Package: sGBJ (via r-universe)

September 2, 2024

Type Package

Title Survival Extension of the Generalized Berk-Jones Test

Version 0.1.0

Description Implements an extension of the Generalized Berk-Jones (GBJ) statistic for survival data, sGBJ. It computes the sGBJ statistic and its p-value for testing the association between a gene set and a time-to-event outcome with possible adjustment on additional covariates. Detailed method is available at Villain L, Ferte T, Thiebaut R and Hejblum BP (2021) <doi:10.1101/2021.09.07.459329>.

License GPL (>= 3)

Depends R (>= 3.5.0)

Imports GBJ, stats, survival

Suggests testthat (>= 3.0.0)

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Encoding UTF-8

LazyData true

RoxygenNote 7.1.2

URL `https://github.com/lauravillain/sGBJ`

BugReports `https://github.com/lauravillain/sGBJ/issues`

Repository https://lauravillain.r-universe.dev

RemoteUrl https://github.com/lauravillain/sgbj

RemoteRef HEAD

RemoteSha 176c792bc1b4dccc1b3192732c1061a1ac582998

Contents

`.epsilon_matrix` *.epsilon_matrix*

Description

Compute the epsilon matrix by permutation for the `sGBJ_scores()` function.

Usage

```
.epsilon_matrix(Z, nperm, surv, factor_matrix, covariates = NULL, dat)
```

Arguments

`Z`	the score vector returned by `.survival_scores()` function.
`nperm`	number of permutations performed to estimate the `epsilon` matrix. Default is `300`.
`surv`	a `Surv` object of length `n`
`factor_matrix`	a `n x p` `data.frame` of the expression for the particular gene set of interest being tested
`covariates`	a `n x l` matrix of the covariates to adjust upon. Default is `NULL`
`dat`	data used to fit survival model returned by `.survival_scores()` function.

Value

The epsilon matrix.

`.survival_scores` *.survival_scores*

Description

Compute the survival score

Usage

```
.survival_scores(factor_matrix, covariates = NULL, surv)
```

Arguments

`factor_matrix` a `n x p` `data.frame` of the expression for the particular gene set of interest being tested

`covariates` a matrix nxl of the covariates to adjust. Default is `NULL`

`surv` a `Surv` object of length `n`

Value

A list of length 3 with the updated factor_matrix (same as factor_matrix but removing columns for which survival model failed to converge), the Z matrix and the data used to fit survival model.

`ls_test_results` *A data file used for testing sGBJ*

Description

A data file used for testing sGBJ

`sGBJ` *Compute the sGBJ statistic and its p-value quantifying a gene set expression association with survival*

Description

This function is the main function of the sGBJ package to perform Gene Set Analysis in the context of time-to-event outcome.

Usage

```
sGBJ(surv, factor_matrix, covariates = NULL, nperm = 300)
```

Arguments

`surv` a `Surv` object of length `n`

`factor_matrix` a `n x p` `data.frame` of the expression for the particular gene set of interest being tested

`covariates` a `n x l` matrix of the covariates to adjust upon. Default is `NULL`

`nperm` number of permutations performed to estimate the `epsilon` matrix. Default is `300`.

Value

The sGBJ statistic and its associated p-value associated

Examples

```
n <- 100
surv_data <- data.frame(Time = runif(n = n, min = 0, max = 100),
                        event = rbinom(n = n, size = 1, prob = 0.5))
surv <- survival::Surv(time = surv_data$Time, event = surv_data$event)

factor_matrix <- data.frame(P1 = rnorm(n = n),
                            P2 = rnorm(n = n))

sGBJ::sGBJ(surv,factor_matrix, nperm = 2)
```

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sGBJ_scores *Compute the sGBJ statistic along with its p-value quantifying the association between a gene set and survival outcome*

Description

Compute the sGBJ statistic along with its p-value quantifying the association between a gene set and survival outcome

Usage

```
sGBJ_scores(surv, factor_matrix, covariates = NULL, nperm = 300)
```

Arguments

surv	a Surv object of length n
factor_matrix	a n x p data.frame of the expression for the particular gene set of interest being tested
covariates	a n x l matrix of the covariates to adjust upon. Default is NULL
nperm	number of permutations performed to estimate the epsilon matrix. Default is 300.

Value

a list containing the sGBJ statistic estimation and its associated p-value

Examples

```
n <- 100
surv_data <- data.frame(Time = runif(n = n, min = 0, max = 100),
                        event = rbinom(n = n, size = 1, prob = 0.5))
surv <- survival::Surv(time = surv_data$Time, event = surv_data$event)

factor_matrix <- data.frame(P1 = rnorm(n = n),
                            P2 = rnorm(n = n))
```

```
sGBJ::sGBJ_scores(surv,factor_matrix, nperm = 2)

# with covariates

covariates <- data.frame(age = runif(n = n, 60, 90))

sGBJ_scores(surv,factor_matrix, nperm = 2, covariates = covariates)
```

surv_calc_scores_stats

surv_calc_scores_stats

Description

An adaptation of `GBJ::calc_scores_stats()` to survival context. Wrapper of sGBJ_scores() function.

Usage

```
surv_calc_scores_stats(null_model, factor_matrix, nperm = 300)
```

Arguments

`null_model`	An R cox model fitted with `survival::coxph()`.
`factor_matrix`	An `n x p` matrix with each factor as one column. There should be no missing data.
`nperm`	Number of permutations (default is 300)

Value

A list with the elements:

`test_stats`	The `p` score test statistics.
`cor_mat`	The `p x p` matrix giving the pairwise correlation of every test statistic pairs.

Examples

```
n <- 100
surv_data <- data.frame(Time = runif(n = n, min = 0, max = 100),
                        event = rbinom(n = n, size = 1, prob = 0.5))
surv <- survival::Surv(time = surv_data$Time, event = surv_data$event)

factor_matrix <- data.frame(P1 = rnorm(n = n),
                             P2 = rnorm(n = n))

covariates <- data.frame(age = runif(n = n, 60, 90))

null_model <- survival::coxph(surv ~ age, data = covariates, x = TRUE)
```

```
surv_reg_stats <- surv_calc_scores_stats(null_model = null_model,
                                          factor_matrix = factor_matrix,
                                          nperm = 2)#nperm = 300)

GBJ::GBJ(test_stats=surv_reg_stats$test_stats, cor_mat=surv_reg_stats$cor_mat)
```

Index