

Package ‘gosset’

June 28, 2022

Type Package

Title Tools for Data Analysis in Experimental Agriculture

Version 0.4

URL <https://agrdatasci.github.io/gosset/>

BugReports <https://github.com/agrdatasci/gosset/issues>

Description Toolkit for a workflow to analyse experimental agriculture data, from data synthesis to model selection and visualisation.

The package is named after W.S. Gosset aka ‘Student’, a pioneer of modern statistics in small sample experimental design and analysis.

License MIT + file LICENSE

Encoding UTF-8

LazyData true

Depends R (>= 3.5.0), methods

Imports BradleyTerry2, DescTools, gnm, ggplot2, ggparty, ggrepel, partykit, PlackettLuce, psychotools, qvcalc, stats, tidyR, utils, patchwork

Suggests climatrends, ClimMobTools, chirps, knitr, psychotree, nasapower, rmarkdown

Language en-GB

RoxygenNote 7.1.2

VignetteBuilder knitr

NeedsCompilation no

Author Kauê de Sousa [aut, cre] (<<https://orcid.org/0000-0002-7571-7845>>),
Jacob van Etten [aut] (<<https://orcid.org/0000-0001-7554-2558>>),
David Brown [aut] (<<https://orcid.org/0000-0003-2859-1618>>),
Jonathan Steinke [aut] (<<https://orcid.org/0000-0001-5742-702X>>)

Maintainer Kauê de Sousa <desousa.kaue@gmail.com>

Repository CRAN

Date/Publication 2022-06-28 07:50:02 UTC

R topics documented:

akaike_weights	2
breadwheat	3
btpermute	5
compare	6
crossvalidation	7
gosset	10
kendallTau	10
kendallW	12
kenyachoice	13
nicabean	14
node_labels	15
pseudoR2	16
pseudo_rank	18
rank_binomial	19
rank_numeric	20
rank_paircomp	21
rank_tricot	23
regret	24
reliability	26
rowbind	28
worth_map	29

Index	32
--------------	-----------

akaike_weights	<i>Akaike weights</i>
----------------	-----------------------

Description

Akaike weights represent the relative likelihood of a model. It can be used in model averaging and selection.

Usage

```
akaike_weights(object)
```

Arguments

object a numerical vector with models goodness of fit coefficients

Value

A data frame containing the coefficients:

delta	the delta overall change in the coefficients
relative_logLik	the relative log-likelihood
akaike_weights	the Akaike weights

Author(s)

Kauê de Sousa and Jacob van Etten

References

Wagenmakers E. J. & Farrell S. (2004). Psychonomic Bulletin and Review, 11(1), 192–196. doi: [10.3758/BF03206482](https://doi.org/10.3758/BF03206482)

Examples

```
data("airquality")

# try three model approaches
mod1 <- glm(Temp ~ 1,
            data = airquality,
            family = poisson())

mod2 <- glm(Temp ~ Ozone,
            data = airquality,
            family = poisson())

mod3 <- glm(Temp ~ Ozone + Solar.R,
            data = airquality,
            family = poisson())

# models AICs together in a single vector
models <- c(mod1 = AIC(mod1),
            mod2 = AIC(mod2),
            mod3 = AIC(mod3))

# calculate akaike weights
aw <- akaike_weights(models)

# the higher the better
names(models[which.max(aw$akaike_weights)])
```

breadwheat

Preferred bread wheat varieties

Description

Data from decentralized on-farm trials of bread wheat (*Triticum aestivum* L.) varieties in Vaishali, India over the 2014's Rabi season. Farmers were asked to test three varieties of bread wheat randomly assigned as incomplete blocks of three varieties (out of 16 varieties) and assess which one had the best and worst performance considering four traits, germination, grain quality, yield and overall performance.

Usage

breadwheat

Format

A data frame with 493 records and 19 variables:

variety_a The name of variety A in the comparison.

variety_b The name of variety B in the comparison.

variety_c The name of variety C in the comparison.

district The administrative region where the experiment was established.

village The village within the administrative region where the experiment was established.

participant_name The participant name (ommitted for protection and privacy).

age The participant age.

gender The participant gender M = Male; F = Female.

planting_date The date which the experiment started.

lon The longitude in which the experiment was established.

lat The latitude in which the experiment was established.

germination_best The variety ranked as best for germination ("A", "B" or "C").

germination_worst The variety ranked as worst for germination ("A", "B" or "C").

grainquality_best The variety ranked as best for grain quality ("A", "B" or "C").

grainquality_worst The variety ranked as worst for grain quality ("A", "B" or "C").

yield_best The variety ranked as best for yield ("A", "B" or "C").

yield_worst The variety ranked as worst for yield ("A", "B" or "C").

overall_best The variety ranked as best for overall performance ("A", "B" or "C").

overall_worst The variety ranked as worst for overall performance ("A", "B" or "C").

Source

The data were provided by Bioversity International <https://www.bioversityinternational.org/>, a CGIAR Research Centre, through the ClimMob platform <https://climmob.net>.

btpermute

*Variable selection with Permuted Inclusion Criterion***Description**

Method of forward variable selection based on deviance for Bradley-Terry models using pairwise ranking data. The selection procedure consists of two steps, first, permuting the variables from the original predictors with `n.iterations`, then performing a forward selection to retain the predictors with highest contribution to the model, see details.

