Package: BRACE (via r-universe)

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Type Package

Title Bias Reduction Through Analysis of Competing Events (BRACE)

Version 0.1.0

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Description Adjusting the bias due to residual confounding (often called treatment selection bias) in estimating the treatment effect in a proportional hazard model, as described in Williamson et al. (2022) <doi:10.1158/1078-0432.ccr-21-2468>.

License GPL (>= 3)

Depends survival, survminer

Suggests knitr, testthat (>= 3.0.0)

Config/testthat/edition 3

Encoding UTF-8

RoxygenNote 7.2.1

VignetteBuilder knitr

NeedsCompilation no

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Contents

brace *Bias Reduction through Analysis of Competing Events*

Description

brace is used to estimate the treatment effect with adjusted confounders on the composite hazard for primary or competing events, and adjust for bias from residual confounding in non-randomized data by BRACE method

Usage

```
brace(
  ftime,
  fstatus,
  covs = NA,
  trt,
  failcode = 1,
  cencode = 0,
  PS = 0,
  B = 1000
)
```

Arguments

ftime	vector of failure/censoring times
fstatus	vector with a unique code for each failure type and a separate code for censored observations (default is primary event = 1, competing event = 2, censored = 0)
covs	matrix (nobs x ncovs) of fixed covariates. If no covariates, set covs = NA (default is NA)
trt	vector of treatment indicator (1 for treatment group)
failcode	code of fstatus that denotes the failure type of interest
cencode	code of fstatus that denotes censored observations
PS	whether to use propensity score method for adjusting the confounding effect (1 for propensity score method, default is 0)
B	bootstrap sample size for calculating the Confidence interval, default is 1000

Value

a list of class brace, with components:

$Summary	summary table of BRACE method
$`BRACE HR Distribution`	the estimated regression coefficients in each bootstrap sample
$`Omega Estimate`	estimate of relative hazards for primary events vs. combined events

`$Epsilon` the estimated bias

`$‘Combined Endpoint Model‘`
the regression model for combined events

`$‘Primary Endpoint Model‘`
the regression model for primary events

`$‘Competing Endpoint Model‘`
the regression model for competing events

`$‘Omega Curve‘` estimate of omega over time

`$‘Combined Endpoint Curve‘`
survival curve for combined events

`$‘Primary Endpoint Curve‘`
survival curve for primary events

`$‘Competing Endpoint Curve‘`
survival curve for competing events

References

Williamson, Casey W., et al. "Bias Reduction through Analysis of Competing Events (BRACE) Correction to Address Cancer Treatment Selection Bias in Observational Data." Clinical Cancer Research 28.9 (2022): 1832-1840.

Examples

```
nsims = 1; nobs = 1500
f = 0.5; g = 0.333; b = 8; w1 = w2 = 0.667
theta1 = 0.5; theta2 = 1; omegaplus = 1; k3 = 0.333
sim1 = gendat(nsims,nobs,f,g,b,w1,w2,omegaplus,theta1,theta2,k3)
ftime = sim1$time
fstatus = sim1$pfs_ci
covs = NA
trt = sim1$group
braceoutput = brace(ftime, fstatus, covs, trt, PS=0, B=10)

nsims = 1; nobs = 1500
f1 = f2 = 0.5; g = 0.333; b1 = 8; b2 = 4; w1 = w2 = 0.667
theta1 = 0.5; theta2 = 1; omegaplus = 1; k3 = 0.333
sim1 = gendat2(nsims,nobs,f1,f2,g,b1,b2,w1,w2,omegaplus,theta1,theta2,k3)
ftime = sim1$time
fstatus = sim1$pfs_ci
covs = sim1$factor2
trt = sim1$group
braceoutput = brace(ftime, fstatus, covs, trt, PS=1, B=10)
```

gendat *simulation data generating function*

Description

generating the simulation data to apply in brace

Usage

```
gendat(nsims, nobs, f, g, b, w1, w2, omegaplus, theta1, theta2, k3)
```

Arguments

nsims	number of simulation datasets
nobs	number of observations for one dataset
f	parameter for generating unmeasured binary confounder
g	parameter for generating group assignment
b	confounder effect on group assignment
w1	shape parameter in generating survival time for event 1 from weibull distribution
w2	shape parameter in generating survival time for event 2 from weibull distribution
omegaplus	multiplier on the baseline hazard for event 1
theta1	multiplier on the baseline hazard for event 1
theta2	multiplier on the baseline hazard for event 2
k3	multiplier on the baseline hazard for event 2

Value

a matrix of nsims*nobs row, which consists of nsims datasets

Examples

```
nsims = 1; nobs = 1500
f = 0.5; g = 0.333; b = 8; w1 = w2 = 0.667
theta1 = 0.5; theta2 = 1; omegaplus = 1; k3 = 0.333
sim1 = gendat(nsims,nobs,f,g,b,w1,w2,omegaplus,theta1,theta2,k3)
```

gendat2 *simulation data generating function (Adding a measured confounder)*

Description

generating the simulation data to apply in brace

Usage

```
gendat2(nsims, nobs, f1, f2, g, b1, b2, w1, w2, omegaplus, theta1, theta2, k3)
```

Arguments

nsims	number of simulation datasets
nobs	number of observations for one dataset
f1	parameter for generating unmeasured binary confounder
f2	parameter for generating measured binary confounder
g	parameter for generating group assignment
b1	unmeasured confounder effect on group assignment
b2	measured confounder effect on group assignment
w1	shape parameter in generating survival time for event 1 from weibull distribution
w2	shape parameter in generating survival time for event 2 from weibull distribution
omegaplus	multiplier on the baseline hazard for event 1
theta1	multiplier on the baseline hazard for event 1
theta2	multiplier on the baseline hazard for event 2
k3	multiplier on the baseline hazard for event 2

Value

a matrix of nsims*nobs row, which consists of nsims datasets

Examples

```
nsims = 1; nobs = 1500
f1 = f2 = 0.5; g = 0.333; b1 = 8; b2 = 4; w1 = w2 = 0.667
theta1 = 0.5; theta2 = 1; omegaplus = 1; k3 = 0.333
sim1 = gendat2(nsims,nobs,f1,f2,g,b1,b2,w1,w2,omegaplus,theta1,theta2,k3)
```

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