

# Package ‘pepa’

October 23, 2015

**Type** Package

**Title** Package for the Execution of Pre Cooked Analysis

**Version** 0.1.0

**Date** 2015-10-22

**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

<b>Index</b>	<b>4</b>
--------------	----------

---

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 or blocks.
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)
```

# Index

pty, [1](#)  
pty\_aovmet, [2](#)  
pty\_rcbd, [3](#)