

Package ‘StatMeasures’

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Type Package

Title Easy Data Manipulation, Data Quality and Statistical Checks

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Description Offers useful functions to perform day-to-day data manipulation operations, data quality checks and post modelling statistical checks. One can effortlessly change class of a number of variables to factor, remove duplicate observations from the data, create deciles of a variable, perform data quality checks for continuous (integer or numeric), categorical (factor) and date variables, and compute goodness of fit measures such as auc for statistical models. The functions are consistent for objects of class 'data.frame' and 'data.table', which is an enhanced 'data.frame' implemented in the package 'data.table'.

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R topics documented:

accuracy	2
actvspred	3
auc	4
contents	5
decile	6
dqcategorical	7
dqcontinuous	8
dqdate	9

factorise	10
gini	11
imputemiss	12
iv	13
ks	14
mape	15
outliers	16
pentile	17
randomise	18
rmdupkey	19
rmdupobs	20
splitdata	21

Index	22
--------------	-----------

accuracy	<i>Confusion matrix and overall accuracy of predicted binary response</i>
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Description

Takes in actual binary response, predicted probabilities and cutoff value, and returns confusion matrix and overall accuracy

Usage

```
accuracy(y, yhat, cutoff)
```

Arguments

y	actual binary response variable
yhat	predicted probabilities corresponding to the actual binary response
cutoff	threshold value in the range 0 to 1

Details

When we predict a binary response, first thing that we want to check is accuracy of the model for a particular cutoff value. This function does just that and provides confusion matrix (numbers and percentage) and overall accuracy. Overall accuracy is calculated as $(TP + TN)/(P + N)$.

The output is a list from which the individual elements can be picked as shown in the example.

Value

a three element list: confusion matrix as a table, confusion matrix (percentages) as a table and overall accuracy value

Author(s)

Akash Jain

See Also

[ks](#), [auc](#), [iv](#), [splitdata](#)

Examples

```
# A 'data.frame' with y and yhat
df <- data.frame(y = c(1, 0, 1, 1, 0),
                  yhat = c(0.86, 0.23, 0.65, 0.92, 0.37))

# Accuracy tables and overall accuracy figures
ltAccuracy <- accuracy(y = df[, 'y'], yhat = df[, 'yhat'], cutoff = 0.7)
accuracyNumber <- ltAccuracy$accuracyNum
accuracyPercentage <- ltAccuracy$accuracyPer
overallAccuracy <- ltAccuracy$overallAcc
```

actvspred

Comparison of actual and predicted linear response

Description

Takes in actual, predicted linear response and quantile value, and returns average actual and predicted response in each quantile

Usage

```
actvspred(y, yhat, n)
```

Arguments

y	actual linear response
yhat	predicted linear response
n	quantiles to be created for comparison

Details

actvspred function divides the data into n (given as input by the user) quantiles and computes mean of y and yhat for each quantile. All NA's in n, y and yhat are removed for calculation.

The function also plots a line chart of average actual response and average predicted response over n quantiles. This plot can be used to visualize how close both the lines are.

Value

a data.frame with average actual and predicted response in each quantile

Author(s)

Akash Jain

See Also

[mape](#), [splitdata](#)

Examples

```
# A 'data.frame' with y and yhat
df <- data.frame(y = c(1, 2, 3, 6, 8, 10, 15),
                  yhat = c(1.2, 2.5, 3.3, 6.9, 9.3, 6.5, 12.3))

# Get actual vs predicted table
ACTVSPRED <- actvspred(y = df[, 'y'], yhat = df[, 'yhat'], n = 5)
```

auc

Area under curve of predicted binary response

Description

Takes in actual binary response and predicted probabilities, and returns auc value

Usage

```
auc(y, yhat)
```

Arguments

y	actual binary response
yhat	predicted probabilities corresponding to the actual binary response

Details

Area under the receiver operating characteristic (ROC) curve is the most sought after criteria for judging how good model predictions are.

auc function calculates the true positive rates (TPR) and false positive rates (FPR) for each cutoff from 0.01 to 1 and calculates the area using trapezoidal approximation. A ROC curve is also generated.

