Package ‘episensr’

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Description Basic sensitivity analysis of the observed relative risks adjusting
      for unmeasured confounding and misclassification of the
      exposure/outcome, or both. It follows the bias analysis methods and
      examples from the book by Lash T.L, Fox M.P, and Fink A.K.
      ``Applying Quantitative Bias Analysis to Epidemiologic Data'',
      ('Springer', 2009).
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R topics documented:

episensr-package .................................................. 2
boot.bias .......................................................... 3
confounders .......................................................... 4
confounders.array ................................................. 5
episensr-package

Description

'episensr' provides basic sensitivity analysis of the observed relative risks adjusting for unmeasured confounding and misclassification of the exposure/outcome, or both.

Author(s)

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References


See Also

Useful links:

- https://github.com/dhaine/episensr
- Report bugs at https://github.com/dhaine/episensr/issues
**boot.bias**

*Bootstrap resampling for selection and misclassification bias models.*

**Description**

Generate $R$ bootstrap replicates of either selection or misclassification bias functions. It then generates a confidence interval of the parameter, by first order normal approximation or the bootstrap percentile interval. Replicates giving negative cell(s) in the adjusted 2-by-2 table are silently ignored.

**Usage**

```r
boot.bias(bias_model, R = 1000, conf = 0.95, ci_type = c("norm", "perc"))
```

**Arguments**

- `bias_model`: An object of class "episensr.boot", i.e. either selection bias function or misclassification bias function.
- `R`: The number of bootstrap replicates.
- `conf`: Confidence level.
- `ci_type`: A character string giving the type of interval required. Values can be either "norm" or "perc", default to "norm".

**Value**

A list with elements:

- `model`: Model ran.
- `boot_mod`: Bootstrap resampled object, of class `boot`.
- `nrep`: Number of replicates used.
- `bias_ciRR`: Bootstrap confidence interval object for relative risk.
- `bias_ciOR`: Bootstrap confidence interval object for odds ratio.
- `ci`: Confidence intervals for the bias adjusted association measures.
- `conf`: Confidence interval.

**See Also**

`boot`, `selection`, `misclassification`
Examples

misclass_eval <- misclassification(matrix(c(215, 1449, 668, 4296),
dimnames = list(c("Breast cancer+", "Breast cancer-"),
c("Smoker+", "Smoker-")),
nrow = 2, byrow = TRUE),
type = "exposure",
bias_parms = c(.78, .78, .99, .99))

set.seed(123)
boot.bias(misclass_eval)

---

**confounders**

*Sensitivity analysis to correct for unknown or unmeasured confounding without effect modification*

**Description**

Simple sensitivity analysis to correct for unknown or unmeasured confounding without effect modification. Implementation for ratio measures (relative risk – RR, or odds ratio – OR) and difference measures (risk difference – RD).

**Usage**

```r
confounders(
  case,
  exposed,
  type = c("RR", "OR", "RD"),
  bias_parms = NULL,
  alpha = 0.05
)
```

**Arguments**

- **case**: Outcome variable. If a variable, this variable is tabulated against.
- **exposed**: Exposure variable.
- **type**: Choice of implementation, with no effect measure modification for ratio measures (relative risk – RR; odds ratio – OR) or difference measures (risk difference – RD).
- **bias_parms**: Numeric vector defining the 3 necessary bias parameters. This vector has 3 elements, in the following order:
  1. the association between the confounder and the outcome among those who were not exposed (RR, OR, or RD according to choice of implementation),
  2. the prevalence of the confounder among the exposed (between 0 and 1), and
  3. the prevalence of the confounder among the unexposed (between 0 and 1).
- **alpha**: Significance level.
confounders.array

Value

A list with elements:

- obs.data: The analyzed 2 x 2 table from the observed data.
- cfder.data: The same table for Confounder +.
- nocfder.data: The same table for Confounder -.
- obs.measures: A table of relative risk with confidence intervals; for Total, Confounder +, and Confounder -.
- bias.parms: Input bias parameters.

References


Examples

```r
confounders(matrix(c(105, 85, 527, 93),
dimnames = list(c("HIV+", "HIV-"), c("Circ+", "Circ-")),
nrow = 2, byrow = TRUE),
type = "RR",
boost_parms = c(.63, .8, .05))
confounders(matrix(c(105, 85, 527, 93),
dimnames = list(c("HIV+", "HIV-"), c("Circ+", "Circ-")),
nrow = 2, byrow = TRUE),
type = "OR",
boost_parms = c(.63, .8, .05))
confounders(matrix(c(105, 85, 527, 93),
dimnames = list(c("HIV+", "HIV-"), c("Circ+", "Circ-")),
nrow = 2, byrow = TRUE),
type = "RD",
boost_parms = c(-.37, .8, .05))
```

Description

Sensitivity analysis to explore effect of residual confounding using simple algebraic transformation (array approach). It indicates the strength of an unmeasured confounder and the necessary imbalance among exposure categories to affect the observed (crude) relative risk.
Usage

```r
confounders.array(
    crude.risk,
    type = c("binary", "continuous", "RD"),
    bias_parms = NULL,
    dec = 2,
    print = TRUE
)
```

Arguments

- **crude.risk**
  Crude (apparent or observed) relative risk between the exposure and the outcome. If type ‘RD’, this is the crude (observed) risk difference.

- **type**
  Choice of implementation, for binary covariates, continuous covariates, or on risk difference scale.

- **bias_parms**
  Numeric vector defining the necessary bias parameters. This vector has 3 elements, in the following order:
  1. the association between the confounder and the outcome (RR, relative risk),
  2. the prevalence of the confounder among the exposed (between 0 and 1, if type ‘binary’), or mean value of the confounder among the exposed (if type ‘continuous’ or ‘RD’), and
  3. the prevalence of the confounder among the unexposed (between 0 and 1, if type ‘binary’), or mean value of the confounder among the unexposed (if type ‘continuous’ or ‘RD’).

- **dec**
  Number of decimals in the printout.

- **print**
  A logical scalar. Should the results be printed?

Value

A vector with elements:

- **crude.risk**
  The crude relative risk or risk difference.

- **RR_CD**
  The association between the confounder and the outcome.

- **P_C1**
  The prevalence of the confounder among the exposed, or mean value of the confounder among the exposed.

- **P_C0**
  The prevalence of the confounder among the unexposed, or mean value of the confounder among the unexposed.

- **risk_adj**
  The adjusted exposure relative risk or risk difference.

- **bias_perc**
  The bias as a percentage: (crude.RR - risk_adj)/risk_adj * 100.

