Package 'PhenStat'

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Type Package

Title Statistical analysis of phenotypic data

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knitr, tools, pingr, ggplot2, reshape, corrplot, graph, lme4,
graphics, grDevices, utils, stats

Suggests RUnit, BiocGenerics

Description Package contains methods for statistical analysis of phenotypic data.

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R topics documented:

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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   *Method "analysisResults"*

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   *Method "batchIn"*

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 [PhenList](#) 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 `PhenList` 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 [PhenList](#) 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 [PhenList](#) 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: "vectorOuput" 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   *Method "comparison"*

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   *Method "dataset"*

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   *Method "finalModel"*

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 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

modelWeight   A vector of positive values for weights mainly used for appliying 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 statisfied 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   *Method "FisherExactTest"*

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 funciton 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 PhenList 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   *Method "generateGraphs"*

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 PhenTestResult class that comes from the function testDataset; 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 *Method "getColumnView"*

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
                                Method "getColumnWeightBatchAdjusted"

Description

Method `getColumnWeightBatchAdjusted` returns column of interest adjusted for weight and batch

Value

This function returns column of interest

Methods

signature(obj = "PhenList")

getCountMatrices   *Method "getCountMatrices"*

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   *Method "getDataset"*

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 *Method "getGenotypeEffect"*

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 *Method "getMatrix"*

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   *Method "getVariables"*

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 *Method "hemiGenotype"*

Description

Method hemiGenotype returns hemi genotype if defined

Value

This function returns hemi genotype if defined

Methods

signature(obj = "PhenList")

signature(obj = "PhenTestResult")

JSONOutput *Method "JSONOutput"*

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 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:::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 abonormal 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   *Method "matrixCount"*

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   *Method "method"*

Description

Method `method` returns method abbriviation, for example: "RR", "MM".

Value

This function returns returns method abbriviation.

Methods

signature(obj = "PhenTestResult")

methodText	*Method "methodText"*

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	*Method "multipleBatches"*

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	*Method "noSexes"*

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   *Method "parameters"*

Description

Method `parameters` returns parameters specific for apllied method/dataset combination

Value

This function returns parameters specific for apllied 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="Oxr1/Oxr1")
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   *Class "PhenList"*

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 orginal 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 weigth values

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

Details

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

Value

PhenlistObject	The input object
depVariable	Dependent variable
texfile	The location of the .tex file, given Clean=FALSE
pdffile	The location of the final pdf file
...	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   *Method "PhenTestResult"*

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

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.`

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)

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(phenTe`

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)$model.effect.batch
# Variance homogeneosity
PhenStat:::analysisResults(result)$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 *Method "pvalue"*

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   *Method "qqplotGenotype"*

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="Cl")
PhenStat:::qqplotRotatedResiduals(result)
```

recommendMethod *Method "recommendMethod"*

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 [PhenList](#) 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   *Method "refGenotype"*

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

phenList	instance of the [PhenList](#) 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
naturalVariation	
	number defining the natural variation range in percents for normal values; default value 95
controlPointsThreshold	
	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 PhenList 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.

Usage

```
scatterplotGenotypeWeightResult(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")
PhenStat:::scatterplotGenotypeWeightResult(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")
PhenStat:::scatterplotGenotypeWeightResult(result_1sex,
        graphingName="Lean Mass")
```

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 [PhenList](#) 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   *Method "setGenotype"*

Description

Method `setGenotype` sets genotype column in the dataset

Value

This function sets genotype column in the dataset.

Methods

signature(obj = "PhenList")

---

setMissingValue   *Method "setMissingValue"*

Description

Method `setMissingValue` sets missing value in the dataset

Value

This function sets missing value in the dataset.

Methods

signature(obj = "PhenList")

---

setSex   *Method "setSex"*

Description

Method `setSex` sets sex column in the dataset

Value

This function sets sex column in the dataset.

Methods

signature(obj = "PhenList")

---

setWeight   *Method "setWeight"*

Description

Method `setWeight` sets weight column in the dataset

Value

This function sets weight column in the dataset.

Methods

signature(obj = "PhenList")

---

startLRModel   *Method "startLRModel"*

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 [PhenList](#) 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   *Method "startModel"*

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 [PhenList](#) 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 | *Method "startTFModel"*

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 [PhenList](#) 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 *Method "subsetText"*

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

summary

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 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

...   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 [PhenList](#) 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" 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^{-18}.
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)
```

---

testFinalLRModel   *Method "testFinalLRModel"*

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   *Method "testFinalModel"*

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   *Method "testGenotype"*

Description

Method `testGenotype` returns test genotype

Value

This function returns test genotype.

Methods

signature(obj = "PhenList")

signature(obj = "PhenTestResult")

TFDataset   *Method "TFDataset"*

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 [PhenList](#) 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   *Method "transformation"*

Description

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

Value

This function returns transformation values.

Methods

signature(obj = "PhenTestResult")

---

transformationJSON   *Method "transformationJSON"*

Description

Method `transformationJSON` returns transformation values as JSON string

Value

This function returns transformation values as JSON string.

Methods

signature(obj = "PhenTestResult")

---

transformationText   *Method "transformationText"*

Description

Method `transformationText` returns transformation values as one string

Value

This function returns transformation values as one string.

Methods

signature(obj = "PhenTestResult")

vectorOutput | *Method "vectorOutput"*

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 charachter 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")

Index