# Package 'Coxwast'

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**Type** Package

**Title** Subgroup testing methods for change-plane Cox models

**Version** 1.0.1

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**Description** Weighted-sum-based subgroup testing method is proposed for change-plane Cox models. Different testing methods are also provided in this package.

**License** GPL (>= 2)

**Imports** survival, simsurv, boot, mvtnorm, parallel

**Depends** R (>= 3.2.0)

**LazyData** true

**NeedsCompilation** yes

**Repository** github

**URL** https://github.com/PanpanRen/Coxwast

**Encoding** UTF-8

**Roxygen** list(markdown = TRUE)

**RoxygenNote** 7.1.1

## R topics documented:

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gam.init                    *Function to select initial gamma values spanning its space*

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## Usage

```
gam.init(n.initials, Z, lb.quantile, ub.quantile, ss=1)
```

## Arguments

| | |
|---|---|
| n.initials | Number of gamma values. |
| Z | The grouping variables. |
| lb.quantile | The lower quantile specified for Z%*%gamma.initials. |
| ub.quantile | The upper quantile specified for Z%*%gamma.initials. |
| ss | A positive integer with n.initials/ss indicating how many sets of gamma are chosen, default to 1. |

## Value

A matrix. A set of gamma values selected for defining subgroup.

## Examples

```
n = 100
p1 = 2
p2 = 1
p3 = 3
alpha = rep(1, p1)
beta  = rep(1, p2)/2
gamma = c(1, seq(-1,1,length.out = p3-1))
rho = 0.3
cenRate = 0.2
set.seed(100)
data = generate_cox_data(n, alpha, beta, gamma, rho, cenRate = cenRate)
K = 1000
qlb = 0.1
cols = apply(data$u, 2, var) != 0
Gamma = gam.init(K, data$u[,cols], lb.quantile=qlb, ub.quantile=1-qlb, ss=1)
```

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generate_cox_data           *Function for generating data from Cox proportional hazard model with a change plane.*

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## Usage

```
generate_cox_data(n, alpha, beta, gamma, rho,
            cenRate = 0.1, censortype = c("RightCensor", "RandomCensor"))
```

## Arguments

| | |
|---|---|
| n | A constant. The sample size. |
| alpha | A vector. The true parameter for baseline covariates. |
| beta | A vector. The true parameter denoting the heterogeneous effect of the subgroup. |
| gamma | A vector. The true parameter for grouping variables. |
| rho | The strength of correlation among covariates. |
| cenRate | A constant. Censoring rate. Default is 0.1. |
| censortype | Censroing type, including "RightCensor" and "RandomCensor". |

## Value

A list.

- y - A length $n$ vector. The survival time.
- x - A matrix. The baseline covariates.
- z - A matrix. The baseline covariates.
- u - A matrix. The grouping variables.
- status - A length $n$ vector. Censoring indicator.

## Examples

```
n = 100
p1 = 2
p2 = 1
p3 = 3
alpha = rep(1, p1)
beta  = rep(1, p2)/2
gamma = c(1, seq(-1,1,length.out = p3-1))
rho = 0.3
cenRate = 0.2
set.seed(100)
data = generate_cox_data(n, alpha, beta, gamma, rho, cenRate = cenRate)
```

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| ST | *The score testing method for change-plane Cox models similar in Kang et al.(2017).* |
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## Usage

```
ST(data, Gamma, B = 1000, K = 1000, qlb = 0.1, tol = 1e-8)
```

## Arguments

| | |
|---|---|
| data | A list, including $y$ (time response), $x$ (predictors), $z$ (predictors), $u$ (grouping variables), status (censoring indicator). |
| Gamma | A matrix for initial gamma values. If not given then it will be automatically generated based on the data. |
| B | A constant. Number of bootstrap samples. Default is 1000. |

| K | A constant. The number of the initial gamma values. Default is 1000. |
|---|---|
| qlb | A constant. The lower quantile specified for Z%*%gamma.initials. Default is 0.1. |
| tol | A constant. The precision of the Newton method. Default is `1e-8`. |

## Value

A list.

