Package 'supervisedPRIM'

October 14, 2022

Title Supervised Classification Learning and Prediction using Patient
Rule Induction Method (PRIM)

Version 2.0.0

Date 2016-10-01

Description The Patient Rule Induction Method (PRIM) is typically
used for ``bump hunting'' data mining to identify regions with abnormally
high concentrations of data with large or small values. This package
extends this methodology so that it can be applied to binary classification
problems and used for prediction.

Depends R (>= 3.1.1), stats, prim (>= 1.0.16)

Suggests kernlab, testthat

License GPL-3

URL https://github.com/dashaub/supervisedPRIM

BugReports https://github.com/dashaub/supervisedPRIM/issues

LazyData true

RoxygenNote 5.0.1

ByteCompile true

NeedsCompilation no

Author David Shaub [aut, cre]

Maintainer David Shaub <davidshaub@gmx.com>

Repository CRAN

Date/Publication 2016-10-01 14:39:25

R topics documented:

---

predict.supervisedPRIM

Model Predictions

Description

Perform prediction on a trained `supervisedPRIM` model. Output to either predicted class or positive class probability is supported.

Usage

```
## S3 method for class 'supervisedPRIM'
predict(object, newdata, classProb = FALSE, ...)
```

Arguments

object	A trained model of class `supervisedPRIM` returned by supervisedPRIM
newdata	The new data on which to create predictions
classProb	Should the function return the estimated class
...	additional arguments (ignored) probabilities instead of the predicted class?

Author(s)

David Shaub

Examples

```
# Train a model to determine if a flower is setosa
data(iris)
yData <- factor(ifelse(iris$Species == "setosa", "setosa", "other"), levels = c("setosa", "other"))
xData <- iris
xData$Species <- NULL
primModel <- supervisedPRIM(x = xData, y = yData)
# Predict on the original dataset
predictions <- predict(primModel, newdata = xData)
```

---

supervisedPRIM   *Fit PRIM model to a labeled dataset*

Description

perform supervised classification using Patient Rule Induction Method (PRIM)

Usage

```
supervisedPRIM(x, y, peel.alpha = 0.05, paste.alpha = 0.01,
  mass.min = 0.05, threshold.type = 1, ...)
```

Arguments

x	matrix of data values
y	binary vector of 0/1 response values
peel.alpha	peeling quantile tuning parameter
paste.alpha	pasting quantile tuning parameter
mass.min	minimum mass tuning parameter
threshold.type	threshold direction indicator: 1 = ">= threshold", -1 = "<= threshold"
...	additional arguments to pass to prim.box

Details

Fit

Value

an object of class supervisedPRIM. See additional details in prim.box

Author(s)

David Shaub

Examples

```
# Train a model to determine if a flower is setosa
data(iris)
yData <- factor(ifelse(iris$Species == "setosa", "setosa", "other"), levels = c("setosa", "other"))
xData <- iris
xData$Species <- NULL
primModel <- supervisedPRIM(x = xData, y = yData)
```

Index