Value

area under the ROC curve

Author(s)

Akash Jain

See Also

[accuracy](#), [ks](#), [iv](#), [gini](#), [splitdata](#)

Examples

```
# A 'data.frame' with y and yhat
df <- data.frame(y = c(1, 0, 1, 1, 0, 0, 1, 0, 1, 0),
                  yhat = c(0.86, 0.23, 0.65, 0.92, 0.37, 0.45, 0.72, 0.19, 0.92, 0.50))

# AUC figure
AUC <- auc(y = df[, 'y'], yhat = df[, 'yhat'])
```

contents

Basic summary of the data

Description

Takes in a data and returns summary of the data

Usage

```
contents(data)
```

Arguments

data	a data.frame or data.table
------	----------------------------

Details

This function helps when one wants to get a quick snapshot of the data such as class, distinct values, missing values and sample value of the variables.

It works for both 'data.frame' and 'data.table' but the output will be a 'data.frame' only.

Value

a data.frame that contains variable, class, distinct values, missing values, percentage of missing value and sample value

Author(s)

Akash Jain

See Also

[dqcontinuous](#), [dqcategorical](#), [dqdate](#)

Examples

```
# A data frame
df <- data.frame(x = c(1, 2, 3, 4, NA),
                  y = c('a', 'b', 'c', 'd', 'e'),
                  z = c(1, 1, 0, 0, 1))

# Summary of the data
dfContents <- contents(data = df)
```

decile	<i>Create deciles of a variable</i>
--------	-------------------------------------

Description

Takes in a vector, and returns the deciles

Usage

```
decile(vector, decreasing = FALSE)
```

Arguments

vector	an integer or numeric vector
decreasing	a logical input, which if set to FALSE puts smallest values in decile 1 and if set to TRUE puts smallest values in decile 10; FALSE is default

Details

`decile` is a convenient function to get integer deciles of an integer or numeric vector. By default, the smallest values are placed in the smallest decile.

Sometimes one may want to put smallest values in the biggest decile, and for that the user can set the `decreasing` argument to TRUE; by default it is FALSE.

Value

an integer vector of decile values

Author(s)

Akash Jain

See Also

[pentile](#), [outliers](#), [imputemiss](#)

Examples

```
# Scores vector
scores <- c(1, 4, 7, 10, 15, 21, 25, 27, 32, 35,
          49, 60, 75, 23, 45, 86, 26, 38, 34, 67)

# Create deciles based on the values of the vector
decileScores <- decile(vector = scores)
decileScores <- decile(vector = scores, decreasing = TRUE)
```

dqcategorical

Data quality check of categorical variables

Description

Takes in a data, and returns summary of categorical variables

Usage

```
dqcategorical(data)
```

Arguments

data	a data.frame or data.table
------	----------------------------

Details

While trying to understand a data, it is important to know the distribution of categorical variables. dqcategorical produces an output which answers a couple of questions regarding such variables - how many distinct categories does the variable have, what are the categories, what is the frequency of each of them and the percentage frequency.

But first, it is critical to identify categorical variables in the data. They may be integer, numeric or character. All such variables should be converted to factor; one may use `factorise` function in this package to do this task easily.

The function identifies all the factor variables and produces an output for each of them and returns a consolidated summary. It works for both 'data.frame' and 'data.table' but the output summary is a 'data.frame' only.

