

# Package ‘PhenStat’

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**Type** Package

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**Suggests** RUnit, BiocGenerics

**Description** Package contains methods for statistical analysis of phenotypic data.

**License** file LICENSE

**NeedsCompilation** no

**biocViews** StatisticalMethod

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analysedDataset *Method "analysedDataset"*

**Description**

Method analysedDataset returns subset of the original dataset that was analysed

**Value**

This function returns the analysed dataset.

**Methods**

signature(obj = "PhenTestResult")

**Examples**

```
# Mixed Model framework
file <- system.file("extdata", "test1.csv", package="PhenStat")
test <- PhenStat::PhenList(dataset=read.csv(file,na.strings = '-'),
  testGenotype="Sparc/Sparc")

result <- PhenStat::testDataset(test,
  depVariable="Lean.Mass")
head(PhenStat::analysedDataset(obj = result))
```

---

analysedDatasetPhenList

*Method "analysedDatasetPhenList"*

---

**Description**

Method analysedDatasetPhenList returns subset of the original dataset that will be analysed

**Value**

The function returns the analysed dataset.

**Methods**

signature(obj = "PhenList")

---

analysedSubset

*Method "analysedSubset"*

---

**Description**

Method analysedSubset returns name of the subset that was analysed by RR or FE frameworks

**Value**

The function returns name of the subset that was analysed by RR or FE frameworks.

**Methods**

signature(obj = "htestPhenStat")

---

analysisResults	<i>Method "analysisResults"</i>
-----------------	---------------------------------

---

**Description**

Method analysisResults returns analysis results

**Value**

The function returns the analysis result.

**Methods**

```
signature(obj = "PhenTestResult")
```

**Examples**

```
# Mixed Model framework
file <- system.file("extdata", "test1.csv", package="PhenStat")
test <- PhenStat::PhenList(dataset=read.csv(file,na.strings = '-'),
                           testGenotype="Sparc/Sparc")

result <- PhenStat::testDataset(test,
                                depVariable="Lean.Mass")
r = PhenStat::analysisResults(obj = result)
```

---

batchIn	<i>Method "batchIn"</i>
---------	-------------------------

---

**Description**

Method batchIn returns TRUE/FALSE values depending on the batch column presence/absence in the dataset

**Value**

TRUE/FALSE

**Methods**

```
signature(obj = "PhenList")
signature(obj = "PhenTestResult")
```

---

boxplotResidualBatch *Method "boxplotResidualBatch"*

---

### Description

Graph function for the Mixed Model framework's results. Creates a box plot with residue versus batch split by genotype.

### Usage

```
boxplotResidualBatch(phenTestResult, outputMessages=TRUE)
```

### Arguments

phenTestResult instance of the [PhenTestResult](#) class that comes from the function [testDataset](#); mandatory argument

outputMessages flag: "FALSE" value to suppress output messages; "TRUE" value to show output messages; default value TRUE

### Value

Empty.

### Author(s)

Natalja Kurbatova, Natasha Karp, Jeremy Mason

### References

Karp N, Melvin D, Sanger Mouse Genetics Project, Mott R (2012): Robust and Sensitive Analysis of Mouse Knockout Phenotypes. *PLoS ONE* 7(12): e52410. doi:10.1371/journal.pone.0052410

West B, Welch K, Galecki A (2007): Linear Mixed Models: A practical guide using statistical software *New York: Chapman & Hall/CRC* 353 p.

### See Also

[PhenList](#) and [PhenTestResult](#)

### Examples

```
file <- system.file("extdata", "test1.csv", package="PhenStat")
test <- PhenStat::PhenList(dataset=read.csv(file, na.strings = '-'),
  testGenotype="Sparc/Sparc")
result <- PhenStat::testDataset(test,
  depVariable="Lean.Mass")
PhenStat::boxplotResidualBatch(result)
```

---

boxplotSexGenotype      *Method "boxplotSexGenotype"*

---

### Description

Graph function for the phenotypic dataset. Creates a box plot split by sex and genotype.

### Usage

```
boxplotSexGenotype(phenList,  
                   depVariable=NULL,  
                   graphingName=NULL,  
                   outputMessages=TRUE)
```

### Arguments

phenList	instance of the <a href="#">PhenList</a> class; mandatory argument
depVariable	a character string defining the dependent variable of interest; mandatory argument
graphingName	a character string defining the name to be used on the graph for the dependent variable; mandatory argument
outputMessages	flag: "FALSE" value to suppress output messages; "TRUE" value to show output messages; default value TRUE

### Value

Empty.

### Author(s)

Natalja Kurbatova, Natasha Karp, Jeremy Mason

### References

Karp N, Melvin D, Sanger Mouse Genetics Project, Mott R (2012): Robust and Sensitive Analysis of Mouse Knockout Phenotypes. *PLoS ONE* 7(12): e52410. doi:10.1371/journal.pone.0052410

West B, Welch K, Galecki A (2007): Linear Mixed Models: A practical guide using statistical software *New York: Chapman & Hall/CRC* 353 p.

### See Also

[PhenList](#)

**Examples**

```

file <- system.file("extdata", "test1.csv", package="PhenStat")
test <- PhenStat::PhenList(dataset=read.csv(file,na.strings = '-'),
                           testGenotype="Sparc/Sparc")
# box plot for dataset with two sexes: males and females
PhenStat::boxplotSexGenotype(test,
                              depVariable="Bone.Mineral.Content",
                              graphingName="BMC")

file <- system.file("extdata", "test4.csv", package="PhenStat")
test_1sex <- PhenStat::PhenList(dataset=read.csv(file,na.strings = '-'),
                                testGenotype="Mysm1/+")
# box plot for females only dataset
PhenStat::boxplotSexGenotype(test_1sex,
                              depVariable="Lean.Mass",
                              graphingName="Lean Mass (g)")

```

---

boxplotSexGenotypeBatch

*Method "boxplotSexGenotypeBatch"*

---

**Description**

NB! Function is deprecated, please use scatterplotSexGenotypeBatch function instead. Graph function for the phenotypic dataset. Creates a box plot split by sex, genotype and batch.

Note: the batches are not ordered with time but allow assessment of how the treatment groups lie relative to the normal control variation.

**Usage**

```

boxplotSexGenotypeBatch(phenList,
  depVariable=NULL,
  graphingName=NULL,
  outputMessages=TRUE)

```

**Arguments**

phenList	instance of the <a href="#">PhenList</a> class; mandatory argument
depVariable	a character string defining the dependent variable of interest; mandatory argument
graphingName	a character string defining the name to be used on the graph for the dependent variable; mandatory argument
outputMessages	flag: "FALSE" value to suppress output messages; "TRUE" value to show output messages; default value TRUE

**Value**

Empty.



**Author(s)**

Natalja Kurbatova, Natasha Karp, Jeremy Mason

**References**

Karp N, Melvin D, Sanger Mouse Genetics Project, Mott R (2012): Robust and Sensitive Analysis of Mouse Knockout Phenotypes. *PLoS ONE* 7(12): e52410. doi:10.1371/journal.pone.0052410

West B, Welch K, Galecki A (2007): Linear Mixed Models: A practical guide using statistical software *New York: Chapman & Hall/CRC* 353 p.

**See Also**

[PhenList](#)

**Examples**

```
file <- system.file("extdata", "test1.csv", package="PhenStat")
test <- PhenStat::PhenList(dataset=read.csv(file,na.strings = '-'),
  testGenotype="Sparc/Sparc")
# box plot for dataset with two sexes: males and females
PhenStat::boxplotSexGenotypeBatch(test,
  depVariable="Bone.Mineral.Content",
  graphingName="BMC" )

file <- system.file("extdata", "test4.csv", package="PhenStat")
test_1sex <- PhenStat::PhenList(dataset=read.csv(file,na.strings = '-'),
  testGenotype="Mysm1/+")
# box plot for females only dataset
PhenStat::boxplotSexGenotypeBatch(test_1sex,depVariable="Lean.Mass",
  graphingName="Lean Mass")
```

---

boxplotSexGenotypeBatchAdjusted

*Method "boxplotSexGenotypeBatchAdjusted"*

---

**Description**

Graph function for the phenotypic dataset. Creates a box plot split by sex and genotype after accounting for batch.

**Usage**

```
boxplotSexGenotypeBatchAdjusted(
  phenList,
  depVariable=NULL,
  graphingName=NULL,
  outputMessages=TRUE)
```

**Arguments**

phenList	instance of the <a href="#">PhenList</a> class; mandatory argument
depVariable	a character string defining the dependent variable of interest; mandatory argument
graphingName	a character string defining the name to be used on the graph for the dependent variable; mandatory argument
outputMessages	flag: "FALSE" value to suppress output messages; "TRUE" value to show output messages; default value TRUE

**Value**

Empty.

**Author(s)**

Natalja Kurbatova, Natasha Karp, Jeremy Mason

**References**

Karp N, Melvin D, Sanger Mouse Genetics Project, Mott R (2012): Robust and Sensitive Analysis of Mouse Knockout Phenotypes. *PLoS ONE* 7(12): e52410. doi:10.1371/journal.pone.0052410

West B, Welch K, Galecki A (2007): Linear Mixed Models: A practical guide using statistical software *New York: Chapman & Hall/CRC* 353 p.

**See Also**

[PhenList](#)

**Examples**

```
file <- system.file("extdata", "test1.csv", package="PhenStat")
test <- PhenStat::PhenList(dataset=read.csv(file,na.strings = '-'),
  testGenotype="Sparc/Sparc")
# box plot for dataset with two sexes: males and females
PhenStat::boxplotSexGenotypeBatchAdjusted(test,
  depVariable="Bone.Mineral.Content",
  graphingName="BMC" )
```

---

boxplotSexGenotypeResult

*Method "boxplotSexGenotypeResult"*

---

**Description**

Graph function for the phenotypic dataset. Creates a box plot split by sex and genotype. Is based on PhenTestResult object.

**Usage**

```
boxplotSexGenotypeResult(phenTestResult,
  graphingName=NULL,
  outputMessages=TRUE)
```

**Arguments**

phenTestResult instance of the [PhenTestResult](#) class; mandatory argument

graphingName a character string defining the name to be used on the graph for the dependent variable; mandatory argument

outputMessages flag: "FALSE" value to suppress output messages; "TRUE" value to show output messages; default value TRUE

**Value**

Empty.

**Author(s)**

Natalja Kurbatova, Natasha Karp, Jeremy Mason

**References**

Karp N, Melvin D, Sanger Mouse Genetics Project, Mott R (2012): Robust and Sensitive Analysis of Mouse Knockout Phenotypes. *PLoS ONE* 7(12): e52410. doi:10.1371/journal.pone.0052410

West B, Welch K, Galecki A (2007): Linear Mixed Models: A practical guide using statistical software *New York: Chapman & Hall/CRC* 353 p.

**See Also**

[PhenList](#)

**Examples**

```
file <- system.file("extdata", "test1.csv", package="PhenStat")
test <- PhenStat::PhenList(dataset=read.csv(file,na.strings = '-'),
  testGenotype="Sparc/Sparc")
result <- PhenStat::testDataset(test,
  depVariable="Lean.Mass")
# box plot for dataset with two sexes: males and females
PhenStat::boxplotSexGenotypeResult(result,
  graphingName="BMC")

file <- system.file("extdata", "test4.csv", package="PhenStat")
test_1sex <- PhenStat::PhenList(dataset=read.csv(file,na.strings = '-'),
  testGenotype="Mysm1/+")
result_1sex <- PhenStat::testDataset(test_1sex,
  depVariable="Lean.Mass")
# box plot for females only dataset
PhenStat::boxplotSexGenotypeResult(result_1sex,
```

```
graphingName="Lean Mass (g)")
```

---

```
boxplotSexGenotypeWeightBatchAdjusted
```

```
Method "boxplotSexGenotypeWeightBatchAdjusted"
```

---

## Description

Graph function for the phenotypic dataset. Creates a box plot split by sex and genotype after accounting for batch and weight.

## Usage

```
boxplotSexGenotypeWeightBatchAdjusted(  
  phenList,  
  depVariable=NULL,  
  graphingName=NULL,  
  outputMessages=TRUE)
```

## Arguments

phenList	instance of the <a href="#">PhenList</a> class; mandatory argument
depVariable	a character string defining the dependent variable of interest; mandatory argument
graphingName	a character string defining the name to be used on the graph for the dependent variable; mandatory argument
outputMessages	flag: "FALSE" value to suppress output messages; "TRUE" value to show output messages; default value TRUE

## Value

Empty.

## Author(s)

Natalja Kurbatova, Natasha Karp, Jeremy Mason

## References

Karp N, Melvin D, Sanger Mouse Genetics Project, Mott R (2012): Robust and Sensitive Analysis of Mouse Knockout Phenotypes. *PLoS ONE* 7(12): e52410. doi:10.1371/journal.pone.0052410

West B, Welch K, Galecki A (2007): Linear Mixed Models: A practical guide using statistical software *New York: Chapman & Hall/CRC* 353 p.

## See Also

[PhenList](#)

**Examples**

```
file <- system.file("extdata", "test1.csv", package="PhenStat")
test <- PhenStat::PhenList(dataset=read.csv(file,na.strings = '-'),
  testGenotype="Sparc/Sparc")
# box plot for dataset with two sexes: males and females
PhenStat::boxplotSexGenotypeWeightBatchAdjusted(test,
  depVariable="Bone.Mineral.Content",
  graphingName="BMC" )
```

---

categoricalBarplot      *Method "categoricalBarplot"*

---

**Description**

Graph function for the Fisher Exact Test framework's results. Creates stacked bar plot(s) to compare proportions seen in a categorical variable between different genotypes. Graphs are created for all data and also for each sex individually.

**Usage**

```
categoricalBarplot(phenTestResult,
  outputMessages=TRUE)
```

**Arguments**

`phenTestResult` instance of the [PhenTestResult](#) class that comes from the function `testDataset`; mandatory argument

`outputMessages` flag: "FALSE" value to suppress output messages; "TRUE" value to show output messages; default value TRUE

**Value**

Empty.

