Package ‘MLSeq’

March 2, 2024

Type Package

Title Machine Learning Interface for RNA-Seq Data

Version 2.20.0

Date 2021-08-14

Depends caret, ggplot2

VignetteBuilder knitr

Suggests knitr, e1071, kernlab

Imports testthat, VennDiagram, pamr, methods, DESeq2, edgeR, limma,
  Biobase, SummarizedExperiment, plyr, foreach, utils, sSeq,
  xtable

biocViews ImmunoOncology, Sequencing, RNASeq, Classification,
  Clustering

Description This package applies several machine learning methods, including SVM, bagSVM, Random
  Forest and CART to RNA-Seq data.

License GPL(>=2)

NeedsCompilation no

Encoding UTF-8

RoxygenNote 7.1.1

Collate 'all_classes.R' 'all_generics.R' 'voomFunctions.R'
  'classify.R' 'helper_functions.R' 'predict.R' 'methods.R'
  'onAttach.R' 'package_and_suppl.R' 'plda_nblda_functions.R'

git_url https://git.bioconductor.org/packages/MLSeq

git_branch RELEASE_3_18

git_last_commit d41d6a4

git_last_commit_date 2023-10-24

Repository Bioconductor 3.18

Date/Publication 2024-03-01
Author  Gokmen Zararsiz [aut, cre],
        Dincer Goksuluk [aut],
        Selcuk Korkmaz [aut],
        Vahap Eldem [aut],
        Izzet Parug Duru [ctb],
        Ahmet Ozturk [aut],
        Ahmet Ergun Karaagaoglu [aut, ths]

Maintainer  Gokmen Zararsiz <gokmenzararsiz@hotmail.com>

R topics documented:

MLSeq-package .............................................. 3
Available-classifiers .................................... 3
cervical .................................................. 4
classify ................................................... 5
confusionMat ............................................... 9
control .................................................... 10
discrete.train-class ..................................... 11
discreteControl .......................................... 12
input ...................................................... 13
isUpdated ................................................ 15
metaData .................................................. 16
method ..................................................... 17
MLSeq-class ............................................... 19
MLSeqMetaData-class ..................................... 20
MLSeqModelInfo-class .................................... 21
modelInfo ................................................ 22
normalization ............................................ 23
plot ....................................................... 24
predict ................................................... 25
preProcessing ............................................ 27
print.confMat ............................................. 28
ref ....................................................... 29
selectedGenes ........................................... 30
show ....................................................... 31
trained .................................................... 32
trainParameters .......................................... 33
transformation .......................................... 35
update ..................................................... 36
voom.train-class ......................................... 38
voomControl .............................................. 38

Index 40
**Description**

This package applies machine learning methods, such as Support Vector Machines (SVM), Random Forest (RF), Classification and Regression Trees (CART), Linear Discriminant Analysis (LDA) and more to RNA-Seq data. MLSeq combines well-known differential expression algorithms from bioconductor packages with functions from a famous package caret, which has comprehensive machine learning algorithms for classification and regression tasks. Although caret has 200+ classification/regression algorithm built-in, approximately 85 classification algorithms are used in MLSeq for classifying gene-expression data. See availableMethods() for further information.

**Author(s)**

Dincer Goksuluk, Gokmen Zararsiz, Selcuk Korkmaz, Vahap Eldem, Ahmet Ozturk and Ahmet Ergun Karaagaoglu

Maintainers:
Dincer Goksuluk <dincer.goksuluk@hacettepe.edu.tr>
Gokmen Zararsiz, <gokmenzararsiz@erciyes.edu.tr>
Selcuk Korkmaz <selcukkorkmaz@hotmail.com>

**See Also**

availableMethods, getModelInfo

---

**Available-classifiers**

*Available classification/regression methods in MLSeq*

**Description**

This function returns a character vector of available classification/regression methods in MLSeq. These methods are imported from caret package. See details below.

**Usage**

```r
availableMethods(model = NULL, regex = TRUE, ...)
printAvailableMethods()
```
Arguments

model  a character string indicating the name of classification model. If NULL, all the available methods from MLSeq is returned. Otherwise, the methods which are complete or partial matches to requested string is returned. See regex for details.

regex a logical: should a regular expressions be used? If FALSE, a simple match is conducted against the whole name of the model.

Details

There are 200+ methods available in caret. We import approximately 85 methods which are available for "classification" task. Some of these methods are available for both classification and regression tasks. availableMethods() returns a character vector of available methods in MLSeq. These names are directly used in classify function with argument method. See http://topepo.github.io/caret/available-models.html for a complete list of available methods in caret. Run printAvailableMethods() to print detailed information about classification methods (prints to R Console).

Value

a requested or complete character vector of available methods.

Note

Available methods in MLSeq will be regularly updated. Some of the methods might be removed as well as some others took its place in MLSeq. Please check the available methods before fitting the model. This function is inspired from the function getModelInfo() in caret and some of the code chunks and help texts are used here.

See Also

classify, getModelInfo, train

cervical

Cervical cancer data

Description

Cervical cancer data measures the expressions of 714 miRNAs of human samples. There are 29 tumor and 29 non-tumor cervical samples and these two groups are treated as two separate classes.

Format

A data frame with 58 observations and 714 variables (i.e. miRNAs of human samples).
classify

Fitting classification models to sequencing data

Description

This function fits classification algorithms to sequencing data and measures model performances using various statistics.

Usage

classify(
  data,
  method = "rpart",
  B = 25,
  ref = NULL,
  class.labels = NULL,
  preProcessing = c("deseq-vst", "deseq-rlog", "deseq-logcpm", "tmm-logcpm", "logcpm"),
  normalize = c("deseq", "TMM", "none"),
  control = NULL,
  ...
)

Arguments

data a DESeqDataSet object, see the constructor functions DESeqDataSet, DESeqDataSetFromMatrix, DESeqDataSetFromHTSeqCount in DESeq2 package.

method a character string indicating the name of classification method. Methods are implemented from the caret package. Run availableMethods() for a list of available methods.

