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.
Ditzhaus, M. and Friedrich, S. (2018) <doi:10.48550/arXiv.1807.05504>.
Ditzhaus, M. and Pauly, M. (2018) <doi:10.48550/arXiv.1808.05627>.

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Imports stats, MASS (>= 7.3-47)

LazyData TRUE

BugReports `http://github.com/marcdii/mdir.logrank/issues`

Suggests RGtk2 (>= 2.20.34), coin

RoxygenNote 6.1.0

NeedsCompilation no

Repository CRAN

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Contents

`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 χ^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.

Details

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 $w(x) = x^r * (1-x)^g$ 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 χ^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

Ditzhaus, M., Friedrich, S. (2018). More powerful logrank permutation tests for two-sample survival data. arXiv preprint arXiv:1807.05504.

See Also

`mdir.onesided` (one-sided test)

Examples

```
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 (neceassary 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 different shape in the list `w.user`. But if the user specified own weights in `w.user` then there is no automatic check for linear independence.

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 the 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

Ditzhaus, M., Pauly, M. (2018). Wild bootstrap logrank tests with broader power functions for testing superiority. arXiv preprint arXiv:arXiv:1808.05627.

See Also

`mdir.onesided`

Examples

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

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

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