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) <arXiv:1807.05504>.
Ditzhaus, M. and Pauly, M. (2018) <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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R topics documented:

| 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)
```

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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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