Package ‘cases’

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Type Package

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RoxygenNote 7.2.0

VignetteBuilder knitr, rmarkdown

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URL https://github.com/maxwestphal/cases

BugReports https://github.com/maxwestphal/cases/issues

Depends R (>= 2.10)

NeedsCompilation no

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**Description**

Enables simultaneous statistical inference for the accuracy of multiple classifiers in multiple subgroups (strata). For instance, allows to perform multiple comparisons in diagnostic accuracy studies with co-primary endpoints sensitivity and specificity. (Westphal, Max, and Antonia Zapf. "Statistical Inference for Diagnostic Test Accuracy Studies with Multiple Comparisons." arXiv:2105.13469 (2021).)

**Details**

See the vignettes vignette()
categorize

Categorize continuous values

Description

This function allows to split continuous values, e.g. (risk) scores or (bio)markers, into two or more categories by specifying one or more cutoff values.

Usage

categorize(
  values,
  cutoffs = rep(0, ncol(values)),
  map = 1:ncol(values),
  labels = NULL
)

Arguments

- **values**: numeric matrix of continuous values to be categorized. Assume an \((n \times r)\) matrix with \(n\) observations (subjects) of \(r\) continuous values.
- **cutoffs**: numeric matrix of dimension \(m \times k\). Each row of cutoffs defines a split into \(k+1\) distinct categories. Each row must contain distinct values. In the simplest case, cutoffs is a single column matrix whereby is row defines a binary split (\(<=t\) vs. \(>t\)). In this case \((k=1)\), cutoffs can also be a numeric vector.
- **map**: integer vector of length \(k\) with values in \(1:r\), whereby \(r = ncol(values)\). \(map\) gives the value which column of values should be categorized by ...
- **labels**: character of length \(m\) (= number of prediction \(r\))

Value

numeric \((n \times k)\) matrix with categorical outcomes after categorizing.

Examples

```r
set.seed(123)
M <- as.data.frame(mvtnorm::rmvnorm(20, mean=rep(0, 3), sigma=2*diag(3)))
M
categorize(M)
C <- matrix(rep(c(-1, 0, 1, -2, 0, 2), 3), ncol=3, byrow = TRUE)
C
w <- c(1, 1, 2, 2, 3, 3)
categorize(M, C, w)
```
**compare**  
*Compare predictions and labels*

**Description**

Compare predictions and labels

**Usage**

```r
compare(
    predictions,
    labels,
    partition = TRUE,
    names = c(specificity = 0, sensitivity = 1)
)
```

**Arguments**

- `predictions`: integer, predicted class
- `labels`: integer, true class state (reference standard)
- `partition`: logical, should result be split into one matrix per class (TRUE; default) or not (FALSE)
- `names`: integer (named), values give data values, names give class names

**Value**

data matrix with values 1 (correct prediction) and 0 (false prediction)

**Examples**

```r
pred <- matrix(c(1,1,0), 5, 3)
labels <- c(1, 1, 0, 0, 1)
compare(pred, labels, FALSE)
compare(pred, labels, TRUE)
```

**complete_results**  
*Complete evaluation results*

**Description**

Complete evaluation results

**Usage**

```r
complete_results(results, benchmark, alpha, analysis)
```
Arguments

results   "cases_results" object, i.e. result of evaluate
benchmark numeric, vector of benchmark values
alpha     numeric, significance level
analysis  character, either "co-primary" or "full"

Details

Not exported, but applied at the end of evaluate by default

Value

"cases_results" object

cormat_ar1

Create an AR(1) correlation matrix

Description

Create an AR(1) correlation matrix

Usage

cormat_ar1(m, rho, d = TRUE)

Arguments

m        integer, dimension
rho      numeric, correlation parameter in (0,1)
d        binary vector of length m, whereby TRUE/FALSE (alternatively 1/0) indicate
        active/inactive components of underlying random vector.

Value

\[ R_{ij} = \rho^{|i-j|} \]
cormat_equi

Create an equicorrelation matrix

Description
Create an equicorrelation matrix

Usage
cormat_equi(m, rho, d = TRUE)

Arguments
- m: integer, dimension
- rho: numeric, correlation parameter in (0,1)
- d: binary vector of length m, whereby TRUE/FALSE (alternatively 1/0) indicate active/inactive components of underlying random vector.

