Package ‘PubBias’

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Type Package

Title Performs simulation study to look for publication bias, using a technique described by Ioannidis and Trikalinos; Clin Trials. 2007;4(3):245-53.

Depends rmeta, R.utils

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Description I adapted a method designed by Ioannidis and Trikalinos, which compares the observed number of positive studies in a meta-analysis with the expected number, if the summary measure of effect, averaged over the individual studies, were assumed true. Excess in the observed number of positive studies, compared to the expected, is taken as evidence of publication bias. The observed number of positive studies, at a given level for statistical significance, is calculated by applying Fisher’s exact test to the reported 2x2 table data of each constituent study, doubling the Fisher one-sided P-value to make a two-sided test. The corresponding expected number of positive studies was obtained by summing the statistical powers of each study. The statistical power depended on a given measure of effect which, here, was the pooled odds ratio of the meta-analysis was used. By simulating each constituent study, with the given odds ratio, and the same number of treated and non-treated as in the real study, the power of the study is estimated as the proportion of simulated studies that are positive, again by a Fisher’s exact test. The simulated number of events in the treated and untreated groups was done with binomial sampling. In the untreated group, the binomial proportion was the percentage of actual events reported in the study and, in the treated group, the binomial sampling proportion was the untreated percentage multiplied by the risk ratio which was derived from the assumed common odds ratio. The statistical significance for judging a positive study may be varied and large differences between expected and observed number of positive studies around the level of 0.05 significance constitutes evidence of publication bias. The difference between the observed and expected is tested by chi-square. A
chi-square test P-value for the difference below 0.05 is suggestive of publication bias, however, a less stringent level of 0.1 is often used in studies of publication bias as the number of published studies is usually small.

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Collate 'process.R'

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BMort

Description
BMort

Format
Brugts meta-analysis study of effect of statins on overall mortality (BMJ 2009).

Source
Chi-square test to test for significant difference between observed and expected number of positive studies (not for end user).

Description

Chi-square test to test for significant difference between observed and expected number of positive studies (not for end user).

Usage

\[
\text{ChisqTest_expect}(\text{vec}\_r\_events\_control, \\
\text{vec}\_n\_sample\_size\_control, \text{vec}\_n\_sample\_size\_treated, \\
\text{OR}\_hat, \text{n, alpha, vec}\_pos)
\]

Arguments

- \text{vec}\_r\_events\_control: an ordered vector of number of events in the untreated group of constituent studies from a meta-analysis.
- \text{vec}\_n\_sample\_size\_control: an ordered vector of the number of participants in the untreated group.
- \text{vec}\_n\_sample\_size\_treated: an ordered vector of the number of participants in the treated group.
- \text{alpha}: Type-1 error rate.
- \text{OR}\_hat: Summary odds ratio from meta-analysis.
- \text{n}: Number of iterations used to generate constituent study power; suggest use 10,000.
- \text{vec}\_pos: Vector of positive results from constituent studies, returned by test.n.treated function.

Value

Vector of p-values for difference between observed and expected number of positive studies from meta-analysis, along with vector of expected values.
expected_events  
calculate the number of expected events from a study included in a meta-analysis assuming summary effect estimate (OR\_hat) is true (not for end user).

Description

calculate the number of expected events from a study included in a meta-analysis assuming summary effect estimate (OR\_hat) is true (not for end user).

Usage

expected_events(vec\_r\_events\_control, 
vec\_n\_sample\_size\_control, vec\_n\_sample\_size\_treated,  
OR\_hat, n, alpha)

Arguments

vec\_r\_events\_control  
an ordered vector of number of events in the untreated group of constituent studies from a meta-analysis.

vec\_n\_sample\_size\_control  
an ordered vector of the number of participants in the untreated group.

vec\_n\_sample\_size\_treated  
an ordered vector of the number of participants in the treated group.

alpha  
Type-1 error rate.

n  
Number of iterations used to generate constituent study power; suggest use 10,000.

OR\_hat  
Summary odds ratio from meta-analysis

Value

Expected number of events at given alpha level.

plot\_chase\_observed\_expected

From a meta-analysis, analyse for publication bias. Calculates observed and expected number of positive studies and P for difference.

Description

From a meta-analysis, analyse for publication bias. Calculates observed and expected number of positive studies and P for difference.
### Usage

```r
plot_chase_observed_expected(vec_r_events_control, 
vec_r_events_treated, vec_n_sample_size_control, 
vec_n_sample_size_treated, n, low.alpha, high.alpha, 
by.alpha)
```

### Arguments

- `vec_r_events_control`: an ordered vector of number of events in the untreated group of constituent studies from a meta-analysis.

- `vec_r_events_treated`: an ordered vector of number of events in the treated group of constituent studies from a meta-analysis.