**Author(s)**

Natalja Kurbatova, Natasha Karp, Jeremy Mason

**References**

Karp N, Melvin D, Sanger Mouse Genetics Project, Mott R (2012): Robust and Sensitive Analysis of Mouse Knockout Phenotypes. *PLoS ONE* 7(12): e52410. doi:10.1371/journal.pone.0052410

West B, Welch K, Galecki A (2007): Linear Mixed Models: A practical guide using statistical software *New York: Chapman & Hall/CRC* 353 p.

**See Also**

[PhenList](#)

## Examples

```
file <- system.file("extdata", "test_categorical.csv", package="PhenStat")
test <- PhenStat::PhenList(dataset=read.csv(file,na.strings = '-'),
  testGenotype="Aff3/Aff3")
result <- PhenStat::testDataset(test,
  depVariable="Thoracic.Processes",
  method="FE")
PhenStat::categoricalBarplot(result)
```

---

checkDataset

*Method "checkDataset"*

---

## Description

Checks dataset for the minimum required info:

1. Column names should present
2. Genotype column should present
3. Sex column should present
4. Two data points for each Genotype/Sex combination
5. Number of Genotype levels should be 2
6. Number of Sex levels should be 1 or 2
7. Sex levels have to be "Female" and/or "Male"
8. Records with reference genotype should be in the dataset
9. Records with test genotype should be in the dataset

Perform the following additional checks:

- presence of Weight column,
- presence of Batch column (Assay.Date).

Warning given in case of missed data indicating that you can only fit a glm or to use MM equation "withoutWeight".

Function [checkDataset](#) is called from [PhenList](#) function.

## Usage

```
checkDataset(dataset,
  testGenotype,
  refGenotype="+/+",
  outputMessages=TRUE,
  dataset.clean=TRUE)
```

**Arguments**

dataset	data frame created from file or from another source; mandatory argument
testGenotype	defines the test genotype to be compared to the reference genotype; mandatory argument
refGenotype	defines the reference genotype; assigned default value is "+/+"
outputMessages	flag: "FALSE" value to suppress output messages; "TRUE" value to show output messages; assigned default value is TRUE
dataset.clean	flag: "FALSE" value for no modification of the dataset; "TRUE" value to clean dataset if needed; assigned default value is TRUE

**Value**

Returns an instance of the [PhenList](#) class.

**Author(s)**

Natalja Kurbatova, Natasha Karp, Jeremy Mason

**References**

Karp N, Melvin D, Sanger Mouse Genetics Project, Mott R (2012): Robust and Sensitive Analysis of Mouse Knockout Phenotypes. *PLoS ONE* 7(12): e52410. doi:10.1371/journal.pone.0052410

West B, Welch K, Galecki A (2007): Linear Mixed Models: A practical guide using statistical software *New York: Chapman & Hall/CRC* 353 p.

**See Also**

[PhenTestResult](#)

**Examples**

```
# "checkDataset" is called internally from "PhenList" function
file <- system.file("extdata", "test1.csv", package="PhenStat")
test <- PhenStat::PhenList(dataset=read.csv(file,na.strings = '-'),
  testGenotype="Sparc/Sparc")
```

---

classificationTag      *Method "classificationTag"*

---

**Description**

Returns a classification tag to assign a sexual dimorphism assessment of the phenotypic change.

**Usage**

```
classificationTag(phenTestResult,
  userMode = "summaryOutput",
  phenotypeThreshold = 0.01,
  outputMessages=TRUE)
```

**Arguments**

`phenTestResult` instance of the [PhenTestResult](#) class that comes from the function `testDataset`; mandatory argument

`userMode` flag: "vectorOutput" a sexual dimorphic classification is assigned with a proviso of later assessing the overall statistical significance; "summaryOutput" the `phenotypeThreshold` is used to assess the overall statistical significance and then if significant the sexual dimorphic classification determined; defaults to `summaryOutput`

`phenotypeThreshold` a numerical value defining the threshold to use in `classificationTag` in determining whether the genotype effect is classed as significant or not; default value 0.01

`outputMessages` flag: "FALSE" value to suppress output messages; "TRUE" value to show output messages ; default value TRUE

**Value**

Returns a classification tag to assign a sexual dimorphism assessment of the phenotypic change.

If you are working interactively with the data, the argument "userMode" set to the value "summaryOutput" will use the "phenotypeThreshold" argument's value to assess statistical significance of the genotype effect and if significant then assign a sexual dimorphic classification. Alternatively, if the "userMode" set to the value "vectorMode", a sexual dimorphic classification will be returned with the MM framework where later you can globally assess whether the variable had a significant genotype effect. With the FE framework and the vectorMode, a NA is returned as the type of the effect cannot be assessed without assessing the statistical significance of the genotype effect.

**Author(s)**

Natalja Kurbatova, Natasha Karp, Jeremy Mason

**References**

Karp N, Melvin D, Sanger Mouse Genetics Project, Mott R (2012): Robust and Sensitive Analysis of Mouse Knockout Phenotypes. *PLoS ONE* 7(12): e52410. doi:10.1371/journal.pone.0052410

West B, Welch K, Galecki A (2007): Linear Mixed Models: A practical guide using statistical software *New York: Chapman & Hall/CRC* 353 p.

**See Also**

[PhenTestResult](#)



**Examples**

```

file <- system.file("extdata", "test1.csv", package="PhenStat")
test <- PhenStat::PhenList(dataset=read.csv(file,na.strings = '-'),
  testGenotype="Sparc/Sparc")
result <- PhenStat::testDataset(test,
  depVariable="Lean.Mass")
PhenStat::classificationTag(result,
  userMode="summaryOutput",
  phenotypeThreshold=0.001)
PhenStat::classificationTag(result,
  userMode="vectorOutput")

```

---

comparison	<i>Method "comparison"</i>
------------	----------------------------

---

**Description**

Method comparison returns name of the comparison that was performed by RR framework: "High vs Normal/Low" or "Low vs Normal/High"

**Value**

returns name of the comparison that was performed by RR framework.

**Methods**

signature(obj = "htestPhenStat")

---

dataset	<i>Method "dataset"</i>
---------	-------------------------

---

**Description**

Method dataset returns data frame stored in the object

**Value**

returns data frame stored in the object

**Methods**

signature(obj = "PhenList")

---

finalLRModel                      Method "finalLRModel"

---

### Description

This is an internal function run within LR framework. It completes the final stage of the LR framework, which builds the final model and estimates effects. As an internal function, it doesn't include extensive error testing of inputs. Please use cautiously if calling directly.

Works with [PhenTestResult](#) object created by [startLRModel](#) function. The creation of LR final model is based on the significance of different fixed effects, depVariable and equation values stored in [PhenTestResult](#) object.

### Usage

```
finalLRModel(phenTestResult,  
outputMessages = TRUE)
```

### Arguments

`phenTestResult` instance of the [PhenTestResult](#) class that comes from the function [testDataset](#); mandatory argument

`outputMessages` flag: "FALSE" value to suppress output messages; "TRUE" value to show output messages; default value TRUE

### Value

Returns results stored in instance of the [PhenTestResult](#) class

### Author(s)

Natalja Kurbatova, Natasha Karp, Jeremy Mason

### References

Karp N, Melvin D, Sanger Mouse Genetics Project, Mott R (2012): Robust and Sensitive Analysis of Mouse Knockout Phenotypes. *PLoS ONE* 7(12): e52410. doi:10.1371/journal.pone.0052410

West B, Welch K, Galecki A (2007): Linear Mixed Models: A practical guide using statistical software *New York: Chapman & Hall/CRC* 353 p.

### See Also

[PhenTestResult](#) and [testDataset](#)

**Examples**

```

file <- system.file("extdata", "testLR.csv", package="PhenStat")
testLR <- PhenStat::PhenList(dataset=read.csv(file,na.strings = '-'),
  testGenotype="Mock")
testLR2 <- PhenStat::LRDataset(testLR,"V2")

# when "testDataset" function's argument "callAll" is set to FALSE
# only "startLRModel" function is called - the first step of LR framework
resultLR <- PhenStat::testDataset(testLR2,
  depVariable="V2",
  callAll=FALSE,
  method="LR")

# print out formula that has been created
PhenStat::analysisResults(resultLR)$model.formula.genotype
# print out batch effect's significance
PhenStat::analysisResults(resultLR)$model.effect.batch
resultLR <- PhenStat::finalLRModel(resultLR)

```

---

finalModel	<i>Method "finalModel"</i>
------------	----------------------------

---

**Description**

This is an internal function run within MM framework. It completes the final stage of the MM framework, which builds the final model and estimates effects. As an internal function, it doesn't include extensive error testing of inputs. Please use cautiously if calling directly.

Works with [PhenTestResult](#) object created by [startModel](#) function. The creation of MM final model is based on the significance of different fixed effects, depVariable and equation values stored in [PhenTestResult](#) object.

**Usage**

```

finalModel(phenTestResult,
  outputMessages = TRUE,
  modelWeight = NULL)

```

**Arguments**

phenTestResult	instance of the <a href="#">PhenTestResult</a> class that comes from the function <a href="#">testDataset</a> ; mandatory argument
outputMessages	flag: "FALSE" value to suppress output messages; "TRUE" value to show output messages; default value TRUE
modelWeight	A vector of positive values for weights mainly used for applying windowing to the data

**Value**

Returns results stored in instance of the [PhenTestResult](#) class

**Author(s)**

Natalja Kurbatova, Natasha Karp, Jeremy Mason

**References**

Karp N, Melvin D, Sanger Mouse Genetics Project, Mott R (2012): Robust and Sensitive Analysis of Mouse Knockout Phenotypes. *PLoS ONE* **7**(12): e52410. doi:10.1371/journal.pone.0052410

West B, Welch K, Galecki A (2007): Linear Mixed Models: A practical guide using statistical software *New York: Chapman & Hall/CRC* 353 p.

**See Also**

[PhenTestResult](#) and [testDataset](#)

**Examples**

```
file <- system.file("extdata", "test1.csv", package="PhenStat")
test <- PhenStat::PhenList(dataset=read.csv(file,na.strings = '-'),
  testGenotype="Sparc/Sparc")
# when "testDataset" function's argument "callAll" is set to FALSE
# only "startModel" function is called - the first step of MM framework
result <- PhenStat::testDataset(test,
  depVariable="Lean.Mass",
  equation="withoutWeight",
  callAll=FALSE)
# print out formula that has been created
# result$model.formula.genotype
# print out batch effect's significance
# result$model.effect.batch
# change the model
# result <- PhenStat::testDataset(test,
#   depVariable="Lean.Mass",
#   equation="withWeight",
#   callAll=FALSE)
# print out new formula
#result$model.formula.genotype
# run the final model fitting when satisfied with the model
result <- PhenStat::finalModel(result)
```

---

finalTFModel

*Method "finalTFModel"*

---

**Description**

This is an internal function run within TF framework. It completes the final stage of the TF framework, which builds the final model and estimates effects. As an internal function, it doesn't include extensive error testing of inputs. Please use cautiously if calling directly.

Works with [PhenTestResult](#) object created by [startTFModel](#) function. The creation of TF final model is based on the significance of different fixed effects, depVariable and equation values stored in [PhenTestResult](#) object.

**Usage**

```
finalTFModel(phenTestResult,
             outputMessages = TRUE)
```

**Arguments**

phenTestResult instance of the [PhenTestResult](#) class that comes from the function [testDataset](#); mandatory argument

outputMessages flag: "FALSE" value to suppress output messages; "TRUE" value to show output messages; default value TRUE

**Value**

Returns results stored in instance of the [PhenTestResult](#) class

**Author(s)**

Natalja Kurbatova, Natasha Karp, Jeremy Mason

**References**

Karp N, Melvin D, Sanger Mouse Genetics Project, Mott R (2012): Robust and Sensitive Analysis of Mouse Knockout Phenotypes. *PLoS ONE* 7(12): e52410. doi:10.1371/journal.pone.0052410

West B, Welch K, Galecki A (2007): Linear Mixed Models: A practical guide using statistical software *New York: Chapman & Hall/CRC* 353 p.

**See Also**

[PhenTestResult](#) and [testDataset](#)

**Examples**

```
file <- system.file("extdata", "test7_TFE.csv", package="PhenStat")
test <- PhenList(dataset=read.csv(file,na.strings = '-'),
                testGenotype="het",
                refGenotype = "WT",
                dataset.colname.sex="sex",
                dataset.colname.genotype="Genotype",
                dataset.values.female="f",
                dataset.values.male= "m",
                dataset.colname.weight="body.weight",
                dataset.colname.batch="Date_of_procedure_start")

test_TF <- PhenStat::TFDataset(test,depVariable="Cholesterol")

# when "testDataset" function's argument "callAll" is set to FALSE
# only "startTFModel" function is called - the first step of TFE framework
result <- PhenStat::testDataset(test_TF,
                               depVariable="Cholesterol",
                               callAll=FALSE,
```

```

                                method="TF")
# print out formula that has been created
PhenStat:::analysisResults(result)$model.formula.genotype
# print out batch effect's significance
PhenStat:::analysisResults(result)$model.effect.batch
result <- PhenStat:::finalTFModel(result)

```

---

FisherExactTest	<i>Method "FisherExactTest"</i>
-----------------	---------------------------------

---

### Description

The main function of the Fisher Exact Test framework. Creates n times 2 matrices with record counts, where n rows represent dependent variable levels and two columns represent genotype levels. Performs Fisher Exact Tests on calculated count matrices.

Three matrices can be created and three tests can be potentially perform depending on the dataset:

- all records together regardless the sex values - combined dataset,
- records where sex value is "Male" (if such exists) - males only dataset,
- records where sex value is "Female" (if such exists) - females only dataset.

Together with count matrices creates percentage matrices, calculates effect sizes and statistics for count matrices. Performs Fisher Exact Tests.

The results (matrices, statistics and Fisher Exact Test outputs) are stored in [PhenTestResult](#) object.

The function is called from "testDataset" function when "method" argument is set to "FE" meaning "Fisher Exact Test".

