

Package ‘tipr’

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Type Package

Title Tipping Point Analyses

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Description The strength of evidence provided by epidemiological and observational studies is inherently limited by the potential for unmeasured confounding.

We focus on three key quantities: the observed bound of the confidence interval closest to the null, a plausible residual effect size for an unmeasured continuous or binary confounder, and a realistic mean difference or prevalence difference for this hypothetical confounder. Building on the methods put forth by Lin, Psaty, & Kronmal (1998) <[doi:10.2307/2533848](https://doi.org/10.2307/2533848)>, we can use these quantities to assess how an unmeasured confounder may tip our result to insignificance, rendering the study inconclusive.

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adjust_coef	<i>Adjust an observed regression coefficient for a normally distributed confounder</i>
-------------	--

Description

Adjust an observed regression coefficient for a normally distributed confounder

Usage

```
adjust_coef(effect, smd, outcome_association, verbose = TRUE)
```

Arguments

effect	Numeric. Observed exposure - outcome effect from a regression model. This can be the beta coefficient, the lower confidence bound of the beta coefficient, or the upper confidence bound of the beta coefficient.
smd	Numeric. Estimated difference in scaled means between the unmeasured confounder in the exposed population and unexposed population
outcome_association	Numeric. Estimated association between the unmeasured confounder and the outcome.
verbose	Logical. Indicates whether to print informative message. Default: TRUE

Value

Data frame.

Examples

```
## Update an observed coefficient of 0.5 with an unmeasured confounder
## with a difference in scaled means between exposure groups of 0.2
## and coefficient of 0.3
adjust_coef(0.5, 0.2, 0.3)
```

```
adjust_coef_with_binary
```

Adjust an observed coefficient from a loglinear model with a binary confounder

Description

Adjust an observed coefficient from a loglinear model with a binary confounder

Usage

```
adjust_coef_with_binary(
  effect,
  exposed_p,
  unexposed_p,
  outcome_association,
  verbose = TRUE
)
```

Arguments

effect	Numeric. Observed exposure - outcome effect from a loglinear model. This can be the beta coefficient, the lower confidence bound of the beta coefficient, or the upper confidence bound of the beta coefficient.
exposed_p	Numeric between 0 and 1. Estimated prevalence of the unmeasured confounder in the exposed population
unexposed_p	Numeric between 0 and 1. Estimated prevalence of the unmeasured confounder in the unexposed population
outcome_association	Numeric. Estimated association between the unmeasured confounder and the outcome.
verbose	Logical. Indicates whether to print informative message. Default: TRUE

Value

Data frame.

Examples

```
adjust_coef_with_binary(1.1, 0.5, 0.3, 1.3)
```

adjust_coef_with_r2	<i>Adjust a regression coefficient using the partial R2 for an unmeasured confounder-exposure relationship and unmeasured confounder- outcome relationship</i>
---------------------	--

Description

This function wraps the [sensemakr::adjusted_estimate\(\)](#) and [sensemakr::adjusted_se\(\)](#) functions.

Usage

```
adjust_coef_with_r2(
  effect,
  se,
  df,
  exposure_r2,
  outcome_r2,
  verbose = TRUE,
  alpha = 0.05,
  ...
)
```

Arguments

effect	Numeric. Observed exposure - outcome effect from a regression model. This is the point estimate (beta coefficient)
se	Numeric. Standard error of the effect in the previous parameter.
df	Numeric positive value. Residual degrees of freedom for the model used to estimate the observed exposure - outcome effect. This is the total number of observations minus the number of parameters estimated in your model. Often for models estimated with an intercept this is $N - k - 1$ where k is the number of predictors in the model.
exposure_r2	Numeric value between 0 and 1. The assumed partial R2 of the unobserved confounder with the exposure given the measured covariates.
outcome_r2	Numeric value between 0 and 1. The assumed partial R2 of the unobserved confounder with the outcome given the exposure and the measured covariates.
verbose	Logical. Indicates whether to print informative message. Default: TRUE
alpha	Significance level. Default = 0.05.
...	Optional arguments passed to the sensemakr::adjusted_estimate() function.

Value

A data frame.

