Package ‘clinfun’

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**Title**  Clinical Trial Design and Data Analysis Functions

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**Imports**  mvtnorm

**Suggests**  survival

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**Description**  Utilities to make your clinical collaborations easier if not fun. It contains functions for designing studies such as Simon 2-stage and group sequential designs and for data analysis such as Jonckheere-Terpstra test and estimating survival quantiles.

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**License**  GPL (>= 2)

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Two-Sample Tests for Growth Curves under Dependent Right Censoring

Description
Permutation test for comparing growth curves across two groups under dependent right censoring.

Usage
\texttt{aucVardiTest(meas, grp, tim=NULL, cgrps=NULL, nperm=5000)}

Arguments
\begin{itemize}
\item \texttt{meas} Matrix of measurements where the rows are the subjects and columns the time-points. At least one value should not be missing in each row. For example they can be tumor sizes measured over time.
\item \texttt{grp} Group indicator for each subject. There must be at least two different groups. This can represent each subject’s treatment.
\item \texttt{tim} Times at which the measurements in \texttt{meas} are taken. If missing, the times are set to 1 through \texttt{ncol(meas)}.
\item \texttt{cgrps} The two groups that are being compared. If missing the first two groups will be compared.
\item \texttt{nperm} Number of permutations for the reference distribution.
\end{itemize}

Details
The test statistic is defined as the sum of pairwise differences in the partial areas under the growth curve. For each pair of subjects the partial area is computed until the smaller of the maximum followup times. For each subject, linear interpolation is used to fill-in missing values prior to the maximum followup time. The reference distribution of obtained by permuting the group labels.

Value
returns a list with objects \texttt{ostat}, \texttt{pstat} and \texttt{p.value} which are the observed test statistic for the two groups being compared, values of the statistics when the group labels are permuted.
**References**


**Examples**

```r
grp <- sample(1:3, 100, replace=TRUE)
grp0 <- LETTERS[grp]
maxfup <- sample(5:20, 100, replace=TRUE)
meas <- matrix(NA, 100, 20)
for(i in 1:100) {
  meas[i, 1:maxfup[i]] <- cumsum(3 + 0.04*grp[i] + rnorm(maxfup[i]))
}
aucVardiTest(meas, grp)
aucVardiTest(meas, grp0, cgrps=c("C", "B"))
```

---

**calogrank**

*Survival curves analysis of covariance*

**Description**

Logrank test to compare survival curves adjusting for covariates

**Usage**

```r
calogrank(ftime, fstatus, grp, cvt, strat=NULL)
```

**Arguments**

- `ftime`: failure times
- `fstatus`: status indicator
- `grp`: group indicator
- `cvt`: continuous covariates used for adjusted analysis
- `strat`: stratification variable

**Details**

`calogrank` is the covariate adjusted version of `k-sample survdiff`. The function in its current form only does basic error checking.

**References**

### Examples

```r
# Not run: library(survival)
data(pbc)
pbc1 <- pbc
pbc1$trt[pbc1$trt == -9] <- NA
pbc1$copper[pbc1$copper == -9] <- NA
calogrank(pbc1$time, pbc1$status, pbc1$trt, pbc1[,c("copper")])
calogrank(pbc1$time, pbc1$status, pbc1$trt, 
         pbc1[,c("protime", "copper")])
# End(Not run)
```

---

### Description

Calculates the Concordance Probability Estimate for a Cox model.

### Usage

```r
coxphCPE(phfit)
```

### Arguments

- `phfit`: output from a proportional hazards fit.

### Value

`coxphCPE` returns a vector with CPE, smooth.CPE & se.CPE which are the estimate, the smoothed estimate and its standard error respectively.

### References


### Examples

```r
# Not run: library(survival)
data(pbc)
pbcfit <- coxph(Surv(time, status==2) ~ trt + log(copper), pbc, 
                 subset=(trt>0 & copper>0))
coxphCPE(pbcfit)
# End(Not run)
```
Description

Calculates the contribution of a subset of covariates to the explained relative risk derived from the full Cox proportional hazards model.

