Package: clubpro (via r-universe)

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Type Package

Title Classification Using Binary Procrustes Rotation

Version 0.6.2

Description Implements a classification method described by Grice (2011, ISBN:978-0-12-385194-9) using binary procrustes rotation; a simplified version of procrustes rotation.

License GPL (>= 3)

URL `https://timbeechey.github.io/clubpro/`

BugReports `https://github.com/timbeechey/clubpro/issues`

Encoding UTF-8

LazyData true

RoxygenNote 7.3.1

LinkingTo Rcpp, RcppArmadillo, RcppProgress

Imports Rcpp, lattice, stats, graphics

Suggests knitr, rmarkdown, tinytest

SystemRequirements C++17

Depends R (>= 2.10)

VignetteBuilder knitr

NeedsCompilation yes

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Repository CRAN

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Contents

`accuracy` *Classification accuracy for each observation.*

Description

Classification accuracy for each observation.

Usage

```
accuracy(m)
```

Arguments

`m`	an object of class "clubprofit" produced by `club()`

Details

Returns a character vector containing a string corresponding to each observation indicating whether classification of that observation was "correct", "incorrect", or "ambigous".

Value

a table

Examples

```
mod <- club(rate ~ dose, data = caffeine)
accuracy(mod)
```

`as.data.frame.clubprocsi`

Convert the output of csi() to a data.frame.

Description

Convert the output of csi() to a data.frame.

Usage

```
## S3 method for class 'clubprocsi'
as.data.frame(x, row.names = NULL, optional = FALSE, ...)
```

Arguments

`x`	an object of class "clubprocsi"
`row.names`	ignored
`optional`	ignored
`...`	ignored

Details

This function is useful to format pcc replicates data for plotting.

Examples

```
mod <- club(rate ~ dose, data = caffeine)
z <- csi(mod)
as.data.frame(z)
```

`as.data.frame.clubprorand` *Convert the output of pcc_replicates() to a data.frame.*

Description

Convert the output of pcc_replicates() to a data.frame.

Usage

```
## S3 method for class 'clubprorand'
as.data.frame(x, row.names = NULL, optional = FALSE, ...)
```

Arguments

`x`	an object of class "clubprorand"
`row.names`	ignored
`optional`	ignored
`...`	ignored

Details

This function is useful to format pcc replicates data for plotting.

Examples

```
mod <- club(rate ~ dose, data = caffeine)
z <- pcc_replicates(mod)
as.data.frame(z)
```

`caffeine` *Caffeine data*

Description

Effect of three different doses of caffeine on finger tapping rate.

Usage

```
caffeine
```

Format

A data frame with 30 rows and 2 columns:

dose dose of caffeine in mg

rate finger taps per minute

Source

Hand D.J., Daly F., Lunn A.D., McConway K.J., Ostrowski E. (1994) A Handbook of Small Data Sets. London: Chapman & Hall. Data set 50.

`club` *Classify observations.*

Description

`club()` is used to classify obervations using binary procrustes rotation.

Usage

```
club(
  f,
  data,
  imprecision,
  nreps,
  normalise_cols,
  reorder_obs,
  display_progress
)
```

Arguments

`f`	a formula.
`data`	a data.frame.
`imprecision`	a number indicting the margin of imprecision allowed in classification.
`nreps`	the number of replicates to use in the randomisation test.
`normalise_cols`	a boolean indicating whether to normalise matrix columns.
`reorder_obs`	a string indicating the method for reordering observations to calculate c-values.
`display_progress`	a boolean indictaing whether a progress bar should be displayed.

Value

an object of class "clubprofit" is a list containing the folllowing components:

prediction a character vector of predicted classifications.

accuracy a character vector indicating whether each classification is "correct", "incorrect", or "ambiguous".

pcc the percentage of correct classifications.

cval the chance of randomly reordered data producing a PCC >= the observed PCC.

pcc_replicates a vector of PCCs generated from randomly reordered data used to calculate `cval`.

call the matched call.

Examples

```
mod <- club(rate ~ dose, data = caffeine)
```

`compare` *Compare models.*

Description

Compare models.

Usage

```
compare(m1, m2)
```

Arguments

`m1`	an object of class "clubprofit" produced by `club()`
`m2`	an object of class "clubprofit" produced by `club()`

Details

Compare the PCC of two clubprofit models and compute the chance-value of the difference.

Value

an object of type "clubprocomparison"

Examples

```
m1 <- club(width ~ location, jellyfish)
m2 <- club(length ~ location, jellyfish)
compare(m1, m2)
```

`csi` *Classification strength indices.*

Description

Classification strength indices.