References

Examples

# Example from Schneeweiss, S. Sensitivity analysis and external adjustment for
# unmeasured confounders in epidemiologic database studies of therapeutics.
confounders.array(crude.risk = 1.5, type = "binary",
    bias_parms = c(5.5, 0.5, 0.1))

# Examples from Patorno E., Gopalakrishnan, C., Franklin, J.M., Brodovicz, K.G.,
# Masso-Gonzalez, E., Bartels, D.B., Liu, J., and Schneeweiss, S. Claims-based
# studies of oral glucose-lowering medications can achieve balance in critical
# clinical variables only observed in electronic health records 2017; 20(4): 974-
# 984.
confounders.array(crude.risk = 1.5, type = "binary",
    bias_parms = c(3.25, 0.333, 0.384))

confounders.array(crude.risk = 1.5, type = "continuous",
    bias_parms = c(1.009, 7.8, 7.9))

confounders.array(crude.risk = 0.05, type = "RD", bias_parms = c(0.009, 8.5, 8),
    dec = 4)


confounders.emm

Sensitivity analysis to correct for unknown or unmeasured confounding in the presence of effect modification

Description

Simple sensitivity analysis to correct for unknown or unmeasured confounding in the presence of effect modification. Implementation for ratio measures (relative risk – RR, or odds ratio – OR) and difference measures (risk difference – RD).

Usage

confounders.emm(
    case,
    exposed,
    type = c("RR", "OR", "RD"),
    bias_parms = NULL,
    alpha = 0.05
)

Arguments

case
    Outcome variable. If a variable, this variable is tabulated against.

exposed
    Exposure variable.

type
    Choice of implementation, with no effect measure modification for ratio measures (relative risk – RR; odds ratio – OR) or difference measures (risk difference – RD).

bias_parms
    Numeric vector defining the 4 necessary bias parameters. This vector has 4 elements, in the following order:
1. the association between the confounder and the outcome among those who were exposed,
2. the association between the confounder and the outcome among those who were not exposed,
3. the prevalence of the confounder among the exposed (between 0 and 1), and
4. the prevalence of the confounder among the unexposed (between 0 and 1).

**alpha**

Significance level.

**Value**

A list with elements:

- **obs.data**: The analyzed 2 x 2 table from the observed data.
- **cfder.data**: The same table for Confounder +.
- **nocfder.data**: The same table for Confounder -.
- **obs.measures**: A table of relative risk with confidence intervals; Total, for Confounder +, and for Confounder -.
- **adj.measures**: A table of Standardized Morbidity Ratio and Mantel-Haenszel estimates.
- **bias.parms**: Input bias parameters.

**References**


**Examples**

```r
# The data for this example come from:
# Tyndall M.W., Ronald A.R., Agoki E., Malisa W., Bwayo J.J., Ndinya-Achola J.O.
# et al.
# Increased risk of infection with human immunodeficiency virus type 1 among
# uncircumcised men presenting with genital ulcer disease in Kenya.
confounders.emm(matrix(c(105, 85, 527, 93),
dimnames = list(c("HIV+", "HIV-"), c("Circ+", "Circ-")),
nrow = 2, byrow = TRUE),
type = "RR",
bias_parms = c(.4, .7, .8, .05))
confounders.emm(matrix(c(105, 85, 527, 93),
dimnames = list(c("HIV+", "HIV-"), c("Circ+", "Circ-")),
nrow = 2, byrow = TRUE),
type = "OR",
bias_parms = c(.4, .7, .8, .05))
confounders.emm(matrix(c(105, 85, 527, 93),
dimnames = list(c("HIV+", "HIV-"), c("Circ+", "Circ-")),
nrow = 2, byrow = TRUE),
type = "RD",
bias_parms = c(-.6, -.3, .8, .05))
```
confounders.evalue

**Compute E-value to assess bias due to unmeasured confounder.**

**Description**

Help to quantify the evidence strength for causality in presence of unmeasured confounding. The E-value is the minimum strength of association that an unmeasured confounder would need to have with both the exposure and the outcome, conditional on the measured covariates, to fully explain away a specific exposure-outcome association.

**Usage**

```r
confounders.evalue(
  est,
  lower_ci = NULL,
  upper_ci = NULL,
  sd = NA,
  type = c("RR", "ORc", "HRc", "diff_RR", "diff_OR"),
  true_est = 1
)
```

**Arguments**

- `est` Point estimate for the effect measure. For difference in continuous outcomes, it is the standardized effect size (i.e. mean of the outcome divided by its standard deviation).
- `lower_ci` Lower limit of the confidence interval for the association (relative risk, odds ratio, hazard ratio, incidence rate ratio, risk difference).
- `upper_ci` Upper limit of the confidence interval for the association (relative risk, odds ratio, hazard ratio, incidence rate ratio, risk difference).
- `sd` For difference in continuous outcomes, the standard error of the outcome divided by its standard deviation.
- `type` Choice of effect measure (relative risk, and odds ratio or hazard ratio for rare outcomes i.e. < 15 outcome – ORc; hazard ratio for common outcome i.e. > 15 difference in continuous outcomes, RR approximation – diff_RR; difference in continuous outcomes, OR approximation – diff_OR).
- `true_est` True estimate to assess E-value for. Default to 1 on risk scale to assess against null value. Set to a different value to assess for non-null hypotheses.

**Value**

A matrix with the observed point estimate and closest confidence interval to the null hypothesis, expressed as a relative risk, and their corresponding E-value.
References

Examples

# The data for this example come from:
# Victoria C.G., Smith P.G., Vaughan J.P., Nobre L.C., Lombardi C., Teixeira A.M.
# et al.
# Evidence for protection by breast-feeding against infant deaths from infectious
# diseases in Brazil.
confounders.evalue(est = 3.9, type = "RR")

# The data for this example come from:
# Oddy W.H, Smith G.J., Jacony P.
# A possible strategy for developing a model to account for attrition bias in a
# longitudinal cohort to investigate associations between exclusive breastfeeding and
# overweight and obesity at 20 years.
confounders.evalue(est = 1.47, lower_ci = 1.12, upper_ci = 1.93, type = "ORc")

# The data for this example come from:
# Reinisch J., Sanders S., Mortensen E., Rubin D.B.
# In-utero exposure to phenobarbital and intelligence deficits in adult men.
# Journal of the American Medical Association 1995;274:1518-1525
confounders.evalue(est = -0.42, sd = 0.14, type = "diff_RR")

confounders.ext  Sensitivity analysis for unmeasured confounders based on external adjustment

Description
Sensitivity analysis to explore effect of residual confounding using simple algebraic transformation. It provides the relative risk adjusted for unmeasured confounders based on available external information (i.e. from the literature) on the relation between confounders and outcome.

