Package ‘survRM2’

February 20, 2017

Type Package
Title Comparing Restricted Mean Survival Time
Version 1.0-2
Date 2017-02-21
Author Hajime Uno, Lu Tian, Angel Cronin, Chakib Battioui, Miki Horiguchi
Maintainer Hajime Uno <huno@jimmy.harvard.edu>
Depends survival
Description Performs two-sample comparisons using the restricted mean survival time (RMST) as a summary measure of the survival time distribution. Three kinds of between-group contrast metrics (i.e., the difference in RMST, the ratio of RMST and the ratio of the restricted mean time lost (RMTL)) are computed. It performs an ANCOVA-type covariate adjustment as well as unadjusted analyses for those measures.
License GPL-2
LazyData true
RoxygenNote 6.0.1
Suggests knitr, rmarkdown
VignetteBuilder knitr
NeedsCompilation no
Repository CRAN
Date/Publication 2017-02-20 17:23:13

R topics documented:

survRM2-package .................................................. 2
plot.rmst2 ......................................................... 3
print.rmst2 ......................................................... 3
rmst2 ............................................................... 4
rmst2.sample.data ................................................ 6

Index 7
Description

Performs two-sample comparisons using the restricted mean survival time (RMST) as a summary measure of the survival time distribution. Three kinds of between-group contrast metrics (i.e., the difference in RMST, the ratio of RMST and the ratio of the restricted mean time lost (RMTL)) are computed. The package has a function to perform an ANCOVA-type covariate adjustment as well as unadjusted analyses for those measures.

Author(s)

Hajime Uno, Lu Tian, Angel Cronin, Chakib Battiouli, Miki Horiguchi
Maintainer: Hajime Uno <huno@jimmy.harvard.edu>

References


Tian L, Zhao L, Wei LJ. Predicting the restricted mean event time with the subject’s baseline co-variates in survival analysis. Biostatistics 2014, 15, 222-233.

See Also

survival

Examples

```r
#--- sample data ---#
D=rmdst2.sample.data()
time=D$time
status=D$status
arm=D$arm
tau=NULL
x=D[,c(4,6,7)]
#--- without covariates ----
a=rmdst2(time, status, arm, tau=10)
print(a)
plot(a, xlab="Years", ylab="Probability", density=60)
#--- with covariates ----
a=rmdst2(time, status, arm, tau=10, covariates=x)
print(a)
```
Description

S3 method for class 'rmst2'

Usage

## S3 method for class 'rmst2'
plot(x, xlab = "", ylab = "", col = "red",
col.RMST = "pink", col.RMTL = "orange", density = 80, angle = 85, ...)

Arguments

x          Results of the unadjusted analyses.
 xlab       x label.
ylab       y label.
col        Color for line. Default is red.
col.RMST   Color for areas of RMST. Default is pink.
col.RMTL   Color for areas of RMTL. Default is orange.
density    Density of shading lines, in lines per inch. Default is 80.
age         Slope of shading lines, given as an angle in degrees (counter-clockwise). Default is 85.
...
 Further arguments ignored in this function.

print.rmst2

Description

S3 method for class 'rmst2'

Usage

## S3 method for class 'rmst2'
print(x, digits = 3, ...)

Arguments

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

Description

Performs two-sample comparisons using the restricted mean survival time (RMST) as a summary measure of the survival time distribution. Three kinds of between-group contrast metrics (i.e., the difference in RMST, the ratio of RMST and the ratio of the restricted mean time lost (RMTL)) are computed. It performs ANCOVA-type adjusted analyses when covariates are passed to it as an argument.

Usage

\texttt{rmst2(time, status, arm, tau = NULL, covariates = NULL, alpha = 0.05)}

Arguments

- \texttt{time}: The follow-up time for right censored data.
- \texttt{status}: The status indicator, 1=event, and 0=right censored.
- \texttt{arm}: The group indicator for comparison. The elements of this vector take either 1 or 0. Normally, 0=control group, 1=active treatment group.
- \texttt{tau}: A scaler value to specify the truncation time point for the RMST calculation. \(\text{tau}\) needs to be smaller than the minimum of the largest observed time in each of the two groups. When \(\text{tau} = \text{NULL}\), the default value (i.e., the minimum of the largest observed time in each of the two groups) is used.
- \texttt{covariates}: This specifies covariates to be used for the adjusted analyses. When \text{NULL}, unadjusted analyses are performed. When non \text{NULL}, the ANCOVA-type adjusted analyses are performed using those variables passed as \text{covariates}. This can be one variable (vector) or more than one variables (matrix).
- \texttt{alpha}: The default is 0.05. \((1{-}\alpha)\) confidence intervals are reported.

Details

For more details, please see the package vignette: \texttt{browseVignettes(package = "survRM2")}

Value

- an object of class \texttt{rmst2}.
- \texttt{tau}: the truncation time used in the analyses
- \texttt{note}: a note regarding the truncation time
- \texttt{RMST.arm1}: RMST results in arm 1. This is generated only when \text{covariates} is not specified.
- \texttt{RMST.arm0}: RMST results in arm 0. This is generated only when \text{covariates} is not specified.
unadjusted.result

Results of the unadjusted analyses. This is generated only when covariates is not specified.

The values below are generated when some covariates are passed to the function.

adjusted.result

Results of the adjusted analyses.

\texttt{RMST.difference.adjusted}

Results of the parameter estimates with the model to derive an adjusted difference in RMST.

\texttt{RMST.ratio.adjusted}

Results of the parameter estimates with the model to derive an adjusted ratio of RMST.

\texttt{RMTL.ratio.adjusted}

Results of the parameter estimates with the model to derive an adjusted ratio of RMTL.

Author(s)

Hajime Uno, Lu Tian, Angel Cronin, Chakib Battioui, Miki Horiguchi

References


Tian L, Zhao L, Wei LJ. Predicting the restricted mean event time with the subject's baseline covariates in survival analysis. Biostatistics 2014, 15, 222-233.

Examples

```r
#--- sample data ---#
D=rmst2.sample.data()
time=D$time
status=D$status
arm=D$arm
tau=NULL
x=D[,c(4,6,7)]
#--- without covariates ----
a=rmst2(time, status, arm, tau=10)
print(a)
plot(a, xlab="Years", ylab="Probability", density=60)
#--- with covariates ----
a=rmst2(time, status, arm, tau=10, covariates=x)
print(a)
```
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

rmst2.sample.data()

Details

The function creates a sample dataset to illustrate the usage of the function rmst2() in this package. The original pbc data in survival package consists of 418 patients data. This function loads the pbc data, select the 312 patients who were randomized. The status variable is edited, so that 1 indicates death and 0 indicates alive.

See Also

pbc in survival package

Examples

D=rmst2.sample.data()
head(D)
Index

*Topic survival
  survRM2-package, 2

plot.rmst2, 3
print.rmst2, 3

rmst2, 4
rmst2.sample.data, 6

survRM2-package, 2