- TestR - The value of test statistic.
- TestB - B values of test statistic obtained from the bootstrap.
- Pvalue - The p-value of the test.
- time - Running time.

## References

Kang, S., Lu, W., and Song, R. (2017). Subgroup detection and sample size calculation with proportional hazards regression for survival data. Statistics in medicine, 36(29), 4646-4659.

## Examples

```
n = 100
p1 = 2
p2 = 1
p3 = 3
alpha = rep(1, p1)
beta  = rep(1, p2)/2
gamma = c(1, seq(-1,1,length.out = p3-1))
rho = 0.3
cenRate = 0.2
set.seed(100)
data = generate_cox_data(n, alpha, beta, gamma, rho, cenRate = cenRate)
fit <- ST(data)
fit$Pvalue
```

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| SUP | *The SUP testing method for change-plane Cox models in Deng et al.(2022).* |
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## Usage

```
SUP(data, Gamma, B = 1000, K = 1000, qlb = 0.1, tol = 1e-8)
```

## Arguments

| data | A list, including $y$ (time response), $x$ (predictors), $z$ (predictors), $u$ (change-plane variables), status (censoring indicator). |
|---|---|
| Gamma | A matrix for initial gamma values. If not given then it will be automatically generated based on the data. |
| B | A constant. Number of bootstrap samples. Default is 1000. |
| K | A constant. The number of the initial gamma values. Default is 1000. |

| qlb | A constant. The lower quantile specified for Z%*%gamma.initials. Default is 0.1. |
|---|---|
| tol | A constant. The precision of the Newton method. Default is `1e-8`. |

## Value

A list.

- TestR - The value of test statistic.
- TestB - B values of test statistic obtained from the bootstrap.
- Pvalue - The p-value of the test.
- time - Running time.

## References

Deng, Y., Cai, J., and Zeng, D. (2022). Maximum Likelihood Estimation for Cox Proportional Hazards Model with a Change Hyperplane. Statistica Sinica, 32(2), 983.

## Examples

```
n = 100
p1 = 2
p2 = 1
p3 = 3
alpha = rep(1, p1)
beta  = rep(1, p2)/2
gamma = c(1, seq(-1,1,length.out = p3-1))
rho = 0.3
cenRate = 0.2
set.seed(100)
data = generate_cox_data(n, alpha, beta, gamma, rho, cenRate = cenRate)
fit <- SUP(data)
fit$Pvalue
```

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| WAST | *The weighted-sum-based subgrouping testing method for change-plane Cox models.* |
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## Usage

```
WAST(data, B = 1000, CoreNum = 4, par = TRUE)
```

## Arguments

| data | A list, including $y$ (time response), $x$ (predictors), $z$ (predictors), $u$ (change-plane variables), status (censoring indicator). |
|---|---|
| B | A constant. Number of bootstrap samples. Default is 1000. |
| CoreNum | A constant. Number of processes to be used in parallel operation. Default is 4. |
| par | A logical value. Whether to conduct the parallel operation. Default is TRUE. |

**Value**

A list.

- alpha_hat - The estimator of alpha under the null hypothesis.
- test_statistic - The value of test statistic.
- test_statistic_boot - B values of test statistic obtained from the bootstrap.
- pval - The p-value of the test.
- time - Running time.

**Examples**

```
n = 100
p1 = 2
p2 = 1
p3 = 3
alpha = rep(1, p1)
beta  = rep(1, p2)/2
gamma = c(1, seq(-1,1,length.out = p3-1))
rho = 0.3
cenRate = 0.2
set.seed(100)
data = generate_cox_data(n, alpha, beta, gamma, rho, cenRate = cenRate)
fit <- WAST(data)
fit$pval
```

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