Package ‘AppliedPredictiveModeling’

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Author Max Kuhn, Kjell Johnson
Maintainer Max Kuhn <mxkuhn@gmail.com>
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AppliedPredictiveModeling-package ................................................. 2
abalone ................................................................. 2
AlzheimerDisease .......................................................... 3
bookTheme ................................................................. 4
ChemicalManufacturingProcess ................................................ 5
concrete ........................................................................ 6
FuelEconomy .................................................................. 7
getPackages .................................................................... 8
hepatic .......................................................................... 9
logisticCreditPredictions ....................................................... 9
permeability ................................................................. 10
Description

This package can be used to reproduce the analyses in the text. Scripts for each chapter are located in the "chapters" directory. Use scriptLocation() to find their exact location.

Details

Package: AppliedPredictiveModeling
Type: Package
Version: 1.1-1
Date: 2013-05-29
License: GPL

Author(s)

Max Kuhn
Maintainer: Max Kuhn <mkuhn@gmail.com>

References

Alzheimer Disease

Description
The Abalone data consist of data from 4177 abalones. The data consist of measurements of the type (male, female and infant), the longest shell measurement, the diameter, height and several weights (whole, shucked, viscera and shell). The outcome is the number of rings. The age of the abalone is the number of rings plus 1.5.

The data are taken from the UCI database (http://archive.ics.uci.edu/ml/datasets/Abalone).

Usage
   data(abalone)

Value
   abalone a data frame with 4177 rows and 9 columns

Examples
   data(abalone)

Alzheimer Disease

Alzheimer's Disease CSF Data

Description
Washington University conducted a clinical study to determine if biological measurements made from cerebrospinal fluid (CSF) can be used to diagnose or predict Alzheimer’s disease (Craig-Schapiro et al. 2011). These data are a modified version of the values used for the publication.

The R factor vector diagnosis contains the outcome data for 333 of the subjects. The demographic and laboratory results are collected in the data frame predictors.

One important indicator of Alzheimer’s disease is the genetic background of a subject. In particular, what versions of the Apolipoprotein E gene inherited from one’s parents has an association with the disease. There are three variants of the gene: E2, E3 and E4. Since a child inherits a version of the gene from each parent, there are six possible combinations (e.g. E2/E2, E2/E3, and so on). This data is contained in the predictor column named Genotype.

Usage
   data(AlzheimerDisease)

Value
   diagnosis labels for the patients, either "Impaired" or "Control".
   predictors predictors for demographic data (eg. age, gender), genotype and assay results.
Source

Examples

```r
data(AlzheimerDisease)
```

<table>
<thead>
<tr>
<th>bookTheme</th>
<th>Lattice Themes</th>
</tr>
</thead>
</table>

Description
Two `lattice` themes used throughout the book.

Usage

```r
bookTheme(set = TRUE)
```

```r
transparentTheme(set = TRUE, pchSize = 1, trans = 0.2)
```

Arguments

- `set` a logical: should these settings be applied to the current device?
- `pchSize` the size of the plot symbols
- `trans` the amount of transparency (via the alpha channel). Note that transparency is not supported by all graphics devices.

Details
When using these functions to save a plot, make sure to invoke them after the device has been opened (e.g. after calls such as `pdf()`).

Value
Each function returns a list of theme parameters. See Sarkar (2008) or `trellis.par.get` for specific details.

Author(s)
Max Kuhn

References
Some of the colors are based on values from ColorBrewer [http://www.colorbrewer.org](http://www.colorbrewer.org).


**Examples**

```r
library(lattice)

example <- quadBoundaryFunc(100)

bookTheme(set = TRUE)
xyplot(X2 ~ X1, data = example, groups = class, auto.key = TRUE)

transparentTheme(set = TRUE, trans = .6)
xyplot(X2 ~ X1, data = example, groups = class, auto.key = TRUE)
```

---

**Chemical Manufacturing Process Data**

**Description**

This data set contains information about a chemical manufacturing process, in which the goal is to understand the relationship between the process and the resulting final product yield. Raw material in this process is put through a sequence of 27 steps to generate the final pharmaceutical product. The starting material is generated from a biological unit and has a range of quality and characteristics. The objective in this project was to develop a model to predict percent yield of the manufacturing process. The data set consisted of 177 samples of biological material for which 57 characteristics were measured. Of the 57 characteristics, there were 12 measurements of the biological starting material, and 45 measurements of the manufacturing process. The process variables included measurements such as temperature, drying time, washing time, and concentrations of by-products at various steps. Some of the process measurements can be controlled, while others are observed. Predictors are continuous, count, categorical; some are correlated, and some contain missing values. Samples are not independent because sets of samples come from the same batch of biological starting material.