### Usage

```

FisherExactTest(phenList,
depVariable,
outputMessages=TRUE)

```

### Arguments

phenList	instance of the <a href="#">PhenList</a> class; mandatory argument
depVariable	a character string defining the dependent variable of interest; mandatory argument
outputMessages	flag: "FALSE" value to suppress output messages; "TRUE" value to show output messages; default value TRUE

### Value

Returns results stored in instance of the [PhenTestResult](#) class

### Author(s)

Natalja Kurbatova, Natasha Karp, Jeremy Mason

## References

Karp N, Melvin D, Sanger Mouse Genetics Project, Mott R (2012): Robust and Sensitive Analysis of Mouse Knockout Phenotypes. *PLoS ONE* 7(12): e52410. doi:10.1371/journal.pone.0052410

West B, Welch K, Galecki A (2007): Linear Mixed Models: A practical guide using statistical software *New York: Chapman & Hall/CRC* 353 p.

## See Also

[PhenTestResult](#)

## Examples

```
file <- system.file("extdata", "test_categorical.csv", package="PhenStat")
test <- PhenStat::PhenList(dataset=read.csv(file,na.strings = '-'),
  testGenotype="Aff3/Aff3")
# "FisherExactTest" function is called from "testDataset" function.
result <- PhenStat::testDataset(test,depVariable="Thoracic.Processes",method="FE")
# Fisher Exact Test results can be printed out using function "summaryOutput"
summary(result)
```

---

generateGraphs	<i>Method "generateGraphs"</i>
----------------	--------------------------------

---

## Description

Function generates graphs for the Mixed Model and Time as Fixed Effect frameworks' results and stores generated graphs in the defined directory.

## Usage

```
generateGraphs(phenTestResult, dir,
  graphingName=NULL, type="Xlib")
```

## Arguments

phenTestResult	instance of the <a href="#">PhenTestResult</a> class that comes from the function <a href="#">testDataset</a> ; mandatory argument
dir	directory where to store generated graphs; mandatory argument
graphingName	a character string defining the name to be used on the graph for the dependent variable; defaults to NULL then the depVariable name will be plotted
type	character string, one of "Xlib" or "quartz" (some OS X builds) or "cairo", or "window", or cairo-png"; mandatory argument

## Value

Empty.

**Author(s)**

Natalja Kurbatova, Natasha Karp, Jeremy Mason

**References**

Karp N, Melvin D, Sanger Mouse Genetics Project, Mott R (2012): Robust and Sensitive Analysis of Mouse Knockout Phenotypes. *PLoS ONE* 7(12): e52410. doi:10.1371/journal.pone.0052410

West B, Welch K, Galecki A (2007): Linear Mixed Models: A practical guide using statistical software *New York: Chapman & Hall/CRC* 353 p.

**See Also**

[PhenTestResult](#)

---

getColumn

*Method "getColumn"*

---

**Description**

Method getColumn returns column of interest

**Value**

This function returns column of interest

**Methods**

signature(obj = "PhenList")

---

getColumnBatchAdjusted

*Method "getColumnBatchAdjusted"*

---

**Description**

Method getColumnBatchAdjusted returns column of interest adjusted for batch

**Value**

This function returns column of interest

**Methods**

signature(obj = "PhenList")



---

getColumnView	<i>Method "getColumnView"</i>
---------------	-------------------------------

---

**Description**

Method getColumnView returns RR or FE frameworks results in a column format

**Value**

This function returns RR or FE frameworks results in a column format

**Methods**

signature(obj = "htestPhenStat")

---

getColumnWeightBatchAdjusted	<i>Method "getColumnWeightBatchAdjusted"</i>
------------------------------	--

---

**Description**

Method getColumnWeightBatchAdjusted returns column of interest adjusted for weight and batch

**Value**

This function returns column of interest

**Methods**

signature(obj = "PhenList")

---

getCountMatrices	<i>Method "getCountMatrices"</i>
------------------	----------------------------------

---

**Description**

Method getCountMatrices returns count matrices for FE and RR frameworks

**Value**

This function returns count matrices for FE and RR frameworks

**Methods**

signature(obj = "PhenTestResult")

---

getDataset	<i>Method "getDataset"</i>
------------	----------------------------

---

**Description**

Method getDataset returns data frame stored in the object

**Value**

This function returns data frame stored in the object.

**Methods**

signature(obj = "PhenList")

---

getGenotypeEffect	<i>Method "getGenotypeEffect"</i>
-------------------	-----------------------------------

---

**Description**

Method getGenotypeEffect returns genotype effect and standard error for the linear regression frameworks

**Value**

This function returns genotype effect and standard error for the linear regression frameworks

**Methods**

signature(obj = "PhenTestResult")

---

getMatrix	<i>Method "getMatrix"</i>
-----------	---------------------------

---

**Description**

Method getMatrix returns RR or FE frameworks results in a matrix format

**Value**

This function returns RR or FE frameworks results in a matrix format

**Methods**

signature(obj = "htestPhenStat")

---

getPercentageMatrix     *Method "getPercentageMatrix"*

---

**Description**

Method getPercentageMatrix returns percentage matrix calculated out of counts

**Value**

This function returns percentage matrix calculated out of counts.

**Methods**

signature(obj = "htestPhenStat")

---

getStat                     *Method "getStat"*

---

**Description**

Method getStat returns simple statistics about variables in the dataset

**Value**

This function returns simple statistics about variables in the dataset

**Methods**

signature(obj = "PhenList")

---

getVariable                 *Method "getVariable"*

---

**Description**

Method getVariable returns dependent variable name

**Value**

This function returns dependent variable name

**Methods**

signature(obj = "PhenTestResult")

---

getVariables	<i>Method "getVariables"</i>
--------------	------------------------------

---

**Description**

Method getVariables returns names of variables in the dataset

**Value**

This function returns names of variables in the dataset

**Methods**

signature(obj = "PhenList")

---

hemiGenotype	<i>Method "hemiGenotype"</i>
--------------	------------------------------

---

**Description**

Method hemiGenotype returns hemi genotype if defined

**Value**

This function returns hemi genotype if defined

**Methods**

signature(obj = "PhenList")

signature(obj = "PhenTestResult")

---

JSONOutput	<i>Method "JSONOutput"</i>
------------	----------------------------

---

**Description**

Wrapper for the model fitting results. Returns model fitting and testing results in a JSON format. Assumes that modelling results are stored in the [PhenTestResult](#) object (output from function [testDataset](#)).

**Usage**

```
JSONOutput(phenTestResult,
phenotypeThreshold = 0.01)
```

**Arguments**

`phenTestResult` instance of the [PhenTestResult](#) class that comes from the function [testDataset](#); mandatory argument

`phenotypeThreshold`  
a numerical value defining the threshold to use in classificationTag; default value 0.01

**Value**

Returns a vector with model fitting results in JSON format: model output summary and other values

**Author(s)**

Natalja Kurbatova

**See Also**

[PhenTestResult](#)

**Examples**

```
## Not run:
# Mixed Model framework
file <- system.file("extdata", "test1.csv", package="PhenStat")
test <- PhenStat::PhenList(dataset=read.csv(file,na.strings = '-'),
  testGenotype="Sparc/Sparc")
result <- PhenStat::testDataset(test,
  depVariable="Lean.Mass")
PhenStat::JSONOutput(result)

# Fishe Exak Test framework
file <- system.file("extdata", "test_categorical.csv", package="PhenStat")
test2 <- PhenStat::PhenList(dataset=read.csv(file,na.strings = '-'),
  testGenotype="Aff3/Aff3")
result2 <- PhenStat::testDataset(test2,
  depVariable="Thoracic.Processes",
  method="FE")
PhenStat::JSONOutput(result2)
## End(Not run)
```

---

LRDataset

*Method "LRDataset"*

---

**Description**

Prepares dataset for the LR framework - maps values of dependent variable to 0/1, where 1 is modeled.

## Usage

```
LRDataset(  
  phenList = NULL,  
  depVariable = NULL,  
  abnormalValues =  
    c("abnormal", "Abnormal", "TRUE", "deviant"),  
  outputMessages = TRUE  
)
```

## Arguments

`phenList` instance of the [PhenList](#) class; mandatory argument

`depVariable` a character string defining the dependent variable of interest; mandatory argument

`abnormalValues` a list of abnormal values that will be mapped to 0; mandatory argument

`outputMessages` flag: "FALSE" value to suppress output messages; "TRUE" value to show output messages; default value TRUE

## Value

Returns dataset suitable for LR framework, where provided abnormal values are mapped to 1 and all other values of dependent variable are assumed to be normal and are mapped to 0.

## Author(s)

Natalja Kurbatova, Natasha Karp, Jeremy Mason

## References

Karp N, Melvin D, Sanger Mouse Genetics Project, Mott R (2012): Robust and Sensitive Analysis of Mouse Knockout Phenotypes. *PLoS ONE* 7(12): e52410. doi:10.1371/journal.pone.0052410

West B, Welch K, Galecki A (2007): Linear Mixed Models: A practical guide using statistical software *New York: Chapman & Hall/CRC* 353 p.

## Examples

```
file <- system.file("extdata", "testLR.csv", package="PhenStat")  
testLR <- PhenStat::PhenList(dataset=read.csv(file,na.strings = '-'),  
  testGenotype="Mock")  
testLR2 <- PhenStat::LRDataset(testLR,"V2")
```

---

matrixCount	<i>Method "matrixCount"</i>
-------------	-----------------------------

---

**Description**

Method matrixCount returns matrix of counts that was created by RR or FE framework.

**Value**

This function returns matrix of counts that was created by RR or FE framework.

**Methods**

signature(obj = "htestPhenStat")

---

method	<i>Method "method"</i>
--------	------------------------

---

**Description**

Method method returns method abbreviation, for example: "RR", "MM".

**Value**

This function returns returns method abbreviation.

**Methods**

signature(obj = "PhenTestResult")

---

methodText	<i>Method "methodText"</i>
------------	----------------------------

---

**Description**

Method methodText returns method's name, for example: "Reference Range Plus", "Linear Mixed Model".

**Value**

This function returns returns method's name.

**Methods**

signature(obj = "PhenTestResult")

---

multipleBatches	<i>Method "multipleBatches"</i>
-----------------	---------------------------------

---

**Description**

Method multipleBatches returns TRUE if there are multiple batches in the dataset, FALSE otherwise

**Value**

This function returns TRUE if there are multiple batches in the dataset.

**Methods**

signature(obj = "PhenList")

---

noSexes	<i>Method "noSexes"</i>
---------	-------------------------

---

**Description**

Method noSexes returns number of sex levels: 1/2

**Value**

This function returns number of sex levels.

**Methods**

signature(obj = "PhenList")  
signature(obj = "PhenTestResult")

---

parameters	<i>Method "parameters"</i>
------------	----------------------------

---

**Description**

Method parameters returns parameters specific for applied method/dataset combination

**Value**

This function returns parameters specific for applied method/dataset combination.

**Methods**

signature(obj = "PhenTestResult")



---

parserOutputSummary    *Method "parserOutputSummary"*

---

**Description**

Parsers model output summary and returns it in readable named vector format

**Usage**

```
parserOutputSummary(linearRegressionOutput)
```

**Arguments**

linearRegressionOutput  
linear regression output that comes from the MM methods; mandatory argument

**Value**

Returns a named vector with linear regression model output summary results

**Author(s)**

Natalja Kurbatova, Natasha Karp, Jeremy Mason

**References**

Karp N, Melvin D, Sanger Mouse Genetics Project, Mott R (2012): Robust and Sensitive Analysis of Mouse Knockout Phenotypes. *PLoS ONE* 7(12): e52410. doi:10.1371/journal.pone.0052410

West B, Welch K, Galecki A (2007): Linear Mixed Models: A practical guide using statistical software *New York: Chapman & Hall/CRC* 353 p.

**See Also**

[PhenTestResult](#)

**Examples**

```
file <- system.file("extdata", "test1.csv", package="PhenStat")
test <- PhenStat::PhenList(dataset=read.csv(file,na.strings = '-'),
  testGenotype="Sparc/Sparc")
result <- PhenStat::testDataset(test,
  depVariable="Lean.Mass")
linearRegressionOutput <- PhenStat::analysisResults(result)
PhenStat::parserOutputSummary(linearRegressionOutput)
```

---

parserOutputSummaryLR *Method "parserOutputSummaryLR"*

---

### Description

Parsers model output summary and returns it in readable named vector format

### Usage

```
parserOutputSummaryLR(linearRegressionOutput)
```

### Arguments

linearRegressionOutput  
linear regression output that comes from the MM methods; mandatory argument

### Value

Returns a named vector with logistic regression model output summary results

### Author(s)

Natalja Kurbatova, Natasha Karp, Jeremy Mason

### References

Karp N, Melvin D, Sanger Mouse Genetics Project, Mott R (2012): Robust and Sensitive Analysis of Mouse Knockout Phenotypes. *PLoS ONE* 7(12): e52410. doi:10.1371/journal.pone.0052410

West B, Welch K, Galecki A (2007): Linear Mixed Models: A practical guide using statistical software *New York: Chapman & Hall/CRC* 353 p.

### See Also

[PhenTestResult](#)

### Examples

```
file <- system.file("extdata", "testLR.csv", package="PhenStat")
testLR <- PhenStat::PhenList(dataset=read.csv(file,na.strings = '-'),
  testGenotype="Mock")
testLR2 <- PhenStat::LRDataset(testLR,"V2")
resultLR <- PhenStat::testDataset(testLR2,
  depVariable="V2",
  method="LR")
linearRegressionOutput <- PhenStat::analysisResults(resultLR)
PhenStat::parserOutputSummaryLR(linearRegressionOutput)
```

---

parserOutputTFSummary *Method "parserOutputTFSummary"*

---

### Description

Parsers model output summary from TF framework and returns it in readable named vector format

### Usage

```
parserOutputTFSummary(linearRegressionOutput)
```

### Arguments

linearRegressionOutput  
linear regression output that comes from the TF method; mandatory argument

### Value

Returns a named vector with model output summary results

### Author(s)

Natalja Kurbatova, Natasha Karp, Jeremy Mason

### References

Karp N, Melvin D, Sanger Mouse Genetics Project, Mott R (2012): Robust and Sensitive Analysis of Mouse Knockout Phenotypes. *PLoS ONE* 7(12): e52410. doi:10.1371/journal.pone.0052410

West B, Welch K, Galecki A (2007): Linear Mixed Models: A practical guide using statistical software *New York: Chapman & Hall/CRC* 353 p.

