Package 'pepa'

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Type Package

Title Package for the Execution of Pre Cooked Analysis

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Description This packages creates automatic reports for different types of statistical methodologies.

Depends R (>= 3.0.0), st4gi

Imports rmarkdown

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LazyData true

Suggests testthat

NeedsCompilation no

R topics documented:

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pty   *Pepa tells you*

Description

Explain an R object in plain English if she knows about it

Usage

```
pty(x, author = "International Potato Center")
```

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Arguments

x	An R object.
author	Author.

Details

It uses a set of templates to explain R objects in plain English. It aims to produce automatic reports for some standard statistical procedures, most of them included in the st4gi package.

Value

It returns an explanation about the selected R object.

Author(s)

Raul Eyzaguirre.

Examples

```
# Pepa tells you something about a data frame:
pty(pjpz09)
```

---

pty.aovmet   *Pepa tells you about a MET with a RCBD*

Description

Explain a fitted model for a multi environment trial (MET) with a RCBD in each environment in plain English.

Usage

```
pty.aovmet(trait, geno, env, rep, data, maxp = 0.1,
  author = "International Potato Center")
```

Arguments

trait	The trait to analize.
geno	The genotypes.
env	The environments.
rep	The replications.
data	The name of the data frame containing the data.
maxp	Maximum allowed proportion of missing values to estimate, default is 10%.
author	Author.

Details

It fits a linear model for a MET with a RCBD and explains the results. If data is unbalanced, missing values are estimated up to an specified maximum proportion, 10% by default. Genotypes and environments are considered as fixed factors while the blocks are considered as random and nested into the environments.

Value

It returns an explanation about the MET with a RCBD fitted model.

Author(s)

Raul Eyzaguirre.

Examples

```
pty.aovmet("y", "geno", "env", "rep", met8x12)
```

---

pty.pesekbaker   *Pepa tells you about the Pesek-Baker index*

Description

Explain the results of the Pesek-Baker index in plain English.

Usage

```
pty.pesekbaker(traits, geno, env, rep = NULL, data, means = "single",
  model = "gxe", dgg = NULL, units = "sdu", sf = 0.1,
  author = "International Potato Center")
```

Arguments

traits	List of traits.
geno	The genotypes.
env	The environments.
rep	The replications. Must be defined if model = "gxe".
data	The name of the data frame containing the data.
means	The genotypic means to compute the index, "single" or "fitted". The default is "single". See details for more information.
model	Type of model, "gxe" for a model with gxe interaction or "g+e" for a model without interaction. The default is "gxe". See details for more information.
dgg	Desired genetic gains. The default is one standard deviation for each trait.
units	Units for dgg, "actual" or "sdu". See details for more information.
sf	Selected fraction. The default is 0.1.
author	Author.

Details

The Pesek-Baker is an index where relative economic weights have been replaced by desired gains.

By default a model with components for genotypes, environments, genotypes by environments interaction and replications nested into environments is fitted (model = "gxe"). If model = "g+e" then a model with components for genotypes and environments is fitted, and in this case the gxe variance includes the gxe plus the error variance. Response to selection is only computed when model = "gxe".

If means = "fitted" then the model specified in model is used to fit the means of the genotypes. Otherwise single arithmetic means are computed over the replications for each genotype at each environment and then for each genotype over environments.

If dgg is not specified, the standard deviations of the traits are used. It means that the desired genetic gains are equal to one standard deviation for each trait. dgg can be specified in actual units (units = "actual") or in standard deviations (units = "sdu"), defaults to "sdu". For example, if you have a trait which is expressed in kilograms and with a standard deviation of 5 kilograms, typing dgg = 2 means a desired genetic gain of 2 standard deviations that corresponds to 10 kilograms. If you type dgg = 2 and units = "actual" then this means a desired genetic gain of 2 kilograms. If dgg = NULL then the desired genetic gain will be one standard deviation, no matter if units is set as "actual" or "sdu".

Value

It returns an explanation about the Pesek-Baker index.

Author(s)

Raul Eyzaguirre.

Examples

```
pty.pesekbaker(c("rytha", "bc", "dm", "star", "nocr"), "geno", "loc", "rep", spg)
```

---

pty.rcbd   *Pepa tells you about RCBD*

Description

Explain a RCBD fitted model in plain English

Usage

```
pty.rcbd(trait, treat, rep, data, maxp = 0.1,
  author = "International Potato Center")
```

Arguments

trait	The trait to analize.
treat	The treatments.
rep	The replications.
data	The name of the data frame.
maxp	Maximum allowed proportion of missing values to estimate, default is 10%.
author	Author.

Details

It fits a linear model for a RCBD and explains the results. It also checks the assumptions.

Value

It returns an explanation about the RCBD fitted model.

Author(s)

Raul Eyzaguirre.

Examples

```
pty.rcbd("trw", "geno", "rep", pjpz09)
```

---

repo.met   *Authomatic report for a MET with a RCBD*

Description

Produces an authomatic report for a selected trait in a multi environment trial (MET) with a RCBD in each environment.

Usage

```
repo.met(trait, geno, env, rep, data, maxp = 0.1,
  author = "International Potato Center")
```

Arguments

trait	The trait to be evaluated.
geno	The genotypes.
env	The environments.
rep	The replications.
data	The name of the data frame containing the data.
maxp	Maximum allowed proportion of missing values to estimate, default is 10%.
author	Author.

Details

It fits a linear model for a MET with a RCBD for the selected trait. If data is unbalanced, missing values are estimated up to an specified maximum proportion, 10% by default. Genotypes and environments are considered as fixed factors while the blocks are considered as random and nested into the environments.

Value

It returns an automatic report about the MET with a RCBD fitted model.

Author(s)

Raul Eyzaguirre.

Examples

```
repo.met("rytha", "geno", "env", "rep", megaclones)
```

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