**Usage**

```r
data(ChemicalManufacturingProcess)
```

**Value**

`ChemicalManufacturingProcess`: a data frame with columns for the outcome (Yield) and the predictors (Biological Material 1 through Biological Material 12 and Manufacturing Process 1 through Manufacturing Process 45)

**Examples**

```r
data(ChemicalManufacturingProcess)
```
Compressive Strength of Concrete from Yeh (1998)

Description

Yeh (1998) describes a collection of data sets from different sources that can be used for modeling the compressive strength of concrete formulations as a functions of their ingredients and age.

Usage

data(concrete)

Details

The data are from Yeh (1998) and taken from the UCI ML website http://archive.ics.uci.edu/ml/datasets/Concrete+Compressive+Strength.

There are 1030 data points from the UCI website, but the paper states that approximately 1,000 samples were made, but only 727 were analyzed in the source material. It is unclear which samples were excluded.

Value

| concrete       | data frame of data with predictor columns Cement, BlastFurnaceSlag, FlyAsh, Water, Superplasticizer, CoarseAggregate, FineAggregate and Age with response column CompressiveStrength. These are the amounts. |
| mixture        | The same data where all the ingredients have been converted to proportions of the total amounts. |

Source


Examples

data(concrete)

library(caret)

### Split used in the book:
set.seed(975)
inTrain <- createDataPartition(mixtures$CompressiveStrength, p = 3/4)[[1]]
training <- mixtures[ inTrain,]
Testing <- mixtures[-inTrain,]
**Fuel Economy Data**

**Description**

The [http://fueleconomy.gov](http://fueleconomy.gov) website, run by the U.S. Department of Energy’s Office of Energy Efficiency and Renewable Energy and the U.S. Environmental Protection Agency, lists different estimates of fuel economy for passenger cars and trucks. For each vehicle, various characteristics are recorded such as the engine displacement or number of cylinders. Along with these values, laboratory measurements are made for the city and highway miles per gallon (MPG) of the car.

Predictors extracted from the website include: `engdispl`, `numcyl`, `transmission`, `airaspirationmethod`, `numgears`, `translockup`, `transcreepergear`, `drivedesc`, `intakevalvepercyl`, `exhaustvalvespercyl`, `carlineclassdesc`, `varvalvetiming` and `varvalvelift`. The outcome used in the book is in column `FE` and is the unadjusted highway data.

**Usage**

```r
data(FuelEconomy)
```

**Value**

- `cars2011`: cars introduced in 2011 that were not in the model year 2010 data.
- `cars2012`: cars introduced in 2012 that were not in the model year 2010 or 2011 data

**Examples**

```r
data(FuelEconomy)
library(lattice)

### Plot shown in the text:

cars2010 <- cars2010[order(cars2010$EngDispl),]
cars2011 <- cars2011[order(cars2011$EngDispl),]

cars2010a <- cars2010
cars2010a$Year <- "2010 Model Year"
cars2011a <- cars2011
cars2011a$Year <- "2011 Model Year"

plotData <- rbind(cars2010a, cars2011a)

plotTheme <- bookTheme(FALSE)
plotTheme$plot.symbol$col <- rgb(.2, .2, .2, .5)
plotTheme$plot.symbol$cex <- 0.7
trellis.par.set(plotTheme)
```
getPackages

Install Packages for Each Chapter

Description

This function identifies the physical location on the user's computer where the chapter R scripts are located.

Usage

getPackages(chapter, ...)

Arguments

chapter an integer vector (or character versions of the integer) for the chapter number. See Details below:

... options to pass to install.packages

Details

Chapter names and packages. about dependencies.