References

Carlos Cinelli, Jeremy Ferwerda and Chad Hazlett (2021). sensemakr: Sensitivity Analysis Tools for Regression Models. R package version 0.1.4. <https://CRAN.R-project.org/package=sensemakr>

Examples

```
adjust_coef_with_r2(0.5, 0.1, 102, 0.05, 0.1)
```

adjust_hr	<i>Adjust an observed hazard ratio for a normally distributed confounder</i>
-----------	--

Description

Adjust an observed hazard ratio for a normally distributed confounder

Usage

```
adjust_hr(  
  effect,  
  smd,  
  outcome_association,  
  verbose = TRUE,  
  hr_correction = FALSE  
)
```

Arguments

effect	Numeric positive value. Observed exposure - outcome hazard ratio. This can be the point estimate, lower confidence bound, or upper confidence bound.
smd	Numeric. Estimated difference in scaled means between the unmeasured confounder in the exposed population and unexposed population
outcome_association	Numeric. Estimated association between the unmeasured confounder and the outcome.
verbose	Logical. Indicates whether to print informative message. Default: TRUE
hr_correction	Logical. Indicates whether to use a correction factor. The methods used for this function are based on relative risks. For rare outcomes, a hazard ratio approximates a relative risk. For common outcomes, a correction factor is needed. If you have a common outcome (>15%), set this to TRUE. Default: FALSE.

Value

Data frame.

Examples

```
adjust_hr(0.9, -0.9, 1.3)
```

adjust_hr_with_binary *Adjust an observed hazard ratio with a binary confounder*

Description

Adjust an observed hazard ratio with a binary confounder

Usage

```
adjust_hr_with_binary(
  effect,
  exposed_p,
  unexposed_p,
  outcome_association,
  verbose = TRUE,
  hr_correction = FALSE
)
```

Arguments

effect	Numeric positive value. Observed exposure - outcome hazard ratio. This can be the point estimate, lower confidence bound, or upper confidence bound.
exposed_p	Numeric between 0 and 1. Estimated prevalence of the unmeasured confounder in the exposed population
unexposed_p	Numeric between 0 and 1. Estimated prevalence of the unmeasured confounder in the unexposed population
outcome_association	Numeric positive value. Estimated association between the unmeasured confounder and the outcome
verbose	Logical. Indicates whether to print informative message. Default: TRUE
hr_correction	Logical. Indicates whether to use a correction factor. The methods used for this function are based on relative risks. For rare outcomes, a hazard ratio approximates a relative risk. For common outcomes, a correction factor is needed. If you have a common outcome (>15%), set this to TRUE. Default: FALSE.

Value

Data frame.

Examples

```
adjust_hr_with_binary(0.8, 0.1, 0.5, 1.8)
```

adjust_or	<i>Adjust an observed odds ratio for a normally distributed confounder</i>
-----------	--

Description

Adjust an observed odds ratio for a normally distributed confounder

Usage

```
adjust_or(  
  effect,  
  smd,  
  outcome_association,  
  verbose = TRUE,  
  or_correction = FALSE  
)
```

Arguments

effect	Numeric positive value. Observed exposure - outcome odds ratio. This can be the point estimate, lower confidence bound, or upper confidence bound.
smd	Numeric. Estimated difference in scaled means between the unmeasured confounder in the exposed population and unexposed population
outcome_association	Numeric. Estimated association between the unmeasured confounder and the outcome.
verbose	Logical. Indicates whether to print informative message. Default: TRUE
or_correction	Logical. Indicates whether to use a correction factor. The methods used for this function are based on relative risks. For rare outcomes, an odds ratio approximates a relative risk. For common outcomes, a correction factor is needed. If you have a common outcome (>15%), set this to TRUE. Default: FALSE.

Value

Data frame.