Value

a data.frame which contains the variable, category index, category, category frequency and percentage frequency of all factor variables

Author(s)

Akash Jain

See Also

[dqcontinuous](#), [dqdate](#), [contents](#)

Examples

```
# A 'data.frame'
df <- data.frame(phone = c('IP', 'SN', 'HO', 'IP', 'SN', 'IP', 'HO', 'SN', 'IP', 'SN'),
                  colour = c('black', 'blue', 'green', 'blue', 'black', 'silver', 'black',
                            'white', 'black', 'green'))

# Factorise categorical variables
df <- factorise(data = df, colNames = c('phone', 'colour'))

# Generate a data quality report of continuous variables
summaryCategorical <- dqcategorical(data = df)
```

dqcontinuous

Data quality check of continuous variables

Description

Takes in a data, and returns summary of continuous variables

Usage

```
dqcontinuous(data)
```

Arguments

data	a data.frame or data.table
------	----------------------------

Details

It is of utmost importance to know the distribution of continuous variables in the data. `dqcontinuous` produces an output which tells - continuous variable, non-missing values, missing values, percentage missing, minimum, average, maximum, standard deviation, variance, common percentiles from 1 to 99, and number of outliers for each continuous variable.

The function tags all integer and numeric variables as continuous, and produces output for them; if you think there are some variables which are integer or numeric in the data but they don't represent a continuous variable, change their type to an appropriate class.

`dqcontinuous` uses the same criteria to identify outliers as the one used for box plots. All values that are greater than 75th percentile value + 1.5 times the inter quartile range or lesser than 25th percentile value - 1.5 times the inter quartile range, are tagged as outliers.

This function works for both 'data.frame' and 'data.table' but returns a 'data.frame' only.

Value

a data.frame which contains the non-missing values, missing values, percentage of missing values, minimum, mean, maximum, standard deviation, variance, percentiles and count of outliers of all integer and numeric variables

Author(s)

Akash Jain

See Also

[dqcategory](#), [dqdate](#), [contents](#)

Examples

```
# A 'data.frame'  
df <- data.frame(x = c(1, 2, 3, 4, 5, 6, 7, 8, 9, 10),  
                  y = c(22, NA, 66, 12, 78, 34, 590, 97, 56, 37))  
  
# Generate a data quality report of continuous variables  
summaryContinuous <- dqcontinuous(data = df)
```

dqdate

Data quality check of date variables

Description

Takes in a data, and returns summary of date variables

Usage

`dqdate(data)`

Arguments

`data` a data.frame or data.table

Details

`dqdate` produces summary of all date variables in the data. The function identifies all variables as date if they are of class 'Date' or 'IDate'.

Generally the dates are imported in R as character. They must be converted to an appropriate date format and then the function should be used.

The summary includes variable, non-missing values, missing values, minimum and maximum of the date variables. Input data can be a 'data.frame' or 'data.table' but the output summary will be a 'data.frame' only.

Value

a data.frame which contains the variable, non-missing values, missing values, minimum and maximum of all date variables

Author(s)

Akash Jain

See Also

[dqcontinuous](#), [dqcategorical](#), [contents](#)

Examples

```
# A 'data.frame'
df <- data.frame(date = c('2012-11-21', '2015-1-4', '1996-4-30', '1979-9-23', '2005-5-13'),
                  temperature = c(26, 32, 35, 7, 14))

# Convert character date to date format
df[, 'date'] <- as.Date(df[, 'date'])

# Generate a data quality report of date variables
summaryDate <- dqdate(data = df)
```

factorise

Change the class of variables to factor

Description

Takes in data and colNames, and returns the data with all variables mentioned in colNames converted to factor

Usage

`factorise(data, colNames)`

Arguments

<code>data</code>	a data.frame or data.table
<code>colNames</code>	a character vector of variable names to be converted to factor

Details

We often face the task of converting a bunch of variables to factor. This function is particularly useful in such a situation. Just specify the data and variable names and all of them will be converted to factor.

It works for both 'data.frame' and 'data.table', and the output is data of the same class as that of input.