Author(s)

Max Kuhn

Examples

## Not run:
getPackages(2)
getPackages(2:3)
getPackages("4")

## End(Not run)
**Hepatic Injury Data**

**Description**

This data set was used to develop a model for predicting compounds’ probability of causing hepatic injury (i.e. liver damage). This data set consisted of 281 unique compounds; 376 predictors were measured or computed for each. The response was categorical (either "None", "Mild" or "Severe"), and was highly unbalanced.

This kind of response often occurs in pharmaceutical data because companies steer away from creating molecules that have undesirable characteristics. Therefore, well-behaved molecules often greatly outnumber undesirable molecules. The predictors consisted of measurements from 184 biological screens and 192 chemical feature predictors. The biological predictors represent activity for each screen and take values between 0 and 10 with a mode of 4. The chemical feature predictors represent counts of important sub-structures as well as measures of physical properties that are thought to be associated with hepatic injury.

**Usage**

data(hepatic)

**Value**

<table>
<thead>
<tr>
<th>bio</th>
<th>Biological screen results.</th>
</tr>
</thead>
<tbody>
<tr>
<td>chem</td>
<td>Chemical fingerprints for sub-structures.</td>
</tr>
<tr>
<td>injury</td>
<td>A factor vector of outcomes.</td>
</tr>
</tbody>
</table>

**Examples**

data(hepatic)

---

**logisticCreditPredictions**

*Logistic Regression Predictions for the Credit Data*

**Description**

add some notes

**Usage**

data(solubility)
Value

A data frame with columns

- **Bad**
  - The predicted class probability for bad credit.
- **Good**
  - The predicted class probability for good credit.
- **pred**
  - The predicted class.
- **obs**
  - The observed class

Examples

```r
## show code to make the predictions

# data frame permeability
```

Description

This pharmaceutical data set was used to develop a model for predicting compounds’ permeability. In short, permeability is the measure of a molecule’s ability to cross a membrane. The body, for example, has notable membranes between the body and brain, known as the blood-brain barrier, and between the gut and body in the intestines. These membranes help the body guard critical regions from receiving undesirable or detrimental substances. For an orally taken drug to be effective in the brain, it first must pass through the intestinal wall and then must pass through the blood-brain barrier in order to be present for the desired neurological target. Therefore, a compound’s ability to permeate relevant biological membranes is critically important to understand early in the drug discovery process. Compounds that appear to be effective for a particular disease in research screening experiments, but appear to be poorly permeable may need to be altered in order improve permeability, and thus the compound’s ability to reach the desired target. Identifying permeability problems can help guide chemists towards better molecules.

Permeability assays such as PAMPA and Caco-2 have been developed to help measure compounds’ permeability (Kansy et al, 1998). These screens are effective at quantifying a compound’s permeability, but the assay is expensive labor intensive. Given a sufficient number of compounds that have been screened, we could develop a predictive model for permeability in an attempt to potentially reduce the need for the assay. In this project there were 165 unique compounds; 1107 molecular fingerprints were determined for each. A molecular fingerprint is a binary sequence of numbers that represents the presence or absence of a specific molecular sub-structure. The response is highly skewed, the predictors are sparse (15.5 percent are present), and many predictors are strongly associated.

Usage

```r
data(permeability)
```

Value

- **permeability**
  - permeability values for each compound.
- **fingerprints**
  - a matrix of binary fingerprint indicator variables.
Source


Examples

data(permeability)

hist(permeability)

summary(apply(fingerprints, 2, mean))

permuteRelief  Permutation Statistics for the Relief Algorithm

Description

This function uses a permutation approach to determining the relative magnitude of Relief scores (Kira and Rendell, 1992 and Kononenko, 1994).

Usage

permuteRelief(x, y, nperm = 100, ...)

Arguments

x  a data frame of predictor data
y  a vector of outcomes
nperm  the number of random permutations of the data
...  options to pass to attrEval, such as the exact Relief algorithm, to use

Details

The scores for each predictor are computed using the original data and after outcome data are randomly scrambled (nperm times). The mean and standard deviation of the permuted values are determined and a standardized version of the observed scores are determined by subtracting the permuted means from the original values, then dividing each by the corresponding standard deviation.

