

Package ‘LLM’

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Title Logit Leaf Model Classifier for Binary Classification

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Description Fits the Logit Leaf Model, makes predictions and visualizes the output. (De Caigny et al., (2018) <DOI:10.1016/j.ejor.2018.02.009>).

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License GPL (>= 3)

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llm *Create Logit Leaf Model*

Description

This function creates the logit leaf model. It takes a dataframe with numeric values as input and a corresponding vector with dependent values. Decision tree parameters threshold for pruning and number of observations per leaf can be set.

Usage

```
llm(X, Y, threshold_pruning = 0.25, nbr_obs_leaf = 100)
```

Arguments

X Dataframe containing numerical independent variables.

Y Numerical vector of dependent variable. Currently only binary classification is supported.

threshold_pruning Set confidence threshold for pruning. Default 0.25.

nbr_obs_leaf The minimum number of observations in a leaf node. Default 100.

Value

An object of class `logitleafmodel`, which is a list with the following components:

DecisionRules The raw decision rules that define segments. Use [table.llm.html](#) to visualize.

Coefficients The segment specific logistic regression coefficients. Use [table.llm.html](#) to visualize.

Author(s)

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References

Arno De Caigny, Kristof Coussement, Koen W. De Bock, A New Hybrid Classification Algorithm for Customer Churn Prediction Based on Logistic Regression and Decision Trees, *European Journal of Operational Research* (2018), doi: 10.1016/j.ejor.2018.02.009.

See Also

[predict.llm](#), [table.llm.html](#), [llm.cv](#)

Examples

```
## Load PimaIndiansDiabetes dataset from mlbench package
if (requireNamespace("mlbench", quietly = TRUE)) {
  library("mlbench")
}
data("PimaIndiansDiabetes")
## Split in training and test (2/3 - 1/3)
idtrain <- c(sample(1:768,512))
PimaTrain <- PimaIndiansDiabetes[idtrain,]
Pimatest <- PimaIndiansDiabetes[-idtrain,]
## Create the LLM
Pima.llm <- llm(X = PimaTrain[,-c(9)], Y = PimaTrain$diabetes,
  threshold_pruning = 0.25, nbr_obs_leaf = 100)
```

llm.cv

Runs v-fold cross validation with LLM

Description

In v -fold cross validation, the data are divided into v subsets of approximately equal size. Subsequently, one of the v data parts is excluded while the remainder of the data is used to create a `logitleafmodel` object. Predictions are generated for the excluded data part. The process is repeated v times.

Usage

```
llm.cv(X, Y, cv, threshold_pruning = 0.25, nbr_obs_leaf = 100)
```

Arguments

<code>X</code>	Dataframe containing numerical independent variables.
<code>Y</code>	Numerical vector of dependent variable. Currently only binary classification is supported.
<code>cv</code>	An integer specifying the number of folds in the cross-validation.
<code>threshold_pruning</code>	Set confidence threshold for pruning. Default 0.25.
<code>nbr_obs_leaf</code>	The minimum number of observations in a leaf node. Default 100.

Value

An object of class `llm.cv`, which is a list with the following components:

<code>foldpred</code>	a data frame with, per fold, predicted class membership probabilities for the left-out observations
<code>pred</code>	a data frame with predicted class membership probabilities.

foldclass	a data frame with, per fold, predicted classes for the left-out observations.
class	a data frame with the predicted classes.
conf	the confusion matrix which compares the real versus the predicted class memberships based on the class object.

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See Also

[predict.llm](#), [table.llm.html](#), [llm](#)

Examples

```
## Load PimaIndiansDiabetes dataset from mlbench package
if (requireNamespace("mlbench", quietly = TRUE)) {
  library("mlbench")
}
data("PimaIndiansDiabetes")
## Create the LLM with 5-cv
Pima.llm <- llm.cv(X = PimaIndiansDiabetes[,-c(9)], Y = PimaIndiansDiabetes$diabetes, cv=5,
  threshold_pruning = 0.25, nbr_obs_leaf = 100)
```

predict.llm

Create Logit Leaf Model Prediction

Description

This function creates a prediction for an object of class `logitleafmodel`. It assumes a dataframe with numeric values as input and an object of class `logitleafmodel`, which is the result of the `llm` function. Currently only binary classification is supported.

Usage

```
## S3 method for class 'llm'
predict(object, X, addrownnumbers = TRUE, ...)
```

Arguments

object	An object of class logitleafmodel, as that created by the function llm.
X	Dataframe containing numerical independent variables.
addrownnumbers	Boolean to add row numbers in output.
...	further arguments passed to or from other methods.

Value

Returns a dataframe containing a probability for every instance based on the LLM model. Optional rownumbers can be added.

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See Also

[llm](#), [table.llm.html](#), [llm.cv](#)

Examples

```
## Load PimaIndiansDiabetes dataset from mlbench package
if (requireNamespace("mlbench", quietly = TRUE)) {
  library("mlbench")
}
data("PimaIndiansDiabetes")
## Split in training and test (2/3 - 1/3)
idtrain <- c(sample(1:768,512))
PimaTrain <-PimaIndiansDiabetes[idtrain,]
Pimatest <-PimaIndiansDiabetes[-idtrain,]
## Create the LLM
Pima.llm <- llm(X = PimaTrain[,-c(9)],Y = PimaTrain$diabetes,
  threshold_pruning = 0.25,nbr_obs_leaf = 100)
## Use the model on the test dataset to make a prediction
PimaPrediction <- predict.llm(object = Pima.llm, X = Pimatest[,-c(9)])
## Optionally add the dependent to calculate performance statistics such as AUC
# PimaPrediction <- cbind(PimaPrediction, "diabetes" = Pimatest["diabetes"])
```

table.llm.html	<i>Create the HTML code for Logit Leaf Model visualization</i>
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Description

This function generates HTML code for a visualization of the logit leaf model.

Usage

```
table.llm.html(object, headertext = "The Logit Leaf Model",  
              footertext = "A table footer comment", roundingnumbers = 2)
```

Arguments

object	An object of class logitleafmodel, as that created by the function llm.
headertext	Allows to provide the table with a header.
footertext	Allows to provide the table with a custom footer.
roundingnumbers	An integer stating the number of decimals in the visualization.

Value

Generates HTML code for a visualization.

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See Also

[predict.llm](#), [llm](#), [llm.cv](#)

Examples

```
## Load PimaIndiansDiabetes dataset from mlbench package  
if (requireNamespace("mlbench", quietly = TRUE)) {  
  library("mlbench")  
}  
data("PimaIndiansDiabetes")  
## Split in training and test (2/3 - 1/3)  
idtrain <- c(sample(1:768,512))
```

```
PimaTrain <-PimaIndiansDiabetes[idtrain,]
Pimatest <-PimaIndiansDiabetes[-idtrain,]
## Create the LLM
Pima.llm <- llm(X = PimaTrain[,-c(9)],Y = PimaTrain$diabetes,
  threshold_pruning = 0.25,nbr_obs_leaf = 100)
## Save the output of the model to a html file
Pima.Viz <- table.llm.html(object = Pima.llm, headertext = "This is an example of the LLM model",
  footertext = "Enjoy the package!")
## Optionally write it to your working directory
# write(Pima.Viz, "Visualization_LLM_on_PimaIndiansDiabetes.html")
```

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