Package: conformalClassification (via r-universe)

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Description Implementation of transductive conformal prediction (see Vovk, 2013, <doi:10.1007/978-3-642-41142-7_36>) and inductive conformal prediction (see Balasubramanian et al., 2014, ISBN:9780124017153) for classification problems.

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Contents

`conformalClassification` *A Conformal Prediction R Package for Classification*

Description

The conformalClassification package implements Transductive Conformal Prediction (TCP) and Inductive Conformal Prediction (ICP) for classification problems.

Details

Currently, the pakcage is built upon random forests method, where voting of random forests for each class is considered as a conformity scores for each data point. Mainly the package generates conformal prediction errors (p-values) for classification problems, it also provides various diagnostic measures such as deviation from alidity, error rate, efficiency, observed fuzziness and calibration plots. In future releases, we plan to extend package to use other machine learning algorithms, (i.e. support vector machine) for model fitting.

`CPCalibrationPlot` *Plots the calibration plot*

Description

Plots the calibration plot

Usage

```
CPCalibrationPlot(pValues, testSet, color = "blue")
```

Arguments

`testSet`	The test set
`color`	colour of the calibration line
`pValues`	Matrix of p-values

See Also

CPEfficiency, CPErrorRate, CPValidity, CPObsFuzziness.

Examples

```
## load the library
library(mlbench)
#library(caret)
library(conformalClassification)

## load the DNA dataset
data(DNA)
originalData <- DNA

## make sure first column is always the label and class labels are always 1, 2, ...
nrAttr = ncol(originalData) #no of attributes
tempColumn = originalData[, 1]
originalData[, 1] = originalData[, nrAttr]
originalData[, nrAttr] = tempColumn
originalData[, 1] = as.factor(originalData[, 1])
originalData[, 1] = as.numeric(originalData[, 1])

## partition the data into training and test set
#result = createDataPartition(originalData[, 1], p = 0.8, list = FALSE)
size = nrow(originalData)
result = sample(1:size,  0.8*size)
trainingSet = originalData[result, ]
testSet = originalData[-result, ]

##ICP classification
pValues = ICPClassification(trainingSet, testSet)
CPCalibrationPlot(pValues, testSet, "blue")
```

`CPEfficiency` *Computes efficiency of a conformal predictor, which is defined as the ratio of predictions with more than one class over the size of the testset*

Description

Computes efficiency of a conformal predictor, which is defined as the ratio of predictions with more than one class over the size of the testset

Usage

```
CPEfficiency(matPValues, testLabels, sigfLevel = 0.05)
```

Arguments

matPValues	Matrix of p-values
testLabels	True labels for the test-set
sigfLevel	Significance level

Value

The efficiency

See Also

CPCalibrationPlot, CPErrorRate, CPValidity, CPObsFuzziness.

Examples

```
## load the library
library(mlbench)
#library(caret)
library(conformalClassification)

## load the DNA dataset
data(DNA)
originalData <- DNA

## make sure first column is always the label and class labels are always 1, 2, ...
nrAttr = ncol(originalData) #no of attributes
tempColumn = originalData[, 1]
originalData[, 1] = originalData[, nrAttr]
originalData[, nrAttr] = tempColumn
originalData[, 1] = as.factor(originalData[, 1])
originalData[, 1] = as.numeric(originalData[, 1])

## partition the data into training and test set
#result = createDataPartition(originalData[, 1], p = 0.8, list = FALSE)
size = nrow(originalData)
result = sample(1:size,  0.8*size)

trainingSet = originalData[result, ]
testSet = originalData[-result, ]

##ICP classification
pValues = ICPClassification(trainingSet, testSet)
testLabels = testSet[,1]
CPEfficiency(pValues, testLabels)
```

CPErrorRate *Computes error rate of a conformal predictor, which is defined as the ratio of predictions with missing true class lables over the size of the testset*

Description

Computes error rate of a conformal predictor, which is defined as the ratio of predictions with missing true class lables over the size of the testset

Usage

```
CPErrorRate(matPValues, testLabels, sigfLevel = 0.05)
```

Arguments

matPValues	Matrix of p-values
testLabels	True labels for the test-set
sigfLevel	Significance level

Value

The error rate

See Also

CPCalibrationPlot, CPEfficiency, CPValidity, CPObsFuzziness.