Usage

```
btpermute(
  contests = NULL,
  predictors = NULL,
  n.iterations = 15,
  seed = NULL,
  ...
)
```

Arguments

<code>contests</code>	a data frame with pairwise binary contests with these variables 'id', 'player1', 'player2', 'win1', 'win2'; in that order. The id should be equivalent to the index of each row in <code>predictors</code>
<code>predictors</code>	a data frame with player-specific variables with row indices that should match with the ids in <code>contests</code> . An id is not required, only the predictor variables, the ids are the index for each row
<code>n.iterations</code>	integer, number of iterations to compute
<code>seed</code>	integer, the seed for random number generation. If NULL (the default), gosset will set the seed randomly
<code>...</code>	additional arguments passed to BradleyTerry2 methods

Details

The selection procedure consists of two steps. In the first step, `btpermute` adds to the set of original (candidate) predictors variables an additional set of 'fake', permuted variables. This set of permuted predictors is created by assigning to each ranking the variables from another, randomly selected ranking. The permuted variables are not expected to have any predictive power for pairwise rankings. In the second step, `btpermute` adds predictors to the Bradley-Terry model in a forward selection procedure. Each predictors (real and permuted) is added to the null model individually, and `btpermute` retains which variable reduces model deviance most strongly. The two-step process is replicated `n` times with argument `n.iterations`. At each iteration, a new random permutation is generated and all variables are tested. Replicability can be controlled using argument `seed`. Across the `n` `n.iterations`, the function identifies the predictor that appeared most often as the most deviance-reducing one. When this is a real variable, it is constantly added to the model and the forward selection procedure moves on – again creating new permutations, adding

real and fake variables individually, and examining model deviance. Variable selection stops when a permuted variable is found to be most frequently the most deviance-reducing predictors across `n.iterations`. In turn, variable selection continuous as long as any real variable has stronger explanatory power for pairwise rankings than the random variables.

Value

an object of class `gosset_btpermute` with the final `BTm()` model, selected variables, seeds (random numbers) used for permutations and deviances

Author(s)

Jonathan Steinke and Kauê de Sousa

References

Lysen, S. (2009) Permuted inclusion criterion: A variable selection technique. University of Pennsylvania <https://repository.upenn.edu/edissertations/28/>

See Also

[rank_binomial](#), [BTm](#)

Other model selection functions: [crossvalidation\(\)](#)

Examples

```
require("BradleyTerry2")

data("kenyachoice", package = "gosset")

mod <- btpermute(contests = kenyachoice$contests,
                 predictors = kenyachoice$predictors,
                 n.iterations = 10,
                 seed = 1)

mod
```

compare

Compare agreement between two methods

Description

Measures the agreement between two methods

Usage

```
compare(x, y, ...)  
  
## Default S3 method:  
compare(x, y, labels = NULL, ...)  
  
## S3 method for class 'PlackettLuce'  
compare(x, y, ...)
```

Arguments

x	a numeric vector, or an object of class PlackettLuce
y	a numeric vector, or an object of class PlackettLuce
...	additional arguments passed to methods
labels	optional, a vector with the same length x to plot values

Value

a ggplot with the agreement

References

Bland, M. J., and Altman, D. G. (1986). *Lancet* (8476):307-10.

Examples

```
set.seed(1)  
x <- runif(10, -1, 2)  
  
set.seed(2)  
y <- runif(10, -1, 2)  
  
compare(x, y)
```

crossvalidation

Cross-validation

Description

Methods for measuring the performance of a predictive model on sets of test data in Bradley-Terry model from **psychotree**, Generalized Linear and Generalized Nonlinear models from **gnm**, and Plackett-Luce model from **PlackettLuce**

Usage

```

crossvalidation(formula, data, k = 10, folds = NULL, seed = NULL, ...)

## S3 method for class 'btree'
AIC(object, newdata = NULL, ...)

## S3 method for class 'btree'
deviance(object, newdata = NULL, ...)

## S3 method for class 'pltree'
deviance(object, newdata = NULL, ...)

## S3 method for class 'gnm'
AIC(object, newdata = NULL, ...)

## S3 method for class 'gnm'
deviance(object, newdata = NULL, ...)

```

Arguments

formula	an object of class "formula" (or one that can be coerced to that class): a symbolic description of the model to be fitted, of the form $y \sim x_1 + \dots + x_n$
data	a data frame (or object coercible by <code>as.data.frame</code> to a data frame) containing the variables in the model
k	an integer for the number of bins in the cross-validation
folds	an optional vector or list of vectors specifying the k -folds in the cross-validation
seed	integer, the seed for random number generation. If NULL (the default), gosset will set the seed randomly
...	additional arguments passed the methods of the chosen model
object	a model object
newdata	a <code>data.frame</code> with test data

Value

an object of class `gosset_cv` with the cross-validation goodness-of-fit estimates, which are:

