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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R topics documented:

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Description

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

- \( p_1 \)
- \( p_0 \)
- \( \gamma \)

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

- \( p_1 \): estimated prevalence of the unmeasured confounder in the exposed population
- \( p_0 \): estimated prevalence of the unmeasured confounder in the unexposed population
- \( \gamma \): estimated size of an unmeasured confounder
- \( \text{lb} \): lower bound of your observed effect
- \( \text{ub} \): upper bound of your observed effect

Details

\( \text{tip}_b() \) is an alias for \( \text{tip}_\text{with}_\text{binary}() \).
**Examples**

```r
# 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)
```

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**Description**

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

- `mean_diff`
- `gamma`

**Usage**

```r
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**

```r
# 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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