

Package ‘Phenotype’

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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](https://doi.org/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)

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RoxygenNote 7.1.1

NeedsCompilation no

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blup	<i>blup</i>
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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)

<code>breaks</code>	The number of bars in the histogram.
<code>ylim</code>	Y axis ranges.
<code>xpos</code>	The horizontal position of the pvalue label. (Default: 0.03)
<code>ypos</code>	The vertical position of the pvalue label. (Default: 0)
<code>cex.text</code>	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	<i>Stripe rust disease severity (leaf areas infected, DS) of the wheat RIL population</i>
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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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