Usage
confounders.ext(RR, bias_parms = NULL, dec = 2, print = TRUE)

Arguments
RR  "True" or fully adjusted exposure relative risk.
bias_parms  Numeric vector defining the necessary bias parameters. This vector has 4 elements, in the following order:
                 1. the association between the confounder and the outcome (RR, relative risk),
2. the association between exposure category and the confounder (OR, odds ratio),
3. the prevalence of the confounder (between 0 and 1), and
4. the prevalence of the exposure (between 0 and 1).

dec Number of decimals in the printout.

print A logical scalar. Should the results be printed?

Value
A vector with elements:

RR True (adjusted) exposure relative risk.

RR_CD The association between the confounder and the outcome.

OR_EC The association between exposure category and the confounder.

P_C The prevalence of the confounder.

P_E The prevalence of the exposure.

crude.RR Crude (observed) exposure relative risk.

bias_perc The bias as a percentage: (crude.RR - RR)/RR * 100.

References

Examples
confounders.ext(RR = 1, bias_parms = c(0.1, 0.9, 0.1, 0.4))

confounders.limit Bounding the bias limits of unmeasured confounding.

Description
Function to elicit the limits on measures of effect corrected for an unmeasured confounder when only some of the bias parameters are known.
### confounders.limit

**Usage**

```r
confounders.limit(
  p = NA,
  RR = NA,
  OR = NA,
  crude.RR = NULL,
  dec = 4,
  print = TRUE
)
```

**Arguments**

- `p` Proportion with the confounder among the unexposed group.
- `RR` Relative risk between the confounder and the outcome.
- `OR` Odds ratio between the confounder and the outcome.
- `crude.RR` Crude relative risk between the exposure and the outcome.
- `dec` Number of decimals in the printout.
- `print` A logical scalar. Should the results be printed?

**Value**

A list with elements:

- `conf.limits` Limits on confounding.
- `bias.parms` Input bias parameters p, RR, OR, and crude RR.

**References**


**Examples**

```r
confounders.limit(OR = 1.65, crude.RR = 1.5)
```
Description

Simple sensitivity analysis to correct for unknown or unmeasured polychotomous (3-level) confounding without effect modification. Implementation for ratio measures (relative risk – RR, or odds ratio – OR) and difference measures (risk difference – RD).

Usage

confounders.poly(
  case,
  exposed,
  type = c("RR", "OR", "RD"),
  bias_parms = NULL,
  alpha = 0.05
)

Arguments

case                   Outcome variable. If a variable, this variable is tabulated against.
exposed                Exposure variable.
type                   Choice of implementation, with no effect measure modification for ratio measures (relative risk – RR; odds ratio – OR) or difference measures (risk difference – RD).
bias_parms             Numeric vector defining the bias parameters. This vector has 6 elements, in the following order:
                        1. the association between the highest level confounder and the outcome,
                        2. the association between the mid-level confounder and the outcome,
                        3. the prevalence of the highest level confounder among the exposed (between 0 and 1),
                        4. the prevalence of the highest level confounder among the unexposed (between 0 and 1),
                        5. the prevalence of the mid-level confounder among the exposed (between 0 and 1), and
                        6. the prevalence of the mid-level confounder among the unexposed (between 0 and 1).
alpha                  Significance level.
### Value

A list with elements:

- `obs.data`: The analyzed 2 x 2 table from the observed data.
- `cfder1.data`: The same table for Mid-level Confounder +.
- `cfder2.data`: The same table for Highest-level Confounder +.
- `nocfder.data`: The same table for Confounder -.
- `obs.measures`: A table of relative risk with confidence intervals; Total and by confounders.
- `bias.parms`: Input bias parameters.

### References


### Examples

```r
# The data for this example come from:
# Tyndall M.W., Ronald A.R., Agoki E., Malisa W., Bwayo J.J., Ndinya-Achola J.O.
# et al.
# Increased risk of infection with human immunodeficiency virus type 1 among
# uncircumcised men presenting with genital ulcer disease in Kenya.
confounders.poly(matrix(c(105, 85, 527, 93),
dimnames = list(c("HIV+", "HIV-"), c("Circ+", "Circ-")),
nrow = 2, byrow = TRUE),
type = "RR",
bias_parms = c(.4, .8, .6, .05, .2, .2))

confounders.poly(matrix(c(105, 85, 527, 93),
dimnames = list(c("HIV+", "HIV-"), c("Circ+", "Circ-")),
nrow = 2, byrow = TRUE),
type = "OR",
bias_parms = c(.4, .8, .6, .05, .2, .2))

confounders.poly(matrix(c(105, 85, 527, 93),
dimnames = list(c("HIV+", "HIV-"), c("Circ+", "Circ-")),
nrow = 2, byrow = TRUE),
type = "RD",
bias_parms = c(-.4, -.2, .6, .05, .2, .2))
```

---

**mbias**

*Sensitivity analysis to correct for selection bias caused by M bias.*

### Description

Simple sensitivity analysis to correct for selection bias caused by M bias using estimates of the odds ratios relating the variables.
mbias

Usage

mbias(or, var)

Arguments

or  Vector defining the input bias parameters, in the following order:
    1. Odds ratio between A and the exposure E,
    2. Odds ratio between A and the collider C,
    3. Odds ratio between B and the collider C,
    4. Odds ratio between B and the outcome D,
    5. Odds ratio observed between the exposure E and the outcome D.

var  Vector defining variable names, in the following order:
     1. Outcome,
     2. Exposure,
     3. A,
     4. B,
     5. Collider.

Value

A list with elements:

mbias.parms  Maximum bias parameters.
adj.measures  Selection bias corrected measures.
bias.parms    Input bias parameters.

References


Examples

mbias(or = c(2, 5.4, 2.5, 1.5, 1),
var = c("HIV", "Circumcision", "Muslim", "Low CD4", "Participation"))
Sensitivity analysis for disease or exposure misclassification.

Description

Simple sensitivity analysis for disease or exposure misclassification. Confidence interval for odds ratio is computed as in Chu et al. (2006), for exposure misclassification.