AIC	Akaike Information Criterion
deviance	Model deviance
logLik	Log-Likelihood
MaxLik	Maximum likelihood pseudo R-squared
CraggUhlen	Cragg and Uhler's pseudo R-squared
McFadden	McFadden pseudo R-squared
kendallTau	the Kendall correlation coefficient

Author(s)

Kauê de Sousa, Jacob van Etten and David Brown

References

Elder J. F. (2003). Journal of Computational and Graphical Statistics, 12(4), 853–864. doi: [10.1198/1061860032733](https://doi.org/10.1198/1061860032733)

James G., et al. (2013). doi: [10.1007/9781461471387](https://doi.org/10.1007/9781461471387)

Whitlock M. C. (2005). Journal of Evolutionary Biology, 18(5), 1368–1373. doi: [10.1111/j.1420-9101.2005.00917.x](https://doi.org/10.1111/j.1420-9101.2005.00917.x)

See Also

[btree](#), [gnm](#), [pltree](#)

Other model selection functions: [btpermute\(\)](#)

Examples

```
# Generalized Linear Models
if (require("gnm")) {
  data("airquality")

  cv <- crossvalidation(Temp ~ Wind + Solar.R,
                       data = airquality,
                       k = 3,
                       seed = 999,
                       family = poisson())
}

# Plackett-Luce Model
if(require("PlackettLuce")) {
  # beans data from PlackettLuce
  data("beans", package = "PlackettLuce")

  G <- rank_tricot(data = beans,
                  items = c(1:3),
                  input = c(4:5),
                  additional.rank = beans[c(6:8)],
                  group = TRUE)

  beans <- cbind(G, beans)

  # take seasons as bins
  k <- length(unique(beans$season))
  folds <- as.integer(as.factor(beans$season))

  cv <- crossvalidation(G ~ maxTN,
                       data = beans,
                       k = k,
                       folds = folds,
```

```
        minsize = 100)  
    }
```

gosset

Tools for Data Analysis in Experimental Agriculture

Description

Toolkit for a workflow to analyse experimental agriculture data, from data synthesis to model selection and visualisation. The package is named after W.S. Gosset aka 'Student', a pioneer of modern statistics in small sample experimental design and analysis.

Author(s)

Kauê de Sousa and Jacob van Etten and David Brown and Jonathan Steinke

See Also

Useful links:

- Development repository: <https://github.com/AgrDataSci/gosset>
- Static documentation: <https://AgrDataSci.github.io/gosset/>
- Report bugs: <https://github.com/AgrDataSci/gosset/issues>

kendallTau

Kendall rank correlation coefficient

Description

Compute Kendall rank correlation coefficient between two objects. Kendall is a coefficient used in statistics to measure the ordinal association between two measured quantities. A tau test is a non-parametric hypothesis test for statistical dependence based on the tau coefficient. The 'kendallTau' function applies the "kendall" method from 'stats::cor' with some previous treatment in the data, such as converting floating numbers into ranks (from the higher being the first and negative being the last) and the possibility to remove zeros from incomplete ranks

Usage

```
kendallTau(x, y, null.rm = TRUE, ...)  
  
## Default S3 method:  
kendallTau(x, y, null.rm = TRUE, ...)  
  
## S3 method for class 'matrix'  
kendallTau(x, y, ...)  
  
## S3 method for class 'rankings'  
kendallTau(x, y, ...)  
  
## S3 method for class 'grouped_rankings'  
kendallTau(x, y, ...)  
  
## S3 method for class 'paircomp'  
kendallTau(x, y, ...)
```

Arguments

x	a numeric vector, matrix or data frame
y	a vector, matrix or data frame with compatible dimensions to x
null.rm	logical, to remove zeros from x and y
...	further arguments affecting the Kendall tau produced. See details

Value

The Kendall correlation coefficient and the Effective N, which is the equivalent N needed if all items were compared to all items. Can be used for significance testing.

Author(s)

Kauê de Sousa and Jacob van Etten

References

Kendall M. G. (1938). *Biometrika*, 30(1–2), 81–93. doi: [10.1093/biomet/30.12.81](https://doi.org/10.1093/biomet/30.12.81)

See Also

[cor](#)

Other goodness-of-fit functions: [kendallW\(\)](#), [pseudoR2\(\)](#)

Examples

```
library("PlackettLuce")  
  
R <- matrix(c(1, 2, 4, 3,
```

```

      1, 4, 2, 3,
      1, 2, 4, 3,
      1, 2, 4, 3,
      1, 3, 4, 2,
      1, 4, 3, 2), nrow = 6, byrow = TRUE)
colnames(R) <- LETTERS[1:4]

G <- group(as.rankings(R), 1:6)

mod <- pltree(G ~ 1, data = G)

preds <- predict(mod)

k <- kendallTau(R, preds)

# also applies to a single observation in the matrix

k <- kendallTau(R[1,], preds[1,])

```

 kendallW

Kendall's W (coefficient of concordance)

Description

Compute Kendall's W , also known as coefficient of concordance among observed rankings and those predicted by the Plackett-Luce model.

Usage

```

kendallW(x, ...)

## Default S3 method:
kendallW(x, y, ...)

## S3 method for class 'pltree'
kendallW(x, newdata = NULL, ...)