B an integer. It is the number of bootstrap samples for bagging classifiers, for example "bagFDA" and "treebag". Default is 25.
classify

ref         a character string indicating the user defined reference class. Default is NULL. If
NULL is selected, first category of class labels is used as reference.

class.labels a character string indicating the column name of colData(...). Should be given
as "character". The column from colData() which matches with given column
name is used as class labels of samples. If NULL, first column is used as class
labels. Default is NULL.

preProcessing a character string indicating the name of the preprocessing method. This option
consists both the normalization and transformation of the raw sequencing data. Available options are:

•  deseq-vst: Normalization is applied with deseq median ratio method.  
   Variance stabilizing transformation is applied to the normalized data.
•  deseq-rlog: Normalization is applied with deseq median ratio method.  
   Regularized logarithmic transformation is applied to the normalized data.
•  deseq-logcpm: Normalization is applied with deseq median ratio method.  
   Log of counts-per-million transformation is applied to the normalized data.
•  tmm-logcpm: Normalization is applied with trimmed mean of M values (TMM) method. Log of counts-per-million transformation is applied to the
   normalized data.
•  logcpm: Normalization is not applied. Log of counts-per-million transfor-
   mation is used for the raw counts.

IMPORTANT: See Details for further information.

normalize a character string indicating the type of normalization. Should be one of 'deseq',  
'tmm' and 'none'. Default is 'deseq'. This option should be used with discrete
and voom-based classifiers since no transformation is applied on raw counts. For
caret-based classifiers, the argument 'preProcessing' should be used.

control a list including all the control parameters passed to model training process. This
argument should be defined using wrapper functions trainControl for caret-
based classifiers, discreteControl for discrete classifiers (PLDA, PLDA2 and
NBLDA) and voomControl for voom-based classifiers (voomDLDA, voomDQDA
and voomNSC). See related functions for further details.

... optional arguments passed to selected classifiers.

Details

MLSeq consists both microarray-based and discrete-based classifiers along with the preprocessing
approaches. These approaches include both normalization techniques, i.e. deseq median ratio (An-
der et al., 2010) and trimmed mean of M values (Robinson et al., 2010) normalization methods,
and the transformation techniques, i.e. variance- stabilizing transformation (vst)(Anders and Hu-
ber, 2010), regularized logarithmic transformation (rlog)(Love et al., 2014), logarithm of counts per
million reads (log-cpm)(Robinson et al., 2010) and variance modeling at observational level
(voom)(Law et al., 2014). Users can directly upload their raw RNA-Seq count data, preprocess
their data, build one of the numerous classification models, optimize the model parameters and
evaluate the model performances.

MLSeq package consists of a variety of classification algorithms for the classification of RNA-Seq
data. These classifiers are categorized into two class: i) microarray-based classifiers after proper
transformation, ii) discrete-based classifiers. First option is to transform the RNA-Seq data to bring
classify

it hierarchically closer to microarrays and apply microarray-based algorithms. These methods are implemented from the caret package. Run availableMethods() for a list of available methods. Note that voom transformation both exports transformed gene-expression matrix as well as the precision weight matrices in same dimension. Hence, the classifier should consider these two matrices. Zararsiz (2015) presented voom-based diagonal discriminant classifiers and the sparse voom-based nearest shrunken centroids classifier. Second option is to build new discrete-based classifiers to classify RNA-Seq data. Two methods are currently available in the literature. Witten (2011) considered modeling these counts with Poisson distribution and proposed sparse Poisson linear discriminant analysis (PLDA) classifier. The authors suggested a power transformation to deal with the overdispersion problem. Dong et al. (2016) extended this approach into a negative binomial linear discriminant analysis (NBLDA) classifier. More detailed information can be found in referenced papers.

Value

an MLSeq object for trained model.

Author(s)

Dincer Goksuluk, Gokmen Zararsiz, Selcuk Korkmaz, Vahap Eldem, Ahmet Ozturk and Ahmet Ergun Karaagaoglu

References


See Also

predictClassify, train, trainControl, voomControl, discreteControl
Examples

## Not run:
library(DESeq2)
data(cervical)

# a subset of cervical data with first 150 features.
data <- cervical[c(1:150), ]

# defining sample classes.
class <- data.frame(condition = factor(rep(c("N","T"), c(29, 29))))

n <- ncol(data) # number of samples
p <- nrow(data) # number of features

# number of samples for test set (30% test, 70% train).
nTest <- ceiling(n*0.3)
ind <- sample(n, nTest, FALSE)

# train set
data.train <- data[-ind]
data.train <- as.matrix(data.train + 1)
classstr <- data.frame(condition = class[-ind, ])

data.trainS4 <- DESeqDataSetFromMatrix(countData = data.train,
colData = classstr, formula(~ 1))

## Number of repeats (repeats) might change model accuracies
## 1. caret-based classifiers:
# Random Forest (RF) Classification
rf <- classify(data = data.trainS4, method = "rf",
   preProcessing = "deseq-vst", ref = "T",
   control = trainControl(method = "repeatedcv", number = 5,
                           repeats = 2, classProbs = TRUE))

rf

# 2. Discrete classifiers:
# Poisson Linear Discriminant Analysis
pmodel <- classify(data = data.trainS4, method = "PLDA", ref = "T",
   class.labels = "condition", normalize = "deseq",
   control = discreteControl(number = 5, repeats = 2,
                            tuneLength = 10, parallel = TRUE))
pmodel

# 3. voom-based classifiers:
# voom-based Nearest Shrunken Centroids
vmodel <- classify(data = data.trainS4, normalize = "deseq",
   method = "voomNSC", class.labels = "condition", ref = "T",
   control = voomControl(number = 5, repeats = 2, tuneLength = 10))
vmodel

## End(Not run)
confusionMat

Accessors for the 'confusionMat' slot.

Description
This slot stores the confusion matrix for the trained model using classify function.

Usage
confusionMat(object)
## S4 method for signature 'MLSeq'
confusionMat(object)
## S4 method for signature 'MLSeqModelInfo'
confusionMat(object)

Arguments
object an MLSeq or MLSeqModelInfo object.

Details
cfconfusionMat slot includes information about cross-tabulation of observed and predicted classes and corresponding statistics such as accuracy rate, sensitivity, specificity, etc. The returned object is in confusionMatrix class of caret package. See confusionMatrix for details.

See Also
confusionMatrix

Examples
## Not run:
library(DESeq2)
data(cervical)

# a subset of cervical data with first 150 features.
data <- cervical[c(1:150), ]

# defining sample classes.
class <- data.frame(condition = factor(rep(c("N","T"), c(29, 29))))

n <- ncol(data)  # number of samples
p <- nrow(data)  # number of features

# number of samples for test set (30% test, 70% train).
nTest <- ceiling(n*0.3)
ind <- sample(n, nTest, FALSE)

# train set
data.train <- data[,-ind]
data.train <- as.matrix(data.train + 1)
classtr <- data.frame(condition = class[-ind, ])

# train set in S4 class
data.trainS4 <- DESeqDataSetFromMatrix(countData = data.train,
    colData = classtr, formula(~ 1))

## Number of repeats (repeats) might change model accuracies ##
# Classification and Regression Tree (CART) Classification
cart <- classify(data = data.trainS4, method = "rpart",
    ref = "T", preProcessing = "deseq-vst",
    control = trainControl(method = "repeatedcv", number = 5,
        repeats = 3, classProbs = TRUE))

confusionMat(cart)

## End(Not run)

classical :: Accessors for the 'control' slot.

