Package 'PubBias'

February 19, 2015

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

Version 1.0

Date 2013-11-18

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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

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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.

License GPL-3

Collate 'process.R'

NeedsCompilation no

Repository CRAN

Date/Publication 2013-11-21 06:48:21

R topics documented:

BMort *BMort*

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	*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

```
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 funtion.

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.

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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

```
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

```
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")
```

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test.n	*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).*

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

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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

```
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.

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

Description

For one constituent study and one simulation of its outcome, test if p<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

Value

Number, 1 if positive, 0 if negative.

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