Package ‘controlTest’

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Type Package
Title Quantile Comparison for Two-Sample Right-Censored Survival Data
Version 1.1.0
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Description Nonparametric two-sample procedure for comparing survival quantiles.
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Imports survival (>= 2.41), graphics (>= 3.4.0), stats (>= 3.4.0)
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R topics documented:

Find standard error for survival quantile

Description

Find standard error for survival quantile
quantileControlTest

Usage
quantileControlTest(timevar1, censor1, timevar2, censor2, q = 0.5, B = 1000, seed = 1234, plots = FALSE)

Arguments
timevar1  Vector of observed survival times for sample 1 (control).
censor1  Vector of censoring indicators for sample 1 (1 = uncensored, 0 = censored).
timevar2  Vector of observed survival times for sample 2 (treatment).
censor2  Vector of censoring indicators for sample 2 (1 = uncensored, 0 = censored).
q  Quantile of interest (Default is median).
B  Number of bootstrap samples.
seed  Seed number (for reproducibility).
plots  Logical. TRUE to show Kaplan-Meier plot

Details
It is important to note the possibility that the estimated quantile may not be estimable in our bootstrap samples. In such cases the largest observed survival time will be considered as an estimate for the quantile.

Value
Returns quantile estimate, bootstrapped standard error, test statistic, and two-sided p-value.

References

Examples
#Reference: Survival Analysis Techniques for Censored and Truncated Data.
#Data: Chapter 7.6 Example 7.9 (p. 211)
library(controlTest)
t1 <- c(1, 63, 105, 129, 182, 216, 250, 262, 301, 301,
      342, 354, 356, 358, 380, 383, 383, 338, 394, 408, 460, 489,
      499, 523, 524, 535, 562, 569, 675, 676, 748, 778, 786, 797,
      955, 968, 1000, 1245, 1271, 1420, 1551, 1694, 2363, 2754, 2950)
t2 <- c(17, 42, 44, 48, 60, 72, 74, 95, 103, 108, 122, 144, 167, 170,
      183, 185, 193, 195, 197, 208, 234, 235, 254, 307, 315, 401, 445,
quantileSE

Find standard error for survival quantile

Description

Find standard error for survival quantile

Usage

quantileSE(timevar, censor, q = 0.5, B = 1000, alpha = 0.05, seed = 1991, plots = FALSE)

Arguments

timevar: Vector of observed survival times.
censor: Vector of censoring indicators (1 = uncensored, 0 = censored).
q: Quantile of interest (Default is median).
B: Number of bootstrap samples.
alpha: Significance level for confidence interval of quantile.
seed: Seed number (for reproducibility).
plots: Logical. TRUE to show Kaplan-Meier plot

Value

Returns quantile estimate, bootstrapped standard error, and (1 - alpha / 2) * 100

Examples

#Reference: Survival Analysis Techniques for Censored and Truncated Data.
#Data: Chapter 7.6 Example 7.9 (p. 211)
library(controlTest)
t1 <- c(1, 63, 105, 129, 182, 216, 250, 262, 301, 301,
       342, 354, 356, 358, 380, 383, 383, 338, 394, 408, 460, 489,
       499, 523, 524, 535, 562, 569, 675, 676, 748, 778, 786, 797,
       955, 968, 1000, 1245, 1271, 1420, 1551, 1694, 2363, 2754, 2950)
c1 <- c(rep(1, 43), 0, 0)
quantileSE(timevar = t1, censor = c1, q = 0.5, B = 500)
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