Package: Phenotype (via r-universe)

August 23, 2024

Type Package

Title A Tool for Phenotypic Data Processing

Version 0.1.0

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Description Large-scale phenotypic data processing is essential in research. Researchers need to eliminate outliers from the data in order to obtain true and reliable results. Best linear unbiased prediction (BLUP) is a standard method for estimating random effects of a mixed model. This method can be used to process phenotypic data under different conditions and is widely used in animal and plant breeding. The 'Phenotype' can remove outliers from phenotypic data and performs the best linear unbiased prediction (BLUP), help researchers quickly complete phenotypic data analysis. H.P.Piepho. (2008) <doi:10.1007/s10681-007-9449-8>.

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Encoding UTF-8

LazyData true

URL `https://github.com/biozhp/Phenotype`

BugReports `https://github.com/biozhp/Phenotype/issues`

Depends R (>= 3.5.0)

Imports lme4, tidyr

RoxygenNote 7.1.1

NeedsCompilation no

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Date/Publication 2020-08-06 14:40:19 UTC

Repository https://biozhp.r-universe.dev

RemoteUrl https://github.com/biozhp/phenotype

RemoteRef HEAD

RemoteSha 21482be2fb92aea1bba8d77e93d62fe0d4b3b063

Contents

`blup` *blup*

Description

Performs the Best Linear Unbiased Prediction (BLUP)

Usage

```
blup(
  x,
  sample = NULL,
  year = NULL,
  loc = NULL,
  rep = NULL,
  phe = NULL,
  fold = 1.5
)
```

Arguments

`x`	Input phenotype data file.
`sample`	The column name of the sample name in phenotypic data. (Default: NULL)
`year`	The column name of the year in phenotypic data. (Default: NULL)
`loc`	The column name of the location in phenotypic data. (Default: NULL)
`rep`	The column name of the replication in phenotypic data. (Default: NULL)
`phe`	The column name of the phenotypic value in data. (Default: NULL)
`fold`	Fold before inter-quartile range. (Default: 1.5)

Value

Estimate BLUPs for a phenotypic data with outliers removed on a per sample basis.

Author(s)

Peng Zhao <pengzhao@nwafu.edu.cn>

Examples

```
data("wheatds")
blup_out <- blup(wheatds, sample = "Line", loc = "Env", rep = "Rep", phe = "DS")
```

`histplot` *histplot*

Description

Histogram drawing

Usage

```
histplot(
  x,
  color = "#99d6e1",
  rug_color = "#f79999",
  freq = FALSE,
  lwd = 2,
  rug_lwd = 1,
  main = "",
  xlab = "",
  ylab = "",
  cex.main = 1.5,
  cex.lab = 1.5,
  cex.axis = 1.5,
  breaks = "Sturges",
  ylim = NULL,
  xpos = 0.03,
  ypos = 0,
  cex.text = 1.2
)
```

Arguments

`x`	Input phenotype data.
`color`	The color of histogram.
`rug_color`	The color of rug under the histogram.
`freq`	If FALSE, the histogram graphic is a representation of frequencies; if TRUE, the histogram graphic is a representation of probability densitie. (Default: FALSE)
`lwd`	The line width of histogram. (Default: 2)
`rug_lwd`	The line width of rug under the histogram. (Default: 1)
`main`	The title of plot.
`xlab`	The X axis labels.

`ylab`	The Y axis labels
`cex.main`	The magnification to be used for title. (Default: 1.5)
`cex.lab`	The magnification to be used for axis labels. (Default: 1.5)
`cex.axis`	The magnification to be used for axis annotation. (Default: 1.5)
`breaks`	The number of bars in the histogram.
`ylim`	Y axis ranges.
`xpos`	The horizontal position of the pvalue label. (Default: 0.03)
`ypos`	The vertical position of the pvalue label. (Default: 0)
`cex.text`	The magnification to be used for pvalue labels. (Default: 1.2)

Value

Histogram and p-value of Shapiro-Wilk Normality Test.

Author(s)

Peng Zhao <pengzhao@nwafu.edu.cn>

Examples

```
data("wheatds")
inlier <- outlier(wheatds, sample = "Line", loc = "Env", rep = "Rep", phe = "DS", mode = "blup")
stat_out <- stat(x = inlier, sample = "Sample", phe = "inlier")
histplot(x = stat_out$mean)
```

`outlier` *outlier*

Description

Remove outliers from phenotypic data

Usage

```
outlier(
  x,
  sample = NULL,
  year = NULL,
  loc = NULL,
  rep = NULL,
  phe = NULL,
  fold = 1.5,
  mode = "normal"
)
```

Arguments

`x`	Input phenotype data file.
`sample`	The column name of the sample name in phenotypic data. (Default: NULL)
`year`	The column name of the year in phenotypic data. (Default: NULL)
`loc`	The column name of the location in phenotypic data. (Default: NULL)
`rep`	The column name of the replication in phenotypic data. (Default: NULL)
`phe`	The column name of the phenotypic value in data. (Default: NULL)
`fold`	Fold before inter-quartile range. (Default: 1.5)
`mode`	Type of input phenotypic data. "normal" means normal data, "blup" means data containing year/location/repetition. (Default: "normal")

Value

phenotypic data with outliers removed.

Author(s)

Peng Zhao <pengzhao@nwafu.edu.cn>

Examples

```
data("wheatds")
inlier <- outlier(wheatds, sample = "Line", loc = "Env", rep = "Rep", phe = "DS", mode = "blup")
```

`stat` *stat*

Description

Calculate statistical indicators of phenotypic data

Usage

```
stat(x, sample = NULL, phe = NULL)
```

Arguments

`x`	Input phenotype data file.
`sample`	The column name of the sample name in phenotypic data. (Default: NULL)
`phe`	The column name of the phenotypic value in data. (Default: NULL)

Value

Mean, median, standard deviation, standard error of phenotypic data for each sample.

Author(s)

Peng Zhao <pengzhao@nwafu.edu.cn>

Examples

```
data("wheatds")
inlier <- outlier(wheatds, sample = "Line", loc = "Env", rep = "Rep", phe = "DS", mode = "blup")
stat_out <- stat(x = inlier, sample = "Sample", phe = "inlier")
```

`wheatds` *Stripe rust disease severity (leaf areas infected, DS) of the wheat RIL population*

Description

Stripe rust disease severity (leaf areas infected, DS) of the wheat RIL population in Yangling, Tianshui, Jiangyou.

Usage

```
data("wheatds")
```

Format

A data frame containing samples, environments, repetitions, and disease severity of the wheat RIL population.

Examples

```
data("wheatds")
```

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