Package 'episensr'

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Type Package

Title Basic Sensitivity Analysis of Epidemiological Results

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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', 2021).

Depends R (>= 4.0.0), ggplot2 (>= 3.4.0)

License GPL-2

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URL https://github.com/dhaine/episensr, https://dhaine.github.io/episensr/

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R topics documented:

`episensr-package` *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.

Author(s)

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References

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

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

```
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

```
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.

Details

The analytic approach uses the "relative risk due to confounding" as defined by Miettinen (1972), i.e. $RR_{adj} = \frac{RR_{crude}}{RR_{conf}}$ where RR_adj is the standardized (adjusted) risk ratio, RR_crude is the crude risk ratio, and RR_conf is the relative risk component attributable to confounding by the stratification factors. The output provides both RR_adj (SMR or Mantel-Haenszel) and the RR_conf.

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.

Miettinen, 1971. Components of the Crude Risk Ratio. *Am J Epidemiol* 96(2):168-172.

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.array` *Sensitivity analysis for unmeasured confounders based on confounding imbalance among exposed and unexposed*

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

```
confounders.array(
  crude.risk,
  type = c("binary", "continuous", "RD"),
  bias_parms = NULL
)
```

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').

Value

A list with elements:

`model`	Bias analysis performed.
`bias.parms`	Input bias parameters.
`adj.measures`	Output results, with bias as a percentage: (crude.RR - risk_adj)/risk_adj * 100.

References

Schneeweiss, S., 2006. Sensitivity analysis and external adjustment for unmeasured confounders in epidemiologic database studies of therapeutics. *Pharmacoepidemiol Drug Safety* 15: 291-303.

Examples

```
# Example from Schneeweiss, S. Sensitivity analysis and external adjustment for
# unmeasured confounders in epidemiologic database studies of therapeutics.
# Pharmacoepidemiol Drug Safety 2006; 15: 291-303.
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))
```

`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

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.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

```
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

VanderWeele T.J and Ding P. Sensitivity analysis in observational research: Introducing the E-value. Annals of Internal Medicine 2017;167:268-274.

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.
# Lancet 1987;2:319-22.
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.
# Annals of Nutrition and Metabolism 2014;65:234-235.
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)
```

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).

Value

A list with elements:

`model`	Bias analysis performed.
`bias.parms`	Input bias parameters.
`adj.measures`	Output results, with bias as a percentage: (crude.RR - RR)/RR * 100.

References

Schneeweiss, S., 2006. Sensitivity analysis and external adjustment for unmeasured confounders in epidemiologic database studies of therapeutics. *Pharmacoepidemiol Drug Safety* 15: 291-303.

Examples

```
# Schneeweiss, S, Glynn, R.J., Tsai, E.H., Avorn, J., Solomon, D.H. Adjusting for
# unmeasured confounders in pharmacoepidemiologic claims data using external
# information. Epidemiology 2005; 16: 17-24.
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. Crude relative risk between exposure and outcome has minimally to be provided. Up to 3 other parameters can be entered.

Usage

```
confounders.limit(p = NA, RR = NA, OR = NA, crude.RR = NULL)
```

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.

Value

A list with elements:

`model`	Bias analysis performed.
`bias.parms`	Input bias parameters.
`adj.measures`	Output results.

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

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.
`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))
```

`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 = c("y", "x", "a", "b", "m"))
```

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 M, 3. Odds ratio between B and the collider M, 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:

`model`	Bias analysis performed.
`mbias.parms`	Three maximum bias parameters: in collider-exposure relationship created by conditioning on the collider, in collider-outcome relationship created by conditioning on the collider, and in exposure-outcome relationship created by conditioning on the collider.

adj.measures	Selection bias corrected odds ratio.
bias.parms	Input bias parameters.
labels	Variables' labels.

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 adjusted using sensitivity and specificity is computed as in Chu et al. (2006), for exposure misclassification.

Usage

```
misclassification(
  case,
  exposed,
  type = c("exposure", "exposure_pv", "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. exposure_pv: bias analysis for exposure misclassification; corrections using PPV/NPV: nondifferential and independent errors, 3. 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).