Examples

```
## load the library
library(mlbench)
#library(caret)
library(conformalClassification)

## load the DNA dataset
data(DNA)
originalData <- DNA

## make sure first column is always the label and class labels are always 1, 2, ...
nrAttr = ncol(originalData) #no of attributes
tempColumn = originalData[, 1]
originalData[, 1] = originalData[, nrAttr]
originalData[, nrAttr] = tempColumn
originalData[, 1] = as.factor(originalData[, 1])
originalData[, 1] = as.numeric(originalData[, 1])

## partition the data into training and test set
#result = createDataPartition(originalData[, 1], p = 0.8, list = FALSE)
```

```
size = nrow(originalData)
result = sample(1:size,  0.8*size)

trainingSet = originalData[result, ]
testSet = originalData[-result, ]

##ICP classification
pValues = ICPClassification(trainingSet, testSet)
testLabels = testSet[,1]
CPErrorRate(pValues, testLabels)
```

`CPObsFuzziness` *Computes observed fuzziness, which is defined as the sum of all p-values for the incorrect class labels.*

Description

Computes observed fuzziness, which is defined as the sum of all p-values for the incorrect class labels.

Usage

```
CPObsFuzziness(matPValues, testLabels)
```

Arguments

`matPValues`	Matrix of p-values
`testLabels`	True labels for the test-set

Value

The observed fuzziness

See Also

`CPCalibrationPlot`, `CPEfficiency`, `CPErrorRate`, `CPValidity`.

Examples

```
## load the library
library(mlbench)
#library(caret)
library(conformalClassification)

## load the DNA dataset
data(DNA)
originalData <- DNA

## make sure first column is always the label and class labels are always 1, 2, ...
```

```
nrAttr = ncol(originalData) #no of attributes
tempColumn = originalData[, 1]
originalData[, 1] = originalData[, nrAttr]
originalData[, nrAttr] = tempColumn
originalData[, 1] = as.factor(originalData[, 1])
originalData[, 1] = as.numeric(originalData[, 1])

## partition the data into training and test set
#result = createDataPartition(originalData[, 1], p = 0.8, list = FALSE)
size = nrow(originalData)
result = sample(1:size,  0.8*size)

trainingSet = originalData[result, ]
testSet = originalData[-result, ]

##ICP classification
pValues = ICPClassification(trainingSet, testSet)
testLabels = testSet[,1]
CPObsFuzziness(pValues, testLabels)
```

`CPValidity` *Computes the deviation from exact validity as the Euclidean norm of the difference of the observed error and the expected error*

Description

Computes the deviation from exact validity as the Euclidean norm of the difference of the observed error and the expected error

Usage

```
CPValidity(matPValues = NULL, testLabels = NULL)
```

Arguments

`matPValues`	Matrix of p-values
`testLabels`	True labels for the test-set

Value

The deviation from exact validity

See Also

`CPCalibrationPlot`, `CPEfficiency`, `CPErrorRate`, `CPObsFuzziness`.

Examples

```
## load the library
library(mlbench)
#library(caret)
library(conformalClassification)

## load the DNA dataset
data(DNA)
originalData <- DNA

## make sure first column is always the label and class labels are always 1, 2, ...
nrAttr = ncol(originalData) #no of attributes
tempColumn = originalData[, 1]
originalData[, 1] = originalData[, nrAttr]
originalData[, nrAttr] = tempColumn
originalData[, 1] = as.factor(originalData[, 1])
originalData[, 1] = as.numeric(originalData[, 1])

## partition the data into training and test set
#result = createDataPartition(originalData[, 1], p = 0.8, list = FALSE)
size = nrow(originalData)
result = sample(1:size,  0.8*size)

trainingSet = originalData[result, ]
testSet = originalData[-result, ]

##ICP classification
pValues = ICPClassification(trainingSet, testSet)
testLabels = testSet[,1]
CPValidity(pValues, testLabels)
```

---

fitModel *Fits the model and returns the fitted model*

Description

Fits the model and returns the fitted model

Usage

```
fitModel(trainingSet=NULL, method = "rf",  nrTrees = 100)
```

Arguments

trainingSet	The training set
method	Method for modeling
nrTrees	Number of trees for RF

Value

The fitted model

`ICPClassification` *Class-conditional Inductive conformal classifier for multi-class problems*

Description

Class-conditional Inductive conformal classifier for multi-class problems

Usage

```
ICPClassification(trainingSet, testSet, ratioTrain = 0.7, method = "rf",
  nrTrees = 100)
```

Arguments

`trainingSet`	Training set
`testSet`	Test set
`ratioTrain`	The ratio for proper training set
`method`	Method for modeling
`nrTrees`	Number of trees for RF

Value

The p-values

See Also

`TCPClassification`, `parTCPClassification`.