Usage

misclassification(
  case,
  exposed,
  type = c("exposure", "outcome"),
  bias_parms = NULL,
  alpha = 0.05
)

Arguments

case  Outcome variable. If a variable, this variable is tabulated against.
exposed Exposure variable.
type  Choice of misclassification:
  1. exposure: bias analysis for exposure misclassification; corrections using sensitivity and specificity: nondifferential and independent errors,
  2. outcome: bias analysis for outcome misclassification.
bias_parms Vector defining the bias parameters. This vector has 4 elements between 0 and 1, in the following order:
  1. Sensitivity of exposure (when type = "exposure") or outcome (when type = "outcome") classification among those with the outcome (when type = "exposure") or exposure (when type = "outcome”),
  2. Sensitivity of exposure (or outcome) classification among those without the outcome (or exposure),
  3. Specificity of exposure (or outcome) classification among those with the outcome (or exposure), and
  4. Specificity of exposure (or outcome) classification among those without the outcome (or exposure).
alpha  Significance level.

Value

A list with elements:

obs.data  The analyzed 2 x 2 table from the observed data.
corr.data The expected observed data given the true data assuming misclassification.
misclassification Cov

obs.measures A table of observed relative risk and odds ratio with confidence intervals.
adj.measures A table of adjusted relative risk and odds ratio with confidence interval for odds ratio.
bias.parms Input bias parameters.

References


Examples

# The data for this example come from:
# Fink, A.K., Lash, T.L. A null association between smoking during pregnancy and breast cancer using Massachusetts registry data (United States).
# Cancer Causes Control 2003;14:497-503.
misclassification(matrix(c(215, 1449, 668, 4296),
dimnames = list(c("Breast cancer+", "Breast cancer-"),
c("Smoker+", "Smoker-")),
nrow = 2, byrow = TRUE),
type = "exposure",
bias_parms = c(.78, .78, .99, .99))
misclassification(matrix(c(4558, 3428, 46305, 46085),
dimnames = list(c("AMI death+", "AMI death-"),
c("Male+", "Male-")),
nrow = 2, byrow = TRUE),
type = "outcome",
bias_parms = c(.53, .53, .99, .99))

# The following example comes from Chu et al. Sensitivity analysis of misclassification: A graphical and a Bayesian approach.
misclassification(matrix(c(126, 92, 71, 224),
dimnames = list(c("Case", "Control"), c("Smoker+", "Smoker-")),
nrow = 2, byrow = TRUE),
type = "exposure",
bias_parms = c(.94, .94, .97, .97))

misclassification_cov Sensitivity analysis for covariate misclassification.

Description

Simple sensitivity analysis to correct for a misclassified covariate (a potential confounder or effect measure modifier).
Usage

misclassification_cov(
  case,
  exposed,
  covariate,
  bias_parms = NULL,
  alpha = 0.05
)

Arguments

case                  Outcome variable. If a variable, this variable is tabulated against.
exposed              Exposure variable.
covariate             Covariate to stratify on.
bias_parms           Vector defining the bias parameters. This vector has 4 elements between 0 and 1, in the following order:
                      1. Sensitivity of confounder classification among those with the outcome,
                      2. Sensitivity of confounder classification among those without the outcome,
                      3. Specificity of confounder classification among those with the outcome,and
                      4. Specificity of confounder classification among those without the outcome.
alpha                 Significance level.

Value

A list with elements:

obs.data            The analyzed stratified 2 x 2 tables from the observed data.
corr.data           The expected stratified observed data given the true data assuming misclassification.
obsmasures          A table of observed relative risk and odds ratio with confidence intervals.
adj.masures         A table of adjusted relative risk and odds ratio.
bias.parms          Input bias parameters.

References


Examples

# The data for this example come from:
# Berry, R.J., Kihlberg, R., and Devine, O. Impact of misclassification of in vitro
# fertilisation in studies of folic acid and twinning: modelling using population
# based Swedish vital records.
# BMJ, doi:10.1136/bmj.38369.437789.82 (published 17 March 2004)
misclassification_cov(array(c(1319, 38054, 5641, 405546,
**multidimBias**

Multidimensional sensitivity analysis for different sources of bias

**Description**

Multidimensional sensitivity analysis for different sources of bias

**Usage**

```r
multidimBias(
  case,
  exposed,
  type = c("exposure", "outcome", "confounder", "selection"),
  se = NULL,
  sp = NULL,
  bias_parms = NULL,
  OR.sel = NULL,
  alpha = 0.05,
  dec = 4,
  print = TRUE
)
```

**Arguments**

- **case**: Outcome variable. If a variable, this variable is tabulated against.
- **exposed**: Exposure variable.
- **type**: Implement analysis for exposure misclassification, outcome misclassification, unmeasured confounder, or selection bias.
- **se**: Numeric vector of sensitivities.
- **sp**: Numeric vector of specificities.
- **bias_parms**: List of bias parameters. The list is made of 3 vectors of the same length:
  1. Prevalence of Confounder in Exposure+ population,
  2. Prevalence of Confounder in Exposure- population, and
  3. Relative risk between Confounder and Outcome.
- **OR.sel**: Selection odds ratios, for selection bias implementation.
- **alpha**: Significance level.
- **dec**: Number of decimals in the printout.
- **print**: A logical scalar. Should the results be printed?
Value

A list with elements:

<table>
<thead>
<tr>
<th>Element</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>obs.data</td>
<td>The analyzed 2 x 2 table from the observed data.</td>
</tr>
<tr>
<td>obs.measures</td>
<td>A table of odds ratios and relative risk with confidence intervals.</td>
</tr>
<tr>
<td>adj.measures</td>
<td>Multidimensional corrected relative risk and/or odds ratio data.</td>
</tr>
<tr>
<td>bias.parms</td>
<td>Bias parameters.</td>
</tr>
</tbody>
</table>