Value

a list with elements

standardized  a vector of standardized predictor scores
permutations  the values of the permuted scores, for plotting to assess the permutation distribution
observed  the observed scores
options  a list of options passed using ...
Author(s)
Max Kuhn

References

See Also
attrEval

Examples
```r
set.seed(874)
reliefEx3 <- easyBoundaryFunc(500)
reliefEx3$X1 <- scale(reliefEx3$X1)
reliefEx3$X2 <- scale(reliefEx3$X2)
reliefEx3$prob <- NULL

standardized <- permuteRelief(reliefEx3[, 1:2], reliefEx3$class,
                               ## For efficiency, a small number of
                               ## permutations are used here.
                               nperm = 50,
                               estimator="ReliefEqualK",
                               ReliefIterations= 50)
```

Description
These functions simulate data that are used in the text.

Usage
```r
quadBoundaryFunc(n)
easyBoundaryFunc(n, intercept = 0, interaction = 2)
```

Arguments
- **n**: the sample size
- **intercept**: the coefficient for the logistic regression intercept term
- **interaction**: the coefficient for the logistic regression interaction term
quadBoundaryFunc

Details

The quadBoundaryFunc function creates a class boundary that is a function of both predictors. The probability values are based on a logistic regression model with model equation: 
\[-1 - 2X_1 - 0.2X_1^2 + 2X_2^2.\]
The predictors here are multivariate normal with mean (1, 0) and a moderate degree of positive correlation.

Similarly, the easyBoundaryFunc uses a logistic regression model with model equation: 
\[\text{intercept} - 4X_1 + 4X_2 + \text{interaction} \times X_1 \times X_2.\]
The predictors here are multivariate normal with mean (1, 0) and a strong positive correlation.

Value

Both functions return data frames with columns

<table>
<thead>
<tr>
<th>Column</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>X1</td>
<td>numeric predictor value</td>
</tr>
<tr>
<td>X2</td>
<td>numeric predictor value</td>
</tr>
<tr>
<td>prob</td>
<td>numeric value reflecting the true probability of the first class</td>
</tr>
<tr>
<td>class</td>
<td>a factor variable with levels 'Class1' and 'Class2'</td>
</tr>
</tbody>
</table>

Author(s)

Max Kuhn

Examples

```r
## in Chapter 11, 'Measuring Performance in Classification Model'
set.seed(975)
training <- quadBoundaryFunc(500)
testing <- quadBoundaryFunc(1000)

## in Chapter 20, 'Factors That Can Affect Model Performance'
set.seed(615)
dat <- easyBoundaryFunc(200, interaction = 3, intercept = 3)
dat$X1 <- scale(dat$X1)
dat$X2 <- scale(dat$X2)
dat$Data <- "Original"
dat$prob <- NULL

## in Chapter X, 'An Introduction to Feature Selection'
set.seed(874)
reliefEx3 <- easyBoundaryFunc(500)
reliefEx3$X1 <- scale(reliefEx3$X1)
reliefEx3$X2 <- scale(reliefEx3$X2)
reliefEx3$prob <- NULL
```
schedulingData

HPC Job Scheduling Data

Description

These data consist of information on 4331 jobs in a high performance computing environment. Seven attributes were recorded for each job along with a discrete class describing the execution time.

The predictors are: Protocol (the type of computation), Compounds (the number of data points for each job), InputFields (the number of characteristic being estimated), Iterations (maximum number of iterations for the computations), NumPending (the number of other jobs pending at the time of launch), Hour (decimal hour of day for launch time) and Day (of launch time).

The classes are: VF (very fast), F (fast), M (moderate) and L (long).

Usage

data(schedulingData)

Value

schedulingData a data frame with 4331 rows and 8 columns

Examples

data(schedulingData)

library(caret)

set.seed(1104)
inTrain <- createDataPartition(schedulingData$Class, p = .8, list = FALSE)

schedulingData$NumPending <- schedulingData$NumPending + 1

trainData <- schedulingData[ inTrain,

testData <- schedulingData[-inTrain,

modForm <- as.formula(Class ~ Protocol + log10(Compounds) + 
  log10(InputFields) + log10(Iterations) + 
  log10(NumPending) + Hour + Day)
**scriptLocation**

| scriptLocation | Find Chapter Script Files |

**Description**

This function identifies the physical location on the user’s computer where the chapter R scripts are located.

