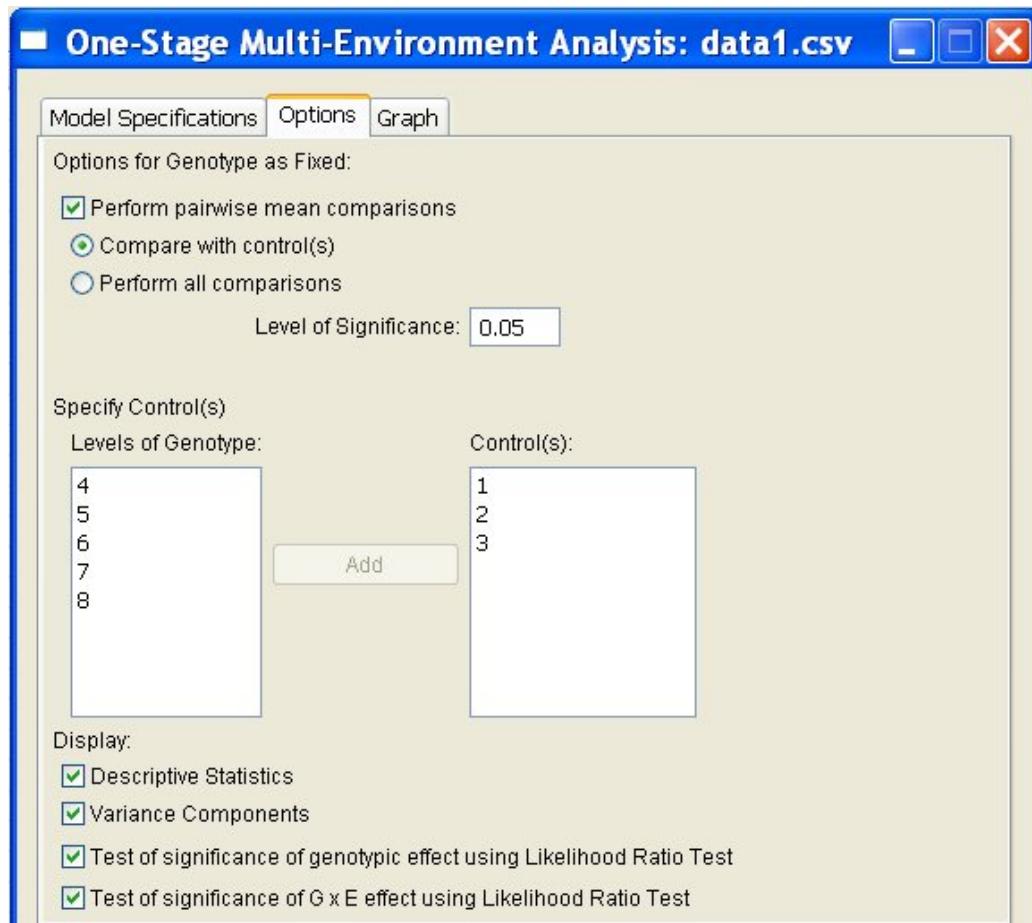
This option is not recommended when the number of genotype levels is very large.

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 (only results from *response variable = Y1*) is shown below:

```
DATA FILE: E:/NSales/juno  
workspace/workspace1/RJavaManager/sample_datasets/RCB_Multi.csv
```

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

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

```
=====
```

```
GENOTYPE AS: Fixed
```

```
=====
```

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

Trial Summary:

```
Number of observations read: 64
```

```
Number of observations used: 64
```

Factors	Number of Levels	Levels
Site	2	Env1 Env2
Gen	8	1 2 3 ... 8
Blk	4	1 2 3 4

Descriptive Statistics

```
Descriptive Statistics:
```

Variable	N_NonMissObs	Mean	StdDev
Y1	64	42.74063	6.215335

Estimates of Variance Components

Variance Components Table:

Groups	Variance	Std.Dev.
1 Gen:Site	7.199774	2.683240
2 Blk:Site	2.496742	1.580108
3 Site	0.000000	0.000000
4 Residual	13.629625	3.691832

Test for Genotypic Effect

Test for Genotype Effect using Maximum likelihood ratio test
Response Variable: Y1

```
Chisq Pr(>Chisq)  
Gen 24.986 0.0007632 ***
```

```
---
```

```
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Test for Genotype x Environment Effect

Test for Genotype X Environment Effect using Maximum likelihood ratio test
Response Variable: Y1

```
          Chisq Pr(>Chisq)
Gen:Site 1.1315      0.2874
```

ANOVA Table:

	Df	Sum Sq	Mean Sq	F value	Chisq	Pr(>Chisq)	
Gen	7	847.25	121.03	8.7731	24.9858	0.0007632	***

							Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Pairwise Mean Comparisons

Significant Pairwise Comparisons (if any):
Compared with control(s)

	Trmt[i]	Trmt[j]	Estimate	lwr	upr
1	4	1	-42.450	-52.31221	-32.58779
2	5	2	-46.600	-56.46221	-36.73779
3	6	3	-30.975	-40.83721	-21.11279
4	7	1	-35.200	-45.06221	-25.33779
5	8	2	-36.850	-46.71221	-26.98779

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

RESPONSE VARIABLE: Y1

Trial Summary:

Number of observations read: 64
Number of observations used: 64

Factors	Number of Levels	Levels
Site	2	Env1 Env2
Gen	8	1 2 3 ... 8
Blk	4	1 2 3 4

Descriptive Statistics

Descriptive Statistics:

Variable	N_NonMissObs	Mean	StdDev
1 Y1	64	42.74063	6.215335

Estimates of Variance Components

Variance Components Table:

	Groups	Variance	Std.Dev.
1	Gen:Site	7.199784	2.683241
2	Blk:Site	2.496750	1.580111
3	Gen	18.223185	4.268862
4	Site	0.000000	0.000000
5	Residual	13.629618	3.691831

Test for Genotypic Effect

Test for Genotype Effect using Maximum likelihood ratio test
Response Variable: Y1

```
          Chisq Pr(>Chisq)
Gen 3.4644      0.0627 .
---
Signif. codes:  0 '****' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Test for Genotype x Environment Effect

Test for Significance of G X E Effect:

Test for Genotype X Environment Effect using Maximum likelihood ratio test
Response Variable: Y1

```
          Chisq Pr(>Chisq)
Gen:Site 5.2812     0.02156 *
---
Signif. codes:  0 '****' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Test for Environment Effect

Test for Environment Effect by Maximum likelihood ratio test
Response Variable: Y1

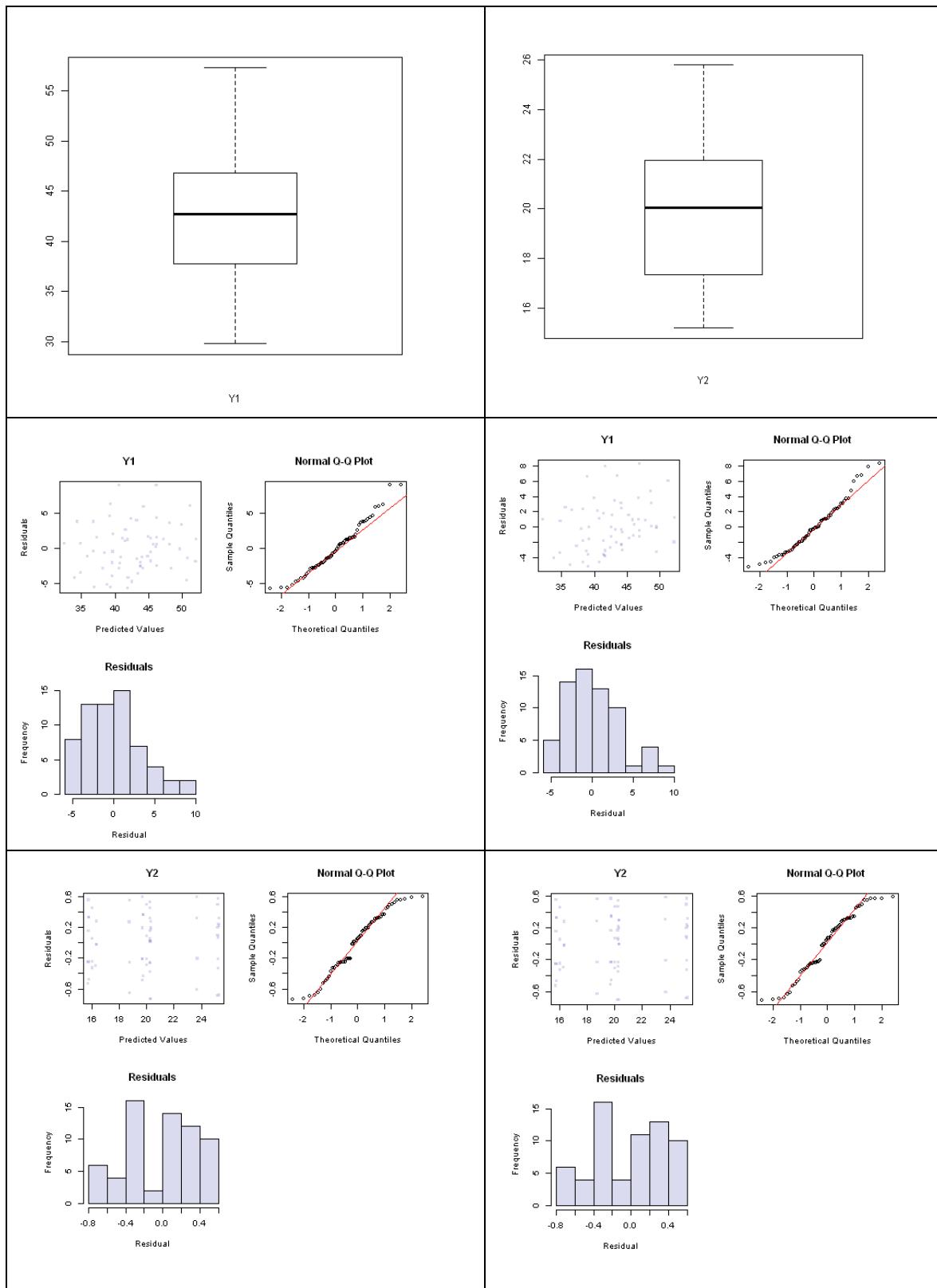
```
          Chisq Pr(>Chisq)
Site      0      0.9997
```

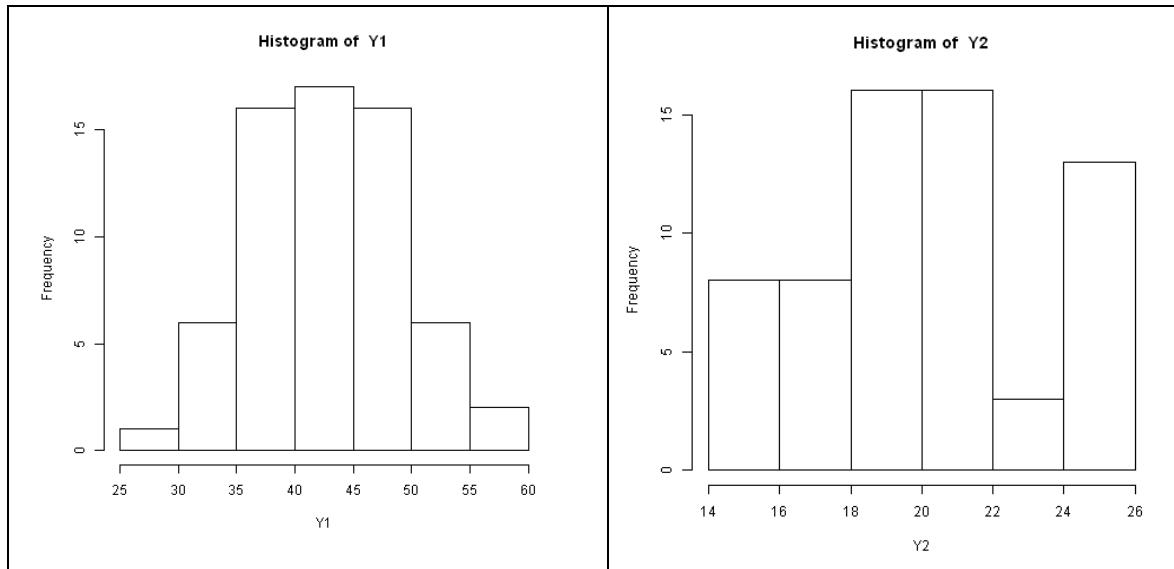
Estimate of Heritability

Heritability:

0.8

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

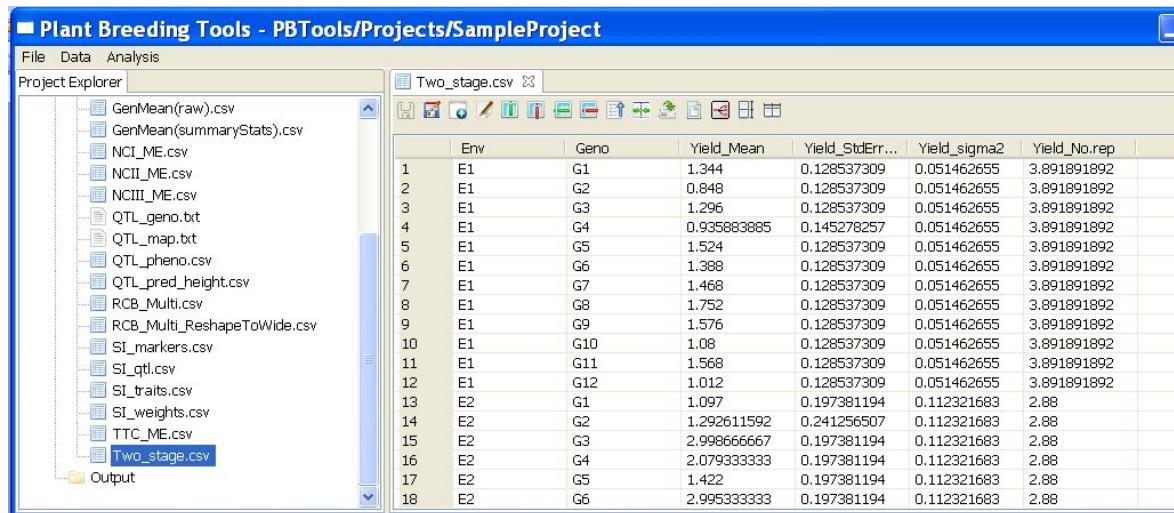




3.2.2. Two-Stage Analysis

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

- On the Project Explorer, locate the *Two_stage.csv* file from the *Data* folder of the project named *SampleProject*. 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 *Geno* factors, with 10 and 12 levels, respectively.



- Choose **Analysis > Multi-environment Analysis > Two-Stage Analysis**

- 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.

For each trait, the user has to specify the response variable which is the mean of the trait, its standard error, residual variance and number of replicates. To indicate that this set of variables correspond to one trait, click the **Add to Table** button. Do the same for the rest of the traits.

'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

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.

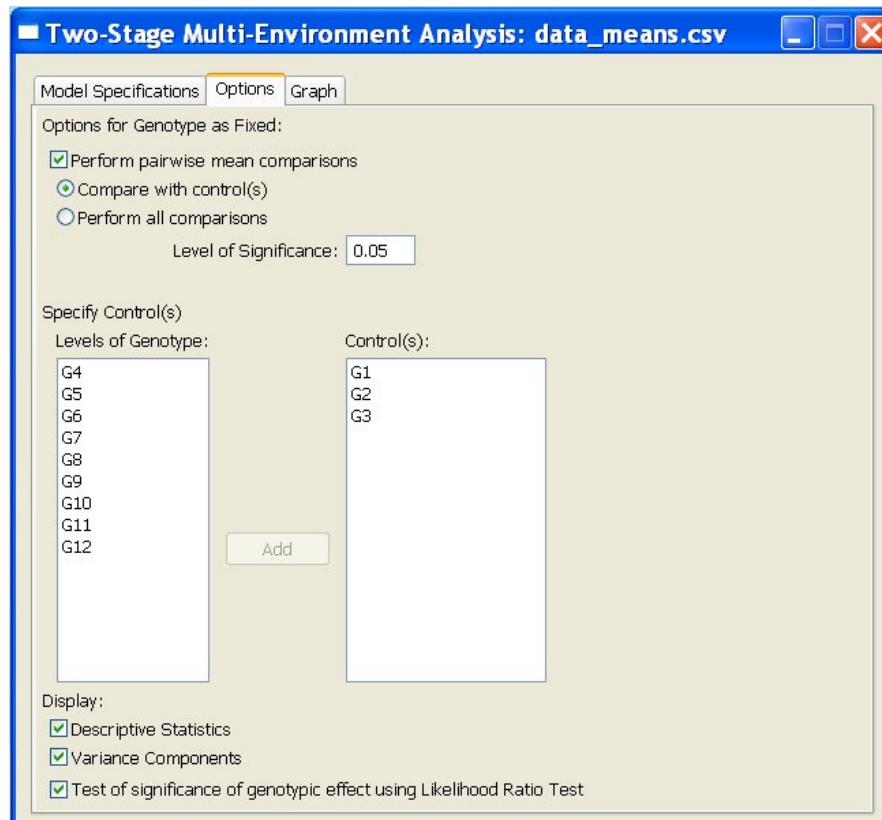
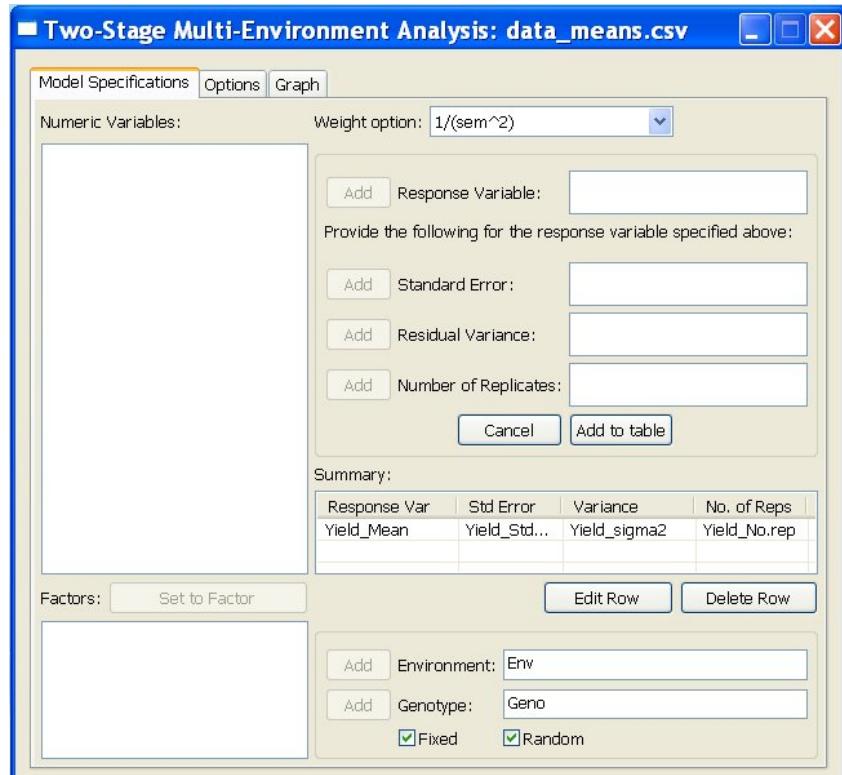
Perform pairwise mean comparisons: Perform all comparisons

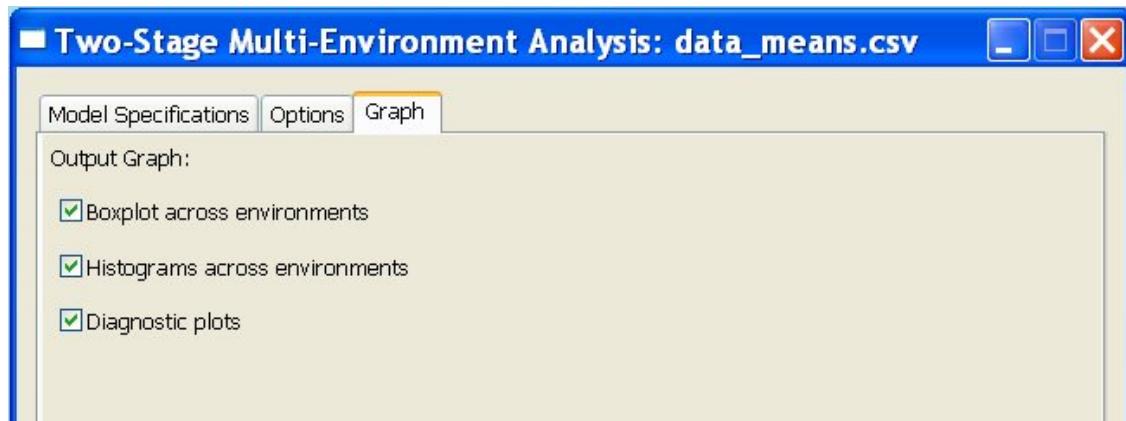
This option is not recommended when the number of genotype levels is very large.

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: C:/Documents and  
Settings/NSales/workspace3/Star/Projects/SampleProject/Data/Two_stage.csv
```