```

Arguments

<code>x</code>	an object of class <code>pltree</code>
<code>...</code>	additional arguments passed to methods
<code>y</code>	an object of class <code>pltree</code>
<code>newdata</code>	data for predictions

Details

It is a wrapper of the function DescTools::KendallW, adapted to compute the Kendall's W on the observed and predicted rankings.

Kendall's W values range between 0 (no agreement) to 1 (full agreement)

Value

Kendall's W (coefficient of concordance)

Author(s)

David Brown, Kauê de Sousa and Jacob van Etten

See Also

Other goodness-of-fit functions: [kendallTau\(\)](#), [pseudoR2\(\)](#)

Examples

```
library("PlackettLuce")
G <- rank_tricot(data = beans,
                items = c(1:3),
                input = c(4:5),
                additional.rank = beans[c(6:8)],
                group = TRUE)

beans <- cbind(G, beans)

beans_plt <- pltree(G ~ maxTN,
                  data = beans)

kendallW(beans_plt)
```

kenyachoice

Kenyan farmers' preferences for agricultural and livelihood practices

Description

Data from a preference experiment in Makeni County, Kenya. Twenty-six smallholder farmers ordered 9 different livelihood improvement practices by their personal preference. Full rankings were broken down into multiple pairwise rankings (`kenyachoice[["contests"]]`). To each respondent, a set of nine socio-economic variables is available (`kenyachoice[["predictors"]]`).

Usage

```
kenyachoice
```

Format

A list with two dataframes. `kenyachoice[["contests"]]` contains the pairwise rankings from farmers choices. `kenyachoice[["predictors"]]` contains the socioeconomic data for each farmer. Codes for contests are described:

- B Opening a business
- D Dry planting
- G Collective crop marketing
- J Finding off-farm job
- M Machine tillage
- O Renting out traction animals
- R Mulching
- T Terracing
- Z Zai pits

Source

Steinke, J., et. al. (2019). Computers and Electronics in Agriculture, 162, 991–1000. doi: [10.1016/j.compag.2019.05.026](https://doi.org/10.1016/j.compag.2019.05.026)

nicabean

Common bean on-farm trial in Nicaragua

Description

Data from decentralized on-farm trials of common bean (*Phaseolus vulgaris* L.) varieties in Nicaragua over five seasons between 2015 and 2016. Following the tricot approach, farmers were asked to test three varieties of common bean randomly assigned as incomplete blocks of three varieties (out of 10 varieties) and assess which of those three had the best and worst performance in nine traits (Vigor, Architecture, Resistance to Pests, Resistance to Diseases, Tolerance to Drought, Yield, Marketability, Taste, and Overall Appreciation).

Usage

nicabean

Format

A list with two data frames, `nicabean[["trial"]]` contains the trial data:

- `id` the plot id
- `item` the variety name
- `trait` the trait for the given variety and plot id
- `rank` the rank for the given variety and trait, with 1 being higher and 3 the lowest

nicabean[["bean_covar"]] contains the covariates associated with the data:

id the plot id
 adm0 the country name where trials were set
 longitude the longitude of the trial plot
 latitude the latitude of the trial plot
 trial the trial name as registered on ClimMob
 variety_a the variety assigned as label A in the incomplete block
 variety_b the variety assigned as label B in the incomplete block
 variety_c the variety assigned as label C in the incomplete block
 planting_date the planting date
 gender the farmer gender
 age the farmer age

Source

van Etten, J., et. al. (2016). Experimental Agriculture, 55, 275-296. doi: [10.1017/S0014479716000739](https://doi.org/10.1017/S0014479716000739)
 van Etten, J., et. al. (2019). PNAS 116(10) 4194-4199 doi: [10.1073/pnas.1813720116](https://doi.org/10.1073/pnas.1813720116)

node_labels	<i>Get node labels and rules used in a party tree</i>
-------------	---

Description

Returns the covariates used to split a recursive partitioning tree and the rules that were applied to build the tree

Usage

```
node_labels(x)

node_rules(x)

top_items(x, top = 5)

## S3 method for class 'pltree'
plot(x, log = TRUE, ref = NULL, ci.level = 0.95, ...)
```

Arguments

x	an object of class party
top	an integer for the number of items to return
log	logical, if TRUE log-worth coefficients are displayed instead of worth
ref	optional, character for the reference item when <i>log = TRUE</i>
ci.level	an integer for the confidence interval levels
...	additional arguments passed to methods

Value

a vector with the node labels, a data.frame with node rules, a ggplot

Author(s)

Kauê de Sousa

Examples

```
library("PlackettLuce")
data("beans", package = "PlackettLuce")
G <- rank_tricot(data = beans,
                 items = c(1:3),
                 input = c(4:5),
                 group = TRUE,
                 additional.rank = beans[c(6:8)])

pld <- cbind(G, beans[,c("maxTN", "season", "lon")])

tree <- pltree(G ~ maxTN + season + lon, data = pld)

node_labels(tree)

node_rules(tree)

top_items(tree)

plot(tree)

plot(tree, log = TRUE)
```

pseudoR2

Pseudo R-squared

Description

Regression coefficient to evaluate goodness-of-fit in a given model when ordinary least squares (OLS) are not available. The algorithm computes estimates from the maximum likelihood through an iterative process. These estimates are called 'pseudo R-squared' because they look like 'R-squared' in the sense that they are on a similar scale (from 0 to 1), with higher values indicating better model fit.

