Package 'MVPBT'

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Type Package

Title Publication Bias Tests for Meta-Analysis of Diagnostic Accuracy Test

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Description Generalized Egger tests for detecting publication bias in meta-analysis for diagnostic accuracy test are implementable. These publication bias tests are generally more powerful compared with the conventional univariate publication bias tests and can incorporate correlation information between the outcome variables.

Depends R (>= 3.5.0)

Imports stats, MASS, metafor, mada, mvmeta

License GPL-3

Encoding UTF-8

LazyData true

RoxygenNote 7.1.1

R topics documented:

MVPBT-package   *The 'MVPBT' package.*

Description

Generalized Egger tests to detect publication bias in meta-analysis for diagnostic accuracy test.

References

Noma, H. (2020). Discussion of "Testing small study effects in multivariate meta-analysis" by Chuan Hong, Georgia Salanti, Sally Morton, Richard Riley, Haitao Chu, Stephen E. Kimmel, and Yong Chen. *Biometrics* **76**: 1255-1259. https://onlinelibrary.wiley.com/doi/abs/10.1111/biom.13343

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davis   *Meta-analysis for diagnostic accuracy of sputum smear microscopy for pulmonary tuberculosis*

Description

Dataset of meta-analysis for diagnostic accuracy of sputum smear microscopy for pulmonary tuberculosis (standard microscopy).

Usage

```
data(taylor)
```

Format

Tabular-type dataset with 8 rows and 4 variables

- TP: A vector of the number of true positives (TP)
- FP: A vector of the number of false positives (FP)
- FN: A vector of the number of false negatives (FN)
- TN: A vector of the number of true negatives (TN)

References

Davis, J. L., Cattamanchi, A., Cuevas, L. E., Hopewell, P. C., and Steingart, K. R. (2013). Diagnostic accuracy of same-day microscopy versus standard microscopy for pulmonary tuberculosis: a systematic review and meta-analysis. *Lancet Infectious Diseases.* **13**: 147-154. https://doi.org/10.1016/s1473-3099(12)70232-3

MVPBT2	*Generalized Egger test to detect publication bias in bivariate meta-analysis for diagnostic accuracy test (MSSET2)*

Description

Generalized Egger test to detect publication bias in bivariate meta-analysis for diagnostic accuracy test (called MSSET2 in Noma (2020)). This test does not consider the uncertainties of heterogeneity variance-covariance parameters, so MVPBT3 is recommended in practice.

Usage

```
MVPBT2(y,S)
```

Arguments

y	Summary outcome statistics
S	Covariance estimates of y

Value

- T: The efficient score statistic.
- P: P-value of the publication bias test (score test).
- b0: Constrained maximum likelihood estimates of the regression intercepts.

References

Noma, H. (2020). Discussion of "Testing small study effects in multivariate meta-analysis" by Chuan Hong, Georgia Salanti, Sally Morton, Richard Riley, Haitao Chu, Stephen E. Kimmel, and Yong Chen. *Biometrics* **76**: 1255-1259. https://onlinelibrary.wiley.com/doi/abs/10.1111/biom.13343

Examples

```
data(taylor)

fit1 <- reitsma(taylor)
summary(fit1)     # results of the bivariate meta-analysis

###

attach(taylor)

dta1 <- sum.dta(TP,FN,TN,FP)

par(mfrow=c(1,3))

plot(fit1, predict=TRUE, cex=1.5, pch=19, sroclty=1, sroclwd=1.5, lty=2,
 main="(a) SROC plot", xlim=c(0,1), ylim=c(0,1))
points(dta1$Fp,dta1$Se,pch=20,col="blue")
#legend(0.2,0.1,legend=c("95% confidence region","95% prediction region"),lty=c(2,3))
```

```
attach(dta1)

res1 <- rma(y[,1], S[,1])
funnel(res1,main="(b) Funnel plot for logit(Se)")
regtest(res1, model="lm") # classical Egger's test

res2 <- rma(y[,2], S[,3])
funnel(res2,main="(c) Funnel plot for logit(FPR)")
regtest(res2, model="lm") # classical Egger's test

###

MVPBT2(y,S)   # Generalized Egger test (MSSET2)
```

| MVPBT3 | *Generalized Egger test to detect publication bias in bivariate meta-analysis for diagnostic accuracy test (MSSET3)* |

Description

Generalized Egger test to detect publication bias in bivariate meta-analysis for diagnostic accuracy test (called MSSET3 in Noma (2020)). This test adequately consider the uncertainties of heterogeneity variance-covariance parameters by bootstrapping.

