

Package ‘Modeler’

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Title Classes and Methods for Training and Using Binary Prediction Models

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Suggests Biobase

Description The Modeler package defines classes and methods to learn models and use them to predict binary outcomes. These are generic tools, but also include specific examples for some common classifiers.

License Apache License (== 2.0)

LazyLoad yes

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Modeler-package	<i>Model for classification and regression</i>
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Description

The Modeler package provides generic tools for learning models and making predictions in the context of high-throughput data sets such as those produced by gene expression microarrays. In order to use this package , you must first prepare a pair of functions (one for learning models from training data, and one for making predictions on test data). These functions, along with any required meta-parameters, are used to create an object of the [Modeler-class](#). That object is then passed to the [Modeler](#) function along with the full training data set.

Details

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Author(s)

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See Also

The following classification methods have been adapted to use the Modeler class: K nearest neighbors ([learnKNN](#)), recursive partitioning and regression trees ([learnRPART](#)),

feature.filters	<i>Feature Filtering</i>
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Description

Functions to create functions that filter potential predictive features using statistics that do not access class labels.

Usage

```
filterMean(cutoff)
filterMedian(cutoff)
filterSD(cutoff)
filterMin(cutoff)
filterMax(cutoff)
filterRange(cutoff)
filterIQR(cutoff)
```

Arguments

cutoff	A real number, the level above which features with this statistic should be retained and below which should be discarded.
--------	---

Details

Following the usual conventions introduced from the world of gene expression microarrays, a typical data matrix is constructed from columns representing samples on which we want to make predictions and rows representing the features used to construct the predictive model. In this context, we define a *filter* to be a function that accepts a data matrix as its only argument and returns a logical vector, whose length equals the number of rows in the matrix, where 'TRUE' indicates features that should be retained. Most filtering functions belong to parametrized families, with one of the most common examples being "retain all features whose mean is above some pre-specified cutoff". We implement this idea using a set of function-generating functions, whose arguments are the parameters that pick out the desired member of the family. The return value is an instantiation of a particular filtering function. The decision to define things this way is to be able to apply the methods in cross-validation (or other) loops where we want to ensure that we use the same filtering rule each time.

Value

Each of the seven functions described here return a filter function, *f*, that can be used by `logicalVector <- filter(data, f)`.

Author(s)

Kevin R. Coombes <krc@silicovore.com>

See Also

See [Modeler-class](#) and [Modeler](#) for details about how to perform cross-validation.

Examples

```
set.seed(246391)
data <- matrix(rnorm(1000*30), nrow=1000, ncol=30)
fm <- filterMean(1)
summary(fm(data))

summary(filterMedian(1)(data))
summary(filterSD(1)(data))
```

Description

Functions to create functions that perform feature selection (or at least feature reduction) using statistics that access class labels.

Usage

```
keepAll(data, group)
fsTtest(fdr, ming=500)
fsModifiedFisher(q)
fsPearson(q = NULL, rho)
fsSpearman(q = NULL, rho)
fsMedSplitOddsRatio(q = NULL, OR)
fsChisquared(q = NULL, cutoff)
fsEntropy(q = 0.9, kind=c("information.gain", "gain.ratio", "symmetric.uncertainty"))
fsFisherRandomForest(q)
fsTailRank(specificity=0.9, tolerance=0.5, confidence=0.5)
```

Arguments

data	A matrix containng the data; columns are samples and rows are features.
group	A factor with two levels defining the sample classes.
fdr	A real number between 0 and 1 specifying the target false discovery rate (FDR).
ming	An integer specifiing the minimum number of features to return; overrides the FDR.
q	A real number between 0.5 and 1 specifying the fraction of features to discard.
rho	A real number between 0 and 1 specifying the absolute value of the correlation coefficient used to filter features.
OR	A real number specifying the desired odds ratio for filtering features.
cutoff	A real number specifiyng the targeted cutoff rate when using the statistic to filter features.
kind	The kind of information metric to use for filtering features.
specificity	See TailRankTest .
tolerance	See TailRankTest .
confidence	See TailRankTest .

Details

Following the usual conventions introduced from the world of gene expression microarrays, a typical data matrix is constructed from columns representing samples on which we want to make predictions amd rows representing the features used to construct the predictive model. In this context, we define a *feature selector* or *pruner* to be a function that accepts a data matrix and a two-level factor as its only arguments and returns a logical vector, whose length equals the number of rows in the matrix, where 'TRUE' indicates features that should be retrained. Most pruning functions belong to parametrized families. We implement this idea using a set of function-generating functions,

whose arguments are the parameters that pick out the desired member of the family. The return value is an instantiation of a particular filtering function. The decision to define things this way is to be able to apply the methods in cross-validation (or other) loops where we want to ensure that we use the same feature selection rule each time.