Usage

```r
coxphERR(phfit, ngamma=NULL)
```

Arguments

- `phfit`: The output from a proportional hazards fit.
- `ngamma`: A vector of indices corresponding to covariates of interest. If missing (default), the explained relative risk is computed for the full model.

Details

The object `phfit` should be the result of a call to `coxph` with the option `x=TRUE`.

Value

The function `coxphERR` returns the vector `(ERR, se.ERR)`. The first component `ERR` represents the contribution of a subset of covariates to the explained relative risk estimate of the full model. If a set of covariates is not provided, then it computes the estimate of the full model. The second component `se.ERR` is the standard error of the estimate.

References

Heller G. (2012) A measure of explained risk in the proportional hazards model. *Biostatistics*

Examples

```r
## Not run:
library(survival)
ovarianfit <- coxph(Surv(futime, fustat) ~ age + resid.ds + rx + ecog.ps, data=ovarian, x=T)

# Compute the explained relative risk (ERR) and
# its standard error (se.ERR) for the full model.
coxphERR(ovarianfit)
# Compute the contribution of age and ECOG performance status to
# the explained relative risk. Age and ECOG performance status are
# the first and fourth covariates in the model.
coxphERR(ovarianfit, c(1,4))

## End(Not run)
```
**Description**

Draws a quantile curve of survival distribution as a function of covariate.

**Usage**

```r
coxphQuantile(phfit, xrange, p=0.5, whichx=1, otherx=NULL, ...)
```

**Arguments**

- `phfit`: output from a proportional hazards fit.
- `xrange`: the range of covariate values for which the quantiles of survival times are computed.
- `p`: the probability level for the quantile (default is median).
- `whichx`: if there are more than one covariates in the Cox model, the one chosen for the quantile plot.
- `otherx`: the values for other covariates in the Cox model. If missing uses their average values.
- `...`: additional parameters to be passed on to the lines command.

**Details**

This function is used to draw quantile curves. It requires a plot of the data (time & covariate of interest) to be present. See example.

It invisibly returns the observed failure times and the covariate values at which the estimated survival probability is (exactly) p.

**References**


**Examples**

```r
# Not run: library(survival)
data(pbc)
pbcfit <- coxph(Surv(time, status==2) ~ trt + log(copper), pbc, subset=(trt>0 & copper>0))
plot(log(pbc$copper[pbc$trt>0 & pbc$copper>0]), pbc$time[pbc$trt>0 & pbc$copper>0], pch=c("o","x")[1+pbc$status[pbc$trt>0 & pbc$copper>0]], xlab="log Copper", ylab="Survival time")
coxphQuantile(pbcfit, c(2.5,6), whichx=2, otherx=1)
coxphQuantile(pbcfit, c(2.5,6), p=0.75, whichx=2, otherx=2, col=2)
# End(Not run)
```
**deltaAUC**  
*Comparing the AUC from ROC curves from nested binary regression*

**Description**
Conducts the test.

**Usage**

```r
deltaAUC(y, x, z)
```

**Arguments**

- `y`: binary response variable
- `x`: matrix of set of covariates that is the basis of the existing (reduced) model
- `z`: matrix of set of covariates that are added to get the new (full) model

**Details**

The models are fit using maximum rank correlation (MRC) method which is an alternate approach to logistic regression. In MRC the area under the ROC curve (AUC) is maximized as opposed to the likelihood in logistic regression. Due to invariance of AUC to location and scale shifts one of the parameters (anchor variable) is set to 1.

The first variable (column) in `x` is used as the anchor variable.

The IPMN data set used as an example in the paper below is included. The columns are high risk lesion (V1), recent weight loss (V2), main duct involvement (V4), presence of a solid component in imaging (V3), and lesion size (V5).

