

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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LazyData true

RoxygenNote 6.0.1

Suggests testthat

Imports broom, tibble, purrr

NeedsCompilation no

Repository CRAN

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tipr	<i>tipr</i>
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Description

tipr

References

Lin, D. Y., Psaty, B. M., & Kronmal, R. A. (1998). Assessing the sensitivity of regression results to unmeasured confounders in observational studies. *Biometrics*, 54(3), 948–963.

tip_with_binary	<i>Tip a result with a binary confounder.</i>
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Description

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

- p1
- p0
- gamma

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

Usage

```
tip_with_binary(p1 = NULL, p0 = NULL, gamma = NULL, lb = NULL,
               ub = NULL)
```

```
tip_b(p1 = NULL, p0 = NULL, gamma = NULL, lb = NULL, ub = NULL)
```

Arguments

p1	estimated prevalence of the unmeasured confounder in the exposed population
p0	estimated prevalence of the unmeasured confounder in the unexposed population
gamma	estimated size of an unmeasured confounder
lb	lower bound of your observed effect
ub	upper bound of your observed effect

Details

[tip_b\(\)](#) is an alias for [tip_with_binary\(\)](#).

Examples

```
#to output the size of an unmeasured confounder needed to tip analysis
tip_with_binary(p1 = .5, p0 = 0, lb = 1.2, ub = 1.5)
```

tip_with_continuous *Tip a result with a continuous confounder.*

Description

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

- mean_diff
- gamma

Usage

```
tip_with_continuous(mean_diff = NULL, gamma = NULL, lb = NULL,
  ub = NULL)
```

```
tip_c(mean_diff = NULL, gamma = NULL, lb = NULL, ub = NULL)
```

Arguments

mean_diff	estimated mean difference of the unmeasured confounder in the exposed population and unexposed population
gamma	estimated size of an unmeasured confounder
lb	lower bound of your observed effect
ub	upper bound of your observed effect

Details

[tip_c\(\)](#) is an alias for [tip_with_continuous\(\)](#).

Value

Numeric. The size of an unmeasured confounder at the given parameters that would tip the observed result.

Examples

```
#to output the size of an unmeasured confounder needed to tip analysis
tip_with_continuous(mean_diff = -2, lb = 1.2, ub = 1.5)
```

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