Usage

```
pseudoR2(object, ...)
```

```
## Default S3 method:
```



```
pseudoR2(object, ...)  
  
## S3 method for class 'pltree'  
pseudoR2(object, newdata = NULL, ...)  
  
## S3 method for class 'bttree'  
pseudoR2(object, ...)
```

Arguments

object	a model object of class glm, gnm, lm, pltree or bttree
...	additional arguments affecting the R-squared produced
newdata	a data.set with testing data

Value

A data frame containing the pseudo R-squared coefficients:

logLik	log-likelihood
logLikNull	Null log-likelihood
MaxLik	maximum likelihood pseudo R-squared
CraggUhler	Cragg and Uhler's pseudo R-squared
McFadden	McFadden pseudo R-squared

Author(s)

Kauê de Sousa and Jacob van Etten

References

Agresti A. (2002). *Categorical Data Analysis*. John Wiley & Sons, Inc., Hoboken, NJ, USA. doi:10.1002/0471249688

Hunter D. R. (2004). *The Annals of Statistics*, 32(1), 384–406. <http://www.jstor.org/stable/3448514>

Cragg, J. G., & Uhler, R. S. (1970). *The Canadian Journal of Economics* 3(3), 386-406. doi:10.2307/133656

McFadden, D. (1973). Conditional logit analysis of qualitative choice behavior.

See Also

Other goodness-of-fit functions: [kendallTau\(\)](#), [kendallW\(\)](#)

Examples

```
data("airquality")  
  
mod <- glm(Temp ~ Wind + Solar.R,  
           data = airquality,  
           family = poisson())
```

```
pseudoR2(mod)
```

pseudo_rank	<i>Add pseudo-rank to missing values</i>
-------------	--

Description

Add pseudo-rank to missing values

Usage

```
pseudo_rank(object, ...)
```

Arguments

object	a matrix or PlackettLuce rank
...	additional arguments passed to methods

Value

a matrix or PlackettLuce rank

Examples

```
library("PlackettLuce")
R <- matrix(c(1, 2, 0, 0,
              4, 1, 0, 3,
              2, 1, 0, 3,
              1, 2, 0, 0,
              2, 1, 0, 0,
              1, 0, 0, 2), nrow = 6, byrow = TRUE)
colnames(R) <- c("apple", "banana", "orange", "pear")

# summary(PlackettLuce(R))

R <- pseudo_rank(R)

summary(PlackettLuce(R))
```

rank_binomial	<i>Binary rankings from pairwise contests</i>
---------------	---

Description

Binary comparisons from a ranking object. Ties are not taken into account, then they are added as NA's.

Usage

```
rank_binomial(object, drop.null = FALSE, disaggregate = FALSE)
```

Arguments

object	an object of class rankings, grouped_rankings or paircomp
drop.null	logical, an optional argument to remove null contests
disaggregate	logical, if TRUE binaries are disaggregated by individual contests

Value

A data.frame with binary rank of pairwise contests:

player1	a factor with n levels for the first player in the contests
player2	a factor with n levels (same as player1) for the second player in the contests
win1	number of times player1 wins against player2
win2	number of times player2 wins against player1

Author(s)

Kauê de Sousa

References

Turner H. & Firth D. (2012). Journal of Statistical Software, 48(9), 1–21. doi: [10.18637/jss.v048.i09](https://doi.org/10.18637/jss.v048.i09)

See Also

Other rank functions: [rank_numeric\(\)](#), [rank_paircomp\(\)](#), [rank_tricot\(\)](#)

Examples

```
library("PlackettLuce")

R <- matrix(c(1, 2, 0, 0,
              4, 1, 2, 3,
              2, 4, 3, 1,
              1, 2, 3, 0,
```

```

      2, 1, 1, 0,
      1, 0, 3, 2), nrow = 6, byrow = TRUE)
colnames(R) <- c("apple", "banana", "orange", "pear")

R <- as.rankings(R)

rank_binomial(R)

rank_binomial(R, disaggregate = TRUE)

```

rank_numeric

Plackett-Luce rankings from numeric values

Description

Group and coerce numeric values into Plackett-Luce rankings.

Usage

```

rank_numeric(
  data,
  items,
  input,
  id = NULL,
  group = FALSE,
  ascending = FALSE,
  ...
)

```

Arguments

data	a data.frame with columns specified by items and input values
items	a character or numerical vector for indexing the column(s) containing the item names in data
input	a character or numerical vector for indexing the column(s) containing the values in data to be ranked
id	an index of data indicating the ids for "long" data
group	logical, if TRUE return an object of class "grouped_rankings"
ascending	logical, only for floating point numbers, to compute rankings from lower to higher values
...	additional arguments passed to methods

Value

a PlackettLuce "rankings" object, which is a matrix of dense rankings

Author(s)