Examples

```
## load the library
library(mlbench)
#library(caret)
library(conformalClassification)

## load the DNA dataset
data(DNA)
originalData <- DNA

## make sure first column is always the label and class labels are always 1, 2, ...
nrAttr = ncol(originalData) #no of attributes
tempColumn = originalData[, 1]
originalData[, 1] = originalData[, nrAttr]
```

```
originalData[, nrAttr] = tempColumn
originalData[, 1] = as.factor(originalData[, 1])
originalData[, 1] = as.numeric(originalData[, 1])

## partition the data into training and test set
#result = createDataPartition(originalData[, 1], p = 0.8, list = FALSE)
size = nrow(originalData)
result = sample(1:size,  0.8*size)

trainingSet = originalData[result, ]
testSet = originalData[-result, ]

##ICP classification
pValues = ICPClassification(trainingSet, testSet)
#perfVlaues = pValues2PerfMetrics(pValues, testSet)
#print(perfVlaues)
#CPCalibrationPlot(pValues, testSet, "blue")
```

`parTCPClassification` *Class-conditional transductive conformal classifier for multi-class problems, paralled computations*

Description

Class-conditional transductive conformal classifier for multi-class problems, paralled computations

Usage

```
parTCPClassification(trainSet, testSet, method = "rf", nrTrees = 100, nrClusters = 12)
```

Arguments

`testSet`	Test set
`method`	Method for modeling
`nrTrees`	Number of trees for RF
`nrClusters`	Number of clusters
`trainSet`	Training set

Value

The p-values

See Also

`TCPClassification`. `ICPClassification`.

Examples

```
## load the library
#library(mlbench)
#library(caret)
#library(conformalClassification)

## load the DNA dataset
#data(DNA)
#originalData <- DNA

## make sure first column is always the label and class labels are always 1, 2, ...
#nrAttr = ncol(originalData) #no of attributes
#tempColumn = originalData[, 1]
#originalData[, 1] = originalData[, nrAttr]
#originalData[, nrAttr] = tempColumn
#originalData[, 1] = as.factor(originalData[, 1])
#originalData[, 1] = as.numeric(originalData[, 1])

## partition the data into training and test set
#result = createDataPartition(originalData[, 1], p = 0.8, list = FALSE)
#trainingSet = originalData[result, ]
#testSet = originalData[-result, ]

##ICP classification
#pValues = parTCPClassification(trainingSet, testSet)
#perfVlaues = pValues2PerfMetrics(pValues, testSet)
#print(perfVlaues)
#CPCalibrationPlot(pValues, testSet, "blue")
#not run
```

`TCPClassification` *Class-conditional transductive conformal classifier for multi-class problems*

Description

Class-conditional transductive conformal classifier for multi-class problems

Usage

```
TCPClassification(trainSet, testSet, method = "rf", nrTrees = 100)
```

Arguments

`testSet`	Test set
`method`	Method for modeling
`nrTrees`	Number of trees for RF
`trainSet`	Training set

Value

The p-values

See Also

parTCPClassification. ICPClassification.

Examples

```
## load the library
#library(mlbench)
#library(caret)
#library(conformalClassification)

## load the DNA dataset
#data(DNA)
#originalData <- DNA

## make sure first column is always the label and class labels are always 1, 2, ...
#nrAttr = ncol(originalData) #no of attributes
#tempColumn = originalData[, 1]
#originalData[, 1] = originalData[, nrAttr]
#originalData[, nrAttr] = tempColumn
#originalData[, 1] = as.factor(originalData[, 1])
#originalData[, 1] = as.numeric(originalData[, 1])

## partition the data into training and test set
#result = createDataPartition(originalData[, 1], p = 0.8, list = FALSE)
#trainingSet = originalData[result, ]
#testSet = originalData[-result, ]

##reduce the size of the training set, because TCP is slow
#result = createDataPartition(trainingSet[, 1], p=0.8, list=FALSE)
#trainingSet = trainingSet[-result, ]

##TCP classification
#pValues = TCPClassification(trainingSet, testSet)
#perfVlaues = pValues2PerfMetrics(pValues, testSet)
#print(perfVlaues)
#CPCalibrationPlot(pValues, testSet, "blue")
#not run
```

---

tcpPValues *Fits the model and computes p-values*

Description

Fits the model and computes p-values

Usage

```
tcpPValues(augTrainSet, method = "rf", nrTrees = 100)
```

Arguments

augTrainSet	Augmented training set
method	Method for modeling
nrTrees	Number of trees for RF

Value

The p-values

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