

# Package ‘episensr’

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**Type** Package

**Title** Basic Sensitivity Analysis of Epidemiological Results

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**Imports** triangle, trapezoid, actuar, llogistic, logitnorm, plyr,  
ggplot2, grid, gridExtra, reshape, boot

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**BugReports** <https://github.com/dhaine/episensr/issues>

**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).

**Depends** R (>= 3.4.1)

**License** GPL-2

**Suggests** testthat, knitr, rmarkdown, aplore3

**RoxygenNote** 6.0.1

**VignetteBuilder** knitr

**NeedsCompilation** no

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boot.bias	<i>Bootstrap resampling for selection and misclassification bias models.</i>
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## 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

```
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	<i>Sensitivity analysis to correct for unknown or unmeasured confounding without effect modification</i>
-------------	--

---

**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**

```

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: <ol style="list-style-type: none"> <li>1. the association between the confounder and the outcome among those who were not exposed,</li> <li>2. the prevalence of the confounder among the exposed, and</li> <li>3. the prevalence of the confounder among the unexposed.</li> </ol>
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; for Total, Confounder +, and Confounder -.
adj.measures	A table of Standardized Morbidity Ratio and Mantel-Haenszel estimates.
bias_parms	Input bias parameters.

**References**

Lash, T.L., Fox, M.P, Fink, A.K., 2009 *Applying Quantitative Bias Analysis to Epidemiologic Data*, pp.59–78, Springer.

**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.
# Clin Infect Dis 1996;23:449-53.
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 = "OR",
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 = "RD",
bias_parms = c(-.37, .8, .05))

```

---

confounders.emm	<i>Sensitivity analysis to correct for unknown or unmeasured confounding with effect modification</i>
-----------------	---

---

### 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

```

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: <ol style="list-style-type: none"> <li>1. the association between the confounder and the outcome among those who were exposed,</li> <li>2. the association between the confounder and the outcome among those who were not exposed,</li> <li>3. the prevalence of the confounder among the exposed, and</li> <li>4. the prevalence of the confounder among the unexposed.</li> </ol>
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

Lash, T.L., Fox, M.P, Fink, A.K., 2009 *Applying Quantitative Bias Analysis to Epidemiologic Data*, pp.59–78, Springer.

## 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.
# Clin Infect Dis 1996;23:449-53.
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.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.

## Usage

```
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**

Lash, T.L., Fox, M.P, Fink, A.K., 2009 *Applying Quantitative Bias Analysis to Epidemiologic Data*, pp.59–78, Springer.

Flanders, W. Dana, Khoury, Muin J., 1990. Indirect Assessment of Confounding: Graphic Description and Limits on Effect of Adjusting for Covariates. *Epidemiology* 1(3): 239–246.

**Examples**

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

---

confounders.poly	<i>Sensitivity analysis to correct for unknown or unmeasured polychotomous confounding without effect modification</i>
------------------	--

---

**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: <ol style="list-style-type: none"> <li>1. the association between the highest level confounder and the outcome,</li> <li>2. the association between the mid-level confounder and the outcome,</li> <li>3. the prevalence of the highest level confounder among the exposed,</li> <li>4. the prevalence of the highest level confounder among the unexposed,</li> <li>5. the prevalence of the mid-level confounder among the exposed, and</li> <li>6. the prevalence of the mid-level confounder among the unexposed.</li> </ol>
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.
adj.measures	A table of Standardized Morbidity Ratio and Mantel-Haenszel estimates.
bias_parms	Input bias parameters.

**References**

Lash, T.L., Fox, M.P, Fink, A.K., 2009 *Applying Quantitative Bias Analysis to Epidemiologic Data*, pp.59–78, Springer.

**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.
# Clin Infect Dis 1996;23:449-53.
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))

```

---

episenr

*Basic sensitivity analysis of epidemiological results*


---

### Description

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

### Details

Package: episenr  
Type: Package  
Version: 0.6  
Date: 2015-03-24  
License: GPL-2

### Author(s)

Denis Haine <denis.haine@gmail.com>

### References

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

---

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:

<code>mbias.parms</code>	Maximum bias parameters.
<code>adj.measures</code>	Selection bias corrected measures.
<code>bias.parms</code>	Input bias parameters.

