Package ‘RatingScaleReduction’

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Type Package

Title Rating Scale Reduction Procedure

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Depends pROC, ggplot2

Description Describes a new procedure of reducing items in a rating scale called Rating Scale Reduction (RSR). The new stop criterion in RSR procedure is added (stop global max).

License GPL-2

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Description

This package describes a procedure of reducing items in a rating scale. It was published in the reference included in this description. The method was proposed by Waldemar W. Koczkodaj and published by a sizable collaboration coordinated by him.

Author(s)

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References


CheckAttr4Inclusion

Description

The attribute checked for AUC before it is added to the running total. The running total is used with the class (decision attribute) to compute AUC. The next attribute is added to the sequence of attributes having the MAX total AUC.
Usage

```
CheckAttr4Inclusion(attribute, D, plotCheck=FALSE, method=c("delong", "bootstrap", "venkatraman", "sensitivity", "specificity"), boot.n, alternative = c("two.sided", "less", "greater"))
```

Arguments

- `attribute`: a matrix or data.frame containing attributes
- `D`: the decision vector
- `plotCheck`: If TRUE the plot with two ROC curves is created
- `method`: the method to use as in the function roc.test(pROC)
- `boot.n`: bootstrap replication number
- `alternative`: the alternative hypothesis

Value

- `test`: the result of the roc.test as in the function roc.test from the package pROC

Author(s)

Waldemar W. Koczkodaj, Feng Li, Alicja Wolny-Dominiak

References


2. W.W. Koczkodaj, T. Kakiashvili, A. Szymaska, J. Montero-Marin, R. Araya, J. Garcia-Campayo, K. Rutkowski, D. Strzalka, How to reduce the number of rating scale items without predictability loss? Scientometrics, 909(2):581-593(open access), 2017

Examples

```
creating the matrix of attributes and the decision vector
must be as.numeric()
data(asSAH)
attach(asSAH)
is.numeric(asSAH)

attribute <- data.frame(as.numeric(gender),
as.numeric(age), as.numeric(wfns), as.numeric(s100b), as.numeric(ndka))
colnames(attribute) <- c("a1", "a2", "a3", "a4", "a5")
decision <- as.numeric(outcome)

delong test, two-side alternative hypothesis
```
diffExamples

CheckAttr4Inclusion(attribute, decision, method=c("delong"),
alternative=c("two.side"))

# bootstrap, two-side alternative hypothesis
# CheckAttr4Inclusion(attribute, decision, method=c("bootstrap"), boot.n=500)
#

diffExamples

The number of different (unique) examples in a dataset

Description
Datasets often contain replications. In particular, one example may be replicated n times, where n
is the total number of examples, so that there are no other examples. Such situation would deviate
computations and should be early detected. Ideally, no example should be replicated but if the rate
is small, we can progress to computing AUC.

Usage
diffExamples(attribute)

Arguments
attribute a matrix or data.frame containing attributes

Value
total.examples a number of examples in a data
diff.examples a number of different examples in a data
dup.examples a number of duplicate examples in a data

Author(s)
Waldemar W. Koczkodaj, Feng Li, Alicja Wolny-Dominiak

Examples

# creating the matrix of attributes and the decision vector
# must be as.numeric()
data(aSAH)
attach(aSAH)
is.numeric(aSAH)

attribute <- data.frame(as.numeric(gender),
as.numeric(age), as.numeric(wfns), as.numeric(s100b), as.numeric(ndka))
colnames(attribute) <- c("a1", "a2", "a3", "a4", "a5")

# show the number of different examples
diffExamples(attribute)
Examples belonging to both classes

Description

A subset of data with examples having identical values on all attributes (excluding the class attribute also called the decision attribute which is different and has two permitted values: positive and negative)

Usage

grayExamples(attribute, D)

Arguments

- attribute: a matrix or data.frame containing attributes
- D: the decision vector

Value

- a list of pairs of identical examples on all attributes

Author(s)

Waldemar W. Koczkodaj, Alicja Wolny-Dominiak

Examples

```r
#generate data
a=c(); attribute=c()
for (i in 1:3){
a <- sample(c(1,2,3), 100, replace=TRUE)
attribute <- cbind(attribute, a)
attribute=data.frame(attribute)
}
colnames(attribute)=c("a1", "a2", "a3")
names(attribute)
decision=sample(c(0,1), 100, replace=TRUE)

#check examples
grayExamples(attribute, decision)
```
Description

This package implements a rather sophisticated method published in (Kocz Kodaj et al., 2017) In essence, it is a stepwise method for maximizing the area under the area (AUC) of receiver operating characteristic (ROC). In this description, data mining terminology will be used:

- examples (observations in statistics),
- variables in statistics,
- class or decision attribute (decision variable may be used statistics).