**Value**

It returns a list with the following elements:

- `par.full`: the MRC estimate of parameters for the full model
- `par.red`: the MRC estimate of parameters for the reduced model
- `results`: matrix of results which gives the full reduced model AUCs along with the test statistic and `p-value`

**References**

Heller G., Seshan V.E., Moskowitz C.S. and Gonen M. (2016) Inference for the difference in the area under the ROC curve derived from nested binary regression models. *Biostatistics* 18, 260-274.

**Examples**

```r
data(ipmn)
deltaAUC(ipmn$v1, cbind(ipmn$v4, ipmn$v3, ipmn$v5), ipmn$v2)
```
Trial Designs Based On Fisher’s Exact Test

Description

Calculates sample size, effect size and power based on Fisher’s exact test

Usage

fe.size(p1, p2, alpha=0.05, power=0.8, r=1, npm=5, mmax=1000)
CPS.size(p1, p2, alpha=0.05, power=0.8, r=1)
fe.mdor(ncase, ncontrol, pcontrol, alpha=0.05, power=0.8)
mdor(n, cprob, presp, alpha=0.05, power=0.8, niter=15)
fe.power(d, n1, n2, p1, alpha = 0.05)
OR2pcase(pcontrol, OR)

Arguments

- p1: response rate of standard treatment
- p2: response rate of experimental treatment
- d: difference = p2-p1
- pcontrol: control group probability
- n1: sample size for the standard treatment group
- n2: sample size for the standard treatment group
- ncontrol: control group sample size
- ncase: case group sample size
- alpha: size of the test (default 5%)
- power: power of the test (default 80%)
- r: treatments are randomized in 1:r ratio (default r=1)
- npm: the sample size program searches for sample sizes in a range (+/- npm) to get the exact power
- mmax: the maximum group size for which exact power is calculated
- n: total number of subjects
- cprob: proportion of patients who are marger positive
- presp: probability of response in all subjects
- niter: number of iterations in binary search
- OR: odds-ratio
Details

CPS.size returns Casagrande, Pike, Smith sample size which is a very close to the exact. Use this for small differences p2-p1 (hence large sample sizes) to get the result instantaneously.

Since Fisher's exact test orders the tables by their probability the test is naturally two-sided.

fe.size return a 2x3 matrix with CPS and Fisher's exact sample sizes with power.

fe.mdr return a 3x2 matrix with Schlesselman, CPS and Fisher's exact minimum detectable odds ratios and the corresponding power.

fe.power returns a Kx2 matrix with probabilities (p2) and exact power.

mdrr computes the minimum detectable P(resplmarker+) and P(resplmarker-) configurations when total sample size (n), P(response) (presp) and proportion of subjects who are marker positive (cprob) are specified.

or2pcase give the probability of disease among the cases for a given probability of disease in controls (pcontrol) and odds-ratio (OR).

References


gsdesign

*Group Sequential Designs*

Description

Functions to calculate sample size for group sequential designs

Usage

gsdesign.binomial(ifrac, pC, pE, sig.level = 0.05, power = 0.8, delta.eb=0.5, delta.fb = NULL, alternative = c("two.sided", "one.sided"), pooled.variance = FALSE, CPS = TRUE, tol=0.00001, ...)
gsdesign.normal(ifrac, delta, sd = 1, sig.level = 0.05, power = 0.8, delta.eb = 0.5, delta.fb = NULL, alternative = c("two.sided", "one.sided"), tol=0.00001, ...)
gsdesign.survival(ifrac, haz.ratio, sig.level = 0.05, power = 0.8, delta.eb = 0.5, delta.fb = NULL, alternative = c("two.sided", "one.sided"), tol=0.00001, ...)
Arguments

ifrac  information fraction or the ratio of current sample size or number of events to the total sample size or number of events. This should be an increasing vector of numbers from 0 to 1 with the last one being 1. If just 1 is given a fixed sample design is derived.

