

Package: dmetatools (via r-universe)

October 24, 2024

Type Package

Title Computational tools for meta-analysis of diagnostic accuracy test

Version 1.1.2

Date 2022-09-13

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Description Computational tools for meta-analysis of diagnostic accuracy test. This package enables computations of confidence interval for the AUC of summary ROC curve and some related AUC-based inference methods.

Depends MASS, doSNOW, doParallel, mada

License GPL-3

Encoding UTF-8

LazyData true

Repository <https://nomahi.r-universe.dev>

RemoteUrl <https://github.com/nomahi/dmetatools>

RemoteRef HEAD

RemoteSha 5d63053d6fa5b95c9df267058afa0556d2cf3ad4

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dmetatools-package *The 'dmetatools' package.*

Description

Computational tools for meta-analysis of diagnostic accuracy test. This package enables computations of confidence interval for the AUC of summary ROC curve and some related AUC-based inference methods.

Author(s)

Hisashi Noma <noma@ism.ac.jp>

References

Noma, H. and Matsushima, Y. (2020). Confidence interval for the AUC of SROC curve and some related methods using bootstrap for meta-analysis of diagnostic accuracy studies. arXiv:2004.04339. <https://arxiv.org/abs/2004.04339>

asthma *Korevaar et al. (2015)'s data of minimally invasive markers for detection of airway eosinophilia in asthma*

Description

- 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)

Usage

```
data(asthma)
```

Format

A data frame with 12 rows and 4 variables

References

Korevaar, D. A., Westerhof, G. A., Wang, J., et al. (2015). Diagnostic accuracy of minimally invasive markers for detection of airway eosinophilia in asthma: a systematic review and meta-analysis. *Lancet Respiratory Medicine*. **3**: 290-300. [https://doi.org/10.1016/S2213-2600\(15\)00050-8](https://doi.org/10.1016/S2213-2600(15)00050-8)

Noma, H. and Matsushima, Y. (2020). Confidence interval for the AUC of SROC curve and some related methods using bootstrap for meta-analysis of diagnostic accuracy studies. arXiv:2004.04339. <https://arxiv.org/abs/2004.04339>

`AUC_boot`*Confidence interval for AUC of summary ROC curve*

Description

Calculating the confidence interval for AUC of summary ROC curve by parametric bootstrap.

Usage

```
AUC_boot(TP, FP, FN, TN, B=2000, alpha=0.95)
```

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)
B	The number of bootstrap resampling (default: 2000)
alpha	The confidence level (default: 0.95)

Value

The confidence interval for AUC of summary ROC curve is calculated.

- AUC: The AUC of the summary ROC curve.
- AUC_CI: The 95% confidence interval for the AUC of the summary ROC curve (the confidence level can be changed by alpha).

Author(s)

Hisashi Noma <noma@ism.ac.jp>

References

Noma, H. and Matsushima, Y. (2020). Confidence interval for the AUC of SROC curve and some related methods using bootstrap for meta-analysis of diagnostic accuracy studies. arXiv:2004.04339. <https://arxiv.org/abs/2004.04339>

Examples

```
data(cervical)

CT <- cervical[cervical$method==1,]
LAG <- cervical[cervical$method==2,]
MRI <- cervical[cervical$method==3,]

fit1 <- reitsma(CT) # DTA meta-analysis using the Reitsma model
```

```

summary(fit1)
fit2 <- reitsma(LAG)
summary(fit2)
fit3 <- reitsma(MRI)
summary(fit3)

plot(fit1) # Plot the SROC curves
lines(sroc(fit2), lty=2, col="blue")
ROCellipse(fit2, lty=2, pch=2, add=TRUE, col="blue")
lines(sroc(fit3), lty=3, col="red")
ROCellipse(fit3, lty=3, pch=3, add=TRUE, col="red")
points(fpr(CT), sens(CT), cex = .5)
points(fpr(LAG), sens(LAG), pch = 2, cex = 0.5, col="blue")
points(fpr(MRI), sens(MRI), pch = 3, cex = 0.5, col="red")
legend("bottomright", c("CT", "LAG", "MRI"), pch = 1:3, lty = 1:3, col=c("black", "blue", "red"))

AUC_boot(CT$TP,CT$FP,CT$FN,CT$TN)
AUC_boot(LAG$TP,LAG$FP,LAG$FN,LAG$TN)
AUC_boot(MRI$TP,MRI$FP,MRI$FN,MRI$TN)

```

AUC_comparison	<i>Bootstrap test for the difference of AUCs of summary ROC curves for multiple diagnostic tests</i>
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Description

Calculating the difference of AUCs of summary ROC curves (dAUC) and its confidence interval, and the p-value for the test of "dAUC=0" by parametric bootstrap.

Usage

```
AUC_comparison(TP1, FP1, FN1, TN1, TP2, FP2, FN2, TN2, B=2000, alpha=0.05)
```

Arguments

TP1	A vector of the number of true positives (TP) of test 1
FP1	A vector of the number of false positives (FP) of test 1
FN1	A vector of the number of false negatives (FN) of test 1
TN1	A vector of the number of true negatives (TN) of test 1
TP2	A vector of the number of true positives (TP) of test 2
FP2	A vector of the number of false positives (FP) of test 2
FN2	A vector of the number of false negatives (FN) of test 2
TN2	A vector of the number of true negatives (TN) of test 2
B	The number of bootstrap resampling (default: 2000)
alpha	The significance level (default: 0.05)

Value

The AUCs of the summary ROC curves and their confidence intervals are calculated. Also, the difference of the AUCs (dAUC) and its confidence interval, and the p-value for the test of "dAUC=0" are provided.