TODO: Describe the various algorithms.

Value

The `keepAll` function is a "pruner"; it takes the data matrix and grouping factor as arguments, and returns a logical vector indicating which features to retain.

Each of the other nine functions described here return uses its arguments to construct and return a pruning function, `f`, that has the same interface as `keepAll`.

Author(s)

Kevin R. Coombes <krc@silicovore.com>

See Also

See [Modeler-class](#) and [Modeler](#) for details about how to perform cross-validation.

Examples

```
set.seed(246391)
data <- matrix(rnorm(1000*36), nrow=1000, ncol=36)
data[1:50, 1:18] <- data[1:50, 1:18] + 1
status <- factor(rep(c("A", "B"), each=18))

fsel <- fsPearson(q = 0.9)
summary(fsel(data, status))
fsel <- fsPearson(rho=0.3)
summary(fsel(data, status))

fsel <- fsEntropy(kind="gain.ratio")
summary(fsel(data, status))
```

FittedModel

Creating FittedModel objects

Description

need a description

Usage

```
FittedModel(predict, data, status, details, ...)
```

Arguments

predict
data
status
details
...

Details

Need some details.

Value

Returns an object of the [FittedModel-class](#).

Author(s)

Kevin R. Coombes <krc@silicovore.com>.

See Also

See the descriptions of the [learn](#) function and the [predict](#) method for details on how to fit models on training data and make predictions on new test data.

See the description of the [Modeler-class](#) for details about the kinds of objects produced by [learn](#).

Examples

```
# right
```

FittedModel-class	Class " <i>FittedModel</i> "
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Description

Objects of this class represent parametrized statistical models (of the [Modeler-class](#)) after they have been fit to a training data set. These objects can be used to [predict](#) binary outcomes on new test data sets.

Objects from the Class

Objects can be created by calls to the constructor function, [FittedModel](#). In practice, however, most [FittedModel](#) objects are created as the result of applying the [learn](#) function to an object of the [Modeler-class](#).

Slots

predictFunction: Object of class "function" that implements the ability to make predictions using the fitted model.

trainData: Object of class "matrix" containing the training data set. Rows are features and columns are samples.

trainStatus: Object of class "vector". Should either be a numeric vector representing outcome or a factor with two levels, containing the classes of the training data set.

details: Object of class "list" containing the fitted parameters for the specific model.

extras: Object of class "list" containing any extra information (such as diagnostics) produced as a result of learning the model from the training data set.

fsVector: Logical vector indicating which features should be retained (TRUE) or discarded (FALSE) after performing feature selection on the training data.

Methods

predict signature(object = "FittedModel"): Predict the binary outcome on a new data set.

Author(s)

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See Also

See [Modeler-class](#) and [learn](#) for details on how to fit a model to data.

See [Modeler-package](#) for a list of the kinds of classifiers that have been adapted for use in this generic framework.

Examples

```
showClass("FittedModel")
```

learn

Learning models from data

Description

The `learn` function provides an abstraction that can be used to fit a binary classification model to a training data set.

Usage

```
learn(model, data, status, prune=keepAll)
```

Arguments

<code>model</code>	An object of the Modeler-class
<code>data</code>	A matrix containing the training data, with rows as features and columns as samples to be classified.
<code>status</code>	A factor, with two levels, containing the known classification of the training data.
<code>prune</code>	A "pruning" function; that is, a function that takes two arguments (a data matrix and a class factor) and returns a logical vector indicating which features to retain.

Details

Objects of the [Modeler-class](#) contain functions to learn models from training data to make predictions on new test data. These functions have to be prepared as pairs, since they have a shared opinion about how to record and use specific details about the parameters of the model. As a result, the learn function is implemented by:

```
learn <- function(model, data, status) {
  model@learn(data, status, model@params, model@predict)
}
```

Value

An object of the [FittedModel-class](#).

Author(s)

Kevin R. Coombes <krc@silicovore.com>

References

See the manual page for the [Modeler-package](#) for a list of related references.

See Also

See [predict](#) for how to make predictions on new test data from an object of the [FittedModel-class](#).

See the manual page for the [Modeler-package](#) for a list of classifiers that have been adapted to work with this cross-validation mechanism.