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

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

```
-----  
RESPONSE VARIABLE: Yield_Mean  
-----
```

```
Trial Summary:
```

```
Number of observations read: 132  
Number of observations used: 132
```

Factors	Number of Levels	Levels
Geno	12	G1 G10 G11 ... G9
Env	10	E1 E10 E2 ... E9

Descriptive Statistics

```
Descriptive Statistics:
```

Variable	N_NonMissObs	Mean	StdDev
Yield_Mean	132	1.302903	0.6795893

Estimates of Variance Components

```
Variance Components Table:
```

Groups	Variance	Std.Dev.
1 Env	0.1897621	0.4356169
2 Geno:Env	0.1571788	0.3964579
3 Residual	0.3061285	0.5532888

Test for Genotypic Effect

Test for Significance of Genotypic Effect using LRT:

Linear Mixed Model fit by Maximum likelihood ratio test
Response Variable: Yield_Mean

Chisq	Pr(>Chisq)	
Geno	7.406	0.7653

Stability Analysis

Stability Analysis using Finlay-Wilkinson Model

	Slope	SE	t.value	Prob	MSReg	MSDev
G1	0.2209859	0.3607000	0.6126583	0.5571122608	0.09453183	0.25184967
G10	0.5349338	0.3399233	1.5736896	0.1542054570	0.55392265	0.22367166
G11	1.2772300	0.2253178	5.6685712	0.0004711780	3.15781997	0.09827434
G12	0.7394037	0.3159928	2.3399384	0.0474202468	1.05830861	0.19328737
G2	0.8758440	0.2448416	3.5771857	0.0072177703	1.48491861	0.11604320
G3	1.5753239	0.2984000	5.2792351	0.0007468977	4.80384350	0.17236411
G4	0.9041620	0.3669859	2.4637509	0.0390894644	1.58249223	0.26070418
G5	1.1692288	0.4292660	2.7237862	0.0260954126	2.64635530	0.35669919
G6	0.8928841	0.3689568	2.4200238	0.0418485379	1.54326087	0.26351181
G7	0.8659759	0.2848161	3.0404736	0.0160517281	1.45164620	0.15702843
G8	1.1409029	0.2507543	4.5498842	0.0018746610	2.51968629	0.12171547
G9	1.3525664	0.3351228	4.0360323	0.0037564081	3.54132913	0.21739874

Stability Analysis using Shukla's model

	lower	est.	upper
G1	0.37799438	0.6914745	1.264932
G10	0.12801056	0.4985676	1.941790
G11	0.08091513	0.3466871	1.485407
G12	0.15972737	0.6173718	2.386241
G2	0.10842668	0.4345654	1.741704
G3	0.16271850	0.6702701	2.760976
G4	0.16836667	0.6421992	2.449534
G5	0.16257788	0.6519746	2.614567
G6	0.12219454	0.4981781	2.031035
G7	0.12996756	0.5252230	2.122524
G8	0.11432187	0.4677800	1.914053
G9	0.11710826	0.4879952	2.033497

AMMI Analysis

AMMI Analysis

Percentage of Total Variation Accounted for by the Principal Components:

	percent	acum	Df	Sum.Sq	Mean.Sq	F.value	Pr.F
PC1	38.2	38.2	19	27.739823	1.459991	9.80	0.0000
PC2	26.8	65.0	17	19.496491	1.146852	7.70	0.0000
PC3	15.9	80.9	15	11.595372	0.773025	5.19	0.0000
PC4	8.0	88.9	13	5.831492	0.448576	3.01	0.0004
PC5	5.3	94.2	11	3.828161	0.348015	2.34	0.0092
PC6	3.3	97.5	9	2.423845	0.269316	1.81	0.0665
PC7	1.6	99.1	7	1.173224	0.167603	1.13	0.3444
PC8	0.8	99.9	5	0.548789	0.109758	0.74	0.5941
PC9	0.1	100.0	3	0.066183	0.022061	0.15	0.9296
PC10	0.0	100.0	1	0.000000	0.000000	0.00	1.0000

ANOVA Table:

Df	Sum Sq	Mean Sq	F value	Chisq	Pr(>Chisq)
Geno	11	2.1267	0.19334	0.6941	7.4060 0.7653

Pairwise Mean Comparisons

Significant Pairwise Comparisons (if any):

Compared with control(s)

	Trmt[i]	Trmt[j]	Estimate	lwr	upr
1	G4	G1	-1.420552	-2.240842	-0.6002629
2	G5	G2	-1.687103	-2.507392	-0.8668134
3	G6	G3	-1.249158	-2.069448	-0.4288690
4	G7	G1	-1.529025	-2.349314	-0.7087356
5	G8	G2	-1.434649	-2.254938	-0.6143595
6	G9	G3	-1.364513	-2.184803	-0.5442240
7	G10	G1	-1.320355	-2.140645	-0.5000660
8	G11	G2	-1.496560	-2.316849	-0.6762705
9	G12	G3	-1.434719	-2.255008	-0.6144296

=====

GENOTYPE AS: Random

=====

RESPONSE VARIABLE: Yield_Mean

Trial Summary:

Number of observations read: 132

Number of observations used: 132

Factors	Number of Levels	Levels
Geno	12	G1 G10 G11 ... G9
Env	10	E1 E10 E2 ... E9

Descriptive Statistics

Descriptive Statistics:

Variable	N_NonMissObs	Mean	StdDev
1 Yield_Mean	132	1.302903	0.6795893

Estimates of Variance Components

Variance Components Table:

	Groups	Variance	Std.Dev.
1	Geno	0.0000000	0.0000000
2	Env	0.1906016	0.4365794
3	Geno:Env	0.1470054	0.3834128
4	Residual	0.2959550	0.5440175

Test for Genotypic Effect

Test for Significance of Genotypic Effect:

Linear Mixed Model fit by Maximum likelihood ratio test

Response Variable: Yield_Mean

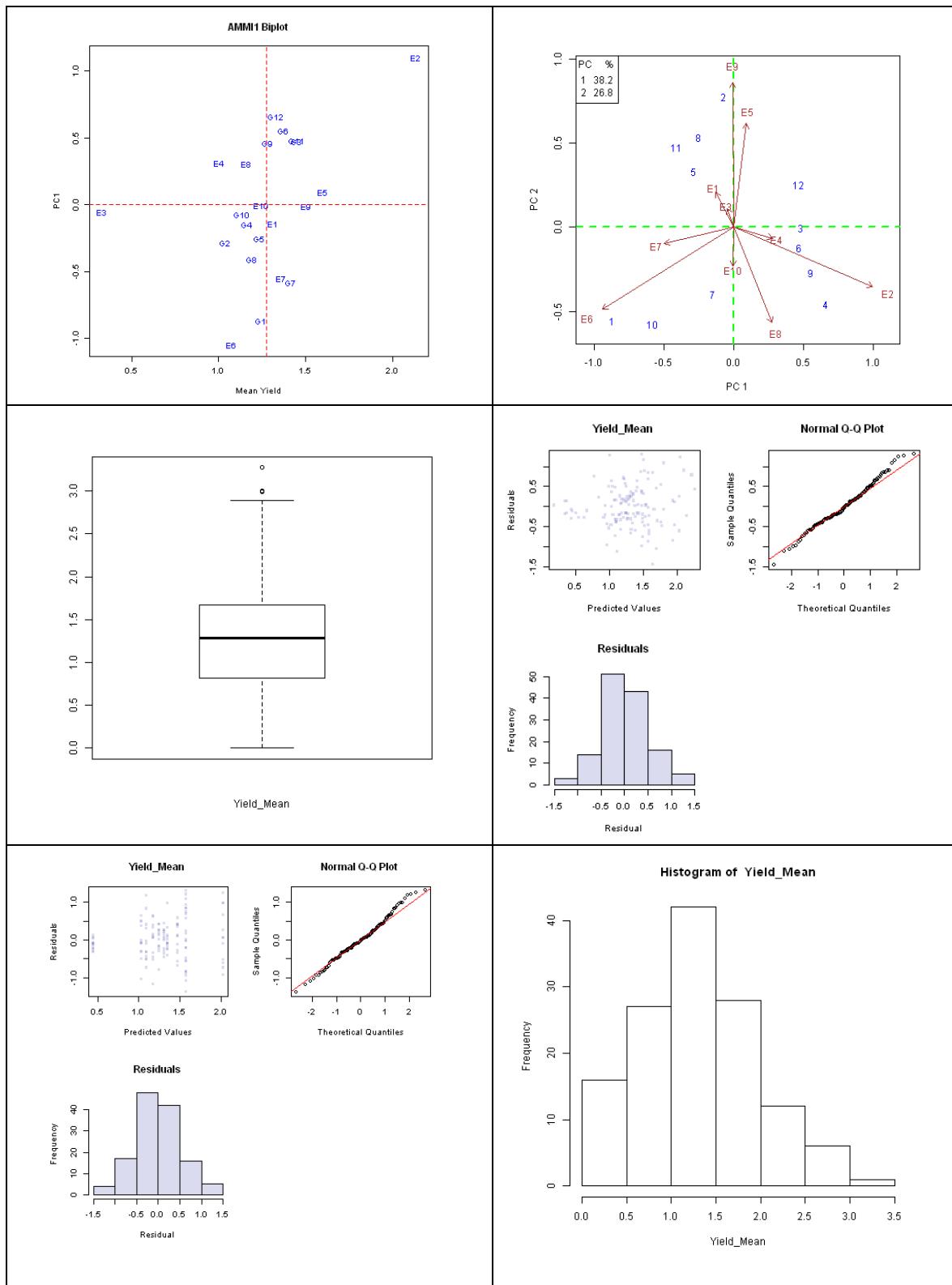
	Chisq	Pr(>Chisq)
Geno	0	1

Estimate of Heritability

Heritability:

0

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



4. QTL ANALYSIS

(NOTE: Currently analysis is done per environment level only)

4.1. Predicted Means as Input

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

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

genotype	pred	ue	env
1 G_001	106.0946921	92.66939637	1
2 G_002	69.115231	92.66939637	1
3 G_003	131.6845468	92.66939637	1
4 G_004	116.5943479	92.66939637	1
5 G_005	110.5828097	92.66939637	1
6 G_006	65.38761326	92.66939637	1
7 G_007	77.01281917	92.66939637	1
8 G_008	99.30493453	92.66939637	1
9 G_009	90.64883245	92.66939637	1
10 G_010	61.68259222	92.66939637	1
11 G_011	76.19990418	92.66939637	1
12 G_012	89.64501032	92.66939637	1
13 G_013	82.91426834	92.66939637	1
14 G_014	107.5512651	92.66939637	1
15 G_015	85.69086803	92.66939637	1
16 G_016	123.3347109	92.66939637	1
17 G_017	73.00071837	92.66939637	1
18 G_018	82.43726154	92.66939637	1

- Choose **Analysis > QTL Analysis**.
- 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* field is regarded by R as numerical variable, it has to be changed as factors. Choose this variable and click on the **Set to Factor** button.
- Specify the response variable and genotype factor. Specifying the Environment factor is optional. For the example, select *pred*, *genotype* and *env* as response variable, genotype and environment factors, respectively.

