Package 'SelectionBias'

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Title Calculates Bounds for the Selection Bias for Binary Treatment and Outcome Variables

Version 1.0.0

Description Computes bounds and sensitivity parameters as part of sensitivity analysis for selection bias. Two bounds are provided: the SV (Smith and VanderWeele) bound and the AF (assumption-free) bound. The SV bound assumes an additional dependence structure in form of a generalized M-structure whereas the AF bound holds for general assumptions in the potential outcomes framework. See Smith and VanderWeele (2019) <doi:10.1097/EDE.0000000000001032> and Zetterstrom and Waernbaum (2022) <doi:10.1515/em-2022-0108>.

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R topics documented:

AFbound *Assumption free bound for a data set*

Description

AFbound() returns the assumption free bound for a dataset that consists of an outcome, a treatment and a selection variable. If the bias is negative, the recoding of the treatment has to be done manually.

Usage

```
AFbound(whichEst, outcome, treatment, selection)
```

Arguments

whichEst	Input string. Defining the population parameter of interest. Available options are as follows. (1) Relative risk in the total population: "RR_tot", (2) Risk difference in the total population: "RD_tot", (3) Relative risk in the subpopulation: "RR_sub", (4) Risk difference in the subpopulation: "RD_sub".
outcome	Input vector. A binary outcome variable.
treatment	Input vector. A binary treatment variable.
selection	Input vector or input scalar. A binary selection variable or a selection probability.

Value

A list with the assumption free bound.

References

Zetterstrom, Stina and Waernbaum, Ingeborg. "Selection bias and multiple inclusion criteria in observational studies" Epidemiologic Methods 11, no. 1 (2022): 20220108.

Examples

```
# Example with selection indicator variable.
y = c(0, 0, 0, 0, 1, 1, 1, 1)
tr = c(0, 0, 1, 1, 0, 0, 1, 1)
sel = c(0, 1, 0, 1, 0, 1, 0, 1)
AFbound(whichEst = "RR_tot", outcome = y, treatment = tr, selection = sel)
```

```
# Example with selection probability.
selprob = mean(sel)
AFbound(whichEst = "RR_tot", outcome = y[sel==1], treatment = tr[sel==1],
 selection = selprob)

# Example with simulated data.
n = 1000
tr = rbinom(n, 1, 0.5)
y = rbinom(n, 1, 0.2 + 0.05 * tr)
sel = rbinom(n, 1, 0.4 + 0.1 * tr + 0.3 * y)
AFbound(whichEst = "RD_tot", outcome = y, treatment = tr, selection = sel)
```

SVbound *Smith and VanderWeele bound*

Description

`SVbound()` returns a list with the SV bound. All sensitivity parameters for the population of interest must be set to numbers, and the rest can be left as `NULL`. The sensitivity parameters can be inserted directly or as output from `SVboundparametersM()`. If the bias is negative, the recoding of the treatment has to be done manually.

Usage

```
SVbound(
  whichEst,
  RR_UY_T1 = NULL,
  RR_UY_T0 = NULL,
  RR_SU_T1 = NULL,
  RR_SU_T0 = NULL,
  RR_UY_S1 = NULL,
  RR_TU_S1 = NULL,
  pY1_T1_S1 = NULL,
  pY1_T0_S1 = NULL
)
```

Arguments

`whichEst`	Input string. Defining the causal estimand of interest. Available options are as follows. (1) Relative risk in the total population: "RR_tot", (2) Risk difference in the total population: "RD_tot", (3) Relative risk in the subpopulation: "RR_sub", (4) Risk difference in the subpopulation: "RD_sub".
`RR_UY_T1`	Input value. The sensitivity parameter RR_UY|T=1. Must be greater than or equal to 1. Used in the bounds for the total population.
`RR_UY_T0`	Input value. The sensitivity parameter RR_UY|T=0. Must be greater than or equal to 1. Used in the bounds for the total population.

RR_SU_T1 Input value. The sensitivity parameter RR_SU|T=1. Must be greater than or equal to 1. Used in the bounds for the total population.

RR_SU_T0 Input value. The sensitivity parameter RR_SU|T=0. Must be greater than or equal to 1. Used in the bounds for the total population.

RR_UY_S1 Input value. The sensitivity parameter RR_UY|S=1. Must be greater than or equal to 1. Used in the bounds for the subpopulation.

RR_TU_S1 Input value. The sensitivity parameter RR_TU|S=1. Must be greater than or equal to 1. Used in the bounds for the subpopulation.

pY1_T1_S1 Input value. The probability P(Y=1|T=1,I_S=1). Must be between 0 and 1. Used in the bounds for the risk difference estimands.

pY1_T0_S1 Input value. The probability P(Y=1|T=0,I_S=1). Must be between 0 and 1. Used in the bounds for the risk difference estimands.

Value

A list containing the Smith and VanderWeele bound.