References


Examples

```r
multidimBias(matrix(c(45, 94, 257, 945),
                  dimnames = list(c("HIV+", "HIV-"), c("Circ+", "Circ-")),
                  nrow = 2, byrow = TRUE),
                  type = "exposure",
                  se = c(1, 1, .9, .9, .8, .8, .8),
                  sp = c(1, .9, .8, 1, .9, .8, 1))
```

```r
multidimBias(matrix(c(105, 85, 527, 93),
                  dimnames = list(c("HIV+", "HIV-"), c("Circ+", "Circ-")),
                  nrow = 2, byrow = TRUE),
                  type = "confounder",
                  bias_parms = list(seq(.72, .92, by = .02),
                                     seq(.01, .11, by = .01),
                                     seq(.13, 1.13, by = .1))
```

```r
multidimBias(matrix(c(136, 107, 297, 165),
                  dimnames = list(c("Uveal Melanoma+", "Uveal Melanoma-"),
                                  c("Mobile Use+", "Mobile Use -")),
                  nrow = 2, byrow = TRUE),
                  type = "selection",
                  OR.sel = seq(1.5, 6.5, by = .5))
```

multiple.bias  

Extract adjusted 2-by-2 table from episensr object

Description

Extract the adjusted 2-by-2 table from an episensr function, so that it can be re-used into an other episensr function when performing multiple (combined) bias analysis. Allowed functions are: 'selection', 'misclassification', 'confounders', 'probsens', 'probsens.sel', and 'probsens.conf'.

```r
multidimBias(matrix(c(45, 94, 257, 945),
                  dimnames = list(c("HIV+", "HIV-"), c("Circ+", "Circ-")),
                  nrow = 2, byrow = TRUE),
                  type = "exposure",
                  se = c(1, 1, .9, .9, .8, .8, .8),
                  sp = c(1, .9, .8, 1, .9, .8, 1))
```
Usage

```r
multiple.bias(
  x,
  bias_function = c("selection", "misclassification", "confounders", "probsens.sel",
                    "probsens.conf", "probsens"),
  ...
)
```

Arguments

- `x`: An object of class `episensr` or `episensr.probsens`.
- `bias_function`: Bias function to be called. Choices between `selection`, `misclassification`, `confounders`, `probsens`, `probsens.sel`, `probsens.conf`.
- `...`: Additional arguments passed on to methods.

Value

A list with the elements corresponding to the bias function called.

See Also

- `selection`, `misclassification`, `confounders`, `probsens`, `probsens.sel`, `probsens.conf`

Examples

```r
dat <- matrix(c(118, 832, 103, 884),
              dimnames = list(c("BC+", "BC-"), c("AD+", "AD-")), nrow = 2, byrow = TRUE)
dat %>%
misclassification(., type = "exposure", bias_parms = c(.56, .58, .99, .97)) %>%
multiple.bias(., bias_function = "selection", bias_parms = c(.73, .61, .82, .76))
```

---

**plot.episensr.booted**

*Plot of bootstrap simulation output for selection and misclassification bias*

**Description**

This takes an episensr bootstrap object and produces the plot of bootstrap replicates for selection or misclassification bias of the variable of interest, either relative risk or odds ratio.

**Usage**

```r
## S3 method for class 'episensr.booted'
plot(x, association = c("rr", "or"), ...)
```
Arguments

- **x**
  An object of class "episensr.booted" returned from the episensr bootstrap generation function.

- **association**
  Choice between bias adjusted relative risk and odds ratio.

- **...**
  Other unused arguments.

See Also

- boot.bias, boot, selection, misclassification

Examples

```r
misclass_eval <- misclassification(matrix(c(215, 1449, 668, 4296),
dimnames = list(c("Breast cancer+", "Breast cancer-"),
c("Smoker+", "Smoker-")),
nrow = 2, byrow = TRUE),
type = "exposure",
bias_parms = c(.78, .78, .99, .99))
set.seed(123)
misclass_boot <- boot.bias(misclass_eval)
plot(misclass_boot, association = "rr")
```

---

**plot.mbias**

*Plot DAGs before and after conditioning on collider (M bias)*

Description

Create two DAGs, before and after conditioning on the collider C, for selection bias caused by M bias, using ggplot2.

Usage

```r
## S3 method for class 'mbias'
plot(
x,
title1 = "DAG before conditioning on C",
title2 = "DAG after conditioning on C",
title.size = 6,
size = 6,
dec = 2,
layout = c("landscape", "portrait"),
...
)
```
Arguments

- `x`: 'mbias' object to plot.
- `title1`: Title of DAG graph before conditioning on C.
- `title2`: Title of DAG graph after conditioning on C.
- `title.size`: Title size.
- `size`: Text size.
- `dec`: Number of digits displayed.
- `layout`: Side-by-side graphs in landscape or portrait layout.
- `...`: Other unused arguments.

Value

Two DAGs for selection bias caused by M bias.

See Also

`mbias`

Examples

```r
plot(mbias(or = c(2, 5.4, 2.5, 1.5, 1),
var = c("HIV", "Circumcision", "Muslim", "Low CD4", "Participation")))
```

---

`print.episensr`  
*Print associations for episensr class*

Description

Print associations for episensr objects.

Usage

```r
## S3 method for class 'episensr'
print(x, digits = getOption("digits"), ...)
```

Arguments

- `x`: An object of class 'episensr'.
- `digits`: Minimal number of _significant_ digits, see 'print.default'.
- `...`: Other unused arguments.

Value

Print the observed and adjusted measures of association.
print.episensr.booted  Print bootstrapped confidence intervals

Description
Print bootstrap-ed confidence intervals for selection and misclassification bias functions.

Usage
```r
## S3 method for class 'episensr.booted'
print(x, digits = getOption("digits"), ...)
```

Arguments
- `x` An object of class 'episensr.booted'.
- `digits` Minimal number of _significant_ digits, see 'print.default'.
- `...` Other unused arguments.

Value
Print the confidence interval of the adjusted measures of association.

print.mbias  Print association corrected for M bias

Description
Print association corrected for M bias.

Usage
```r
## S3 method for class 'mbias'
print(x, ...)
```

Arguments
- `x` An object of class 'mbias'.
- `...` Other unused arguments.

Value
Print the observed and adjusted measures of association.
Probsens

Probabilistic sensitivity analysis. 

Description

Probabilistic sensitivity analysis to correct for exposure misclassification or outcome misclassification and random error. Non-differential misclassification is assumed when only the two bias parameters seca.parms and spca.parms are provided. Adding the 2 parameters seexp.parms and spexp.parms (i.e. providing the 4 bias parameters) evaluates a differential misclassification.

Usage

probsens(
  case, 
  exposed, 
  type = c("exposure", "outcome"), 
  reps = 1000, 
  seca.parms = list(dist = c("constant", "uniform", "triangular", "trapezoidal", "logit-logistic", "logit-normal"), parms = NULL), 
  seexp.parms = NULL, 
  spca.parms = list(dist = c("constant", "uniform", "triangular", "trapezoidal", "logit-logistic", "logit-normal"), parms = NULL), 
  spexp.parms = NULL, 
  corr.se = NULL, 
  corr.sp = NULL, 
  discard = TRUE, 
  alpha = 0.05
)

Arguments

case Outcome variable. If a variable, this variable is tabulated against.
exposed Exposure variable.
type Choice of correction for exposure or outcome misclassification.
reps Number of replications to run.
seca.parms List defining:
  1. The sensitivity of exposure classification among those with the outcome (when type = "exposure"), or
  2. The sensitivity of outcome classification among those with the exposure (when type = "outcome").