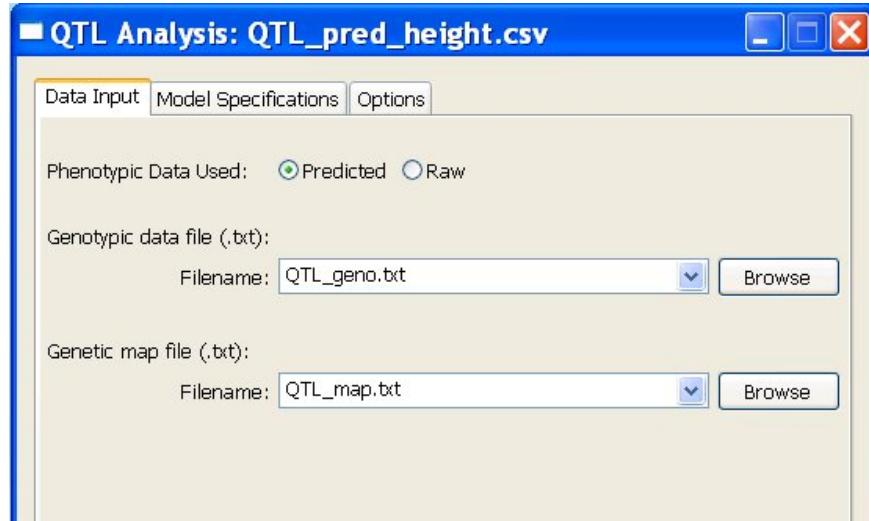
Environment Level(s)

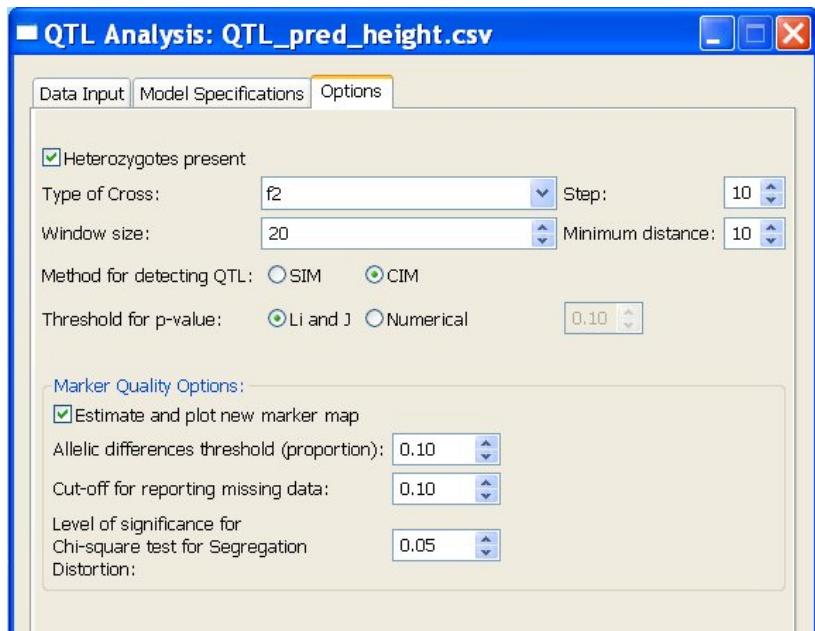
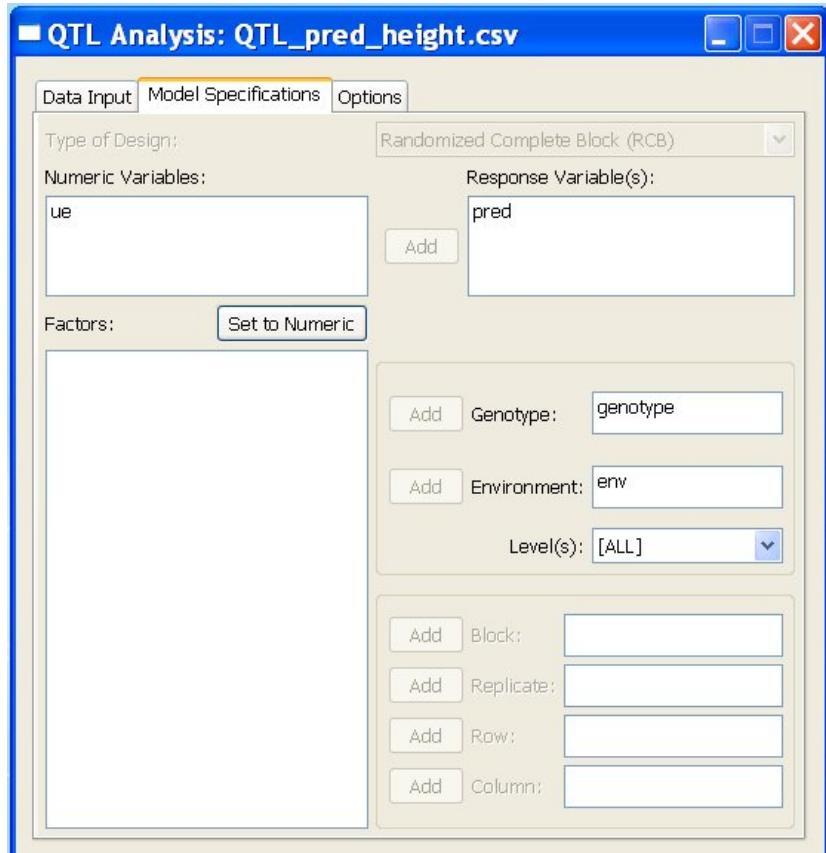
If the Environment factor is specified, the user has the option to perform the analysis for each of the environment levels by selecting “[ALL]”. To perform the analysis on a specific environment level, select environment level of interest in the combo box.

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: C:/Documents and  
Settings/NSales/workspace3/Star/Projects/SampleProject/Data/QTL_pred_height.csv  
  
QTL ANALYSIS  
  
Method: CIM  
  
TRAIT: pred  
  
ENVIRONMENT: 1
```

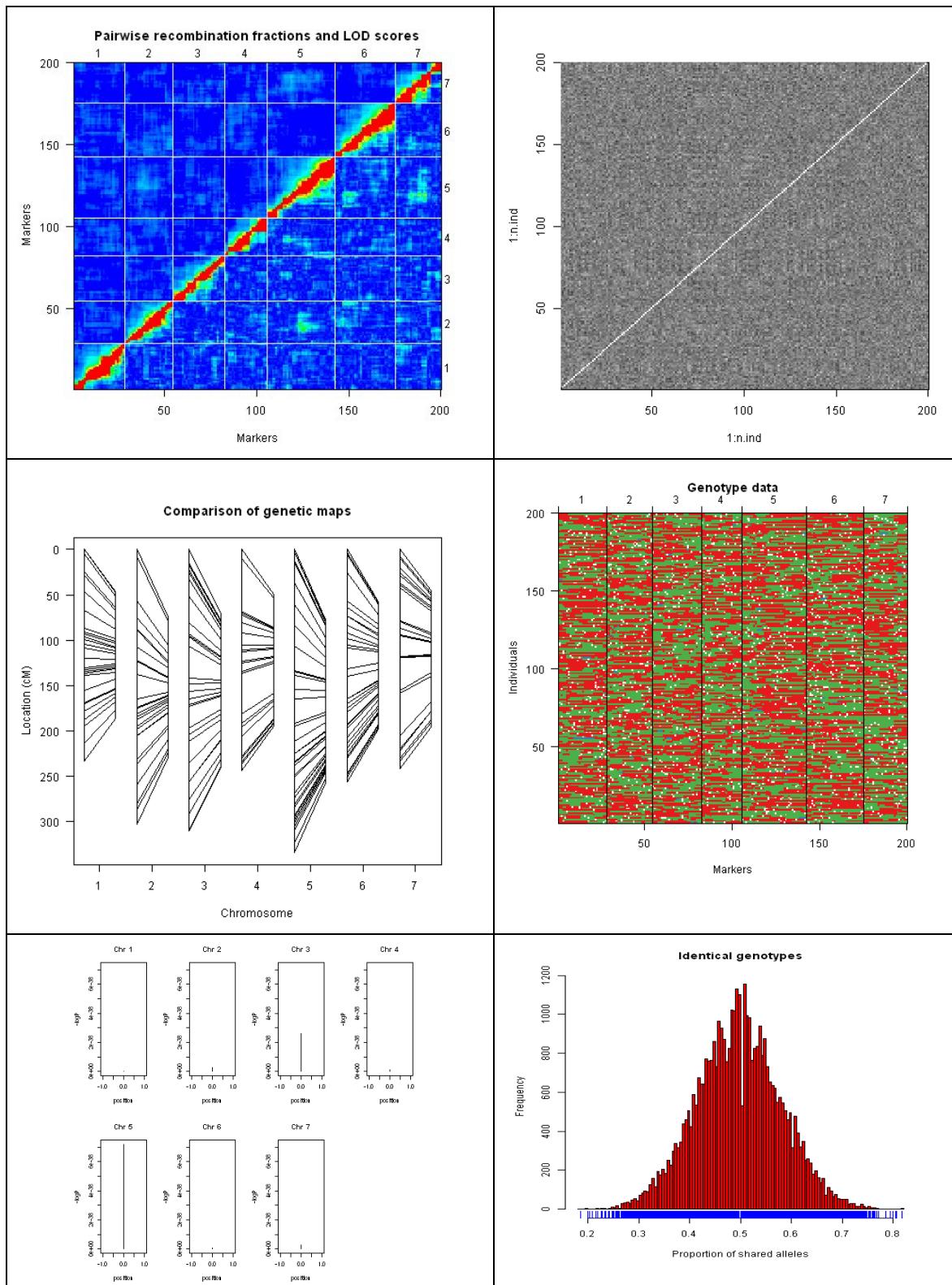
LOD of All Markers (partial results are shown below)

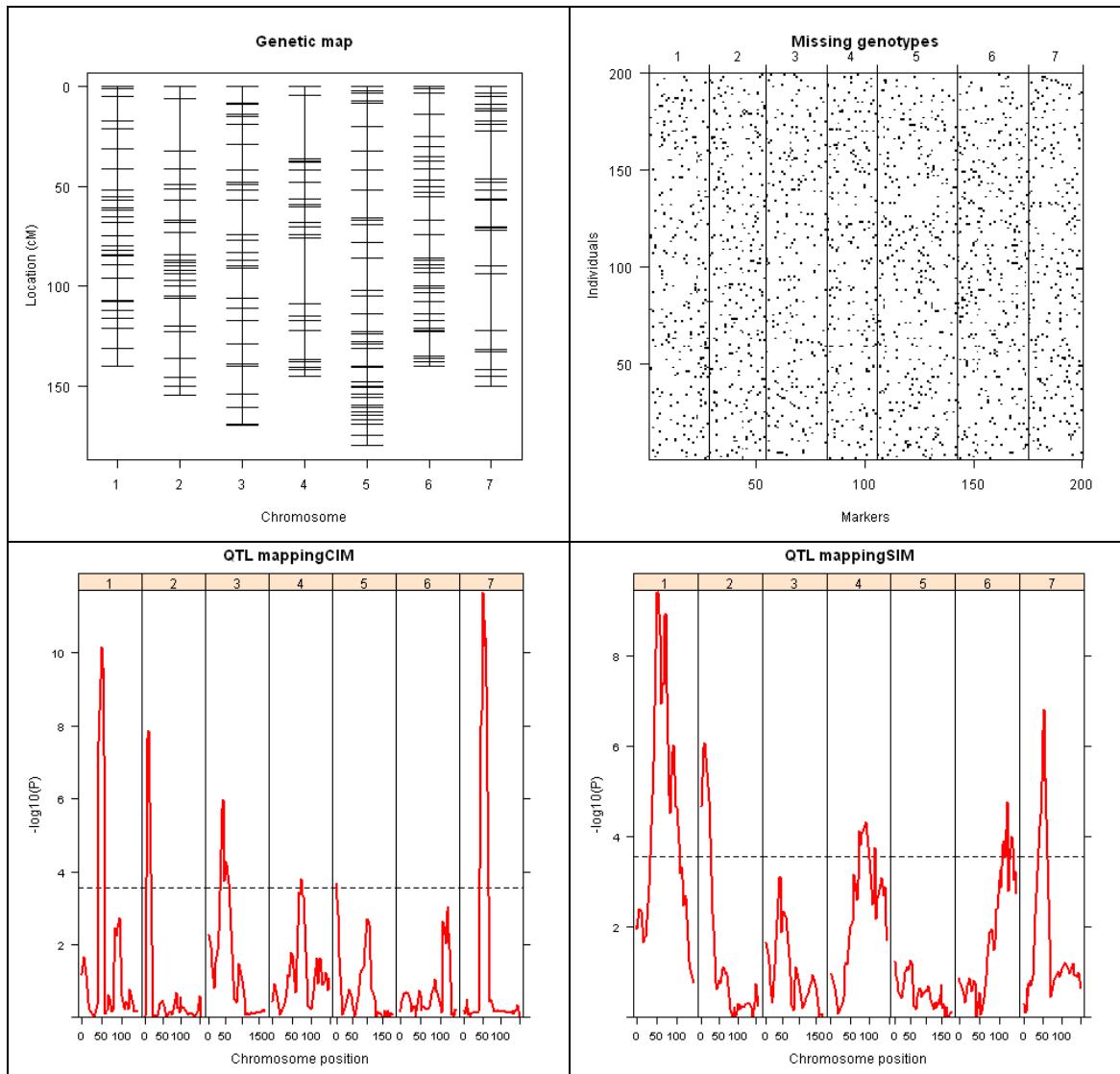
```
QTL RESULT (ALL):  
marker Chr Pos LOD  
1 M_0001 1 0 1.174800566  
2 M_0002 1 1 1.203821631  
3 M_0006 1 5 1.668347468  
4 1_loc10 1 10 1.188279464  
5 M_0018 1 17 0.402935738  
6 1_loc20 1 20 0.225377662  
7 M_0022 1 21 0.167893203  
8 1_loc30 1 30 0.027011398  
9 M_0032 1 31 0.010962483  
10 1_loc40 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:





4.2. Raw Data as Input

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

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

ENV	REP	PLOTS	GENOTYPE	HEIGHT	FTIME
1	1	1	G_016	117.4237093	60
2	1	1	G_086	82.47428239	44
3	1	1	G_081	91.91906885	48
4	1	1	G_152	119.0191347	61
5	1	1	G_113	121.623271	62
6	1	1	G_085	93.37929492	48
7	1	1	G_082	105.644906	54
8	1	1	G_035	58.96327784	31
9	1	1	G_011	77.92405473	40
10	1	1	G_058	60.07218663	32
11	1	1	G_097	90.1238785	46
12	1	1	G_200	109.2684327	57
13	1	1	G_071	95.83671078	50
14	1	1	G_037	103.0534553	53
15	1	1	G_111	92.76190898	47
16	1	1	G_087	64.92688445	34
17	1	1	G_120	113.5499252	59
18	1	1	G_136	59.42130001	31

- Choose **Analysis > QTL Analysis**.
- 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

Type of Design

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

- Opening the data for the first time, *ENV* and *REP* fields are regarded by R as numerical variables, they need to be changed as factors. Choose these variable and click on the **Set to Factor** button.
- Specify the response variable and genotype factor. Specifying the Environment factor is optional. Additional fields are required depending on the type of design selected. For the example, select *HEIGHT* and *FTIME* as response variables, *GENOTYPE* as genotype factor and *ENV* as environment factor.

