Package 'mdir.logrank'

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Type Package
Title Multiple-Direction Logrank Test
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Depends R (>= 3.4.0)
Description Implemented are the one-sided and two-sided multiple-direction logrank test for two-sample right censored data. In addition to the statistics p-values are calculated: 1. For the one-sided testing problem one p-value based on a wild bootstrap approach is determined. 2. In the two-sided case one p-value based on a chi-squared approximation and a second p-values based on a permutation approach are calculated.
License GPL-2 | GPL-3
Imports stats, MASS (>= 7.3-47)
LazyData TRUE
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calculateGUI

A graphical user interface for the package mdir.logrank

Description

This function provides a graphical user interface for calculating multiple-direction logrank test for the two-sided and the one-sided testing problem.

Usage

calculateGUI()

mdir.logrank

Two-sample multiple-direction log rank test

Description

The mdir.logrank function calculates the multiple-direction logrank statistic and its corresponding p-values based on a $\chi^2$-approximation and a permutation approach

Usage

mdir.logrank(data, cross = TRUE, rg = list(c(0, 0)), nperm = 10000, dig_p = 3, dig_stat = 3)

Arguments

data A data.frame, list or environment containing the variables time, event (with values 0 for censored and 1 for uncensored) and group.
cross logical. Should the weight corresponding to crossing hazards be included? The default is TRUE.
rg A list (or NULL) containing the exponents c(r, g) of the directions $w(x) = x^r(1 - x)^g$. Both exponents r,g need to be natural numbers including 0. Default is list(c(0, 0)) corresponding to proportional hazards.
nperm The number of permutations used for calculating the permuted p-value. The default option is 10000.
dig_p The p-values are rounded to dig_p digits, the default is 3.
dig_stat The test statistic is rounded to dig_stat digits, the default is 3.
The package provides the multiple-direction logrank statistic for the two sample testing problem within right-censored survival data. Directions of the form $w(x) = 1 - 2x$ (cross = TRUE) and $w(x) = x^r \cdot (1-x)^g$ for natural numbers $r,g$ (including 0) can be specified. The multiple-direction logrank test needs linearly independent directions. A check for this is implemented. If the directions chosen by the user are linearly dependent then a subset consisting of linearly independent directions is selected automatically.

The `mdir.logrank` function returns the test statistic as well as two corresponding p-values: the first is based on a $\chi^2$ approximation and the second one is based on a permutation procedure.

### Value

An `mdirLR` object containing the following components:

- **Descriptive**
  - The directions used and whether the directions specified by the user were linearly independent.
- **p.values**
  - The p-values of the multiple-direction logrank test using the $\chi^2$-approximation (Approx.) as well as the one using the permutation approach (Perm.).
- **stat**
  - Value of the multiple-direction logrank statistic.
- **rg**
  - A list containing the exponents of the direction considered in the statistical analysis.
- **cross**
  - logical. Was the crossing direction considered in the statistical analysis?
- **indep**
  - logical. Were the directions specified by the user linearly independent?
- **nperm**
  - The number of permutations used for calculating the permuted p-value.

### References


### See Also

- `mdir.onesided` (one-sided test)

### Examples

```r
library(coin)
data(GTSG)
out <- mdir.logrank(data = GTSG, nperm = 1000)

## Detailed information:
summary(out)
```
mdir.onesided

Two-sample multiple-direction log rank test for stochastic ordered alternatives

Description

The mdir.onesided function calculates the multiple-direction logrank statistic for (one-sided) stochastic ordered alternatives and its p-value based on a wild bootstrap approach.

Usage

mdir.onesided(data, group1, rg = list(c(0, 0), c(0, 4), c(4, 0)),
    w.user = NA, wild = "rade", iter = 10000, dig_p = 3,
    dig_stat = 3)

Arguments

data A data.frame, list or environment containing the variables time, event (with values 0 for censored and 1 for uncensored) and group.
group1 The name or the coding for the first group in the data set (necessary for a one-sided testing problem).
rg A list containing the exponents \( c(r, g) \) of the directions \( w(x) = x^r(1-x)^g \) or NA. Both exponents r,g need to be natural numbers including 0. Default is list(c(0, 0), c(0, 4), c(4, 0)) corresponding to the choice of the proportional, early and late direction/weight.
w.user A list containing the user specified functions or NA (default).
wild The wild bootstrap approach used for estimating the p-value. The Rademacher (rade, default), the normal distribution (norm) or the centred Poisson distribution (pois) approach can be selected.
iter The number of iteration used for calculating the wild bootstrap p-value. The default option is 10000.
dig_p The p-values are rounded to dig_p digits, the default is 3.
dig_stat The test statistic is rounded to dig_stat digits, the default is 3.

Details

The function provides the multiple-direction logrank statistic for the two sample one-sided testing problem of stochastic ordering within right-censored survival data. The null hypothesis \( H : F_1 = F_2 \) is tested against the one-sided alternative \( K : F_1 \geq F_2, F_1 \neq F_2 \). The first group corresponding to \( F_1 \) can be specified by the argument group1. An arbitrary amount of directions/weights of the form \( w(x) = x^r(1-x)^g \) for natural numbers r,g (including 0) can be chosen in the list rg. The multiple-direction onesided logrank test needs linearly independent directions. A check for this is implemented. If the directions chosen by the user are linearly dependent then a subset consisting of linearly independent directions is selected automatically. The user can also specify weights of a
The `mdir.onesided` function returns the test statistic and the p-value based on a wild bootstrap procedure `wild`.

**Value**

An `mdirone` object containing the following components:

- **Descriptive**
  - `The directions used and whether the directions specified by the user were linearly independent.`
  - `p.value`:
    - The p-value of the one-sided multiple-direction logrank test using the permutation approach (Perm.).
  - `wild`:
    - The wild bootstrap approach which was used.
  - `stat`:
    - Value of the one-sided multiple-direction logrank statistic.
  - `rg`:
    - The argument `rg`.
  - `w.user`:
    - The argument `w.user`.
  - `group1`:
    - The name of the first group.
  - `indep`:
    - Logical or NA. `indep=TRUE/FALSE` when the directions specified by `rg` were linearly independent. `indep=NA` when `rg=NA`.
  - `iter`:
    - The number of iterations used for calculating the wild bootstrap p-value.

**References**


**See Also**

`mdir.onesided`

**Examples**

```r
library(coin)
data(GTSG)
out <- mdir.onesided(data = GTSG, group1 = "Chemotherapy+Radiation", iter = 1000)

## Detailed information:
summary(out)
```
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