Value
$R_{ij} = \rho, i \neq j$

data_wdbc

Breast Cancer Wisconsin (Diagnostic) Data Set

Description
Dataset documentation can be found at the source website and references below.

Usage
data_wdbc

Format
data_wdbc:
A data frame with 569 rows (patients) and 31 columns (1 target, 30 features).

Details
The ID variable was removed. Diagnosis (1 = malignant, 0 = benign). Feature variables have been renamed.

Source
References


---

**define_contrast**

Define a contrast (matrix) to specify exact hypothesis system

---

**Description**

Define a contrast (matrix) to specify exact hypothesis system

**Usage**

```r
define_contrast(type = c("raw", "dunnett", "tukey"), comparator = NA)
```

**Arguments**

- `type` character, either "Raw", "dunnett" or "tukey"
- `comparator` either integer (index of comparator) or character (name of comparator)

**Details**

- "raw" contrast: compare all candidates against specified benchmark values
- "dunnett" (all vs. one) contrast: compare all candidates to a single comparator.
- "tukey" (all vs. all) contrast: compare all candidates against each other.

**Value**

cases_contrast object to be passed to `evaluate`

**Examples**

```r
define_contrast("dunnett", 1)
```
draw_data  Generate binary data

Description

Generate binary data

Usage

draw_data(
  n = 200,
  prev = c(0.5, 0.5),
  random = FALSE,
  m = 10,
  method = c("roc", "lfc", "pr"),
  pars = list(),
  ...
)

Arguments

  n          integer, overall sample size
  prev       numeric, vector of class prevalences (adding up to 1)
  random     logical, random sampling (TRUE) or fixed group sample sizes
  m          integer, number of models
  method     character, either "roc", "lfc" (multiple subgroups) or "prob" (no subgroups)
  pars       list, containing further named parameters passed to draw_data_roc, draw_data_lfc
  ...        further named parameters passed

Value

  generated binary data (possibly stratified for subgroups)

Examples

draw_data()
draw_data_lfc

Generate binary data (LFC model)

Description
Generate binary data (LFC model)

Usage

\[
\text{draw_data_lfc}(\n, \text{n} = 100, \\
, \text{prev} = c(0.5, 0.5), \\
, \text{random} = \text{FALSE}, \\
, \text{m} = 10, \\
, \text{se} = 0.8, \\
, \text{sp} = 0.8, \\
, \text{B} = \text{round(m/2)}, \\
, \text{L} = 1, \\
, \text{Rse} = \text{diag(rep(1, m)),} \\
, \text{Rsp} = \text{diag(rep(1, m)),} \\
, \text{modnames} = \text{paste0("model", 1:m),} \\
, \text{...} \\
\)

Arguments

\text{n} integer, total sample size
\text{prev} numeric, disease and healthy prevalence (adds up to 1)
\text{random} logical, random sampling (TRUE) or fixed prevalence (FALSE)
\text{m} integer, number of models
\text{se} numeric, sensitivity (length 1)
\text{sp} numeric, specificity (length 1)
\text{B} integer, between 1 and \text{m}, specifies how many sensitivity values are projected to 1
\text{L} numeric, worst alternative is computed under side condition \text{Acc} \leq \text{L} (default value \text{L}=1 corresponds to true LFC where values are projected to 1)
\text{Rse} matrix, correlation matrix for empirical sensitivities (\text{m} x \text{m})
\text{Rsp} matrix, correlation matrix for empirical specificities (\text{m} x \text{m})
\text{modnames} character, model names (length \text{m})
... further arguments (currently unused)

Value
Generated binary dataset
draw_data_roc

Examples

data <- draw_data_lfc()
head(data)

draw_data_prb

Sample binary data (single sample)

Description

This function is wrapper for rmvbin.