The first argument provides the probability distribution function (constant, uniform, triangular, trapezoidal, logit-logistic, or logit-normal) and the second its parameters as a vector. Logit-logistic and logit-normal distributions can be shifted by providing lower and upper bounds. Avoid providing these values if a non-shifted distribution is desired.
1. Constant: constant value,
2. Uniform: min, max,
3. Triangular: lower limit, upper limit, mode,
4. Trapezoidal: min, lower mode, upper mode, max,
5. Logit-logistic: location, scale, lower bound shift, upper bound shift,

seexp.parms List defining:
1. The sensitivity of exposure classification among those without the outcome (when type = "exposure"), or
2. The sensitivity of outcome classification among those without the exposure (when type = "outcome").

spca.parms List as above for seca.parms but for specificity.

spexp.parms List as above for seexp.parms but for specificity.

corr.se Correlation between case and non-case sensitivities.

corr.sp Correlation between case and non-case specificities.
discard A logical scalar. In case of negative adjusted count, should the draws be discarded? If set to FALSE, negative counts are set to zero.

alpha Significance level.

Value
A list with elements:

obs.data The analyzed 2 x 2 table from the observed data.

obs.measures A table of observed relative risk and odds ratio with confidence intervals.

adj.measures A table of corrected relative risks and odds ratios.

sim.df Data frame of random parameters and computed values.

treps Number of replications.

References

Examples
# The data for this example come from:
# Greenland S., Salvan A., Wegman D.H., Hallock M.F., Smith T.J.
# A case-control study of cancer mortality at a transformer-assembly facility.
set.seed(123)
# Exposure misclassification, non-differential
probsens(matrix(c(45, 94, 257, 945),
dimnames = list(c("BC+", "BC-"), c("Smoke+", "Smoke-")), nrow = 2, byrow = TRUE),
type = "exposure",
reps = 20000,
seca.parms = list("trapezoidal", c(.75, .85, .95, 1)),
spca.parms = list("trapezoidal", c(.75, .85, .95, 1)))
# Exposure misclassification, differential
probsens(matrix(c(45, 94, 257, 945),
dimnames = list(c("BC+", "BC-"), c("Smoke+", "Smoke-")), nrow = 2, byrow = TRUE),
type = "exposure",
reps = 20000,
seca.parms = list("trapezoidal", c(.75, .85, .95, 1)),
seexp.parms = list("trapezoidal", c(.7, .8, .9, .95)),
spca.parms = list("trapezoidal", c(.75, .85, .95, 1)),
spexp.parms = list("trapezoidal", c(.7, .8, .9, .95)),
corr.se = .8,
corr.sp = .8)
# Disease misclassification
probsens(matrix(c(173, 602, 134, 663),
dimnames = list(c("BC+", "BC-"), c("Smoke+", "Smoke-")), nrow = 2, byrow = TRUE),
type = "outcome",
reps = 20000,
seca.parms = list("uniform", c(.8, 1)),
spca.parms = list("uniform", c(.8, 1)))

---

**probsens.conf**

Probabilistic sensitivity analysis for unmeasured confounding.

**Description**

Probabilistic sensitivity analysis to correct for unknown or unmeasured confounding and random error simultaneously.

**Usage**

```r
probsens.conf(
  case,
  exposed,
  reps = 1000,
  prev.exp = list(dist = c("constant", "uniform", "triangular", "trapezoidal",
                          "logit-logistic", "logit-normal"), parms = NULL),
  prev.nexp = list(dist = c("constant", "uniform", "triangular", "trapezoidal",
                         "logit-logistic", "logit-normal"), parms = NULL),
  risk = list(dist = c("constant", "uniform", "triangular", "trapezoidal",
                     "log-logistic", "log-normal"), parms = NULL),
  corr.p = NULL,
  discard = TRUE,
  alpha = 0.05
)
```
Arguments

- **case**: Outcome variable. If a variable, this variable is tabulated against.
- **exposed**: Exposure variable.
- **reps**: Number of replications to run.
- **prev.exp**: List defining the prevalence of exposure among the exposed. The first argument provides the probability distribution function (constant, uniform, triangular, trapezoidal, logit-logistic, or logit-normal) and the second its parameters as a vector. Logit-logistic and logit-normal distributions can be shifted by providing lower and upper bounds. Avoid providing these values if a non-shifted distribution is desired.
  1. Constant: constant value,
  2. Uniform: min, max,
  3. Triangular: lower limit, upper limit, mode,
  4. Trapezoidal: min, lower mode, upper mode, max.
  5. Logit-logistic: location, scale, lower bound shift, upper bound shift,
- **prev.nexp**: List defining the prevalence of exposure among the unexposed.
- **risk**: List defining the confounder-disease relative risk or the confounder-exposure odds ratio. The first argument provides the probability distribution function (constant, uniform, triangular, trapezoidal, log-logistic, or log-normal) and the second its parameters as a vector:
  1. Constant: constant value,
  2. Uniform: min, max,
  3. Triangular: lower limit, upper limit, mode,
  4. Trapezoidal: min, lower mode, upper mode, max.
  5. Log-logistic: shape, rate. Must be strictly positive,
  6. Log-normal: meanlog, sdlog. This is the mean and standard deviation on the log scale.
- **corr.p**: Correlation between the exposure-specific confounder prevalences.
- **discard**: A logical scalar. In case of negative adjusted count, should the draws be discarded? If set to FALSE, negative counts are set to zero.
- **alpha**: Significance level.

Value

A list with elements:

- **obs.data**: The analyzed 2 x 2 table from the observed data.
- **obs.measures**: A table of observed relative risk and odds ratio with confidence intervals.
- **adj.measures**: A table of corrected relative risks and odds ratios.
- **sim.df**: Data frame of random parameters and computed values.
- **reps**: Number of replications.
References


Examples

# The data for this example come from:
# Increased risk of infection with human immunodeficiency virus type 1 among
# uncircumcised men presenting with genital ulcer disease in Kenya.
set.seed(123)
probsens.conf(matrix(c(105, 85, 527, 93),
dimnames = list(c("HIV+", "HIV-"), c("Circ+", "Circ-")), nrow = 2, byrow = TRUE),
reps = 20000,
prev.exp = list("triangular", c(.7, .9, .8)),
prev.nexp = list("trapezoidal", c(.03, .04, .05, .06)),
risk = list("triangular", c(.6, .7, .63)),
corr.p = .8)

probsens.irr

Probabilistic sensitivity analysis for exposure misclassification of
person-time data and random error.