If PPV/NPV is chosen in case of exposure misclassification, this vector is the following:

1. Positive predictive value among those with the outcome,
2. Positive predictive value among those without the outcome,
3. Negative predictive value among those with the outcome,
4. Negative predictive value among those without the outcome.

`alpha` Significance level.

Details

For exposure misclassification, bias-adjusted measures are available using sensitivity and specificity, or using predictive values.

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))

# The next example, using PPV/NPV, comes from Bodnar et al. Validity of birth
# certificate-derived maternal weight data.
# Paediatric and Perinatal Epidemiology 2014;28:203-212.
misclassification(matrix(c(599, 4978, 31175, 391851),
dimnames = list(c("Preterm", "Term"), c("Underweight", "Normal weight")),
nrow = 2, byrow = TRUE),
type = "exposure_pv",
bias_parms = c(0.65, 0.74, 1, 0.98))
```

`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.
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, where the bias analysis is repeated within a range of values for the bias parameter(s).

Usage

```
multidimBias(
  case,
  exposed,
  type = c("exposure", "outcome", "confounder", "selection"),
  se = NULL,
  sp = NULL,
  bias_parms = NULL,
  OR.sel = 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. Parameter used with exposure or outcome misclassification.
`sp`	Numeric vector of specificities. Parameter used with exposure or outcome misclassification. Should be the same length as 'se'.
`bias_parms`	List of bias parameters used with unmeasured confounder. 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`	Deprecated; please use OR_sel instead.
`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.

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))
```

---

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.

Usage

```
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.

Details

For probabilistic bias analyses, median of cells are passed to the next function as starting 2-by-2 table.

Value

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

See Also

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

Examples

```
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. It also draws the confidence interval.

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 (rr) and odds ratio (or).
...	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.episensr.probsens

Plot(s) of probabilistic bias analyses

Description

This takes a probsens-family object and produces the distribution plot of chosen bias parameters, as well as distribution of adjusted measures (with confidence interval).

Usage

```
## S3 method for class 'episensr.probsens'
plot(
  x,
 parms = c("rr", "or", "rr_tot", "or_tot", "irr", "irr_tot", "seca", "seexp", "spca",
    "spexp", "or_sel", "prev.exp", "prev.nexp", "risk"),
  ...
)
```

Arguments

x	An object of class "episensr.probsens" returned from the episensr probsens, probsens.sel, probsens.conf, probsens.irr, probsens.irr.conf functions.
parms	Choice between adjusted relative risk (rr) and odds ratio (or), total error relative risk and odds ratio (rr_tot and or_tot), seca, seexp, spca, or_sel, and spexp, prev.exp, prev.nexp and risk, irr and irr_tot.
...	Other unused arguments.

See Also

probsens, probsens.sel, probsens.conf, probsens.irr, probsens.irr.conf

Examples

```
set.seed(123)
risk <- 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)))
plot(risk, "rr")

set.seed(123)
odds <- 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("beta", c(908, 16)),
seexp.parms = list("beta", c(156, 56)),
spca.parms = list("beta", c(153, 6)),
spexp.parms = list("beta", c(205, 18)),
corr.se = .8,
corr.sp = .8)
plot(odds, "seca")

set.seed(123)
select <- 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)))
plot(select, "or_sel")

set.seed(123)
conf <- 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)
plot(conf, "prev.exp")
```

```
set.seed(123)
inc1 <- 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))
plot(inc1, "irr")

set.seed(123)
inc2 <- 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)
plot(inc2, "risk")
```

`plot.mbias` *Plot DAGs before and after conditioning on collider (M bias)*

Description

Create two Directed Acyclic Graphs (DAGs), before and after conditioning on the collider M, for selection bias caused by M bias, using 'ggdag'.

Usage

```
## S3 method for class 'mbias'
plot(x, type = c("before", "after"), dec = 2, ...)
```

Arguments

`x`	'mbias' object to plot.
`type`	DAG before or after conditioning on M.
`dec`	Number of digits displayed.
`...`	Other unused arguments.

Value

A DAG 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 _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 '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

```
## 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", "beta"), parms = NULL),
  seexp.parms = NULL,
  spca.parms = list(dist = c("constant", "uniform", "triangular", "trapezoidal",
    "logit-logistic", "logit-normal", "beta"), 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, logit-normal, or beta) 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, 6. logit-normal: location, scale, lower bound shift, upper bound shift. 7. beta: alpha, beta.
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.
reps	Number of replications.

