

Package ‘EValue’

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Type Package

Title Sensitivity Analyses for Unmeasured Confounding and Other Biases
in Observational Studies and Meta-Analyses

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Description Conducts sensitivity analyses for unmeasured confounding, selection bias, and measurement error (individually or in combination) in individual studies. Also conducts sensitivity analyses for unmeasured confounding in meta-analyses.

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R topics documented:

bias_plot	2
confounded_meta	3
confounding	8
convert_measures	9
effect_measures	10

evaluate	12
evaluate.HR	14
evaluate.MD	15
evaluate.OLS	16
evaluate.OR	17
evaluate.RD	18
evaluate.RR	19
lead	20
misclassification	21
multi_bias	22
multi_bound	23
multi_evaluate	24
selection	26
selection_evaluate	27
sens_plot	29
soyMeta	33
svalues.HR	34
svalues.OR	35
svalues.RR	36
toyMeta	38
twoXtwoRR	38

Index	40
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bias_plot	<i>Plot bias factor as function of confounding relative risks</i>
-----------	---

Description

Plots the bias factor required to explain away a provided relative risk.

Usage

```
bias_plot(RR, xmax)
```

Arguments

RR	The relative risk
xmax	Upper limit of x-axis.

Examples

```
# recreate the plot in VanderWeele and Ding (2017)
bias_plot(RR=3.9, xmax=20)
```

Description

This function implements the sensitivity analyses of Mathur & VanderWeele (2020a, 2020b). It computes point estimates, standard errors, and confidence intervals for (1) Prop, the proportion of studies with true causal effect sizes above or below a chosen threshold q as a function of the bias parameters; (2) the minimum bias factor on the relative risk scale (T_{min}) required to reduce to less than r the proportion of studies with true causal effect sizes more extreme than q ; and (3) the counterpart to (2) in which bias is parameterized as the minimum relative risk for both confounding associations (G_{min}).

Usage

```
confounded_meta(
  method = "calibrated",
  q,
  r = NA,
  tail = NA,
  CI.level = 0.95,
  give.CI = TRUE,
  R = 1000,
  muB = NA,
  muB.toward.null = FALSE,
  dat = NA,
  yi.name = NA,
  vi.name = NA,
  sigB = NA,
  yr = NA,
  vyr = NA,
  t2 = NA,
  vt2 = NA,
  ...
)
```

Arguments

<code>method</code>	"calibrated" or "parametric". See Details.
<code>q</code>	True causal effect size chosen as the threshold for a meaningfully large effect.
<code>r</code>	For T_{min} and G_{min} , value to which the proportion of meaningfully strong effect sizes is to be reduced.
<code>tail</code>	"above" for the proportion of effects above q ; "below" for the proportion of effects below q . By default, is set to "above" if the pooled point estimate (<code>method = "parametric"</code>) or median of the calibrated estimates (<code>method = "calibrated"</code>) is above 1 on the relative risk scale and is set to "below" otherwise.

CI.level	Confidence level as a proportion (e.g., 0.95).
give.CI	Logical. If TRUE, confidence intervals are provided. Otherwise, only point estimates are provided.
R	Number of bootstrap iterates for confidence interval estimation. Only used if method = "calibrated" and give.CI = TRUE.
muB	Mean bias factor on the log scale across studies (greater than 0). When considering bias that is of homogeneous strength across studies (i.e., method = "calibrated" or method = "parametric" with sigB = 0), muB represents the log-bias factor in each study. If muB is not specified, then only Tmin and Gmin will be returned, not Prop.
muB.toward.null	Whether you want to consider bias that has on average shifted studies' point estimates away from the null (FALSE; the default) or that has on average shifted studies' point estimates toward the null (TRUE). See Details.
dat	Dataframe containing studies' point estimates and variances. Only used if method = "calibrated".
yi.name	Name of variable in dat containing studies' point estimates on the log-relative risk scale. Only used if method = "calibrated".
vi.name	Name of variable in dat containing studies' variance estimates. Only used if method = "calibrated".
sigB	Standard deviation of log bias factor across studies. Only used if method = "parametric".
yr	Pooled point estimate (on log-relative risk scale) from confounded meta-analysis. Only used if method = "parametric".
vyr	Estimated variance of pooled point estimate from confounded meta-analysis. Only used if method = "parametric".
t2	Estimated heterogeneity (τ^2) from confounded meta-analysis. Only used if method = "parametric".
vt2	Estimated variance of τ^2 from confounded meta-analysis. Only used if method = "parametric".
...	Additional arguments passed to confounded_meta.

Details

Specifying the sensitivity parameters on the bias:

By convention, the average log-bias factor, muB, is taken to be greater than 0 (Mathur & VanderWeele, 2020a; Ding & VanderWeele, 2017). Confounding can operate on average either away from or toward the null, a choice specified via muB.toward.null. The most common choice for sensitivity analysis is to consider bias that operates on average away from the null, which is confounded_meta's default. In such an analysis, correcting for the bias involves shifting studies' estimates back toward the null by muB (i.e., if $yr > 0$, the estimates will be corrected downward; if $yr < 0$, they will be corrected upward). Alternatively, to consider bias that operates on average away from the null, you would still specify $muB > 0$ but would also specify muB.toward.null = TRUE. For detailed guidance on choosing the sensitivity parameters muB and sigB, see Section 5 of Mathur & VanderWeele (2020a).

Specifying the threshold q:

For detailed guidance on choosing the threshold q , see the Supplement of Mathur & VanderWeele (2020a).

Specifying the estimation method:

By default, `confounded_meta` performs estimation using a **calibrated method** (Mathur & VanderWeele, 2020b) that extends work by Wang et al. (2019). This method makes no assumptions about the distribution of population effects and performs well in meta-analyses with as few as 10 studies, and performs well even when the proportion being estimated is close to 0 or 1. However, it only accommodates bias whose strength is the same in all studies (homogeneous bias). When using this method, the following arguments need to be specified:

- `q`
- `r` (if you want to estimate T_{min} and G_{min})
- `muB`
- `dat`
- `yi.name`
- `vi.name`

The **parametric method** assumes that the population effects are approximately normal and that the number of studies is large. Parametric confidence intervals should only be used when the proportion estimate is between 0.15 and 0.85 (and `confounded_meta` will issue a warning otherwise). Unlike the calibrated method, the parametric method can accommodate bias that is heterogeneous across studies (specifically, bias that is log-normal across studies). When using this method, the following arguments need to be specified:

- `q`
- `r` (if you want to estimate T_{min} and G_{min})
- `muB`
- `sigB`
- `yr`
- `vyr` (if you want confidence intervals)
- `t2`
- `vt2` (if you want confidence intervals)

Effect size measures other than log-relative risks:

If your meta-analysis uses effect sizes other than log-relative risks, you should first approximately convert them to log-relative risks, for example via `convert_measures()` and then pass the converted point estimates or meta-analysis estimates to `confounded_meta`.

Interpreting T_{min} and G_{min} :

T_{min} is defined as the minimum bias factor on the relative risk scale, common to all meta-analyzed studies, that would be required to reduce to less than r the proportion of studies with true causal effect sizes stronger than the threshold q . G_{min} is defined as the minimum confounding strength on the relative risk scale – that is, the relative risk relating unmeasured confounder(s) to both the exposure and the outcome – common to all meta-analyzed studies, that would be required to reduce to less than r the proportion of studies with true causal effect sizes stronger than the threshold q . G_{min} is a one-to-one transformation of T_{min} given by $G_{min} = T_{min} + \sqrt{T_{min} * (T_{min} - 1)}$.