**References**

Greenland S. Quantifying biases in causal models: classical confounding vs. collider-stratification bias. *Epidemiology* 2003;14:300-6.

**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: <ol style="list-style-type: none"> <li>1. exposure: bias analysis for exposure misclassification; corrections using sensitivity and specificity: nondifferential and independent errors,</li> <li>2. outcome: bias analysis for outcome misclassification.</li> </ol>
bias_parms	Vector defining the bias parameters. This vector has 4 elements between 0 and 1, in the following order: <ol style="list-style-type: none"> <li>1. Sensitivity of exposure (or outcome) classification among those with the outcome (or exposure),</li> <li>2. Sensitivity of exposure (or outcome) classification among those without the outcome (or exposure),</li> <li>3. Specificity of exposure (or outcome) classification among those with the outcome (or exposure), and</li> <li>4. Specificity of exposure (or outcome) classification among those without the outcome (or exposure).</li> </ol>
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.
bias_parms	Input bias parameters.

## References

Lash, T.L., Fox, M.P, Fink, A.K., 2009 *Applying Quantitative Bias Analysis to Epidemiologic Data*, pp.79–108, Springer.

Chu, H., Zhaojie, W., Cole, S.R., Greenland, S., *Sensitivity analysis of misclassification: A graphical and a Bayesian approach*, *Annals of Epidemiology* 2006;16:834-841.

## 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.
# Annals of Epidemiology 2006;16:834-841.
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: <ol style="list-style-type: none"> <li>1. Sensitivity of confounder classification among those with the outcome,</li> <li>2. Sensitivity of confounder classification among those without the outcome,</li> <li>3. Specificity of confounder classification among those with the outcome, and</li> <li>4. Specificity of confounder classification among those without the outcome.</li> </ol>
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.
bias_parms	Input bias parameters.

**References**

Lash, T.L., Fox, M.P, Fink, A.K., 2009 *Applying Quantitative Bias Analysis to Epidemiologic Data*, pp.79–108, Springer.

**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,
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

```
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: <ol style="list-style-type: none"> <li>1. Prevalence of Confounder in Exposure+ population,</li> <li>2. Prevalence of Confounder in Exposure- population, and</li> <li>3. Relative risk between Confounder and Outcome.</li> </ol>
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

Lash, T.L., Fox, M.P, Fink, A.K., 2009 *Applying Quantitative Bias Analysis to Epidemiologic Data*, pp.109–116, Springer.

**Examples**

```

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, 1, .9, .9, .9, .8, .8, .8),
sp = c(1, .9, .8, 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, 1, .9, .9, .9, .8, .8, .8),
sp = c(1, .9, .8, 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))

```

---

plot.episensr.booted *Plot of bootstrap simulation output for selection and misclassification bias*

---

**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**

```

## 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**

```

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.



**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 <code>_significant_</code> 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 '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	<i>Print association corrected for M bias</i>
-------------	---

---

**Description**

Print association corrected for M bias.

**Usage**

```
## 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	<i>Probabilistic sensitivity analysis.</i>
----------	--

---

**Description**

Probabilistic sensitivity analysis to correct for exposure misclassification or outcome misclassification and random error.

**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 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. <ol style="list-style-type: none"> <li>1. Constant: constant value,</li> <li>2. Uniform: min, max,</li> <li>3. Triangular: lower limit, upper limit, mode,</li> <li>4. Trapezoidal: min, lower mode, upper mode, max,</li> <li>5. Logit-logistic: location, scale, lower bound shift, upper bound shift,</li> <li>6. Logit-normal: location, scale, lower bound shift, upper bound shift.</li> </ol>
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**

Lash, T.L., Fox, M.P, Fink, A.K., 2009 *Applying Quantitative Bias Analysis to Epidemiologic Data*, pp.117–150, Springer.