### See Also

[PhenTestResult](#)

### Examples

```
file <- system.file("extdata", "test6_RR.csv", package="PhenStat")
test <- PhenStat::PhenList(dataset=read.csv(file,na.strings = '-'),
  testGenotype="0xr1/0xr1")
result <- PhenStat::testDataset(test,
  depVariable="Ca",
  method="TF",
  dataPointsThreshold=2)
linearRegressionOutput <- PhenStat::analysisResults(result)
PhenStat::parserOutputTFSummary(linearRegressionOutput)
```

PhenList

*Method "PhenList"***Description**

Function to create data object from the data frame.

In addition to dependent variable column (the variable of interest) mandatory columns that should present in the data frame are "Genotype" and "Sex". The "Assay.Date" column is used to model "Batch" effect if not specified differently. "Weight" column is used to model body weight effect.

Function creates [PhenList](#) object, checks data integrity, renames columns when requested, provides simple statistics about dataset.

Returns an instance of the [PhenList](#) object created from the data file.

Dataset is cleaned to ensure there is a maximum two sex levels and there are exactly two levels for genotype. Data cleaning can be switched off by defining the argument "dataset.clean" as FALSE.

**Usage**

```
PhenList(dataset, testGenotype, refGenotype="+/+", hemiGenotype=NULL,
         outputMessages=TRUE, dataset.clean=TRUE,
         dataset.colname.batch=NULL, dataset.colname.genotype=NULL,
         dataset.colname.sex=NULL, dataset.colname.weight=NULL,
         dataset.values.missingValue=" ", dataset.values.male=NULL,
         dataset.values.female=NULL)
```

**Arguments**

dataset	data frame created from file or from another source; mandatory argument
testGenotype	defines the test genotype to be compared to the reference genotype; mandatory argument
refGenotype	defines the reference genotype; assigned default value is "+/+"
hemiGenotype	defines the genotype value for hemizygous that will be changed to test genotype value
outputMessages	flag: "FALSE" value to suppress output messages; "TRUE" value to show output messages; assigned default value is TRUE
dataset.clean	flag: "FALSE" value for no modification of the dataset; "TRUE" value to clean dataset if needed; assigned default value is TRUE
dataset.colname.batch	column name within dataset for the batch effect
dataset.colname.genotype	column name within dataset for the genotype info
dataset.colname.sex	column name within dataset for the sex info

`dataset.colname.weight`  
column name within dataset for the weight info

`dataset.values.missingValue`  
value used as missing value in the dataset

`dataset.values.male`  
value used to label "males" in the dataset

`dataset.values.female`  
value used to label "females" in the dataset

### Value

Returns an instance of the [PhenList](#) class.

### Author(s)

Natalja Kurbatova, Natasha Karp, Jeremy Mason

### References

Karp N, Melvin D, Sanger Mouse Genetics Project, Mott R (2012): Robust and Sensitive Analysis of Mouse Knockout Phenotypes. *PLoS ONE* 7(12): e52410. doi:10.1371/journal.pone.0052410

West B, Welch K, Galecki A (2007): Linear Mixed Models: A practical guide using statistical software *New York: Chapman & Hall/CRC* 353 p.

### See Also

[PhenList](#)

### Examples

```
file <- system.file("extdata", "test1.csv", package="PhenStat")
test <- PhenStat::PhenList(dataset=read.csv(file, na.strings = '-'),
  testGenotype="Sparc/Sparc")

file <- system.file("extdata", "test2.csv", package="PhenStat")
test2 <- PhenStat::PhenList(dataset=read.csv(file, na.strings = '-'),
  testGenotype="Arid4a/Arid4a",
  refGenotype="+/+",
  hemiGenotype="Arid4a/+",
  dataset.colname.weight="Weight.Value")

file <- system.file("extdata", "test3.csv", package="PhenStat")
test3 <- PhenStat::PhenList(dataset=read.csv(file, na.strings = '-'),
  dataset.clean=TRUE,
  dataset.values.female=1,
  dataset.values.male=2,
  testGenotype="Mysm1/+")
```

---

PhenList-class	<i>Class "PhenList"</i>
----------------	-------------------------

---

### Description

A list-based S4 class for storing phenotypic data. Helps to support data integrity checks and statistics calculation. The PhenList object can be created by using function [PhenList](#).

### Explore PhenList object

PhenList object instance contains the following slots:

1. "datasetPL" where cleaned and checked dataset is stored: `getDataset(phenList)`
2. "testGenotype" where the genotype level to test is stored: `testGenotype(phenList)`
3. "refGenotype" where reference genotype value is stored with default value set to "+/+":  
`refGenotype(phenList)`
4. "hemiGenotype" if defined contains the genotype value for hemizygous: `hemiGenotype(phenList)`
6. "dataset.clean" flag value is stored, see [PhenList](#) for more details:  
`phenList@dataset.clean`
7. "dataset.colname" if defined contains dataset column names that have been renamed:
  - `phenList@dataset.colname.batch` column name for batch values
  - `phenList@dataset.colname.genotype` column name for genotype values
  - `phenList@dataset.colname.sex` column name for sex values
  - `phenList@dataset.colname.weight` column name for weight values
8. "dataset.values" if defined contains dataset values that have been changed during dataset cleaning process:
  - `phenList@dataset.values.missingValue` value used as missing value in the original dataset
  - `phenList@dataset.values.male` value used to label "males" in the original dataset
  - `phenList@dataset.values.female` value used to label "females" in the original dataset

### Slots

`datasetPL`: Object of class "data.frame" ~~ dataset to work with  
`refGenotype`: Object of class "character" ~~ reference genotype  
`testGenotype`: Object of class "character" ~~ test genotype  
`hemiGenotype`: Object of class "character" ~~ hemi genotype  
`dataset.colname.batch`: Object of class "character" ~~ column name for batch values  
`dataset.colname.genotype`: Object of class "character" ~~ column name for genotype values  
`dataset.colname.sex`: Object of class "character" ~~ column name for sex values  
`dataset.colname.weight`: Object of class "character" ~~ column name for weight values

`dataset.values.missingValue`: Object of class "character" ~~ value used as missing value in the original dataset

`dataset.values.male`: Object of class "character" ~~ value used to label "males" in the original dataset

`dataset.values.female`: Object of class "character" ~~ value used to label "females" in the original dataset

`dataset.clean`: Object of class "logical" ~~ flag value is stored

`datasetUNF`: Object of class "data.frame" ~~ unfiltered dataset

## Methods

**getDataset** (accessor): Returns dataset

**refGenotype** (accessor): Returns reference genotype

**testGenotype** (accessor): Returns test genotype

**hemiGenotype** (accessor): Returns hemi genotype if specified

**getColumn** Returns specified column if exists

**getColumnBatchAdjusted** Returns specified column adjusted for batch effect

**getColumnWeightBatchAdjusted** Returns specified column adjusted for batch and weight effects

**getStat** Returns simple dataset statistics

**getVariables** Returns dataset column names

**batchIn** Returns TRUE if the batch is in the dataset, FALSE otherwise

**weightIn** Returns TRUE if the weight is in the dataset, FALSE otherwise

**multipleBatches** Returns TRUE if the batches are variable in the dataset, FALSE otherwise

**noSexes** Returns number of sexes in the dataset

**setBatch** Sets the batch column - change the column names

**setGenotype** Sets the genotype column - change the column names

**setMissingValue** Sets the missing value

**setSex** Sets the sex column - change the column names

**setWeight** Sets the weight column - change the column names

## Author(s)

Natalja Kurbatova

## See Also

[PhenList](#)

**Examples**

```

file <- system.file("extdata", "test1.csv", package="PhenStat")
test <- PhenStat::PhenList(dataset=read.csv(file,na.strings = '-'),
  testGenotype="Sparc/Sparc")
class(test)

file <- system.file("extdata", "test2.csv", package="PhenStat")
test2 <- PhenStat::PhenList(dataset=read.csv(file,na.strings = '-'),
  testGenotype="Arid4a/Arid4a",
  refGenotype="+/+",
  hemiGenotype="Arid4a/+",
  dataset.colname.weight="Weight.Value")
PhenStat::getStat(test2)
PhenStat::testGenotype(test2)
PhenStat::refGenotype(test2)
PhenStat::hemiGenotype(test2)

```

PhenStatReport

*Generating a pdf report from a PhenList object***Description**

This function takes a Phenlist object and generates a pdf report containing several statistical methods.

**Usage**

```

PhenStatReport(
  PhenlistObject      ,
  depVariable = NULL  ,
  other.response = NULL ,
  update = TRUE      ,
  Gene.Symbol = NULL  ,
  Response.name = NULL ,
  destination = NULL  ,
  reportTitle = "Extended Statistical Report",
  DataRelease = NULL  ,
  Showsource = FALSE  ,
  open = FALSE        ,
  clean = TRUE         ,
  verbos = FALSE      ,
  ...
)

```

**Arguments**

**PhenlistObject** A phenlist object that is already created by PhenList() function in PhenStat.  
**depVariable** String. Name of the dependent variable.



<code>other.response</code>	The vector of strings. A vector of names containing the other dependent variables in the data set. Default NULL
<code>update</code>	Logical flag. Set to TRUE to get the latest version of the report on the fly. Default is TRUE
<code>Gene.Symbol</code>	Optional string. Gene symbol. Default NULL
<code>Response.name</code>	Optional string. Name of the dependent variable. Default NULL
<code>destination</code>	Location of the final report file. The default is the working directory of R.
<code>reportTitle</code>	The title of the report that is printed on the top of the first page of the report.
<code>DataRelease</code>	Optional flag. Data release version. Default NULL
<code>Showsource</code>	Logical flag. Set to TRUE to see the actual R codes that generate each section of the report. Default FALSE
<code>open</code>	Logical flag. Set to TRUE to open the report after it is generated. Default FALSE
<code>clean</code>	Logical flag. Set to TRUE to remove the auxiliary files after successfully generating the report. Default TRUE
<code>verbos</code>	Logical flag. Setting to TRUE shows the details and progress of the report generating function on screen. Default FALSE
<code>...</code>	List of other parameters that can be passed to the functions.

### Details

See [PhenStatReport page on the IMPC website](#)

### Value

<code>PhenlistObject</code>	The input object
<code>depVariable</code>	Dependent variable
<code>texfile</code>	The location of the .tex file, given Clean=FALSE
<code>pdffile</code>	The location of the final pdf file
<code>...</code>	The same as the input parameters

### Author(s)

Hamed Haselimashhadi <hamedhm@ebi.ac.uk>

### See Also

[PhenList](#)

**Examples**

```

file <- system.file("extdata", "test1.csv", package = "PhenStat")
test = PhenStat:::PhenList(dataset = read.csv(file,na.strings = '-'),
                           testGenotype = "Sparc/Sparc")

## Not run:
PhenStatReport(test,
                depVariable = 'Bone.Area',
                open = TRUE)

## End(Not run)

```

---

PhenTestResult	<i>Method "PhenTestResult"</i>
----------------	--------------------------------

---

**Description**

Creates [PhenTestResult](#) object based on test results or model building results. Internal function for the package. Not build for users to directly call.

**Usage**

```

PhenTestResult(model.output=NULL, model.dataset=NULL,
               depVariable=NULL,
               refGenotype=NULL,
               equation="withWeight",
               method="MM", model.effect.batch=NULL,
               model.effect.variance=NULL,model.effect.sex=NULL,
               model.effect.interaction=NULL, model.output.interaction=NULL,
               model.effect.weight=NULL, numberSexes=NULL,pThreshold=0.05,
               model.formula.null=NULL,model.formula.genotype=NULL,
               model.output.genotype.nulltest.pVal=NULL,
               model.output.quality=NULL,model.output.summary=NULL,
               model.output.averageRefGenotype = NULL,
               model.output.percentageChanges = NULL)

```

**Arguments**

model.output	representing the model fit gls object or lme object
model.dataset	dataset used for modeling
depVariable	depending variable in the model
refGenotype	reference genotype in the model
equation	possible values: "withWeight" to include weight effect into model, "withoutWeight" to exclude weight effect from the model
method	possible values: "MM" to work with Mixed Model framework, "FE" to work with Fisher Exact Test framework

<code>model.effect.batch</code>	Result of the test for batch effect significance
<code>model.effect.variance</code>	Result of the test for residual variance effect
<code>model.effect.sex</code>	Result of the test for sex effect significance
<code>model.effect.weight</code>	Result of the test for weight effect significance
<code>model.effect.interaction</code>	Result of the test for genotype by sex interaction significance
<code>model.output.interaction</code>	Interaction test result: p-value
<code>numberSexes</code>	number of possible sex values in the dataset
<code>pThreshold</code>	p-value threshold used to evaluate the effect significance, default value 0.05
<code>model.formula.null</code>	formula for the model without genotype effect
<code>model.formula.genotype</code>	formula for the model with genotype effect
<code>model.output.genotype.nulltest.pVal</code>	Genotype test results: p-value
<code>model.output.quality</code>	vector that contains diagnostic test output for mixed model quality of fit
<code>model.output.summary</code>	named vector that contains summary of the model output
<code>model.output.averageRefGenotype</code>	named vector that contains mean values calculated for reference genotype records
<code>model.output.percentageChanges</code>	named vector that contains percentage changes values per sex

**Value**

Returns an instance of the [PhenTestResult](#) class.

**Author(s)**

Natalja Kurbatova, Natasha Karp, Jeremy Mason

**References**

- Karp N, Melvin D, Sanger Mouse Genetics Project, Mott R (2012): Robust and Sensitive Analysis of Mouse Knockout Phenotypes. *PLoS ONE* 7(12): e52410. doi:10.1371/journal.pone.0052410
- West B, Welch K, Galecki A (2007): Linear Mixed Models: A practical guide using statistical software *New York: Chapman & Hall/CRC* 353 p.