Description

This slot stores the information about control parameters of selected classification model.

Usage

control(object)
control(object) <- value

## S4 method for signature 'MLSeq'
control(object)

## S4 replacement method for signature 'MLSeq,list'
control(object) <- value

Arguments

object an MLSeq or MLSeqModelInfo object.

value a list with elements for controlling trained model. It should be a list returned from one of discreteControl, voomControl, trainControl functions.
discrete.train-class

See Also
discreteControl, voomControl, trainControl

Examples

## Not run:
library(DESeq2)
data(cervical)

# a subset of cervical data with first 150 features.
data <- cervical[c(1:150), ,]

# defining sample classes.
class <- data.frame(condition = factor(rep(c("N","T"), c(29, 29))))

n <- ncol(data) # number of samples
p <- nrow(data) # number of features

# number of samples for test set (30% test, 70% train).
nTest <- ceiling(n*0.3)
ind <- sample(n, nTest, FALSE)

# train set
data.train <- data[,] -ind]
data.train <- as.matrix(data.train + 1)
classstr <- data.frame(condition = class[-ind, ,]

# train set in S4 class
data.trainS4 <- DESeqDataSetFromMatrix(countData = data.train,
colData = classstr, formula(~ 1))

## Number of repeats (repeats) might change model accuracies ##
# Classification and Regression Tree (CART) Classification
cart <- classify(data = data.trainS4, method = "rpart",
ref = "T", preProcessing = "deseq-vst",
control = trainControl(method = "repeatedcv", number = 5,
repeats = 3, classProbs = TRUE))

control(cart)

## End(Not run)

discrete.train-class discrete.train object

Description

This object is the subclass for the MLSeq.train class. It contains trained model information for discrete classifiers such as Poisson Linear Discriminant Analysis (PLDA) and Negative Binomial Linear Discriminant Analysis (NBLDA).
discreteControl

Slots
inputs: a list with elements used as input for classification task.
control: a list with control parameters for discrete classifiers, e.g. PLDA, PLDA2 and NBLDA.
crossValidatedModel: a list. It stores the results for cross validation.
finalModel: a list. This is the trained model with optimum parameters.
tuningResults: a list. It stores the results for tuning parameter if selected classifier has one or more parameters to be optimized.
callInfo: a list. call info for selected method.

| discreteControl       | Define controlling parameters for discrete classifiers (NBLDA and PLDA) |

Description
This function sets the control parameters for discrete classifiers (PLDA and NBLDA) while training the model.

Usage

discreteControl(
  method = "repeatedcv",
  number = 5,
  repeats = 10,
  rho = NULL,
  rhos = NULL,
  beta = 1,
  prior = NULL,
  alpha = NULL,
  truephi = NULL,
  foldIdx = NULL,
  tuneLength = 30,
  parallel = FALSE,
  ...
)

Arguments

method validation method. Support repeated cross validation only ("repeatedcv").
number a positive integer. Number of folds.
repeats a positive integer. Number of repeats.
rho a single numeric value. This parameter is used as tuning parameter in PLDA classifier. It does not effect NBLDA classifier.
**input**

Accessors for the 'inputObject' slot of an MLSeq object

---

**Description**

MLSeq package benefits from DESeqDataSet structure from bioconductor package DESeq2 for storing gene expression data in a comprehensive structure. This object is used as an input for classification task through `classify`. The input is stored in `inputObject` slot of MLSeq object.

**Usage**

```r
input(object)
```

## S4 method for signature 'MLSeq'

```r
input(object)
```
Arguments

doctarget an MLSeq object.

See Also

classify, DESeqDataSet

Examples

```r
## Not run:
library(DESeq2)
data(cervical)

# a subset of cervical data with first 150 features.
data <- cervical[c(1:150),]

# defining sample classes.
class <- data.frame(condition = factor(rep(c("N","T"), c(29, 29))))

n <- ncol(data) # number of samples
p <- nrow(data) # number of features

# number of samples for test set (30% test, 70% train).
nTest <- ceiling(n*0.3)
ind <- sample(n, nTest, FALSE)

# train set
data.train <- data[,-ind]
data.train <- as.matrix(data.train + 1)
classstr <- data.frame(condition = class[-ind,])

data.trainS4 <- DESeqDataSetFromMatrix(countData = data.train,
colData = classstr, formula(~ 1))

## Number of repeats (repeats) might change model accuracies ##
# Classification and Regression Tree (CART) Classification
cart <- classify(data = data.trainS4, method = "rpart",
ref = "T", preProcessing = "deseq-vst",
control = trainControl(method = "repeatedcv", number = 5,
repeats = 3, classProbs = TRUE))

input(cart)

## End(Not run)
```
isUpdated

Checks if MLSeq object is updated/modified or not.

Description

These functions are used to check whether the MLSeq object is modified and/or updated. It is possible to update classification parameters of MLSeq object which is returned by `classify()` function.

Usage

isUpdated(object)

isUpdated(object) <- value

isModified(object)

isModified(object) <- value

## S4 method for signature 'MLSeq'

isUpdated(object)

## S4 replacement method for signature 'MLSeq,logical'

isUpdated(object) <- value

## S4 method for signature 'MLSeq'

isModified(object)

## S4 replacement method for signature 'MLSeq,logical'

isModified(object) <- value

Arguments

object     an MLSeq object.

value      a logical. Change the state of update info.

Value

a logical.