Usage

draw_data_prb(n = 100, pr = c(0.8, 0.8), R = diag(length(pr)))

Arguments

n integer, sample size
pr numeric, vector with marginal success probabilities
R matrix, square correlation matrix

Value

a matrix with n rows and length(pr) columns of randomly generated binary (0, 1) data

draw_data_roc

Generate binary data (ROC model)

Description

Generate binary data (ROC model)

Usage

draw_data_roc(
    n = 100,
    prev = c(0.5, 0.5),
    random = FALSE,
    m = 10,
    auc = seq(0.85, 0.95, length.out = 5),
    rho = c(0.25, 0.25),
    dist = c("normal", "exponential"),
    e = 10,
    k = 100,
    delta = 0,
)
evaluate

modnames = paste0("model", 1:m),
corrplot = FALSE,
...
)

Arguments

n integer, total sample size
prev numeric, disease and healthy prevalence (adds up to 1)
random logical, random sampling (TRUE) or fixed prevalence (FALSE)
m integer, number of models
auc numeric, vector of AUCs of biomarkers
rho numeric, vector (length 2) of correlations between biomarkers
dist character, either "normal" or "exponential" specifying the subgroup biomarker distributions
e numeric, emulates better (worse) model selection quality with higher (lower) values of e
k integer, technical parameter which adjusts grid size
delta numeric, specify importance of sensitivity and specificity (default 0)
modnames character, model names (length m)
corrplot logical (default: FALSE), if TRUE do not return data but instead plot correlation matrices for final binary data
...
 further arguments (currently unused)

Value

Generated binary dataset

Examples

data <- draw_data_roc()
head(data)

evaluate Evaluate the accuracy of multiple (candidate) classifiers in several subgroups

Description

Assess classification accuracy of multiple classification rules stratified by subgroups, e.g. in diseased (sensitivity) and healthy (specificity) individuals.
Usage

evaluate(
  data,
  contrast = define_contrast("raw"),
  benchmark = 0.75,
  alpha = 0.05,
  alternative = c("two.sided", "greater", "less"),
  adjustment = c("none", "bonferroni", "maxt", "bootstrap", "mbeta"),
  transformation = c("none", "logit"),
  analysis = c("co-primary", "full"),
  regu = FALSE,
  pars = list(),
  ...
)

Arguments

data list of n_g x m binary matrix or data.frame (n_g observations of m binary decisions), g is the index of subgroups/classes, usually created via compare.
contrast cases_contrast object, specified via define_contrast
benchmark value to compare against (RHS), should have same length as data.
alpha numeric, significance level (default: 0.05)
alternative character, specify alternative hypothesis
adjustment character, specify type of statistical adjustment taken to address multiplicity
transformation character, define transformation to ensure results (e.g. point estimates, confidence limits) lie in unit interval ("none" (default) or "logit")
analysis character, "co-primary" or "full"
regu numeric vector of length 3, specify type of shrinkage. Alternatively, logical of length one (TRUE := c(2, 1, 1/2), FALSE := c(0, 0, 0))
pars further parameters given as named list list(type="pairs", nboot=10000)
... additional named parameters, can be used instead of (in in conjunction with) pars

Details

Adjustment methods (adjustment) and additional parameters (pars or ...):

"none" (default): no adjustment for multiplicity

"bonferroni": Bonferroni adjustment

"maxt": maxT adjustment

"bootstrap": Bootstrap approach
generate_instance_lfc

- type: "pairs" (default) or "wild" = type (for adjustment="bootstrap"
- nboot: number of bootstrap draws (default: 5000)
- res_tra: = 0, 1, 2 or 3 = type of residual transformation of wild bootstrap (default = 0: no transformation) (see https://www.math.kth.se/matstat/gru/sf2930/papers/wild.bootstrap.pdf)

"mbeta": A heuristic Bayesian approach which is based on a multivariate beta-binomial model.
- nrep: number of posterior draws (default: 5000)
- lfc_pr: prior probability of 'least-favorable parameter configuration' (default: 1).

Value

cases_results object, which is a list of analysis results

Examples

```r
#
data <- draw_data_roc()
evaluate(data)
```

---

**generate_instance_lfc**  Generate data sets under least favorable parameter configurations

**Description**

Generates a (simulation) instance, a list of multiple datasets to be processed (analyzed) with `process_instance`. Ground truth parameters (Sensitivity & Specificity) are least-favorable in the sense that the type-I error rate of the subsequently applied multiple test procedures is maximized.