The implemented algorithm (when reduced to its minimum) comes to using a loop for all attributes (with the class excluded) to compute AUC. Subsequently, attributes are sorted in the descending order by AUC. The attribute with the largest AUC is added to a subset of all attributes (evidently, it cannot be empty since it is supposed to be the minimum subset S of all attributes with the maximum AUC). We keep adding the next in line (according to AUC) attribute to the subset S checking AUC. If it decreases, we stop the procedure. The above procedure can be described by the following algorithm.

Algorithm:

1. compute AUC of all attributes excluding class
2. sort attributes by their AUC in the ascending order
3. select the attribute with the largest AUC to subset S
4. select the next attribute A with the largest AUC to subset S
5. if the AUC of the subset S is larger that AUC of the former AUC then go to 3

There are a lot of checking (e.g., if the dataset is not empty or full of replications) involved.

Usage

rsr(attribute, D, plotRSR = FALSE, method = c('Stop1Max', 'StopGlobalMax'))

Arguments

attribute: a matrix or data.frame containing attributes
D: the decision vector
plotRSR: If TRUE the ROC curve is plotted
method: the Stop reduction criteria: First Max of AUC or Global Max of AUC

Value

rsr.auc: total AUC of attributes
rsr.label: attribute labels
summary: a summary table
startAuc

Author(s)

Waldemar W. Koczkodaj, Alicja Wolny-Dominiak

References


https://link.springer.com/article/10.1007/s11199-017-2283-4


DOI: http://dx.doi.org/10.1016/j.cmpb.2011.09.011


https://bmcbioinformatics.biomedcentral.com/articles/10.1186/1471-2105-12-77

Examples

#creating the matrix of attributes and the decision vector
#must be as.numeric()
data(aSAH)
attach(aSAH)
is.numeric(aSAH)

attribute <- data.frame(as.numeric(gender),
as.numeric(age), as.numeric(wfns), as.numeric(s100b), as.numeric(ndka))
colnames(attribute) <- c("a1", "a2", "a3", "a4", "a5")
decision <- as.numeric(outcome)

#rating scale reduction procedure
rsred <- rsr(attribute, decision, plotRSR=TRUE)
rsred

startAuc

AUC of a single attribute

Description

Compute AUC of every single attribute

Usage

startAuc(attribute, D)
startAuc

Arguments

attribute a matrix or data.frame containing attributes
D the decision vector

Value

auc AUC of a single attribute
item attribute labels
summary a summary table

Author(s)

Waldemar W. Koczkodaj, Alicja Wolny-Dominiak

References

1. W.W. Koczkodaj, T. Kakiashvili, A. Szymanska, J. Montero-Marin, R. Araya, J. Garcia-Campayo, K. Rutkowski, D. Strzalka, How to reduce the number of rating scale items without predictability loss? Scientometrics, 909(2):581-593(open access), 2017  
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Examples

#creating the matrix of attributes and the decision vector
#must be as.numeric()
data(aSAH)
attach(aSAH)
is.numeric(aSAH)

attribute <- data.frame(as.numeric(gender), as.numeric(age), as.numeric(wfns), as.numeric(s100b), as.numeric(ndka))
colnames(attribute) <- c("a1", "a2", "a3", "a4", "a5")
decision <- as.numeric(outcome)

#compute AUC of all attributes
start <- startAuc(attribute, decision)
start$summary
**totalAuc**

*AUC of the running total of attributes*

**Description**

AUC values are computed for all individual attributes. We sort them in an ascending order. We begin with the attribute having the largest AUC and add to it the second, third,... attribute until AUC of the total of them decreases.

**Usage**

`totalAuc(attribute, D, plotT = FALSE)`

**Arguments**

- `attribute`: a matrix or data.frame containing attributes
- `D`: the decision vector
- `plotT`: If TRUE the plot is created: x - labels of attributes, y - total AUC in ascending order

**Value**

- `ordered.attribute`: ordered attribute matrix
- `total.auc`: total AUC
- `item`: ordered attribute labels
- `summary`: a summary table

**Author(s)**

Waldemar W. Koczkodaj, Alicja Wolny-Dominiak

**References**

   [https://link.springer.com/article/10.1007/s11199-017-2283-4](https://link.springer.com/article/10.1007/s11199-017-2283-4)


   [https://bmcgenomics.biomedcentral.com/articles/10.1186/1471-2105-12-77](https://bmcgenomics.biomedcentral.com/articles/10.1186/1471-2105-12-77)
Examples

```r
# creating the matrix of attributes and the decision vector
# must be as.numeric()
data(aSAH)
attach(aSAH)
is.numeric(aSAH)

attribute <- data.frame(as.numeric(gender),
                        as.numeric(age), as.numeric(wfns), as.numeric(s100b), as.numeric(ndka))
colnames(attribute) <- c("a1", "a2", "a3", "a4", "a5")
decision <- as.numeric(outcome)

# arrange start AUC in an ascending order and compute total AUC according to
# Rating Scale Reduction procedure

tot <- totalAuc(attribute, decision, plotT=TRUE)
tot$summary
```
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