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

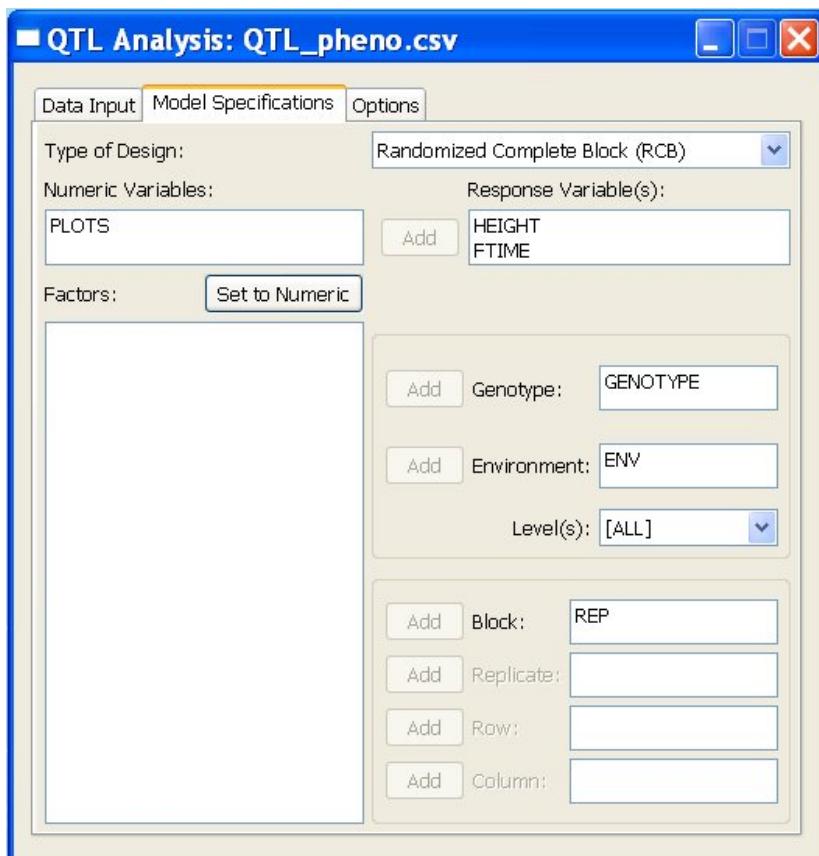
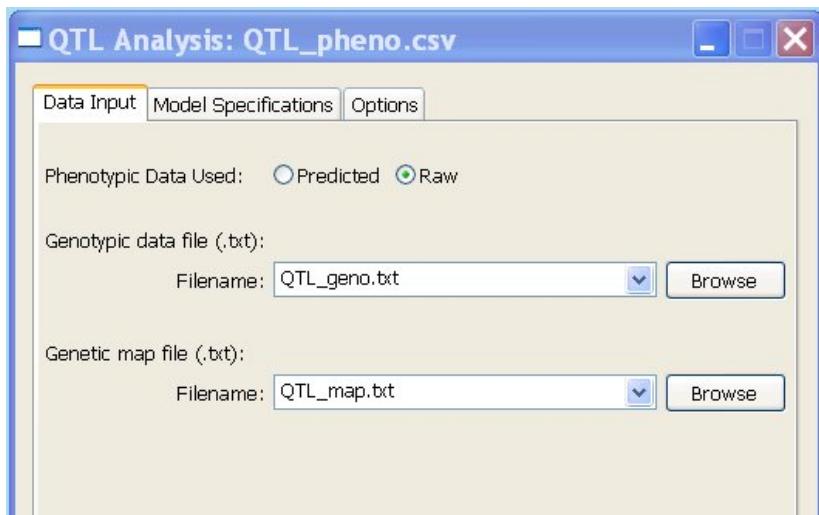
This field is required if the design is Augmented Latin Square or Row-Column.

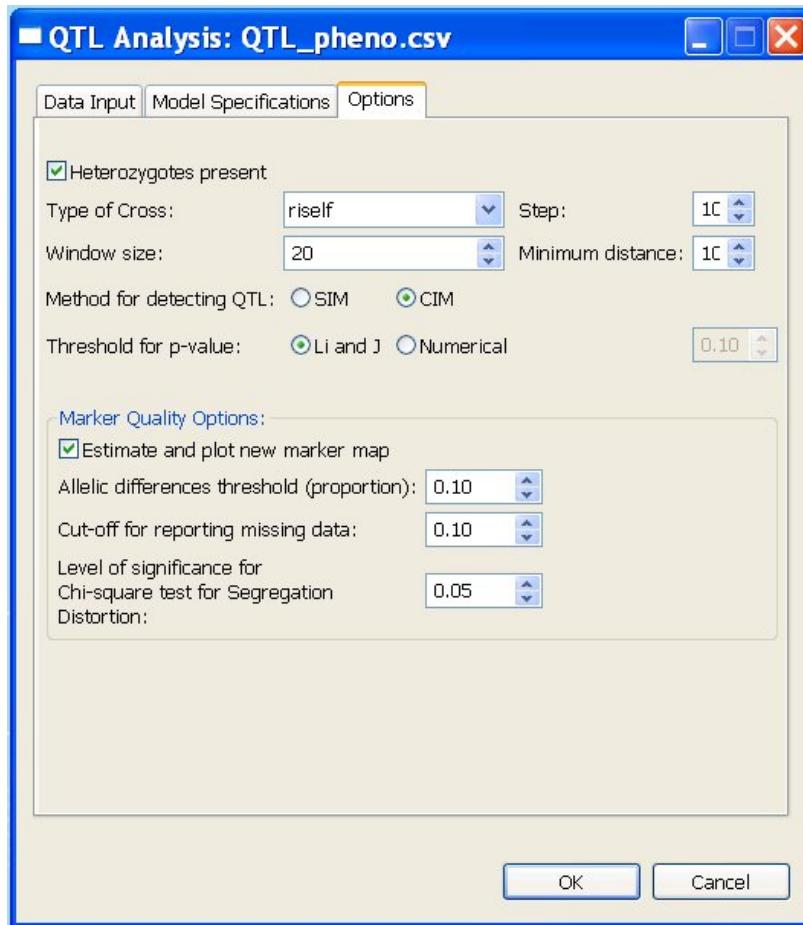
- For the example, select *REP* as blocking factor.

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* and *ENV = 1*) is shown below:

```
DATA FILE: C:/Documents and  
Settings/NSales/workspace3/Star/Projects/SampleProject/Data/QTL_pheno.csv  
  
QTL ANALYSIS  
  
Method: CIM  
  
TRAIT: HEIGHT  
  
ENVIRONMENT: 1
```

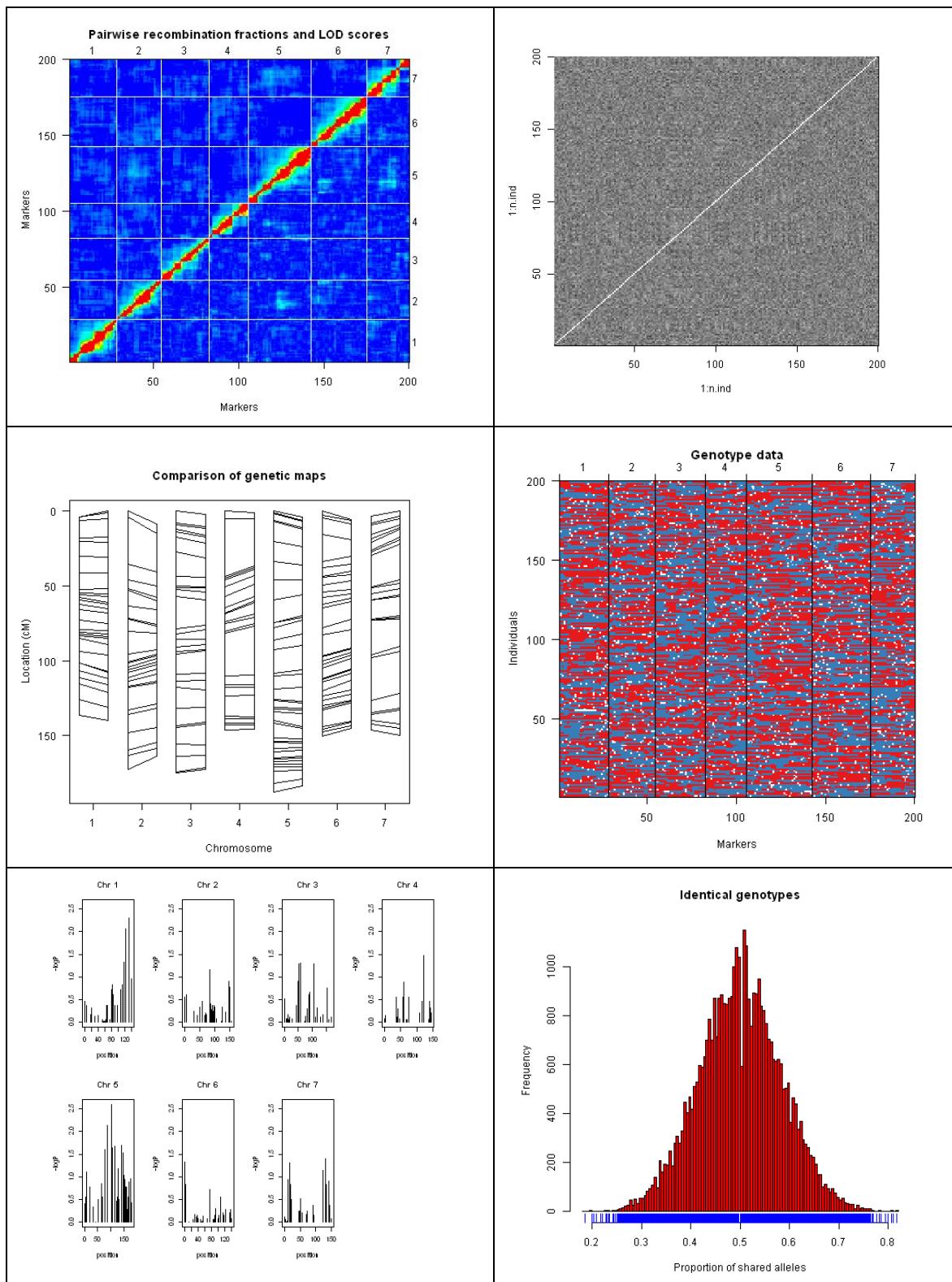
LOD of All Markers (partial results are shown below)

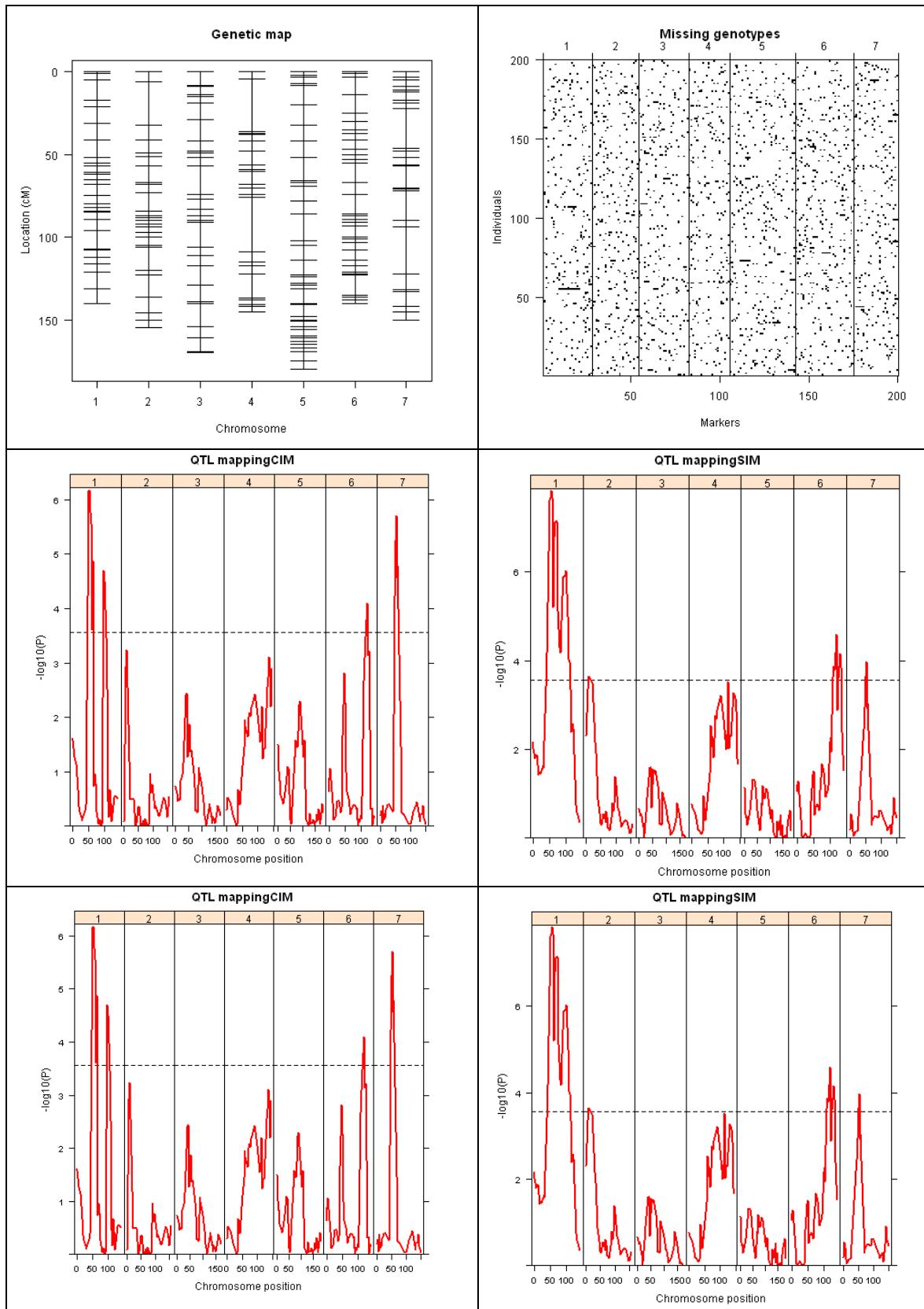
```
QTL RESULT (ALL):
marker Chr Pos      LOD
1       M_0001   1    0 1.719838121
2       M_0002   1    1 1.677144227
3       M_0006   1    5 1.391695682
4       1_loc10  1   10 1.305053123
5       M_0018   1   17 0.822234428
6       1_loc20  1   20 0.490251111
7       M_0022   1   21 0.378632136
8       1_loc30  1   30 0.033990981
9       M_0032   1   31 0.076251512
10      1_loc40  1   40 0.412881994
11      M_0042   1   41 0.481624267
12      1_loc50  1   50 3.032312237
13      M_0053   1   52 2.993300100
14      M_0056   1   55 2.393748375
15      M_0058   1   57 2.050005978
16      1_loc60  1   60 0.800187756
17      M_0062   1   61 1.027929889
18      M_0063   1   62 0.004544941
19      M_0066   1   65 0.814112679
20      M_0069   1   68 1.007243321
21      1_loc70  1   70 0.802144754
22      M_0076   1   75 0.223197350
23      M_0081   1   80 0.642217439
24      M_0083   1   82 0.575348973
25      M_0085   1   84 0.295955315
26      M_0086   1   85 0.178233708
27      M_0090   1   89 0.260128196
28      1_loc90  1   90 0.223594713
29      M_0097   1   96 4.349593525
30      1_loc100 1  100 4.212653085
31      M_0108   1  107 2.806241230
32      M_0109   1  108 2.437075463
33      1_loc110 1  110 0.343900108
34      M_0113   1  112 0.087243507
35      M_0117   1  116 0.602507003
36      1_loc120 1  120 0.122423501
37      M_0122   1  121 0.038678013
38      1_loc130 1  130 0.450427269
39      M_0132   1  131 0.485505126
40      M_0141   1  140 0.447614411
41      M_0142   2    0 0.139913839
42      M_0148   2    6 2.879883229
43      2_loc10  2   10 3.193303564
44      2_loc20  2   20 0.550213145
45      2_loc30  2   30 0.550213145
```

Characteristics of the Selected Markers

```
QTL RESULT (SELECTED):
marker Chr Pos      LOD      m.eff      Rsq
1 M_0097   1  96 4.349594 8.140951 0.06140629
2 M_0913   6 117 4.174088 6.884556 0.08838039
3 M_0989   7  52 5.281438 6.001867 0.11451457
```

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





5. SELECTION INDEX

The steps to perform Selection Index Analysis using *PBTools* are listed below:

- On the Project Explorer, locate the *SI_traits.csv* file from the *Data* folder of the project named *SampleProject*. Double-click the 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*, ...).