**Usage**

```r
generate_instance_lfc(
  nrep = 10,
  n = 100,
  prev = 0.5,
  random = FALSE,
  m = 10,
  se = 0.8,
  sp = 0.8,
  L = 1,
  rhose = 0,
  rhosp = 0,
  cortype = "equi",
  ...
  data = NULL,
  job = NULL
)
```
Arguments

- **nrep**: integer, number of instances
- **n**: integer, total sample size
- **prev**: numeric, disease prevalence
- **random**: logical, fixed prevalence (FALSE) or simple random sampling (TRUE)
- **m**: integer, number of candidates
- **se**: numeric
- **sp**: numeric
- **L**: numeric
- **rhose**: numeric
- **rhosp**: numeric
- **cortype**: character, "equi" or "ak1"
- **...**: further arguments
- **data**: ignored (for batchtools compatibility)
- **job**: ignored (for batchtools compatibility)

Details

Utilizes same arguments as `draw_data_lfc` unless mentioned above.

Value

a list, a single (LFC) simulation instance

---

**generate_instance_roc**  
*Generate data sets under realistic parameter configurations*

Description

Generates a (simulation) instance, a list of multiple datasets to be processed (analyzed) with `process_instance`. Ground truth parameters (Sensitivity & Specificity) are initially generated according to a generative model whereby multiple decision rules (with different parameter values) are derived by thresholding multiple biomarkers.

Usage

```r
generate_instance_roc(
  nrep = 10,
  n = 100,
  prev = 0.5,
  random = FALSE,
  m = 10,
  auc = "seq(0.85, 0.95, length.out = 5)"
)```
\begin{verbatim}
  rhose = 0.5,
  rhosp = 0.5,
  dist = "normal",
  e = 10,
  k = 100,
  delta = 0,
  ...
  data = NULL,
  job = NULL
"
\end{verbatim}

**Arguments**

- `nrep` integer, number of instances
- `n` integer, total sample size
- `prev` numeric, disease prevalence
- `random` logical, fixed prevalence (FALSE) or simple random sampling (TRUE)
- `m` integer, number of candidates
- `auc` numeric
- `rhose` numeric
- `rhosp` numeric
- `dist` character
- `e` numeric
- `k` numeric
- `delta` numeric
- `...` further arguments
- `data` ignored (for batchtools compatibility)
- `job` ignored (for batchtools compatibility)

**Details**

Utilizes same arguments as \texttt{draw_data_roc} unless mentioned above.

**Value**

- a list, a single (ROC) simulation instance
**process_instance**

Analyze simulated synthetic datasets.

### Description

Process data instances, a list of multiple datasets generated via `generate_instance_lfc` or `generate_instance_roc`. This function applies `evaluate` to all datasets.

### Usage

```r
process_instance(
  instance = NULL,
  contrast = "cases::define_contrast('raw', NA)",
  benchmark = 0.5,
  alpha = 0.05,
  alternative = "greater",
  adjustment = "none",
  transformation = "none",
  analysis = "co-primary",
  regu = "c(1,1/2,1/4)",
  pars = "list()",
  ...
)
```

### Arguments

- **instance**: generated via `generate_instance_lfc` or `generate_instance_roc`.
- **contrast**: `cases::define_contrast('raw', NA)`.
- **benchmark**: numeric, value to compare against (RHS), should have same length as data.
- **alpha**: numeric, significance level (default: 0.05)
- **alternative**: character, specify alternative hypothesis
- **adjustment**: character, specify type of statistical adjustment taken to address multiplicity
- **transformation**: character, define transformation to ensure results (e.g. point estimates, confidence limits) lie in unit interval ("none" (default) or "logit")
- **analysis**: character, "co-primary" (default; only option currently)
- **regu**: numeric vector of length 3, specify type of shrinkage. Alternatively, logical of length one (TRUE := c(2, 1, 1/2), FALSE := c(0, 0, 0))
- **pars**: further parameters given as named list
- **...**: additional named parameters
- **data**: ignored (for batchtools compatibility)
- **job**: for batchtools compatibility, do not change
visualize

Details
Utilizes same arguments as evaluate unless mentioned above.

Value

standardized evaluation results

---

visualize Visualize evaluation results

---

Description

Visualize evaluation results

Usage

visualize(x, ...)

Arguments

x, a cases_results object, see evaluate

... further arguments (currently ignored)

Details

+++ early development version (only alternative = "greater" is supported) +++

Value

a ggplot
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