If the estimated proportion of meaningfully strong effect sizes is already less than r even without the introduction of any bias, T_{\min} and G_{\min} will be set to 1.

The direction of bias represented by T_{\min} and G_{\min} is dependent on the argument `tail`: when `tail = "above"`, these metrics consider bias that had operated to *increase* studies' point estimates, and when `tail = "below"`, these metrics consider bias that had operated to *decrease* studies' point estimates. Such bias could operate toward or away from the null depending on whether the pooled point estimate `yr` happens to fall above or below the null. As such, the direction of bias represented by T_{\min} and G_{\min} may or may not match that specified by the argument `muB.toward.null` (which is used only for estimation of `Prop`).

When these methods should be used:

These methods perform well only in meta-analyses with at least 10 studies; we do not recommend reporting them in smaller meta-analyses. Additionally, it only makes sense to consider proportions of effects stronger than a threshold when the heterogeneity estimate t_2 is greater than 0. For meta-analyses with fewer than 10 studies or with a heterogeneity estimate of 0, you can simply report E-values for the point estimate via `evaluate()` (VanderWeele & Ding, 2017; see Mathur & VanderWeele (2020a), Section 7.2 for interpretation in the meta-analysis context).

References

- Mathur MB & VanderWeele TJ (2020a). Sensitivity analysis for unmeasured confounding in meta-analyses. *Journal of the American Statistical Association*.
- Mathur MB & VanderWeele TJ (2020b). Robust metrics and sensitivity analyses for meta-analyses of heterogeneous effects. *Epidemiology*.
- Mathur MB & VanderWeele TJ (2019). New statistical metrics for meta-analyses of heterogeneous effects. *Statistics in Medicine*.
- Ding P & VanderWeele TJ (2016). Sensitivity analysis without assumptions. *Epidemiology*.
- VanderWeele TJ & Ding P (2017). Introducing the E-value. *Annals of Internal Medicine*.
- Wang C-C & Lee W-C (2019). A simple method to estimate prediction intervals and predictive distributions: Summarizing meta-analyses beyond means and confidence intervals. *Research Synthesis Methods*.

Examples

```
##### Using Calibrated Method #####
d = metafor::escalc(measure="RR", ai=tpos, bi=tneg,
                  ci=cpos, di=cneg, data=metafor::dat.bcg)

# obtaining all three estimators and inference
# number of bootstrap iterates
# should be larger in practice
R = 100
confounded_meta( method="calibrated", # for both methods
                q = log(0.90),
                r = 0.20,
                tail="below",
                muB = log(1.5),
```

```

    dat = d,
    yi.name = "yi",
    vi.name = "vi",
    R = 100 )

# passing only arguments needed for prop point estimate
confounded_meta( method="calibrated",
  q = log(0.90),
  tail="below",
  muB = log(1.5),
  give.CI = FALSE,
  dat = d,
  yi.name = "yi",
  vi.name = "vi" )

# passing only arguments needed for Tmin, Gmin point estimates
confounded_meta( method="calibrated",
  q = log(0.90),
  r = 0.10,
  tail="below",
  give.CI = FALSE,
  dat = d,
  yi.name = "yi",
  vi.name = "vi" )

##### Using Parametric Method #####
# fit random-effects meta-analysis
m = metafor::rma.uni(yi= d$yi,
  vi=d$vi,
  knha=TRUE,
  measure="RR",
  method="REML" )

yr = as.numeric(m$b) # metafor returns on log scale
vyr = as.numeric(m$vb)
t2 = m$tau2
vt2 = m$se.tau2^2

# obtaining all three estimators and inference
# now the proportion considers heterogeneous bias
confounded_meta( method = "parametric",
  q=log(0.90),
  r=0.20,
  tail = "below",
  muB=log(1.5),
  sigB=0.1,
  yr=yr,
  vyr=vyr,
  t2=t2,
  vt2=vt2,
  CI.level=0.95 )

# passing only arguments needed for prop point estimate

```

```

confounded_meta( method = "parametric",
                 q=log(0.90),
                 tail = "below",
                 muB=log(1.5),
                 sigB = 0,
                 yr=yr,
                 t2=t2,
                 CI.level=0.95 )

# passing only arguments needed for Tmin, Gmin point estimates
confounded_meta( method = "parametric",
                 q=log(0.90),
                 r = 0.10,
                 tail = "below",
                 yr=yr,
                 t2=t2,
                 CI.level=0.95 )

```

confounding

Unmeasured confounding

Description

A type of bias. Declares that unmeasured confounding will be a component of interest in the multi-bias sensitivity analysis. Generally used within other functions, its output is returned invisibly.

Usage

```
confounding(..., verbose = FALSE)
```

Arguments

...	Other arguments. Not currently used for this function.
verbose	Logical. If TRUE, returns warnings and messages immediately. Defaults to FALSE because it is generally used within the <code>multi_bias()</code> function, which will print the same messages/warnings.

Value

Invisibly returns a list with components `n` (2, the degree of the polynomial in the numerator), `d` (1, the degree of the polynomial in the denominator), `mess` (any messages/warnings that should be printed for the user), and `bias` ("confounding").

Examples

```

# returns invisibly without print()
print(confounding())

# Calculate an E-value for unmeasured confounding only

```



```
multi_evalue(est = RR(4), biases = confounding())
```

convert_measures *Convert an effect measure*

Description

These helper functions are mostly used internally to convert [effect measures](#) for the calculation of E-values. The approximate conversion of odds and hazard ratios to risk ratios depends on whether the rare outcome assumption is made.

Usage

```
toRR(est, rare, delta = 1, ...)
```

```
toMD(est, delta = 1, ...)
```

Arguments

est	The effect estimate; constructed with one of RR() , OR() , HR() , MD() , OLS() .
rare	When converting a OR() or HR() estimate, a logical indicating whether the outcome is sufficiently rare to approximate a risk ratio.
delta	When converting an OLS() estimate, the contrast of interest in the exposure. Defaults to 1 (a 1-unit contrast in the exposure).
...	Arguments passed to other methods.

Details

Uses the conversions listed in Table 2 of VanderWeele TJ, Ding P. *Sensitivity Analysis in Observational Research: Introducing the E-Value*. *Annals of Internal Medicine*. 2017;167(4):268–75.

See references.

Regarding the continuous outcome, the function uses the effect-size conversions in Chinn (2000) and VanderWeele (2017) to approximately convert the mean difference between these exposure "groups" to the odds ratio that would arise from dichotomizing the continuous outcome.

Value

An object of class "estimate" and the desired effect measure. Also includes as an attribute its conversion history.

References

- Chinn, S (2000). A simple method for converting an odds ratio to effect size for use in meta-analysis. *Statistics in Medicine*, 19(22), 3127-3131.
- VanderWeele, TJ (2017). On a square-root transformation of the odds ratio for a common outcome. *Epidemiology*, 28(6), e58.
- VanderWeele TJ (2020). *Optimal approximate conversions of odds ratios and hazard ratios to risk ratios*. Biometrics.

Examples

```
# Both odds ratios are 3, but will be treated differently
# depending on whether rare outcome assumption is reasonable
OR(3, rare = FALSE)
OR(3, rare = TRUE)
toRR(OR(3, rare = FALSE))
toRR(OR(3, rare = TRUE))
attributes(toRR(toMD(OLS(3, sd = 1.2), delta = 1)))
```

```
effect_measures      Declare an effect measure
```

Description

These functions allow the user to declare that an estimate is a certain type of effect measure: risk ratio (RR), odds ratio (OR), hazard ratio (HR), risk difference (RD), linear regression coefficient (OLS), or mean standardized difference (MD).

