Package ‘MultSurvTests’

June 18, 2021

Title     Permutation Tests for Multivariate Survival Analysis
Version  0.2
Description Multivariate version of the two-sample Gehan and logrank tests, as de-
Encoding UTF-8
LazyData true
RoxygenNote 7.1.1
Imports Rcpp (>= 0.12.9), Rdpack
LinkingTo Rcpp, RcppArmadillo
RdMacros Rdpack
URL https://github.com/lukketotte/MultSurvTests
BugReports https://github.com/lukketotte/MultSurvTests/issues
Depends R (>= 2.10)
License MIT + file LICENSE
NeedsCompilation yes
Author Lukas Arnroth [aut, cre],
          Måns Thulin [aut]
Maintainer Lukas Arnroth <lukas.arnroth@gmail.com>
Repository CRAN
Date/Publication 2021-06-18 07:50:02 UTC

R topics documented:

choose_B ................................................................. 2
diabetes ................................................................. 3
gehan ................................................................. 3
mvlogrank .............................................................. 4
perm_gehan ............................................................ 5
perm_mvlogrank ....................................................... 6
wltestdata ............................................................... 7

choose_B

Description

Computes the value of B for a permutation test required to obtain a specified accuracy when approximating the permutation p-values using B random permutations.

Usage

choose_B(p0 = 0.05, width = 0.01, conf.level = 0.95)

Arguments

- **p0**: A guess for the p-value. Can be based e.g. on a small number of simulations. The default is 0.05.
- **width**: The desired width of the Clopper-Pearson interval. The default is 0.01.
- **conf.level**: The confidence level of the Clopper-Pearson interval. The default is 0.95.

Details

Computations are based on the Clopper-Pearson interval, using a formula from Thulin (2014). The procedure is described in Section 3.3 in Persson et al. (2019).

Value

B

References


Examples

# B required to achieve an expected width of 0.02 when
# the p-value is approximately 0.1:
choose_B(p0 = 0.1, width = 0.02)
**Diabetes Data**

**Description**

Diabetic retinopathy: how strongly are times to blindness of a treated and an untreated eye correlated in patients suffering from diabetic retinopathy? The analysis is based on a sample of n=197 paired failure times (censoring 73% and 49% for the treated and untreated eyes, respectively) described by Huster, Brookmeyer, and Self (1989). Both eyes of an individual are observed for the same time, and therefore dots on the diagonal generally indicate pairs of censored times.

**Usage**

diabetes

**Format**

A data.frame containing 197 rows.

**Source**

https://www.mayo.edu/research/documents/diabeteshtml/DOC-10027460/

**References**


---

**Gehan test**

**Description**

Computes the multivariate Gehan test statistic.

**Usage**

gehan(x, y, delta_x, delta_y, n1, n2, p, k = 1L, l = 1L)
Arguments

\(x\) Matrix
\(y\) Matrix
\(\text{delta}_x\) Matrix
\(\text{delta}_y\) Matrix
\(n_1\) Integer. Set as the number of rows in \(x\)
\(n_2\) Integer. Set as the number of rows in \(y\)
\(p\) Integer. Set as the number of columns in \(x\) and \(y\)
\(k\) Integer.
\(l\) Integer.

Value

1x1 matrix containing a numeric

---

**mvlogrank**  
*Mvlogrank test*

**Description**

Computes the multivariate logrank test statistic.

**Usage**

\[ \text{mvlogrank}(x, y, \text{delta}_x, \text{delta}_y, n_1, n_2, p, k = 1L, l = 1L) \]

**Arguments**

\(x\) Matrix
\(y\) Matrix
\(\text{delta}_x\) Matrix
\(\text{delta}_y\) Matrix
\(n_1\) Integer. Set as the number of rows in \(x\)
\(n_2\) Integer. Set as the number of rows in \(y\)
\(p\) Integer. Set as the number of columns in \(x\) and \(y\)
\(k\) Integer.
\(l\) Integer.

