

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'

NeedsCompilation no

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BMort	<i>BMort</i>
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Description

BMort

Format

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

Source

Brugts JJ, Yetgin T, Hoeks SE, Gotto AM, Shepherd J, Westendorp RGJ, et al. The benefits of statins in people without established cardiovascular disease but with cardiovascular risk factors: meta-analysis of randomised controlled trials. *BMJ* 2009;338

ChisqTest_expect	<i>Chi-square test to test for significant difference between observed and expected number of positive studies (not for end user).</i>
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Description

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

Usage

```
ChisqTest_expect(vec_r_events_control,
  vec_n_sample_size_control, vec_n_sample_size_treated,
  OR_hat, n, alpha, vec_pos)
```

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.
OR_hat	Summary odds ratio from meta-analysis
n	Number of iterations used to generate constituent study power; suggest use 10,000.
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	<i>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).</i>
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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	<i>From a meta-analysis, analyse for publication bias. Calculates observed and expected number of positive studies and P for difference.</i>
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Description

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

Usage

```
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

<code>vec_r_events_control</code>	an ordered vector of number of events in the untreated group of constituent studies from a meta-analysis.
<code>vec_r_events_treated</code>	an ordered vector of number of events in the treated group of constituent studies from a meta-analysis.
<code>vec_n_sample_size_control</code>	an ordered vector of the number of participants in the untreated group.
<code>vec_n_sample_size_treated</code>	an ordered vector of the number of participants in the treated group.
<code>n</code>	Number of iterations used to generate constituent study power; suggest use 10,000.
<code>low.alpha</code>	Lower limit of type-1 error rate used to judge whether constituent studies are positive; suggest 0.001.
<code>high.alpha</code>	Upper limit of type-1 error rate used to judge whether constituent studies are positive; suggest 0.3.
<code>by.alpha</code>	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

```
data("BMort") ## Meta-analysis of statin use (Brugts 2009, BMJ)
Btmort<-with(BMort, 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(Btmort$alpha, Btmort$observed, type="l", las=1, lwd=2, xlim=c(.0001,0.3),
  xlab=c("Significance level"), ##### Brugts study mortality outcome; n set low for speed.
  ylab=c(""), main=c("(a) Brugts; all-cause mortality.))
lines(Btmort$alpha,Btmort$observed)
lines(Btmort$alpha,Btmort$expected, lty=3)
abline(v=0.05, lty=2)
par(new=TRUE)
plot(Btmort$alpha, Btmort$p.value, type="l", xlab="", lty=4, lwd=2,
  col="grey", axes=FALSE, ylab="")
```

```
abline(h=0.1, lty=2)
axis(4,las=1)
mtext(side=4,line=2.5,"P for difference")
```

test.n	<i>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).</i>
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Description

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

```
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	<i>Observed number of positive by testing for significance from observed findings at given alpha level (not intended for end user).</i>
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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	<i>Is one constituent study observed significant, in favour of treatment, at a given alpha level? (Not intended for end user)</i>
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Description

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

Usage

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

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

Usage

```
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

test_one

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Value

Number, 1 if positive, 0 if negative.

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