Kauê de Sousa

See Also[rankings](#)Other rank functions: [rank_binomial\(\)](#), [rank_paircomp\(\)](#), [rank_tricot\(\)](#)**Examples**

```
# A matrix with 10 rankings of 5 items (A, B, C, D, E)
# with numeric values as "rank"
set.seed(123)
df <- cbind(id = rep(1:10, each = 5),
            items = rep(LETTERS[1:5], times = 10),
            input = runif(50, 1, 3))

# return an object of class 'rankings'
R <- rank_numeric(df,
                 items = 2,
                 input = 3,
                 id = 1)

# rankings can be computed in ascending order
R <- rank_numeric(df,
                 items = 2,
                 input = 3,
                 id = 1,
                 ascending = TRUE)

# return an object of class 'grouped_rankings'
R <- rank_numeric(df,
                 items = 2,
                 input = 3,
                 id = 1,
                 group = TRUE)
```

rank_paircomp*Pairwise comparison rankings*

Description

Pairwise comparisons from a ranking object. Ties are not taken into account, then they are added as NA's.

Usage

```
rank_paircomp(object)
```

Arguments

object an object of class "rankings" or "grouped_rankings" which is a matrix of dense rankings.

Value

an object of class "paircomp" which is a matrix of pairwise comparisons

Author(s)

Kauê de Sousa and Jacob van Etten

References

Strobl C., Wickelmaier F. & Zeileis A. (2011). Journal of Educational and Behavioral Statistics, 36(2), 135–153. doi:10.3102/1076998609359791

See Also

[rankings](#), [paircomp](#)

Other rank functions: [rank_binomial\(\)](#), [rank_numeric\(\)](#), [rank_tricot\(\)](#)

Examples

```
library("PlackettLuce")

R <- matrix(c(1, 2, 0, 0,
             4, 1, 2, 3,
             2, 4, 3, 1,
             1, 2, 3, 0,
             2, 1, 1, 0,
             1, 0, 3, 2), nrow = 6, byrow = TRUE)
colnames(R) <- c("apple", "banana", "orange", "pear")
R <- as.rankings(R)

PC <- rank_paircomp(R)

#####

# using breadwheat data
data("breadwheat", package = "gosset")

# convert the tricot rankings from breadwheat data
# into a object of class 'rankings' from PlackettLuce
R <- rank_tricot(breadwheat,
                 items = c("variety_a", "variety_b", "variety_c"),
                 input = c("overall_best", "overall_worst"))

PC <- rank_paircomp(R)
```

rank_tricot

*Build Plackett-Luce rankings from tricot dataset***Description**

Create an object of class "rankings" from tricot data. Tricot stands for "triadic comparison of technologies". Is a methodology to carry out large agronomic field experiments allowing the comparison between many alternative technologies, in many different environments. Each participant evaluates a set of three randomised technologies from a larger set. A comparison with a local item can be added as additional rankings with the argument `additional.rank`.

Usage

```
rank_tricot(data, items, input, group = FALSE, additional.rank = NULL, ...)
```

Arguments

<code>data</code>	a data.frame with columns specified by <code>items</code> and <code>input</code> values
<code>items</code>	a character or numerical vector for indexing the column(s) containing the item names in <code>data</code>
<code>input</code>	a character or numerical vector for indexing the column(s) containing the values in <code>data</code> to be ranked
<code>group</code>	logical, if TRUE return an object of class "grouped_rankings"
<code>additional.rank</code>	optional, a data frame for the comparisons between tricot items and the local item
<code>...</code>	additional arguments passed to methods. See details

Details

`full.output`: logical, to return a list with a "rankings", a "grouped_rankings" and the ordered items

Value

a PlackettLuce "rankings" object, which is a matrix of dense rankings

Author(s)

Kauê de Sousa and Jacob van Etten, with ideas from Heather Turner

References

van Etten J., et al. (2016). Experimental Agriculture, 55(S1), 275–296. doi: [10.1017/S0014479716000739](https://doi.org/10.1017/S0014479716000739)

See Also

[rankings](#), [breadwheat](#)

Other rank functions: [rank_binomial\(\)](#), [rank_numeric\(\)](#), [rank_paircomp\(\)](#)

Examples

```
# using breadwheat data
data("breadwheat", package = "gosset")

# convert the tricot rankings from breadwheat data
# into a object of class 'rankings' from PlackettLuce
R <- rank_tricot(data = breadwheat,
                 items = c("variety_a", "variety_b", "variety_c"),
                 input = c("overall_best", "overall_worst"))

#####

# beans data where each observer compares 3 varieties randomly distributed
# from a list of 11 and additionally compares these 3 varieties
# with their local variety
library("PlackettLuce")
data("beans", package = "PlackettLuce")

# first build rankings with only tricot items
# and return an object of class 'rankings'
R <- rank_tricot(data = beans,
                 items = c(1:3),
                 input = c(4:5))

head(R)

#####

# pass the comparison with local item as an additional rankings, then
# each of the 3 varieties are compared separately with the local item
# and return an object of class grouped_rankings
G <- rank_tricot(data = beans,
                 items = c(1:3),
                 input = c(4:5),
                 group = TRUE,
                 additional.rank = beans[c(6:8)])

head(G)
```


Description

Regret is an important heuristic in the behavioural sciences. Minimizing worst regret (the loss under the worst possible outcome) is a criterion that takes a conservative approach to risk analysis in diversification strategies.

