Package ‘supervisedPRIM’

October 1, 2016

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

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Repository CRAN

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

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**supervisedPRIM**

### Model Predictions

**Description**

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

**Usage**

```r
## 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 probabilities instead of the predicted class?

**Author(s)**

David Shaub

**Examples**

```r
# 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)
```

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**supervisedPRIM**

**Fit PRIM model to a labeled dataset**

**Description**

perform supervised classification using Patient Rule Induction Method (PRIM)

**Usage**

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

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)
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