Package ‘survAWKMT2’

November 25, 2016

Type Package
Title Two-Sample Tests Based on Differences of Kaplan-Meier Curves
Version 1.0.0
Date 2016-11-24
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Description Tests for equality of two survival functions based on integrated weighted differences of two Kaplan-Meier curves.
Imports survival
License GPL-2
LazyData TRUE
RoxygenNote 5.0.1
NeedsCompilation no
Repository CRAN
Date/Publication 2016-11-25 12:55:52

R topics documented:

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Two-Sample Tests Based on Weighted Differences of Kaplan-Meier Curves

Description

Tests for equality of two survival functions based on integrated weighted differences of two Kaplan-Meier curves.
Author(s)
Miki Horiguchi, Hajime Uno

References

See Also
survival

Examples

d = survival::pbc[1:312, c(2,3,4)] #The pbc data from 'survival' package
d$status = as.numeric(D$status==2)
d$trt = as.numeric(D$trt==2)
names(D) = c("time", "status", "arm")
tau = max(D[,2]==1,1])
nmethod = 10 #Recommended to specify at least 10000 (default) or larger.

a = AWKMT2(indata=D, tau=tau, c_first=0, c_last=4, c_by=0.1, method=\"permutation\",
nmethod=nmethod, seed=1, v1=TRUE, v2=TRUE, test=\"1\_side\")
print(a)

AWKMT2
Adaptively Weighted Kaplan-Meier Tests

Description
Performs the two-sample tests based on adaptively weighted differences between two Kaplan-Meier curves proposed by Uno, Tian, Claggett and Wei (2015).

Usage

AWKMT2(indata, tau, c_first=0, c_last=4, c_by=0.1, method=\"permutation\",
nmethod=10000, seed=1, v1=TRUE, v2=TRUE, test=\"1\_side\")

Arguments

indata A data matrix (data frame). The 1st column is time-to-event variable, the 2nd column is event indicator (1=event, 0=censor), and the 3rd column is the treatment indicator (1=treat, 0=control). No missing values are allowed in this data matrix.

tau A numeric value to specify the time interval of interest. The end of study time will be a general choice.
c_first A first number in range to specify the search area of "c" for the versatile tests by Uno et al. (2015). Default is 0.
c_last
A last number in range to specify the search area of "c" for the versatile tests by Uno et al. (2015). Default is 4.
c_by
A number to specify the search area of "c" for the versatile tests by Uno et al. (2015). Default is 0.1.
method
A name of the resampling method. It supports "permutation" (default) and "perturbation".
nmethod
A number of iterations for the resampling. Recommended to specify at least 10000 (default) or larger.
seed
An integer value, used for the random number generation in the resampling procedures. Default is 1.

v1
Choice of the test statistic. When TRUE (default), v1 proposed by Uno et al. (2015) is used as a test statistic.

v2
Choice of the test statistic. When TRUE (default), v2 proposed by Uno et al. (2015) is used as a test statistic.

test
Specify "1_side" for the one-sided test where the alternative hypothesis is that treatment group is superior to control group with respect to survival. Specify "2_side" for the two-sided test where the alternative hypothesis is that treatment group is not equal to control group with respect to survival. Default is "1_side".

Value
A list with components:

resampling_method
The resampling method.

crude_pvalue_T1_1_side
The one-sided crude p-value of the test based on v1 in Uno et al. (2015).

crude_pvalue_T2_1_side
The one-sided crude p-value of the test based on v2 in Uno et al. (2015).

crude_pvalue_T1_2_side
The two-sided crude p-value of the test based on v1 in Uno et al. (2015).

crude_pvalue_T2_2_side
The two-sided crude p-value of the test based on v2 in Uno et al. (2015).

bona_fide_pvalue_T1_1_side
The one-sided bona-fide p-value of the test based on v1 in Uno et al. (2015).

bona_fide_pvalue_T2_1_side
The one-sided bona-fide p-value of the test based on v2 in Uno et al. (2015).

bona_fide_pvalue_T1_2_side
The two-sided bona-fide p-value of the test based on v1 in Uno et al. (2015).

bona_fide_pvalue_T2_2_side
The two-sided bona-fide p-value of the test based on v2 in Uno et al. (2015).

References
See Also

survival

Examples

```r
D = survival::pbc[1:312, c(2,3,4)] # The pbc data from 'survival' package
D$status = as.numeric(D$status==2)
D$trt  = as.numeric(D$trt==2)
names(D) = c("time", "status", "arm")
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         nmethod=nmethod, seed=1, v1=TRUE, v2=TRUE, test="1_side")
print(a)
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