**See Also**

[PhenTestResult](#)

**Examples**

```

file <- system.file("extdata", "test1.csv", package="PhenStat")
test <- PhenStat::PhenList(dataset=read.csv(file,na.strings = '-'),
  testGenotype="Sparc/Sparc")
# "testDataset" function calls "PhenTestResult" function internally
result <- PhenStat::testDataset(test,
  equation="withoutWeight",
  depVariable="Lean.Mass")
class(result)

```

---

PhenTestResult-class    *Class "PhenTestResult"*

---

**Description**

A list-based S4 class for storing of model fitting results and other information like dependent variable, method used to build a model, etc. Helps to support operations needed for model fitting process and modelling/testing results storage. In the package PhenTestResult object is created by function [testDataset](#).

**Explore PhenTestResult object**

PhenTestResults object instance contains the following slots:

1. "analysedDataset" contains subdataset that was used for the modelling/testing:  
analysedDataset(phenTestResult)
2. "depVariable" contains dependent variable that was tested: getVariable(phenTestResult)
3. "refGenotype" contains reference genotype which is usually is wildtype: refGenotype(phenTestResult)
4. "testGenotype" contains test genotype: testGenotype(phenTestResult)
5. "method" contains method name that was used for modelling/testing: method(phenTestResult)
6. "transformationRequired" contains TRUE/FALSE value indicating transformation of dependent variable:  
transformationText(phenTestResult) or phenTestResult@transformationRequired
7. "lambdaValue" contains lambda value for the Box-Cox transformation:  
transformationText(phenTestResult) or phenTestResult\$lambdaValue
8. "scaleShift" contains the value of scale shift for Box-Cox transformation:  
transformationText(phenTestResult) or phenTestResult@scaleShift
9. "transformationCode" contains the code of transformation. Possible values:  
0 - transformation is not applicable (methods "FE", "RR", "LR") or switched off by user  
1 - transformation is not needed (1 is within the 95% - log transformation)  
2 - log transformation  
3 - power transformation  
4 - transformation is not performed since optimal lambda value is not found (-5 > lambda > 5)  
transformationText(phenTestResult) or phenTestResult@transformationCode

10. "parameters" contains the parameters used during method application, e.g. pThreshold for MM and TF:

`parameters(phenTestResult)`

11. Modelling/testing results are stored in the sections "analysisResults": `analysisResults(phenTestResult)`

The contents of the analysisResults slot depend on framework that was used.

The results of MM and TF frameworks: 1. Equation used during linear modeling: `analysisResults(phenTestResult)$equation`

2. Batch effect significance: `analysisResults(phenTestResult)$model.effect.batch`

3. Variance equality: `analysisResults(phenTestResult)$model.effect.variance`

4. Weight effect significance: `analysisResults(phenTestResult)$model.effect.weight`

5. Sex effect significance: `analysisResults(phenTestResult)$model.effect.interaction`

6. Evidence of sex effect (p-value): `analysisResults(phenTestResult)$model.output.interaction`

7. Evidence of genotype effect (p-value): `analysisResults(phenTestResult)$model.output.genotype.nulltest.pValue`

8. Formula for the final genotype model: `analysisResults(phenTestResult)$model.formula.genotype`

9. Formula for the final null model: `analysisResults(phenTestResult)$model.formula.null`

10. Model fitting output: `analysisResults(phenTestResult)$model.output`

11. Model fitting summary: `summary(analysisResults(phenTestResult)$model.output)$tTable`

The results of FE and RR frameworks are stored as a list of `hTestPhenStat` S4 objects: `analysisResults(phenTestResult)[1:length(analysisResults(phenTestResult))]$hTestPhenStat`

Each one `hTestPhenStat` object contains:

1. Output of Fisher Exact Test: `pvalue(analysisResults(phenTestResult)[[1]])`.

2. Effect size: `ES(analysisResults(phenTestResult)[[1]])`.

3. Name of the table analysed (all, males, females): `analysedSubset(analysisResults(phenTestResult)[[1]])`.

4. Comparison, used for RR only (High vs Normal/Low, Low vs High/Normal): `comparison(analysisResults(phenTestResult)[[1]])`.

5. Matrix of counts: `matrixCount(analysisResults(phenTestResult)[[1]])`.

## Slots

**analysedDataset:** Object of class "data.frame" ~~ analysed dataset

**transformationRequired:** Object of class "logical" ~~ flag indicating was or not transformation performed

**lambdaValue:** Object of class "numeric" ~~ Box-Cox transform lambda value

**scaleShift:** Object of class "numeric" ~~ Box-Cox transform scale shift

**transformationCode:** Object of class "numeric" ~~ code explaining the transformation output

**depVariable:** Object of class "character" ~~ dependent variable

**refGenotype:** Object of class "character" ~~ reference genotype

**testGenotype:** Object of class "character" ~~ test genotype

**method:** Object of class "character" ~~ analysis method

**parameters:** Object of class "matrix" ~~ parameters of method

**analysisResults:** Object of class "list" ~~ results of the analysis

**Methods**

**getVariable** (accessor): Returns dependent variable  
**refGenotype** (accessor): Returns reference genotype  
**testGenotype** (accessor): Returns test genotype  
**method** (accessor): Returns method used  
**methodText** (accessor): Returns full name of the method used  
**parameters** (accessor): Returns parameteres used during the method application  
**analysisResults** (accessor): Returns analysis results depending on method  
**analysedDataset** (accessor): Returns analysed dataset  
**transformationText** (accessor): Returns the info about transformation  
**batchIn** Returns TRUE if the batch is in the dataset, FALSE otherwise  
**weightIn** Returns TRUE if the weight is in the dataset, FALSE otherwise  
**noSexes** Returns number of sexes in the dataset  
**show** Prints out the PhenTestResult object  
**getCountMatrices** Returns count matrices if they are present (for methods "FE" and "RR"), NULL otherwise.

**Author(s)**

Natalja Kurbatova

**Examples**

```
# Mixed Model framework
file <- system.file("extdata", "test1.csv", package="PhenStat")
test <- PhenStat::PhenList(dataset=read.csv(file,na.strings = '-'),
  testGenotype="Sparc/Sparc")
result <- PhenStat::testDataset(test,
  equation="withoutWeight",
  depVariable="Bone.Area")
PhenStat::getVariable(result)
PhenStat::method(result)
# Batch effect is significant
PhenStat::analysisResults(result)$model.effect.batch
# Variance homogeneity
PhenStat::analysisResults(result)$model.effect.variance
# Weight effect is significant
PhenStat::analysisResults(result)$model.effect.weight
# Sex effect is significant
PhenStat::analysisResults(result)$model.effect.interaction
# Sex effect p-value - the result of the test
PhenStat::analysisResults(result)$model.output.interaction
# Genotype effect p-value
PhenStat::analysisResults(result)$model.output.genotype.nulltest.pVal
# Final model formula with genotype
PhenStat::analysisResults(result)$model.formula.genotype
```

```

# Final model formula without genotype
PhenStat::analysisResults(result)$model.formula.null
# Final model fitting output
# result$model.output
# Final model fitting summary
# summary(result$model.output)$tTable

# Fisher Exact Test framework
file <- system.file("extdata", "test_categorical.csv", package="PhenStat")
test <- PhenStat::PhenList(dataset=read.csv(file,na.strings = '-'),
  testGenotype="Aff3/Aff3")
result <- PhenStat::testDataset(test,
  depVariable="Thoracic.Processes",
  method="FE")
PhenStat::getVariable(result)
PhenStat::method(result)
for (i in seq_along(analysisResults(result))) {
  val <- PhenStat::analysisResults(result)[[i]]
  val
}

```

---

plot.PhenList

*Plot Phenlist object*


---

## Description

Plot method for objects of class "PhenList".

## Usage

```

## S3 method for class 'PhenList'
plot(
  x
  ,
  depVariable = 'Value',
  graphingName = NULL ,
  outputMessages = TRUE,
  type = NULL,
  ...
)

```

## Arguments

x	instance of the PhenList class mandatory argument
depVariable	a character string defining the dependent variable of interest mandatory argument
graphingName	character string defining the name to be used on the graph for the dependent variable

`outputMessages` flag: "FALSE" value to suppress output messages "TRUE" value to show output messages default value TRUE

`type` a vector of names. Select one or more from the list below to only get those plots.

- `boxplotSexGenotype`. See documentations for `boxplotSexGenotype`
- `boxplotSexGenotypeBatchAdjusted`. See documentations for `boxplotSexGenotypeBatchAdjusted`
- `boxplotSexGenotypeWeightBatchAdjusted`. See documentations for `boxplotSexGenotypeWeightBatchAdjusted`
- `scatterplotSexGenotypeBatch`. See documentations for `scatterplotSexGenotypeBatch`
- `scatterplotGenotypeWeight`. See documentations for `scatterplotGenotypeWeight`
- `boxplotSexGenotypeBatch`. See documentations for `boxplotSexGenotypeBatch`

...

**Value**

Empty.

**Author(s)**

Hamed Haselimashhadi <hamedhm@eb.ac.uk >

**See Also**

[PhenList](#),

**Examples**

```
example(testDataset)
```

---

`plot.PhenTestResult`    *Plot phenTestResult object*

---

**Description**

Plot method for objects of class "phenTestResult".



**Usage**

```
## S3 method for class 'PhenTestResult'
plot(
  x
  ,
  graphingName = NULL
  ,
  outputMessages = TRUE,
  type = NULL,
  ...
)
```

**Arguments**

**x** instance of the PhenTestResult class mandatory argument

**graphingName** character string defining the name to be used on the graph for the dependent variable

**outputMessages** flag:"FALSE" value to suppress output messages "TRUE" value to show output messages default value TRUE

**type** a vector of names. Select one or more from the list below to only get those plots.

- boxplotSexGenotypeResult. See documentations for boxplotSexGenotypeResult
- scatterplotSexGenotypeBatchResult. See documentations for scatterplotSexGenotypeBatchResult
- scatterplotGenotypeWeightResult. See documentations for scatterplotGenotypeWeightResult
- plotResidualPredicted. See documentations for plotResidualPredicted
- qqplotRandomEffects. See documentations for qqplotRandomEffects
- boxplotResidualBatch. See documentations for boxplotResidualBatch
- qqplotRotatedResiduals. See documentations for qqplotRotatedResiduals
- qqplotGenotype. See documentations for qqplotGenotype
- categoricalBarplot. See documentations for categoricalBarplot

...

**Value**

Empty.

**Author(s)**

Hamed Haselimashhadi <hamedhm@eb.ac.uk >

**See Also**

[testDataset](#)

**Examples**

```
example(testDataset)
```

---

plotResidualPredicted *Method "plotResidualPredicted"*

---

**Description**

Graph function for the Mixed Model framework's results. Creates predicted versus residual values plots split by genotype.

**Usage**

```
plotResidualPredicted(phenTestResult, outputMessages=TRUE)
```

**Arguments**

`phenTestResult` instance of the [PhenTestResult](#) class that comes from the function [testDataset](#); mandatory argument

`outputMessages` flag: "FALSE" value to suppress output messages; "TRUE" value to show output messages; default value TRUE

**Value**

Empty.

**Author(s)**

Natalja Kurbatova, Natasha Karp, Jeremy Mason

**References**

Karp N, Melvin D, Sanger Mouse Genetics Project, Mott R (2012): Robust and Sensitive Analysis of Mouse Knockout Phenotypes. *PLoS ONE* 7(12): e52410. doi:10.1371/journal.pone.0052410

West B, Welch K, Galecki A (2007): Linear Mixed Models: A practical guide using statistical software *New York: Chapman & Hall/CRC* 353 p.

**See Also**

[PhenList](#) and [PhenTestResult](#)

**Examples**

```
file <- system.file("extdata", "test1.csv", package="PhenStat")
test <- PhenStat::PhenList(dataset=read.csv(file,na.strings = '-'),
  testGenotype="Sparc/Sparc")
result <- PhenStat::testDataset(test,
  depVariable="Lean.Mass")
PhenStat::plotResidualPredicted(result)
```

---

pvalue	<i>Method "pvalue"</i>
--------	------------------------

---

**Description**

Method pvalue returns p-value that was calculate by RR or FE framework.

**Value**

This function returns p-value that was calculate by RR or FE framework.

**Methods**

signature(obj = "htestPhenStat")

---

qqplotGenotype	<i>Method "qqplotGenotype"</i>
----------------	--------------------------------

---

**Description**

Graph function for the Mixed Model framework's results. Creates a Q-Q plot of residuals for each genotype.

**Usage**

```
qqplotGenotype(phenTestResult, outputMessages=TRUE)
```

**Arguments**

phenTestResult instance of the [PhenTestResult](#) class that comes from the function [testDataset](#); mandatory argument

outputMessages flag: "FALSE" value to suppress output messages; "TRUE" value to show output messages; default value TRUE

**Value**

Empty.

**Author(s)**

Natalja Kurbatova, Natasha Karp, Jeremy Mason

**References**

Karp N, Melvin D, Sanger Mouse Genetics Project, Mott R (2012): Robust and Sensitive Analysis of Mouse Knockout Phenotypes. *PLoS ONE* 7(12): e52410. doi:10.1371/journal.pone.0052410

West B, Welch K, Galecki A (2007): Linear Mixed Models: A practical guide using statistical software *New York: Chapman & Hall/CRC* 353 p.

**See Also**

[PhenList](#) and [PhenTestResult](#)

**Examples**

```
file <- system.file("extdata", "test1.csv", package="PhenStat")
test <- PhenStat::PhenList(dataset=read.csv(file,na.strings = '-'),
  testGenotype="Sparc/Sparc")
result <- PhenStat::testDataset(test,
  depVariable="Lean.Mass")
PhenStat::qqplotGenotype(result)
```

---

qqplotRandomEffects *Method "qqplotRandomEffects"*

---

**Description**

Graph function for the Mixed Model framework's results. Creates a Q-Q plot of blups (best linear unbiased predictions).

**Usage**

```
qqplotRandomEffects(phenTestResult, outputMessages=TRUE)
```

**Arguments**

`phenTestResult` instance of the [PhenTestResult](#) class that comes from the function [testDataset](#); mandatory argument

`outputMessages` flag: "FALSE" value to suppress output messages; "TRUE" value to show output messages; default value TRUE

**Value**

Empty.