Usage

```
RR(est)
```

```
OR(est, rare)
```

```
HR(est, rare)
```

```
RD(est)
```

```
OLS(est, sd)
```

```
MD(est)
```

Arguments

- | | |
|------|--|
| est | The effect estimate (numeric). |
| rare | Logical. Whether the outcome is sufficiently rare for use of risk ratio approximates; if not, approximate conversions are used. Used only for <code>HR()</code> and <code>OR()</code> ; see Details. |

sd The standard deviation of the outcome (or residual standard deviation). Used only for `OLS()`; see Details.

Details

The [conversion functions](#) use these objects to convert between effect measures when necessary to calculate E-values. Read more about the conversions in Table 2 of VanderWeele TJ, Ding P. *Sensitivity Analysis in Observational Research: Introducing the E-Value*. *Annals of Internal Medicine*. 2017;167(4):268–75.

See also VanderWeele TJ. *Optimal approximate conversions of odds ratios and hazard ratios to risk ratios*. *Biometrics*. 2019 Jan 6;(September 2018):1–7.

For `OLS()`, `sd` must be specified. A true standardized mean difference for linear regression would use $sd = SD(Y | X, C)$, where Y is the outcome, X is the exposure of interest, and C are any adjusted covariates. See Examples for how to extract this from `lm`. A conservative approximation would instead use $sd = SD(Y)$. Regardless, the reported E-value for the confidence interval treats `sd` as known, not estimated.

Value

An object of classes "estimate" and the measure of interest, containing the effect estimate and any other attributes to be used in future calculations.

Examples

```
# Both odds ratios are 3, but will be treated differently in E-value calculations
# depending on whether rare outcome assumption is reasonable
OR(3, rare = FALSE)
OR(3, rare = TRUE)
evaluate(OR(3, rare = FALSE))
evaluate(OR(3, rare = TRUE))
attributes(OR(3, rare = FALSE))

# If an estimate was constructed via conversion from another effect measure,
# we can see the history of a conversion using the summary() function
summary(toRR(OR(3, rare = FALSE)))
summary(toRR(OLS(3, sd = 1)))

# Estimating sd for an OLS estimate
# first standardizing conservatively by SD(Y)
data(lead)
ols = lm(age ~ income, data = lead)
est = ols$coefficients[2]
sd = sd(lead$age)
summary(evaluate(OLS(est, sd)))
# now use residual SD to avoid conservatism
# here makes very little difference because income and age are
# not highly correlated
sd = summary(ols)$sigma
summary(evaluate(OLS(est, sd)))
```

evalue	<i>Compute an E-value for unmeasured confounding</i>
--------	--

Description

Returns a data frame containing point estimates, the lower confidence limit, and the upper confidence limit on the risk ratio scale (possibly through an approximate conversion) as well as E-values for the point estimate and the confidence interval limit closer to the null.

Usage

```
evalue(est, lo = NA, hi = NA, se = NA, delta = 1, true = c(0, 1), ...)
```

Arguments

est	The effect estimate that was observed but which is suspected to be biased. A number of class "estimate" (constructed with RR() , OR() , HR() , OLS() , or MD() ; for E-values for risk differences, see evalues.RD()).
lo	Optional. Lower bound of the confidence interval. If not an object of class "estimate", assumed to be on the same scale as est.
hi	Optional. Upper bound of the confidence interval. If not an object of class "estimate", assumed to be on the same scale as est.
se	The standard error of the point estimate, for est of class "OLS"
delta	The contrast of interest in the exposure, for est of class "OLS"
true	A number to which to shift the observed estimate to. Defaults to 1 for ratio measures (RR() , OR() , HR()) and 0 for additive measures (OLS() , MD()).
...	Arguments passed to other methods.

Details

An E-value for unmeasured confounding is minimum strength of association, on the risk ratio scale, that an unmeasured confounder would need to have with both the treatment and the outcome to fully explain away a specific treatment–outcome association, conditional on the measured covariates.

The estimate is converted appropriately before the E-value is calculated. See [conversion functions](#) for more details. The point estimate and confidence limits after conversion are returned, as is the E-value for the point estimate and the confidence limit closest to the proposed "true" value (by default, the null value.)

For an [OLS\(\)](#) estimate, the E-value is for linear regression with a continuous exposure and outcome. Regarding the continuous exposure, the choice of `delta` defines essentially a dichotomization in the exposure between hypothetical groups of subjects with exposures equal to an arbitrary value c versus to another hypothetical group with exposures equal to $c + \text{delta}$.

For example, if resulting E-value is 2, this means that unmeasured confounder(s) would need to double the probability of a subject's having exposure equal to $c + \text{delta}$ instead of c , and would also need to double the probability of being high versus low on the outcome, in which the cutoff for "high" versus "low" is arbitrary subject to some distributional assumptions (Chinn, 2000).

Examples

```

# compute E-value for leukemia example in VanderWeele and Ding (2017)
evaluate(RR(0.80), 0.71, 0.91)

# you can also pass just the point estimate
# and return just the E-value for the point estimate with summary()
summary(evaluate(RR(0.80)))

# demonstrate symmetry of E-value
# this apparently causative association has same E-value as the above
summary(evaluate(RR(1 / 0.80)))

# E-value for a non-null true value
summary(evaluate(RR(2), true = 1.5))

## Hsu and Small (2013 Biometrics) Data
## sensitivity analysis after log-linear or logistic regression
head(lead)

## log linear model -- obtain the conditional risk ratio
lead.loglinear = glm(lead ~ ., family = binomial(link = "log"),
                    data = lead[,-1])
est_se = summary(lead.loglinear)$coef["smoking", c(1, 2)]

est      = RR(exp(est_se[1]))
lowerRR  = exp(est_se[1] - 1.96*est_se[2])
upperRR  = exp(est_se[1] + 1.96*est_se[2])
evaluate(est, lowerRR, upperRR)

## logistic regression -- obtain the conditional odds ratio
lead.logistic = glm(lead ~ ., family = binomial(link = "logit"),
                   data = lead[,-1])
est_se = summary(lead.logistic)$coef["smoking", c(1, 2)]

est      = OR(exp(est_se[1]), rare = FALSE)
lowerOR  = exp(est_se[1] - 1.96*est_se[2])
upperOR  = exp(est_se[1] + 1.96*est_se[2])
evaluate(est, lowerOR, upperOR)

## linear regression
# standardizing conservatively by SD(Y)
ols = lm(age ~ income, data = lead)
est = OLS(ols$coefficients[2], sd = sd(lead$age))

# for a 1-unit increase in income
evaluate(est = est,
        se = summary(ols)$coefficients['income', 'Std. Error'])

# for a 0.5-unit increase in income
evaluate(est = est,
        se = summary(ols)$coefficients['income', 'Std. Error'],
        delta = 0.5)

```

```
# E-value for Cohen's d = 0.5 with SE = 0.25
value(est = MD(.5), se = .25)

# compute E-value for HR = 0.56 with CI: [0.46, 0.69]
# for a common outcome
value(HR(0.56, rare = FALSE), lo = 0.46, hi = 0.69)
# for a rare outcome
value(HR(0.56, rare = TRUE), lo = 0.46, hi = 0.69)
```

evalues.HR

Compute E-value for a hazard ratio and its confidence interval limits

Description

Returns a data frame containing point estimates, the lower confidence limit, and the upper confidence limit on the risk ratio scale (through an approximate conversion if needed when outcome is common) as well as E-values for the point estimate and the confidence interval limit closer to the null.

