Package: ROCpAI (via r-universe)

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Type Package

Title Receiver Operating Characteristic Partial Area Indexes for evaluating classifiers

Version 1.26.0

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 standarizate proper and improper pAUC.

License GPL-3

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

Config/pak/sysreqs zlib1g-dev

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mcpAUC *Clasification 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

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 mcpAUC scores,and the TPR and FPR values for each ROC curve generated

Examples

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

mcpAUCboot *mcpAUCboot*

Description

Calculates the confidence interval using a boot analysis

Usage

```
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 objetc
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

```
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 the ROC curve

Usage

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

Arguments

x	It is the vector of the status (gold standar)
y	It is the vector with the values of a predictor variable or clasificator

Value

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

Examples

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

tpAUC *Tigher partial area under the ROC curve*

Description

It standarizes the partial area under the ROC curve by the tigher 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 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

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.1080","SPAC186.08c"), variable="strain")
```

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tpAUCboot *tpAUCboot*

Description

Calculates the confidence interval using a boot analysis

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 objetc
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 desviation, 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")
```

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