- `vec_n_sample_size_control`: an ordered vector of the number of participants in the untreated group.

- `vec_n_sample_size_treated`: an ordered vector of the number of participants in the treated group.

- `n`: Number of iterations used to generate constituent study power; suggest use 10,000.

- `low.alpha`: Lower limit of type-1 error rate used to judge whether constituent studies are positive; suggest 0.001.

- `high.alpha`: Upper limit of type-1 error rate used to judge whether constituent studies are positive; suggest 0.3.

- `by.alpha`: Interval of type-2 error rate at which observed and expected values and P for difference evaluated.

### Value

a dataframe with columns which include alpha level, observed number of positive studies, expected number, and P for difference, OR_hat (summary measure of effect for meta-analysis) with varying levels of significance for constituent studies.

### Examples

```r
data("Bmortality") # Meta-analysis of statin use (Brugts 2009, BMJ)
Bmortality$with(Bmortality, plot_chase_observed_expected(r_events_control, 
  r_events_treated, n_sample_size_control, n_sample_size_treated, n=10, 
  low.alpha=.001, high.alpha=0.3, by.alpha=0.01))
plot(Bmortality$alpha, Bmortality$observed, type="l", las=1, lwd=2, xlab=c("Significance level"), 
  xlab=c("Significance level"), main=c("(a) Brugts study mortality outcome; n set low for speed.
  ylab=c(""), main=c("(a) Brugts all-cause mortality."))
lines(Bmortality$alpha,Bmortality$observed)
lines(Bmortality$alpha,Bmortality$expected, lty=3)
abline(v=0.05, lty=2)
par(new=TRUE)
plot(Bmortality$alpha, Bmortality$p.value, type="l", xlab="", ylab="", lty=4,lwd=2, 
col="grey", axes=FALSE, ylab="")
```

This runs `test_one` function for many replicates, usually 10,000, for example, to generate the type-2 error rate for one constituent study (not for end user).

**Usage**

```r
test.n(r_events_control, n_sample_size_control, 
n_sample_size_treated, OR_hat, n, alpha)
```

**Arguments**

- `r_events_control` Number of events in untreated
- `n_sample_size_control` Sample size in untreated group
- `n_sample_size_treated` Sample size in treated group
- `alpha` Type-1 error rate.
- `n` Number of iterations used to generate constituent study power; suggest use 10,000.
- `OR_hat` Summary odds ratio from meta-analysis

**Value**

Type-2 error for one constituent study
test.n.treated

Observed number of positive by testing for significance from observed findings at given alpha level (not intended for end user).

Description

Observed number of positive by testing for significance from observed findings at given alpha level (not intended for end user).

Usage

test.n.treated(vec_r_events_control, 
    vec_r_events_treated, vec_n_sample_size_control, 
    vec_n_sample_size_treated, alpha)

Arguments

vec_r_events_control
    an ordered vector of number of events in the untreated group of constituent studies from a meta-analysis.

vec_r_events_treated
    an ordered vector of number of events in the treated group of constituent studies from a meta-analysis.

vec_n_sample_size_control
    an ordered vector of the number of participants in the untreated group.

vec_n_sample_size_treated
    an ordered vector of the number of participants in the treated group.

alpha
    Type-1 error rate.

Value

Vector of results, 1 if positive, 0 if negative.

---

test.one.treated

Is one constituent study observed significant, in favour of treatment, at a given alpha level? (Not intended for end user)

Description

Is one constituent study observed significant, in favour of treatment, at a given alpha level? (Not intended for end user)
**Usage**

```r
test_one.treated(r_events_control, r_events_treated, n_sample_size_control, n_sample_size_treated, alpha = 0.05)
```

**Arguments**

- `r_events_control`: Number of events in untreated
- `r_events_treated`: Number of events in treated group
- `n_sample_size_control`: Sample size in untreated group
- `n_sample_size_treated`: Sample size in treated group
- `alpha`: Type-1 error rate.

**Value**

Number, 1 if positive, 0 if negative.

---

**test_one**

*For one constituent study and one simulation of its outcome, test if \( p < \text{type-1 error rate} \) (not for end user).*

---

**Description**

For one constituent study and one simulation of its outcome, test if \( p < \text{type-1 error rate} \) (not for end user).

**Usage**

```r
test_one(r_events_control, n_sample_size_control, n_sample_size_treated, OR_hat, alpha)
```

**Arguments**

- `r_events_control`: Number of events in untreated
- `n_sample_size_control`: Sample size in untreated group
- `n_sample_size_treated`: Sample size in treated group
- `alpha`: Type-1 error rate.
- `OR_hat`: Summary odds ratio from meta-analysis
Value

Number, 1 if positive, 0 if negative.
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