Usage

```
evalues.HR(est, lo = NA, hi = NA, rare = NA, true = 1, ...)
```

Arguments

est	The point estimate
lo	The lower limit of the confidence interval
hi	The upper limit of the confidence interval
rare	1 if outcome is rare (<15 percent at end of follow-up); 0 if outcome is not rare (>15 percent at end of follow-up)
true	The true HR to which to shift the observed point estimate. Typically set to 1 to consider a null true effect.
...	Arguments passed to other methods.

Examples

```
# compute E-value for HR = 0.56 with CI: [0.46, 0.69]
# for a common outcome
evalues.HR(0.56, 0.46, 0.69, rare = FALSE)
```

evalues.MD	<i>Compute E-value for a difference of means and its confidence interval limits</i>
------------	---

Description

Returns a data frame containing point estimates, the lower confidence limit, and the upper confidence limit on the risk ratio scale (through an approximate conversion) as well as E-values for the point estimate and the confidence interval limit closer to the null.

Usage

```
evalues.MD(est, se = NA, true = 0, ...)
```

Arguments

est	The point estimate as a standardized difference (i.e., Cohen's d)
se	The standard error of the point estimate
true	The true standardized mean difference to which to shift the observed point estimate. Typically set to 0 to consider a null true effect.
...	Arguments passed to other methods.

Details

Regarding the continuous outcome, the function uses the effect-size conversions in Chinn (2000) and VanderWeele (2017) to approximately convert the mean difference between the exposed versus unexposed groups to the odds ratio that would arise from dichotomizing the continuous outcome.

For example, if resulting E-value is 2, this means that unmeasured confounder(s) would need to double the probability of a subject's being exposed versus not being exposed, and would also need to double the probability of being high versus low on the outcome, in which the cutoff for "high" versus "low" is arbitrary subject to some distributional assumptions (Chinn, 2000).

References

Chinn, S (2000). A simple method for converting an odds ratio to effect size for use in meta-analysis. *Statistics in Medicine*, 19(22), 3127-3131.

VanderWeele, TJ (2017). On a square-root transformation of the odds ratio for a common outcome. *Epidemiology*, 28(6), e58.

Examples

```
# compute E-value if Cohen's d = 0.5 with SE = 0.25
evalues.MD(.5, .25)
```

 evalues.OLS

 Compute E-value for a linear regression coefficient estimate

Description

Returns a data frame containing point estimates, the lower confidence limit, and the upper confidence limit on the risk ratio scale (through an approximate conversion) as well as E-values for the point estimate and the confidence interval limit closer to the null.

Usage

```
evalues.OLS(est, se = NA, sd, delta = 1, true = 0, ...)
```

Arguments

<code>est</code>	The linear regression coefficient estimate (standardized or unstandardized)
<code>se</code>	The standard error of the point estimate
<code>sd</code>	The standard deviation of the outcome (or residual standard deviation); see Details
<code>delta</code>	The contrast of interest in the exposure
<code>true</code>	The true standardized mean difference to which to shift the observed point estimate. Typically set to 0 to consider a null true effect.
<code>...</code>	Arguments passed to other methods.

Details

This function is for linear regression with a continuous exposure and outcome. Regarding the continuous exposure, the choice of `delta` defines essentially a dichotomization in the exposure between hypothetical groups of subjects with exposures equal to an arbitrary value c versus to another hypothetical group with exposures equal to $c + \text{delta}$. Regarding the continuous outcome, the function uses the effect-size conversions in Chinn (2000) and VanderWeele (2017) to approximately convert the mean difference between these exposure "groups" to the odds ratio that would arise from dichotomizing the continuous outcome.

For example, if resulting E-value is 2, this means that unmeasured confounder(s) would need to double the probability of a subject's having exposure equal to $c + \text{delta}$ instead of c , and would also need to double the probability of being high versus low on the outcome, in which the cutoff for "high" versus "low" is arbitrary subject to some distributional assumptions (Chinn, 2000).

A true standardized mean difference for linear regression would use $\text{sd} = \text{SD}(Y | X, C)$, where Y is the outcome, X is the exposure of interest, and C are any adjusted covariates. See Examples for how to extract this from `lm`. A conservative approximation would instead use $\text{sd} = \text{SD}(Y)$. Regardless, the reported E-value for the confidence interval treats `sd` as known, not estimated.

References

Chinn, S (2000). A simple method for converting an odds ratio to effect size for use in meta-analysis. *Statistics in Medicine*, 19(22), 3127-3131.

VanderWeele, TJ (2017). On a square-root transformation of the odds ratio for a common outcome. *Epidemiology*, 28(6), e58.

Examples

```
# first standardizing conservatively by SD(Y)
data(lead)
ols = lm(age ~ income, data = lead)

# for a 1-unit increase in income
evalues.OLS(est = ols$coefficients[2],
            se = summary(ols)$coefficients['income', 'Std. Error'],
            sd = sd(lead$age))

# for a 0.5-unit increase in income
evalues.OLS(est = ols$coefficients[2],
            se = summary(ols)$coefficients['income', 'Std. Error'],
            sd = sd(lead$age),
            delta = 0.5)

# now use residual SD to avoid conservatism
# here makes very little difference because income and age are
# not highly correlated
evalues.OLS(est = ols$coefficients[2],
            se = summary(ols)$coefficients['income', 'Std. Error'],
            sd = summary(ols)$sigma)
```

evalues.OR

Compute E-value for an odds ratio and its confidence interval limits

Description

Returns a data frame containing point estimates, the lower confidence limit, and the upper confidence limit on the risk ratio scale (through an approximate conversion if needed when outcome is common) as well as E-values for the point estimate and the confidence interval limit closer to the null.

Usage

```
evalues.OR(est, lo = NA, hi = NA, rare = NA, true = 1, ...)
```

Arguments

est	The point estimate
lo	The lower limit of the confidence interval
hi	The upper limit of the confidence interval
rare	1 if outcome is rare (<15 percent at end of follow-up); 0 if outcome is not rare (>15 percent at end of follow-up)
true	The true OR to which to shift the observed point estimate. Typically set to 1 to consider a null true effect.
...	Arguments passed to other methods.

Examples

```
# compute E-values for OR = 0.86 with CI: [0.75, 0.99]
# for a common outcome
evalues.OR(0.86, 0.75, 0.99, rare = FALSE)

## Example 2
## Hsu and Small (2013 Biometrics) Data
## sensitivity analysis after log-linear or logistic regression

head(lead)

## log linear model -- obtain the conditional risk ratio
lead.loglinear = glm(lead ~ ., family = binomial(link = "log"),
                    data = lead[,-1])
est = summary(lead.loglinear)$coef["smoking", c(1, 2)]

RR      = exp(est[1])
lowerRR = exp(est[1] - 1.96*est[2])
upperRR = exp(est[1] + 1.96*est[2])
evalues.RR(RR, lowerRR, upperRR)

## logistic regression -- obtain the conditional odds ratio
lead.logistic = glm(lead ~ ., family = binomial(link = "logit"),
                   data = lead[,-1])
est = summary(lead.logistic)$coef["smoking", c(1, 2)]

OR      = exp(est[1])
lowerOR = exp(est[1] - 1.96*est[2])
upperOR = exp(est[1] + 1.96*est[2])
evalues.OR(OR, lowerOR, upperOR, rare=FALSE)
```

evalues.RD

Compute E-value for a population-standardized risk difference and its confidence interval limits

Description

Returns E-values for the point estimate and the lower confidence interval limit for a positive risk difference. If the risk difference is negative, the exposure coding should be first be reversed to yield a positive risk difference.