**Value**

1x1 matrix containing a numeric
**perm_gehan**  
*Multivariate permutation Gehan test*

**Description**

Computes the p-value of the multivariate permutation Gehan test described in Persson et al. (2019).

**Usage**

```r
perm_gehan(B = 999, z, delta.z, n1)
```

**Arguments**

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>B</td>
<td>An integer specifying the number of permutations to perform. The default is 999. It is recommended to use <code>choose_B</code> for choosing B.</td>
</tr>
<tr>
<td>z</td>
<td>A matrix containing the observed (possibly censored) survival times for the two groups. The observations for the first group should be one the first n1 rows.</td>
</tr>
<tr>
<td>delta.z</td>
<td>A matrix containing the censoring status of each observation in z.</td>
</tr>
<tr>
<td>n1</td>
<td>An integer specifying the sample size of the first group.</td>
</tr>
</tbody>
</table>

**Details**

Multivariate version of the logrank and Gehan tests were described by Wei & Lachin (1984). Persson et al. (2019) described permutation versions of these tests, with improved performance.

**Value**

A p-value.

**References**


**Examples**

```r
# Diabetes data:
?diabetes
# Survival times for the two groups:
x <- as.matrix(subset(diabetes, LASER==1)[c(6,8)])
y <- as.matrix(subset(diabetes, LASER==2)[c(6,8)])
# Censoring status for the two groups:
delta.x <- as.matrix(subset(diabetes, LASER==1)[c(7,9)])
```
```
delta.y <- as.matrix(subset(diabetes, LASER==2)[c(7,9)])
# Create the input for the test:
z <- rbind(x, y)
delta.z <- rbind(delta.x, delta.y)
# Run the test with 50 permutations:
perm_gehan(B = 50, z, delta.z, n1 = nrow(x))
# In most cases, it is preferable to use more than 50
# permutations for computing p-values. choose_B() can
# be used to determine how many permutations are needed.
```

---

## perm_mvlogrank

### Multivariate permutation logrank test

**Description**

Computes the p-value of the multivariate permutation logrank test described in Persson et al. (2019).

**Usage**

```
perm_mvlogrank(B, z, delta.z, n1)
```

**Arguments**

- `B`: An integer specifying the number of permutations to perform. The default is 999. It is recommended to use `choose_B` for choosing `B`.
- `z`: A matrix containing the observed (possibly censored) survival times for the two groups. The observations for the first group should be one the first `n1` rows.
- `delta.z`: A matrix containing the censoring status of each observation in `z`.
- `n1`: An integer specifying the sample size of the first group.

**Details**

Multivariate version of the logrank and Gehan tests were described by Wei & Lachin (1984). Persson et al. (2019) described permutation versions of these tests, with improved performance.

**Value**

A p-value.

**References**


Examples

# Diabetes data:
?diabetes

# Survival times for the two groups:
x <- as.matrix(subset(diabetes, LASER==1)[c(6,8)])
y <- as.matrix(subset(diabetes, LASER==2)[c(6,8)])

# Censoring status for the two groups:
delta.x <- as.matrix(subset(diabetes, LASER==1)[c(7,9)])
delta.y <- as.matrix(subset(diabetes, LASER==2)[c(7,9)])

# Create the input for the test:
z <- rbind(x, y)
delta.z <- rbind(delta.x, delta.y)

# Run the test with 50 permutations:
perm_mvlogrank(B = 50, z, delta.z, n1 = nrow(x))

# In most cases, it is preferable to use more than 50
# permutations for computing p-values. choose_B() can
# be used to determine how many permutations are needed.

-------------------------

wltestdata

Data randomly generated.

-------------------------

Description

Data randomly generated.

Usage

wltestdata

Format

A dataframe containing 47 rows and 9 columns

V1:V9 Randomly generated integers
Index

* datasets
  diabetes, 3
  wltestdata, 7

choose_B, 2, 5, 6

diabetes, 3

gehan, 3

mvlogrank, 4

perm_gehan, 5

perm_mvlogrank, 6

wltestdata, 7