**Author(s)**

Natalja Kurbatova, Natasha Karp, Jeremy Mason

**References**

Karp N, Melvin D, Sanger Mouse Genetics Project, Mott R (2012): Robust and Sensitive Analysis of Mouse Knockout Phenotypes. *PLoS ONE* 7(12): e52410. doi:10.1371/journal.pone.0052410

West B, Welch K, Galecki A (2007): Linear Mixed Models: A practical guide using statistical software *New York: Chapman & Hall/CRC* 353 p.

**See Also**

[PhenList](#) and [PhenTestResult](#)

**Examples**

```
file <- system.file("extdata", "test1.csv", package="PhenStat")
test <- PhenStat::PhenList(dataset=read.csv(file,na.strings = '-'),
  testGenotype="Sparc/Sparc")
result <- PhenStat::testDataset(test,
  depVariable="Lean.Mass")
PhenStat::qqplotRandomEffects(result)
```

---

qqplotRotatedResiduals

*Method "qqplotRotatedResiduals"*

---

**Description**

Graph function for the Mixed Model framework's results. Creates a Q-Q plot of rotated residuals.

**Usage**

```
qqplotRotatedResiduals(phenTestResult, outputMessages=TRUE)
```

**Arguments**

`phenTestResult` instance of the [PhenTestResult](#) class that comes from the function [testDataset](#); mandatory argument

`outputMessages` flag: "FALSE" value to suppress output messages; "TRUE" value to show output messages; default value TRUE

**Value**

Empty.

**Author(s)**

Natalja Kurbatova, Natasha Karp, Jeremy Mason

**References**

Karp N, Melvin D, Sanger Mouse Genetics Project, Mott R (2012): Robust and Sensitive Analysis of Mouse Knockout Phenotypes. *PLoS ONE* 7(12): e52410. doi:10.1371/journal.pone.0052410

Houseman, E. A., Ryan, L. M., Coull, B. A. (2004): Cholesky residuals for assessing normal errors in a linear model with correlated outcomes. *Journal of the American Statistical Association* 99:466: pg 383-394. Doi 10.1198

West B, Welch K, Galecki A (2007): Linear Mixed Models: A practical guide using statistical software *New York: Chapman & Hall/CRC* 353 p.

**See Also**

[PhenList](#) and [PhenTestResult](#)

**Examples**

```
file <- system.file("extdata", "test2.csv", package="PhenStat")
test <- PhenStat::PhenList(dataset=read.csv(file,na.strings = '-'),
  dataset.colname.weight="Weight.Value",
  testGenotype="Arid4a/Arid4a",
  hemiGenotype="Arid4a/+")
result <- PhenStat::testDataset(test,
  depVariable="C1")
PhenStat::qqplotRotatedResiduals(result)
```

---

recommendMethod	<i>Method "recommendMethod"</i>
-----------------	---------------------------------

---

**Description**

Checks the dependent variable and dataset to make choose the appropriate statistical method. Returns the method or the list of methods that are appropriate for statistical analysis.

**Usage**

```
recommendMethod(phenList = NULL,
  depVariable = NULL,
  outputMessages = TRUE,
  upper = 5)
```

**Arguments**

phenList	instance of the <a href="#">PhenList</a> class; mandatory argument
depVariable	a character string defining the dependent variable of interest; mandatory argument
outputMessages	flag: "FALSE" value to suppress output messages; "TRUE" value to show output messages; default value TRUE
upper	Single integer: maximum allowed number of levels for the Batch in the TF framework

**Value**

Returns the method or the list of methods that are appropriate for statistical analysis.

**Author(s)**

Natalja Kurbatova, Natasha Karp, Jeremy Mason

**References**

Karp N, Melvin D, Sanger Mouse Genetics Project, Mott R (2012): Robust and Sensitive Analysis of Mouse Knockout Phenotypes. *PLoS ONE* 7(12): e52410. doi:10.1371/journal.pone.0052410

West B, Welch K, Galecki A (2007): Linear Mixed Models: A practical guide using statistical software *New York: Chapman & Hall/CRC* 353 p.

**See Also**

[PhenList](#)

**Examples**

```
file <- system.file("extdata", "test1.csv", package="PhenStat")
test <- PhenStat::PhenList(dataset=read.csv(file,na.strings = '-'),
  testGenotype="Sparc/Sparc")
PhenStat::recommendMethod(test,"Lean.Mass")
```

---

refGenotype	<i>Method "refGenotype"</i>
-------------	-----------------------------

---

**Description**

Method refGenotype returns reference genotype

**Value**

This function returns reference genotype.

**Methods**

```
signature(obj = "PhenList")
signature(obj = "PhenTestResult")
```

---

RRTest

*Method "RRTest"*


---

**Description**

This is an internal function run within RR framework. It performs Reference Ranges Plus test and after that Fisher Exact test on calculated count matrices. As an internal function, it doesn't include extensive error testing of inputs. Please use cautiously if calling directly.

Works with [PhenList](#) object created by [PhenList](#) function.

**Usage**

```
RRTest(
  phenList,
  depVariable,
  outputMessages = TRUE,
  naturalVariation = 95,
  controlPointsThreshold = 60
)
```

**Arguments**

<code>phenList</code>	instance of the <a href="#">PhenList</a> class; mandatory argument
<code>depVariable</code>	a character string defining the dependent variable of interest; mandatory argument
<code>outputMessages</code>	flag: "FALSE" value to suppress output messages; "TRUE" value to show output messages; default value TRUE
<code>naturalVariation</code>	number defining the natural variation range in percents for normal values; default value 95
<code>controlPointsThreshold</code>	number defining how many control points is needed to perform RR plus method; default value 60

**Value**

Returns results stored in instance of the [PhenTestResult](#) class

**Author(s)**

Natalja Kurbatova, Natasha Karp, Jeremy Mason



## References

Karp N, Melvin D, Sanger Mouse Genetics Project, Mott R (2012): Robust and Sensitive Analysis of Mouse Knockout Phenotypes. *PLoS ONE* 7(12): e52410. doi:10.1371/journal.pone.0052410

West B, Welch K, Galecki A (2007): Linear Mixed Models: A practical guide using statistical software *New York: Chapman & Hall/CRC* 353 p.

## See Also

[PhenList](#) and [testDataset](#)

## Examples

```
file <- system.file("extdata", "test1.csv", package="PhenStat")
test <- PhenStat::PhenList(dataset=read.csv(file,na.strings = '-'),
  testGenotype="Sparc/Sparc")
# "RRTest" function is called from "testDataset" function
result <- PhenStat::testDataset(test,
  depVariable="Lean.Mass",
  method="RR")
# RR test results can be printed out using function "summaryOutput"
summary(result)
```

---

scatterplotGenotypeWeight

*Method "scatterplotGenotypeWeight"*

---

## Description

Graph function for the phenotypic dataset. Creates a scatter plot body weight versus dependent variable.

Both a regression line and a loess line (locally weighted line) is fitted for each genotype.

## Usage

```
scatterplotGenotypeWeight(
  phenList,
  depVariable = NULL,
  graphingName = NULL,
  outputMessages = TRUE
)
```

## Arguments

phenList	instance of the <a href="#">PhenList</a> class; mandatory argument
depVariable	a character string defining the dependent variable of interest; mandatory argument

graphingName a character string defining the name to be used on the graph for the dependent variable; mandatory argument

outputMessages flag: "FALSE" value to suppress output messages; "TRUE" value to show output messages; default value TRUE

**Value**

Empty.

**Author(s)**

Natalja Kurbatova, Natasha Karp, Jeremy Mason

**References**

Karp N, Melvin D, Sanger Mouse Genetics Project, Mott R (2012): Robust and Sensitive Analysis of Mouse Knockout Phenotypes. *PLoS ONE* 7(12): e52410. doi:10.1371/journal.pone.0052410

West B, Welch K, Galecki A (2007): Linear Mixed Models: A practical guide using statistical software *New York: Chapman & Hall/CRC* 353 p.

**See Also**

[PhenList](#)

**Examples**

```
file <- system.file("extdata", "test1.csv", package="PhenStat")
test <- PhenStat::PhenList(dataset=read.csv(file,na.strings = '-'),
  testGenotype="Sparc/Sparc")
PhenStat::scatterplotGenotypeWeight(test,
  depVariable="Bone.Mineral.Content",
  graphingName="BMC" )
file <- system.file("extdata", "test4.csv", package="PhenStat")
test_1sex <- PhenStat::PhenList(dataset=read.csv(file,na.strings = '-'),
  testGenotype="Mysm1/+")
PhenStat::scatterplotGenotypeWeight(test_1sex,
  depVariable="Lean.Mass",
  graphingName="Lean Mass")
```

---

scatterplotGenotypeWeightResult

*Method "scatterplotGenotypeWeightResult"*

---

**Description**

Graph function for the phenotypic dataset. Creates a scatter plot body weight versus dependent variable. It is based on PhenTestResult object. Both a regression line and a loess line (locally weighted line) is fitted for each genotype.



---

`scatterplotSexGenotypeBatch`*Method "scatterplotSexGenotypeBatch"*

---

### Description

Graph function for the phenotypic dataset. Creates a scatterplot split by sex, genotype and batch. refGenotype data points are shown in black and the testGenotype data points are shown in red.

Note: the batches are not ordered with time but allow assessment of how the testGenotype data lie relative to the variation within the refGenotype data.

### Usage

```
scatterplotSexGenotypeBatch(  
  phenList,  
  depVariable = NULL,  
  graphingName = NULL,  
  outputMessages = TRUE  
)
```

### Arguments

phenList	instance of the <a href="#">PhenList</a> class; mandatory argument
depVariable	a character string defining the dependent variable of interest; mandatory argument
graphingName	a character string defining the name to be used on the graph for the dependent variable; mandatory argument
outputMessages	flag: "FALSE" value to suppress output messages; "TRUE" value to show output messages; default value TRUE

### Value

Empty.

### Author(s)

Natalja Kurbatova, Natasha Karp, Jeremy Mason

### References

Karp N, Melvin D, Sanger Mouse Genetics Project, Mott R (2012): Robust and Sensitive Analysis of Mouse Knockout Phenotypes. *PLoS ONE* 7(12): e52410. doi:10.1371/journal.pone.0052410

West B, Welch K, Galecki A (2007): Linear Mixed Models: A practical guide using statistical software *New York: Chapman & Hall/CRC* 353 p.

**See Also**[PhenList](#)**Examples**

```

file <- system.file("extdata", "test1.csv", package="PhenStat")
test <- PhenStat::PhenList(dataset=read.csv(file,na.strings = '-'),
  testGenotype="Sparc/Sparc")
# box plot for dataset with two sexes: males and females
PhenStat::scatterplotSexGenotypeBatch(test,
  depVariable="Bone.Mineral.Content",
  graphingName="BMC" )

file <- system.file("extdata", "test4.csv", package="PhenStat")
test_1sex <- PhenStat::PhenList(dataset=read.csv(file,na.strings = '-'),
  testGenotype="Mysm1/+")
# box plot for females only dataset
PhenStat::scatterplotSexGenotypeBatch(test_1sex,depVariable="Lean.Mass",
  graphingName="Lean Mass")

```

---

scatterplotSexGenotypeBatchResult

*Method "scatterplotSexGenotypeBatchResult"*


---

**Description**

Graph function for the phenotypic dataset. Creates a scatterplot split by sex, genotype and batch. refGenotype data points are shown in black and the testGenotype data points are shown in red. It is based on PhenTestResult object.

Note: the batches are not ordered with time but allow assessment of how the testGenotype data lie relative to the variation within the refGenotype data.

**Usage**

```

scatterplotSexGenotypeBatchResult(phenTestResult,
  graphingName = NULL,
  outputMessages = TRUE)

```

**Arguments**

phenTestResult instance of the [PhenTestResult](#) class; mandatory argument

graphingName a character string defining the name to be used on the graph for the dependent variable; mandatory argument

outputMessages flag: "FALSE" value to suppress output messages; "TRUE" value to show output messages; default value TRUE

**Value**

Empty.

**Author(s)**

Natalja Kurbatova, Natasha Karp, Jeremy Mason

**References**

Karp N, Melvin D, Sanger Mouse Genetics Project, Mott R (2012): Robust and Sensitive Analysis of Mouse Knockout Phenotypes. *PLoS ONE* 7(12): e52410. doi:10.1371/journal.pone.0052410

West B, Welch K, Galecki A (2007): Linear Mixed Models: A practical guide using statistical software *New York: Chapman & Hall/CRC* 353 p.

**See Also**

[PhenList](#)

**Examples**

```
file <- system.file("extdata", "test1.csv", package="PhenStat")
test <- PhenStat::PhenList(dataset=read.csv(file,na.strings = '-'),
  testGenotype="Sparc/Sparc")
result <- PhenStat::testDataset(test,
  depVariable="Lean.Mass")
# box plot for dataset with two sexes: males and females
PhenStat::scatterplotSexGenotypeBatchResult(result,
  graphingName="BMC" )

file <- system.file("extdata", "test4.csv", package="PhenStat")
test_1sex <- PhenStat::PhenList(dataset=read.csv(file,na.strings = '-'),
  testGenotype="Mysm1/+")
result_1sex <- PhenStat::testDataset(test_1sex,
  depVariable="Lean.Mass")
# box plot for females only dataset
PhenStat::scatterplotSexGenotypeBatchResult(result_1sex,
  graphingName="Lean Mass")
```

---

setBatch

*Method "setBatch"*

---

**Description**

Method setBatch sets batch column in the dataset

**Value**

This function sets batch column in the dataset.

**Methods**

signature(obj = "PhenList")

---

setGenotype	<i>Method "setGenotype"</i>
-------------	-----------------------------

---

**Description**

Method setGenotype sets genotype column in the dataset

**Value**

This function sets genotype column in the dataset.

**Methods**

signature(obj = "PhenList")

---

setMissingValue	<i>Method "setMissingValue"</i>
-----------------	---------------------------------

---

**Description**

Method setMissingValue sets missing value in the dataset

**Value**

This function sets missing value in the dataset.

**Methods**

signature(obj = "PhenList")

---

setSex	<i>Method "setSex"</i>
--------	------------------------

---

**Description**

Method setSex sets sex column in the dataset

**Value**

This function sets sex column in the dataset.

