Package ‘mdir.logrank’

September 29, 2018

Type Package
Title Multiple-Direction Logrank Test
Version 0.0.4
Date 2018-09-28
Author Marc Ditzhaus and Sarah Friedrich
Maintainer Sarah Friedrich <sarah.friedrich@alumni.uni-ulm.de>
Depends R (>= 3.4.0)
License GPL-2 | GPL-3
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
Date/Publication 2018-09-29 15:30:02 UTC

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<td>A graphical user interface for the package <code>mdir.logrank</code></td>
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**Description**

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

**Usage**

```r
calculateGUI()
```

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**mdir.logrank**

**Two-sample multiple-direction log rank test**

**Description**

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

**Usage**

```r
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.
**mdir.logrank**

**Details**

The package provides the multiple-direction logrank statistic for the two sample testing problem within right-censored survival data. Directions of the form \( w(x) = 1 - 2x \) (\( \text{cross} = \text{TRUE} \)) 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:

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<thead>
<tr>
<th>Field</th>
<th>Description</th>
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<tr>
<td>descriptive</td>
<td>The directions used and whether the directions specified by the user were linearly independent.</td>
</tr>
<tr>
<td>p.values</td>
<td>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.).</td>
</tr>
<tr>
<td>stat</td>
<td>Value of the multiple-direction logrank statistic.</td>
</tr>
<tr>
<td>rg</td>
<td>A list containing the exponents of the direction considered in the statistical analysis.</td>
</tr>
<tr>
<td>cross</td>
<td>logical. Was the crossing direction considered in the statistical analysis?</td>
</tr>
<tr>
<td>indep</td>
<td>logical. Were the directions specified by the user linearly independent?</td>
</tr>
<tr>
<td>nperm</td>
<td>The number of permutations used for calculating the permuted p-value.</td>
</tr>
</tbody>
</table>

**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
different shape in the list \texttt{w.user}. But if the user specified own weights in \texttt{w.user} then there is no automatic check for linear independence.

The \texttt{mdir.onesided} function returns the test statistic and the p-value based on a wild bootstrap procedure \texttt{wild}.

\textbf{Value}

An \texttt{mdirone} object containing the following components:

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

\textbf{References}


\textbf{See Also}

\texttt{mdir.onesided}

\textbf{Examples}

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

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