Examples

## Not run:
library(DESeq2)
data(cervical)

# a subset of cervical data with first 150 features.
data <- cervical[c(1:150), ]
# defining sample classes.
class <- data.frame(condition = factor(rep(c("N","T"), c(29, 29))))

n <- ncol(data) # number of samples
p <- nrow(data) # number of features

# number of samples for test set (30% test, 70% train).
ntest <- ceiling(n*0.3)
ind <- sample(n, ntest, FALSE)

# train set
data.train <- data[ , -ind]
data.train <- as.matrix(data.train + 1)
classtr <- data.frame(condition = class[-ind, ])

# train set in S4 class
data.trainS4 <- DESeqDataSetFromMatrix(countData = data.train,
colData = classtr, formula(~ 1))

## Number of repeats (repeats) might change model accuracies ##
# Classification and Regression Tree (CART) Classification
cart <- classify(data = data.trainS4, method = "rpart",
ref = "T", preProcessing = "deseq-vst",
control = trainControl(method = "repeatedcv", number = 5,
repeats = 3, classProbs = TRUE))

isUpdated(cart)
isModified(cart)

## End(Not run)
method

Examples

```
## Not run:
library(DESeq2)
data(cervical)

# a subset of cervical data with first 150 features.
data <- cervical[c(1:150), ]

# defining sample classes.
class <- data.frame(condition = factor(rep(c("N","T"), c(29, 29))))

n <- ncol(data)  # number of samples
p <- nrow(data)  # number of features

# number of samples for test set (30% test, 70% train).
nTest <- ceiling(n*0.3)
ind <- sample(n, nTest, FALSE)

# train set
data.train <- data[,-ind]
data.train <- as.matrix(data.train + 1)
classstr <- data.frame(condition = class[-ind, ])

# train set in S4 class
data.trainS4 <- DESeqDataSetFromMatrix(countData = data.train,
                                      colData = classstr, formula(~ 1))

## Number of repeats (repeats) might change model accuracies ##
# Classification and Regression Tree (CART) Classification
cart <- classify(data = data.trainS4, method = "rpart",
                 ref = "T", preProcessing = "deseq-vst",
                 control = trainControl(method = "repeatedcv", number = 5,
                                         repeats = 3, classProbs = TRUE))

metaData(cart)

## End(Not run)
```

method

Accessors for the 'method'.

Description

This slot stores the name of selected model which is used in classify function. The trained model is stored in slot trainedModel. See trained for details.
**Usage**

```r
method(object)
method(object) <- value
```

## S4 method for signature 'MLSeq'

```r
method(object)
```

## S4 method for signature 'MLSeqModelInfo'

```r
method(object)
```

## S4 replacement method for signature 'MLSeq,character'

```r
method(object) <- value
```

**Arguments**

- **object**: an MLSeq object.
- **value**: a character string. One of the available classification methods to replace with current method stored in MLSeq object.

**Details**

The `method` slot stores the name of the classification method such as "svmRadial" for Radial-based Support Vector Machines, "rf" for Random Forests, "voomNSC" for voom-based Nearest Shrunken Centroids, etc. For the complete list of available methods, see `printAvailableMethods` and `availableMethods`.

**See Also**

- `trained`

**Examples**

```r
## Not run:
library(DESeq2)
data(cervical)

# a subset of cervical data with first 150 features.
data <- cervical[c(1:150), ]

# defining sample classes.
class <- data.frame(condition = factor(rep(c("N","T"), c(29, 29))))

n <- ncol(data)  # number of samples
p <- nrow(data)  # number of features

# number of samples for test set (30% test, 70% train).
nTest <- ceiling(n*0.3)
ind <- sample(n, nTest, FALSE)
```
### MLSeq-class

For classification, this is the main class for the MLSeq package. It contains all the information including trained model, selected genes, cross-validation results, etc.

#### Details

Objects can be created by calls of the form `new("MLSeq", ...)`. This type of objects is created as a result of `classify` function of MLSeq package. It is then used in `predict` or `predictClassify` function for predicting the class labels of new samples.

#### Slots

- `inputObject`: stores the data in `DESeqDataSet` object.
- `modelInfo`: stores all the information about classification model. The object is from subclass `MLSeqModelInfo`. See `MLSeqModelInfo-class` for details.
- `metaData`: metadata for MLSeq object. The object is from subclass `MLSeqMetaData`. See `MLSeqMetaData-class` for details.

#### Note

An MLSeq class stores the results of `classify` function and offers further slots that are populated during the analysis. The slot `inputObject` stores the raw and transformed data throughout the classification. The slot `modelInfo` stores all the information about classification model. These results...
may contain the classification table and performance measures such as accuracy rate, sensitivity, specificity, positive and negative predictive values, etc. It also contains information on classification method, normalization and transformation used in the classification model. Lastly, the slot metaData stores the information about modified or updated slots in MLSeq object.

Author(s)
Dincer Goksuluk, Gokmen Zararsiz, Selcuk Korkmaz, Vahap Eldem, Ahmet Ozturk and Ahmet Ergun Karaagaoglu

See Also
MLSeqModelInfo-class, MLSeqMetaData-class

Description
This object is a subclass for the MLSeq class. It contains metadata information, i.e., information on modified and/or updated elements, raw data etc..

Details
Objects can be created by calls of the form new("MLSeqMetaData", ...). This type of objects is created as a result of classify function of MLSeq package. It is then used in update function for updating the object in given object.

Slots
updated, modified: a logical. See notes for details.
modified.elements: a list containing the modified elements in MLSeq object.
rawData.DESeqDataSet: raw data which is used for classification.
classLabel: a character string indicating the name of class variable.

Note
The function update is used to re-run classification task with modified elements in MLSeq object. This function is useful when one wish to perform classification task with modified options without running classify function from the beginning. MLSeqMetaData object is used to store information on updated and/or modified elements in MLSeq object.

If an MLSeq object is modified, i.e. one or more elements in MLSeq object is replaced using related setter functions such as method, ref etc., the slot modified becomes TRUE. Similarly, the slot updated stores the information that the MLSeq object is updated (or classification task is re-runned) or not. If updated slot is FALSE and modified slot is TRUE, one should run update to obtain the classification results by considering the modified elements.
**MLSeqModelInfo-class**

**Description**

For classification, this is the subclass for the MLSeq class. This object contains all the information about classification model.

**Details**

Objects can be created by calls of the form `MLSeqModelInfo(...)`. This type of objects is created as a result of `classify` function of MLSeq package. It is then used in `predictClassify` function for predicting the class labels of new samples.

**Slots**

- `method`, `transformation`, `normalization`: these slots store the classification method, transformation technique and normalization method respectively. See notes for details.
- `preProcessing`: See `classify` for details.
- `ref`: a character string indicating the reference category for cases (diseased subject, tumor sample, etc.)
- `control`: a list with controlling parameters for classification task.
- `confusionMat`: confusion table and accuracy measures for the predictions.
- `trainedModel`: an object of `MLSeq.train` class. It contains the trained model. See notes for details.
- `trainParameters`: a list with training parameters from final model. These parameters are used for test set before predicting class labels.
- `call`: a call object for classification task.