Usage

```
evaluates.RD(n11, n10, n01, n00, true = 0, alpha = 0.05, grid = 1e-04, ...)
```

Arguments

n11	Number of exposed, diseased individuals
n10	Number of exposed, non-diseased individuals
n01	Number of unexposed, diseased individuals
n00	Number of unexposed, non-diseased individuals
true	True value of risk difference to which to shift the point estimate. Usually set to 0 to consider the null.
alpha	Alpha level
grid	Spacing for grid search of E-value
...	Arguments passed to other methods.

Examples

```
## example 1
## Hammond and Holl (1958 JAMA) Data
## Two by Two Table
##      Lung Cancer   No Lung Cancer
##Smoker   397         78557
##Nonsmoker 51         108778

# E-value to shift observed risk difference to 0
evaluates.RD(397, 78557, 51, 108778)

# E-values to shift observed risk difference to other null values
evaluates.RD(397, 78557, 51, 108778, true = 0.001)
```

evaluates.RR	<i>Compute E-value for a risk ratio or rate ratio and its confidence interval limits</i>
--------------	--

Description

Returns a data frame containing point estimates, the lower confidence limit, and the upper confidence limit for the risk ratio (as provided by the user) as well as E-values for the point estimate and the confidence interval limit closer to the null.

Usage

```
evalues.RR(est, lo = NA, hi = NA, true = 1, ...)
```

Arguments

<code>est</code>	The point estimate
<code>lo</code>	The lower limit of the confidence interval
<code>hi</code>	The upper limit of the confidence interval
<code>true</code>	The true RR to which to shift the observed point estimate. Typically set to 1 to consider a null true effect.
<code>...</code>	Arguments passed to other methods.

Examples

```
# compute E-value for leukemia example in VanderWeele and Ding (2017)
evalues.RR(0.80, 0.71, 0.91)

# you can also pass just the point estimate
evalues.RR(0.80)

# demonstrate symmetry of E-value
# this apparently causative association has same E-value as the above
evalues.RR(1 / 0.80)
```

<code>lead</code>	<i>An example dataset</i>
-------------------	---------------------------

Description

An example dataset from Hsu and Small (Biometrics, 2013).

Usage

```
lead
```

Format

An object of class `data.frame` with 3340 rows and 18 columns.

misclassification	<i>Misclassification</i>
-------------------	--------------------------

Description

A type of bias. Declares that (differential) misclassification will be a component of interest in the multi-bias sensitivity analysis. Generally used within other functions; its output is returned invisibly.

Usage

```
misclassification(
  ...,
  rare_outcome = FALSE,
  rare_exposure = FALSE,
  verbose = FALSE
)
```

Arguments

...	Arguments describing the type of misclassification. Currently two options: "outcome" or "exposure".
rare_outcome	Logical. Is the outcome rare enough that outcome odds ratios approximate risk ratios? Only needed when considering exposure misclassification. Note that rare_outcome = FALSE returns an error, as this option is not currently available.
rare_exposure	Logical. Is the exposure rare enough that exposure odds ratios approximate risk ratios? Only needed when considering exposure misclassification.
verbose	Logical. If TRUE, returns warnings and messages immediately. Defaults to FALSE because it is generally used within the <code>multi_bias()</code> function, which will print the same messages/warnings.

Value

Invisibly returns a list with components whose values depend on the options chosen: n (the degree of the polynomial in the numerator), d (the degree of the polynomial in the denominator), m (the parameters in the bias factor), mess (any messages/warnings that should be printed for the user), and bias("misclassification").

Examples

```
# returns invisibly without print()
print(misclassification("outcome"))

# Calculate an E-value for misclassification
multi_value(est = RR(4),
  biases = misclassification("exposure",
    rare_outcome = TRUE, rare_exposure = TRUE))
```

`multi_bias`*Create a set of biases for a multi-bias sensitivity analysis*

Description

Multiple biases (`confounding()`, `selection()`, and/or `misclassification()`) can be assessed simultaneously after creating a `multi_bias` object using this function.

Usage

```
multi_bias(..., verbose = TRUE)
```

Arguments

`...` Biases (`confounding()`, `selection()`, and/or `misclassification()`), each possibly including arguments specifying more detail about the bias of interest. Selection and confounding should be listed in the order in which they affect the data (see [ordering of the biases](#))

`verbose` Logical. If TRUE, returns warnings and messages immediately. Defaults to TRUE.

Value

Invisibly returns a list with components whose values depend on the options chosen: `n` (the degree of the polynomial in the numerator), `d` (the degree of the polynomial in the denominator), `m` (the parameters in the bias factor), `mess` (any messages/warnings that should be printed for the user), and `bias` ("misclassification").

Examples

```
biases <- multi_bias(confounding(),
                    selection("general"))

# print() lists the arguments for the multi_bound() function
print(biases)

# summary() provides more information
# with parameters in latex notation if latex = TRUE
summary(biases, latex = TRUE)

# Calculate a bound
multi_bound(biases = biases,
            RRAUc = 1.5, RRUCY = 2, RRUsYA1 = 1.25,
            RRSUsA1 = 4, RRUsYA0 = 3, RRSUsA0 = 2)
```

multi_bound

Calculate a bound for the bias

Description

Function used to calculate the maximum factor by which a risk ratio is biased, given possible values for each of the parameters that describe the bias factors for each type of bias.

Usage

```
multi_bound(
  biases,
  RRAUc = NULL,
  RRUCy = NULL,
  RRUsYA1 = NULL,
  RRSUsA1 = NULL,
  RRUsYA0 = NULL,
  RRSUsA0 = NULL,
  RRAUscS = NULL,
  RRUscYS = NULL,
  RRAYy = NULL,
  ORYAa = NULL,
  RRYAa = NULL,
  RRAYyS = NULL,
  ORYAaS = NULL,
  RRYAaS = NULL,
  RRAUsS = NULL,
  RRUsYS = NULL
)
```

Arguments

biases	A set of biases (or single bias) to include in the calculation of the bound. A single object constructed with the <code>multi_bias()</code> function, it may include any or all of <code>confounding()</code> , <code>selection()</code> , and <code>misclassification()</code> , and any of the options described in the documentation for those functions.
RRAUc	Named parameter values with which to calculate a bound. Names must correspond to the parameters defining the biases provided by <code>biases</code> . Help with names can be found by running <code>print(multi_bias(...))</code> for the biases of interest. Unnecessary parameters are ignored with a warning.
RRUCy	See RRAUc
RRUsYA1	See RRAUc
RRSUsA1	See RRAUc
RRUsYA0	See RRAUc
RRSUsA0	See RRAUc

RRAUscS	See RRAUc
RRUscYS	See RRAUc
RRAYy	See RRAUc
ORYAa	See RRAUc
RRYAa	See RRAUc
RRAYyS	See RRAUc
ORYAaS	See RRAUc
RRYAaS	See RRAUc
RRAUsS	See RRAUc
RRUsYS	See RRAUc

Details

The names of the parameters in the bound can be found for a given set of biases with `print(biases)`. Running `summary(biases)` shows the equivalent notation used in the output of the `multi_evalue()` function.

Value

Returns the value of the bound formed as a function of the provided parameters.

Examples

```
multi_bound(multi_bias(confounding()),
            RRAUc = 2.2, RRUcY = 1.7)

biases <- multi_bias(confounding(), selection("S = U"),
                    misclassification("exposure",
                    rare_outcome = TRUE, rare_exposure = FALSE))

print(biases)

multi_bound(biases,
            RRAUc = 3, RRUcY = 2, RRSUsA1 = 2.3,
            RRSUsA0 = 1.7, ORYAaS = 5.2)
```

multi_evalue

Calculate a multiple-bias E-value

Description

Calculate an E-value for a specified set of biases.