Examples

```
adjust_or(1.2, 0.9, 1.3)
```

adjust_or_with_binary *Adjust an observed odds ratio with a binary confounder*

Description

Adjust an observed odds ratio with a binary confounder

Usage

```
adjust_or_with_binary(  
  effect,  
  exposed_p,  
  unexposed_p,  
  outcome_association,  
  verbose = TRUE,  
  or_correction = FALSE  
)
```

Arguments

effect	Numeric positive value. Observed exposure - outcome odds ratio. This can be the point estimate, lower confidence bound, or upper confidence bound.
exposed_p	Numeric between 0 and 1. Estimated prevalence of the unmeasured confounder in the exposed population
unexposed_p	Numeric between 0 and 1. Estimated prevalence of the unmeasured confounder in the unexposed population
outcome_association	Numeric positive value. Estimated association between the unmeasured confounder and the outcome
verbose	Logical. Indicates whether to print informative message. Default: TRUE
or_correction	Logical. Indicates whether to use a correction factor. The methods used for this function are based on relative risks. For rare outcomes, an odds ratio approximates a relative risk. For common outcomes, a correction factor is needed. If you have a common outcome (>15%), set this to TRUE. Default: FALSE.

Value

Data frame.

Examples

```
adjust_or_with_binary(3, 1, 0, 3)  
adjust_or_with_binary(3, 1, 0, 3, or_correction = TRUE)
```

adjust_rr	<i>Adjust an observed relative risk for a normally distributed confounder</i>
-----------	---

Description

Adjust an observed relative risk for a normally distributed confounder

Usage

```
adjust_rr(effect, smd, outcome_association, verbose = TRUE)
```

Arguments

effect	Numeric positive value. Observed exposure - outcome relative risk. This can be the point estimate, lower confidence bound, or upper confidence bound.
smd	Numeric. Estimated difference in scaled means between the unmeasured confounder in the exposed population and unexposed population
outcome_association	Numeric. Estimated association between the unmeasured confounder and the outcome.
verbose	Logical. Indicates whether to print informative message. Default: TRUE

Value

Data frame.

Examples

```
adjust_rr(1.2, 0.5, 1.1)
```

adjust_rr_with_binary	<i>Adjust an observed relative risk with a binary confounder</i>
-----------------------	--

Description

Adjust an observed relative risk with a binary confounder

Usage

```
adjust_rr_with_binary(
  effect,
  exposed_p,
  unexposed_p,
  outcome_association,
  verbose = TRUE
)
```

Arguments

effect	Numeric positive value. Observed exposure - outcome relative risk. This can be the point estimate, lower confidence bound, or upper confidence bound.
exposed_p	Numeric between 0 and 1. Estimated prevalence of the unmeasured confounder in the exposed population
unexposed_p	Numeric between 0 and 1. Estimated prevalence of the unmeasured confounder in the unexposed population
outcome_association	Numeric positive value. Estimated association between the unmeasured confounder and the outcome
verbose	Logical. Indicates whether to print informative message. Default: TRUE

Value

Data frame.

Examples

```
adjust_rr_with_binary(1.1, 0.5, 0.3, 1.3)
```

e_value

Calculate an E-value

Description

Calculate an E-value

Usage

```
e_value(effect)
```

Arguments

effect	Numeric positive value. Observed exposure - outcome effect (assumed to be the exponentiated coefficient, so a relative risk, odds ratio, or hazard ratio). This can be the point estimate, lower confidence bound, or upper confidence bound.
--------	---

Value

Numeric value

Examples

```
e_value(0.9)
e_value(1.3)
```

observed_bias_order *Order observed bias data frame for plotting*

Description

Order observed bias data frame for plotting

Usage

```
observed_bias_order(d, by)
```

Arguments

d	Observed bias data frame. Must have columns dropped and type
by	Character. Variable in d to order by.

Value

Data frame in the correct order

observed_bias_tbl *Create a data frame to assist with creating an observed bias plot*

Description

Create a data frame to assist with creating an observed bias plot

Usage

```
observed_bias_tbl(ps_mod, outcome_mod, drop_list = NULL)
```

Arguments

ps_mod	Model object for the propensity score model
outcome_mod	Model object for the outcome model
drop_list	Named list of covariates or groups of covariates to drop if NULL, will default to dropping each covariate one at a time.