Examples

```
# set up a generic RPART model
rpart.mod <- Modeler(learnRPART, predictRPART, minsplit=2, minbucket=1)

# simulate fake data
data <- matrix(rnorm(100*20), ncol=20)
status <- factor(rep(c("A", "B"), each=10))

# learn the specific RPART model
fm <- learn(rpart.mod, data, status)

# show the predicted results from the model on the training data
predict(fm)

# set up a nearest neighbor model
knn.mod <- Modeler(learnKNN, predictKNN, k=3)

# fit the 3NN model on the same data
fm3 <- learn(knn.mod, data, status)
# show its performance
predict(fm3)
```


learnCCP

*Fit models and make predictions with a PCA-LR classifier***Description**

These functions are used to apply the generic cross-validation mechanism to a classifier that combines principal component analysis (PCA) with logistic regression (LR).

Usage

```
learnCCP(data, status, params, pfun)
predictCCP(newdata, details, status, ...)
```

Arguments

data	The data matrix, with rows as features ("genes") and columns as the samples to be classified.
status	A factor, with two levels, classifying the samples. The length must equal the number of data columns.
params	A list of additional parameters used by the classifier; see Details.
pfun	The function used to make predictions on new data, using the cross-validated classifier. Should always be set to predictCCP.
newdata	Another data matrix, with the same number of rows as data.
details	A list of additional parameters describing details about the particular classifier; see Details.
...	Optional extra parameters required by the generic "predict" method.

Details

The input arguments to both learnCCP and predictCCP are dictated by the requirements of the general cross-validation mechanism provided by the [Modeler-class](#).

The CCP classifier is similar in spirit to the "supervised principal components" method implemented in the superpc package. We start by performing univariate two-sample t-tests to identify features that are differentially expressed between two groups of training samples. We then set a cutoff to select features using a bound (alpha) on the false discovery rate (FDR). If the number of selected features is smaller than a prespecified goal (minNgenes), then we increase the FDR until we get the desired number of features. Next, we perform PCA on the selected features from the training data. we retain enough principal components (PCs) to explain a prespecified fraction of the variance (perVar). We then fit a logistic regression model using these PCs to predict the binary class of the training data. In order to use this model to make binary predictions, you must specify a prior probability that a sample belongs to the first of the two groups (where the ordering is determined by the levels of the classification factor, status).

In order to fit the model to data, the params argument to the learnCCP function should be a list containing components named alpha, minNgenes, perVar, and prior. It may also contain a logical value called verbose, which controls the amount of information that is output as the algorithm runs.

The result of fitting the model using learnCCP is a member of the [FittedModel-class](#). In addition to storing the prediction function (pfun) and the training data and status, the FittedModel stores those details about the model that are required in order to make predictions of the outcome on

new data. In this case, the details are: the prior probability, the set of selected features (`sel`, a logical vector), the principal component decomposition (`spca`, an object of the [SamplePCA](#) class), the logistic regression model (`mmod`, of class [glm](#)), the number of PCs used (`nCompUsed`) as well as the number of components available (`nCompAvail`) and the number of gene-features selected (`nGenesSelected`). The `details` object is appropriate for sending as the second argument to the `predictCCP` function in order to make predictions with the model on new data. Note that the status vector here is the one used for the *training* data, since the prediction function only uses the *levels* of this factor to make sure that the direction of the predictions is interpreted correctly.

Value

The `learnCCP` function returns an object of the [FittedModel-class](#), representing a CCP classifier that has been fitted on a training data set.

The `predictCCP` function returns a factor containing the predictions of the model when applied to the new data set.

Author(s)

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See Also

See [Modeler-class](#) and [Modeler](#) for details about how to perform cross-validation. See [FittedModel-class](#) and [FittedModel](#) for details about the structure of the object returned by `learnCCP`.

Examples

```
# simulate some data
data <- matrix(rnorm(100*20), ncol=20)
status <- factor(rep(c("A", "B"), each=10))

# set up the parameter list
ccp.params <- list(minNgenes=10, alpha=0.10, perVar=0.80, prior=0.5)

# learn the model
fm <- learnCCP(data, status, ccp.params, predictCCP)

# Make predictions on some new simulated data
newdata <- matrix(rnorm(100*30), ncol=30)
predictCCP(newdata, fm@details, status)
```

learnKNN

Fit models and make predictions with a KNN classifier

Description

These functions are used to apply the generic cross-validation mechanism to a K-nearest neighbors (KNN) classifier.

