

Package ‘sensRMST’

May 12, 2022

Title What the Package Does (One Line, Title Case)

Version 0.0.0.9000

Description What the package does (one paragraph).

License MIT + file LICENSE

Encoding UTF-8

Roxygen list(markdown = TRUE)

RoxygenNote 7.1.2

URL <https://github.com/seungjae2525/sensRMST>

BugReports <https://github.com/seungjae2525/sensRMST/issues>

Imports optimParallel,
parallel,
stats,
survival

Suggests doParallel

R topics documented:

adj_rmst	1
print.RMSTsensitivity	3
RMSTsensitivity	4
Index	7

adj_rmst	<i>Adjusted RMST</i>
----------	----------------------

Description

Function for RMST estimate from adjusted Kaplan-Meier curve via SIPW (or IPW)

Usage

```
adj_rmst(
  time,
  status,
  exposure,
  data,
  ps = NULL,
  stabilize = TRUE,
  tau = NULL,
  var.est = FALSE,
  alpha = 0.05
)
```

Arguments

time	The name of the variable for time to event
status	The name of the variable for status (0 if censored, 1 if event)
exposure	The name of the variable for exposure (0 if unexposed, 1 if exposed)
data	A data frame in which contains the follow-up time (time), the event (status), the exposure (exposure), and the optional propensity score (ps)
ps	The name of the variable for propensity score variable $P(A=1 L)>0$, Default: NULL
stabilize	A logical value. If true, stabilized ipw., Default: TRUE
tau	pre-specified time point to estimate of restricted mean survival time (RMST), Default: NULL
var.est	A logical value. variance of RMST via xie (2005) is calculated., Default: FALSE
alpha	A significance level, Default: 0.05

Details

DETAILS

Value

OUTPUT_DESCRIPTION

Examples

```
## Not run:
if(interactive()){
  # EXAMPLE
  library(survival)

  dat <- gbsg
  dat$size2 <- ifelse(dat$size <= 20, 0,
                     ifelse(dat$size > 20 & dat$size <= 50, 1, 2))
  dat$age2 <- dat$age/100
  dat$er2 <- dat$er/1000

  ## Estimation of propensity score
  denom.fit <- glm(hormon ~ (age2)^3 + (age2)^3*log(age2) + meno + factor(size2) + sqrt(nodes) + er2,
```

```

      data=dat, family=binomial(link='logit'))
dat$Ps <- predict(denom.fit, type='response')

## Adjusted RMST with tau qual to 5-year
rr <- adj_rmst(data=dat, time='rfstime', status='status', exposure='hormon',
              ps='Ps', stabilize=FALSE, tau=365.25*5, alpha=.05, var.est = TRUE)
round(c(rr$rmst_diff, rr$rmst_diff_low, rr$rmst_diff_upp, rr$rmst_diff_pval), 3)
}

## End(Not run)

```

print.RMSTsensitivity *Print for "senRMST" objects*

Description

Print for objects of class "senRMST".

Usage

```

## S3 method for class 'RMSTsensitivity'
print(x, digits = max(1L, getOption("digits") - 3L), ...)

```

Arguments

x	an object of class "senRMST"
digits	print digits, Default: max(1L, getOption("digits") - 3L)
...	PARAM_DESCRIPTION

Details

DETAILS

Value

OUTPUT_DESCRIPTION

Examples

```

## Not run:
if(interactive()){
  #EXAMPLE1
}

## End(Not run)

```

Description

Function for sensitivity analysis of unmeasured confounding for restricted mean survival time using propensity score

Usage

```
RMSTsensitivity(
  time,
  status,
  exposure,
  exposed.ref.level = 1,
  ps,
  data,
  methods = "Approx",
  use.multicore = TRUE,
  n.core = parallel::detectCores()/2,
  lambda = 2,
  tau = NULL,
  ini.par = 1,
  verbose = FALSE
)
```