Usage

```
csi(m)
```

Arguments

`m`	an object of class "clubprofit" produced by `club()`

Details

Returns a vector containing the classification strength index for each observation.

Value

a numeric vector.

Examples

```
mod <- club(rate ~ dose, data = caffeine)
csi(mod)
```

`cval` *Chance value.*

Description

Chance value.

Usage

```
cval(m)
```

Arguments

`m`	an object of class "clubprofit" produced by `club()`

Details

Compute the chance that randomly reordered data results in a percentage of correctly classified observations at least as high as the observed data.

Value

a numeric value.

Examples

```
mod <- club(rate ~ dose, data = caffeine)
cval(mod)
```

`individual_results` *Individual level classification results.*

Description

Individual level classification results.

Usage

```
individual_results(m, digits)
```

Arguments

`m`	an object of class "clubprofit" produced by `club()`
`digits`	an integer

Details

Returns a data.frame containing predicted classifications and classification accuracy for each individual observation.

Value

a data.frame containing a columns of predictions and prediction accuracy

Examples

```
mod <- club(rate ~ dose, data = caffeine)
individual_results(mod)
```

`jellyfish` *Jellyfish dimension data*

Description

Sizes of jellyfish from two locations in the Hawkesbury River, New South Wales, Australia.

Usage

```
jellyfish
```

Format

A data frame with 46 rows and 3 columns:

location location where jellyfish was caught

width jellyfish width in mm

length jellyfish length in mm

Source

Hand D.J., Daly F., Lunn A.D., McConway K.J., Ostrowski E. (1994) A Handbook of Small Data Sets. London: Chapman & Hall. Data set 225.

`median_csi` *Median classification strength index.*

Description

Median classification strength index.

Usage

```
median_csi(m)
```

Arguments

`m`	an object of class "clubprofit" produced by `club()`

Details

Returns the median classification strength index.

Value

a numeric vector.

Examples

```
mod <- club(rate ~ dose, data = caffeine)
median_csi(mod)
```

`n_ambiguous` *Number of ambiguous classifications.*

Description

Number of ambiguous classifications.

Usage

```
n_ambiguous(m)
```

Arguments

`m`	an object of class "clubprofit" produced by `club()`

Details

Returns the number of observations which were classified ambiguously by the model.

Value

an integer.

Examples

```
mod <- club(rate ~ dose, data = caffeine)
n_ambiguous(mod)
```

`n_correct` *Number of correct classifications.*

Description

Number of correct classifications.

Usage

```
n_correct(m)
```

Arguments

`m`	an object of class "clubprofit" produced by `club()`

Details

Returns the number of observations which were classified correctly by the model.

Value

an integer.

Examples

```
mod <- club(rate ~ dose, data = caffeine)
n_correct(mod)
```

`n_incorrect` *Number of incorrect classifications.*

Description

Number of incorrect classifications.

Usage

```
n_incorrect(m)
```

Arguments

`m`	an object of class "clubprofit" produced by `club()`

Details

Returns the number of observations which were classified incorrectly by the model.

Value

an integer.

Examples

```
mod <- club(rate ~ dose, data = caffeine)
n_incorrect(mod)
```

`pcc` *Percentage of correct classifications.*

Description

Percentage of correct classifications.

Usage

```
pcc(m)
```

Arguments

`m`	an object of class "clubprofit" produced by `club()`

Details

Returns the percentage of correctly classified observations.

Value

a numeric value.

Examples

```
mod <- club(rate ~ dose, data = caffeine)
pcc(mod)
```

`pcc_replicates` *PCC replicates.*

Description

PCC replicates.

Usage

```
pcc_replicates(m)
```

Arguments

`m`	an object of class "clubprofit" produced by `club()`

Details

Returns an object containing a vector of PCC replicates used to calculate the chance-value.

Value

an object of class clubprorand.

Examples

```
mod <- club(rate ~ dose, data = caffeine)
head(pcc_replicates(mod))
```

`plot.clubproaccuracy` *Plot accuracy.*

Description

Plot accuracy.

Usage

```
## S3 method for class 'clubproaccuracy'
plot(x, ...)
```

Arguments

`x`	an object of class "clubproaccuracy"
`...`	ignored

Details

Produces a mosaic plot of predictio naccuracy by category

Value

called for side-effects only

Examples

```
mod <- club(rate ~ dose, data = caffeine)
z <- accuracy(mod)
plot(z)
```

`plot.clubprocomparison` *Plot model comparison.*

Description

Plot model comparison.