Value

data of same class as input with specified variables converted to factor

Author(s)

Akash Jain

See Also

[randomise](#), [rmdupkey](#), [rmdupobs](#)

Examples

```
# A 'data.frame'  
df <- data.frame(x = c(1, 2, 3, 4, 5),  
                  y = c('a', 'b', 'c', 'd', 'e'),  
                  z = c(1, 1, 0, 0, 1))  
  
# Change the class of variables y and z to factors  
dfFac <- factorise(data = df, colNames = c('y', 'z'))
```

gini

Gini coefficient of a distribution

Description

Takes in a distribution and returns gini coefficient

Usage

gini(y)

Arguments

y an integer or numeric distribution

Details

To compute the gini coefficient of a distribution, gini is the right function. It uses trapezoidal approximation to calculate the area of the curve.

Lorenz curve is also plotted as output.

Value

gini coefficient of the distribution

Author(s)

Akash Jain

See Also[auc](#)**Examples**

```
# Distribution
dist <- c(1, 4, 7, 15, 10)

# Gini coefficient
GINI <- gini(y = dist)
```

imputemiss*Impute missing values in a variable***Description**

Takes in a vector and a value, and returns the vector with missing values imputed with that value

Usage

```
imputemiss(vector, value)
```

Arguments

<code>vector</code>	a vector with missing values
<code>value</code>	the value to be used for imputation

Details

`imputemiss` imputes the missing (NA) values in the vector with a specified value. The function simplifies the code for imputation.

Value

`vector` of the same class as input vector with imputed missing values

Author(s)

Akash Jain

See Also[decile](#), [pentile](#), [outliers](#)

Examples

```
# Scores vector
scores <- c(1, 2, 3, NA, 4, NA)

# Imputd scores vector
scoresImp <- imputemiss(vector = scores, value = 5)
```

iv

Information value of an independent variable in predicting a binary response

Description

Takes in independent and dependent variable and returns IV value

Usage

```
iv(x, y)
```

Arguments

- | | |
|---|----------------------------|
| x | an independent variable |
| y | a binary response variable |

Details

Information value of a variable is a significant indicator of its relevance in the prediction of a binary response variable. iv computes that value using the formula, $IV = \text{summation}[(\text{Responders} - \text{Non-responders}) * \ln(\text{Responders} / \text{Non-responders})]$ for each bin].

Ten bins are created for continuous variables while categories themselves are used as bins for categorical independent variables.

Value

information value of x

Author(s)

Akash Jain

See Also

[accuracy](#), [auc](#), [ks](#), [splitdata](#)

Examples

```
# A 'data.frame'
df <- data.frame(x = c('a', 'a', 'a', 'b', 'b', 'b'),
                  y = c(0, 1, 0, 1, 0, 1))

# Information value
IV <- iv(x = df[, 'x'], y = df[, 'y'])
```

ks

Kolmogorov-Smirnov statistic for predicted binary response

Description

Takes in actual binary response and predicted probabilities, and returns table used for KS computation and KS value

Usage

```
ks(y, yhat)
```

Arguments

y	actual binary response
yhat	predicted probabilities corresponding to the actual binary response

Details

Kolmogorov-Smirnov statistic can be easily computed using ks function. It not only computes the statistic but also returns the table used for ks computation. A chart is also plotted for quick visualization of split between percentage of responders and non-responders. Deciles are used for computation.

Appropriate elements of the 2 element list (ie. ksTable or ks) can be picked using the code given in the example.

Value

a two element list: table for KS computation and KS value itself

Author(s)

Akash Jain

See Also

[accuracy](#), [auc](#), [iv](#), [splitdata](#)

Examples

```
# A 'data.frame' with y and yhat
df <- data.frame(y = c(1, 0, 1, 1, 0),
                  yhat = c(0.86, 0.23, 0.65, 0.92, 0.37))

# KS table and value
ltKs <- ks(y = df[, 'y'], yhat = df[, 'yhat'])
ksTable <- ltKs$ksTable
KS <- ltKs$ks
```

mape

Compute mean absolute percentage error

Description

Takes in actual and predicted linear response, and returns MAPE value

Usage

```
mape(y, yhat)
```

Arguments

y	actual linear response
yhat	predicted linear response

Details

mape calculates the mean absolute percentage error in a predicted linear response.