Usage

```

multi_evalue(biases, est, ...)

multi_values.HR(
  biases,
  est,
  lo = NA,
  hi = NA,
  rare = NULL,
  true = 1,
  verbose = TRUE,
  ...
)

multi_values.OR(
  biases,
  est,
  lo = NA,
  hi = NA,
  rare = NULL,
  true = 1,
  verbose = TRUE,
  ...
)

multi_values.RR(biases, est, lo = NA, hi = NA, true = 1, verbose = TRUE, ...)

```

Arguments

biases	An object created by <code>multi_bias()</code> (or a single bias) to include in the calculation of the E-value. May include any or all of <code>confounding()</code> , <code>selection()</code> , and <code>misclassification()</code> , and any of the options described in the documentation for those functions.
est	The effect estimate that was observed but which is suspected to be biased. This may be of class "estimate" (constructed with <code>RR()</code> , <code>OR()</code> , or <code>HR()</code> , or more information can be provided using the other arguments.
...	Arguments passed to other methods.
lo	Optional. Lower bound of the confidence interval. If not an object of class "estimate", assumed to be on the same scale as est.
hi	Optional. Upper bound of the confidence interval. If not an object of class "estimate", assumed to be on the same scale as est.
rare	Logical indicating whether outcome is sufficiently rare for risk ratio approximation to hold.
true	A number to which to shift the observed estimate to. Defaults to 1. If not an object of class "estimate", assumed to be on the same scale as est.
verbose	Logical indicating whether or not to print information about which parameters the multi-bias E-value refers to. Defaults to TRUE.

Value

Returns a multiple bias E-value, of class "multi_evalue", describing the value that each of a number of parameters would have to have for the observed effect measure to be completely explained by bias.

Examples

```
# Calculate an E-value for unmeasured confounding
multi_evalue(est = RR(4), biases = confounding())
# Equivalent to
evaluates.RR(4)

# Calculate a multi-bias E-value for selection bias
# and misclassification
multi_evalue(est = RR(2.5),
             biases = multi_bias(selection("selected"),
                                misclassification("outcome")))

# Calculate a multi-bias E-value for all three
# available types of bias
biases <- multi_bias(confounding(),
                    selection("general", "S = U"),
                    misclassification("exposure",
                                     rare_outcome = TRUE))
multi_evalue(est = RR(2.5), biases = biases)

# Calculate a multi-bias E-value for a non-rare OR
# using the square root approximation
multi_evalue(est = OR(2.5, rare = FALSE), biases = biases)

# Calculate a non-null multi-bias E-value
multi_evalue(est = RR(2.5), biases = biases, true = 2)
```

selection

Selection bias

Description

A type of bias. Declares that selection bias will be a component of interest in the multi-bias sensitivity analysis. Generally used within other functions; its output is returned invisibly.

Usage

```
selection(..., verbose = FALSE)
```

Arguments

- ... Optional arguments describing the type of potential selection bias. Options are "general" (general selection bias, the default if no options are chosen), "increased risk" and "decreased risk" (assumptions about the direction of risk in the selected population), "S = U" (simplification used if the biasing characteristic is common to the entire selected population), and "selected" (when the target of inference is the selected population only). Errors are produced when incompatible assumptions are chosen.
- verbose Logical. If TRUE, returns warnings and messages immediately. Defaults to FALSE because it is generally used within the `multi_bias()` function, which will print the same messages/warnings.

Value

Invisibly returns a list with components whose values depend on the options chosen: n (the degree of the polynomial in the numerator), d (the degree of the polynomial in the denominator), mess (any messages/warnings that should be printed for the user), and bias("selection").

Examples

```
# returns invisibly without print()
print(selection("general", "increased risk"))

# Calculate an E-value for selection bias only
multi_evalue(est = RR(4),
             biases = selection("general", "increased risk"))
```

selection_evalue	<i>Compute selection bias E-value for a hazard ratio and its confidence interval limits</i>
------------------	---

Description

Returns a data frame containing point estimates, the lower confidence limit, and the upper confidence limit on the risk ratio scale (through an approximate conversion if needed when outcome is common) as well as E-values for the point estimate and the confidence interval limit closer to the null.

Usage

```
selection_evalue(
  est,
  lo = NA,
  hi = NA,
  true = 1,
  sel_pop = FALSE,
```

```

    S_eq_U = FALSE,
    risk_inc = FALSE,
    risk_dec = FALSE,
    ...
  )

```

Arguments

<code>est</code>	The point estimate: a risk, odds, or hazard ratio. An object of class "estimate", it should be constructed with functions <code>RR()</code> , <code>OR()</code> , or <code>HR()</code> .
<code>lo</code>	The lower limit of the confidence interval
<code>hi</code>	The upper limit of the confidence interval
<code>true</code>	The true value to which to shift the observed point estimate. Typically set to 1 to consider a null true effect.
<code>sel_pop</code>	Whether inference is specific to selected population (TRUE) or entire population (FALSE). Defaults to FALSE.
<code>S_eq_U</code>	Whether the unmeasured factor is assumed to be a defining characteristic of the selected population. Defaults to FALSE.
<code>risk_inc</code>	Whether selection is assumed to be associated with increased risk of the outcome in both exposure groups. Defaults to FALSE.
<code>risk_dec</code>	Whether selection is assumed to be associated with decreased risk of the outcome in both exposure groups. Defaults to FALSE.
<code>...</code>	Arguments passed to other methods.

Details

A selection bias E-value is a summary measure that helps assess susceptibility of a result to selection bias. Each of one or more parameters characterizing the extent of the bias must be greater than or equal to this value to be sufficient to shift an estimate (`est`) to the null or other true value (`true`). The parameters, as defined in Smith and VanderWeele 2019, depend on assumptions an investigator is willing to make (see arguments `sel_pop`, `S_eq_U`, `risk_inc`, `risk_dec`). The function prints a message about which parameters the selection bias E-value refers to given the assumptions made. See the cited article for details.

Examples

```

# Examples from Smith and VanderWeele 2019

# Zika virus example
selection_evalue(OR(73.1, rare = TRUE), lo = 13.0)

# Endometrial cancer example
selection_evalue(OR(2.30, rare = TRUE), true = 11.98, S_eq_U = TRUE, risk_inc = TRUE)

# Obesity paradox example
selection_evalue(RR(1.50), lo = 1.22, sel_pop = TRUE)

```

Description

Produces line plots (type="line") showing the average bias factor across studies on the relative risk (RR) scale vs. the estimated proportion of studies with true RRs above or below a chosen threshold q . The plot secondarily includes a X-axis showing the minimum strength of confounding to produce the given bias factor. The shaded region represents a pointwise confidence band. Alternatively, produces distribution plots (type="dist") for a specific bias factor showing the observed and true distributions of RRs with a red line marking $\exp(q)$.

