Package ‘ROCpAI’

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Type Package

Title Receiver Operating Characteristic Partial Area Indexes for evaluating classifiers

Version 1.14.0

BugReports https://github.com/juanpegarcia/ROCpAI/tree/master/issues

Description The package analyzes the Curve ROC, identificates it among different types of Curve ROC and calculates the area under de curve through the method that is most accuracy. This package is able to standardize proper and improper pAUC.

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Encoding UTF-8

LazyData TRUE

Depends boot, SummarizedExperiment, fission, knitr, methods
import boot, SummarizedExperiment, fission, knitr, methods
bioCViews Software, StatisticalMethod, Classification

RoxygenNote 7.0.2

VignetteBuilder knitr

Suggests BiocStyle, knitr, rmarkdown

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R topics documented:

mcpAUC .................................................. 2
mcpAUCboot .................................................. 3
pointsCurve .................................................. 4
tpAUC .................................................. 4
tpAUCboot .................................................. 5

Index 7

mcpAUC  Classification of area under ROC curve following McClish method

Description

Calculate the area under the ROC curve following McClish methodologic from a dataset and a sample from that dataset.

Usage

mcpAUC(
  dataset,
  low.value = NULL,
  up.value = NULL,
  plot = FALSE,
  selection = NULL,
  variable = NULL
)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>dataset</td>
<td>Dataframe of the complete information of the samples</td>
</tr>
<tr>
<td>low.value</td>
<td>lower false positive rate value that the function will use to calculate the pAUC</td>
</tr>
<tr>
<td>up.value</td>
<td>upper false positive rate value that the function will use to calculate the pAUC</td>
</tr>
<tr>
<td>plot</td>
<td>ROC plot</td>
</tr>
<tr>
<td>selection</td>
<td>vector that will only be used if the parameter &quot;dataset&quot; is a RangedSummarizedExperiment object. This parameter is used to select the variables that will be analysed</td>
</tr>
<tr>
<td>variable</td>
<td>in case that dataset is a SummarizedExperiment, indicate the Gold Standard</td>
</tr>
</tbody>
</table>

Value

RangedSummarizedExperiment object with the pAUC and the mcpAUC scores, and the TPR and FPR values for each ROC curve generated
**Examples**

```r
library(fission)
data("fission")
resultsMC <- mcpAUC(fission, low.value = 0, up.value = 0.25, plot = TRUE,
                   selection = c("SPNCRNA.1080","SPAC186.08c"), variable="strain")
```

**Description**

Calculates the confidence interval using a boot analysis

**Usage**

```r
mcpAUCboot(
  dataset,
  low.value = NULL,
  up.value = NULL,
  r = 50,
  level = 0.95,
  type.interval = "perc",
  selection = NULL,
  variable = NULL
)
```

**Arguments**

- `dataset`: dataframe or RangedSummarizedExperiment object
- `low.value`: lower false positive rate value that the function will use to calculate the pAUC
- `up.value`: upper false positive rate value that the function will use to calculate the pAUC
- `r`: number of iterations.
- `level`: confidence level
- `type.interval`: String that represent the type of intervals required. The value should be any subset of the values c("norm","basic","stud","perc","bca") or simply "all" which will compute all five types of intervals.
- `selection`: vector that will only be used if the parameter "dataset" is a RangedSummarizedExperiment object. This parameter is used to select the variables that will be analysed
- `variable`: in case that dataset is a SummarizedExperiment, indicate the Gold Standard

**Value**

SummarizedExperiment object with the mcpAUC, the standard desviation, and the lower and upper limits of the confidence interval.
Examples

```r
library(fission)
data("fission")
resultsMCboot <- mcpAUCboot(fission, low.value = 0, up.value = 0.25,
selection = c("SPNCRNA.1080", "SPAC186.08c"), variable="strain")
```

**pointsCurve**

**Points of the ROC curve**

Description

It calculates the coordinates (fpr, sen) of the ROC curve. This function sorts the scores of a model test and generates the points which will be used to plot its ROC curve.

Usage

```r
pointsCurve(x, y)
```

Arguments

- **x**: It is the vector of the status (gold standard).
- **y**: It is the vector with the values of a predictor variable or classifier.

Value

return a matrix with the points of 1-specificity and sensitivity that will be used to generate a ROC curve.

Examples

```r
library(fission)
data("fission")
strain <- fission@colData@listData$strain
pointsCurve <- pointsCurve(strain, t(assay(fission))[, "SPNCRNA.1080"])
```

**tpAUC**

**Tighter partial area under the ROC curve**

Description

It standardizes the partial area under the ROC curve by the tighter index.
Usage

```
tpAUC(
  dataset,
  low.value = NULL,
  up.value = NULL,
  plot = FALSE,
  selection = NULL,
  variable = NULL
)
```

Arguments

- **dataset**
  Dataframe of the complete information of the samples
- **low.value**
  lower false positive rate value that the function will use to calculate the pAUC
- **up.value**
  upper false positive rate value that the function will use to calculate the pAUC
- **plot**
  ROC plot
- **selection**
  vector that will only be used if the parameter "dataset" is a RangedSummarized-Experiment object. This parameter is used to select the variables that will be analysed
- **variable**
  in case that dataset is a SummarizedExperiment, indicate the Gold Standard

Value

RangedSummarizedExperiment object with the pAUC and the tpAUC scores, and the TPR and FPR values for each ROC curve generated

Examples

```
library(fission)
data("fission")
resultsT <- tpAUC(fission, low.value = 0, up.value = 0.25, plot = TRUE,
  selection = c("SPNCRNA.1000","SPAC186.08c"), variable="strain")
```

Description

Calculates the confidence interval using a boot analysis
tpAUCboot

Usage

```
tpAUCboot(
  dataset,
  low.value = NULL,
  up.value = NULL,
  r = 50,
  level = 0.95,
  type.interval = "perc",
  selection = NULL,
  variable = NULL
)
```

Arguments

dataset dataframe or RangedSummarizedExperiment object
low.value lower false positive rate value that the function will use to calculate the pAUC
up.value upper false positive rate value that the function will use to calculate the pAUC
r number of iterations.
level confidence level
type.interval String that represent the type of intervals required. The value should be any subset of the values c("norm","basic","stud","perc","bca") or simply "all" which will compute all five types of intervals.
selection vector that will only be used if the parameter "dataset" is a RangedSummarizedExperiment object. This parameter is used to select the variables that will be analysed
variable in case that dataset is a SummarizedExperiment, indicate the Gold Standard

Value

SummarizedExperiment object with the Tp_AUC, the standard deviation, and the lower and upper limits of the confidence interval

Examples

```
library(fission)
data("fission")
resultstboot<- tpAUCboot(fission,low.value = 0, up.value = 0.25,
selection = c("SPNCRNA.1080","SPAC186.08c"), variable="strain")
```
Index

mcpAUC, 2
mcpAUCboot, 3
pointsCurve, 4
tpAUC, 4
tpAUCboot, 5