The screenshot shows the PBTools software interface. The title bar reads "Plant Breeding Tools - PBTools/Projects/SampleProject". The left pane is the "Project Explorer" showing a list of files and folders: GenMean(raw).csv, GenMean(summaryStats).csv, NC1_ME.csv, NCII_ME.csv, NCIII_ME.csv, QTL_genotype.txt, QTL_map.txt, QTL_pheno.csv, QTL_pred_height.csv, RCB_Multi.csv, RCB_Multi_ReshapeToWide.csv, SI_markers.csv, SI_qtl.csv, SI_traits.csv (which is selected), SI_weights.csv, TTC_ME.csv, Two_stage.csv, and Output. The right pane is the "Data Viewer" showing a table titled "SI_traits.csv" with the following data:

	REP	Block	ENTRY	MFL1	FFL1	EHT1	PHT1	GY1
1	1	12	1	103	101	64	11	10
2	1	12	2	106.86	106.67	96.43	14	11
3	1	24	3	97.75	101.67	78.33	15	10
4	1	10	4	103.33	105.14	74.44	13	10
5	1	19	5	95.3	99.33	85	15	10
6	1	22	6	102.25	104.33	78.57	12	10
7	1	19	8	103.25	104	81.5	13	10
8	1	14	9	100	100.6	73.89	13	10
9	1	8	10	106.33	105	77.5	12	10
10	1	17	12	102	103.5	77.22	13	10
11	1	24	13	98	99.8	77.5	15	10
12	1	1	14	109	101.98416	55	77	10
13	1	5	15	101.63	101.25	73.75	14	10
14	1	21	16	108.75	101.98416	80	14	10
15	1	14	17	106.2	97.67	41.88	99	10
16	1	6	18	111.5	109.5	75	11	10
17	1	4	19	102	102.2	71.11	13	10

- Choose **Analysis > Selection Index**.
- 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.

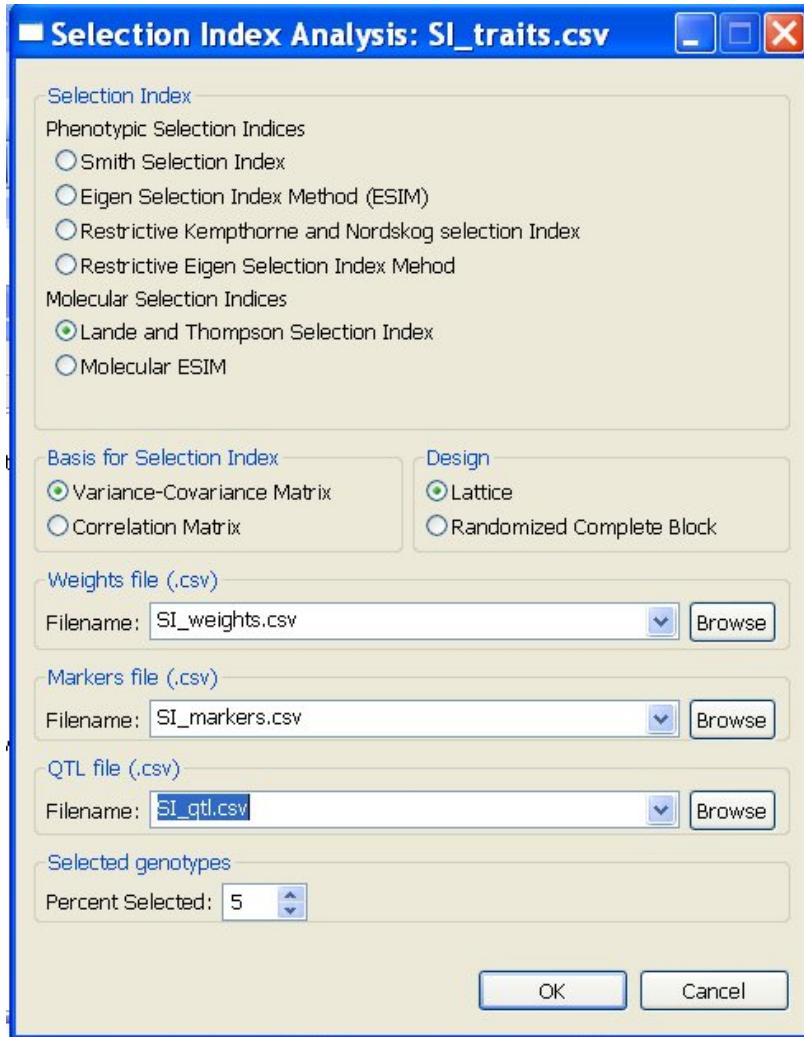
Markers file and QTL file

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.

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



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

```
DATA FILE: C:/Documents and  
Settings/NSales/workspace3/Star/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
Entry 8	99.96	100.72	77.75	138.50	85.50	104.25	101.70	80.68	126.22	71.43
Entry 9	100.58	99.97	90.20	149.33	42.06	98.47	98.62	98.32	154.44	40.00
Entry 10	103.81	103.00	87.36	146.25	27.22	103.28	104.50	90.87	143.69	11.50
Entry 12	102.50	105.75	72.86	117.78	0.00	100.70	101.12	74.69	125.84	0.00
Entry 13	96.14	96.10	81.75	162.75	126.75	96.17	96.41	78.00	146.50	41.00
Entry 14	107.15	104.16	53.25	91.50	33.00	107.00	111.50	47.44	85.25	0.00
Entry 15	97.00	95.00	84.93	159.10	387.09	97.00	95.31	88.51	153.27	183.41
Entry 16	106.25	102.49	83.75	137.88	15.50	101.84	103.82	80.89	145.22	88.00
Entry 17	101.53	97.25	53.72	121.36	177.22	99.72	98.53	65.70	138.14	268.78
Entry 18	108.03	108.41	93.00	144.56	11.94	108.87	100.74	95.97	139.69	0.00

6. MATING DESIGNS

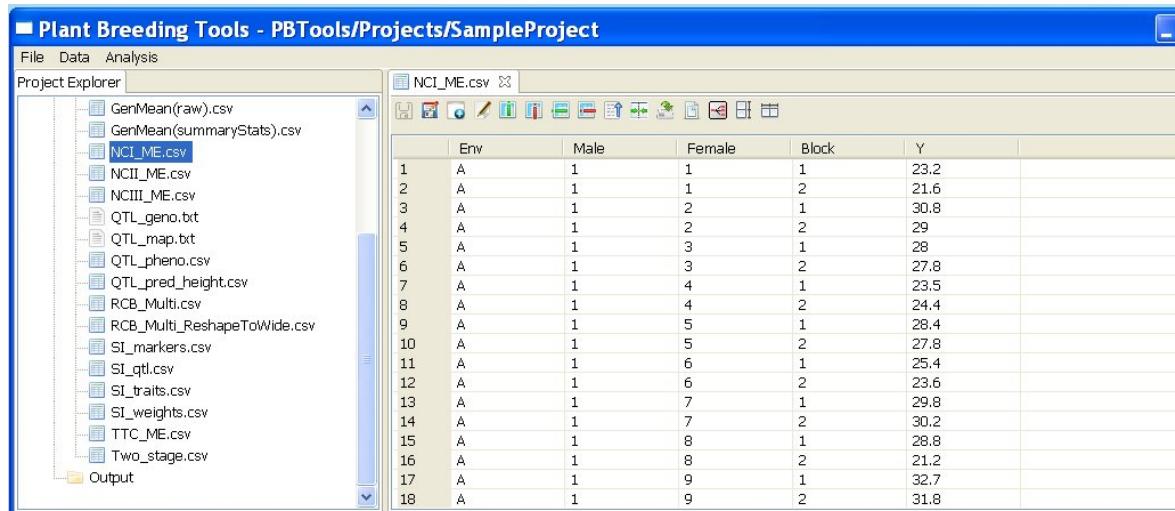
(NOTE: Currently multiple-environment analyses can only handle balanced data)

6.1. 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 using *PBTools* are listed below:

- On the Project Explorer, locate the *NCI_ME.csv* file from the *Data* folder of the project named *SampleProject*. 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**
- Opening the data for the first time, *Block*, *Male* and *Female* 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 two available experimental designs, Completely Randomized Design (CRD) and Randomized Complete Block Design (RCB).

Data Input

The input data for the analysis may be plot-means or observations of individual plants (*not yet implemented*). If the selected design is CRD, the required fields are the *Female*, *Male* and *Replicate* for plot-mean data and the *Female*, *Male*, *Replicate* and *Individual* for the individual data. If the design is RCB, the required fields are the *Female*, *Male* and *Block* for plot-mean data and the *Female*, *Male*, *Block* and *Individual* for the individual data.

'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).

'Perform Analysis Per Site' Option

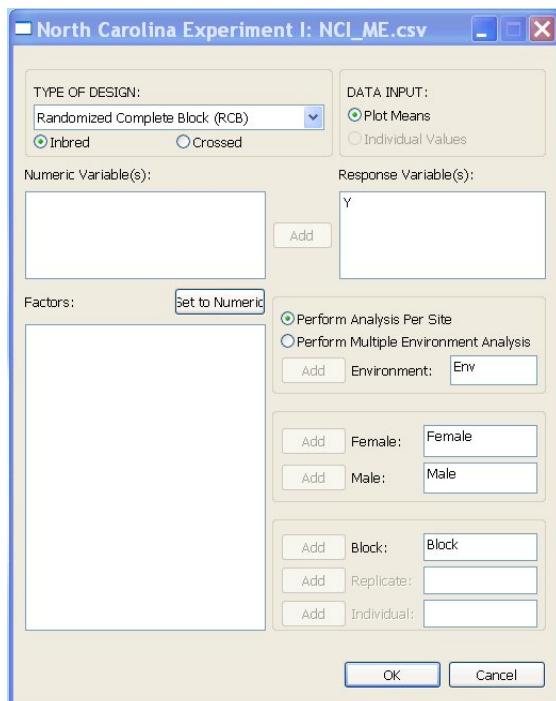
If this option is selected and the *Environment* factor is specified, *PBTools* will perform the analysis for each level of the *Environment* factor.

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.

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

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

```
RESPONSE VARIABLE: Y
```

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

```
DATA SUMMARY:
```

Factors	Number of Levels	Levels
Env	1	A
Male	4	1 2 3 4
Female	11	1 10 11 2 3 ... 9
Block	2	1 2

```
Number of observations read: 88
```

```
Number of missing observations: 0
```

Analysis of Variance Table

```
ANOVA TABLE FOR THE EXPERIMENT
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Block	1	16.0	15.98	2.167	0.148
Male	3	479.9	159.98	21.696	1.04e-08
Male:Female	40	1161.7	29.04	3.939	9.90e-06
Residuals	43	317.1	7.37		

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

Estimated Variance Components of Random Effects and the Estimated Effects of the Fixed 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

```
Fixed Effects:
```

	Estimate	Std. Error	t value
(Intercept)	28.2989	1.3841	20.4459

```
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 and Heritability

ESTIMATES OF GENETIC VARIANCE COMPONENTS:

	Estimate
VA	11.9036
VD	4.8824
h ² -narrow sense	0.4927
H ² -broad sense	0.6948
Dominance Ratio	0.9057

ESTIMATES OF HERITABILITY:

	Family Selection	Narrow Sense	Broad sense
Male	0.82	0.25	0.69
Female	0.75	0.90	1.10
Full-sib	0.82	0.69	0.90

6.2. 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 using *PBTools* are listed below:

- On the Project Explorer, locate the *NCII_ME.csv* file from the *Data* folder of the project named *SampleProject*. 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*.

Env	Female	Male	Block	Y
1	A	1	9	59.17
2	A	1	9	61.62
3	A	1	9	48.15
4	A	1	10	55.87
5	A	1	10	58.48
6	A	1	10	55.83
7	A	1	11	42.4
8	A	1	11	49.77
9	A	1	11	33.17
10	A	1	12	50.11
11	A	1	12	54.32
12	A	1	12	53.22
13	A	1	13	56.65
14	A	1	13	57.1
15	A	1	13	54.65
16	A	1	14	56.88
17	A	1	14	59.53
18	A	1	14	56.61

- Choose **Analysis > Mating Designs > North Carolina II**
- Opening the data for the first time, *Block*, *Male* and *Female* fields in the data file 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 two available experimental designs, Completely Randomized Design (CRD) and Randomized Complete Block Design (RCB).

Data Input

The input data for the analysis may be plot-means or observations of individual plants (*not yet implemented*). If the selected design is CRD, the required fields are the *Female*, *Male* and *Replicate* for plot-mean data and the *Female*, *Male*, *Replicate* and *Individual* for the individual data. If the design is RCB, the required fields are the *Female*, *Male* and *Block* for plot-mean data and the *Female*, *Male*, *Block* and *Individual* for the individual data.

'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).

'Perform Analysis Per Site' Option

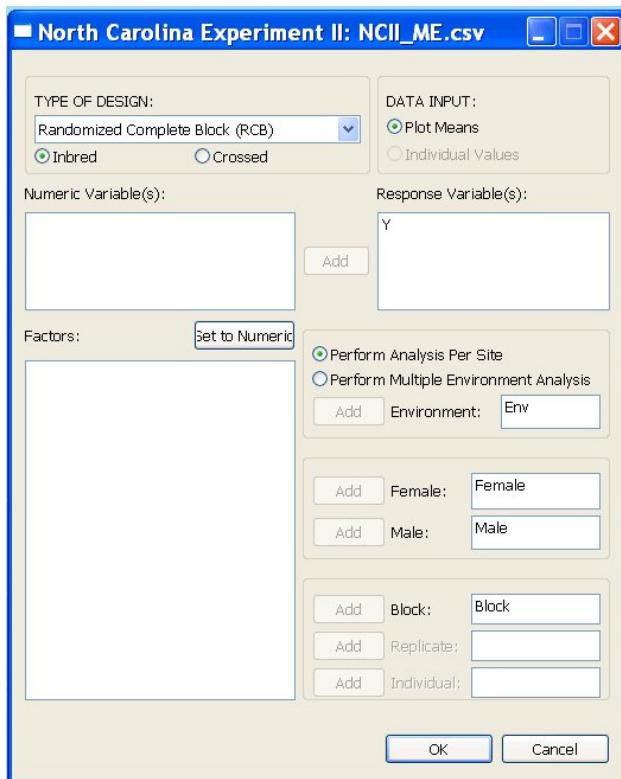
If this option is selected and the *Environment* factor is specified, *PBTools* will perform the analysis for each level of the *Environment* factor.

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.

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

DESIGN: NORTH CAROLINA EXPERIMENT II IN RCB (INBRED)

RESPONSE VARIABLE: Y

ANALYSIS FOR: Env = A

DATA SUMMARY:

Factors	Number of Levels	Levels
Env	1	A
Female	8	1 2 3 4 5 ... 8
Male	8	10 11 12 13 14 ... 9
Block	3	1 2 3

Number of observations read: 192

Number of missing observations: 0

Analysis of Variance Table

```
ANOVA TABLE FOR THE EXPERIMENT
  Df Sum Sq Mean Sq F value    Pr(>F)
Block      2   22.4   11.18   1.144  0.32197
Male       7 1112.6  158.95  16.263 4.02e-15
Female     7  735.3  105.04  10.747 1.44e-10
Male:Female 49  823.1   16.80   1.719  0.00857
Residuals 126 1231.5    9.77
-----
```

REMARK: Raw dataset is balanced.

Estimated Variance Components of Random Effects and the Estimated Effects of the Fixed 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
```

Fixed Effects:

	Estimate	Std. Error	t value
(Intercept)	55.6076	1.1379	48.8702

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 and Heritability

ESTIMATES OF GENETIC VARIANCE COMPONENTS:

	Estimate
VA	9.5997
VD	2.3418
Narrow sense heritability(plot-mean based)	0.4421
Broad sense heritability(plot-mean based)	0.5499
Dominance Ratio	0.6985

ESTIMATES OF HERITABILITY:

	Family	Selection	Narrow Sense	Broad sense
Male		0.89	0.66	0.79
Female		0.84	0.47	0.61
Full-sib		0.96	0.44	0.55

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

Data Summary

MULTIPLE ENVIRONMENT ANALYSIS

DESIGN: NORTH CAROLINA EXPERIMENT II IN RCB (INBRED)

RESPONSE VARIABLE: Y

DATA SUMMARY:

Factors	Number of Levels	Levels
Env	2	A B
Female	8	1 2 3 4 5 ... 8
Male	8	10 11 12 13 14 ... 9
Block	3	1 2 3

Number of observations read: 384

Estimated Variance Components of Random Effects and the Estimated Effects of the Fixed Effects

LINEAR MIXED MODEL FIT BY RESTRICTED MAXIMUM LIKELIHOOD:

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

AIC BIC logLik deviance REMLdev
2147.079 2186.586 -1063.54 2128.376 2127.079

Fixed Effects:

	Estimate	Std. Error	t value
(Intercept)	55.7587	0.7634	73.0416

Random Effects:

Groups	Variance	Std. Deviation
Env:Female:Male	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
Block:Env	0.1792	0.4233
Env	0.0000	0.0000
Residual	10.5157	3.2428

Genetic Variance Components and Heritability

ESTIMATES OF GENETIC VARIANCE COMPONENTS:

	Estimate
VA	2.7773
VAxE	2.2427
VD	0.8681
VDxE	3.1506
h2-narrow sense	0.1420
H2-broad sense	0.1864
Dominance Ratio	0.7907

ESTIMATES OF HERITABILITY:

	Family	Selection	Narrow Sense	Broad sense
Male	0.67	0.12	0.17	
Female	0.77	0.21	0.26	
Full-sib	0.68	0.14	0.19	

6.3. 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 *PBTools* are listed below:

- On the Project Explorer, locate the *NCIII_ME.csv* file from the *Data* folder of the project named *SampleProject*. 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*.