Usage

```
sens_plot(
  method = "calibrated",
  type,
  q,
  CI.level = 0.95,
  tail = NA,
  muB.toward.null = FALSE,
  give.CI = TRUE,
  Bmin = 0,
  Bmax = log(4),
  breaks.x1 = NA,
  breaks.x2 = NA,
  muB,
  sigB,
  yr,
  vyr = NA,
  t2,
  vt2 = NA,
  R = 1000,
  dat = NA,
  yi.name = NA,
  vi.name = NA
)
```

Arguments

method	"calibrated" or "parametric". See Details.
type	dist for distribution plot; line for line plot (see Details)
q	True causal effect size chosen as the threshold for a meaningfully large effect
CI.level	Pointwise confidence level as a proportion (e.g., 0.95).

tail	"above" for the proportion of effects above q; "below" for the proportion of effects below q. By default, is set to "above" if the pooled point estimate (method = "parametric") or median of the calibrated estimates (method = "calibrated") is above 1 on the relative risk scale and is set to "below" otherwise.
muB.toward.null	Whether you want to consider bias that has on average shifted studies' point estimates away from the null (FALSE; the default) or that has on average shifted studies' point estimates toward the null (TRUE). See Details.
give.CI	Logical. If TRUE, a pointwise confidence intervals is plotted.
Bmin	Lower limit of lower X-axis on the log scale (only needed if type = "line").
Bmax	Upper limit of lower X-axis on the log scale (only needed if type = "line")
breaks.x1	Breaks for lower X-axis (bias factor) on RR scale. (optional for type = "line"; not used for type = "dist").
breaks.x2	Breaks for upper X-axis (confounding strength) on RR scale (optional for type = "line"; not used for type = "dist")
muB	Single mean bias factor on log scale (only needed if type = "dist")
sigB	Standard deviation of log bias factor across studies (only used if method = "parametric")
yr	Pooled point estimate (on log scale) from confounded meta-analysis (only used if method = "parametric")
vyr	Estimated variance of pooled point estimate from confounded meta-analysis (only used if method = "parametric")
t2	Estimated heterogeneity (τ^2) from confounded meta-analysis (only used if method = "parametric")
vt2	Estimated variance of τ^2 from confounded meta-analysis (only used if method = "parametric")
R	Number of bootstrap iterates for confidence interval estimation. Only used if method = "calibrated" and give.CI = TRUE.
dat	Dataframe containing studies' point estimates and variances. Only used if method = "calibrated".
yi.name	Name of variable in dat containing studies' point estimates. Only used if method = "calibrated".
vi.name	Name of variable in dat containing studies' variance estimates. Only used if method = "calibrated".

Details

This function calls `confounded_meta` to get the point estimate and confidence interval at each value of the bias factor. See `?confounded_meta` for details.

Note that `Bmin` and `Bmax` are specified on the log scale for consistency with the `muB` argument and with the function `confounded_meta`, whereas `breaks.x1` and `breaks.x2` are specified on the relative risk scale to facilitate adjustments to the plot appearance.


```

                                data=metafor::dat.bcg)

# without confidence band
sens_plot( method = "calibrated",
           type="line",
           tail = "below",
           q=log(1.1),
           dat = d,
           yi.name = "yi",
           vi.name = "vi",
           give.CI = FALSE )

## with confidence band
## commented out because it takes a while
## this example gives bootstrap warnings because of its small sample size
# sens_plot( method = "calibrated",
#           type="line",
#           q=log(1.1),
#           R = 500, # should be higher in practice (e.g., 1000)
#           dat = d,
#           yi.name = "yi",
#           vi.name = "vi",
#           give.CI = TRUE )

# now with heterogeneous bias across studies (via sigB) and with confidence band
sens_plot( method = "parametric",
           type="line",
           q=log(1.1),
           yr=log(1.3),
           vyr = .05,
           vt2 = .001,
           t2=0.4,
           sigB = 0.1,
           Bmin=0,
           Bmax=log(4) )

##### Distribution Line Plot #####

# distribution plot: apparently causative
sens_plot( type="dist",
           q=log(1.1),
           muB=log(2),
           sigB = 0.1,
           yr=log(1.3),
           t2=0.4 )

# distribution plot: apparently preventive
sens_plot( type="dist",
           q=log(0.90),
           muB=log(1.5),
           sigB = 0.1,
           yr=log(0.7),

```


t2=0.2)

soyMeta	<i>A meta-analysis on soy intake and breast cancer risk (Trock et al., 2006)</i>
---------	--

Description

A meta-analysis of observational studies (12 case-control and six cohort or nested case-control) on the association of soy-food intake with breast cancer risk. Data are from Trock et al.'s (2006) Table 1. This dataset was used as the applied example in Mathur & VanderWeele (2020a).

Usage

soyMeta

Format

An object of class `data.frame` with 20 rows and 3 columns.

Details

The variables are as follows:

- `author` Last name of the study's first author.
- `est` Point estimate on the log-relative risk or log-odds ratio scale.
- `var` Variance of the log-relative risk or log-odds ratio.

References

Trock BJ, Hilakivi-Clarke L, Clark R (2006). Meta-analysis of soy intake and breast cancer risk. *Journal of the National Cancer Institute*.

Mathur MB & VanderWeele TJ (2020a). Sensitivity analysis for unmeasured confounding in meta-analyses. *Journal of the American Statistical Association*.

svalues.HR

Compute selection bias E-value for an estimate and its confidence interval limits

Description

Returns a data frame containing point estimates, the lower confidence limit, and the upper confidence limit on the risk ratio scale (through an approximate conversion if needed when outcome is common) as well as selection bias E-values for the point estimate and the confidence interval limit closer to the null.

Usage

```
svalues.HR(
  est,
  lo = NA,
  hi = NA,
  rare = NA,
  true = 1,
  sel_pop = FALSE,
  S_eq_U = FALSE,
  risk_inc = FALSE,
  risk_dec = FALSE,
  ...
)
```

Arguments

est	The point estimate
lo	The lower limit of the confidence interval
hi	The upper limit of the confidence interval
rare	1 if outcome is rare (<15 percent at end of follow-up); 0 if outcome is not rare (>15 percent at end of follow-up)
true	The true HR to which to shift the observed point estimate. Typically set to 1 to consider a null true effect.
sel_pop	Whether inference is specific to selected population (TRUE) or entire population (FALSE). Defaults to FALSE.
S_eq_U	Whether the unmeasured factor is assumed to be a defining characteristic of the selected population. Defaults to FALSE.
risk_inc	Whether selection is assumed to be associated with increased risk of the outcome in both exposure groups. Defaults to FALSE.
risk_dec	Whether selection is assumed to be associated with decreased risk of the outcome in both exposure groups. Defaults to FALSE.
...	Arguments passed to other methods.

Details

A selection bias E-value is a summary measure that helps assess susceptibility of a result to selection bias. Each of one or more parameters characterizing the extent of the bias must be greater than or equal to this value to be sufficient to shift an estimate (`est`) to the null or other true value (`true`). The parameters, as defined in Smith and VanderWeele 2019, depend on assumptions an investigator is willing to make (see arguments `sel_pop`, `S_eq_U`, `risk_inc`, `risk_dec`). The `svalues.XX` functions print a message about which parameters the selection bias E-value refers to given the assumptions made. See the cited article for details.

Examples

```
# Examples from Smith and VanderWeele 2019

# Obesity paradox example
svalues.RR(est = 1.50, lo = 1.22, sel_pop = TRUE)
```

<code>svalues.OR</code>	<i>Compute selection bias E-value for an odds ratio and its confidence interval limits</i>
-------------------------	--

Description

Returns a data frame containing point estimates, the lower confidence limit, and the upper confidence limit on the risk ratio scale (through an approximate conversion if needed when outcome is common) as well as E-values for the point estimate and the confidence interval limit closer to the null.

Usage

```
svalues.OR(
  est,
  lo = NA,
  hi = NA,
  rare = NA,
  true = 1,
  sel_pop = FALSE,
  S_eq_U = FALSE,
  risk_inc = FALSE,
  risk_dec = FALSE,
  ...
)
```

Arguments

<code>est</code>	The point estimate
<code>lo</code>	The lower limit of the confidence interval
<code>hi</code>	The upper limit of the confidence interval

rare	1 if outcome is rare (<15 percent at end of follow-up); 0 if outcome is not rare (>15 percent at end of follow-up)
true	The true OR to which to shift the observed point estimate. Typically set to 1 to consider a null true effect.
sel_pop	Whether inference is specific to selected population (TRUE) or entire population (FALSE). Defaults to FALSE.
S_eq_U	Whether the unmeasured factor is assumed to be a defining characteristic of the selected population. Defaults to FALSE.
risk_inc	Whether selection is assumed to be associated with increased risk of the outcome in both exposure groups. Defaults to FALSE.
risk_dec	Whether selection is assumed to be associated with decreased risk of the outcome in both exposure groups. Defaults to FALSE.
...	Arguments passed to other methods.