Usage

```
learnKNN(data, status, params, pfun)
predictKNN(newdata, details, status, ...)
```

Arguments

data	The data matrix, with rows as features and columns as the samples to be classified.
status	A factor, with two levels, classifying the samples. The length must equal the number of data columns.
params	A list of additional parameters used by the classifier; see Details.
pfun	The function used to make predictions on new data, using the cross-validated classifier.
newdata	Another data matrix, with the same number of rows as data.
details	A list of additional parameters describing details about the particular classifier; see Details.
...	Optional extra parameters required by the generic "predict" method.

Details

The input arguments to both `learnKNN` and `predictKNN` are dictated by the requirements of the general cross-validation mechanism provided by the [Modeler-class](#).

The implementation uses the `knn` method from the `class` package. The `params` argument to `learnKNN` must be a list that at least includes the component `k` that specifies the number of neighbors used.

Value

The `learnKNN` function returns an object of the [FittedModel-class](#), logically representing a KNN classifier that has been fitted on a training data set.

The `predictKNN` function returns a factor containing the predictions of the model when applied to the new data set.

Author(s)

Kevin R. Coombes <krc@silicovore.com>

References

- Ripley, B. D. (1996) *Pattern Recognition and Neural Networks*. Cambridge.
 Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

See Also

See [Modeler-class](#) and [Modeler](#) for details about how to perform cross-validation. See [FittedModel-class](#) and [FittedModel](#) for details about the structure of the object returned by `learnPCALR`.

Examples

```
# simulate some data
data <- matrix(rnorm(100*20), ncol=20)
status <- factor(rep(c("A", "B"), each=10))

# set up the parameter list
knn.params <- list(k=5)
```

```
# learn the model
fm <- learnKNN(data, status, knn.params, predictKNN)

# Make predictions on some new simulated data
newdata <- matrix(rnorm(100*30), ncol=30)
predictKNN(newdata, fm@details, status)
```

learnLR

Fit models and make predictions with a logistic regression classifier

Description

These functions are used to apply the generic cross-validation mechanism to a logistic regression (LR) classifier.

Usage

```
learnLR(data, status, params, pfun)
predictLR(newdata, details, status, type = "response", ...)
```

Arguments

data	The data matrix, with rows as features ("genes") and columns as the samples to be classified.
status	A factor, with two levels, classifying the samples. The length must equal the number of data columns.
params	A list of additional parameters used by the classifier; see Details.
pfun	The function used to make predictions on new data, using the cross-validated classifier. Should always be set to predictLR.
newdata	Another data matrix, with the same number of rows as data.
details	A list of additional parameters describing details about the particular classifier; see Details.
type	A character string indicating the type of prediction to make.
...	Optional extra parameters required by the generic "predict" method.

Details

The input arguments to both learnLR and predictLR are dictated by the requirements of the general cross-validation mechanism provided by the [Modeler-class](#).

The LR classifier is similar in spirit to the "supervised principal components" method implemented in the superpc package. We start by performing univariate two-sample t-tests to identify features that are differentially expressed between two groups of training samples. We then set a cutoff to select features using a bound (alpha) on the false discovery rate (FDR). If the number of selected features is smaller than a prespecified goal (minNgenes), then we increase the FDR until we get the desired number of features. Next, we perform PCA on the selected features from the training data. We retain enough principal components (PCs) to explain a prespecified fraction of the variance (perVar). We then fit a logistic regression model using these PCs to predict the binary class of the training data. In order to use this model to make binary predictions, you must specify a prior probability that a sample belongs to the first of the two groups (where the ordering is determined by the levels of the classification factor, status).

In order to fit the model to data, the `params` argument to the `learnLR` function should be a list containing components named `alpha`, `minNgenes`, `perVar`, and `prior`. It may also contain a logical value called `verbose`, which controls the amount of information that is output as the algorithm runs.

The result of fitting the model using `learnLR` is a member of the [FittedModel-class](#). In addition to storing the prediction function (`pfun`) and the training data and status, the `FittedModel` stores those details about the model that are required in order to make predictions of the outcome on new data. In this case, the details are: the prior probability, the set of selected features (`sel`, a logical vector), the principal component decomposition (`spca`, an object of the [SamplePCA](#) class), the logistic regression model (`mmod`, of class `glm`), the number of PCs used (`nCompUsed`) as well as the number of components available (`nCompAvail`) and the number of gene-features selected (`nGenesSelected`). The `details` object is appropriate for sending as the second argument to the `predictLR` function in order to make predictions with the model on new data. Note that the status vector here is the one used for the *training* data, since the prediction function only uses the *levels* of this factor to make sure that the direction of the predictions is interpreted correctly.