**Usage**

scriptLocation()

**Author(s)**

Max Kuhn

**Examples**

scriptLocation()

---

**segmentationOriginal**  
**Cell Body Segmentation**

**Description**

Hill, LaPan, Li and Haney (2007) develop models to predict which cells in a high content screen were well segmented. The data consists of 119 imaging measurements on 2019. The original analysis used 1009 for training and 1010 as a test set (see the column called Case).

The outcome class is contained in a factor variable called Class with levels "PS" for poorly segmented and "WS" for well segmented.

A pre-processed version of these data can be found in the caret package.

**Usage**

data(segmentationOriginal)

**Value**

segmentationOriginal  
data frame of cells

**Source**

Description

Tetko et al. (2001) and Huuskonen (2000) investigated a set of compounds with corresponding experimental solubility values using complex sets of descriptors. They used linear regression and neural network models to estimate the relationship between chemical structure and solubility. For our analyses, we will use 1267 compounds and a set of more understandable descriptors that fall into one of three groups: 208 binary "fingerprints" that indicate the presence or absence of a particular chemical sub-structure, 16 count descriptors (such as the number of bonds or the number of Bromine atoms) and 4 continuous descriptors (such as molecular weight or surface area).

Usage

data(solubility)

Value

solTrainX  training set predictors in their natural units.
solTrainXtrans  training set predictors after transformations for skewness and centering/scaling.
solTrainY  a vector of log10 solubility values for the training set.
solTestX  test set predictors in their natural units.
solTestXtrans  test set predictors after the same transformations used on the training set are applied.
solTestY  a vector of log10 solubility values for the training set.

Source


Examples

data(solubility)

library(caret)

### Cross-validation splits used in the book:
set.seed(100)
indx <- createFolds(solTrainY, returnTrain = TRUE)
### Description

These data contain two predictors measured for 208 samples. Of these, 111 samples are labeled as Class1 and the remaining 97 are Class2.

### Usage

```r
data(twoClassData)
```

### Value

- **predictors**: data frame of two predictors
- **classes**: a factor vector of class labeled

### Examples

```r
data(twoClassData)
library(lattice)
xyplot(PredictorB ~ PredictorA,
       data = predictors,
       groups = classes,
       auto.key = TRUE)
```
Index

*Topic datasets
  abalone, 2
  AlzheimerDisease, 3
  ChemicalManufacturingProcess, 5
  concrete, 6
  FuelEconomy, 7
  hepatic, 9
  logisticCreditPredictions, 9
  permeability, 10
  schedulingData, 14
  segmentationOriginal, 15
  solubility, 16
  twoClassData, 17

*Topic hplot
  bookTheme, 4

*Topic htest
  permuteRelief, 11

*Topic package
  AppliedPredictiveModeling-package, 2

*Topic utilities
  getPackages, 8
  quadBoundaryFunc, 12
  scriptLocation, 15
  translationalTheme (bookTheme), 4

abalone, 2
AlzheimerDisease, 3
AppliedPredictiveModeling
  (AppliedPredictiveModeling-package), 2
AppliedPredictiveModeling-package, 2
attrEval, //, /2
bio (hepatic), 9
bookTheme, 4
cars2010 (FuelEconomy), 7
cars2011 (FuelEconomy), 7
cars2012 (FuelEconomy), 7
chem (hepatic), 9
ChemicalManufacturingProcess, 5
classes (twoClassData), 17
concrete, 6
diagnosis (AlzheimerDisease), 3
easyBoundaryFunc (quadBoundaryFunc), 12
fingerprints (permeability), 10
FuelEconomy, 7
getPackages, 8
hepatic, 9
injury (hepatic), 9
install.packages, 8
logisticCreditPredictions, 9
mixtures (concrete), 6
permeability, 10
permuteRelief, 11
predictors (AlzheimerDisease), 3
quadBoundaryFunc, 12
schedulingData, 14
scriptLocation, 15
segmentationOriginal, 15
solTestX (solubility), 16
solTestXtrans (solubility), 16
solTestY (solubility), 16
solTrainX (solubility), 16
solTrainXtrans (solubility), 16
solTrainY (solubility), 16
solubility, 16
trainX (solubility), 16
translationalTheme (bookTheme), 4
trellis.par.get, 4
twoClassData, 17