**Note**

`method`, `transformation`, `normalization` slots give the information on classifier, transformation and normalization techniques. Since all possible pairs of transformation and normalization are not available in practice, we specify appropriate transformations and normalization techniques with `preProcessing` argument in `classify` function. Finally, the information on normalization and transformation is extracted from `preProcessing` argument.

`MLSeq.train` is a union class of `train` from caret package, `voom.train` and `discrete.train` from MLSeq package. See related class manuals for details.

**See Also**

`update`, `isUpdated`, `isModified`
modelInfo

Accessors for the ‘modelInfo’ slot of an MLSeq object

Description

This slot stores all the information about classification model.

Usage

modelInfo(object)

## S4 method for signature 'MLSeq'
modelInfo(object)

Arguments

object an MLSeq object.

Examples

## Not run:
library(DESeq2)
data(cervical)

# a subset of cervical data with first 150 features.
data <- cervical[c(1:150), ]

# defining sample classes.
class <- data.frame(condition = factor(rep(c("N","T"), c(29, 29))))

n <- ncol(data) # number of samples
p <- nrow(data) # number of features

# number of samples for test set (30% test, 70% train).
nTest <- ceiling(n*0.3)
ind <- sample(n, nTest, FALSE)

# train set
data.train <- data[,-ind]
data.train <- as.matrix(data.train + 1)
classtr <- data.frame(condition = class[-ind, ])

# train set in S4 class
data.trainS4 <- DESeqDataSetFromMatrix(countData = data.train,
colData = classtr, formula(~ 1))

## Number of repeats (repeats) might change model accuracies ##
# Classification and Regression Tree (CART) Classification
cart <- classify(data = data.trainS4, method = "rpart",
ref = "T", preProcessing = "deseq-vst",

---

---
control = trainControl(method = "repeatedcv", number = 5,
repeat = 3, classProbs = TRUE))

modelInfo(cart)

## End(Not run)

normalization

Accessors for the 'normalization' slot.

Description

This slot stores the name of normalization method which is used while normalizing the count data such as "deseq", "tmm" or "none"

Usage

normalization(object)

normalization(object) <- value

## S4 method for signature 'MLSeq'
normalization(object)

## S4 method for signature 'MLSeqModelInfo'
normalization(object)

## S4 replacement method for signature 'MLSeq,character'
normalization(object) <- value

Arguments

object an MLSeq or MLSeqModelInfo object.
value a character string. One of the available normalization methods for voom-based classifiers.

Examples

## Not run:
library(DESeq2)
data(cervical)

# a subset of cervical data with first 150 features.
data <- cervical[c(1:150), ]

# defining sample classes.
class <- data.frame(condition = factor(rep(c("N","T"), c(29, 29))))
n <- ncol(data)  # number of samples
p <- nrow(data)  # number of features

# number of samples for test set (30% test, 70% train).
nTest <- ceiling(n*0.3)
ind <- sample(n, nTest, FALSE)

# train set
data.train <- data[, -ind]
data.train <- as.matrix(data.train + 1)
classstr <- data.frame(condition = class[-ind, ])

# train set in S4 class
data.trainS4 <- DESeqDataSetFromMatrix(countData = data.train,
colData = classstr, formula(~ 1))

## Number of repeats (repeats) might change model accuracies ##
# Classification and Regression Tree (CART) Classification
cart <- classify(data = data.trainS4, method = "rpart",
                 ref = "T", preProcessing = "deseq-vst",
                 control = trainControl(method = "repeatedcv", number = 5,
                                            repeats = 3, classProbs = TRUE))

normalization(cart)

## End(Not run)##

---

**plot**

*Plot accuracy results from 'MLSeq' object*

**Description**

This generic function is used to plot accuracy results from 'MLSeq' object returned by classify function.

**Usage**

```r
## S3 method for class 'MLSeq'
plot(x, y, ...)

## S4 method for signature 'MLSeq,ANY'
plot(x, y, ...)
```

**Arguments**

- `x` an MLSeq object returned from classify function.
- `y` this parameter is not used. Deprecated.
- `...` further arguments. Deprecated.
**Author(s)**
Dincer Goksuluk, Gokmen Zararsiz, Selcuk Korkmaz, Vahap Eldem, Ahmet Ozturk and Ahmet Ergun Karaagaoglu

**Description**
This function predicts the class labels of test data for a given model.

`predictClassify` and `predict` functions return the predicted class information along with trained model. Predicted values are given either as class labels or estimated probabilities of each class for each sample. If `type = "raw"`, as can be seen in the example below, the predictions are extracted as raw class labels. In order to extract estimated class probabilities, one should follow the steps below:

- set `classProbs = TRUE` within control argument in `classify`
- set `type = "prob"` within `predictClassify`

**Usage**
```r
## S3 method for class 'MLSeq'
predict(object, test.data, ...)
predictClassify(object, test.data, ...)
## S4 method for signature 'MLSeq'
predict(object, test.data, ...)
```

**Arguments**
- `object` a model of MLSeq class returned by `classify`
- `test.data` a DESeqDataSet instance of new observations.
- `...` further arguments to be passed to or from methods. These arguments are used in `predict.train` from caret package.

**Value**
- `MLSeqObject` an MLSeq object returned from `classify`. See details.
- `Predictions` a data frame or vector including either the predicted class probabilities or class labels of given test data.

**Note**
predictClassify(...) function was used in MLSeq up to package version 1.14.x. This function is aliased with generic function `predict`. In the upcoming versions of MLSeq package, predictClassify function will be omitted. Default function for predicting new observations will be `predict` from version 1.16.x and later.
## Not run:
library(DESeq2)
data(cervical)

# a subset of cervical data with first 150 features.
data <- cervical[,1:150,]

# defining sample classes.
class <- data.frame(condition = factor(rep(c("N","T"), c(29, 29))))

n <- ncol(data) # number of samples
p <- nrow(data) # number of features

# number of samples for test set (30% test, 70% train).
nTest <- ceiling(n*0.3)
ind <- sample(n, nTest, FALSE)

# train set
data.train <- data[, -ind]
data.train <- as.matrix(data.train + 1)
classtr <- data.frame(condition = class[-ind, ])

# train set in S4 class
data.trainS4 <- DESeqDataSetFromMatrix(countData = data.train,
colData = classtr, formula(~ 1))

# test set
data.test <- data[, ind]
data.test <- as.matrix(data.test + 1)
classt <- data.frame(condition = class[ind, ])

data.testS4 <- DESeqDataSetFromMatrix(countData = data.test,
colData = classt, formula(~ 1))

