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

Noma, H. (2022). MVPBT: R package for publication bias tests in meta-analysis of diagnostic accuracy studies. arXiv:2209.07270. https://arxiv.org/abs/2209.07270

`cervical` *Scheidler et al. (1997)'s cervical cancer data*

Description

Dataset of a meta-analysis of diagnostic accuracy for radiological evaluation of lymph node metastases in patients with cervical cancer.

Usage

```
data(cervical)
```

Format

A data frame with 44 rows and 8 variables

- `id`: identification number
- `author`: The first author name of the corresponding study
- `year`: The published year of the corresponding study
- `method`: The diagnostic method; 1=CT (computed tomography), 2=LAG (lymphangiography), 3=MRI (magnetic resonance imaging)
- `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

Scheidler, J., Hricak, H., Yu, K. K., Subak, L., and Segal, M. R. (1997). Radiological evaluation of lymph node metastases in patients with cervical cancer. A meta-analysis. *JAMA* **278**: 1096-1101. https://jamanetwork.com/journals/jama/fullarticle/vol/278/pg/1096

Reitsma, J. B., Glas, A. S., Rutjes, A. W., Scholten, R. J., Bossuyt, P. M., and Zwinderman, A. H. (2005). Bivariate analysis of sensitivity and specificity produces informative summary measures in diagnostic reviews. *Journal of Clinical Epidemiology* **58**: 982-990. https://doi.org/10.1016/j.jclinepi.2005.02.022

`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

Noma, H. (2022). MVPBT: R package for publication bias tests in meta-analysis of diagnostic accuracy studies. arXiv:2209.07270. https://arxiv.org/abs/2209.07270

Examples

```
require(metafor)
require(mada)

data(cervical)

LAG <- cervical[cervical$method==2,]

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

###

attach(LAG)

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(0.4,0.1,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") # univariate Egger's test

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

Noma, H. (2022). MVPBT: R package for publication bias tests in meta-analysis of diagnostic accuracy studies. arXiv:2209.07270. https://arxiv.org/abs/2209.07270

Examples

```
require(metafor)
require(mada)

data(cervical)

LAG <- cervical[cervical$method==2,]

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

###

attach(LAG)

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(0.4,0.1,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") # univariate Egger's test

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

###

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

`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(cervical)
LAG <- cervical[cervical$method==2,]

attach(LAG)

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

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