## 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.
# Int Arch Occup Environ Health 1994; 66(1):49-54.
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

```
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. <ol style="list-style-type: none"> <li>1. Constant: constant value,</li> <li>2. Uniform: min, max,</li> <li>3. Triangular: lower limit, upper limit, mode,</li> <li>4. Trapezoidal: min, lower mode, upper mode, max.</li> <li>5. Logit-logistic: location, scale, lower bound shift, upper bound shift,</li> <li>6. Logit-normal: location, scale, lower bound shift, upper bound shift.</li> </ol>
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: <ol style="list-style-type: none"> <li>1. Constant: constant value,</li> <li>2. Uniform: min, max,</li> <li>3. Triangular: lower limit, upper limit, mode,</li> <li>4. Trapezoidal: min, lower mode, upper mode, max.</li> <li>5. Log-logistic: shape, rate. Must be strictly positive,</li> <li>6. Log-normal: meanlog, sdlog. This is the mean and standard deviation on the log scale.</li> </ol>
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

Lash, T.L., Fox, M.P, Fink, A.K., 2009 *Applying Quantitative Bias Analysis to Epidemiologic Data*, pp.117–150, Springer.

## 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.
# Clin Infect Dis 1996;23:449-53.
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 contains person-time at risk, and first and second columns are exposed and unexposed observations, as:

	Exposed	Unexposed
Cases	a	b
Person-time	N1	N0

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. <ol style="list-style-type: none"> <li>1. Constant: constant value,</li> <li>2. Uniform: min, max,</li> <li>3. Triangular: lower limit, upper limit, mode,</li> <li>4. Trapezoidal: min, lower mode, upper mode, max,</li> <li>5. Logit-logistic: location, scale, lower bound shift, upper bound shift,</li> <li>6. Logit-normal: location, scale, lower bound shift, upper bound shift.</li> </ol>
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

Lash, T.L., Fox, M.P, Fink, A.K., 2009 *Applying Quantitative Bias Analysis to Epidemiologic Data*, pp.117–150, Springer.

## Examples

```
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	<i>Probabilistic sensitivity analysis for unmeasured confounding of person-time data and random error.</i>
-------------------	--

---

## 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:

	Exposed	Unexposed
Cases	a	b
Person-time	N1	N0

**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.



	<ol style="list-style-type: none"> <li>1. Constant: value,</li> <li>2. Uniform: min, max,</li> <li>3. Triangular: lower limit, upper limit, mode,</li> <li>4. Trapezoidal: min, lower mode, upper mode, max.</li> <li>5. Logit-logistic: location, scale, lower bound shift, upper bound shift,</li> <li>6. Logit-normal: location, scale, lower bound shift, upper bound shift.</li> </ol>
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: <ol style="list-style-type: none"> <li>1. Constant: value,</li> <li>2. Uniform: min, max,</li> <li>3. Triangular: lower limit, upper limit, mode,</li> <li>4. Trapezoidal: min, lower mode, upper mode, max.</li> <li>5. Log-logistic: shape, rate. Must be strictly positive,</li> <li>6. Log-normal: meanlog, sdlog. This is the mean and standard deviation on the log scale.</li> </ol>
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

Lash, T.L., Fox, M.P, Fink, A.K., 2009 *Applying Quantitative Bias Analysis to Epidemiologic Data*, pp.117–150, Springer.

### 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(.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)
```

---

probsens.sel                      *Probabilistic sensitivity analysis for selection bias.*

---

## Description

Probabilistic sensitivity analysis to correct for selection bias.

## Usage

```
probsens.sel(case, exposed, reps = 1000, 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: <ol style="list-style-type: none"> <li>1. Constant: constant value,</li> <li>2. Uniform: min, max,</li> <li>3. Triangular: lower limit, upper limit, mode,</li> <li>4. Trapezoidal: min, lower mode, upper mode, max.</li> <li>5. Log-logistic: shape, rate. Must be strictly positive,</li> <li>6. Log-normal: meanlog, sdlog. This is the mean and standard deviation on the log scale.</li> </ol>
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*, pp.117–150, Springer.

**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.
# Eur J Cancer Prev 2006;15:165-70.
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)))
```

---

selection

*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	Numeric vector defining the selection probabilities. This vector has 4 elements between 0 and 1, in the following order: <ol style="list-style-type: none"> <li>1. Selection probability among cases exposed,</li> <li>2. Selection probability among cases unexposed,</li> <li>3. Selection probability among noncases exposed, and</li> <li>4. Selection probability among noncases unexposed.</li> </ol>
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.
# Eur J Cancer Prev 2006;15:165-70.
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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