Package 'rocNIT'

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Type Package

Title Non-Inferiority Test for Paired ROC Curves

Version 1.0

Author Zhicheng Du, Yuantao Hao

Maintainer Zhicheng Du<dgdzc@hotmail.com>

Description Non-inferiority test and diagnostic test are very important in clinical trails.
This package is to get a p value from the non-inferiority test for ROC curves from diagnostic test.

License GPL-3

Depends R (>= 3.3.2)

LazyData TRUE

NeedsCompilation no

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R topics documented:

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rocNIT	*Non-Inferiority Test for Paired ROC Curves*

Description

Non-inferiority test and diagnostic test are very important in clinical trails. This package is to get a
p value of the non-inferiority test for ROC curves from diagnostic test using the bootstrap method.

Usage

```
rocNIT(BNO,DATA,cVAL1,cVAL2,cGOLD,DELTA,ALPHA,seed)
```

Arguments

BNO	the times of the sampling of bootstrap
DATA	the dataset including 3 variables at least: VAL1,VAL2,GOLD
cVAL1	the column number of the first numeric variable
cVAL2	the column number of the second numeric variable
cGOLD	the column number of the golden variable which should be binary
DELTA	the non-inferiority margin, default is 0.05
ALPHA	the significant level, default is 0.05
seed	the seed for the sampling of bootstrap, default is 2016

Value

AREA1	the AUC for the first variable
AREASE1	the SE of the AUC for the first variable
AREA2	the AUC for the second variable
AREASE2	the SE of the AUC for the second variable
bCIL	the lower limit of CI from bootstrap sampling
bCIU	the upper limit of CI from bootstrap sampling
Z	the statistic to get the p value
P	the p value of the non-inferiority test, $P < ALPHA$ means a significant non-inferiority

Note

Referenced from Jen-Pei Liu et al. Tests of equivalence and non-inferiority for diagnostic accuracy based on the paired areas under ROC curves. STATISTICS IN MEDICINE. DOI: 10.1002/sim.2358

Author(s)

Zhicheng Du<dgdzc@hotmail.com>, Yuantao Hao<haoyt@mail.sysu.edu.cn>

See Also

nothing

Examples

```
VAL1=c(rnorm(50,mean=0),rnorm(50,mean=0)+0.5)
VAL2=c(rnorm(50,mean=0),rnorm(50,mean=0)+1)
GOLD=rep(1:2,each=50)
data=data.frame(GOLD,VAL1,VAL2)
rocNIT(BNO=200,DATA=data,cVAL1=2,cVAL2=3,cGOLD=1,DELTA=0.05,ALPHA=0.05,seed=2016)
```

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