Value

mean absolute percentage error

Author(s)

Akash Jain

See Also

[actvspred](#), [splitdata](#)

Examples

```
# A 'data.frame' with y and yhat
df <- data.frame(y = c(1.5, 2, 3.2),
                  yhat = c(3.4, 2.2, 2.7))

# Compute mape
MAPE <- mape(y = df[, 'y'], yhat = df[, 'yhat'])
```

outliers	<i>Identify outliers in a variable</i>
----------	--

Description

Takes in a vector, and returns count and index of outliers

Usage

```
outliers(vector)
```

Arguments

vector	an integer or numeric vector
--------	------------------------------

Details

The function uses the same criteria to identify outliers as the one used for box plots. All values that are greater than 75th percentile value + 1.5 times the inter quartile range or lesser than 25th percentile value - 1.5 times the inter quartile range, are tagged as outliers.

The individual elements (number of outliers and index of outliers) of the two element output list can be picked using the code given in example. The index of outliers can be used to get a vector of all outliers.

Value

a list with two elements: count and index of outliers

Author(s)

Akash Jain

See Also

[decile](#), [pentile](#), [imputemiss](#)

Examples

```
# Scores vector
scores <- c(1, 4, 7, 10, 566, 21, 25, 27, 32, 35,
         49, 60, 75, 23, 45, 86, 26, 38, 34, 223, -3)

# Identify the count of outliers and their index
ltOutliers <- outliers(vector = scores)
numOutliers <- ltOutliers$numOutliers
idxOutliers <- ltOutliers$idxOutliers
valOutliers <- scores[idxOutliers]
```

pentile	<i>Create pentiles of a variable</i>
---------	--------------------------------------

Description

Takes in a vector, and returns a vector of pentiles

Usage

```
pentile(vector, decreasing = FALSE)
```

Arguments

vector	an integer or numeric vector
decreasing	a logical input, which if set to FALSE puts smallest values in pentile 1 and if set to TRUE puts smallest values in pentile 5; FALSE is default

Details

pentile is a convenient function to get integer pentiles of an integer or numeric vector. By default, the smallest values are placed in the smallest pentile.

Sometimes one may want to put smallest values in the biggest pentile, and for that the user can set the decreasing argument to TRUE; by default it is FALSE.

Value

an integer vector of pentile values

Author(s)

Akash Jain

See Also

[decile](#), [outliers](#), [imputemiss](#)

Examples

```
# Scores vector
scores <- c(1, 4, 7, 10, 15, 21, 25, 27, 32, 35,
          49, 60, 75, 23, 45, 86, 26, 38, 34, 67)

# Create pentiles based on the values of the vector
pentileScores <- pentile(vector = scores)
pentileScores <- pentile(vector = scores, decreasing = TRUE)
```

randomise*Order the rows of a data randomly***Description**

Takes in data and seed, and returns the data with randomly ordered observations

Usage

```
randomise(data, seed = NULL)
```

Arguments

data	a matrix, data.frame or data.table
seed	an integer value

Details

Some of the modeling algorithms pick top p percent of the observations for training the model, which could lead to skewed predictions. This function solves that problem by randomly ordering the observations so that the response variable has more or less the same distribution even if the algorithms don't pick training observations randomly.

Value

data of same class as input with randomly ordered observations

Author(s)

Akash Jain

See Also

[factorise](#), [rmdupkey](#), [rmdupobs](#)

Examples

```
# A 'data.frame'
df <- data.frame(x = c(1, 2, 3, 4, 5), y = c('a', 'b', 'c', 'd', 'e'))

# Change the order of the observations randomly
dfRan <- randomise(data = df)
dfRan <- randomise(data = df, seed = 150)
```

rmdupkey*Remove observations with duplicate keys from data*

Description

Takes in a data and key, and returns data with duplicate observations by key removed

Usage

```
rmdupkey(data, by)
```

Arguments

data	a data.frame or data.table
by	a character vector of keys to be used

Details

Remove duplicate observations by key(s) is what this function does. How it is different from other functions that remove duplicates is that `rmdupkey` works for both 'data.frame' and 'data.table', and it also returns the duplicated observations.