Usage

```
## S3 method for class 'clubprocomparison'
plot(x, ...)
```

Arguments

`x`	an object of class "clubprocomparison".
`...`	ignored

Details

Plot a distribution of PCCs computed from randomly reordered data used to calculate the chance-value for a model comparison.

Value

no return value, called for side effects only.

Examples

```
m1 <- club(width ~ location, jellyfish)
m2 <- club(length ~ location, jellyfish)
z <- compare(m1, m2)
plot(z)
```

`plot.clubprocsi` *Plot classification strength indices.*

Description

Plot classification strength indices.

Usage

```
## S3 method for class 'clubprocsi'
plot(x, ...)
```

Arguments

`x`	an object of class "clubprocsi"
`...`	ignored

Details

Produces dotplot showing classification strength for each individual.

Value

called for side-effects only

Examples

```
mod <- club(rate ~ dose, data = caffeine)
z <- csi(mod)
plot(z)
```

`plot.clubprofit` *Plot classification accuracy.*

Description

Plot classification accuracy.

Usage

```
## S3 method for class 'clubprofit'
plot(x, ...)
```

Arguments

`x`	an object of class "clubprofit" produced by `club()`
`...`	ignored

Details

Produces bar plot showing counts of individuals against observed values within each target grouping. Fill colours indicate whether each individual was classified correctly, incorrectly or ambiguously.

Value

called for side-effects only

Examples

```
mod <- club(rate ~ dose, data = caffeine)
plot(mod)
```

`plot.clubpropredictions` *Plot predictions.*

Description

Plot predictions.

Usage

```
## S3 method for class 'clubpropredictions'
plot(x, ...)
```

Arguments

`x`	an object of class "clubpropredictions"
`...`	ignored

Details

Produces a mosaic plot of observed versus predicted categories

Value

called for side-effects only

Examples

```
mod <- club(rate ~ dose, data = caffeine)
z <- predict(mod)
plot(z)
```

`plot.clubprorand` *Plot PCC replicates.*

Description

Plot PCC replicates.

Usage

```
## S3 method for class 'clubprorand'
plot(x, ...)
```

Arguments

`x`	an object of class "clubprofit" produced by `club()`
`...`	ignored

Details

Plot the distribution of PCCs computed from randomly reordered data used to calculate the chance-value.

Value

no return value, called for side effects only.

Examples

```
mod <- club(rate ~ dose, data = caffeine)
plot(pcc_replicates(mod))
```

`plot.clubprothreshold` *Plot PCC as a function of binary category boundary location.*

Description

Plot PCC as a function of binary category boundary location.

Usage

```
## S3 method for class 'clubprothreshold'
plot(x, ...)
```

Arguments

`x`	an object of class "clubprothreshold"
`...`	ignored

Details

Produces an xyplot showing the PCC returned for each possible category boundary.

Value

called for side-effects only

Examples

```
mod <- club(rate ~ dose, data = caffeine)
z <- threshold(mod)
plot(z)
```

`predict.clubprofit` *Predicted category for each observation.*

Description

Predicted category for each observation.

Usage

```
## S3 method for class 'clubprofit'
predict(object, ...)
```

Arguments

`object`	an object of class "clubprofit" produced by `club()`
`...`	ignored

Details

Returns a character vector containing the name of the predicted category for each observed value.

Value

a table

Examples

```
mod <- club(rate ~ dose, data = caffeine)
predict(mod)
```

`summary.clubprocomparison` *Generate a summary of a comparison of clubprofit models.*

Description

Generate a summary of a comparison of clubprofit models.

Usage

```
## S3 method for class 'clubprocomparison'
summary(object, ...)
```

Arguments

`object`	an object of class "clubprocomparison".
`...`	ignored

Value

No return value, called for side effects.

Examples

```
m1 <- club(width ~ location, jellyfish)
m2 <- club(length ~ location, jellyfish)
z <- compare(m1, m2)
summary(z)
```

`summary.clubprofit` *Generate a summary of results from a fitted clubpro model.*

Description

Generate a summary of results from a fitted clubpro model.

Usage

```
## S3 method for class 'clubprofit'
summary(object, ...)
```

Arguments

`object`	an object of class "clubprofit".
`...`	ignored

Value

No return value, called for side effects.

Examples

```
mod <- club(rate ~ dose, data = caffeine)
summary(mod)
```

`threshold` *Classification strength indices.*

Description

Classification strength indices.

Usage

```
threshold(m)
```

Arguments

`m`	an object of class "clubprofit" produced by `club()`

Details

Returns a vector containing the classification strength index for each observation.

Value

an object of class clubprothreshold

Examples

```
mod <- club(width ~ location, data = jellyfish)
threshold(mod)
```

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