References

Smith, Louisa H., and Tyler J. VanderWeele. "Bounding bias due to selection." Epidemiology (Cambridge, Mass.) 30.4 (2019): 509.

Zetterstrom, Stina and Waernbaum, Ingeborg. "Selection bias and multiple inclusion criteria in observational studies" Epidemiologic Methods 11, no. 1 (2022): 20220108.

Examples

```
# Example for relative risk in the total population.
SVbound(whichEst = "RR_tot", RR_UY_T1 = 2, RR_UY_T0 = 2,
 RR_SU_T1 = 1.7, RR_SU_T0 = 1.5)

# Example for risk difference in the total population.
SVbound(whichEst = "RD_tot", RR_UY_T1 = 2, RR_UY_T0 = 2,
 RR_SU_T1 = 1.7, RR_SU_T0 = 1.5, pY1_T1_S1 = 0.05, pY1_T0_S1 = 0.01)

# Example for relative risk in the subpopulation.
SVbound(whichEst = "RR_sub", RR_UY_S1 = 2.71, RR_TU_S1 = 2.33)

# Example for risk difference in the subpopulation.
SVbound(whichEst = "RD_sub", RR_UY_S1 = 2.71, RR_TU_S1 = 2.33,
 pY1_T1_S1 = 0.05, pY1_T0_S1 = 0.01)
```

SVboundparametersM *Sensitivity parameters for the Smith and VanderWeele bound*

Description

SVboundparametersM() returns a list with the sensitivity parameters and an indicator if bias is negative and the treatment coding is reversed for an assumed model.

Usage

```
SVboundparametersM(
  whichEst,
  Vval,
  Uval,
  Tcoef,
  Ycoef,
  Scoef,
  Mmodel,
  pY1_T1_S1,
  pY1_T0_S1
)
```

Arguments

whichEst	Input string. Defining the causal estimand of interest. Available options are as follows. (1) Relative risk in the total population: "RR_tot", (2) Risk difference in the total population: "RD_tot", (3) Relative risk in the subpopulation: "RR_sub", (4) Risk difference in the subpopulation: "RD_sub".
Vval	Input matrix. The first column is the values of the categories of V. The second column is the probabilities of the categories of V. If V is continuous, use a fine grid of values and probabilities.
Uval	Input matrix. The first column is the values of the categories of U. The second column is the probabilities of the categories of U. If U is continuous, use a fine grid of values and probabilities.
Tcoef	Input vector. Two numerical elements. The first element is the intercept in the model for the treatment. The second element is the slope in the model for the treatment.
Ycoef	Input vector. Three numerical elements. The first element is the intercept in the model for the outcome. The second element is the slope for T in the model for the outcome. The third element is the slope for U in the model for the outcome.
Scoef	Input matrix. Numerical matrix of size K by 4, where K is the number of selection variables. Each row is the coefficients for one selection variable. The first column is the intercepts in the models for the selection variables. The second column is the slopes for V in the models for the selection variables. The third column is the slopes for U in the models for the selection variables. The fourth column is the slopes for T in the models for the selection variables.

Mmodel	Input string. Defining the models for the variables in the M structure. If "P", the probit model is used. If "L", the logit model is
pY1_T1_S1	Input scalar. The observed probability P(Y=1|T=1,I_S=1).
pY1_T0_S1	Input scalar. The observed probability P(Y=1|T=0,I_S=1). used.

Value

A list containing the sensitivity parameters and an indicator if the treatment has been reversed.

References

Smith, Louisa H., and Tyler J. VanderWeele. "Bounding bias due to selection." Epidemiology (Cambridge, Mass.) 30.4 (2019): 509.

Zetterstrom, Stina and Waernbaum, Ingeborg. "Selection bias and multiple inclusion criteria in observational studies" Epidemiologic Methods 11, no. 1 (2022): 20220108.

Examples

```
# Example with no selection bias.
V = matrix(c(1, 0, 0.1, 0.9), ncol = 2)
U = matrix(c(1, 0, 0.1, 0.9), ncol = 2)
Tr = c(0, 1)
Y = c(0, 0, 1)
S = matrix(c(1, 0, 0, 0, 1, 0, 0, 0), nrow = 2, byrow = TRUE)
probT1 = 0.534
probT0 = 0.534
SVboundparametersM(whichEst = "RR_tot", Vval = V, Uval = U, Tcoef = Tr,
  Ycoef = Y, Scoef = S, Mmodel = "P", pY1_T1_S1 = probT1, pY1_T0_S1 = probT0)

# Example with selection bias. DGP from the zika example.
V = matrix(c(1, 0, 0.85, 0.15), ncol = 2)
U = matrix(c(1, 0, 0.5, 0.5), ncol = 2)
Tr = c(-6.2, 1.75)
Y = c(-5.2, 5.0, -1.0)
S = matrix(c(1.2, 2.2, 0.0, 0.5, 2.0, -2.75, -4.0, 0.0), ncol = 4)
probT1 = 0.286
probT0 = 0.004
SVboundparametersM(whichEst = "RR_sub", Vval = V, Uval = U, Tcoef = Tr,
  Ycoef = Y, Scoef = S, Mmodel = "L", pY1_T1_S1 = probT1, pY1_T0_S1 = probT0)
```

SVboundsharp *Check if the Smith and VanderWeele bound in the subpopulation is sharp*

Description

SVboundsharp() returns a string that indicates if the SV bound is sharp, if it's inconclusive or if it's not sharp. If the bias is negative, the recoding of the treatment has to be done manually.

