

# Package: mrPStrata (via r-universe)

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**Type** Package

**Title** Multiply Robust Estimation in Causal Survival Analysis with Treatment Noncompliance

**Version** 0.1.0

**Description** Provides multiply robust estimators of principal survival causal effects among always-takers, compliers, and never-takers in studies with treatment noncompliance. The methods are based on Cheng et al. (2026) <[doi:10.1214/25-AOAS2117](https://doi.org/10.1214/25-AOAS2117)>.

**License** GPL (>= 2)

**Encoding** UTF-8

**LazyData** true

**Depends** R (>= 2.10)

**Imports** dplyr, ggplot2, magrittr, progress, survival

**Suggests** knitr, rmarkdown, testthat (>= 3.0.0)

**Config/testthat/edition** 3

**RoxygenNote** 7.3.3

**VignetteBuilder** knitr

**NeedsCompilation** no

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**Repository** <https://cran.r-universe.dev>

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BootEst.MO.SA	<i>Bootstrap confidence intervals for the bias-corrected multiply robust estimator under violations of monotonicity</i>
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### Description

Bootstrap confidence intervals for the bias-corrected multiply robust estimator under violations of monotonicity

### Usage

```

BootEst.MO.SA(
  times,
  propensity.model,
  principal.model,
  censor.model,
  failure.model,
  data,
  zeta,
  estimand = c("NACE", "CACE", "ACE", "DACE"),
  bootstrap = 50
)

```

### Arguments

times	a vector of time when the principal survival causal effects (PSCEs) are of interest
propensity.model	propensity score model
principal.model	principal score model
censor.model	censoring model
failure.model	outcome model
data	dataset

zeta	the sensitivity parameter zeta
estimand	the estimands of interest
bootstrap	number of bootstrap replications

**Value**

The bootstrap confidence intervals

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BootEst.PI.SA	<i>Bootstrap confidence intervals for the multiply robust estimator</i>
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**Description**

Bootstrap confidence intervals for the multiply robust estimator

**Usage**

```

BootEst.PI.SA(
  times,
  propensity.model,
  principal.model,
  censor.model,
  failure.model,
  data,
  xi0,
  xi1,
  eta0,
  eta1,
  estimand = c("NACE", "CACE", "AAE"),
  bootstrap
)
    
```

**Arguments**

times	a vector of time when the principal survival causal effects (PSCEs) are of interest
propensity.model	propensity score model
principal.model	principal score model
censor.model	censoring model
failure.model	outcome model
data	dataset
xi0	sensitivity parameter xi_0
xi1	sensitivity parameter xi_1

eta0	sensitivity parameter eta_0
eta1	sensitivity parameter eta_1
estimand	the estimands of interest
bootstrap	number of bootstrap replications

**Value**

The bootstrap confidence intervals

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mrPStrata	<i>Multiply robust estimator for calculating the principal survival causal effects among always takers, compliers, and never takers</i>
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---

**Description**

Multiply robust estimator for calculating the principal survival causal effects among always takers, compliers, and never takers

**Usage**

```
mrPStrata(
  times,
  data,
  Xpi_names,
  Xe_names,
  Xc_names,
  Xt_names,
  Z_name,
  S_name,
  U_name,
  delta_name,
  B = 100
)
```

**Arguments**

times	a vector of time when the principal survival causal effects (PSCEs) are of interest
data	the dataset
Xpi_names	names of the covariates for the propensity score model
Xe_names	names of the covariates for the principal score model
Xc_names	names of the covariates for the censoring model
Xt_names	names of the covariates for the failure outcome model
Z_name	name of the treatment assignment status
S_name	name of the true treatment receipt status
U_name	name of the observed failure time
delta_name	name of the censoring indicator
B	number of the bootstrap replications (default 100)

**Value**

The PSCE estimates and their 95% confidence intervals

**Examples**

```
# example code
attach(sim_data)
sim_data = sim_data[1:1000,]
res = mrPStrata(times=c(1,2,3,4,5,6,7,8),
               data = sim_data,
               Xpi_names = c("X1","X2","X3","X4","X5"),
               Xe_names = c("X1","X2","X3","X4","X5"),
               Xc_names = c("X1","X2","X3","X4","X5"),
               Xt_names = c("X1","X2","X3","X4","X5"),
               Z_name = "z",
               S_name = "s",
               U_name = "U",
               delta_name = "delta",
               B=3)
res
```

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mrPStrata_MO_SA	<i>Bias-corrected multiply robust estimator of the PSCE under violation of monotonicity</i>
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**Description**

Bias-corrected multiply robust estimator of the PSCE under violation of monotonicity

**Usage**

```
mrPStrata_MO_SA(
  times,
  data,
  Xpi_names,
  Xe_names,
  Xc_names,
  Xt_names,
  Z_name,
  S_name,
  U_name,
  delta_name,
  zeta = 0.01,
  B = 100
)
```