## Number of repeats (repeats) might change model accuracies ##
# Classification and Regression Tree (CART) Classification
cart <- classify(data = data.trainS4, method = "rpart",
ref = "T", preProcessing = "deseq-vst",
control = trainControl(method = "repeatedcv", number = 5,
repeats = 3, classProbs = TRUE))
cart
```r
# predicted classes of test samples for CART method (class probabilities)
pred.cart = predictClassify(cart, data.testS4, type = "prob")
pred.cart

# predicted classes of test samples for RF method (class labels)
pred.cart = predictClassify(cart, data.testS4, type = "raw")
pred.cart

## End(Not run)
```

---

### preProcessing

**Accessors for the ‘preProcessing’ slot of an MLSeq object**

#### Description

MLSeq package benefits from DESeqDataSet structure from bioconductor package DESeq2 for storing gene expression data in a comprehensive structure. This object is used as an input for classification task through `classify`. The input is stored in `inputObject` slot of MLSeq object.

#### Usage

```r
preProcessing(object)

preProcessing(object) <- value
```

#### Arguments

- `object`  
  an MLSeq object.

- `value`  
  a character string. Which preProcessing should be replaced with current one?

#### See Also

`classify`, `DESeqDataSet`

#### Examples

```r
## Not run:
library(DESeq2)
data(cervical)

data(cervical)

# a subset of cervical data with first 150 features.
```
```r
data <- cervical[c(1:150), ]

# defining sample classes.
class <- data.frame(condition = factor(rep(c("N","T"), c(29, 29))))

n <- ncol(data)  # number of samples
p <- nrow(data)  # number of features

# number of samples for test set (30% test, 70% train).
nTest <- ceiling(n*0.3)
ind <- sample(n, nTest, FALSE)

# train set
data.train <- data[, -ind]
data.train <- as.matrix(data.train + 1)
classtr <- data.frame(condition = class[-ind, ])

# train set in S4 class
data.trainS4 <- DESeqDataSetFromMatrix(countData = data.train, colData = classtr, formula(~ 1))

## Number of repeats (repeats) might change model accuracies ##
# Classification and Regression Tree (CART) Classification
cart <- classify(data = data.trainS4, method = "rpart", ref = "T", preProcessing = "deseq-vst", control = trainControl(method = "repeatedcv", number = 5, repeats = 3, classProbs = TRUE))

preProcessing(cart)

## End(Not run)
```

### print.confMat

**Print method for confusion matrix**

**Description**

This function prints the confusion matrix of the model.

**Usage**

```r
## S3 method for class 'confMat'
print(x, ..., mode = x$mode, digits = max(3,getOption("digits") - 3))

## S4 method for signature 'confMat'
print(x, ..., mode = x$mode, digits = max(3,getOption("digits") - 3))
```
Arguments

- \texttt{x} \hspace{1cm} an object of class \texttt{confMat}
- \texttt{...} \hspace{1cm} further arguments to be passed to \texttt{print.table}
- \texttt{mode} \hspace{1cm} see \texttt{print.confusionMatrix}
- \texttt{digits} \hspace{1cm} see \texttt{print.confusionMatrix}

\begin{description}
\item[ref] Accessors for the \texttt{ref} slot.
\end{description}

Description

This slot stores the information about reference category. Confusion matrix and related statistics are calculated using the user-defined reference category.

Usage

\begin{verbatim}
ref(object)
ref(object) <- value
\end{verbatim}

## S4 method for signature 'MLSeq'
ref(object)

## S4 method for signature 'MLSeqModelInfo'
ref(object)

## S4 replacement method for signature 'MLSeq,character'
ref(object) <- value

Arguments

- \texttt{object} \hspace{1cm} an MLSeq or MLSeqModelInfo object.
- \texttt{value} \hspace{1cm} a character string. Select reference category for class labels.

Examples

\begin{verbatim}
## Not run:
library(DESeq2)
data(cervical)

# a subset of cervical data with first 150 features.
data <- cervical[1:150,]

# defining sample classes.
class <- data.frame(condition = factor(rep(c("N","T"), c(29, 29))))
\end{verbatim}
n <- ncol(data)  # number of samples
p <- nrow(data)  # number of features

# number of samples for test set (30% test, 70% train).
nTest <- ceiling(n*0.3)
ind <- sample(n, nTest, FALSE)

# train set
data.train <- data[, -ind]
data.train <- as.matrix(data.train + 1)
classtr <- data.frame(condition = class[-ind, ])

# train set in S4 class
data.trainS4 <- DESeqDataSetFromMatrix(countData = data.train,
           colData = classtr, formula(~ 1))

## Number of repeats (repeats) might change model accuracies ##
# Classification and Regression Tree (CART) Classification
cart <- classify(data = data.trainS4, method = "rpart",
               ref = "T", preProcessing = "deseq-vst",
               control = trainControl(method = "repeatedcv", number = 5,
                                       repeats = 3, classProbs = TRUE))

ref(cart)

## End(Not run)##

-----

**selectedGenes**

*Accessors for the 'selectedGenes'.*

**Description**

This slot stores the name of selected genes which are used in the classifier. The trained model is stored in slot `trainedModel`. See `trained` for details.

**Usage**

```r
selectedGenes(object)
```

```r
## S4 method for signature 'MLSeq'
selectedGenes(object)
```

**Arguments**

- `object` an MLSeq object.

**See Also**

- `trained`
## Examples

```r
## Not run:
library(DESeq2)
data(cervical)

# a subset of cervical data with first 150 features.
data <- cervical[c(1:150), ]

# defining sample classes.
class <- data.frame(condition = factor(rep(c("N","T"), c(29, 29))))

n <- ncol(data) # number of samples
p <- nrow(data) # number of features

# number of samples for test set (30% test, 70% train).
nTest <- ceiling(n*0.3)
ind <- sample(n, nTest, FALSE)

# train set
data.train <- data[,-ind]
data.train <- as.matrix(data.train + 1)
classtr <- data.frame(condition = class[-ind, ])

# train set in S4 class
data.trainS4 <- DESeqDataSetFromMatrix(countData = data.train,
colData = classtr, formula(~ 1))

## Number of repeats (repeats) might change model accuracies ##
# Classification and Regression Tree (CART) Classification
cart <- classify(data = data.trainS4, method = "rpart",
ref = "T", preProcessing = "deseq-vst",
control = trainControl(method = "repeatedcv", number = 5,
repeats = 3, classProbs = TRUE))

selectedGenes(cart)

## End(Not run)
```

---

**show**  
*Show method for MLSeq objects*

**Description**  
Prints out the information from the trained model using classify function.

**Usage**  
`show.MLSeq(object)`
## S4 method for signature 'MLSeq'
show(object)

## S4 method for signature 'MLSeqModelInfo'
show(object)

## S4 method for signature 'MLSeqMetaData'
show(object)

## S4 method for signature 'voom.train'
show(object)

## S4 method for signature 'discrete.train'
show(object)

### Arguments

object an MLSeq object returned from classify function.