pC  prob of success of the standard therapy (for binomial data)

pE  prob of success of the experimental therapy (for binomial data)

delta  true difference in means (for normal data)

sd  standard deviation (for normal data)

haz.ratio  hazard ratio (for survival comparison)

sig.level  significance level (type I error probability)

power  power of test (1 minus type II error probability)

delta.eb  power for efficacy boundary in the Pocock (=0) to O’Brien-Fleming (=0.5) family (default is 0.5)

delta.fb  power for futility boundary in the Pocock (=0) to O’Brien-Fleming (=0.5) family (default is NULL i.e. no futility boundary is requested.)

alternative  one- or two-sided test.
pooled.variance  whether the test statistic is standardized by pooled (2*pbar*(1-pbar)) or unpooled variance (pC*(1-pC) + pE*(1-pE)). Default is unpooled variance.

CPS  whether continuity correction is used for sample size calculation as in Casagrande, Pike & Smith. Default is to use it.
tol  tolerance level for multivariate normal probability computation.
...

Details

The futility boundary is not returned when delta.fb is not specified i.e. stopping for futility is not requested. The futility boundary is non-binding. That is the significance level is not adjusted to account for early stopping for utility. This makes the test a bit conservative in that the true size is less than the nominal level.

The Casagrande-Pike-Smith type continuity correction is obtained using the formula n*1 + sqrt1+4/abs(pC-pE)*n^2 where n is the uncorrected sample size.

Value

a list with ifrac, sig.level, power, alternative, delta.eb, delta.fb and:

efbdry  the critical value to use at the different looks.

futbdry  the critical value to use at the different looks.
sample.size  the sample size per arm for binomial/normal data.

num.events  the total number of failures which should be converted to number of subjects using censoring proportion.
**jonckheere.test**

*Exact/permutation version of Jonckheere-Terpstra test*

**Description**

Jonckheere-Terpstra test to test for ordered differences among classes

**Usage**

```r
jonckheere.test(x, g, alternative = c("two.sided", "increasing", "decreasing"), nperm=NULL)
```

**Arguments**

- `x, g` data and group vector
- `alternative` means are monotonic (two.sided), increasing, or decreasing
- `nperm` number of permutations for the reference distribution. The default is null in which case the permutation p-value is not computed. Recommend that the user set nperm to be 1000 or higher if permutation p-value is desired.

**Details**

`jonckheere.test` is the exact (permutation) version of the Jonckheere-Terpstra test. It uses the statistic

\[
\sum_{k<l} \sum_{ij} I(X_{ik} < X_{jl}) + 0.5I(X_{ik} = X_{jl}),
\]

where \(i, j\) are observations in groups \(k\) and \(l\) respectively. The asymptotic version is equivalent to `cor.test(x, g, method="k`). The exact calculation requires that there be no ties and that the sample size is less than 100. When data are tied and sample size is at most 100 permutation p-value is returned.

**References**


Terpstra, T. J. (1952). The asymptotic normality and consistency of Kendall’s test against trend, when ties are present in one ranking. *Indagationes Mathematicae* 14:327-333.

**Examples**

```r
set.seed(1234)
g <- rep(1:5, rep(10,5))
x <- rnorm(50)
jonckheere.test(x+0.3*g, g)
x[1:2] <- mean(x[1:2]) # tied data
jonckheere.test(x+0.3*g, g)
jonckheere.test(x+0.3*g, g, nperm=5000)
```
**Description**

Calculates the Kendall’s tau-b.

**Usage**

\[ \texttt{ktau(x, y)} \]

**Arguments**

- \( x \): first variable
- \( y \): second variable

**Details**

\( \texttt{ktau} \) computes the same quantity as \( \texttt{cor(x, y, method=\text{"kendall"})} \). It uses a faster algorithm than pairwise comparisons used by \( \texttt{cor} \).

**Value**

\( \texttt{ktau} \) returns Kendall’s tau-b.

