

Package ‘pepa’

October 26, 2015

Type Package

Title Package for the Execution of Pre Cooked Analysis

Version 0.2.0

Date 2015-10-26

Author Raul Eyzaguirre

Maintainer Raul Eyzaguirre <R.EYZAGUIRRE@CGIAR.ORG>

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

Depends R (>= 3.0.0), st4gi

Imports rmarkdown

License MIT + file LICENSE

Copyright International Potato Center (2015)

LazyData true

Suggests testthat

NeedsCompilation no

R topics documented:

pty	1
pty.aovmet	2
pty.rcbd	3
repo.met	4
Index	5

pty	<i>Pepa tells you</i>
-----	-----------------------

Description

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

Usage

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

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 automatic report about the selected R object.

Author(s)

Raul Eyzaguirre.

Examples

```
# Pepa tells you something about a data frame:
pty(pjz09)
```

```
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 analyze.
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 automatic report about the MET with a RCBD fitted model.

Author(s)

Raul Eyzaguirre.

Examples

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

pty.rcbd	<i>Pepa tells you about RCBD</i>
----------	----------------------------------

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 analyze.
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 automatic report about the RCBD fitted model.

Author(s)

Raul Eyzaguirre.

Examples

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

`repo.met`*Automatic report for a MET with a RCBD*

Description

Produces an automatic 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

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

Index

pty, [1](#)
pty.aovmet, [2](#)
pty.rcbd, [3](#)
repo.met, [4](#)