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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**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

```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)
boot.bias(misclass_eval)
```

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,
  2. the prevalence of the confounder among the exposed, and
  3. the prevalence of the confounder among the unexposed.
- **alpha**: Significance level.

Value

A list with elements:

- **obs.data**: The analyzed 2 x 2 table from the observed data.
- **confder.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 -.
- **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:
# Increased risk of infection with human immunodeficiency virus type 1 among # uncircumcised men presenting with genital ulcer disease in Kenya.
confounders(matrix(c(105, 85, 527, 93),
dimnames = list(c("HIV+", "HIV-"), c("Circ+", "Circ-")),
nrow = 2, byrow = TRUE),
type = "RR",
bias_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 = "RR",
bias_parms = c(.63, .8, .05))
```
confounders.emm

Sensitivity analysis to correct for unknown or unmeasured confounding with effect modification

Description

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

Usage

```r
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, and
  4. the prevalence of the confounder among the unexposed.
- `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
# 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))
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
cconfounders.limit(OR = 1.65, crude.RR = 1.5)
```

Description

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

Usage

```r
cconfounders.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,
  4. the prevalence of the highest level confounder among the unexposed,
  5. the prevalence of the mid-level confounder among the exposed, and
  6. the prevalence of the mid-level confounder among the unexposed.
- **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 +.
- **nolcfder.data**: The same table for Confounder -.
- **obs.measures**: A table of relative risk with confidence intervals; Total and by confounders.
- **adj.measures**: A table of Standardized Morbidity Ratio and Mantel-Haenszel estimates.
- **bias parms**: Input bias parameters.

References


Examples

# 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(0.4, 0.8, 0.6, 0.05, 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))

episensr

**Basic sensitivity analysis of epidemiological results**

**Description**

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

**Details**

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**References**


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.
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"))
misclassification

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 (or outcome) classification among those with the outcome (or exposure),
  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.

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.

biasparms
  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))

# 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, biasParms = 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,
    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.

- **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.

- **biasparms**
  - Input bias parameters.

**References**


**Examples**

```r
# 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,
                        565, 3583, 781, 21958,
                        754, 34471, 4860, 383588),
                      dimnames = list(c("Twins+", "Twins-"),
                                      c("Folic acid+", "Folic acid-"),
                                      c("Total", "IVF+", "IVF-")),
                      dim = c(2, 2, 3)),
bias_parms = c(.6, .6, .95, .95))
```
**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 = 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**: Deprecated, please use bias_parms instead.
- **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:

- **obs.data**: The analyzed 2 x 2 table from the observed data.
- **obs.measures**: A table of odds ratios and relative risk with confidence intervals.
- **adj.measures**: Multidimensional corrected relative risk and/or odds ratio data.
- **bias parms**: Bias parameters.

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

Description

This takes an episensr bootstrap object and produces the pot 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.
plot.mbias

See Also

boot.bias, 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)
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

## 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.
print.episensr

See Also

mbias

Examples

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

## 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

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


Arguments

- `x`: An object of class 'episens.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'
prompt(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.

Usage

```r
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.
sec parms  List defining the sensitivity of exposure classification among those with the 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 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 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.

References

Examples

C The data for this example come from:
C A case-control study of cancer mortality at a transformer-assembly facility.
C set.seed(123)
C 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)))

C 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)

C Disease misclassification
probsens(matrix(c(173, 682, 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

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.
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)

# 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.

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 con-
tains person-time at risk, and first and second columns are exposed and unex-
posed 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

set.seed(123)
# Exposure misclassification, non-differential
probsens.irr.conf(matrix(c(2, 67232, 58, 18539000),
dimnames = list(c("GBS+", "Person-time"), c("HPV+", "HPV-")), ncol = 2),
reps = 20000,
secaparms = list("trapezoidal", c(.4, .45, .55, .6)),
spcaparms = list("constant", 1))

Description

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

Usage

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.
albedo 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

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(0.01, .2, .3, .51)),
prev.nexp = list("trapezoidal", c(0.09, .27, .35, .59)),
risk = list("trapezoidal", c(2, 2.5, 3.5, 4.5)),
corr.p = .8)
probsens.sel  

Probabilistic sensitivity analysis for selection bias.

Description

Probabilistic sensitivity analysis to correct for selection bias.

Usage

probsens.sel(case, exposed, reps = 100, or.parms = list(dist =
c("constant", "uniform", "triangular", "trapezoidal", "log-logistic", 
"log-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.

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.

References

Lash, T.L., Fox, M.P, Fink, A.K., 2009 Applying Quantitative Bias Analysis to Epidemiologic Data, 
Examples

# The data for this example come from:
# Population-based incidence estimates of uveal melanoma in Germany.
# Supplemeting 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, biasParms = NULL, alpha = 0.05)

Arguments

case Outcome variable. If a variable, this variable is tabulated against.
exposed Exposure variable.
bias_parms Numeric vector defining the selection probabilities. This vector has 4 elements between 0 and 1, in the following order:
   1. Selection probability among cases exposed,
   2. Selection probability among cases unexposed,
   3. Selection probability among noncases exposed, and
   4. Selection probability among noncases unexposed.
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.
bias.parms 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:
# Stang A., Schmidt-Pokrzywniak A., Lehnert M., Parkin D.M., Ferlay J., Bornfeld N.
# et al.
# Population-based incidence estimates of uveal melanoma in Germany. Supplementing
# cancer registry data by case-control data.
selection(matrix(c(136, 107, 297, 165),
dimnames = list(c("UM+", "UM-"), c("Mobile+", "Mobile-")),
nrow = 2, byrow = TRUE),
bias_parms = c(.94, .85, .64, .25))
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