**Methods**

signature(obj = "PhenList")

---

setWeight	<i>Method "setWeight"</i>
-----------	---------------------------

---

**Description**

Method setWeight sets weight column in the dataset

**Value**

This function sets weight column in the dataset.

**Methods**

signature(obj = "PhenList")

---

startLRModel	<i>Method "startLRModel"</i>
--------------	------------------------------

---

**Description**

This is an internal function run within LR framework. It completes the testing stage of which effects are significant. As an internal function, it doesn't include extensive error testing of inputs. Please use cautiously if calling directly.

It creates start model and modify it after testing of different hypothesis.

The tested effects are:

-batch effect (TRUE if batch variation is significant, FALSE if not), though it is never used in final LR model;

-interaction effect (TRUE if genotype by sex interaction is significant),

-sex effect (TRUE if sex is significant),

-weight effect and variance effect are not tested and used in LR model.

**Usage**

```
startLRModel(phenList,
  depVariable,
  outputMessages = TRUE,
  pThreshold = 0.05)
```



**Arguments**

phenList	instance of the <a href="#">PhenList</a> class; mandatory argument
depVariable	a character string defining the dependent variable of interest; mandatory argument
outputMessages	flag: "FALSE" value to suppress output messages; "TRUE" value to show output messages ; default value TRUE
pThreshold	a numerical value for the p-value threshold used to determine which fixed effects to keep in the model, default value 0.05

**Value**

Returns results stored in instance of the [PhenTestResult](#) class

**Author(s)**

Natalja Kurbatova, Natasha Karp, Jeremy Mason

**References**

Karp N, Melvin D, Sanger Mouse Genetics Project, Mott R (2012): Robust and Sensitive Analysis of Mouse Knockout Phenotypes. *PLoS ONE* 7(12): e52410. doi:10.1371/journal.pone.0052410

West B, Welch K, Galecki A (2007): Linear Mixed Models: A practical guide using statistical software *New York: Chapman & Hall/CRC* 353 p.

**See Also**

[PhenList](#)

**Examples**

```
file <- system.file("extdata", "testLR.csv", package="PhenStat")
testLR <- PhenStat::PhenList(dataset=read.csv(file,na.strings = '-'),
                             testGenotype="Mock")
testLR2 <- PhenStat::LRDataset(testLR,"V2")

# when "testDataset" function's argument "callAll" is set to FALSE
# only "startLRModel" function is called - the first step of LR framework
resultLR <- PhenStat::testDataset(testLR2,
                                  depVariable="V2",
                                  callAll=FALSE,
                                  method="LR")
# print out formula that has been created
PhenStat::analysisResults(resultLR)$model.formula.genotype
# print out batch effect's significance
PhenStat::analysisResults(resultLR)$model.effect.batch
```

---

startModel	<i>Method "startModel"</i>
------------	----------------------------

---

### Description

This is an internal function run within MM framework. It completes the testing stage of which effects are significant. As an internal function, it doesn't include extensive error testing of inputs. Please use cautiously if calling directly.

It creates start model and modify it after testing of different hypothesis (the model fixed effects).

The model random effects are:

-batch effect (TRUE if batch variation is significant, FALSE if not)

The model fixed effects are:

-variance effect (TRUE if residual variances for genotype groups are homogeneous and FALSE if they are heterogeneous),

-interaction effect (TRUE if genotype by sex interaction is significant),

-sex effect (TRUE if sex is significant),

-weight effect (TRUE if weight is significant).

If user would like to assign other TRUE/FALSE values to the fixed effects of the model then he or she has to define keepList argument which is vector of TRUE/FALSE values.

If user has defined model fixed effects (keepList argument) then function prints out calculated and user defined effects (only when outputMessages argument is set to TRUE), checks user defined effects for consistency (for instance, if there are no "Weight" column in the dataset then weight effect can't be assigned to TRUE, etc.) and modifies start model according to user defined effects.

As the result PhenTestResult object that contains calculated or user defined model fixed effects and MM start model is created.

### Usage

```
startModel(phenList, depVariable,
           equation="withWeight", outputMessages=TRUE,
           pThreshold=0.05, keepList=NULL, modelWeight = NULL,
           threshold = 10^-18,
           check = 1)
```

### Arguments

phenList	instance of the <a href="#">PhenList</a> class; mandatory argument
depVariable	a character string defining the dependent variable of interest; mandatory argument
equation	a character string defining the equation to use. Possible values "withWeight" (default), "withoutWeight"
outputMessages	flag: "FALSE" value to suppress output messages; "TRUE" value to show output messages ; default value TRUE

pThreshold	a numerical value for the p-value threshold used to determine which fixed effects to keep in the model, default value 0.05
keepList	a logical vector defining the significance of different model effects: keep_batch, keep_equalvar, keep_weight, keep_sex, keep_interaction; default value NULL
modelWeight	a vector of positive values for weights in the mixed model. The sum of the values must be one.
threshold	a single positive value. The threshold for the ModelWeights to consider as zero (see modelWeight)
check	Only useful when modelWeight is included. Select between 0, 1, 2 to impose different weighting strategies on the Linear Mixed model. check=1 (default) selects the weights that are greater than the threshold (above) and keeps the batches that include more than one single sample. check=2 keeps only the weights that are greater than the threshold but ignores the single sample batches. check=0 to disable the function.

### Value

Returns results stored in instance of the [PhenTestResult](#) class

### Author(s)

Natalja Kurbatova, Natasha Karp, Jeremy Mason

### References

Karp N, Melvin D, Sanger Mouse Genetics Project, Mott R (2012): Robust and Sensitive Analysis of Mouse Knockout Phenotypes. *PLoS ONE* 7(12): e52410. doi:10.1371/journal.pone.0052410

West B, Welch K, Galecki A (2007): Linear Mixed Models: A practical guide using statistical software *New York: Chapman & Hall/CRC* 353 p.

### See Also

[PhenList](#)

### Examples

```
file <- system.file("extdata", "test1.csv", package="PhenStat")
test <- PhenStat::PhenList(dataset=read.csv(file,na.strings = '-'),
  testGenotype="Sparc/Sparc")
# when "testDataset" function's argument "callAll" is set to FALSE
# only "startModel" function is called - the first step of MM framework
result <- PhenStat::testDataset(test,
  depVariable="Lean.Mass",
  callAll=FALSE)
# print out formula that has been created
PhenStat::analysisResults(result)$model.formula.genotype
# print out batch effect's significance
PhenStat::analysisResults(result)$model.effect.batch
# change the model
```

```

result <- PhenStat:::testDataset(test,
  depVariable="Lean.Mass",
  equation="withWeight",
  callAll=FALSE)
# print out new formula
PhenStat:::analysisResults(result)$model.formula.genotype

```

---

startTFModel	<i>Method "startTFModel"</i>
--------------	------------------------------

---

### Description

This is an internal function run within TF framework. It completes the testing stage of which effects are significant. As an internal function, it doesn't include extensive error testing of inputs. Please use cautiously if calling directly.

It creates start model and modify it after testing of different hypothesis.

The tested fixed effects are:

- batch effect (TRUE if batch variation is significant, FALSE if not),
- variance effect (TRUE if residual variances for genotype groups are homogeneous and FALSE if they are heterogeneous),
- interaction effect (TRUE if genotype by sex interaction is significant),
- sex effect (TRUE if sex is significant),
- weight effect (TRUE if weight is significant).

### Usage

```

startTFModel(phenList, depVariable,
  equation="withWeight", outputMessages=TRUE,
  pThreshold=0.05, keepList=NULL)

```

### Arguments

phenList	instance of the <a href="#">PhenList</a> class; mandatory argument
depVariable	a character string defining the dependent variable of interest; mandatory argument
equation	a character string defining the equation to use. Possible values "withWeight" (default), "withoutWeight"
outputMessages	flag: "FALSE" value to suppress output messages; "TRUE" value to show output messages ; default value TRUE
pThreshold	a numerical value for the p-value threshold used to determine which fixed effects to keep in the model, default value 0.05
keepList	a logical vector defining the significance of different model effects: keep_batch, keep_equalvar, keep_weight, keep_sex, keep_interaction; default value NULL

**Value**

Returns results stored in instance of the [PhenTestResult](#) class

**Author(s)**

Natalja Kurbatova, Natasha Karp, Jeremy Mason

**References**

Karp N, Melvin D, Sanger Mouse Genetics Project, Mott R (2012): Robust and Sensitive Analysis of Mouse Knockout Phenotypes. *PLoS ONE* 7(12): e52410. doi:10.1371/journal.pone.0052410

West B, Welch K, Galecki A (2007): Linear Mixed Models: A practical guide using statistical software *New York: Chapman & Hall/CRC* 353 p.

**See Also**

[PhenList](#)

**Examples**

```
file <- system.file("extdata", "test7_TFE.csv", package="PhenStat")
test <- PhenStat::PhenList(dataset=read.csv(file,na.strings = '-'),
  testGenotype="het",
  refGenotype = "WT",
  dataset.colname.sex="sex",
  dataset.colname.genotype="Genotype",
  dataset.values.female="f",
  dataset.values.male= "m",
  dataset.colname.weight="body.weight",
  dataset.colname.batch="Date_of_procedure_start")

test_TF <- PhenStat::TFDataset(test,depVariable="Cholesterol")

# when "testDataset" function's argument "callAll" is set to FALSE
# only "startTFModel" function is called - the first step of TFE framework
result <- PhenStat::testDataset(test_TF,
  depVariable="Cholesterol",
  callAll=FALSE,
  method="TF")
# print out formula that has been created
PhenStat::analysisResults(result)$model.formula.genotype
# print out batch effect's significance
PhenStat::analysisResults(result)$model.effect.batch
```

---

subsetText	<i>Method "subsetText"</i>
------------	----------------------------

---

**Description**

Method subsetText returns full name of subset that was analysed by RR or FE framework: Males only, Females only, All.

**Value**

This function returns full name of subset that was analysed by RR or FE framework.

**Methods**

signature(obj = "htestPhenStat")

---

summary.PhenTestResult	<i>summary</i>
------------------------	----------------

---

**Description**

Wrapper for the model fitting results. Returns model fitting and testing results in a user friendly format.

**Usage**

```
## S3 method for class 'PhenTestResult'
summary(object, phenotypeThreshold = 0.01, ...)
```

**Arguments**

object	instance of the <a href="#">PhenTestResult</a> class that comes from the function <a href="#">testDataset</a> ; mandatory argument
phenotypeThreshold	a numerical value defining the threshold to use in classificationTag; default value 0.01
...	Not applicable

**Value**

Returns model fitting results in a text format for the screen

**Author(s)**

Natalja Kurbatova, Natasha Karp, Jeremy Mason

## References

Karp N, Melvin D, Sanger Mouse Genetics Project, Mott R (2012): Robust and Sensitive Analysis of Mouse Knockout Phenotypes. *PLoS ONE* 7(12): e52410. doi:10.1371/journal.pone.0052410

West B, Welch K, Galecki A (2007): Linear Mixed Models: A practical guide using statistical software *New York: Chapman & Hall/CRC* 353 p.

## See Also

[PhenTestResult](#)

## Examples

```
# Mixed Model framework
file <- system.file("extdata", "test1.csv", package="PhenStat")
test <- PhenStat::PhenList(dataset=read.csv(file,na.strings = '-'),
  testGenotype="Sparc/Sparc")
result <- PhenStat::testDataset(test,
  depVariable="Lean.Mass")
summary(result)

# Fishe Exact Test framework
file <- system.file("extdata", "test_categorical.csv", package="PhenStat")
test2 <- PhenStat::PhenList(dataset=read.csv(file,na.strings = '-'),
  testGenotype="Aff3/Aff3")
result2 <- PhenStat::testDataset(test2,
  depVariable="Thoracic.Processes",
  method="FE")
summary(result2)
```

---

summaryOutput

*Method "summaryOutput"*

---

## Description

Wrapper for the model fitting results. Returns model fitting and testing results in a user friendly format.

## Usage

```
summaryOutput(phenTestResult, phenotypeThreshold = 0.01)
```

## Arguments

`phenTestResult` instance of the [PhenTestResult](#) class that comes from the function [testDataset](#); mandatory argument

`phenotypeThreshold`  
a numerical value defining the threshold to use in classificationTag; default value 0.01

**Value**

Returns model fitting results in a text format for the screen

**Author(s)**

Natalja Kurbatova, Natasha Karp, Jeremy Mason

**References**

Karp N, Melvin D, Sanger Mouse Genetics Project, Mott R (2012): Robust and Sensitive Analysis of Mouse Knockout Phenotypes. *PLoS ONE* **7**(12): e52410. doi:10.1371/journal.pone.0052410

West B, Welch K, Galecki A (2007): Linear Mixed Models: A practical guide using statistical software *New York: Chapman & Hall/CRC* 353 p.

**See Also**

[PhenTestResult](#)

**Examples**

```
# Mixed Model framework
file <- system.file("extdata", "test1.csv", package="PhenStat")
test <- PhenStat:::PhenList(dataset=read.csv(file,na.strings = '-'),
  testGenotype="Sparc/Sparc")
result <- PhenStat:::testDataset(test,
  depVariable="Lean.Mass")
PhenStat:::summaryOutput(result)

# Fishe Exact Test framework
file <- system.file("extdata", "test_categorical.csv", package="PhenStat")
test2 <- PhenStat:::PhenList(dataset=read.csv(file,na.strings = '-'),
  testGenotype="Aff3/Aff3")
result2 <- PhenStat:::testDataset(test2,
  depVariable="Thoracic.Processes",
  method="FE")
PhenStat:::summaryOutput(result2)
```

---

testDataset

*Method "testDataset"*

---

**Description**

Statistical analysis manager function in PhenStat package.

Firstly, it performs the checks for dependent variable in the dataset. Some checks are generic, some depends on selected statistical framework/method.

Secondly, if checks are passed it runs the stages of selected framework to analyse dependent variable.



For instance, runs startModel and finalModel for the MM framework if the argument "callAll" is set to TRUE. If framework contains only one stage like in Fisher Exact Test case then runs that one stage regardless "callAll" value.