Value

Data frame with the following columns:

- `dropped`: The covariate or group of covariates that were dropped
- `type`: Explanation of dropped, whether it refers to a single covariate (`covariate`) or a group of covariates (`group`)
- `ps_formula`: The new formula for the updated propensity score model
- `outcome_formula`: The new formula for the updated outcome model
- `ps_model`: The new model object for the updated propensity score model
- `p`: The updated propensity score

Examples

```
ps_mod <- glm(am ~ mpg + cyl + I(hp^2), data = mtcars)
outcome_mod <- lm(qsec ~ am + hp + disp + wt, data = mtcars)
observed_bias_tbl(
  ps_mod,
  outcome_mod,
  drop_list = list(
    group_one = c("mpg", "hp"),
    group_two = c("cyl", "wt")
  )
)
```

<code>observed_bias_tip</code>	<i>Create a data frame to combine with an observed bias data frame demonstrating a hypothetical unmeasured confounder</i>
--------------------------------	---

Description

Create a data frame to combine with an observed bias data frame demonstrating a hypothetical unmeasured confounder

Usage

```
observed_bias_tip(
  tip,
  point_estimate,
  lb,
  ub,
  tip_desc = "Hypothetical unmeasured confounder"
)
```

Arguments

tip	Numeric. Value you would like to tip to.
point_estimate	Numeric. Result estimate from the full model.
lb	Numeric. Result lower bound from the full model.
ub	Numeric. Result upper bound from the full model.
tip_desc	Character. A description of the tipping point.

Value

A data frame with five columns:

- dropped: the input from tip_desc
- type: Explanation of dropped, here tip to clarify that this was calculated as a tipping point.
- point_estimate: the shifted point estimate
- lb: the shifted lower bound
- ub: the shifted upper bound

observed_covariate_e_value

Calculate the Observed Covariate E-value

Description

Calculate the Observed Covariate E-value

Usage

```
observed_covariate_e_value(lb, ub, lb_adj, ub_adj, transform = NULL)
```

Arguments

lb	Numeric. The lower bound of the full model
ub	Numeric. The upper bound of the full model
lb_adj	Numeric. The lower bound of the adjusted model
ub_adj	Numeric. The upper bound of the adjusted model
transform	Character. If your effect is an odds ratio or hazard ratio, this will perform the transformation suggested by VanderWeele and Ding. Allowed values are: <ul style="list-style-type: none"> • "OR" • "HR"

Value

The Observed Covariate E-value

r_value	<i>Robustness value</i>
---------	-------------------------

Description

This function wraps the `sensemkr::robustness_value()` function

Usage

```
r_value(effect, se, df, ...)
```

Arguments

effect	Numeric. Observed exposure - outcome effect from a regression model. This is the point estimate (beta coefficient)
se	Numeric. Standard error of the effect in the previous parameter.
df	Numeric positive value. Residual degrees of freedom for the model used to estimate the observed exposure - outcome effect. This is the total number of observations minus the number of parameters estimated in your model. Often for models estimated with an intercept this is $N - k - 1$ where k is the number of predictors in the model.
...	Optional arguments passed to the <code>sensemkr::robustness_value()</code> function.

Value

Numeric. Robustness value

References

Carlos Cinelli, Jeremy Ferwerda and Chad Hazlett (2021). `sensemkr`: Sensitivity Analysis Tools for Regression Models. R package version 0.1.4. <https://CRAN.R-project.org/package=sensemkr>

Examples

```
r_value(0.5, 0.1, 102)
```

 tip

Tip a result with a normally distributed confounder.

Description

choose one of the following, and the other will be estimated:

- `smd`
- `outcome_association`

Usage

```
tip(
  effect,
  smd = NULL,
  outcome_association = NULL,
  verbose = TRUE,
  correction_factor = "none"
)
```

```
tip_with_continuous(
  effect,
  smd = NULL,
  outcome_association = NULL,
  verbose = TRUE,
  correction_factor = "none"
)
```

```
tip_c(
  effect,
  smd = NULL,
  outcome_association = NULL,
  verbose = TRUE,
  correction_factor = "none"
)
```