Usage

```
SVboundsharp(BF_U, pY1_T0_S1, SVbound = NULL, AFbound = NULL)
```

Arguments

BF_U	Input scalar. The bounding factor for the SV bounds in the subpopulation. Must be equal to or above 1. Can be inserted directly or as output from SVboundparametersM().
pY1_T0_S1	Input scalar. The probability P(Y=1|T=0,I_S=1).
SVbound	Optional input scalar. The SV bound, can be inserted directly or as output from SVbound(). Only necessary if one wants to know if the SV bound is not sharp.
AFbound	Optional input scalar. The AF bound, can be inserted directly or as output from AFbound(). Only necessary if one wants to know if the SV bound is not sharp.

Value

A string stating if the SV bound is sharp, inconclusive or not sharp.

References

Smith, Louisa H., and Tyler J. VanderWeele. "Bounding bias due to selection." Epidemiology (Cambridge, Mass.) 30.4 (2019): 509.

Zetterstrom, Stina and Waernbaum, Ingeborg. MANUSCRIPT XXX

Examples

```
# Example where the SV bound is sharp.
SVboundsharp(BF_U = 1.56, pY1_T0_S1 = 0.33, SVbound = 1.56, AFbound = 3.0)

# Example where the SV bound is not sharp.
SVboundsharp(BF_U = 2, pY1_T0_S1 = 0.9, SVbound = 2, AFbound = 1.8)

# Example where the SV bound is inconclusive.
SVboundsharp(BF_U = 2, pY1_T0_S1 = 0.8, SVbound = 2, AFbound = 3)
```

`zika_learner` *Simulated data set emulating a zika outbreak in Brazil*

Description

The data set is simulated to mimic real data. For the data generating process, see the vignette.

Usage

```
data(zika_learner)
```

Format

A data frame with 5,000 observations on the following 7 binary variables:

mic_ceph Indication if the baby has microcephaly (1=microcephaly, 0=not microcephaly)

zika Indication if the mother is infected by zika (1=infected, 0=not infected)

urban Indication of the living area of the subject (1=urban, 0=rural)

SES Indication of the socioeconomic status of the subject (1=high, 0=low)

birth First selection variable. Indication if the baby is born (1=birth, 0=terminated birth)

hospital Second selection variable. Indication if the delivery is in a public hospital (1=public, 0=private)

sel_ind Selection indicator variable. Indication if the subject is included in the study (1=included, 0=not included)

Details

The data set is created to use in examples of selection bias. A similar example has previously been used in articles that construct bounds for selection bias (Smith and VanderWeele, 2019; Zetterstrom and Waernbaum, 2022).

References

de Araújo, Thalia Velho Barreto, et al. "Association between microcephaly, Zika virus infection, and other risk factors in Brazil: final report of a case-control study." The Lancet infectious diseases 18.3 (2018): 328-336.

de Oliveira, Wanderson Kleber, et al. "Infection-related microcephaly after the 2015 and 2016 Zika virus outbreaks in Brazil: a surveillance-based analysis." The Lancet 390.10097 (2017): 861-870.

Ali, Sofia, et al. "Environmental and social change drive the explosive emergence of Zika virus in the Americas." PLoS neglected tropical diseases 11.2 (2017): e0005135.

Lebov, Jill F., et al. "International prospective observational cohort study of Zika in infants and pregnancy (ZIP study): study protocol." BMC Pregnancy and Childbirth 19.1 (2019): 1-10.

Malta, Monica, et al. "Abortion in Brazil: the case for women's rights, lives, and choices." The Lancet Public Health 4.11 (2019): e552.

Smith, Louisa H., and Tyler J. VanderWeele. "Bounding bias due to selection." Epidemiology (Cambridge, Mass.) 30.4 (2019): 509.

Zetterstrom, Stina and Waernbaum, Ingeborg. "Selection bias and multiple inclusion criteria in observational studies" Epidemiologic Methods 11, no. 1 (2022): 20220108.

https://data.worldbank.org/indicator/SP.URB.TOTL.IN.ZS?locations=BR

https://agenciabrasil.ebc.com.br/en/geral/noticia/2020-12/number-births-registered-brazil-down-2019

https://www.angloinfo.com/how-to/brazil/healthcare/health-system

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