- AUC1: The AUC of the summary ROC curve for test 1.
- AUC1_CI: The 95% confidence interval for the AUC of the summary ROC curve for test 1 (the confidence level can be changed by alpha).
- AUC2: The AUC of the summary ROC curve for test 2.
- AUC2_CI: The 95% confidence interval for the AUC of the summary ROC curve for test 2 (the confidence level can be changed by alpha).
- dAUC: The difference of the AUC1 and AUC2.
- dAUC_CI: The 95% confidence interval for dAUC (the confidence level can be changed by alpha).
- pvalue: The p-value of the test of dAUC=0.

Author(s)

Hisashi Noma <noma@ism.ac.jp>

References

Noma, H. and Matsushima, Y. (2020). Confidence interval for the AUC of SROC curve and some related methods using bootstrap for meta-analysis of diagnostic accuracy studies. arXiv:2004.04339. <https://arxiv.org/abs/2004.04339>

Examples

```
data(cervical)

CT <- cervical[cervical$method==1,]
LAG <- cervical[cervical$method==2,]
MRI <- cervical[cervical$method==3,]

fit1 <- reitsma(CT) # DTA meta-analysis using the Reitsma model
summary(fit1)
fit2 <- reitsma(LAG)
summary(fit2)
fit3 <- reitsma(MRI)
summary(fit3)

plot(fit1) # Plot the SROC curves
lines(sroc(fit2), lty=2, col="blue")
ROCellipse(fit2, lty=2, pch=2, add=TRUE, col="blue")
lines(sroc(fit3), lty=3, col="red")
ROCellipse(fit3, lty=3, pch=3, add=TRUE, col="red")
points(fpr(CT), sens(CT), cex = .5)
points(fpr(LAG), sens(LAG), pch = 2, cex = 0.5, col="blue")
points(fpr(MRI), sens(MRI), pch = 3, cex = 0.5, col="red")
```

```

legend("bottomright", c("CT", "LAG", "MRI"), pch = 1:3, lty = 1:3, col=c("black","blue","red"))

AUC_comparison(CT$TP,CT$FP,CT$FN,CT$TN,LAG$TP,LAG$FP,LAG$FN,LAG$TN) # Comparison of the AUCs
AUC_comparison(MRI$TP,MRI$FP,MRI$FN,MRI$TN,LAG$TP,LAG$FP,LAG$FN,LAG$TN)
AUC_comparison(MRI$TP,MRI$FP,MRI$FN,MRI$TN,CT$TP,CT$FP,CT$FN,CT$TN)

```

AUC_IF

Influence diagnostics based on the AUC of summary ROC curve

Description

Influence diagnostics based on AUC of the summary ROC curve by leave-one-out analysis. The threshold to determine influential outlying study is computed by parametric bootstrap.

Usage

```
AUC_IF(TP, FP, FN, TN, B=2000, alpha=0.95, Cores=detectCores())
```

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)
B	The number of bootstrap resampling (default: 2000)
alpha	The error level to be calculated for the bootstrap interval of <code>deltaAUC</code> (default: 0.95)
Cores	The number of cores to be used for parallel computations (if the user don't want to implement parallel computations, please set to 1).

Value

Influence diagnostic statistics based on the AUC of the summary ROC curve. The output is sorted by the absolute size of `deltaAUC`.

- AUC: The AUC of the summary ROC curve.
- id: identification number.
- AUC(-i): The AUC estimate if *i*th study is excluded.
- `deltaAUC`: The difference of AUC estimates for all study and for the subpopulation that *i*th study is excluded.
- Q1: Default 2.5th percentile of the bootstrap distribution of `deltaAUC` (can be changed by `alpha`).
- Q2: Default 97.5th percentile of the bootstrap distribution of `deltaAUC` (can be changed by `alpha`).

Author(s)

Hisashi Noma <noma@ism.ac.jp>

References

Noma, H. and Matsushima, Y. (2020). Confidence interval for the AUC of SROC curve and some related methods using bootstrap for meta-analysis of diagnostic accuracy studies. arXiv:2004.04339. <https://arxiv.org/abs/2004.04339>

Examples

```
data(asthma)

fit1 <- reitsma(asthma) # DTA analysis using the Reitsma model
summary(fit1)

plot(fit1) # Plot the SROC curves
points(fpr(asthma), sens(asthma), cex = .5)

attach(asthma)
AUC_IF(TP, FP, FN, TN) # Influential analysis based on the AUC
detach(asthma)
```

cervical

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

Description

- 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)

Usage

```
data(cervical)
```

Format

A data frame with 44 rows and 8 variables

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>
- Noma, H. and Matsushima, Y. (2020). Confidence interval for the AUC of SROC curve and some related methods using bootstrap for meta-analysis of diagnostic accuracy studies. arXiv:2004.04339. <https://arxiv.org/abs/2004.04339>

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