Arguments

<code>effect</code>	Numeric positive value. Observed exposure - outcome effect (assumed to be the exponentiated coefficient, so a relative risk, odds ratio, or hazard ratio). This can be the point estimate, lower confidence bound, or upper confidence bound.
<code>smd</code>	Numeric. Estimated difference in scaled means between the unmeasured confounder in the exposed population and unexposed population
<code>outcome_association</code>	Numeric positive value. Estimated association between the unmeasured confounder and the outcome

`verbose` Logical. Indicates whether to print informative message. Default: TRUE

`correction_factor` Character string. Options are "none", "hr", "or". For common outcomes (>15%), the odds ratio or hazard ratio is not a good estimate for the relative risk. In these cases, we can apply a correction factor. If you are supplying a hazard ratio for a common outcome, set this to "hr"; if you are supplying an odds ratio for a common outcome, set this to "or"; if you are supplying a risk ratio or your outcome is rare, set this to "none" (default).

Value

Data frame.

Examples

```
## to estimate the association between an unmeasured confounder and outcome
## needed to tip analysis
tip(1.2, smd = -2)

## to estimate the number of unmeasured confounders specified needed to tip
## the analysis
tip(1.2, smd = -2, outcome_association = .99)

## Example with broom
if (requireNamespace("broom", quietly = TRUE) &&
    requireNamespace("dplyr", quietly = TRUE)) {
  glm(am ~ mpg, data = mtcars, family = "binomial") %>%
  broom::tidy(conf.int = TRUE, exponentiate = TRUE) %>%
  dplyr::filter(term == "mpg") %>%
  dplyr::pull(conf.low) %>%
  tip(outcome_association = 2.5)
}
```

tipr

tipr

Description

The tipr package.

References

D'Agostino McGowan, L. (2018). Improving Modern Techniques of Causal Inference: Finite Sample Performance of ATM and ATO Doubly Robust Estimators, Variance Estimation for ATO Estimators, and Contextualized Tipping Point Sensitivity Analyses for Unmeasured Confounding. PhD thesis, Vanderbilt University.

VanderWeele, TJ, and Peng D (2017). Sensitivity Analysis in Observational Research: Introducing the E-Value. *Ann Intern Med*, 167(4), 268–74.

Lin, DY, Psaty, BM, & Kronmal, RA. (1998). Assessing the sensitivity of regression results to unmeasured confounders in observational studies. *Biometrics*, 54(3), 948–963.

tip_coef_with_r2	<i>Tip a regression coefficient using the partial R2 for an unmeasured confounder-exposure relationship and unmeasured confounder- outcome relationship</i>
------------------	---

Description

Choose one of the following, and the other will be estimated:

- exposure_r2
- outcome_r2

Usage

```
tip_coef_with_r2(
  effect,
  se,
  df,
  exposure_r2 = NULL,
  outcome_r2 = NULL,
  verbose = TRUE,
  alpha = 0.05,
  tip_bound = FALSE,
  ...
)
```

Arguments

effect	Numeric. Observed exposure - outcome effect from a regression model. This is the point estimate (beta coefficient)
se	Numeric. Standard error of the effect in the previous parameter.
df	Numeric positive value. Residual degrees of freedom for the model used to estimate the observed exposure - outcome effect. This is the total number of observations minus the number of parameters estimated in your model. Often for models estimated with an intercept this is $N - k - 1$ where k is the number of predictors in the model.
exposure_r2	Numeric value between 0 and 1. The assumed partial R2 of the unobserved confounder with the exposure given the measured covariates.
outcome_r2	Numeric value between 0 and 1. The assumed partial R2 of the unobserved confounder with the outcome given the exposure and the measured covariates.
verbose	Logical. Indicates whether to print informative message. Default: TRUE
alpha	Significance level. Default = 0.05.

tip_bound Do you want to tip at the bound? Default = FALSE, will tip at the point estimate
 ... Optional arguments passed to the `sensemkr::adjusted_estimate()` function.

Value

A data frame.

Examples

```
tip_coef_with_r2(0.5, 0.1, 102, 0.5)
```

tip_hr	<i>Tip an observed hazard ratio with a normally distributed confounder.</i>
--------	---

Description

choose one of the following, and the other will be estimated:

- `smd`
- `outcome_association`

Usage

```
tip_hr(  
  effect,  
  smd = NULL,  
  outcome_association = NULL,  
  verbose = TRUE,  
  hr_correction = FALSE  
)
```

Arguments

`effect` Numeric positive value. Observed exposure - outcome hazard ratio. This can be the point estimate, lower confidence bound, or upper confidence bound.

