

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, 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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Encoding UTF-8

LazyData true

RoxygenNote 7.1.1

Suggests testthat, broom, dplyr, MASS

Imports glue, tibble, purrr

NeedsCompilation no

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 tip

Tip a result with a continuous confounder.

Description

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

- `smd`
- `outcome_association`

Usage

```
tip(
  d,
  smd = NULL,
  outcome_association = NULL,
  verbose = TRUE,
  lb_name = "conf.low",
  ub_name = "conf.high"
)
```

```
tip_with_continuous(
  d,
  smd = NULL,
  outcome_association = NULL,
  verbose = TRUE,
  lb_name = "conf.low",
  ub_name = "conf.high"
)
```

```
tip_c(
  d,
  smd = NULL,
  outcome_association = NULL,
  verbose = TRUE,
  lb_name = "conf.low",
  ub_name = "conf.high"
)
```

Arguments

- | | |
|------------------|---|
| <code>d</code> | Data frame. A data frame with the observed effect(s). This should have at least two columns with the lower and upper confidence bounds. These columns are assumed to be called <code>conf.low</code> and <code>conf.high</code> . If this is not the case, the names can be changed using the <code>lb_name</code> and <code>ub_name</code> parameters. |
| <code>smd</code> | 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
lb_name	Character. Column name of d that holds the lower confidence bound. Default: conf.low based on broom defaults.
ub_name	Character. Column name of d that holds the upper confidence bound. Default: conf.high based on broom defaults.

Value

Data frame.

Examples

```
d <- data.frame(conf.low = 1.2, conf.high = 1.5)
## to estimate the association between an unmeasured confounder and outcome
## needed to tip analysis
tip(d, smd = -2)

## to estimate the number of unmeasured confounders specified needed to tip
## the analysis
tip(d, 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") %>%
  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_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(
  d,
  exposed_p = NULL,
  unexposed_p = NULL,
  outcome_association = NULL,
  verbose = TRUE,
  lb_name = "conf.low",
  ub_name = "conf.high"
)
```

```
tip_b(
  d,
  exposed_p = NULL,
  unexposed_p = NULL,
  outcome_association = NULL,
  verbose = TRUE,
  lb_name = "conf.low",
  ub_name = "conf.high"
)
```

Arguments

d	Data frame. A data frame with the observed effect(s). This should have at least two columns with the lower and upper confidence bounds. These columns are assumed to be called <code>conf.low</code> and <code>conf.high</code> . If this is not the case, the names can be changed using the <code>lb_name</code> and <code>ub_name</code> parameters.
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
lb_name	Character. Column name of d that holds the lower confidence bound. Default: conf.low based on broom defaults.
ub_name	Character. Column name of d that holds the upper confidence bound. Default: conf.high based on broom defaults.

Details

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

Examples

```
d <- data.frame(conf.low = 1.2, conf.high = 1.5)
## to estimate the association between an unmeasured confounder and outcome
## needed to tip analysis
tip_with_binary(d, exposed_p = 0.5, unexposed_p = 0)

## to estimate the number of unmeasured confounders specified needed to tip
## the analysis
tip_with_binary(d, 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") %>%
  tip_with_binary(exposed_p = 1, outcome_association = 1.15)
}
```

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