Package ‘ROC’

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Title utilities for ROC, with microarray focus
Author Vince Carey <stvjc@channing.harvard.edu>, Henning Redestig for
C++ language enhancements
Maintainer Vince Carey <stvjc@channing.harvard.edu>
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AUC functionals of ROC curve

Description

various functionals of ROC (Receiver Operating Characteristic) curves

Usage

AUC(rocobj)
AUCi(rocobj)
pAUC(rocobj, t0)
pAUCi(rocobj, t0)

Arguments

rocobj element of class rocc

Details

AUC, pAUC, AUCi and pAUCi compute the Area Under the Curve.
AUC and pAUC employ the trapezoidal rule. AUCi and pAUCi use integrate().
AUC and AUCi compute the area under the curve from 0 to 1 on the x-axis (i.e., the 1 - specificity axis).
pAUC and pAUCi compute the area under the curve from 0 to argument t0 on the x-axis (i.e., the 1 - specificity axis).

Elements of class rocc can be created by rocdemo.sca() or other constructors you might make using the code of rocdemo.sca() as a template.

Author(s)

Vince Carey (stvjc@channing.harvard.edu)

References

Duda, R. O., Hart, P. E., Stork, D. G., 2001 Pattern Classification, 2nd Ed., p. 49

See Also

rocdemo.sca
Examples

set.seed(123)
R1 <- rocdemo.sca( rbinom(40,1,.3), rnorm(40), dxrule.sca,
  caseLabel="new case", markerLabel="demo Marker" )
print(AUC(R1))
print(pAUC(R1,.3))
print(pAUCi(R1,.3))
print(ROC(R1,.3))

plot-methods

plot method for ROC curves

Description

plot method for ROC curves

Methods

x = rocc plots an ROC curve object, with additional parameters available:

show.thresh (logical): should marker threshold values be plotted?
jit (logical): should plotted points be jittered?
add (logical): increment to current plot?
line (logical): plot points or lines?
threshCex (numeric): if showing threshold values, set character expansion in text call to
  this value
threshYsh (numeric): if showing threshold values, add this quantity to y coordinate of curve
  to plot the threshold value (should be negative for printing below point)
threshDig (numeric): if showing threshold values, use this as the digits parameter to round
to display the threshold
... extra parameters passed to base plot, lines or points as needed

Examples

set.seed(123)
R1 <- rocdemo.sca( rbinom(40,1,.3), rnorm(40), dxrule.sca,
  caseLabel="new case", markerLabel="demo Marker" )
plot(R1, line=TRUE, show.thresh=TRUE, lwd=2, threshDig=2)
R2 <- rocdemo.sca( rbinom(40,1,.3), rnorm(40), dxrule.sca,
  caseLabel="new case", markerLabel="demo Marker" )
plot(R2, line=TRUE, add=TRUE, col="green", lwd=2 )
R3 <- rocdemo.sca( rbinom(40,1,.4), rnorm(40), dxrule.sca,
  caseLabel="new case", markerLabel="demo Marker" )
points(R3, col="red", pch=19)
rocc-class

Class rocc, ROC curve representation

Description

object representing ROC curve, typically created using rocdemo.sca

Creating Objects

new('rocc',
    sens = ...., # Object of class numeric
    spec = ...., # Object of class numeric
    rule = ...., # Object of class function
    cuts = ...., # Object of class numeric
    markerLabel = ...., # Object of class character
    caseLabel = ...., # Object of class character
)

Slots

sens: Object of class "numeric" sensitivity values
spec: Object of class "numeric" specificity values
rule: Object of class "function" rule to classify objects
cuts: Object of class "numeric" thresholds defining curve
markerLabel: Object of class "character" name of measured marker
caseLabel: Object of class "character" name of condition

Methods

plot (rocc, missing): a plotting function with some additional parameters

Examples

set.seed(123)
R1 <- rocdemo.sca( rbinom(40,1,.3), rnorm(40), dxrule.sca,
                   caseLabel="new case", markerLabel="demo Marker" )
plot( R1, show.thresh=TRUE )
rocdemo.sca — demonstrate 'rocc' class construction using a scalar marker and simple functional rule

Usage

rocdemo.sca(truth, data, rule=NULL, cutpts=NA, markerLabel="unnamed marker", caseLabel="unnamed diagnosis", quiet=TRUE)

Arguments

truth true classification of objects. Must take values 0 or 1.
data quantitative markers used to classify
rule rule: a function with arguments (x, thresh) returning 0 or 1. If no rule is provided or the standard rule dxrule.sca is passed, a faster C-based implementation is used to compute sensitivity and specificity.
cutpts values of thresholds; no NA allowed, or they will be recomputed using smallest gap between data points with distinct values
markerLabel textual label describing marker
caseLabel textual label describing classification
quiet defaults to TRUE, suppressing message about discovery of NA in cutpts

Details

dxrule.sca is function (x, thresh) ifelse(x > thresh, 1, 0)
The default value of argument cutpts is a point less than min(data), points separating the unique values of data and a point greater than max(data).

Value

an object of S4 class rocc

Author(s)

Vince Carey (stvjc@channing.harvard.edu)

See Also

AUC
Examples

```r
set.seed(123)
R1 <- rocdemo.sca(rbinom(40,1,.3), rnorm(40), caseLabel="new case", markerLabel="demo Marker")
plot(R1, line=TRUE, show.thresh=TRUE)

truth <- c(0, 1, 0, 1, 0, 1, 1)
data <- c(2, 3, 4, 4, 5, 6, 7, 8)
R2 <- rocdemo.sca(truth, data, dxrule.sca)
plot(R2, line=TRUE, show.thresh=TRUE)
R3 <- rocdemo.sca(truth, data, function(x, thresh) 1 - dxrule.sca(x, thresh))
if (AUC(R2) + AUC(R3) != 1) stop('Sum of AUCs should be 1. ')

# # more involved
#
set.seed(1234)
x = runif(1000)
w = runif(1000)
z = rbinom(1000, 1, plogis(-2.7+6.2*x + .3*w))
m1 = glm(z~x, fam=binomial)
demorule.glm.clo = function(model) function(w,thresh)
  ifelse(predict(model, newdata=list(x=w), type="response">thresh, 1, 0)
demorule.glm = demorule.glm.clo(m1)
R4 = rocdemo.sca(z, x, demorule.glm )
plot(R4)
```

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**trapezint**

*trapezoidal rule for AUC*

Description

trapezoidal rule for AUC

Usage

```r
trapezint(x, y, a, b)
```

Arguments

- `x`: x - abscissae
- `y`: y - ordinates
- `a`: a - lower limit of integration
- `b`: b - upper limit of integration

Details

uses approx
Value

estimated AUC

Examples

```r
x <- sort(runif(30))
y <- sin(x)
print(trapezint(x, y, 0, 1))
```
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