### See Also

classify

### Description

This slot stores the trained model. This object is returned from train function in caret package. Any further request using caret functions is available for trainedModel since this object is in the same class as the returned object from train. See train for details.

### Usage

trained(object)

## S4 method for signature 'MLSeq'
trained(object)

## S4 method for signature 'MLSeqModelInfo'
trained(object)

### Arguments

object an MLSeq or MLSeqModelInfo object.
trainParameters

See Also

train.default, voom.train-class, discrete.train-class

Examples

```r
## Not run:
library(DESeq2)
data(cervical)

# a subset of cervical data with first 150 features.
data <- cervical[c(1:150), ]

# defining sample classes.
class <- data.frame(condition = factor(rep(c("N","T"), c(29, 29))))

n <- ncol(data) # number of samples
p <- nrow(data) # number of features

# number of samples for test set (30% test, 70% train).
NTest <- ceiling(n*0.3)
ind <- sample(n, NTest, FALSE)

# train set
data.train <- data[, -ind]
data.train <- as.matrix(data.train + 1)
classtr <- data.frame(condition = class[-ind, ])

# train set in S4 class
data.trainS4 <- DESeqDataSetFromMatrix(countData = data.train,
                                      colData = classtr, formula(~ 1))

## Number of repeats (repeats) might change model accuracies ##
# Classification and Regression Tree (CART) Classification
cart <- classify(data = data.trainS4, method = "rpart",
                 ref = "T", preProcessing = "deseq-vst",
                 control = trainControl(method = "repeatedcv", number = 5,
                                       repeats = 3, classProbs = TRUE))

trained(cart)

## End(Not run)
```

---

trainParameters

Accessors for the ’trainParameters’ slot.

Description

This slot stores the transformation and normalization parameters from train set. These parameters are used to normalize and transform test set using train set parameters.
trainParameters

Usage

trainParameters(object)

## S4 method for signature 'MLSeq'
trainParameters(object)

## S4 method for signature 'MLSeqModelInfo'
trainParameters(object)

Arguments

object an MLSeq or MLSeqModelInfo object.

Examples

## Not run:
library(DESeq2)
data(cervical)

# a subset of cervical data with first 150 features.
data <- cervical[,c(1:150),]

# defining sample classes.
class <- data.frame(condition = factor(rep(c("N","T"), c(29, 29))))

n <- ncol(data) # number of samples
p <- nrow(data) # number of features

# number of samples for test set (30% test, 70% train).
nTest <- ceiling(n*0.3)
ind <- sample(n, nTest, FALSE)

# train set
data.train <- data[,,-ind]
data.train <- as.matrix(data.train + 1)
classstr <- data.frame(condition = class[-ind,])

# train set in S4 class
data.trainS4 <- DESeqDataSetFromMatrix(countData = data.train, colData = classstr, formula(~ 1))

## Number of repeats (repeats) might change model accuracies ##
# Classification and Regression Tree (CART) Classification
cart <- classify(data = data.trainS4, method = "rpart", ref = "T", preProcessing = "deseq-vst", control = trainControl(method = "repeatedcv", number = 5, repeats = 3, classProbs = TRUE))

trainParameters(cart)

## End(Not run)
transformation

Accessors for the 'transformation' slot.

Description

This slot stores the name of transformation method which is used while transforming the count data (e.g. "vst", "rlog", etc.)

Usage

transformation(object)

## S4 method for signature 'MLSeq'
transformation(object)

## S4 method for signature 'MLSeqModelInfo'
transformation(object)

Arguments

object an MLSeq or MLSeqModelInfo object.

Examples

## Not run:
library(DESeq2)
data(cervical)

# a subset of cervical data with first 150 features.
data <- cervical[1:150, ,]

# defining sample classes.
class <- data.frame(condition = factor(rep(c("N","T"), c(29, 29))))

n <- ncol(data)  # number of samples
p <- nrow(data)  # number of features

# number of samples for test set (30% test, 70% train).
nTest <- ceiling(n*0.3)
ind <- sample(n, nTest, FALSE)

# train set
data.train <- data[, -ind]
data.train <- as.matrix(data.train + 1)
classstr <- data.frame(condition = class[-ind, ])

# train set in S4 class
data.trainS4 <- DESeqDataSetFromMatrix(countData = data.train, 
  colData = classtr, formula(~ 1))

## Number of repeats (repeats) might change model accuracies ##
# Classification and Regression Tree (CART) Classification
cart <- classify(data = data.trainS4, method = "rpart",
  ref = "T", preProcessing = "deseq-vst",
  control = trainControl(method = "repeatedcv", number = 5,
    repeats = 3, classProbs = TRUE))

transformation(cart)

## End(Not run)

---

update

Update MLSeq objects returned from classify()

### Description

This function updates the MLSeq object. If one of the options is changed inside MLSeq object, it should be updated to pass its effects into classification results.

### Usage

```r
## S3 method for class 'MLSeq'
update(object, ..., env = .GlobalEnv)

## S4 method for signature 'MLSeq'
update(object, ..., env = .GlobalEnv)
```

### Arguments

- `object`: a model of MLSeq class returned by `classify`
- `...`: optional arguments passed to `classify` function.
- `env`: an environment. Define the environment where the trained model is stored.

### Value

same object as an MLSeq object returned from `classify`.