Usage

```
regret(object, ..., bootstrap = TRUE, normalize = TRUE)

## Default S3 method:
regret(object, ..., values, items, group, bootstrap = TRUE, normalize = TRUE)

## S3 method for class 'pltree'
regret(object, bootstrap = TRUE, normalize = TRUE, ...)

## S3 method for class 'list'
regret(object, bootstrap = TRUE, normalize = TRUE, ...)
```

Arguments

<code>object</code>	a data.frame, an object of class <code>pltree</code> , or a list with PlackettLuce models
<code>...</code>	further arguments passed to methods
<code>bootstrap</code>	logical, to run a bayes bootstrap on <i>object</i>
<code>normalize</code>	logical, to normalize values to sum to 1
<code>values</code>	an index in <i>object</i> with the values to compute regret
<code>items</code>	an index in <i>object</i> for the different items
<code>group</code>	an index in <i>object</i> for the different scenarios

Value

	A data frame with regret estimates
<code>items</code>	the item names
<code>worth</code>	the worth parameters
<code>regret</code>	the squared regret
<code>worst_regret</code>	the worst regret

Author(s)

Jacob van Etten and Kauê de Sousa

References

Loomes G. & Sugden R. (1982). The Economic Journal, 92(368), 805. doi: [10.2307/2232669](https://doi.org/10.2307/2232669)
 Bleichrodt H. & Wakker P. P. (2015). The Economic Journal, 125(583), 493–532. doi: [10.1111/eoj.12200](https://doi.org/10.1111/eoj.12200)

Examples

```

# Case 1 ####
library("PlackettLuce")
data("breadwheat", package = "gosset")

# convert the tricot rankings from breadwheat data
# into a object of class 'grouped_rankings'

G <- rank_tricot(breadwheat,
                 items = c("variety_a", "variety_b", "variety_c"),
                 input = c("overall_best", "overall_worst"),
                 group = TRUE)

# combine grouped rankings with temperature indices
mydata <- cbind(G, breadwheat[c("lon", "lat")])

# fit a pltree model using geographic data
mod <- pltree(G ~ ., data = mydata)

regret(mod)

# Case 2 ####
# list of PlackettLuce models
R <- matrix(c(1, 2, 3, 0,
              4, 1, 2, 3,
              2, 1, 3, 4,
              1, 2, 3, 0,
              2, 1, 3, 0,
              1, 0, 3, 2), nrow = 6, byrow = TRUE)
colnames(R) <- c("apple", "banana", "orange", "pear")

mod1 <- PlackettLuce(R)

R2 <- matrix(c(1, 2, 0, 3,
              2, 1, 0, 3,
              2, 1, 0, 3,
              1, 2, 0, 3,
              2, 1, 0, 3,
              1, 3, 4, 2), nrow = 6, byrow = TRUE)
colnames(R2) <- c("apple", "banana", "orange", "pear")

mod2 <- PlackettLuce(R2)

mod <- list(mod1, mod2)

regret(mod, n1 = 500)

```

Description

Measures the precision of estimated values, and the potential response to selection on those estimated values compared to a check

Usage

```
reliability(x, ...)  
  
## Default S3 method:  
reliability(x, y = NULL, ...)  
  
## S3 method for class 'PlackettLuce'  
reliability(x, ref, ...)  
  
## S3 method for class 'pltree'  
reliability(x, ref, ...)
```

Arguments

x	a numeric vector, or an object of class PlackettLuce or pltree
...	additional arguments passed to methods
y	numeric, the reference value
ref	a character or integer for indexing the element containing reference values in x

Value

the reliability based on the worth parameters

Author(s)

Kauê de Sousa, David Brown, Jacob van Etten

References

Eskridge and Mumm (1992). Theoret. Appl. Genetics 84, 494–500 doi: [10.1007/BF00229512](https://doi.org/10.1007/BF00229512).

Examples

```
# Case 1. vector example  
  
x <- c(9.5, 12, 12.3, 17)  
  
y <- 11.2  
  
reliability(x, y)  
  
# Case 2. PlackettLuce model  
  
library("PlackettLuce")
```

```

R <- matrix(c(1, 2, 4, 3,
             4, 1, 2, 3,
             2, 3, 1, 4,
             4, 2, 3, 1,
             2, 1, 4, 3,
             1, 4, 3, 2), nrow = 6, byrow = TRUE)
colnames(R) <- c("apple", "banana", "orange", "pear")

mod <- PlackettLuce(R)

reliability(mod, ref = "orange")

# Case 3. PlackettLuce tree

data("beans", package = "PlackettLuce")

G <- rank_tricot(data = beans,
                 items = c(1:3),
                 input = c(4:5),
                 group = TRUE,
                 additional.rank = beans[c(6:8)])

pld <- cbind(G, beans[,c("maxTN", "season", "lon")])

tree <- pltree(G ~ maxTN + season + lon, data = pld)

reliability(tree, ref = "INTA Matagalpa")

```

rowbind

Combine R objects by rows

Description

Combine R objects when number and names of columns do not match

Usage

```

rowbind(x, ...)

## Default S3 method:
rowbind(x, y, ...)

## S3 method for class 'list'
rowbind(x, ...)