Env	Male	Female	Block	Y
1	A	1	1	3.1
2	A	2	1	3.8
3	A	3	1	3.9
4	A	4	1	3.7
5	A	5	1	3.4
6	A	6	1	3.2
7	A	7	1	3.3
8	A	8	1	3.5
9	A	9	1	3.8
10	A	10	1	3.6
11	A	11	1	3.6
12	A	12	1	2.5
13	A	13	1	3.5
14	A	14	1	3.7
15	A	15	1	4.5
16	A	16	1	3.2
17	A	1	2	3.6
18	A	2	2	4.2

- Choose **Analysis > Mating Designs > North Carolina III**.
- Opening the data for the first time, *Block*, *Male* and *Female* 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 two available experimental designs, Completely Randomized Design (CRD) and Randomized Complete Block Design (RCB).

Data Input

The input data for the analysis may be plot-means or observations of individual plants (*not yet implemented*). If the selected design is CRD, the required fields are the *Tester*, *F2* and *Replicate* for plot-mean data and the *Tester*, *F2*, *Replicate* and *Individual* for the individual data. If the design is RCB, the required fields are the *Tester*, *F2* and *Block* for plot-mean data and the *Tester*, *F2*, *Block* and *Individual* for the individual data.

'Perform Analysis Per Site' Option

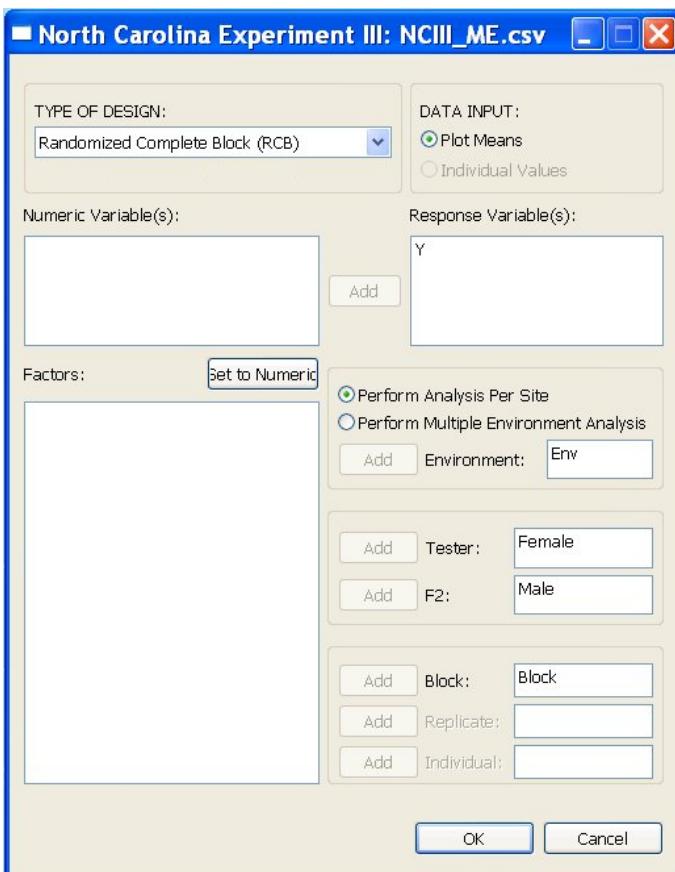
If this option is selected and the *Environment* factor is specified, *PBTools* will perform the analysis for each level of the *Environment* factor.

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.

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

```
DESIGN: NORTH CAROLINA EXPERIMENT III IN RCB
```

```
RESPONSE VARIABLE: Y
```

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

```
DATA SUMMARY:
```

Factors	Number of Levels	Levels
Env	1	A
Female	2	1 2
Block	2	1 2

```
Number of observations read: 64
```

```
Number of missing observations: 0
```

Analysis of Variance Table

```
ANOVA TABLE FOR THE EXPERIMENT  
Df Sum Sq Mean Sq F value Pr(>F)  
Block      1  3.803   3.803  11.046 0.00151  
Female     1  0.903   0.903   2.622 0.11058  
Residuals  61 20.999   0.344  
-----
```

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

Estimated Variance Components of Random Effects and the Estimated Effects of the Fixed Effects

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

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

```
AIC      BIC      logLik deviance  REMLdev  
131.1663 144.1196 -59.58313 118.3868 119.1663
```

```
Fixed Effects:
```

	Estimate	Std. Error	t value
(Intercept)	3.9969	0.3495	11.4371
Female	0.2375	0.3690	0.6436

```
Random Effects:
```

Groups	Variance	Std. Deviation
Block	0.1081	0.3287
Female	0.0287	0.1694
Female:Female	0.0287	0.1694
Residual	0.3443	0.5867

Genetic Variance Components and Heritability

ESTIMATES OF GENETIC VARIANCE COMPONENTS:

	Estimate
VA	0.1148
VD	0.2161
h ² -narrow sense	0.1700
H ² -broad sense	0.4901
h ² -family	0.1429
Dominance Ratio	1.9409

6.4. Triple Test Cross

This design involves taking a number of F₂ individuals from a cross between two inbred lines (P₁ and P₂) and crossing each back to these same two parental lines and F₁. The two parental inbreds and F₁ thus act as testers against which the F₂ are assessed.

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

- On the Project Explorer, locate the *TTC_ME.csv* file from the *Data* folder of the project named *SampleProject*. 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 F₂ 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.

	Env	Block	Female	Male	Y
1	A	1	P1	1	3.6
2	A	1	P1	2	4.5
3	A	1	P1	3	3.7
4	A	1	P1	4	4.2
5	A	1	P1	5	4.3
6	A	1	P1	6	4.2
7	A	1	P1	7	3.7
8	A	1	P1	8	3.9
9	A	1	P1	9	4.5
10	A	1	P1	10	4.9
11	A	1	P2	1	3.2
12	A	1	P2	2	3.6
13	A	1	P2	3	3.7
14	A	1	P2	4	3.6
15	A	1	P2	5	3.8
16	A	1	P2	6	3.1
17	A	1	P2	7	3.5
18	A	1	P2	8	3.8

- Choose **Analysis > Mating Designs > Triple Test Cross > Triple Test Cross (no parents)**.

- 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 two available experimental designs, Completely Randomized Design (CRD) and Randomized Complete Block Design (RCB).

Data Input

The input data for the analysis may be plot-means or observations of individual plants (*not yet implemented*). If the selected design is CRD, the required fields are the *Tester*, *F2* and *Replicate* for plot-mean data and the *Tester*, *F2*, *Replicate* and *Individual* for the individual data. If the design is RCB, the required fields are the *Tester*, *F2* and *Block* for plot-mean data and the *Tester*, *F2*, *Block* and *Individual* for the individual data.

‘Perform Analysis Per Site’ Option

If this option is selected and the *Environment* factor is specified, *PBTools* will perform the analysis 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.

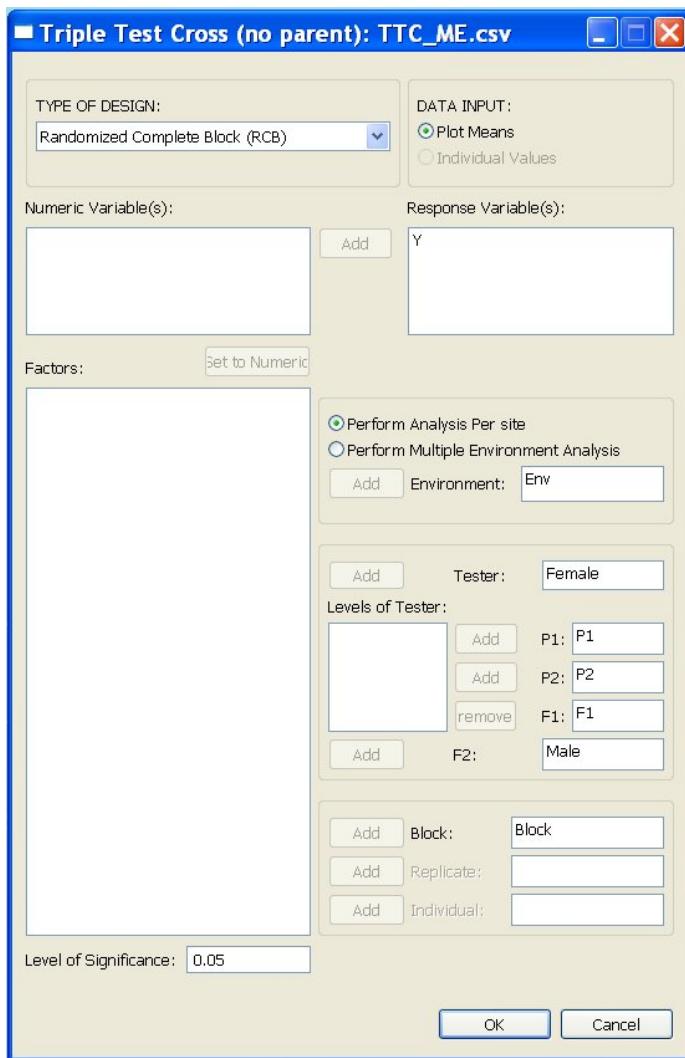
Levels of Tester

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.

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

DESIGN: TRIPLE TEST CROSS (NO PARENTS) IN RCB

RESPONSE VARIABLE: Y

ANALYSIS FOR: Env = A

DATA SUMMARY:
Factors Number of Levels Levels
Env 1 A
Block 3 1 2 3
Female 3 F1 P1 P2
Male 10 1 10 2 3 4 ... 9

Number of observations read: 90
Number of missing observations: 0

Analysis of Variance Table

ANOVA TABLE FOR THE EXPERIMENT
Df Sum Sq Mean Sq F value Pr(>F)
Block 2 1.884 0.9421 12.047 4.21e-05
Female 2 1.071 0.5354 6.847 0.00214
Male 9 9.443 1.0492 13.417 2.62e-11
Female:Male 18 1.989 0.1105 1.413 0.16042
Residuals 58 4.536 0.0782

REMARK: Raw dataset is balanced.

Testing the Significance of Genotypic Differences

ANOVA TABLE: (Trt = Female:Male)
Formula for Model 1: Y ~ Trt + (1|Block)
Formula for Model 2: Y ~ (1|Block)

Df	AIC	BIC	logLik	Chisq	Chi	Df	Pr(>Chisq)
model2	3	118.38	125.88	-56.19			
model1	32	61.02	141.02	1.49	115.36	29	0.0000

Testing for Epistasis

ANOVA FOR TESTING EPISTASIS:
SV 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
Residual 18 1.3149 0.0730

REMARK: Raw dataset is balanced.

ANOVA TABLE:
SV 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

Genetic Variance Components and Heritability

ESTIMATES OF GENETIC VARIANCE COMPONENTS:
VA = 0.4376; se = 0.03962
VD = 0.0054; se = 0.00023
VE = 0.0646
VP = 0.5076
Heritability, Broad sense = 0.8728; se = 0.00452
Heritability, Narrow sense = 0.8622; se = 0.00522
Dominance Ratio = 0.1567

6.5. Diallel Analysis (Griffing Method)

6.5.1 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 using *PBTools* are listed below:

- On the Project Explorer, locate the *Diallel_M1.csv* file from the *Data* folder of the project named *SampleProject*. 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*.

	Env	P1	P2	Block	Plant_height	Grain_yield
1	Normal	1	1	1	147.7	26.58
2	Normal	1	1	2	147.3	9.7
3	Normal	1	1	3	133.7	17.75
4	Normal	1	2	1	145	56.14
5	Normal	1	2	2	153	48.46
6	Normal	1	2	3	147	28.98
7	Normal	1	3	1	170.3	38.42
8	Normal	1	3	2	159.7	23.14
9	Normal	1	3	3	161.7	32.34

- Choose **Analysis > Mating Designs > Diallel Analysis > Griffing Method I**
- 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 two available experimental designs, Completely Randomized Design (CRD) and Randomized Complete Block Design (RCB).

Data Input

The input data for the analysis may be plot-means or observations of individual plants (*not yet implemented*). If the selected design is CRD, the required fields are the *P1*, *P2* and *Replicate* for plot-mean data and the *P1*, *P2*, *Replicate* and *Individual* for the individual data. If the design is RCB, the required fields are the *P1*, *P2* and *Block* for plot-mean data and the *P1*, *P2*, *Block* and *Individual* for the individual data.

'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.

'Perform Analysis Per Site' Option

If this option is selected and the *Environment* factor is specified, *PBTools* will perform the analysis 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.

