Package: varoc (via r-universe)

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Type Package

Title Value Added Receiver Operating Characteristics Curve

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Description A continuous version of the receiver operating characteristics (ROC) curve to assess both classification and continuity performances of biomarkers, diagnostic tests, or risk prediction models.

License GPL (>= 2)

Depends R (>= 4.5.0), pROC, graphics, stats, utils, plot3D

NeedsCompilation no

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varoc *VAROC: value added receiver operating characteristics (ROC) curve*

Description

ROC curve to visualize classification and continuity performances of biomarkers, diagnostic tests, or risk prediction models.

Usage

```
varoc(y,x,zlim=NULL,plot=TRUE,digits=2,pval="no",B=2000)
```

Arguments

y	binary outcome, where y=1 if disease (or case) and y=0 if non-disease (or control).
x	continuous score, e.g. biomarker, diagnostic test, risk score.
zlim	minimum and maximum values of TMD, useful when comparing more than two scores (see Examples below).
plot	TRUE if VAROC curve is displayed.
digits	number of decimals.
pval	Bootstrap one-sided p-value if pval="yes".
B	Number of bootstrap samples.

Details

The varoc function summarizes and visualizes continuity performance of x at each threshold (or cutoff) c using two key metrics: (i) tail mean difference (tmd) (or above md (amd)) and (ii) intergrated tmd (itmd). For (i), tmd(c) is true positive mean(tpm)(c) minus false positive mean(fpm)(c), where tpm(c) is E(x>c|y=1) and fpm(c) is E(x>c|y=0). For (ii), itmd is a global measure of evaluating continuity performance of x over all cutoff values, where itmd is integrated tpm minus integrated fpm.

These measures are continuous versions of ROC curve-based measures. Specifically, tpm(c) and fpm(c) are continuous versions of true positive fraction (tpf)(c) and false positive fraction (fpf)(c), where tpf(c)=P(x>c|y=1) and fpf(c)=P(x>c|y=0). Thus, the useful (or useless) x has J(c)=tpf(c)-fpf(c)>0 and tmd(c)>0 (or J(c)=0 and tmd(c)=0); and useful (or useless) x has area under the ROC curve (auc)>0.5 and itmd(c)>0 (or auc=0.5 and itmd(c)=0).

Value

res1	Metrics at each th (threshold): tpf, fpf, tmd=tpm-fpm, pvalue (alternative hypothesis: tpm>fpm (or tpm>0))
res2	Global metrics: auc, iptm, ifpm, itmd=itpm-ifpm, pvalue (alternative hypothesis: itpm>ifpm (or itmd>0))

Author(s)

Yunro Chung [aut, cre]

References

Danielle Brister and Yunro Chung, VAROC: value added receiver operating characteristics curve, Journal of Data Science (under review)

Examples

```
set.seed(10)

n1=n0=25
y=c(rep(1,n1),rep(0,n0))

#1. useless marker
x1=abs(c(rnorm(n1,0,1),rnorm(n0,0,1)))
fit1=varoc(y=y,x=x1,plot=FALSE)

#2. useful marker
x2=abs(c(rnorm(n1,2,1),rnorm(n0,0,1)))
fit2=varoc(y=y,x=x2,plot=FALSE)

#3. markers 1 vs 2
opar=par(mfrow=c(1,2))
zlim=range(c(fit1$res1$tmd,fit2$res1$tmd))
fit1=varoc(y=y,x=x1,zlim=zlim)
fit2=varoc(y=y,x=x2,zlim=zlim)
on.exit(par(opar))
```

`varoc3d` *VAROC: value added receiver operating characteristics (ROC) curve*

Description

Three-dimensional VAROC curve.

Usage

```
varoc3d(y,x,zlim=NULL,plot=TRUE,digits=2,pval="no",B=2000)
```

Arguments

`y`	binary outcome, where y=1 if disease (or case) and y=0 if non-disease (or control).
`x`	continuous score, e.g. biomarker, diagnostic test, risk score.
`zlim`	minimum and maximum values of TMD, useful when comparing more than two scores (see Examples below).

plot	TRUE if three-dimensional VAROC curve is displayed.
digits	number of decimals.
pval	Bootstrap one-sided p-value if pval="yes".
B	Number of bootstrap samples.

Details

Three-dimensional version of the VAROC curve. See the varoc function in details.

Value

res1	Metrics at each th (threshold): tpf, fpf, tmd=tpm-fpm, pvalue (alternative hypothesis: tpm>fpm (or tpm>0))
res2	Global metrics: auc, iptm, ifpm, itmd=itpm-ifpm, pvalue (alternative hypothesis: itpm>ifpm (or itmd>0))

Author(s)

Yunro Chung [aut, cre]

References

Danielle Brister and Yunro Chung, Value added receiver operating characteristics curve, Journal of Data Science (under review)

Examples

```
set.seed(10)

n1=n0=25
y=c(rep(1,n1),rep(0,n0))

#1. useless marker
x1=abs(c(rnorm(n1,0,1),rnorm(n0,0,1)))
fit1=varoc3d(y=y,x=x1,plot=FALSE)

#2. useful marker
x2=abs(c(rnorm(n1,2,1),rnorm(n0,0,1)))
fit2=varoc3d(y=y,x=x2,plot=FALSE)

#3. markers 1 vs 2
opar=par(mfrow=c(1,2))
zlim=range(c(fit1$res1$tmd,fit2$res1$tmd))
fit1=varoc3d(y=y,x=x1,zlim=zlim)
fit2=varoc3d(y=y,x=x2,zlim=zlim)
on.exit(par(opar))
```

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