Usage

```
MVPBT3(y,S,B=2000)
```

Arguments

y	Summary outcome statistics
S	Covariance estimates of y
B	Number of bootstrap resampling (default: 2000)

Value

- `T.b`: Bootstrap samples of the efficient score statistic.
- `T`: The efficient score statistic.
- `P`: P-value of the publication bias test (bootstrap test).

References

Noma, H. (2020). Discussion of "Testing small study effects in multivariate meta-analysis" by Chuan Hong, Georgia Salanti, Sally Morton, Richard Riley, Haitao Chu, Stephen E. Kimmel, and Yong Chen. *Biometrics* **76**: 1255-1259. https://onlinelibrary.wiley.com/doi/abs/10.1111/biom.13343

Examples

```
data(taylor)

fit1 <- reitsma(taylor)
summary(fit1)      # results of the bivariate meta-analysis

###

attach(taylor)

dta1 <- sum.dta(TP,FN,TN,FP)

par(mfrow=c(1,3))

plot(fit1, predict=TRUE, cex=1.5, pch=19, sroclty=1, sroclwd=1.5, lty=2,
 main="(a) SROC plot", xlim=c(0,1), ylim=c(0,1))
points(dta1$Fp,dta1$Se,pch=20,col="blue")
#legend(0.2,0.1,legend=c("95% confidence region","95% prediction region"),lty=c(2,3))

attach(dta1)

res1 <- rma(y[,1], S[,1])
funnel(res1,main="(b) Funnel plot for logit(Se)")
regtest(res1, model="lm") # classical Egger's test

res2 <- rma(y[,2], S[,3])
funnel(res2,main="(c) Funnel plot for logit(FPR)")
regtest(res2, model="lm") # classical Egger's test

###

MVPBT3(y,S)   # Generalized Egger test (MSSET3)
```

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sum.dta	*Transforming contingency table data to summary statistics in diagnostic studies*

Description

Transforming contingency table data to summary statistics in diagnostic studies.

Usage

```
sum.dta(TP,FN,TN,FP)
```

Arguments

TP   A vector of the number of true positives (TP)

FP   A vector of the number of false positives (FP)

FN   A vector of the number of false negatives (FN)

TN   A vector of the number of true negatives (TN)

Value

Summary statistics for meta-analysis are generated.

- y: Logit-transformed sensitivities and false positive rates.
- S: Within-study variances and covariances.
- Se: Sensitivities.
- Fp: False positive rates.

Examples

```
data(taylor)
attach(taylor)

edat <- sum.dta(TP,FN,TN,FP)
```

---

taylor   *Meta-analysis for diagnostic accuracy of point-of-care natriuretic peptide tests for chronic heart failure*

Description

Dataset of meta-analysis for diagnostic accuracy of point-of-care natriuretic peptide tests for chronic heart failure (B-type natriuretic peptide < 100 pg/mL).

Usage

```
data(taylor)
```

Format

Tabular-type dataset with 18 rows and 4 variables

- TP: A vector of the number of true positives (TP)
- FP: A vector of the number of false positives (FP)
- FN: A vector of the number of false negatives (FN)
- TN: A vector of the number of true negatives (TN)

References

Taylor, K. S., Verbakel, J. Y., Feakins, B. G., et al. (2018). Diagnostic accuracy of point-of-care natriuretic peptide testing for chronic heart failure in ambulatory care: systematic review and meta-analysis. *BMJ*. **361**: k1450. https://www.bmj.com/content/361/bmj.k1450

Index