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)

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("beta", c(908, 16)),
seexp.parms = list("beta", c(156, 56)),
spca.parms = list("beta", c(153, 6)),
spexp.parms = list("beta", c(205, 18)),
corr.se = .8,
```

```
corr.sp = .8)

probsens(matrix(c(338, 490, 17984, 32024),
dimnames = list(c("BC+", "BC-"), c("Smoke+", "Smoke-")), nrow = 2, byrow = TRUE),
type = "exposure",
reps = 1000,
seca.parms = list("trapezoidal", c(.8, .9, .9, 1)),
spca.parms = list("trapezoidal", c(.8, .9, .9, 1)))

# 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(matrix(c(338, 490, 17984, 32024),
dimnames = list(c("BC+", "BC-"), c("Smoke+", "Smoke-")), nrow = 2, byrow = TRUE),
type = "outcome",
reps = 20000,
seca.parms = list("uniform", c(.2, .6)),
seexp.parms = list("uniform", c(.1, .5)),
spca.parms = list("uniform", c(.99, 1)),
spexp.parms = list("uniform", c(.99, 1)),
corr.se = .8,
corr.sp = .8)

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("beta", c(100, 5)),
seexp.parms = list("beta", c(110, 10)),
spca.parms = list("beta", c(120, 15)),
spexp.parms = list("beta", c(130, 30)),
corr.se = .8,
corr.sp = .8)
```

`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", "beta"), parms = NULL),
  prev.nexp = list(dist = c("constant", "uniform", "triangular", "trapezoidal",
    "logit-logistic", "logit-normal", "beta"), 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, logit-normal, or beta) 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, 6. logit-normal: location, scale, lower bound shift, upper bound shift. 7. beta: alpha, beta.
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

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)

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("beta", c(200, 56)),
prev.nexp = list("beta", c(10, 16)),
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", "beta"), parms = NULL),
  seexp.parms = NULL,
  spca.parms = list(dist = c("constant", "uniform", "triangular", "trapezoidal",
    "logit-logistic", "logit-normal", "beta"), 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, logit-normal, or beta) 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,
6. logit-normal: location, scale, lower bound shift, upper bound shift,
7. beta: alpha, beta.

`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 *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

```
probsens.irr.conf(
  counts,
  pt = NULL,
  reps = 1000,
  prev.exp = list(dist = c("constant", "uniform", "triangular", "trapezoidal",
    "logit-logistic", "logit-normal", "beta"), parms = NULL),
  prev.nexp = list(dist = c("constant", "uniform", "triangular", "trapezoidal",
    "logit-logistic", "logit-normal", "beta"), 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

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, logit-normal, or beta) 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,
6. logit-normal: location, scale, lower bound shift, upper bound shift,
7. beta: alpha, beta.

`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.

`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)
# 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),
  case.exp = list(dist = c("constant", "uniform", "triangular", "trapezoidal",
    "logit-logistic", "logit-normal", "beta"), parms = NULL),
  case.nexp = list(dist = c("constant", "uniform", "triangular", "trapezoidal",
    "logit-logistic", "logit-normal", "beta"), parms = NULL),
  ncase.exp = list(dist = c("constant", "uniform", "triangular", "trapezoidal",
    "logit-logistic", "logit-normal", "beta"), parms = NULL),
  ncase.nexp = list(dist = c("constant", "uniform", "triangular", "trapezoidal",
    "logit-logistic", "logit-normal", "beta"), 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,
6. logit-normal: location, scale, lower bound shift, upper bound shift,
7. beta: alpha, beta.

`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

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`	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 [(1*4)/(2*3) from above].
`alpha`	Significance level.

Value

A list with elements:

`model`	Bias analysis performed.
`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))


selection(matrix(c(136, 107, 297, 165),
dimnames = list(c("UM+", "UM-"), c("Mobile+", "Mobile-")),
nrow = 2, byrow = TRUE),
bias_parms = 0.43)
```

`%>%` *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))
```

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