Details

A selection bias E-value is a summary measure that helps assess susceptibility of a result to selection bias. Each of one or more parameters characterizing the extent of the bias must be greater than or equal to this value to be sufficient to shift an estimate (`est`) to the null or other true value (`true`). The parameters, as defined in Smith and VanderWeele 2019, depend on assumptions an investigator is willing to make (see arguments `sel_pop`, `S_eq_U`, `risk_inc`, `risk_dec`). The `svalues.XX` functions print a message about which parameters the selection bias E-value refers to given the assumptions made. See the cited article for details.

Examples

```
# Examples from Smith and VanderWeele 2019

# Zika virus example
svalues.OR(est = 73.1, rare = TRUE, lo = 13.0)

# Endometrial cancer example
svalues.OR(est = 2.30, rare = TRUE, true = 11.98, S_eq_U = TRUE, risk_inc = TRUE)
```

svalues.RR	<i>Compute selection bias E-value for a risk ratio or rate ratio and its confidence interval limits</i>
------------	---

Description

Returns a data frame containing point estimates, the lower confidence limit, and the upper confidence limit for the risk ratio (as provided by the user) as well as selection bias E-values for the point estimate and the confidence interval limit closer to the null.

Usage

```
svalues.RR(
  est,
  lo = NA,
  hi = NA,
  true = 1,
  sel_pop = FALSE,
  S_eq_U = FALSE,
  risk_inc = FALSE,
  risk_dec = FALSE,
  ...
)
```

Arguments

<code>est</code>	The point estimate
<code>lo</code>	The lower limit of the confidence interval
<code>hi</code>	The upper limit of the confidence interval
<code>true</code>	The true RR to which to shift the observed point estimate. Typically set to 1 to consider a null true effect.
<code>sel_pop</code>	Whether inference is specific to selected population (TRUE) or entire population (FALSE). Defaults to FALSE.
<code>S_eq_U</code>	Whether the unmeasured factor is assumed to be a defining characteristic of the selected population. Defaults to FALSE.
<code>risk_inc</code>	Whether selection is assumed to be associated with increased risk of the outcome in both exposure groups. Defaults to FALSE.
<code>risk_dec</code>	Whether selection is assumed to be associated with decreased risk of the outcome in both exposure groups. Defaults to FALSE.
<code>...</code>	Arguments passed to other methods.

Details

A selection bias E-value is a summary measure that helps assess susceptibility of a result to selection bias. Each of one or more parameters characterizing the extent of the bias must be greater than or equal to this value to be sufficient to shift an estimate (`est`) to the null or other true value (`true`). The parameters, as defined in Smith and VanderWeele 2019, depend on assumptions an investigator is willing to make (see arguments `sel_pop`, `S_eq_U`, `risk_inc`, `risk_dec`). The `svalues.XX` functions print a message about which parameters the selection bias E-value refers to given the assumptions made. See the cited article for details.

Examples

```
# Examples from Smith and VanderWeele 2019

# Zika virus example
svalues.RR(est = 73.1, lo = 13.0)
```

```
# Endometrial cancer example
svalues.RR(est = 2.30, true = 11.98, S_eq_U = TRUE, risk_inc = TRUE)

# Obesity paradox example
svalues.RR(est = 1.50, lo = 1.22, sel_pop = TRUE)
```

 toyMeta

An example meta-analysis

Description

A simple simulated meta-analysis of 50 studies with exponentially distributed population effects.

Usage

```
toyMeta
```

Format

An object of class `data.frame` with 50 rows and 2 columns.

Details

The variables are as follows:

- `est` Point estimate on the log-relative risk scale.
- `var` Variance of the log-relative risk.

 twoXtwoRR

Estimate risk ratio and compute CI limits from two-by-two table

Description

Given counts in a two-by-two table, computes risk ratio and confidence interval limits.

Usage

```
twoXtwoRR(n11, n10, n01, n00, alpha = 0.05)
```

Arguments

<code>n11</code>	Number exposed (X=1) and diseased (D=1)
<code>n10</code>	Number exposed (X=1) and not diseased (D=0)
<code>n01</code>	Number unexposed (X=0) and diseased (D=1)
<code>n00</code>	Number unexposed (X=0) and not diseased (D=0)
<code>alpha</code>	Alpha level associated with confidence interval

Examples

```
# Hammond and Holl (1958 JAMA) Data
# Two by Two Table
#      Lung Cancer   No Lung Cancer
# Smoker   397       78557
# Nonsmoker 51       108778

twoXtwoRR(397, 78557, 51, 108778)
```

Index

- * **confounding**
 - sens_plot, 29
 - * **datasets**
 - lead, 20
 - soyMeta, 33
 - toyMeta, 38
 - * **e-value**
 - bias_plot, 2
 - evaluate, 12
 - evaluate.HR, 14
 - evaluate.MD, 15
 - evaluate.OLS, 16
 - evaluate.OR, 17
 - evaluate.RD, 18
 - evaluate.RR, 19
 - * **meta-analysis**
 - confounded_meta, 3
 - sens_plot, 29
 - * **multi-bias**
 - confounding, 8
 - misclassification, 21
 - multi_bias, 22
 - multi_bound, 23
 - multi_evaluate, 24
 - selection, 26
 - * **selection-bias**
 - selection_evaluate, 27
 - svalues.HR, 34
 - svalues.OR, 35
 - svalues.RR, 36
 - * **sensitivity**
 - sens_plot, 29
- bias_plot, 2
- confounded_meta, 3
- confounding, 8
- confounding(), 22, 23, 25
- conversion functions, 11, 12
- convert_measures, 9
- convert_measures(), 5
- effect measures, 9
- effect_measures, 10
- evaluate, 12
- evaluate(), 6
- evaluate.HR, 14
- evaluate.MD, 15
- evaluate.OLS, 16
- evaluate.OR, 17
- evaluate.RD, 18
- evaluate.RD(), 12
- evaluate.RR, 19
- HR (effect_measures), 10
- HR(), 9, 10, 12, 25, 28
- lead, 20
- MD (effect_measures), 10
- MD(), 9, 12
- misclassification, 21
- misclassification(), 22, 23, 25
- multi_bias, 22
- multi_bias(), 8, 21, 23, 25, 27
- multi_bound, 23
- multi_evaluate, 24
- multi_evaluate(), 24
- multi_evaluate.HR (multi_evaluate), 24
- multi_evaluate.OR (multi_evaluate), 24
- multi_evaluate.RR (multi_evaluate), 24
- OLS (effect_measures), 10
- OLS(), 9, 11, 12
- OR (effect_measures), 10
- OR(), 9, 10, 12, 25, 28
- RD (effect_measures), 10
- RR (effect_measures), 10
- RR(), 9, 12, 25, 28

selection, [26](#)
selection(), [22](#), [23](#), [25](#)
selection_evalue, [27](#)
sens_plot, [29](#)
soyMeta, [33](#)
svalues.HR, [34](#)
svalues.OR, [35](#)
svalues.RR, [36](#)

toMD (convert_measures), [9](#)
toRR (convert_measures), [9](#)
toyMeta, [38](#)
twoXtwoRR, [38](#)