### Note

When an MLSeq object is updated, new results are updated on the given object. The results before update process are lost when update is done. To keep the results before update, one should copy the MLSeq object to a new object in global environment.
## Not run:
library(DESeq2)
data(cervical)

# a subset of cervical data with first 150 features.
data <- cervical[c(1:150), ]

# defining sample classes.
class <- data.frame(condition = factor(rep(c("N","T"), c(29, 29))))

n <- ncol(data)  # number of samples
p <- nrow(data)  # number of features

# number of samples for test set (30% test, 70% train).
nTest <- ceiling(n*0.3)
ind <- sample(n, nTest, FALSE)

# train set
data.train <- data[,-ind]
data.train <- as.matrix(data.train + 1)
classtr <- data.frame(condition = class[-ind, ])

data.trainS4 <- DESeqDataSetFromMatrix(countData = data.train,
colData = classtr, formula(~ 1))

# test set
data.test <- data[,ind]
data.test <- as.matrix(data.test + 1)
classts <- data.frame(condition=class[ind, ])

data.testS4 <- DESeqDataSetFromMatrix(countData = data.test,
colData = classts, formula(~ 1))

## Number of repeats (repeats) might change model accuracies ##

# Classification and Regression Tree (CART) Classification
cart <- classify(data = data.trainS4, method = "rpart",
ref = "T", preProcessing = "deseq-vst",
control = trainControl(method = "repeatedcv", number = 5,
repeats = 3, classProbs = TRUE))
cart

# Change classification model into "Random Forests" (rf)
method(cart) <- "rf"
rf <- update(cart)

rf
voomControl

## Description

This object is the subclass for the MLSeq.train class. It contains trained model information for voom based classifiers, i.e. "voomDLDA", "voomDQDA" and "voomNSC".

### Slots

- `weigtedStats`: a list with elements of weighted statistics which are used for training the model. Weights are calculated from voom transformation.
- `foldInfo`: a list containing information on cross-validated folds.
- `control`: a list with control parameters for voom based classifiers.
- `tuningResults`: a list. It stores the cross-validation results for tuning parameter(s).
- `finalModel`: a list. It stores results for trained model with optimum parameters.
- `callInfo`: a list. Call info for related function.

---

### voomControl

Define controlling parameters for voom-based classifiers

### Description

This function sets the control parameters for voom based classifiers while training the model.

### Usage

```r
voomControl(method = "repeatedcv", number = 5, repeats = 10, tuneLength = 10)
```

### Arguments

- `method`: validation method. Support repeated cross validation only ("repeatedcv").
- `number`: a positive integer. Number of folds.
- `repeats`: a positive integer. Number of repeats.
- `tuneLength`: a positive integer. If there is a tuning parameter in the classifier, this value is used to define total number of tuning parameter to be searched.

### Author(s)

Dincer Goksuluk, Gokmen Zararsiz, Selcuk Korkmaz, Vahap Eldem, Ahmet Ozturk and Ahmet Ergun Karaagaoglu
See Also

classify, trainControl, discreteControl

Examples

1L
Index

* RNA-seq
  classify, 5
discreteControl, 12
predict, 25
voomControl, 38
* classification
  classify, 5
discreteControl, 12
predict, 25
voomControl, 38
* package
  MLSeq-package, 3
Available-classifiers, 3
availableMethods, 3, 18
availableMethods
  (Available-classifiers), 3
cervical, 4
classify, 4, 5, 13, 14, 21, 25–27, 32, 36, 37, 39
classify, 5
confusionMat, 9
confusionMat, MLSeq-method
  (confusionMat), 9
confusionMat, MLSeqModelInfo-method
  (confusionMat), 9
confusionMatrix, 9
control, 10
control, MLSeq-method (control), 10
control<-(control), 10
control<-, MLSeq, list-method (control), 10
DESeqDataSet, 5, 14, 19, 27
DESeqDataSetFromHTSeqCount, 5
DESeqDataSetFromMatrix, 5
discrete.train-class, 11
discreteControl, 6, 7, 10, 11, 12, 13, 39
grepl, 4
input, 13
input, MLSeq-method (input), 13
isModified, 21
isModified (isUpdated), 15
isModified, MLSeq-method (isUpdated), 15
isModified<-(isUpdated), 15
isModified<-, MLSeq, logical-method
  (isUpdated), 15
isUpdated, 15, 21
isUpdated, MLSeq-method (isUpdated), 15
isUpdated<-(isUpdated), 15
isUpdated<-, MLSeq, logical-method
  (isUpdated), 15
metaData, 16
metaData, MLSeq-method (metaData), 16
method, 17, 20
method, MLSeq-method (method), 17
method, MLSeqModelInfo-method (method), 17
method<-(method), 17
method<-, MLSeq, character-method
  (method), 17
MLSeq-class, 19
MLSeq-package, 3
MLSeqMetaData-class, 20
MLSeqModelInfo-class, 21
modelInfo, 22
modelInfo, MLSeq-method (modelInfo), 22
normalization, 23
normalization, MLSeq-method
  (normalization), 23
normalization, MLSeqModelInfo-method
  (normalization), 23
normalization<-(normalization), 23
normalization<-, MLSeq, character-method
  (normalization), 23
plot, 24
plot,MLSeq,ANY-method (plot), 24
plot,MLSeq (plot), 24
predict, 19, 25
predict,MLSeq-method (predict), 25
predict,MLSeq (predict), 25
predict.train, 25
predictClassify, 7, 19
predictClassify (predict), 25
preProcessing,MLSeq-method
(preProcessing), 27
preProcessing<- (preProcessing), 27
preProcessing<-,MLSeq,character-method
(preProcessing), 27
print.confMat-method (print.confMat), 28
print.confMat, 28
print.confusionMatrix, 29
printAvailableMethods, 18
printAvailableMethods
(Available-classifiers), 3
ref, 20, 29
ref,MLSeq-method (ref), 29
ref,MLSeqModelInfo-method (ref), 29
ref<- (ref), 29
ref<-,MLSeq,character-method (ref), 29

selectedGenes, 30
selectedGenes,MLSeq-method
(selectedGenes), 30
show, 31
show,discrete.train-method (show), 31
show,MLSeq-method (show), 31
show,MLSeqMetaData-method (show), 31
show,MLSeqModelInfo-method (show), 31
show,voom.train-method (show), 31
show,MLSeq (show), 31

train, 4, 7, 21, 26, 32
train.default, 33
trainControl, 6, 7, 10, 11, 13, 26, 39
trained, 17, 18, 30, 32
trained,MLSeq-method (trained), 32
trained,MLSeqModelInfo-method
(trained), 32
trainParameters, 33
trainParameters,MLSeq-method
(trainParameters), 33

transformation, 35
transformation,MLSeq-method
(transformation), 35
transformation,MLSeqModelInfo-method
(transformation), 35

update, 20, 21, 36
update,MLSeq-method (update), 36
update,MLSeq (update), 36

voom.train-class, 38
voomControl, 6, 7, 10, 11, 38