```

Arguments

x	a R object, typically a data.frame, matrix or list
...	additional arguments passed to methods
y	a matrix, a data.frame (or any other object that can be coerced to data.frame)

Value

a data.frame with the combined data

Examples

```
# two data frames
rowbind(airquality, mtcars)

# a list of data frames
l <- list(airquality, mtcars)
rowbind(l)
```

worth_map

Plot worth parameters

Description

Produces plots to highlight worth coefficients of items in a party tree of a list of PlackettLuce models

Usage

```
worth_map(object, ...)

## Default S3 method:
worth_map(object, ...)

## S3 method for class 'list'
worth_map(object, labels, ...)

worth_bar(object, ...)
```

Arguments

object	an object of class party or an object of class PlackettLuce or a list objects of class PlackettLuce
...	additional arguments passed to methods
labels	a vector with the name of models in <i>object</i>

Examples

```

library("psychotree")
library("PlackettLuce")
data("Topmodel2007", package = "psychotree")
R <- as.grouped_rankings(Topmodel2007$preference)

tm_tree <- pltree(R ~ ., data = Topmodel2007[, -1],
                 minsize = 5,
                 npseudo = 0)

worth_map(tm_tree)

#####

# Ranking of preference on four fruits
# based on traits taste, texture,
# price and storability

# taste
R1 <- matrix(c(1, 2, 3, 4,
              4, 1, 3, 2,
              4, 1, 2, 3,
              1, 2, 0, 3), nrow = 4, byrow = TRUE)
colnames(R1) <- c("apple", "banana", "orange", "pear")
mod1 <- PlackettLuce(R1)

# texture
R2 <- matrix(c(1, 4, 2, 3,
              1, 4, 3, 2,
              1, 4, 2, 3,
              1, 4, 2, 3), nrow = 4, byrow = TRUE)
colnames(R2) <- c("apple", "banana", "orange", "pear")
mod2 <- PlackettLuce(R2)

# price
R3 <- matrix(c(2, 4, 3, 1,
              4, 1, 2, 3,
              3, 4, 2, 1,
              4, 3, 1, 2), nrow = 4, byrow = TRUE)
colnames(R3) <- c("apple", "banana", "orange", "pear")
mod3 <- PlackettLuce(R3)

# storability
R4 <- matrix(c(1, 4, 3, 2,
              3, 4, 1, 2,
              1, 3, 2, 4,
              2, 3, 4, 1), nrow = 4, byrow = TRUE)
colnames(R4) <- c("apple", "banana", "orange", "pear")
mod4 <- PlackettLuce(R4)

# models in a list
mods <- list(mod1, mod2, mod3, mod4)

```

```
# name for each model
labels <- c("Taste", "Texture", "Price", "Storability")

worth_map(mods, labels)

# plot only one model as bar
worth_bar(mod1)
```

Index

- * **dataset**
 - breadwheat, [3](#)
 - kenyachoice, [13](#)
 - nicabean, [14](#)
 - * **goodness-of-fit functions**
 - kendallTau, [10](#)
 - kendallW, [12](#)
 - pseudoR2, [16](#)
 - * **model selection functions**
 - btpermute, [5](#)
 - crossvalidation, [7](#)
 - * **rank functions**
 - rank_binomial, [19](#)
 - rank_numeric, [20](#)
 - rank_paircomp, [21](#)
 - rank_tricot, [23](#)
 - * **utility functions**
 - rowbind, [28](#)
- AIC.btree (crossvalidation), [7](#)
AIC.gnm (crossvalidation), [7](#)
akaike_weights, [2](#)
- breadwheat, [3](#), [24](#)
BTm, [6](#)
btpermute, [5](#), [9](#)
btree, [9](#)
- compare, [6](#)
cor, [11](#)
crossvalidation, [6](#), [7](#)
- deviance.btree (crossvalidation), [7](#)
deviance.gnm (crossvalidation), [7](#)
deviance.pltree (crossvalidation), [7](#)
- gnm, [9](#)
gosset, [10](#)
gosset-package (gosset), [10](#)
- kendallTau, [10](#), [13](#), [17](#)
- kendallW, [11](#), [12](#), [17](#)
kenyachoice, [13](#)
- nicabean, [14](#)
node_labels, [15](#)
node_rules (node_labels), [15](#)
- paircomp, [22](#)
plot.pltree (node_labels), [15](#)
pltree, [9](#)
pseudo_rank, [18](#)
pseudoR2, [11](#), [13](#), [16](#)
- rank_binomial, [6](#), [19](#), [21](#), [22](#), [24](#)
rank_numeric, [19](#), [20](#), [22](#), [24](#)
rank_paircomp, [19](#), [21](#), [21](#), [24](#)
rank_tricot, [19](#), [21](#), [22](#), [23](#)
rankings, [21](#), [22](#), [24](#)
regret, [24](#)
reliability, [26](#)
rowbind, [28](#)
- top_items (node_labels), [15](#)
- worth_bar (worth_map), [29](#)
worth_map, [29](#)