Package 'ROC'

December 11, 2024

Version 1.83.0

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>

Description Provide utilities for ROC, with microarray focus.

Depends R (>= 1.9.0), utils, methods

Imports knitr

Suggests rmarkdown, Biobase, BiocStyle

License Artistic-2.0

URL http://www.bioconductor.org

LazyLoad Yes

biocViews DifferentialExpression

VignetteBuilder knitr

git_url https://git.bioconductor.org/packages/ROC

git_branch devel

git_last_commit 1857a19

git_last_commit_date 2024-10-29

Repository Bioconductor 3.21

Date/Publication 2024-12-10

Contents

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
t0	FPR point at which TPR is evaluated or limit in (0,1) to integrate to

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 are 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

Rosner, B., 2000, *Fundamentals of Biostatistics, 5th Ed.*, pp. 63–65

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 *function to build objects of class 'rocc'*

Description

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

```
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, 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)
```

`trapezint` *trapezoidal rule for AUC*

Description

trapezoidal rule for AUC

Usage

```
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

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

Index