

# Package ‘ROCwoGS’

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**Type** Package  
**Title** Non-parametric estimation of ROC curves without Gold Standard Test  
**Version** 1.0  
**Date** 2010-10-13  
**Author** Chong Wang <chwang@iastate.edu>  
**Maintainer** Chong Wang <chwang@iastate.edu>  
**Description** Function to estimate the ROC Curve of a continuous-scaled diagnostic test with the help of a second imperfect diagnostic test with binary responses.  
**License** GPL (>= 2)  
**LazyLoad** yes  
**Repository** CRAN  
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**NeedsCompilation** no

## R topics documented:

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## Description

Function to estimate the ROC Curve of a continuous-scaled diagnostic test with the help of a second imperfect diagnostic test with binary responses.

**Details**

```

Package:   ROCwoGS
Type:      Package
Version:   1.0
Date:      2010-09-13
License:   GPL (>= 2)
LazyLoad:  no

```

This package contains one function. `NPROCwoGS` estimates the ROC Curve of a continuous-scaled diagnostic test with the help of a second imperfect diagnostic test with binary responses

### Author(s)

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### References

Wang, C., Turnbull, B. W., Grohn, Y. T. and Nielsen, S. S. (2007). Nonparametric Estimation of ROC Curves Based on Bayesian Models When the True Disease State Is Unknown. *Journal of Agricultural, Biological and Environmental Statistics* 12, 128-146.

### Examples

```

data(score)
score$r <- (score$r >= 3)
ncutoff<- 20
ROC.est<-NPROCwoGS (score, ncutoff, niter=2000, Clevel=0.95)
#Print results on R screen
ROC.est
#Calculate area under the curve
AUC<- sum((ROC.est$T.Se[1,-1]+ROC.est$T.Se[1,-(ncutoff+2)])*(ROC.est$T.Sp[1,-1]-ROC.est$T.Sp[1,-(ncutoff+2)])/
#Find the optimal cutoff to maximize
#Youden Index
opt.cut<- ROC.est$cutoff[which.max(ROC.est$T.Se[1,]+ROC.est$T.Sp[1,])-1]
# Plot ROC curve
plot(1-ROC.est$T.Sp[1,],ROC.est$T.Se[1,],"l", xlab="1-Specificities",ylab="Sensitivities", main=paste("AUC=", f
", Optimal Cutoff=",opt.cut))
data.frame(1-ROC.est$T.Sp)[c(3,2),]>ci.tsp
data.frame(ROC.est$T.Se)[c(2,3),]>ci.tse
#Write Sensitivities and Specificities to
#".csv" files, saved in the R library path
#write.csv(ROC.est$T.Se,
#paste(.Library,"/ROCwoGS/data/T_Se.csv",sep=''))
#write.csv(ROC.est$T.Sp,
#paste(.Library,"/ROCwoGS/data/T_Sp.csv",sep=''))

```

NPROCwoGS

*Non-parametric estimation of ROC curves without Gold Standard***Description**

Function to estimate the ROC Curve of a continuous-scaled diagnostic test with the help of a second imperfect diagnostic test with binary responses.

**Usage**

```
NPROCwoGS(score, ncutoff, niter, CIlevel)
```

**Arguments**

score	A data frame with the first column of the continuous-scaled diagnostic test scores; the second column of the binary reference scores; the third column of a factor vector to indicate the population that the observations come from.
ncutoff	Desired number of cutoff values. This determines the number of estimated pairs of (sensitivity, specificity) along the ROC curve.
niter	Desired number of iterations for the Markov Chain Monte Carlo method.
CIlevel	Desired level of credible intervals. A numeric value between 0 and 1.

**Details**

The method is based on a multinomial model for the joint distribution of test-positive and test-negative observations. The estimated ROC curve of the continuous-scaled test is in the form of pairs of sensitivities and specificities. Also estimated are the sensitivity and specificity of the binary reference test and the population disease prevalences.

**Value**

NPROCwoGS produces an ordinary list with the following components.

cutoff	Cutoff values for the continuous-scaled diagnostic test. The length of cutoff is the same as the input ncutoff
T.Se	Point estimates (first row) and credible intervals (second and third rows) of the sensitivities for the continuous-scaled diagnostic test
T.Sp	Point estimates (first row) and credible intervals (second and third rows) of the specificities for the continuous-scaled diagnostic test
R.Se	Point estimate and the lower bound and upper bound of the credible interval of the sensitivity for the binary reference test
R.Sp	Point estimate and the lower bound and upper bound of the credible interval of the specificity for the binary reference test
Prev	Point estimates (first row) and credible intervals (second and third rows) of the population disease prevalences. Each column represents a population
flag	Flag for potential nonidentifiable configurations. flag=0: no flag is raised, flag=1: Flag 1 is raised; flag=2: Flag 2 is raised; flag=3: both flags are raised

Author(s)

Chong Wang <<chwang@iastate.edu>>

References

Wang, C., Turnbull, B. W., Grohn, Y. T. and Nielsen, S. S. (2007). Nonparametric Estimation of ROC Curves Based on Bayesian Models When the True Disease State Is Unknown. Journal of Agricultural, Biological and Environmental Statistics 12, 128-146.

Examples

```
data(score)
score$r <- (score$r >= 3)
ncutoff<- 20
ROC.est<-NPROCwoGS (score, ncutoff, niter=2000, Clevel=0.95)
#Print results on R screen
ROC.est
#Calculate area under the curve
AUC<- sum((ROC.est$T.Se[1,-1]+ROC.est$T.Se[1,-(ncutoff+2)])*(ROC.est$T.Sp[1,-1]-ROC.est$T.Sp[1,-(ncutoff+2)])/2)
#Find the optimal cutoff to maximize
#Youden Index
opt.cut<- ROC.est$cutoff[which.max(ROC.est$T.Se[1,]+ROC.est$T.Sp[1,])-1]
# Plot ROC curve
plot(1-ROC.est$T.Sp[1,],ROC.est$T.Se[1,],"l", xlab="1-Specificities",ylab="Sensitivities", main=paste("AUC=", f
    ", Optimal Cutoff=",opt.cut))
data.frame(1-ROC.est$T.Sp)[c(3,2),]->ci.tsp
data.frame(ROC.est$T.Se)[c(2,3),]->ci.tse
#Write Sensitivities and Specificities to
#" .csv" files, saved in the R library path
#write.csv(ROC.est$T.Se,
#paste(.Library,"/ROCwoGS/data/T_Se.csv",sep=' '))
#write.csv(ROC.est$T.Sp,
#paste(.Library,"/ROCwoGS/data/T_Sp.csv",sep=' '))
```

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score	<i>score data</i>
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Description

A data frame with the first column of the continuous-scaled diagnostic test scores; the second column of the binary reference scores; the third column of a factor vector to indicate the population that the observations come from.

Usage

```
data(score)
```

**Format**

A data frame with 4214 observations on the following 3 variables.

t a numeric vector

r a numeric vector

Group a factor with levels 1 2 3

**Examples**

```
data(score)
## maybe str(score) ; plot(score) ...
```

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