`smd` Numeric. Estimated difference in scaled means between the unmeasured confounder in the exposed population and unexposed population

`outcome_association` Numeric positive value. Estimated association between the unmeasured confounder and the outcome

`verbose` Logical. Indicates whether to print informative message. Default: TRUE

`hr_correction` Logical. Indicates whether to use a correction factor. The methods used for this function are based on relative risks. For rare outcomes, a hazard ratio approximates a relative risk. For common outcomes, a correction factor is needed. If you have a common outcome (>15%), set this to TRUE. Default: FALSE.

Value

Data frame.

Examples

```
## to estimate the association between an unmeasured confounder and outcome
## needed to tip analysis
tip_hr(1.2, smd = -2)

## to estimate the number of unmeasured confounders specified needed to tip
## the analysis
tip_hr(1.2, smd = -2, outcome_association = .99)
```

tip_hr_with_binary	<i>Tip an observed hazard ratio with a binary confounder.</i>
--------------------	---

Description

Choose two of the following three to specify, and the third will be estimated:

- exposed_p
- unexposed_p
- outcome_association

Alternatively, specify all three and the function will return the number of unmeasured confounders specified needed to tip the analysis.

Usage

```
tip_hr_with_binary(
  effect,
  exposed_p = NULL,
  unexposed_p = NULL,
  outcome_association = NULL,
  verbose = TRUE,
  hr_correction = FALSE
)
```

Arguments

effect	Numeric positive value. Observed exposure - outcome hazard ratio. This can be the point estimate, lower confidence bound, or upper confidence bound.
exposed_p	Numeric between 0 and 1. Estimated prevalence of the unmeasured confounder in the exposed population
unexposed_p	Numeric between 0 and 1. Estimated prevalence of the unmeasured confounder in the unexposed population

outcome_association	Numeric positive value. Estimated association between the unmeasured confounder and the outcome
verbose	Logical. Indicates whether to print informative message. Default: TRUE
hr_correction	Logical. Indicates whether to use a correction factor. The methods used for this function are based on relative risks. For rare outcomes, a hazard ratio approximates a relative risk. For common outcomes, a correction factor is needed. If you have a common outcome (>15%), set this to TRUE. Default: FALSE.

Value

Data frame.

Examples

```
tip_hr_with_binary(0.9, 0.9, 0.1)
```

tip_lm	<i>Tip a linear model result with a continuous confounder.</i>
--------	--

Description

choose one of the following, and the other will be estimated:

- smd
- outcome_association

Usage

```
tip_lm(
  effect,
  smd = NULL,
  outcome_association = NULL,
  verbose = TRUE,
  correction_factor = "none"
)
```

```
lm_tip(effect, smd, outcome_association, verbose = TRUE)
```

Arguments

effect	Numeric. Observed exposure - outcome effect from a regression model. This can be the beta coefficient, the lower confidence bound of the beta coefficient, or the upper confidence bound of the beta coefficient.
smd	Numeric. Estimated scaled mean difference between the unmeasured confounder in the exposed population and unexposed population

outcome_association
 Numeric positive value. Estimated association between the unmeasured confounder and the outcome

verbose
 Logical. Indicates whether to print informative message. Default: TRUE

correction_factor
 Character string. Options are "none", "hr", "or". For common outcomes (>15%), the odds ratio or hazard ratio is not a good estimate for the relative risk. In these cases, we can apply a correction factor. If you are supplying a hazard ratio for a common outcome, set this to "hr"; if you are supplying an odds ratio for a common outcome, set this to "or"; if you are supplying a risk ratio or your outcome is rare, set this to "none" (default).

Value

Data frame.