**Examples**

```r
set.seed(1234)
x <- rnorm(10000); y <- x+rnorm(10000)
cor(x, y, method=\text{"k"})
clinfun::ktau(x,y)
```

---

**oc.twostage.bdry**

**Two-stage boundary operating characteristics**

**Description**

Calculates the operating characteristics of a two-stage boundary.

**Usage**

\[ \texttt{oc.twostage.bdry(pu, pa, r1, n1, r, n)} \]
**permlogrank**

**Arguments**

- `pu`: unacceptable response rate
- `pa`: response rate that is desirable
- `r1`: first stage threshold to declare treatment undesirable
- `n1`: first stage sample size
- `r`: overall threshold to declare treatment undesirable
- `n`: total sample size

**Value**

`oc.twostage.bdry` returns the type I and II error rates as well as the probability of early termination and expected sample size under `pu` for a specific boundary.

---

**permlogrank**

*Permutation version of survdiff*

**Description**

Small sample `survdiff` using permutation reference distributions.

**Usage**

```r
permlogrank(formula, data, subset, na.action, rho=0, nperm=5000)
```

**Arguments**

- `nperm`: number of permutations for the reference distribution
- `formula, data, subset, na.action, rho`
  see `survdiff` for details

**Details**

`permlogrank` is the permutation version of k-sample `survdiff`. see `survdiff` in survival package for details.

**References**

**Description**

Calculates Optimal and Minimax 2-stage Phase II designs given by Richard Simon

**Usage**

```r
ph2simon(pu, pa, ep1, ep2, nmax=100)
## S3 method for class 'ph2simon'
print(x, ...)
## S3 method for class 'ph2simon'
plot(x, ...)
```

**Arguments**

- `pu` unacceptable response rate
- `pa` response rate that is desirable
- `ep1` threshold for the probability of declaring drug desirable under p0
- `ep2` threshold for the probability of rejecting the drug under p1
- `nmax` maximum total sample size (default 100; can be at most 500)
- `x` object returned by `ph2simon`
- `...` arguments to be passed onto plot and print commands called within

**Value**

`ph2simon` returns a list with `pu`, `pa`, `alpha`, `beta` and `nmax` as above and:

- `out` matrix of best 2 stage designs for each value of total sample size n. the 6 columns are: r1, n1, r, n, EN(p0), PET(p0)

Trial is stopped early if <= r1 responses are seen in the first stage and treatment is considered desirable only when >r responses seen.

The "print" method formats and returns the minimax and optimal designs. The "plot" plots the expected sample size agains the maximum sample size as in Jung et al., 2001

**References**


**ph2single**

**See Also**

twostage.inference, oc.twostage.bdary

**Examples**

```r
ph2simon(0.2, 0.4, 0.1, 0.1)
ph2simon(0.2, 0.35, 0.05, 0.05)
ph2simon(0.2, 0.35, 0.05, 0.05, nmax=150)
```

---

**ph2single**

*Exact single stage Phase II design*

**Description**

Calculates the exact one stage Phase II design

**Usage**

```r
ph2single(pu, pa, ep1, ep2, nsoln=5)
```

**Arguments**

- `pu`: unacceptable response rate
- `pa`: response rate that is desirable
- `ep1`: threshold for the probability of declaring drug desirable under p0
- `ep2`: threshold for the probability of rejecting the drug under p1
- `nsoln`: number of designs with given alpha and beta

**Value**

`ph2single` returns a data frame with variables: n, r, and the Type I and Type II errors. Treatment desirable if >r responses seen.
power.ladesign

Power of k-sample rank test under Lehmann alternative

Description

Functions to calculate the power of rank tests for animal studies.

