# Package 'pepa'

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**Type** Package

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

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**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** agricolae, rmarkdown

**License** MIT + file LICENSE



**LazyData** true

**Suggests** testthat

**RoxygenNote** 5.0.1.9000

**NeedsCompilation** no

## R topics documented:

## pty *Pepa tells you*

### 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 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.elston *Pepa tells you about the Elston index*

---

### Description

Explain the results of the Elston index in plain English.

### Usage

```
pty.elston(traits, geno, env = NULL, rep = NULL, data, means = "single",
  model = "gxe", lb = 1, author = "International Potato Center")
```

### Arguments

| | |
|---|---|
| traits | List of traits. |
| geno | The genotypes. |
| env | The environments. |
| rep | The replications. |
| 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 to fit means, "gxe" for a model with gxe interaction or "g+e" for a model without interaction. The default is "gxe". See details for more information. |
| lb | Lower bound. 1 for $k = min(x)$ and 2 for $k = (n \times min(x) - max(x))/(n-1)$ |
| author | Author. |

## Details

Type ?elston for additional details.

## Value

It returns an explanation about the Elston index.

## Author(s)

Raul Eyzaguirre.

## Examples

```
pty.elston(c("rytha", "bc", "dm", "star", "nocr"), "geno", data = spg)
```

---

# 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

Type ?pesekbaker for additional details.

### 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.spconsis *Pepa tells you about the consistency of your data*

---

### Description

It checks your data for inconsistencies.

### Usage

```
pty.spconsis(data, plot.size, f = 3, author = "International Potato Center")
```

### Arguments

| | |
|---|---|
| data | The name of the data frame. |
| plot.size | Plot size in square meters. |
| f | Factor for extreme values detection. See details. |
| author | Author. |

### Details

The data frame must use the labels (lower or upper case) specified in the function spconsis of package st4gi. Type ?spconsis to see the list and for additional details.

### Value

It returns a list of all rows with some kind of inconsistency and all rows with outliers.

### Author(s)

Raul Eyzaguirre.

### Examples

```
pty.spconsis(pjpz09, 4.5)
```

repo.abd *Automatic report for an augmented block design (ABD)*

## Description

Produces an automatic report for selected traits in an experiment with an ABD.

## Usage

```
repo.abd(traits, treat, rep, data, author = "International Potato Center")
```

## Arguments

| | |
|---|---|
| traits | The traits to analize. |
| treat | The treatments. |
| rep | The replications. |
| data | The name of the data frame. |
| author | Author. |

## Details

It fits a linear model for an ABD and explains the results.

The Tukey HSD method for pairwise differences is applied. Assumptions of the model are evaluated with residual plots.

## Value

It returns an explanation about the ABD fitted model.

## Author(s)

Raul Eyzaguirre.

## Examples

```
# A subset that looks like an ABD
temp <- pjpz09[c(1, 2, 9, 10, 13, 14, 27, 29, 31, 33, 35, 37, 40, 42, 44, 46, 48, 50, 203, 204), ]
repo.abd(c("trw", "vw", "crw"), "geno", "rep", temp)

# With some missing values
temp[c(1, 2, 3, 4), "trw"] <- NA
temp[c(1, 2, 3), "vw"] <- NA
temp[c(1, 10, 15), "crw"] <- NA
repo.abd(c("nocr", "trw", "vw", "crw"), "geno", "rep", temp)
```

repo.crd *Automatic report for a Completely Randomized Design (CRD)*

## Description

Produces an automatic report for selected traits in an experiment with a CRD.

## Usage

```
repo.crd(traits, treat, data, maxp = 0.1,
  author = "International Potato Center")
```

## Arguments

| | |
|---|---|
| traits | The traits to analize. |
| treat | The treatments. |
| 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 CRD and explains the results.

Under the assumption of fixed effects an ANOVA table is computed. If the ANOVA results in a significant value then the Tukey HSD method for pairwise differences is applied. Assumptions of the model are evaluated with residual plots.

Under the assumption of random effects the model is estimated using REML and the variance components are shown.

## Value

It returns an explanation about the CRD fitted model.

## Author(s)

Raul Eyzaguirre.

## Examples

```
repo.crd(c("trw", "vw", "crw"), "geno", pjpz09)

# With a small data set
temp <- pjpz09[1:18, ]
repo.crd(c("trw", "vw", "crw"), "geno", temp)
```

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

## Description

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

## Usage

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

## Arguments

| | |
|---|---|
| traits | The traits 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 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 for ANOVA. For variance components estimation all the factors are treated as random.

## Value

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

## Author(s)

Raul Eyzaguirre.

## Examples

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

repo.rcbd *Automatic report for a Randomized Complete Block Design (RCBD)*

## Description

Produces an automatic report for selected traits in an experiment with a RCBD.

## Usage

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

## Arguments

| | |
|---|---|
| traits | The traits 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.

Under the assumption of fixed effects an ANOVA table is computed with missing values estimated up to a specified percentage (10% by default). If the ANOVA results in a significant value for treatments then the Tukey HSD method for pairwise differences is applied. Assumptions of the model are evaluated with residual plots.

Under the assumption of random effects the model is estimated using REML and the variance components are shown. Missing values are not estimated in this case.

## Value

It returns an explanation about the RCBD fitted model.

## Author(s)

Raul Eyzaguirre.

## Examples

```
repo.rcbd(c("trw", "vw", "crw"), "geno", "rep", pjpz09)

# With a small data set
temp <- pjpz09[1:18, ]
repo.rcbd(c("trw", "vw", "crw"), "geno", "rep", temp)
```

# Index