Examples

```
## to estimate the association between an unmeasured confounder and outcome
## needed to tip analysis
tip_lm(1.2, smd = -2)

## to estimate the number of unmeasured confounders specified needed to tip
## the analysis
tip_lm(1.2, smd = -2, outcome_association = -0.05)

## Example with broom
if (requireNamespace("broom", quietly = TRUE) &&
    requireNamespace("dplyr", quietly = TRUE)) {
  lm(wt ~ mpg, data = mtcars) %>%
  broom::tidy(conf.int = TRUE) %>%
  dplyr::filter(term == "mpg") %>%
  dplyr::pull(conf.low) %>%
  tip_lm(outcome_association = 2.5)
}
```

tip_or

Tip an observed odds ratio with a normally distributed confounder.

Description

choose one of the following, and the other will be estimated:

- smd
- outcome_association

Usage

```
tip_or(
  effect,
  smd = NULL,
  outcome_association = NULL,
  verbose = TRUE,
  or_correction = FALSE
)
```

Arguments

effect	Numeric positive value. Observed exposure - outcome odds ratio. This can be the point estimate, lower confidence bound, or upper confidence bound.
smd	Numeric. Estimated difference in scaled means between the unmeasured confounder in the exposed population and unexposed population
outcome_association	Numeric positive value. Estimated association between the unmeasured confounder and the outcome
verbose	Logical. Indicates whether to print informative message. Default: TRUE
or_correction	Logical. Indicates whether to use a correction factor. The methods used for this function are based on relative risks. For rare outcomes, an odds ratio approximates a relative risk. For common outcomes, a correction factor is needed. If you have a common outcome (>15%), set this to TRUE. Default: FALSE.

Value

Data frame.

Examples

```
## to estimate the association between an unmeasured confounder and outcome
## needed to tip analysis
tip_or(1.2, smd = -2)

## to estimate the number of unmeasured confounders specified needed to tip
## the analysis
tip_or(1.2, smd = -2, outcome_association = .99)

## Example with broom
if (requireNamespace("broom", quietly = TRUE) &&
    requireNamespace("dplyr", quietly = TRUE)) {
  glm(am ~ mpg, data = mtcars, family = "binomial") %>%
  broom::tidy(conf.int = TRUE, exponentiate = TRUE) %>%
  dplyr::filter(term == "mpg") %>%
  dplyr::pull(conf.low) %>%
  tip_or(outcome_association = 2.5, or_correction = TRUE)
}
```

tip_or_with_binary *Tip an observed odds ratio with a binary confounder.*

Description

Choose two of the following three to specify, and the third will be estimated:

- exposed_p
- unexposed_p
- outcome_association

Alternatively, specify all three and the function will return the number of unmeasured confounders specified needed to tip the analysis.

Usage

```
tip_or_with_binary(
  effect,
  exposed_p = NULL,
  unexposed_p = NULL,
  outcome_association = NULL,
  verbose = TRUE,
  or_correction = FALSE
)
```

Arguments

effect	Numeric positive value. Observed exposure - outcome odds ratio. This can be the point estimate, lower confidence bound, or upper confidence bound.
exposed_p	Numeric between 0 and 1. Estimated prevalence of the unmeasured confounder in the exposed population
unexposed_p	Numeric between 0 and 1. Estimated prevalence of the unmeasured confounder in the unexposed population
outcome_association	Numeric positive value. Estimated association between the unmeasured confounder and the outcome
verbose	Logical. Indicates whether to print informative message. Default: TRUE
or_correction	Logical. Indicates whether to use a correction factor. The methods used for this function are based on relative risks. For rare outcomes, an odds ratio approximates a relative risk. For common outcomes, a correction factor is needed. If you have a common outcome (>15%), set this to TRUE. Default: FALSE.

Value

Data frame.

Examples

```
tip_or_with_binary(0.9, 0.9, 0.1)
```

tip_rr	<i>Tip an observed relative risk with a normally distributed confounder.</i>
--------	--

Description

choose one of the following, and the other will be estimated:

- smd
- outcome_association

Usage

```
tip_rr(effect, smd = NULL, outcome_association = NULL, verbose = TRUE)
```

Arguments

effect	Numeric positive value. Observed exposure - outcome relative risk. This can be the point estimate, lower confidence bound, or upper confidence bound.
smd	Numeric. Estimated difference in scaled means between the unmeasured confounder in the exposed population and unexposed population
outcome_association	Numeric positive value. Estimated association between the unmeasured confounder and the outcome
verbose	Logical. Indicates whether to print informative message. Default: TRUE

Value

Data frame.