Description

Probabilistic sensitivity analysis to correct for exposure misclassification when person-time data has been collected. Non-differential misclassification is assumed when only the two bias parameters seca.parms and spca.parms are provided. Adding the 2 parameters seexp.parms and spexp.parms (i.e. providing the 4 bias parameters) evaluates a differential misclassification.

Usage

probsens.irr(
  counts,
  pt = NULL,
  reps = 1000,
  seca.parms = list(dist = c("constant", "uniform", "triangular", "trapezoidal", 
    "logit-logistic", "logit-normal"), parms = NULL),
  seexp.parms = NULL,
  spca.parms = list(dist = c("constant", "uniform", "triangular", "trapezoidal", 
    "logit-logistic", "logit-normal"), parms = NULL),
  spexp.parms = NULL,
  corr.se = NULL,
  corr.sp = NULL,
  discard = TRUE,
  alpha = 0.05
)
**Arguments**

- **counts**: A table or matrix where first row contains disease counts and second row contains person-time at risk, and first and second columns are exposed and unexposed observations, as:

<table>
<thead>
<tr>
<th></th>
<th>Exposed</th>
<th>Unexposed</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cases</td>
<td>a</td>
<td>b</td>
</tr>
<tr>
<td>Person-time</td>
<td>N1</td>
<td>N0</td>
</tr>
</tbody>
</table>

- **pt**: A numeric vector of person-time at risk. If provided, **counts** must be a numeric vector of disease counts.

- **reps**: Number of replications to run.

- **seca.parms**: List defining the sensitivity of exposure classification among those with the outcome. The first argument provides the probability distribution function (uniform, triangular, trapezoidal, logit-logistic, or logit-normal) and the second its parameters as a vector. Logit-logistic and logit-normal distributions can be shifted by providing lower and upper bounds. Avoid providing these values if a non-shifted distribution is desired.

  1. Constant: constant value,
  2. Uniform: min, max,
  3. Triangular: lower limit, upper limit, mode,
  4. Trapezoidal: min, lower mode, upper mode, max,
  5. Logit-logistic: location, scale, lower bound shift, upper bound shift,

- **seexp.parms**: List defining the sensitivity of exposure classification among those without the outcome.

- **spca.parms**: List defining the specificity of exposure classification among those with the outcome.

- **spexp.parms**: List defining the specificity of exposure classification among those without the outcome.

- **corr.se**: Correlation between case and non-case sensitivities.

- **corr.sp**: Correlation between case and non-case specificities.

- **discard**: A logical scalar. In case of negative adjusted count, should the draws be discarded? If set to FALSE, negative counts are set to zero.

- **alpha**: Significance level.

**Value**

A list with elements:

- **obs.data**: The analyzed 2 x 2 table from the observed data.

- **obs.measures**: A table of observed incidence rate ratio with exact confidence interval.

- **adj.measures**: A table of corrected incidence rate ratios.

- **sim.df**: Data frame of random parameters and computed values.
References

Examples

```r
set.seed(123)
# Exposure misclassification, non-differential
probsens.irr(matrix(c(2, 67232, 58, 10539000),
dimnames = list(c("GBS+", "Person-time"), c("HPV+", "HPV-")), ncol = 2),
reps = 20000,
seca.parms = list("trapezoidal", c(.4, .45, .55, .6)),
spca.parms = list("constant", 1))
```

probsens.irr.conf Probabilistic sensitivity analysis for unmeasured confounding of person-time data and random error.

Description
Probabilistic sensitivity analysis to correct for unmeasured confounding when person-time data has been collected.

Usage

```r
probsens.irr.conf(
  counts,
  pt = NULL,
  reps = 1000,
  prev.exp = list(dist = c("constant", "uniform", "triangular", "trapezoidal", "logit-logistic", "logit-normal"), parms = NULL),
  prev.nexp = list(dist = c("constant", "uniform", "triangular", "trapezoidal", "logit-logistic", "logit-normal"), parms = NULL),
  risk = list(dist = c("constant", "uniform", "triangular", "trapezoidal", "log-logistic", "log-normal"), parms = NULL),
  corr.p = NULL,
  alpha = 0.05
)
```

Arguments
counts A table or matrix where first row contains disease counts and second row contains person-time at risk, and first and second columns are exposed and unexposed observations, as:

<table>
<thead>
<tr>
<th></th>
<th>Exposed</th>
<th>Unexposed</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cases</td>
<td>a</td>
<td>b</td>
</tr>
<tr>
<td>Person-time</td>
<td>N1</td>
<td>N0</td>
</tr>
</tbody>
</table>
**pt**
A numeric vector of person-time at risk. If provided, `counts` must be a numeric vector of disease counts.

**reps**
Number of replications to run.

**prev.exp**
List defining the prevalence of exposure among the exposed. The first argument provides the probability distribution function (constant, uniform, triangular, trapezoidal, logit-logistic, or logit-normal) and the second its parameters as a vector. Logit-logistic and logit-normal distributions can be shifted by providing lower and upper bounds. Avoid providing these values if a non-shifted distribution is desired.

1. Constant; value,
2. Uniform: min, max,
3. Triangular: lower limit, upper limit, mode,
4. Trapezoidal: min, lower mode, upper mode, max.
5. Logit-logistic: location, scale, lower bound shift, upper bound shift,

**prev.nexp**
List defining the prevalence of exposure among the unexposed.

**risk**
List defining the confounder-disease relative risk or the confounder-exposure odds ratio. The first argument provides the probability distribution function (constant, uniform, triangular, trapezoidal, log-logistic, or log-normal) and the second its parameters as a vector:

1. Constant: value,
2. Uniform: min, max,
3. Triangular: lower limit, upper limit, mode,
4. Trapezoidal: min, lower mode, upper mode, max.
5. Log-logistic: shape, rate. Must be strictly positive,
6. Log-normal: meanlog, sdlog. This is the mean and standard deviation on the log scale.

**corr.p**
Correlation between the exposure-specific confounder prevalences.

**alpha**
Significance level.

**Value**
A list with elements:

- **obs.data**
  The analyzed 2 x 2 table from the observed data.

- **obs.measures**
  A table of observed incidence rate ratio with exact confidence interval.

- **adj.measures**
  A table of corrected incidence rate ratios.

- **sim.df**
  Data frame of random parameters and computed values.

