

Package ‘survRM2adapt’

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Type Package

Title Flexible and Coherent Test/Estimation Procedure Based on
Restricted Mean Survival Times

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Imports survival

Description Performs the procedure proposed by Horiguchi et al. (2018) <[doi:10.1002/sim.7661](https://doi.org/10.1002/sim.7661)>. The method specifies a set of truncation time points tau's for calculating restricted mean survival times (RMST), performs testing for equality, and estimates the difference in RMST between two groups at the specified tau's. Multiplicity by specifying several tau's is taken into account in this procedure.

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R topics documented:

survRM2adapt-package	2
print.rmst2adapt	2
rmst2adapt	3
rmst2adapt.sample.data	4

Index	6
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survRM2adapt-package *Flexible and Coherent Test/Estimation Procedure Based on Restricted Mean Survival Times*

Description

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Author(s)

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References

Horiguchi M, Cronin A, Takeuchi M, Uno H. A flexible and coherent test/estimation procedure based on restricted mean survival times for censored time-to-event data in randomized clinical trials. *Statistics in Medicine* 2018. doi:10.1002/sim.7661.

See Also

survival survRM2

Examples

```
#--- sample data ---#
data = rmst2adapt.sample.data()
nmethod = 100 #This is only for example use.
           #Recommended to specify at least 100000 (default) or larger.

a = rmst2adapt(indata=data, tau_star=seq(6,12,2), method="perturbation",
              nmethod=nmethod, test="2_side")
print(a)
```

print.rmst2adapt *print.rmst2adapt*

Description

S3 method for class 'rmst2adapt'

Usage

```
## S3 method for class 'rmst2adapt'
print(x, digits = 3, ...)
```

Arguments

x	Object to be printed
digits	Integer indicating the number of decimal places
...	Further arguments ignored in this function

rmst2adapt	<i>Flexible and Coherent Test/Estimation Procedure Based on Restricted Mean Survival Times</i>
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Description

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Usage

```
rmst2adapt(indata, tau_star, method="perturbation", nmethod=100000,
           seed=NULL, test="2_side", conf.int=0.95)
```

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=treatment, 0=control). No missing values are allowed in this data matrix.
tau_star	A vector indicating a set of tau's. All elements in tau_star need to be shorter than or equal to the minimum of the largest observed time on each of the two groups.
method	A name of the resampling method. It supports "perturbation" (default) and "permutation".
nmethod	A number of iterations for the resampling. Recommended to specify at least 100000 (default) or larger.
seed	An integer value, used for the random number generation in the resampling procedures. Default is NULL.
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 "2_side".

conf.int Specify confidence coefficient for confidence bands of the differences in RMST. Default is 0.95.

Value

an object of class rmst2adapt.

method	The resampling method used in the analyses
nmethod	The number of iterations for the resampling
test	The type of test used in the analyses
candidate_taus	The set of tau's used in the analyses
observed_z	The observed test statistic Z_{star}
p_value	The p-value of testing for equality
conf_band	The difference in RMST between two groups at the specified tau's
selected_tau	The value of tau selected to summarize the treatment effect

Author(s)

Miki Horiguchi, Hajime Uno

References

Horiguchi M, Cronin A, Takeuchi M, Uno H. A flexible and coherent test/estimation procedure based on restricted mean survival times for censored time-to-event data in randomized clinical trials. *Statistics in Medicine* 2018. doi:10.1002/sim.7661.

Examples

```
#--- sample data ---#
data = rmst2adapt.sample.data()
nmethod = 100 #This is only for example use.
           #Recommended to specify at least 100000 (default) or larger.

a = rmst2adapt(indata=data, tau_star=seq(6,12,2), method="perturbation",
              nmethod=nmethod, test="2_side")
print(a)
```

rmst2adapt.sample.data

Generate a sample data from the pbc data

Description

This is a function to retrieve 312 randomized patients from the pbc data in survival package.

Usage

```
rmst2adapt.sample.data()
```

Details

The function creates a sample dataset to illustrate the usage of the function `rmst2adapt()` in this package. The original `pbcc` data in `survival` package consists of 418 patients data. This function loads the `pbcc` data, select the 312 patients who were randomized. The status variable is edited, so that 1 indicates death and 0 indicates alive.

See Also

`pbcc` in `survival` package

Examples

```
D=rmst2adapt.sample.data()  
head(D)
```

Index

* **survival**

survRM2adapt-package, [2](#)

print.rmst2adapt, [2](#)

rmst2adapt, [3](#)

rmst2adapt.sample.data, [4](#)

survRM2adapt-package, [2](#)