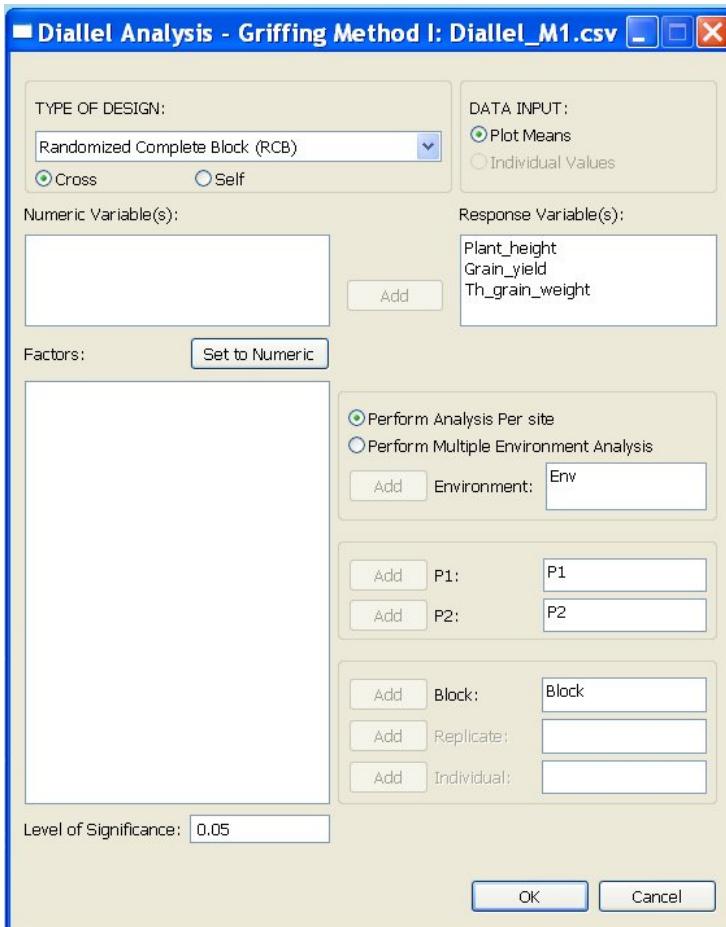
'Perform Multiple Environment Analysis' Option

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

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 Summary

```
DIALLEL ANALYSIS: GRIFFING METHOD I IN RCB (CROSS)
```

```
RESPONSE VARIABLE: Plant_height
```

```
-----
ANALYSIS FOR: Env = Normal
-----
```

```
DATA SUMMARY:
```

Factors	Number 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 missing observations: 0
```

Analysis of Variance Table

```
ANOVA TABLE FOR THE EXPERIMENT
   Df Sum Sq Mean Sq F value    Pr(>F)
Block      2   3027   1513  19.745 6.57e-08
P1          6   32497   5416  70.668 < 2e-16
P2          6   21855   3643  47.527 < 2e-16
P1:P2      36  22865     635   8.287 < 2e-16
Residuals  96   7358      77
-----
REMARK: Raw dataset is balanced.
```

Testing the Significance of Genotypic Differences

```
ANOVA TABLE FOR TESTING SIGNIFICANCE OF GENOTYPIC EFFECT
Formula: Plant_height ~ Block + P1:P2
```

```
   Df Sum Sq Mean Sq F value    Pr(>F)
Block      2  3026.53  1513.27   19.74  0.0000
P1:P2      48 77217.05 1608.69   20.99  0.0000
Residuals  96  7357.58   76.64
```

```
MATRIX OF MEANS:
```

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

Combining Ability Analysis

ANALYSIS OF VARIANCE:

SV	Df	Sum Sq	Mean Sq	F value	Pr(>F)
GCA	6	17675.67	2945.94	9.05	0.0000
SCA	21	6983.51	332.55	13.02	0.0000
Reciprocal	21	1079.84	51.42	2.01	0.0118
Error	96	2452.53	25.55		

NOTE: MS* = 325.4087 Error used for GCA MS with df = 1920.5

ESTIMATES OF VARIANCE COMPONENTS:

	Variance Component	Std. Error
GCA	187.1811	121.6995
SCA	174.9192	58.5110
Reciprocal	12.9368	8.1458
Error	25.5471	3.6874

ESTIMATES OF GENETIC VARIANCE COMPONENTS:

	Estimate
VA	748.7245
VD	699.6769
h2-narrow sense	0.5080
H2-broad sense	0.9827
Dominance Ratio	1.3671

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

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

TABLE OF STANDARD ERRORS AND LSDs:

	Std. Error	LSD
Gi	1.2506	
Sii	4.3324	
Sij	3.1057	
Rij	3.5740	
Gi-Gj	1.9104	3.7921
Sii-Sjj	6.0412	11.9917
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

6.5.2 Method 2

If no reciprocal differences exist, there is no need to make reciprocal crosses. The parents and one set of F₁'s can be analyzed.

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

- On the Project Explorer, locate the *Diallel_M2.csv* file from the *Data* folder of the project named *SampleProject*. 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 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*.

Env	P1	P2	Block	Plant_height	Grain_yield	Th
1	Normal	1	2	145	56.14	32.
2	Normal	1	2	153	48.46	25.
3	Normal	1	2	147	28.98	28.
4	Normal	1	3	170.3	38.42	23.
5	Normal	1	3	159.7	23.14	23.
6	Normal	1	3	161.7	32.34	25.
7	Normal	1	4	151	47.88	27.
8	Normal	1	4	162	19.09	26.
9	Normal	1	4	145.7	15.99	26.
10	Normal	1	5	142.7	51.27	25.

- Choose **Analysis > Mating Designs > Diallel Analysis > Griffing Method II**
- 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 two available experimental designs, Completely Randomized Design (CRD) and Randomized Complete Block Design (RCB).

Data Input

The input data for the analysis may be plot-means or observations of individual plants (*not yet implemented*). If the selected design is CRD, the required fields are the *P1*, *P2* and *Replicate* for plot-mean data and the *P1*, *P2*, *Replicate* and *Individual* for the individual data. If the design is RCB, the required fields are the *P1*, *P2* and *Block* for plot-mean data and the *P1*, *P2*, *Block* and *Individual* for the individual data.

'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.

'Perform Analysis Per Site' Option

If this option is selected and the *Environment* factor is specified, *PBTools* will perform the analysis 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.

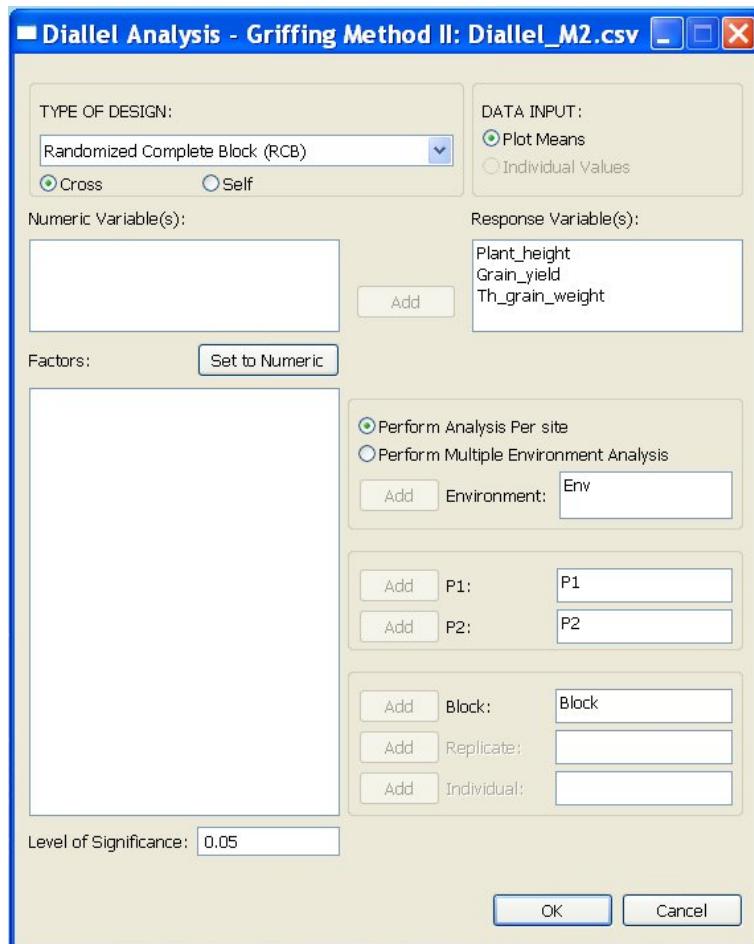
'Perform Multiple Environment Analysis' Option

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

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 Summary

```
DIALLEL ANALYSIS: GRIFFING METHOD II IN RCB (CROSS)
```

```
RESPONSE VARIABLE: Plant_height
```

```
-----  
ANALYSIS FOR: Env = Normal  
-----
```

```
DATA SUMMARY:
```

Factors	Number 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: 84
```

```
Number of missing observations: 0
```

Testing the Significance of Genotypic Differences

```
ANOVA TABLE FOR TESTING SIGNIFICANCE OF GENOTYPIC EFFECT  
Formula: Plant_height ~ Block + P1:P2
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Block	2	852.45	426.22	9.65	0.0003
P1:P2	27	36854.84	1364.99	30.92	0.0000
Residuals	54	2383.98	44.15		

```
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

Combining Ability Analysis

```
ANALYSIS OF VARIANCE:
```

SV	Df	Sum Sq	Mean Sq	F value	Pr(>F)
GCA	6	7784.37	1297.39	6.05	0.0008
SCA	21	4500.58	214.31	14.56	0.0000
Error	54	794.66	14.72		

```
ESTIMATES OF VARIANCE COMPONENTS:
```

	Estimate	Std. Error
GCA	120.3424	217.0737
SCA	199.5974	66.1426
Error	14.7159	2.8321

ESTIMATES OF GENETIC VARIANCE COMPONENTS:

	Estimate
VA	481.3695
VD	798.3895
h2-narrow sense	0.3719
H2-broad sense	0.9886
Dominance Ratio	1.8213

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

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	4.0436	8.1070
Sij-Sik	5.1148	10.2546
Sij-Skl	4.7845	9.5923

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

Data Summary

MULTIPLE ENVIRONMENT ANALYSIS
DIALLEL ANALYSIS: GRIFFING METHOD II IN RCB (CROSS)
RESPONSE VARIABLE: Plant_height

DATA SUMMARY:
Factors Number 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

Testing the Significance of Genotypic Differences

ANOVA TABLE

SV	Df	Sum Sq	Mean Sq	F	value	Pr(>F)
Env	1	17111.43	17111.43	28.18	0.0061	
Block(Env)	4	2429.29	607.32	14.44	0.0000	
Hybrid	27	80041.58	2964.50	31.42	0.0000	
HybridxE	27	2547.46	94.35	2.24	0.0018	
Error	108	4543.85	42.07			

Combining Ability Analysis

ANOVA TABLE

SV	Df	Sum Sq	Mean Sq	F value	Pr(>F)
GCA	6	54367.67	9061.28	51.14	0.0001
SCA	21	25673.91	1222.57	17.30	0.0000
GCAxE	6	1063.14	177.19	4.21	0.0008
SCAxE	21	1484.32	70.68	1.68	0.0451
Error	108	4543.85	42.07		

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

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	71.5945
SCA	191.9809
GCAxE	3.9448
SCAxE	9.5363
Error	42.0727

ESTIMATES OF GENETIC VARIANCE COMPONENTS:

	Estimate
VA	286.3779
VD	767.9238
VAE	15.7791
VDE	38.1453
h2-narrow sense	0.2490
H2-broad sense	0.9165
Dominance Ratio	2.3158

6.5.3 Method 3

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

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

- On the Project Explorer, locate the *Diallel_M3.csv* file from the *Data* folder of the project named *SampleProject*. 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*.

Env	P1	P2	Block	Plant_height	Grain_yield	Th
1	Normal	1	2	1	145	56.14
2	Normal	1	2	2	153	48.46
3	Normal	1	2	3	147	28.98
4	Saline	1	2	1	117.7	33.63
5	Saline	1	2	2	125.3	26.67
6	Saline	1	2	3	115	19.21
7	Normal	1	3	1	170.3	38.42
8	Normal	1	3	2	159.7	23.14
9	Normal	1	3	3	161.7	32.34
10	Saline	1	3	1	135	30.57
11	Saline	1	3	2	154.3	25.91
12	Saline	1	3	3	140.3	26.73

- Choose **Analysis > Mating Designs > Diallel Analysis > Griffing Method III**.
- 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 two available experimental designs, Completely Randomized Design (CRD) and Randomized Complete Block Design (RCB).

Data Input

The input data for the analysis may be plot-means or observations of individual plants (*not* yet implemented). If the selected design is CRD, the required fields are the *P1*, *P2* and *Replicate* for plot-mean data and the *P1*, *P2*, *Replicate* and *Individual* for the individual data. If the design is RCB, the required fields are the *P1*, *P2* and *Block* for plot-mean data and the *P1*, *P2*, *Block* and *Individual* for the individual data.

'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.

'Perform Analysis Per Site' Option

If this option is selected and the *Environment* factor is specified, *PBTools* will perform the analysis 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.

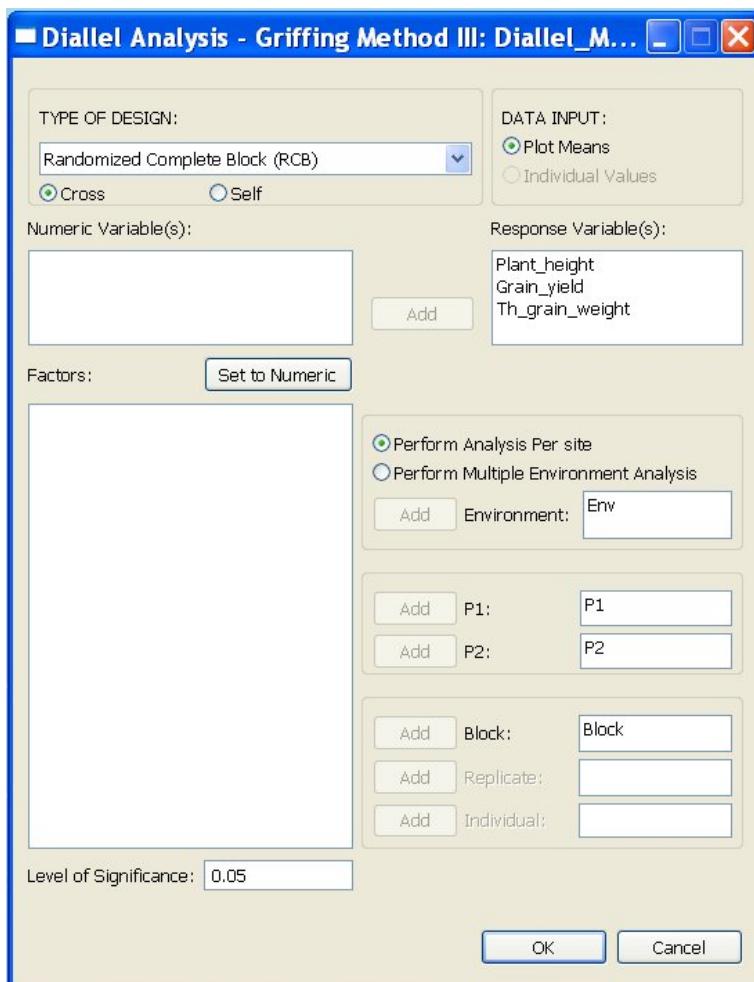
'Perform Multiple Environment Analysis' Option

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

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 Summary

```
DIALLEL ANALYSIS: GRIFFING METHOD III IN RCB (CROSS)
```

```
RESPONSE VARIABLE: Plant_height
```

```
-----  
ANALYSIS FOR: Env = Normal  
-----
```

```
DATA SUMMARY:
```

Factors	Number 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 missing observations: 0
```

Testing the Significance of Genotypic Differences

```
ANOVA TABLE FOR TESTING SIGNIFICANCE OF GENOTYPIC EFFECT  
Formula: Plant_height ~ Block + P1:P2
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Block	2	3024.48	1512.24	18.44	0.0000
P1:P2	41	64423.40	1571.30	19.16	0.0000
Residuals	82	6723.23	81.99		

```
MATRIX OF MEANS:
```

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

Combining Ability Analysis

```
ANALYSIS OF VARIANCE:
```

SV	Df	Sum Sq	Mean Sq	F value	Pr(>F)
GCA	6	19425.23	3237.54	46.76	0.0000
SCA	14	969.40	69.24	2.53	0.0047
Reciprocal	21	1079.84	51.42	1.88	0.0231
Error	82	2241.08	27.33		

ESTIMATES OF VARIANCE COMPONENTS:

	Variance Component	Std. Error
GCA	316.8295	186.9377
SCA	20.9563	13.2586
Reciprocal	12.0453	8.2164
Error	27.3302	4.2683

ESTIMATES OF GENETIC VARIANCE COMPONENTS:

	Estimate
VA	1267.3182
VD	83.8254
h2-narrow sense	0.9194
H2-broad sense	0.9802
Dominance Ratio	0.3637

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

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

TABLE OF STANDARD ERRORS AND LSDs:

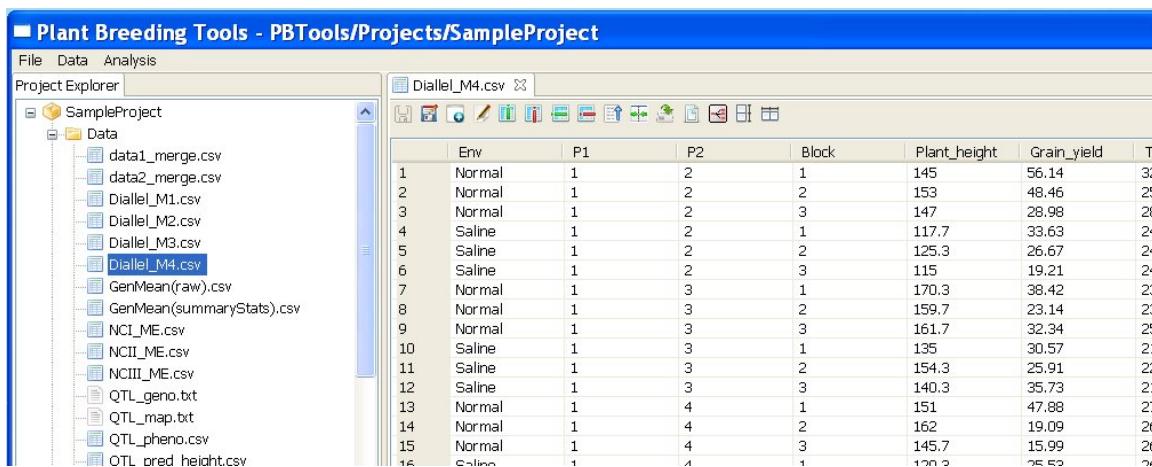
	Std. Error	LSD
Gi	1.5306	
Sii	3.0183	
Rij	3.6966	
Gi-Gj	2.3380	4.6509
Sij-Sik	4.6759	9.3019
Sij-Skl	4.0495	8.0557

6.5.4 Method 4

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

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

- On the Project Explorer, locate the *Diallel_M4.csv* file from the *Data* folder of the project named *SampleProject*. 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*.



