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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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

```r
## 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

```r
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)
```
SANOV A

Generalized Test for Survival ANOVA

Description

SANOV A performs generalized test for survival ANOVA.

Usage

SANOV A(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

SANOV A performs parametric survival ANOVA when the underlying data are distributed as Weibull or Gumbel. SANOV A 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


Examples

```r
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**

```r
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)

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**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

```r
## 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
weibull.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)
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.
weibull.test

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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