Package: MultSurvTests (via r-universe)

October 21, 2024

Title Permutation Tests for Multivariate Survival Analysis

Version 0.2

Description Multivariate version of the two-sample Gehan and logrank tests, as described in L.J Wei & J.M Lachin (1984) and Persson et al. (2019).

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)

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NeedsCompilation yes

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Repository CRAN

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Contents

`choose_B` *Choose B for permutation tests*

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

Persson I, Arnroth L, Thulin M (2019). “Multivariate two sample permutation tests for trials with multiple time to event outcomes.” *Pharmaceutical Statistics*, **18**, 476–485. doi: 10.1002/pst.1938, `https://doi.org/10.1002/pst.1938`.

Thulin M (2014). “The cost of using exact confidence intervals for a binomial proportion.” *Electronic Journal of Statistics*, **8(1)**, 817–840. doi: 10.1214/14EJS909, `https://doi.org/10.1214/14-EJS909`.

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` *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

Huster WJ, Brookmeyer R, Self SG (1989). “Modelling paired survival data with covariates.” *Biometrics*, **45**, 145–156. doi: 10.2307/2532041, `https://doi.org/10.2307/2532041`.

`gehan` *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
`delta_x`	Matrix
`delta_y`	Matrix
`n1`	Integer. Set as the number of rows in x
`n2`	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

```
mvlogrank(x, y, delta_x, delta_y, n1, n2, p, k = 1L, l = 1L)
```

Arguments

`x`	Matrix
`y`	Matrix
`delta_x`	Matrix
`delta_y`	Matrix
`n1`	Integer. Set as the number of rows in x
`n2`	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

```
perm_gehan(B = 999, 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

Persson I, Arnroth L, Thulin M (2019). “Multivariate two sample permutation tests for trials with multiple time to event outcomes.” *Pharmaceutical Statistics*, **18**, 476–485. doi: 10.1002/pst.1938, `https://doi.org/10.1002/pst.1938`.

Wei LJ, Lachin JM (1984). “Two sample asymptotically distribution free tests for incomplete multivariate observations.” *Journal of the American Statistical Association*, **79(387)**, 653–661. doi: 10.1080/01621459.1984.10478093, `https://doi.org/10.1080/01621459.1984.10478093`.

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_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

Persson I, Arnroth L, Thulin M (2019). “Multivariate two sample permutation tests for trials with multiple time to event outcomes.” *Pharmaceutical Statistics*, **18**, 476–485. doi: 10.1002/pst.1938, `https://doi.org/10.1002/pst.1938`.

Wei LJ, Lachin JM (1984). “Two sample asymptotically distribution free tests for incomplete multivariate observations.” *Journal of the American Statistical Association*, **79(387)**, 653–661. doi: 10.1080/01621459.1984.10478093, `https://doi.org/10.1080/01621459.1984.10478093`.

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

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