The screenshot shows the PBTools software interface. The Project Explorer on the left lists several CSV files under the 'Data' folder, including 'Diallel_M1.csv', 'Diallel_M2.csv', 'Diallel_M3.csv', and 'Diallel_M4.csv'. The main window displays a table titled 'Diallel_M4.csv' with the following data:

	Env	P1	P2	Block	Plant_height	Grain_yield	Tk
1	Normal	1	2	1	145	56.14	32
2	Normal	1	2	2	153	48.46	25
3	Normal	1	2	3	147	28.98	28
4	Saline	1	2	1	117.7	33.63	24
5	Saline	1	2	2	125.3	26.67	24
6	Saline	1	2	3	115	19.21	24
7	Normal	1	3	1	170.3	38.42	23
8	Normal	1	3	2	159.7	23.14	23
9	Normal	1	3	3	161.7	32.34	25
10	Saline	1	3	1	135	30.57	21
11	Saline	1	3	2	154.3	25.91	22
12	Saline	1	3	3	140.3	35.73	21
13	Normal	1	4	1	151	47.88	27
14	Normal	1	4	2	162	19.09	26
15	Normal	1	4	3	145.7	15.99	26
16	Saline	1	4	1	120.2	38.62	26

- Choose **Analysis > Mating Designs > Diallel Analysis > Griffing Method IV**
- 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 two available experimental designs, Completely Randomized Design (CRD) and Randomized Complete Block Design (RCB).

Data Input

The input data for the analysis may be plot-means or observations of individual plants (*not yet implemented*). If the selected design is CRD, the required fields are the *P1*, *P2* and *Replicate* for plot-mean data and the *P1*, *P2*, *Replicate* and *Individual* for the individual data. If the design is RCB, the required fields are the *P1*, *P2* and *Block* for plot-mean data and the *P1*, *P2*, *Block* and *Individual* for the individual data.

'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.

'Perform Analysis Per Site' Option

If this option is selected and the *Environment* factor is specified, *PBTools* will perform the analysis 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.

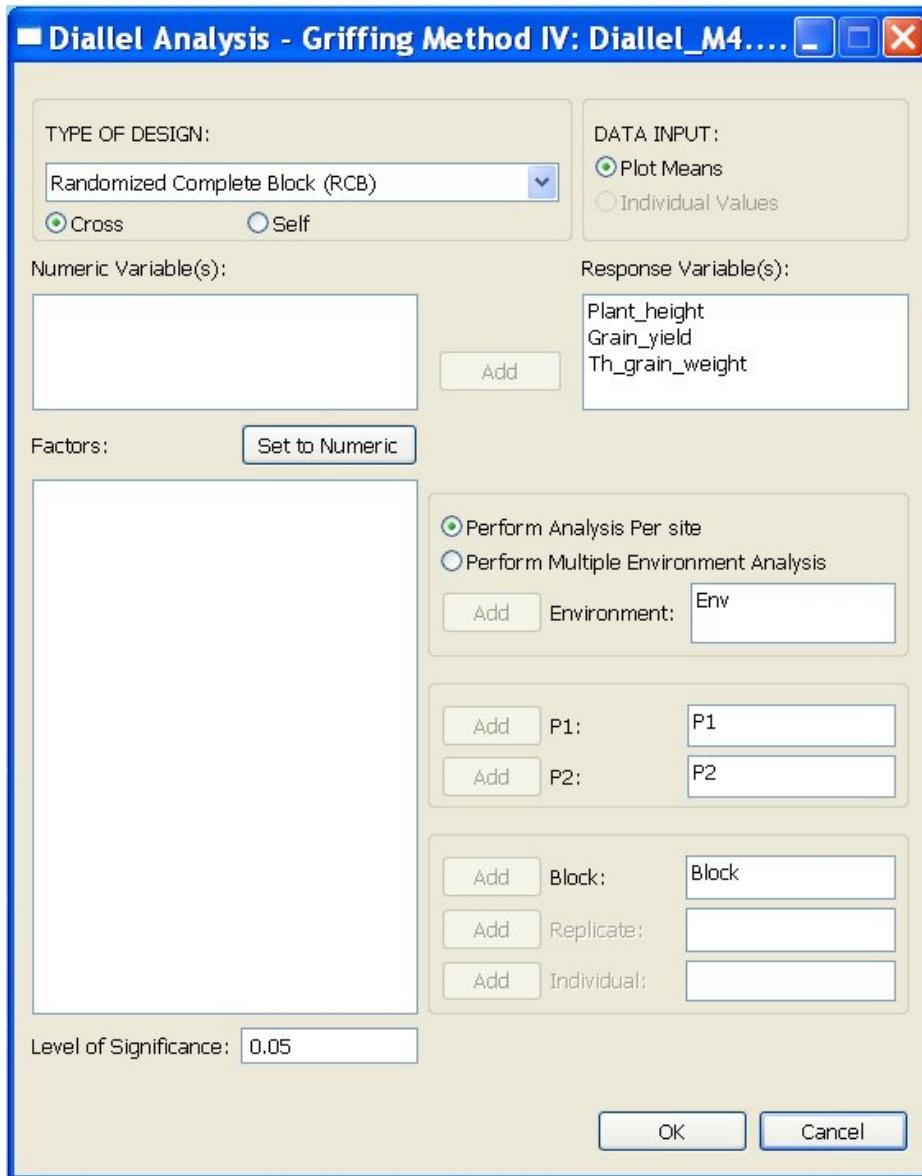
'Perform Multiple Environment Analysis' Option

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

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 Summary

```
DIALLEL ANALYSIS: GRIFFING METHOD IV IN RCB (CROSS)
```

```
RESPONSE VARIABLE: Plant_height
```

```
-----  
ANALYSIS FOR: Env = Normal  
-----
```

```
DATA SUMMARY:
```

Factors	Number 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 missing observations: 0
```

Testing the Significance of Genotypic Differences

```
ANOVA TABLE FOR TESTING SIGNIFICANCE OF GENOTYPIC EFFECT
```

```
Formula: Plant_height ~ Block + P1:P2
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Block	2	869.06	434.53	10.04	0.0003
P1:P2	20	26919.89	1345.99	31.1	0.0000
Residuals	40	1730.97	43.27		

```
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							

Combining Ability Analysis

```
ANALYSIS OF VARIANCE:
```

SV	Df	Sum Sq	Mean Sq	F value	Pr(>F)
GCA	6	8630.00	1438.33	58.66	0.0000
SCA	14	343.29	24.52	1.70	0.0945
Error	40	576.99	14.42		

```
ESTIMATES OF VARIANCE COMPONENTS:
```

	Variance Component	Std. Error
GCA	282.7625	166.0948
SCA	10.0963	9.8133
Error	14.4248	0.8493

ESTIMATES OF GENETIC VARIANCE COMPONENTS:

	Estimate
VA	1131.0501
VD	40.3851
h ² -narrow sense	0.9538
H ² -broad sense	0.9878
Dominance Ratio	0.2672

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

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	8.4087

7. 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.

7.1. Raw Data as Input

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

- On the Project Explorer, locate the *GenMean(raw).csv* file from the *Data* folder of the project named *SampleProject*. Double-click the file to view it in the Data Viewer.

rep	P1	P2	F1	F2	F3	BC
1	3.968	4.526	3.333	3.522	4.122	3.6
2	3.578	4.566	3.345	3.421	4.066	3.8
3	3.628	4.677	3.222	3.453	4.177	3.9
4	3.622	4.675	3.234	3.234	4.175	3.8
5	4.111	4.545	3.222	3.553	4.045	3.5
6	3.544	4.544	3.004	3.547	4.044	3.6
7	3.666	4.666	3.126	3.669	4.166	3.7
8	3.754	4.754	3.214	3.757	4.254	3.7
9	3.456	4.456	2.916	3.459	3.956	3.4
10	10			3.027	3.571	4.497

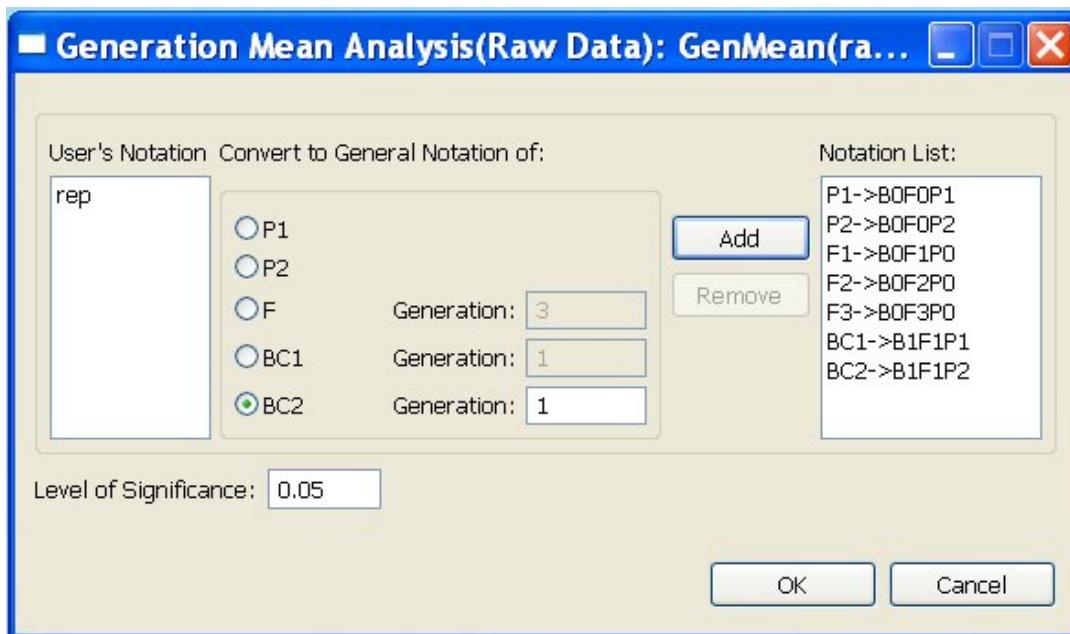
- Choose **Analysis > Generation Mean Analysis > Raw data as input**.
- For each column that represents a generation, convert it to the general notation that *PBTools* recognizes by clicking one variable in the user’s notation box, selecting the appropriate radio button that corresponds to its generation 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

-----
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     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

SET A MODEL 2 :

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

SET A MODEL 3 :

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

SET A MODEL 4 :

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

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	4.2285	0.6493	6.5122	0.0228
a	-0.3635	0.2842	-1.2789	0.3293
d	-0.7595	2.2763	-0.3337	0.7704
aa	0.0150	0.6402	0.0235	0.9834
dd	-0.2641	1.8178	-0.1453	0.8978

```
Residual Standard Error: 8.1854
Multiple R-square: 0.998
Adjusted R-square: 0.9931
F-value: 203.7846
p-value: 0.0049
```

Observed and Predicted Values of Generation Means:

	Generation	Observed	Predicted
1	P1	3.703000	3.879968
2	P2	4.601000	4.607007
3	F1	3.231667	3.204911
4	F2	3.515867	3.782703
5	F3	4.140600	4.022087
6	BC1	3.775600	3.604700
7	BC2	4.483000	3.968219

Goodness-of-fit Test

```
Chi-square value: 134.0001
p-value: 7.984403e-30
```

SET B MODEL 2 :

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

Regression Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
m	4.2421	0.2373	17.8775	0.0004
a	-0.3635	0.2321	-1.5660	0.2153
d	-0.8026	1.0989	-0.7303	0.5181
dd	-0.2335	1.0367	-0.2253	0.8363

Residual Standard Error: 6.6842

```
Multiple R-square: 0.998
Adjusted R-square: 0.9954
F-value: 381.9907
p-value: 0.0002
```

Observed and Predicted Values of Generation Means:

	Generation	Observed	Predicted
1	P1	3.703000	3.878601
2	P2	4.601000	4.605581
3	F1	3.231667	3.205987
4	F2	3.515867	3.782421
5	F3	4.140600	4.026852
6	BC1	3.775600	3.600676
7	BC2	4.483000	3.964166

Goodness-of-fit Test

```
Chi-square value: 134.037
p-value: 7.294329e-29
```

SET B MODEL 3 :

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
```

SET B MODEL 4 :

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
```

7.2. Summary Statistics as Input

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

- On the Project Explorer, locate the *GenMean(summaryStats).csv* file from the *Data* folder of the project named *SampleProject*. Double-click the file to view it in the Data Viewer.

generation	mean	stddev	n	Weights	
1	P1	3.676	0.1973879	15	384.9905
2	P2	4.6342	0.1296397	15	892.5141
3	F1	3.231667	0.1696558	15	521.1392
4	F2	3.515867	0.1262848	15	940.5664
5	BC1	3.7756	0.1501788	15	665.0798
6	BC2	4.483	0.379357	15	104.2306

- Choose **Analysis > Generation Mean Analysis > Summary statistics as input**.
- 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

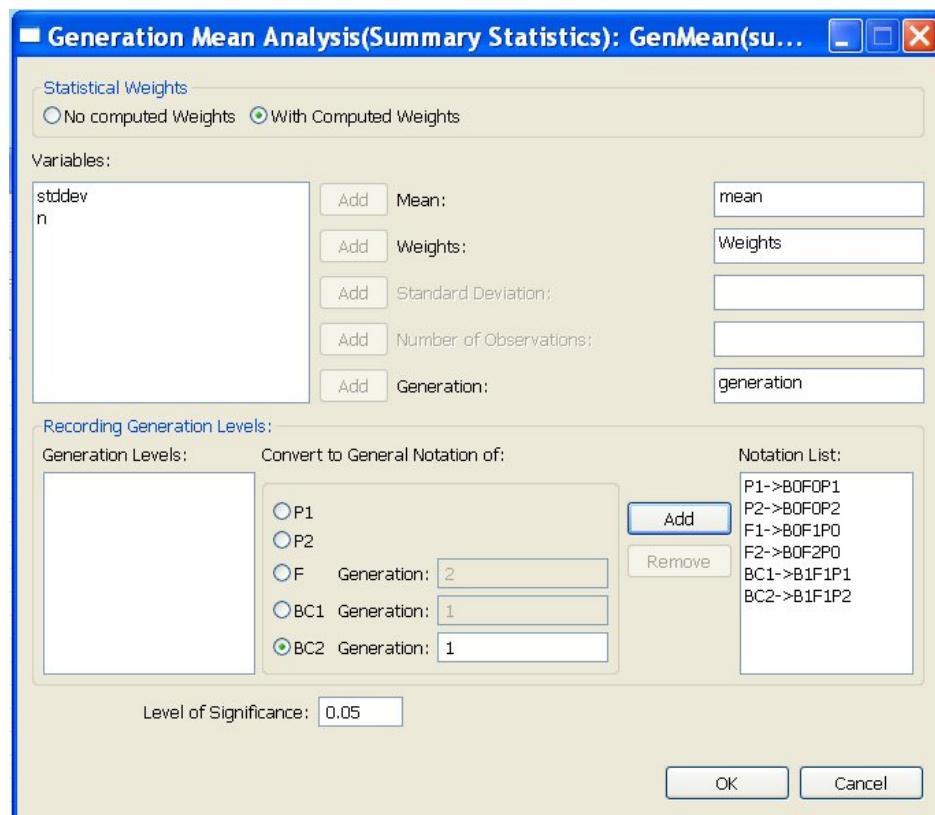
This is the column that corresponds to the generation classification.

- 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     0.42423  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

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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
```