Usage

```r
power.ladesign(gsize, odds.ratio, sig.level = 0.05, statistic =
c("Kruskal-Wallis", "Jonckheere-Terpstra"), alternative =
c("two.sided", "one.sided"), nrep=1e+6)
```

```
## S3 method for class 'ladesign'
print(x, ...)
```

Arguments

- `gsize`: sample size of the k (= length of vector) groups.
- `odds.ratio`: odds ratio parameters for the k-1 groups. The first group is considered the control.
- `sig.level`: the significance level of the test (default = 0.05)
- `statistic`: the test statistic for the k-group comparison. Is one of Kruskal-Wallis (default) or Jonckheere-Terpstra.
- `alternative`: one- or two-sided test. Valid only for the Jonckheere-Terpstra test.
- `nrep`: number of reps (default 1 million) for Monte Carlo.
- `x`: object of class ladesign returned by power.ladesign
- `...`: arguments to be passed on left for S3 method consistency.

Details

Although the power for Jonckheere-Terpstra test is calculated for any set of odds ratio, the test is meant for monotone alternative. Thus it is preferable to specify odds ratios that are monotonically increasing with all values larger than 1 or decreasing with all values smaller than 1.

Value

returns a list with objects group.size, odds.ratio, statistic, sig.level and power. The "print" method formats the output.

References

**pselect**

### Examples

```r
c(9,7, 4, statistic="K")
c(9,7,9), c(2,4), statistic="J")
c(9,7,9), c(2,4), statistic="J", alt="o")
```

### Description

Calculates the probability of selecting the treatment with the higher response rate under the pick the winner rule.

### Usage

```r
pselect(n, p, min.diff=NULL, min.resp=NULL)
```

### Arguments

- `n` sample size for each treatment arm. This is either a single integer or a vector of two integers for the special case of comparing two treatments with unequal sample sizes.
- `p` vector of response rates for the treatments.
- `min.diff` this is the number of responses or the rate by which the best treatment should be superior to the others to be chosen. This must be a positive integer or a rate between 0 and 1. If missing it defaults to 1 for the equal sample size case but quits with a warning for the unequal sample size case.
- `min.resp` the minimum number of responses in each treatment arm for it to be considered further. If missing defaults to 0.

### Value

The function returns a list with:

- `prob.none.worthy` is the probability that no treatment has the minimum number of responses specified in `min.resp`. This element is present only if `min.resp` is greater than 0 for at least one arm.
- `prob.inconclusive` this is the probability that the best treatment has the requisite `min.resp` responses but exceeds the second best by less than `min.diff` responses (rate) provided the second best also has at least `min.resp` responses.
- `prob.selection` this is a matrix which for each treatment gives the response probability and the probability of selecting it i.e. the number of responses in the chosen arm is at least `min.resp` and either none of the remaining arms exceed the `min.resp` threshold or the chosen (best) arm is better than the second best by at least `min.diff` responses (rate).
References


Examples

# selection when no difference i.e. type I error
pselect(18, c(0.2, 0.2, 0.2))
# selection probability
pselect(18, c(0.2, 0.2, 0.4))
pselect(26, c(0.2, 0.2, 0.4), min.diff=2, min.resp=3)
# unequal sample size case
pselect(c(27,54), c(0.5, 0.65), min.diff=0.05)
# unequal sample size case
pselect(c(27,54), c(0.5, 0.65), min.diff=0.05, min.resp=c(14,27))

---

roc.area.test                Nonparametric area under the ROC curve

Description

Computes the nonparametric area under the ROC curve and its variance based on U-statistic theory (DDCP).

Usage

roc.area.test(markers, status)
## S3 method for class 'roc.area.test'
print(x, ...)

Arguments

markers    The marker values for each subject. If there are more than one markers then this should be a matrix.
status     binary disease status indicator
x          object of class roc.area.test output from this function.
...        optional arguments to the print function.

Details

It calculates the area and its variance. For more than one marker it calculates the statistic to test for the equality of all AUCs. This statistic has a standard normal reference distribution for two variables and chi-square with number of variables minus 1.
Value

a list with the following elements

area estimated area.
var estimated variance (matrix).
stat test statistic for equality of AUCs. Is not returned when only one diagnostic marker is present.
p.value the p-value for the test of equality (2-sided).
df the degrees of freedom of the chi-square.