**Arguments**

times	a vector of time when the principal survival causal effects (PSCEs) are of interest
data	the dataset
Xpi_names	names of the covariates for the propensity score model
Xe_names	names of the covariates for the principal score model
Xc_names	names of the covariates for the censoring model
Xt_names	names of the covariates for the outcome model
Z_name	name of the treatment assignment status
S_name	name of the true treatment receipt status
U_name	name of the observed failure time
delta_name	name of the censoring indicator
zeta	sensitivity parameter zeta
B	number of the bootstrap replications (default 100)

**Value**

The PSCE estimates and their 95% confidence intervals

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mrPStrata_PI_SA	<i>Bias-corrected multiply robust estimator of the PSCE under violation of the principal ignorability assumption</i>
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---

**Description**

Bias-corrected multiply robust estimator of the PSCE under violation of the principal ignorability assumption

**Usage**

```
mrPStrata_PI_SA(
  times,
  data,
  Xpi_names,
  Xe_names,
  Xc_names,
  Xt_names,
  Z_name,
  S_name,
  U_name,
  delta_name,
  xi0 = 0,
  xi1 = 0,
  eta0 = 1,
  eta1 = 1,
  B = 100
)
```

**Arguments**

times	a vector of time when the principal survival causal effects (PSCEs) are of interest
data	the dataset
Xpi_names	names of the covariates for the propensity score model
Xe_names	names of the covariates for the principal score model
Xc_names	names of the covariates for the censoring model
Xt_names	names of the covariates for the outcome model
Z_name	name of the treatment assignment status
S_name	name of the true treatment receipt status
U_name	name of the observed failure time
delta_name	name of the censoring indicator
xi0	sensitivity parameter xi_0
xi1	sensitivity parameter xi_1
eta0	sensitivity parameter eta_0
eta1	sensitivity parameter eta_1
B	number of the bootstrap replications (default 100)

**Value**

The PSCE estimates and their 95% confidence intervals

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plot.psce	<i>Plot of the PSCEs and their associated 95% pointwise confidence intervals</i>
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---

**Description**

Plot of the PSCEs and their associated 95% pointwise confidence intervals

**Usage**

```
## S3 method for class 'psce'
plot(res)
```

**Arguments**

res	an output from mrPStrata
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**Value**

The PSCE point estimates and 95% pointwise confidence intervals

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PointEst.MO.SA	<i>Point estimation for the multiply robust estimator under violation of monotonicity assumption</i>
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### Description

Point estimation for the multiply robust estimator under violation of monotonicity assumption

### Usage

```
PointEst.MO.SA(
  times,
  propensity.model,
  principal.model,
  censor.model,
  failure.model,
  data,
  zeta,
  estimand = c("NACE", "CACE", "ACE", "DACE")
)
```

### Arguments

times	a vector of time when the principal survival causal effects (PSCEs) are of interest
propensity.model	propensity score model
principal.model	principal score model
censor.model	censoring model
failure.model	outcome model
data	dataset
zeta	the sensitivity parameter zeta
estimand	the estimands of interest

### Value

The PSCE point estimates

---

PointEst.PI.SA      *Point estimation for the multiply robust estimator*

---

## Description

Point estimation for the multiply robust estimator

## Usage

```
PointEst.PI.SA(  
  times,  
  propensity.model,  
  principal.model,  
  censor.model,  
  failure.model,  
  data,  
  xi0,  
  xi1,  
  eta0,  
  eta1,  
  estimand = c("NACE", "CACE", "ACE")  
)
```

## Arguments

times	a vector of time when the principal survival causal effects (PSCEs) are of interest
propensity.model	propensity score model
principal.model	principal score model
censor.model	censoring model
failure.model	outcome model
data	dataset
xi0	sensitivity parameter xi_0
xi1	sensitivity parameter xi_1
eta0	sensitivity parameter eta_0
eta1	sensitivity parameter eta_1
estimand	the estimands of interest

## Value

The PSCE point estimates

---

`sim_data`*Simulated survival dataset*

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**Description**

A simulated dataset used to illustrate the functions in this package.

**Usage**

```
sim_data
```

**Format**

A data frame with rows corresponding to individuals and the following variables:

**U** Observed event time.

**delta** Event indicator, where 1 indicates that the event was observed and 0 indicates censoring.

**z** Treatment assignment status.

**s** Treatment receipt status.

**X1** Baseline covariate 1.

**X2** Baseline covariate 2.

**X3** Baseline covariate 3.

**X4** Baseline covariate 4.

**X5** Baseline covariate 5.

**Details**

The dataset contains simulated observations with an observed event time, event indicator, treatment assignment status, treatment receipt status, and five baseline covariates.

**Source**

Simulated by the package authors for illustration purposes.

**Examples**

```
data(sim_data)
head(sim_data)
```

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