### Usage

```
testDataset(
  phenList = NULL           ,
  depVariable = NULL       ,
  equation = "withWeight"  ,
  outputMessages = TRUE   ,
  pThreshold = 0.05       ,
  method = "MM"           ,
  modelWeight = NULL      ,
  callAll = TRUE          ,
  keepList = NULL         ,
  dataPointsThreshold = 4 ,
  RR_naturalVariation = 95 ,
  RR_controlPointsThreshold = 60 ,
  transformValues = FALSE ,
  useUnfiltered = FALSE   ,
  threshold = 10 ^ -18    ,
  check = 1               ,
  upper = 5
)
```

### Arguments

phenList	instance of the <a href="#">PhenList</a> class; mandatory argument
depVariable	a character string defining the dependent variable of interest; mandatory argument
equation	a character string defining the equation to use. Possible values "withWeight" (default), "withoutWeight"
outputMessages	flag: "FALSE" value to suppress output messages; "TRUE" value to show output messages; default value TRUE
pThreshold	a numerical value for the p-value threshold used to determine which fixed effects to keep in the model, default value 0.05
method	a character string ("MM", "FE", "TF" or "RR") defining the method to use for model building; default value "MM" for mixed model
modelWeight	a vector of possible weights (the same length as the response) that are imposed on the weighted MM. Only works when method="MM". The default is NULL that leads to normal (non-weighted) MM.
callAll	flag: "FALSE" value to run only the first stage of the selected framework; "TRUE" value (default) to run all stages of framework one after another
keepList	a logical vector defining the significance of different model effects: keep_batch, keep_equalvar, keep_weight, keep_sex, keep_interaction; default value NULL

dataPointsThreshold	threshold for the number of data points in the MM framework; default value is 4 ; minimal value is 2
RR_naturalVariation	threshold for the variation ranges in the RR framework; default value is 95 ; minimal value is 60
RR_controlPointsThreshold	threshold for the number of control data points in the RR framework ; default value is 60; minimal value is 40
transformValues	flag: "FALSE" value to suppress transformation; "TRUE" value to perform transformation if needed; default value FALSE
useUnfiltered	flag: "FALSE" value to use filtered dataset; "TRUE" value to use unfiltered dataset; default value FALSE
threshold	The threshold for the model weights to be considered as zero. It only works when method="MM" and modelWeight is not null. Default is 10 <sup>-18</sup> .
check	Only useful when modelWeight is included. Select between 0, 1, 2 to impose different weighting strategies on the Linear Mixed model. check=1 (default) selects the weights that are greater than the threshold (above) and keeps the batches that include more than one single sample. check=2 keeps only the weights that are greater than the threshold but ignores the single sample batches. check=0 to disable the function.
upper	Single integer: maximum allowed number of levels for the Batch in the TF framework. Default 5

### Value

Returns results stored in instance of the [PhenTestResult](#) class

### Author(s)

Natalja Kurbatova, Natasha Karp, Jeremy Mason

### References

Karp N, Melvin D, Sanger Mouse Genetics Project, Mott R (2012): Robust and Sensitive Analysis of Mouse Knockout Phenotypes. *PLoS ONE* 7(12): e52410. doi:10.1371/journal.pone.0052410

West B, Welch K, Galecki A (2007): Linear Mixed Models: A practical guide using statistical software *New York: Chapman & Hall/CRC* 353 p.

### See Also

[PhenList](#), [plot.PhenTestResult](#), [plot.PhenList](#)

**Examples**

```

# Mixed Model framework
file <- system.file("extdata", "test1.csv", package="PhenStat")
test <- PhenStat::PhenList(dataset=read.csv(file,na.strings = '-'),
  testGenotype="Sparc/Sparc")
plot(test,depVariable="Lean.Mass")

result <- PhenStat::testDataset(test,
  depVariable="Lean.Mass")
# print out formula that has been created
PhenStat::analysisResults(result)$model.formula.genotype
summary(result)
plot(result)

# Mixed Model framework with user defined effects
user_defined_effects <- c(keep_batch=TRUE,
  keep_equalvar=TRUE,
  keep_weight=TRUE,
  keep_sex=TRUE,
  keep_interaction=TRUE)
result3 <- PhenStat::testDataset(test,
  depVariable="Lean.Mass",
  keepList=user_defined_effects)
# print out formula that has been created
PhenStat::analysisResults(result3)$model.formula.genotype
summary(result3)
plot(result3)

# Fisher Exact Test framework
file <- system.file("extdata", "test_categorical.csv", package="PhenStat")
test2 <- PhenStat::PhenList(dataset=read.csv(file,na.strings = '-'),
  testGenotype="Aff3/Aff3")
plot(test2,depVariable="Thoracic.Processes")
result2 <- PhenStat::testDataset(test2,
  depVariable="Thoracic.Processes",
  method="FE")
summary(result2)
plot(result2)

```

**Description**

Performs diagnostic tests for Logistic Regression model quality of fit. There are no arguments checks assuming that function is called internally from the "finalLRModel" function. Otherwise should be used with precaution.

**Usage**

```
testFinalLRModel(phenTestResult)
```

**Arguments**

phenTestResult instance of the [PhenTestResult](#) class that comes from the function testDataset  
; mandatory argument

**Value**

Returns a vector with model fitting results

**Author(s)**

Natalja Kurbatova, Natasha Karp, Jeremy Mason

**References**

Karp N, Melvin D, Sanger Mouse Genetics Project, Mott R (2012): Robust and Sensitive Analysis of Mouse Knockout Phenotypes. *PLoS ONE* 7(12): e52410. doi:10.1371/journal.pone.0052410

West B, Welch K, Galecki A (2007): Linear Mixed Models: A practical guide using statistical software *New York: Chapman & Hall/CRC* 353 p.

**See Also**

[PhenTestResult](#)

**Examples**

```
file <- system.file("extdata", "testLR.csv", package="PhenStat")
testLR <- PhenStat::PhenList(dataset=read.csv(file,na.strings = '-'),
  testGenotype="Mock")
testLR2 <- PhenStat::LRDataset(testLR,"V2")
resultLR <- PhenStat::testDataset(testLR2,
  depVariable="V2",
  method="LR")
PhenStat::testFinalLRModel(resultLR)
```

---

testFinalModel	<i>Method "testFinalModel"</i>
----------------	--------------------------------

---

### Description

Performs diagnostic tests for Mixed Model quality of fit. There are no arguments checks assuming that function is called internally from the "finalModel" function. Otherwise should be used with precaution.

### Usage

```
testFinalModel(phenTestResult)
```

### Arguments

phenTestResult instance of the [PhenTestResult](#) class that comes from the function testDataset ; mandatory argument

### Value

Returns a vector with model fitting results

### Author(s)

Natalja Kurbatova, Natasha Karp, Jeremy Mason

### References

Karp N, Melvin D, Sanger Mouse Genetics Project, Mott R (2012): Robust and Sensitive Analysis of Mouse Knockout Phenotypes. *PLoS ONE* 7(12): e52410. doi:10.1371/journal.pone.0052410

West B, Welch K, Galecki A (2007): Linear Mixed Models: A practical guide using statistical software *New York: Chapman & Hall/CRC* 353 p.

### See Also

[PhenTestResult](#)

### Examples

```
file <- system.file("extdata", "test1.csv", package="PhenStat")
test <- PhenStat::PhenList(dataset=read.csv(file,na.strings = '-'),
  testGenotype="Sparc/Sparc")
result <- PhenStat::testDataset(test,
  depVariable="Lean.Mass")
PhenStat::testFinalModel(result)
```

---

testGenotype	<i>Method "testGenotype"</i>
--------------	------------------------------

---

**Description**

Method testGenotype returns test genotype

**Value**

This function returns test genotype.

**Methods**

signature(obj = "PhenList")

signature(obj = "PhenTestResult")

---

TFDataset	<i>Method "TFDataset"</i>
-----------	---------------------------

---

**Description**

Removes of all non-concurrent batches from the dataset. Returns dataset suitable for TF framework or original dataset if data removal was not successful.

**Usage**

```
TFDataset(phenList,
          depVariable,
          outputMessages = TRUE,
          forDecisionTree = FALSE,
          upper           = 5)
```

**Arguments**

phenList	instance of the <a href="#">PhenList</a> class; mandatory argument
depVariable	a character string defining the dependent variable of interest; mandatory argument
outputMessages	flag: "FALSE" value to suppress output messages; "TRUE" value to show output messages; default value TRUE
forDecisionTree	flag: "FALSE" value for normal procedure; "TRUE" value to indicate that is called form decisionTree function; default value FALSE
upper	Single integer: maximum allowed number of levels for the Batch in the TF framework. Default 5.

**Value**

Returns dataset suitable for TF framework or original dataset if data removal was not successful.

**Author(s)**

Natalja Kurbatova, Natasha Karp, Jeremy Mason

**References**

Karp N, Melvin D, Sanger Mouse Genetics Project, Mott R (2012): Robust and Sensitive Analysis of Mouse Knockout Phenotypes. *PLoS ONE* 7(12): e52410. doi:10.1371/journal.pone.0052410

West B, Welch K, Galecki A (2007): Linear Mixed Models: A practical guide using statistical software *New York: Chapman & Hall/CRC* 353 p.

**See Also**

[PhenList](#)

**Examples**

```
file <- system.file("extdata", "test1.csv", package="PhenStat")
test <- PhenStat::PhenList(dataset=read.csv(file,na.strings = '-'),
  testGenotype="Sparc/Sparc")
test2 <- PhenStat::TFDataset(test,"Lean.Mass")
```

---

transformation	<i>Method "transformation"</i>
----------------	--------------------------------

---

**Description**

Method transformation returns transformation values: lamda=value, scaleShift=value

**Value**

This function returns transformation values.

**Methods**

signature(obj = "PhenTestResult")

---

transformationJSON	<i>Method "transformationJSON"</i>
--------------------	------------------------------------

---

**Description**

Method transformationJSON returns transformation values as JSON string

**Value**

This function returns transformation values as JSON string.

**Methods**

signature(obj = "PhenTestResult")

---

transformationText	<i>Method "transformationText"</i>
--------------------	------------------------------------

---

**Description**

Method transformationText returns transformation values as one string

**Value**

This function returns transformation values as one string.

**Methods**

signature(obj = "PhenTestResult")

---

vectorOutput	<i>Method "vectorOutput"</i>
--------------	------------------------------

---

**Description**

Wrapper for the model fitting results. Returns model fitting and testing results in a vector format. Assumes that modelling results are stored in the [PhenTestResult](#) object (output from function [testDataset](#)).



**Usage**

```
vectorOutput(  
  phenTestResult,  
  phenotypeThreshold = 0.01,  
  othercolumns = NULL,  
  quote = ''  
)
```

**Arguments**

**phenTestResult** instance of the [PhenTestResult](#) class that comes from the function [testDataset](#); mandatory argument

**phenotypeThreshold** a numerical value defining the threshold to use in classificationTag; default value 0.01

**othercolumns** a vector of column names that needs to be included in the function output

**quote** The character that is used to encompass the JSON keys in summary statistics. The default is quotation

**Value**

Returns a vector with model fitting results: model output summary and other values

**Author(s)**

Natalja Kurbatova, Natasha Karp, Jeremy Mason

**References**

Karp N, Melvin D, Sanger Mouse Genetics Project, Mott R (2012): Robust and Sensitive Analysis of Mouse Knockout Phenotypes. *PLoS ONE* 7(12): e52410. doi:10.1371/journal.pone.0052410

West B, Welch K, Galecki A (2007): Linear Mixed Models: A practical guide using statistical software *New York: Chapman & Hall/CRC* 353 p.

**See Also**

[PhenTestResult](#)

**Examples**

```
# Mixed Model framework  
file <- system.file("extdata", "test1.csv", package="PhenStat")  
test <- PhenStat::PhenList(dataset=read.csv(file,na.strings = '-'),  
  testGenotype="Sparc/Sparc")  
result <- PhenStat::testDataset(test,  
  depVariable="Lean.Mass")  
PhenStat::vectorOutput(result)  
  
# Fishe Exact Test framework
```

```
file <- system.file("extdata", "test_categorical.csv", package="PhenStat")
test2 <- PhenStat:::PhenList(dataset=read.csv(file,na.strings = '-'),
  testGenotype="Aff3/Aff3")
result2 <- PhenStat:::testDataset(test2,
  depVariable="Thoracic.Processes",
  method="FE")
PhenStat:::vectorOutput(result2)
```

---

vectorOutputMatrices *Method "vectorOutputMatrices"*

---

### Description

Returns count matrices from Fisher Exact Test framework in a vector form.

Note: Maximal supported number of dependent variable levels is 10.

### Usage

```
vectorOutputMatrices(phenTestResult, outputMessages=TRUE)
```

### Arguments

`phenTestResult` instance of the [PhenTestResult](#) class that comes from the function [testDataset](#); mandatory argument

`outputMessages` flag: "FALSE" value to suppress output messages; "TRUE" value to show output messages; default value TRUE

### Value

Returns a vector with count values.

### Author(s)

Natalja Kurbatova, Natasha Karp, Jeremy Mason

### References

Karp N, Melvin D, Sanger Mouse Genetics Project, Mott R (2012): Robust and Sensitive Analysis of Mouse Knockout Phenotypes. *PLoS ONE* 7(12): e52410. doi:10.1371/journal.pone.0052410

West B, Welch K, Galecki A (2007): Linear Mixed Models: A practical guide using statistical software *New York: Chapman & Hall/CRC* 353 p.

### See Also

[PhenTestResult](#)

**Examples**

```
file <- system.file("extdata", "test_categorical.csv", package="PhenStat")
test <- PhenStat::PhenList(dataset=read.csv(file,na.strings = '-'),
  testGenotype="Aff3/Aff3")
result <- PhenStat::testDataset(test,
  depVariable="Thoracic.Processes",
  method="FE")
PhenStat::vectorOutputMatrices(result)
```

---

weightIn

*Method "weightIn"*

---

**Description**

Returns TRUE if the weight is in the dataset, FALSE otherwise

**Value**

TRUE/FALSE

**Methods**

signature(obj = "PhenList")

signature(obj = "PhenTestResult")

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