**References**
Examples

```r
set.seed(123)
# Unmeasured confounding
probsens.irr.conf(matrix(c(77, 10000, 87, 10000),
dimnames = list(c("D+", "Person-time"), c("E+", "E-")), ncol = 2),
reps = 20000,
prev.exp = list("trapezoidal", c(.01, .2, .3, .51)),
prev.nexp = list("trapezoidal", c(.09, .27, .35, .59)),
risk = list("trapezoidal", c(2, 2.5, 3.5, 4.5)),
corr.p = .8)
```

Description

Probabilistic sensitivity analysis for selection bias.

Usage

```r
probsens.sel(
  case,
  exposed,
  reps = 1000,
  or.parms = list(dist = c("constant", "uniform", "triangular", "trapezoidal", "log-logistic", "log-normal"), parms = NULL),
  case.exp = list(dist = c("constant", "uniform", "triangular", "trapezoidal", "logit-logistic", "logit-normal"), parms = NULL),
  case.nexp = list(dist = c("constant", "uniform", "triangular", "trapezoidal", "logit-logistic", "logit-normal"), parms = NULL),
  ncase.exp = list(dist = c("constant", "uniform", "triangular", "trapezoidal", "logit-logistic", "logit-normal"), parms = NULL),
  ncase.nexp = list(dist = c("constant", "uniform", "triangular", "trapezoidal", "logit-logistic", "logit-normal"), parms = NULL),
  alpha = 0.05
)
```

Arguments

- **case**
  - Outcome variable. If a variable, this variable is tabulated against.
- **exposed**
  - Exposure variable.
- **reps**
  - Number of replications to run.
- **or.parms**
  - List defining the selection bias odds. The first argument provides the probability distribution function (constant, uniform, triangular, trapezoidal, log-logistic or log-normal) and the second its parameters as a vector:
    1. Constant: constant value,
2. Uniform: min, max,
3. Triangular: lower limit, upper limit, mode,
4. Trapezoidal: min, lower mode, upper mode, max.
5. Log-logistic: shape, rate. Must be strictly positive,
6. Log-normal: meanlog, sdlog. This is the mean and standard deviation on the log scale.

case.exp

If or.parms not provided, defines the selection probability among case exposed. The first argument provides the probability distribution function and the second its parameters as a vector:
1. Constant: constant value,
2. Uniform: min, max,
3. Triangular: lower limit, upper limit, mode,
4. Trapezoidal: min, lower mode, upper mode, max.
5. Logit-logistic: location, scale, lower bound shift, upper bound shift,

case.nexp

Same among cases non-exposed.

ncase.exp

Same among non-cases exposed.

ncase.nexp

Same among non-cases non-exposed.

alpha

Significance level.

Value

A list with elements:

obs.data

The analyzed 2 x 2 table from the observed data.

obs.measures

A table of observed odds ratio with confidence intervals.

adj.measures

A table of corrected odds ratios.

sim.df

Data frame of random parameters and computed values.

reps

Number of replications.

References


Examples

# The data for this example come from:
# Population-based incidence estimates of uveal melanoma in Germany.
# Supplementing cancer registry data by case-control data.
set.seed(123)
probsens.sel(matrix(c(136, 107, 297, 165),
dimnames = list(c("Melanoma+", "Melanoma-"), c("Mobile+", "Mobile-")), nrow = 2, byrow = TRUE),
reps = 20000,
or.parms = list("triangular", c(.35, 1.1, .43)))
Sensitivity analysis to correct for selection bias.

Description

Simple sensitivity analysis to correct for selection bias using estimates of the selection proportions.

Usage

```
selection(case, exposed, bias_parms = NULL, alpha = 0.05)
```

Arguments

- `case`: Outcome variable. If a variable, this variable is tabulated against.
- `exposed`: Exposure variable.
- `bias_parms`: Selection probabilities. Either a vector of 4 elements between 0 and 1 defining the following probabilities in this order can be provided:
  1. Selection probability among cases exposed (1),
  2. Selection probability among cases unexposed (2),
  3. Selection probability among noncases exposed (3), and
  4. Selection probability among noncases unexposed (4).
  or a single positive selection-bias factor which is the ratio of the exposed versus unexposed selection probabilities comparing cases and noncases \[\frac{1*4}{2*3}\] from above.
- `alpha`: Significance level.

Value

A list with elements:

- `obs.data`: The analyzed 2 x 2 table from the observed data.
- `corr.data`: The same table corrected for selection proportions.
- `obs.measures`: A table of odds ratios and relative risk with confidence intervals.
- `adj.measures`: Selection bias corrected measures of outcome-exposure relationship.
- `biasparms`: Input bias parameters: selection probabilities.
- `selbias.or`: Selection bias odds ratio based on the bias parameters chosen.

Examples

```
# The data for this example come from:
# Population-based incidence estimates of uveal melanoma in Germany. Supplementing cancer registry data by case-control data.
```
Pipe bias functions

Description

episensr also uses the pipe function, %>% to turn function composition into a series of imperative statements.

Arguments

lhs, rhs Data or bias function and a function to apply to it

Examples

# Instead of
misclassification(matrix(c(118, 832, 103, 884),
dimnames = list(c("BC+", "BC-"), c("AD+", "AD-")), nrow = 2, byrow = TRUE),
type = "exposure", bias_parms = c(.56, .58, .99, .97))
# you can write
dat <- matrix(c(118, 832, 103, 884),
dimnames = list(c("BC+", "BC-"), c("AD+", "AD-")), nrow = 2, byrow = TRUE)
dat %>% misclassification(., type = "exposure", bias_parms = c(.56, .58, .99, .97))
# also for multiple bias:
dat %>% misclassification(., type = "exposure", bias_parms = c(.56, .58, .99, .97)) %>%
multiple.bias(., bias_function = "selection", bias_parms = c(.73, .61, .82, .76))
Index

\%\% \quad 36

boot, 3, 22
boot.bias, 3, 22

confounders, 4, 21
confounders.array, 5
confounders.emm, 7
confounders.evalue, 9
confounders.ext, 10
confounders.limit, 11
confounders.poly, 13

episensr (episensr-package), 2
episensr-package, 2

mbias, 14, 23
misclassification, 3, 16, 21, 22
misclassification_cov, 17
multidimBias, 19
multiple.bias, 20

plot.episensr.booted, 21
plot.mbias, 22
print.episensr, 23
print.episensr.booted, 24
print.mbias, 24
probsens, 21, 25
probsens.conf, 21, 27
probsens.irr, 29
probsens.irr.conf, 31
probsens.sel, 21, 33

selection, 3, 21, 22, 35