Many a times we want to go back to the duplicated observations and see why that duplication occurred. One can pick the duplicated observations using the code given in example.

Value

a two element list: unique data and duplicate data

Author(s)

Akash Jain

See Also

`randomise`, `factorise`, `rmdupobs`

Examples

```
# A 'data.frame'  
df <- data.frame(x = c(1, 2, 1, 1), y = c(3, 3, 1, 3))  
  
# Remove duplicate observations by key from data  
ltDf <- rmdupkey(data = df, by = c('x'))  
unqDf <- ltDf$unqData  
dupDf <- ltDf$dupData
```

rmdupobs*Remove duplicate observations from data***Description**

Takes in a data, and returns it with duplicate observations removed

Usage

```
rmdupobs(data)
```

Arguments

data	a data.frame or data.table
------	----------------------------

Details

Duplicate observations are redundant and they need to be removed from the data. `rmdupobs` does just that; it removes the duplicated observations (the ones in which value of every variable is duplicated) and returns the data with only unique observations.

It works for both 'data.frame' and 'data.table' and returns the data with same class as that of input.

Value

a data of same class as input with only unique observations

Author(s)

Aakash Jain

See Also

[randomise](#), [rmdupkey](#), [factorise](#)

Examples

```
# A 'data.frame'
df <- data.frame(x = c(1, 2, 5, 1), y = c(3, 3, 1, 3))

# Remove duplicate observations from data
dfUnq <- rmdupobs(data = df)
```

splitdata	<i>Split modeling data into test and train set</i>
-----------	--

Description

Takes in data, fraction (for train set) and seed, and returns train and test set

Usage

```
splitdata(data, fraction, seed = NULL)
```

Arguments

data	a matrix, data.frame or data.table
fraction	proportion of observations that should go in the train set
seed	an integer value

Details

An essential task before doing modeling is to split the modeling data into train and test sets. splitdata is built for this task and returns a list with train and test sets, which can be picked using the code given in example.

fraction corresponds to the train dataset, while the rest of the observations go to the test dataset. If the user wants to generate the same test and train dataset everytime, he should specify a seed value.

Value

a list with two elements: train and test set

Author(s)

Akash Jain

See Also

[actvspred](#), [mape](#), [accuracy](#), [auc](#), [iv](#), [ks](#)

Examples

```
# A 'data.frame'  
df <- data.frame(x = c(1, 2, 3, 4, 5, 6, 7, 8, 9, 10),  
                  y = c('a', 'b', 'c', 'd', 'e', 'f', 'g', 'h', 'i', 'j'),  
                  z = c(1, 1, 0, 0, 1, 0, 0, 1, 1, 0))  
  
# Split data into train (70%) and test (30%)  
ltData <- splitdata(data = df, fraction = 0.7, seed = 123)  
trainData <- ltData$train  
testData <- ltData$test
```

Index

accuracy, 2, 4, 13, 14, 21
actvspred, 3, 15, 21
auc, 3, 4, 12–14, 21

contents, 5, 8–10

decile, 6, 12, 16, 17
dqcategorical, 5, 7, 9, 10
dqcontinuous, 5, 8, 8, 10
dqdate, 5, 8, 9, 9

factorise, 10, 18–20

gini, 4, 11

imputemiss, 6, 12, 16, 17
iv, 3, 4, 13, 14, 21

ks, 3, 4, 13, 14, 21

mape, 4, 15, 21

outliers, 6, 12, 16, 17

pentile, 6, 12, 16, 17

randomise, 11, 18, 19, 20
rmdupkey, 11, 18, 19, 20
rmdupobs, 11, 18, 19, 20

splitdata, 3, 4, 13–15, 21