Examples

```
## to estimate the association between an unmeasured confounder and outcome
## needed to tip analysis
tip_rr(1.2, smd = -2)

## to estimate the number of unmeasured confounders specified needed to tip
## the analysis
tip_rr(1.2, smd = -2, outcome_association = .99)
```

tip_rr_with_binary *Tip an observed relative risk with a binary confounder.*

Description

Choose two of the following three to specify, and the third will be estimated:

- exposed_p
- unexposed_p
- outcome_association

Alternatively, specify all three and the function will return the number of unmeasured confounders specified needed to tip the analysis.

Usage

```
tip_rr_with_binary(  
  effect,  
  exposed_p,  
  unexposed_p,  
  outcome_association,  
  verbose = TRUE  
)
```

Arguments

effect	Numeric positive value. Observed exposure - outcome relative risk. This can be the point estimate, lower confidence bound, or upper confidence bound.
exposed_p	Numeric between 0 and 1. Estimated prevalence of the unmeasured confounder in the exposed population
unexposed_p	Numeric between 0 and 1. Estimated prevalence of the unmeasured confounder in the unexposed population
outcome_association	Numeric positive value. Estimated association between the unmeasured confounder and the outcome
verbose	Logical. Indicates whether to print informative message. Default: TRUE

tip_with_binary *Tip a result with a binary confounder.*

Description

Choose two of the following three to specify, and the third will be estimated:

- exposed_p
- unexposed_p
- outcome_association

Alternatively, specify all three and the function will return the number of unmeasured confounders specified needed to tip the analysis.

Usage

```
tip_with_binary(
  effect,
  exposed_p = NULL,
  unexposed_p = NULL,
  outcome_association = NULL,
  verbose = TRUE,
  correction_factor = "none"
)
```

```
tip_b(
  effect,
  exposed_p = NULL,
  unexposed_p = NULL,
  outcome_association = NULL,
  verbose = TRUE,
  correction_factor = "none"
)
```

Arguments

effect	Numeric positive value. Observed exposure - outcome effect (assumed to be the exponentiated coefficient, so a relative risk, odds ratio, or hazard ratio). This can be the point estimate, lower confidence bound, or upper confidence bound.
exposed_p	Numeric between 0 and 1. Estimated prevalence of the unmeasured confounder in the exposed population
unexposed_p	Numeric between 0 and 1. Estimated prevalence of the unmeasured confounder in the unexposed population
outcome_association	Numeric positive value. Estimated association between the unmeasured confounder and the outcome

verbose Logical. Indicates whether to print informative message. Default: TRUE

correction_factor Character string. Options are "none", "hr", "or". For common outcomes (>15%), the odds ratio or hazard ratio is not a good estimate for the relative risk. In these cases, we can apply a correction factor. If you are supplying a hazard ratio for a common outcome, set this to "hr"; if you are supplying an odds ratio for a common outcome, set this to "or"; if you are supplying a risk ratio or your outcome is rare, set this to "none" (default).

Details

`tip_b()` is an alias for `tip_with_binary()`.

Examples

```
## to estimate the association between an unmeasured confounder and outcome
## needed to tip analysis
tip_with_binary(1.2, exposed_p = 0.5, unexposed_p = 0)

## to estimate the number of unmeasured confounders specified needed to tip
## the analysis
tip_with_binary(1.2,
  exposed_p = 0.5,
  unexposed_p = 0,
  outcome_association = 1.1)

## Example with broom
if (requireNamespace("broom", quietly = TRUE) &&
  requireNamespace("dplyr", quietly = TRUE)) {
  glm(am ~ mpg, data = mtcars, family = "binomial") %>%
  broom::tidy(conf.int = TRUE, exponentiate = TRUE) %>%
  dplyr::filter(term == "mpg") %>%
  dplyr::pull(conf.low) %>%
  tip_with_binary(exposed_p = 1, outcome_association = 1.15)
}
```

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