The "print" method formats and returns the output.

References


Examples

```r
  g <- rep(0:1, 50)
  x <- rnorm(100) + g
  y <- rnorm(100) + g
  z <- rnorm(100) + g
  roc.area.test(cbind(x, y), g)
  roc.area.test(cbind(x, y, z), g)
  y1 <- y + 0.75*g
  roc.area.test(cbind(x, y1), g)
```

---

roc.curve | Empirical ROC curve

Description

Computes the empirical ROC curve for a diagnostic tool.

Usage

```r
roc.curve(marker, status, method=c("empirical"))
```

## S3 method for class 'roc.curve'

print(x, ...)

## S3 method for class 'roc.curve'

plot(x, ...)

## S3 method for class 'roc.curve'

lines(x, ...)
Arguments

- **marker**: the marker values for each subject.
- **status**: binary disease status indicator
- **method**: the method for estimating the ROC curve. Currently only the empirical curve is implemented.
- **x**: object of class roc.area.test output from this function.
- ... optional arguments to the print, plot and lines functions.

Details

The computation is based on assuming that larger values of the marker is indicative of the disease. So for a given threshold \( x_0 \), TPR is \( P(\text{marker} \geq x_0 | \text{status} = 1) \) and FPR is \( P(\text{marker} \geq x_0 | \text{status} = 0) \). This function computes the empirical estimates of TPR and FPR.

Value

A list with the following elements:

- **tpr**: true positive rates for all thresholds.
- **fpr**: true positive rates for all thresholds.
- **marker**: the diagnostic marker being studied.
- **status**: binary disease

The "print" method returns the nonparametric AUC and its s.e.

The "plot" and "lines" methods can be used to draw a new plot and add to an existing plot of ROC curve.

Examples

```r
  g <- rep(0:1, 50)
  x <- rnorm(100) + g
  y <- rnorm(100) + 1.5*g
  o <- roc.curve(x, g)
  plot(o)
  lines(roc.curve(y, g, col=2))
```

---

**roc.perm.test**

*Permutation test to compare ROC curve*

Description

Computes the test statistic and permutation reference distribution for comparing paired or unpaired ROC curves.
roc.perm.test

Usage

roc.perm.test(marker, status, marker2=NULL, group=NULL, nperm=2500, mp=NULL)
## S3 method for class 'roc.perm.test'
print(x, ...)
## S3 method for class 'roc.perm.test'
plot(x, ...)

Arguments

marker  
marker values for each subject.

status  
binary disease status indicator.

marker2  
second diagnostic marker for the same subjects (paired).

group  
indicator of which diagnostic test was used (unpaired).

nperm  
number of permutations for the reference distribution.

mp  
mixing proportion for the unpaired case when proportion of diseased subjects can differ.

x  
object of class roc.perm.test output from this function.

...  
optional arguments to print and plot functions.

Details

This function implements the permutation method described in the Venkatraman and Begg (1996) paper for the paired case and the Venkatraman (2000) paper for the unpaired case.

The function detects whether the data are paired or unpaired by testing which of the options marker2 and group is specified. If both are missing it will stop with an error message. At present exactly one should be missing.

Value

an object of class roc.perm.test with the following elements

ostat  
test statistic from the observed data.

pstat  
test statistic from permuted data.

p.value  
the p-value for the test of equality (2-sided).

The "print" method formats and returns the statistic and p-value. The "plot" method plots the density from the permutation reference distribution and marks the location of the observed statistic.

References


Examples

\[
\begin{align*}
d & \leftarrow \text{rep}(0:1, 50) \\
x & \leftarrow \text{rnorm}(100) + 1.2 \times d \\
y & \leftarrow \text{rnorm}(100) + 1.2 \times d \\
oo & \leftarrow \text{roc.perm.test}(x, d, \text{marker2}=y) \\
\text{plot}(oo) \\
oo & \leftarrow \text{roc.perm.test}(c(x,y), c(d,d), \text{group}=\text{rep}(1:2, \text{each}=100)) \\
\text{plot}(oo)
\end{align*}
\]

RCanalysis

*Functions to plot and compare ROC curves.*

Description

These functions can be used for nonparametric analysis of ROC curves.

