Package ‘SurvivalTests’

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Type Package

Title Survival Tests for One-Way Layout

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Depends R (>= 3.2.0), weibullness

Imports stats, ggplot2

Suggests survival, arules

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Description Performs survival analysis for one-way layout. The package includes the generalized test for survival ANOVA (Tsui and Weerahandi (1989) <doi:10.2307/2289949> and (Weerahandi, 2004; ISBN:978-0471470175)). It also performs pairwise comparisons and graphical approaches. Moreover, it assesses the weibullness of data in each group via test. The package computes mean and confidence interval under Weibull distribution.

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NeedsCompilation no

Repository CRAN

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Contents

`plot.Sdescribe` *Error Bars with Means and Confidence Limits*

Description

`plot.Sdescribe` produce error bars with means and confidence limits of the given grouped values.

Usage

```
## S3 method for class 'Sdescribe'
plot(x, ylim = NULL, xlab = NULL, ylab = NULL, title = NULL, width = NULL, ...)
```

Arguments

`x`	a Sdescribe object.
`ylim`	a limit for y axes.
`xlab`	a label for the x axis.
`ylab`	a label for the y axis.
`title`	a main title for the plot.
`width`	the little lines at the tops and bottoms of the error bars (defaults to 0.80).
`...`	additional arguments.

Value

No return value, called for side effects

Author(s)

Osman Dag

Examples

```
library(survival)
lung$status <- ifelse(lung$status == 2, 1, 0)
lung$age <- arules::discretize(lung$age, breaks = 3, labels = c("Low","Medium","High"))


library(SurvivalTests)

out <- Sdescribe(time~age+status, lung)

plot(out, ylim = c(0,500))
plot(out)
```

`SANOVA` *Generalized Test for Survival ANOVA*

Description

`SANOVA` performs generalized test for survival ANOVA.

Usage

```
SANOVA(formula, data, nM = 5000, seed = 123, alpha = 0.05, na.rm = TRUE, verbose = TRUE)
```

Arguments

`formula`	a formula of the form `lhs ~ rhs` where `lhs` gives the survival times and `rhs` the corresponding groups + the status variable (1: non-censored, 0: censored).
`data`	a data frame containing the variables in `formula`.
`nM`	a number of bootstrap samples.
`seed`	a seed number for the reproducibility of results. Default is set to 123.
`alpha`	the level of significance to assess the statistical difference. Default is set to alpha = 0.05.
`na.rm`	a logical value indicating whether NA values should be stripped before the computation proceeds.
`verbose`	a logical for printing output to R console.

Details

SANOVA performs parametric survival ANOVA when the underlying data are distributed as Weibull or Gumbel. SANOVA tests are based on generalized p-value approach (cf. Tsui and Weerahandi (1989) and Weerahandi (2004)) extended for situations of affine invariance.

Value

A list with class "survtests" containing the following components:

`p.value`	the p-value of the test.
`alpha`	the level of significance to assess the statistical difference.
`method`	the character string "Generalized Test for Survival ANOVA".
`data`	a data frame containing the variables in which NA values (if exist) are removed.
`formula`	a formula of the form `lhs ~ rhs` where `lhs` gives the sample values and `rhs` the corresponding groups + the status variable (1: non-censored, 0: censored).
`seed`	a seed number for the reproducibility of results.

Author(s)

Sam Weerahandi, Malwane Ananda, Osman Dag

References

Tsui K. and Weerahandi, S. (1989). Generalized P-values in Significance Testing of Hypotheses in the Presence of Nuisance Parameters. *Journal of the American Statistical Association*, **84**, 602-607.

Weerahandi, S. (2004). Generalized Inference in Repeated Measures: Exact Methods in MANOVA and Mixed Models, Wiley.

Examples

```
library(survival)
lung$status <- ifelse(lung$status == 2, 1, 0)
lung$age <- arules::discretize(lung$age, breaks = 3, labels = c("Low","Medium","High"))

library(SurvivalTests)

SANOVA(time~age+status, lung, alpha = 0.05)
```

`Sdescribe` *Descriptive Statistics*

Description

`Sdescribe` produces number of observations (n), number of events (nE), and the mean survival with confidence limits for the mean.

Usage

```
Sdescribe(formula, data, level = 0.95, nM = 5000, na.rm = TRUE,
  verbose = TRUE)
```

Arguments

`formula`	a formula of the form `lhs ~ rhs` where `lhs` gives the survival times and `rhs` the corresponding groups + the status variable (1: non-censored, 0: censored).
`data`	a data frame containing the variables in `formula`.
`level`	the confidence level.
`nM`	a number of bootstrap samples.
`na.rm`	a logical value indicating whether NA values should be stripped before the computation proceeds.
`verbose`	a logical for printing output to R console.

Value

Returns a data.frame of output with class "Sdescribe".

Author(s)

Malwane Ananda, Osman Dag

Examples

```
library(survival)
lung$status <- ifelse(lung$status == 2, 1, 0)
lung$age <- arules::discretize(lung$age, breaks = 3, labels = c("Low","Medium","High"))

library(SurvivalTests)

Sdescribe(time~age+status, lung)
```

`Spaircomp` *Pairwise Comparisons of Survival Tests for One-Way Layout*

Description

`Spaircomp` is a generic function for pairwise comparisons of survival tests in one-way layout by adjusting p-values.

Usage

```
## S3 method for class 'survtests'
Spaircomp(x, adjust.method = c("bonferroni", "holm", "hochberg", "hommel", "BH",
  "BY", "fdr", "none"), verbose = TRUE, ...)
```

Arguments

`x`	a `survtests` object.
`adjust.method`	Method for adjusting p values (see `p.adjust`). Default is set to "bonferroni".
`verbose`	a logical for printing output to R console.
`...`	Additional arguments affecting multiple comparisons of groups in one-way independent designs.

Value

Returns a data.frame of output.

Author(s)

Osman Dag

Examples

```
library(survival)
lung$status <- ifelse(lung$status == 2, 1, 0)
lung$age <- arules::discretize(lung$age, breaks = 3, labels = c("Low","Medium","High"))

library(SurvivalTests)

out = SANOVA(time~age+status, lung, alpha = 0.05)

Spaircomp(out, adjust.method = "bonferroni")


# to illustrate pairwise comparison, alpha is set to 0.5
out2 = SANOVA(time~age+status, lung, alpha = 0.5)

Spaircomp(out2, adjust.method = "bonferroni")

Spaircomp(out2, adjust.method = "hochberg")

Spaircomp(out2, adjust.method = "hommel")

Spaircomp(out2, adjust.method = "holm")
```

`weibull.test` *Weibullness Test*

Description

`weibull.test` performs weibullness test from weibull plot in each group.

Usage

```
weibull.test(formula, data, alpha = 0.05, na.rm = TRUE, verbose = TRUE)
```

Arguments

`formula`	a formula of the form `lhs ~ rhs` where `lhs` gives the survival times and `rhs` the corresponding groups.
`data`	a tibble or data frame containing the variables in `formula`.
`alpha`	the level of significance to assess normality. Default is set to alpha = 0.05.
`na.rm`	a logical value indicating whether NA values should be stripped before the computation proceeds.
`verbose`	a logical for printing output to R console.

Value

A data frame gives the test results for the weibullness of groups.

Author(s)

Osman Dag

See Also

`wp.test`

Examples

```
library(survival)
lung$status <- ifelse(lung$status == 2, 1, 0)
lung$age <- arules::discretize(lung$age, breaks = 3, labels = c("Low","Medium","High"))

library(SurvivalTests)

weibull.test(time~age, lung)
```

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