Arguments

time	The name of the variable for time to event
status	The name of the variable for status (0 if censored, 1 if event)
exposure	The name of the variable for exposure (0 if unexposed, 1 if exposed)
exposed.ref.level	Reference level in exposure variable, Default: 1
ps	The name of the variable for propensity score variable i.e., $P(A=1 L)>0$
data	A data frame in which contains the follow-up time (time), the event (status), the exposure (exposure), and the propensity score (ps)
methods	A character with the methods how to calculate the adjusted RMST ("Optim", "Approx", "LP1", "LP2"), Default: 'Approx'
use.multicore	Logical scalar indicating whether to parallelize our optimization problem, Default: TRUE
n.core	The number of usable cores, Default: <code>parallel::detectCores()/2</code>
lambda	The sensitivity parameter, Default: 1.5
tau	User-specific time point, If tau not specified (NULL), use the minimum of the largest observed event time in both groups.
ini.par	Initial parameter for direct optimization method, Default: 1
verbose	Conditional on the verbose level, print the message that each optimization (minimization or maximization) for each group was ended, Default: FALSE

Details

To assess details of method of sensitivity analysis, see Lee et al. (2022) for details.

Value

An object of class `senRMST`. The object is a `data.frame` with the following components:

<code>N</code>	Total number of subjects
<code>N.exposed</code>	The number of subjects in exposed group
<code>N.unexposed</code>	The number of subjects in unexposed group
<code>N.event.exposed</code>	The number of events in exposed group
<code>N.event.unexposed</code>	The number of events in unexposed group
<code>cen.rate</code>	Total censoring rate
<code>cen.rate.exposed</code>	Censoring rate in exposed group
<code>cen.rate.unexposed</code>	Censoring rate in unexposed group
<code>Lambda</code>	A used sensitivity parameter
<code>Tau</code>	User-specific time point, If tau not specified (NULL), use the minimum of the largest observed event time in both groups
<code>Method</code>	A used method
<code>min.exposed</code>	The minimum of adjusted RMST based on the shifted propensity score for exposed group
<code>max.exposed</code>	The maximum of adjusted RMST based on the shifted propensity score for exposed group
<code>min.unexposed</code>	The minimum of adjusted RMST based on the shifted propensity score for unexposed group
<code>max.unexposed</code>	The maximum of adjusted RMST based on the shifted propensity score for unexposed group
<code>RMST.diff.min</code>	The minimum of between-group difference in adjusted RMST based on shifted propensity score
<code>RMST.diff.max</code>	The maximum of between-group difference in adjusted RMST based on shifted propensity score

The results for the `RMST_sensitivity` are printed with the `print.RMSTsensitivity` functions. To generate graphs comparing Lambda with interval of adjusted RMST based on shifted propensity score use the `aaa` functions.

Author(s)

Seungjae Lee <seungjae2525@gmail.com>

References

Bakbergenuly I, Hoaglin DC, Kulinskaya E (2020): Methods for estimating between-study variance and overall effect in meta-analysis of odds-ratios. *Research Synthesis Methods*, DOI: 10.1002/jrsm.1404

See Also

[detectCores](#), [makeCluster](#)

Examples

```
if(interactive()){
  ## EXAMPLE
  library(survival)

  dat <- gbsg
  dat$size2 <- ifelse(dat$size <= 20, 0,
                     ifelse(dat$size > 20 & dat$size <= 50, 1, 2))
  dat$age2 <- dat$age/100
  dat$er2 <- dat$er/1000

  ## Estimation of propensity score
  denom.fit <- glm(hormon ~ (age2)^3 + (age2)^3*log(age2) + meno + factor(size2) + sqrt(nodes) + er2,
                  data=dat, family=binomial(link='logit'))
  dat$Ps <- predict(denom.fit, type='response')

  ## Between-group difference in adjusted RMST based on shifted propensity score
  # Using approximate optimization method
  results.approx <- RMST_sensitivity(time='rfstime', status='status', exposure='hormon',
                                   exposed.ref.level=1, ps='Ps', data=dat, methods="Approx",
                                   use.multicore=TRUE, n.core=parallel::detectCores()/2,
                                   lambda=1.5, tau=365.25*5)

  results.approx
  ## Adjusted RMST with tau equal to 5-year
  # Using direct optimization method
  results.optim <- RMST_sensitivity(time='rfstime', status='status', exposure='hormon',
                                   exposed.ref.level=1, data=dat, ps='Ps', methods="Optim",
                                   use.multicore=TRUE, n.core=parallel::detectCores()/2,
                                   lambda=1.5, tau=365.25*5)

  results.optim
}
```

Index

`adj_rmst`, [1](#)

`detectCores`, [6](#)

`makeCluster`, [6](#)

`print.RMSTsensitivity`, [3](#), [5](#)

`RMSTsensitivity`, [4](#)