Details

The relevant functions are `roc.curve`, `roc.area.test` and `roc.perm.test`. See the individual functions for usage details.

toxbdry

*Stopping rule for toxicity monitoring*

Description

Computes a stopping rule and its operating characteristics for toxicity monitoring based repeated significance testing.

Usage

\[
\text{toxbdry}(\text{pLo}, \text{pHi}, n, \text{cP0}=0.1, \text{cP1}=0.9, \text{ngrid}=6, \text{niter}=10, \text{delta}=0, \\
\text{priority}=c(\text{"null","alt"})) \\
\text{bdrycross.prob}(n, r, \text{ptoxt}) \\
\text{## S3 method for class 'toxbdry'} \\
\text{print}(x, ...) \\
\]

Arguments

- `pLo`: the toxicity rate that is acceptable.
- `pHi`: the toxicity rate that is too high and hence unacceptable.
- `n`: vector of times (sample size) when toxicity is monitored.
- `r`: vector of maximum acceptable toxicities corresponding to `n`.
- `ptoxt`: the toxicity rates for which the operating characteristics are calculated.
boundary crossing probability under pLo i.e. type I error or the probability of declaring a treatment with toxicity rate pLo unacceptable.

boundary crossing probability under pHi i.e. power or the probability of declaring a treatment with toxicity rate pHi unacceptable.

the number of toxicity rates from pLo to pHi for which the operating characteristics are computed.

the number of iterations run to obtain the boundary.

power determining the shape of the boundary. Should be between 0 (default) and 0.5.

the error threshold to prioritize when the max sample size is too small to have both error thresholds satisfied. Default is the null i.e. error under pLo.

object returned by the function toxbdry.

additional arguments to print.

Default value of boundary shape corresponds to the Pocock boundary where the same significance level is used for all looks. For a more conservative stopping rule use delta greater than 0 where 0.5 corresponds to the O’Brien-Fleming boundary which is extremely conservative in the early looks. Value between 0.1 and 0.2 is a reasonable compromise.

The exact calculations in this function are done along the lines of the method in Chapter 12 of Jennison and Turnbull (2000). Ivanova, Qaqish and Schell (2005) have an illustrative paper.

the function returns a list with:

- lower boundary is a vector of maximum acceptable number of toxicities corresponding the number of subjects in n. The boundary crossing probability for this is slightly above cP0.
- upper boundary is a vector of maximum acceptable number of toxicities corresponding the number of subjects in n. The boundary crossing probability for this is slightly below cP0.
- the operating characteristics i.e the toxicity rate, the probability of crossing, stopping (i.e. cross before the last observation) and the expected sample size for both the low (lo) and high (hi) boundaries.
- the alpha levels for testing at each look for the two boundaries.

stopping for toxicity is done when the number of toxicities exceeda the boundary i.e. the boundary gives the maximum acceptable number.


twostage.inference

Inference following a two-stage design for binary response

Description

Calculates the p-value, UMVUE and CI for the data from a study using a two stage design for response.

Usage

```
twostage.inference(x, r1, n1, n, pu, alpha=0.05)
```

Arguments

- `x`: number of responses observed at the end of the study
- `r1`: first stage threshold to declare treatment undesirable
- `n1`: first stage sample size
- `n`: total sample size
- `pu`: unacceptable response rate (null hypothesis)
- `alpha`: the confidence level. For consistency with the design use the same value from the design. (default is 0.05)

Value

twostage.inference returns the UMVUE (Jung & Kim, 2004), p-value and CI (Koyama & Chen, 2008). The CI has confidence level 1-2*alpha and the one-sided (1-alpha) interval consistent with the design is obtained by changing the upper confidence limit (UCL) to 1.

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