Package ‘adjROC’

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Type Package

Title Computing Sensitivity at a Fix Value of Specificity and Vice Versa as Well as Bootstrap Metrics for ROC Curves

Version 0.3

Author E. F. Haghish

Maintainer E. F. Haghish <`haghish@uio.no`>

Description For a binary classification the adjusted sensitivity and specificity are measured for a given fixed threshold. If the threshold for either sensitivity or specificity is not given, the crossing point between the sensitivity and specificity curves are returned. For bootstrap procedures, mean and CI bootstrap values of sensitivity, specificity, crossing point between specificity and specificity as well as AUC and AUCPR can be evaluated.

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Imports ROCit, ggplot2, boot, yardstick

Encoding UTF-8

RoxygenNote 7.2.3

URL `https://github.com/haghish/adjROC`, `https://www.sv.uio.no/psi/english/people/aca/haghish/`

BugReports `https://github.com/haghish/adjROC/issues`

NeedsCompilation no

Repository CRAN

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R topics documented:

`adjroc` *adjroc*

Description

computes adjusted sensitivity, adjusted specificity, or the crossing point between sensitivity and specificity for different thresholds

Usage

```
adjroc(
  score,
  class,
  method = "emp",
  sensitivity = NULL,
  specificity = NULL,
  plot = FALSE
)
```

Arguments

`score`	A numeric array of diagnostic score i.e. the estimated probability of each diagnosis
`class`	A numeric array of equal length of `"score"`, including the actual class of the observations
`method`	Specifies the method for estimating the ROC curve. Three methods are supported, which are `"empirical"`, `"binormal"`, and `"nonparametric"`
`sensitivity`	numeric. Specify the threshold of sensitivity
`specificity`	numeric. Specify the threshold of specificity
`plot`	logical. if TRUE, the sensitivity and specificity will be plotted

Value

data.frame including cutoff point, and adjusted sensitivity and specificity based on the specified threshold

Examples

```
# random classification and probability score
score <- runif(10000, min=0, max=1)
class <- sample(x = c(1,0), 10000, replace=TRUE)

# calculate adjusted sensitivity, when specificity threshold is 0.90:
adjroc(score = score, class = class, specificity = 0.9, plot = TRUE)

# calculate adjusted specificity, when sensitivity threshold equals 0.9
```

```
adjroc(score = score, class = class, sensitivity = 0.9, plot = TRUE)

# calculate the meeting point between sensitivity and specificity
adjroc(score = score, class = class, plot = TRUE)
```

`boot.adjroc` *boot.adjroc*

Description

computes bootstrap adjusted sensitivity, bootstrap adjusted specificity, or bootstrap crossing point between sensitivity and specificity for different thresholds

Usage

```
boot.adjroc(
  score,
  class,
  n = 100,
  method = "emp",
  sensitivity = NULL,
  specificity = NULL
)
```

Arguments

`score`	A numeric array of diagnostic score i.e. the estimated probability of each diagnosis
`class`	A numeric array of equal length of `"score"`, including the actual class of the observations
`n`	number of bootstrap samples.
`method`	Specifies the method for estimating the ROC curve. Three methods are supported, which are `"empirical"`, `"binormal"`, and `"nonparametric"`
`sensitivity`	numeric. Specify the threshold of sensitivity.
`specificity`	numeric. Specify the threshold of specificity.

Value

list including mean and CI of bootstrap value (sensitivity, specificity, or the crossing point) and the bootstrap data.

Examples

```
# random classification and probability score
score <- runif(10000, min=0, max=1)
class <- sample(x = c(1,0), 10000, replace=TRUE)

# calculate adjusted sensitivity, when specificity threshold is 0.90:
adjroc(score = score, class = class, specificity = 0.9, plot = TRUE)

# calculate adjusted specificity, when sensitivity threshold equals 0.9
boot.adjroc(score = score, class = class, n = 100, sensitivity = 0.9)

# calculate the bootstrap meeting point between sensitivity and specificity
boot.adjroc(score = score, class = class, n = 100)
```

`boot.roc` *boot.roc*

Description

computes bootstrap AUC and AUCPR for the ROC curve

Usage

```
boot.roc(
  score,
  class,
  metric = "AUC",
  n = 100,
  method = "emp",
  event_level = "first"
)
```

Arguments

`score`	A numeric array of diagnostic score i.e. the estimated probability of each diagnosis
`class`	A numeric array of equal length of `"score"`, including the actual class of the observations
`metric`	character. specify the metric of interest which can be `"AUC"` (Area Under the Curve, default) or `"AUCPR"` (Area Under the Precision-Recall Curve).
`n`	number of bootstrap samples.
`method`	Specifies the method for estimating the ROC curve. Three methods are supported, which are `"empirical"`, `"binormal"`, and `"nonparametric"`
`event_level`	character. only needed for bootstrapping AUCPR. this argument specifies which level of the "class" should be considered the positive event. the values can only be `"first"` or `"second"`.

Value

list including mean and CI of bootstrap value (sensitivity, specificity, or the crossing point) and the bootstrap data.

Examples

```
# random classification and probability score
score <- runif(10000, min=0, max=1)
class <- sample(x = c(1,0), 10000, replace=TRUE)

# calculate bootstrap AUC of the ROC curve
boot.roc(score = score, class = class, n = 100, metric = "AUC")

# calculate bootstrap AUCPR of the ROC curve
boot.roc(score = score, class = class, n = 100, metric = "AUCPR")
```

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