Value

The `learnLR` function returns an object of the [FittedModel-class](#), representing a LR classifier that has been fitted on a training data set.

The `predictLR` function returns a factor containing the predictions of the model when applied to the new data set.

Author(s)

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See Also

See [Modeler-class](#) and [Modeler](#) for details about how to perform cross-validation. See [FittedModel-class](#) and [FittedModel](#) for details about the structure of the object returned by `learnLR`.

Examples

```
# simulate some data
data <- matrix(rnorm(100*20), ncol=20)
status <- factor(rep(c("A", "B"), each=10))

# set up the parameter list
lr.params <- list(minNgenes=10, alpha=0.10, perVar=0.80, prior=0.5)

# learn the model
fm <- learnLR(data, status, lr.params, predictLR)

# Make predictions on some new simulated data
newdata <- matrix(rnorm(100*30), ncol=30)
predictLR(newdata, fm@details, status)
```

learnNNET

*Fit models and make predictions with a PCA-LR classifier***Description**

These functions are used to apply the generic cross-validation mechanism to a classifier that combines principal component analysis (PCA) with logistic regression (LR).

Usage

```
learnNNET(data, status, params, pfun)
predictNNET(newdata, details, status, ...)
```

Arguments

data	The data matrix, with rows as features ("genes") and columns as the samples to be classified.
status	A factor, with two levels, classifying the samples. The length must equal the number of data columns.
params	A list of additional parameters used by the classifier; see Details.
pfun	The function used to make predictions on new data, using the cross-validated classifier. Should always be set to predictNNET.
newdata	Another data matrix, with the same number of rows as data.
details	A list of additional parameters describing details about the particular classifier; see Details.
...	Optional extra parameters required by the generic "predict" method.

Details

The input arguments to both learnNNET and predictNNET are dictated by the requirements of the general cross-validation mechanism provided by the [Modeler-class](#).

The NNET classifier is similar in spirit to the "supervised principal components" method implemented in the superpc package. We start by performing univariate two-sample t-tests to identify features that are differentially expressed between two groups of training samples. We then set a cutoff to select features using a bound (alpha) on the false discovery rate (FDR). If the number of selected features is smaller than a prespecified goal (minNgenes), then we increase the FDR until we get the desired number of features. Next, we perform PCA on the selected features from the training data. we retain enough principal components (PCs) to explain a prespecified fraction of the variance (perVar). We then fit a logistic regression model using these PCs to predict the binary class of the training data. In order to use this model to make binary predictions, you must specify a prior probability that a sample belongs to the first of the two groups (where the ordering is determined by the levels of the classification factor, status).

In order to fit the model to data, the params argument to the learnNNET function should be a list containing components named alpha, minNgenes, perVar, and prior. It may also contain a logical value called verbose, which controls the amount of information that is output as the algorithm runs.

The result of fitting the model using learnNNET is a member of the [FittedModel-class](#). In addition to storing the prediction function (pfun) and the training data and status, the FittedModel stores those details about the model that are required in order to make predictions of the outcome on

new data. In this case, the details are: the prior probability, the set of selected features (`sel`, a logical vector), the principal component decomposition (`spca`, an object of the [SamplePCA](#) class), the logistic regression model (`mmod`, of class [glm](#)), the number of PCs used (`nCompUsed`) as well as the number of components available (`nCompAvail`) and the number of gene-features selected (`nGenesSelected`). The `details` object is appropriate for sending as the second argument to the `predictNNET` function in order to make predictions with the model on new data. Note that the `status` vector here is the one used for the *training* data, since the prediction function only uses the *levels* of this factor to make sure that the direction of the predictions is interpreted correctly.

Value

The `learnNNET` function returns an object of the [FittedModel-class](#), representing a NNET classifier that has been fitted on a training data set.

The `predictNNET` function returns a factor containing the predictions of the model when applied to the new data set.

Author(s)

Kevin R. Coombes <krc@silicovore.com>

See Also

See [Modeler-class](#) and [Modeler](#) for details about how to perform cross-validation. See [FittedModel-class](#) and [FittedModel](#) for details about the structure of the object returned by `learnNNET`.

Examples

```
# simulate some data
data <- matrix(rnorm(100*20), ncol=20)
status <- factor(rep(c("A", "B"), each=10))

# set up the parameter list
nnet.params <- list()

# learn the model
#fm <- learnNNET(data, status, nnet.params, predictNNET)

# Make predictions on some new simulated data
#newdata <- matrix(rnorm(100*30), ncol=30)
#predictNNET(newdata, fm@details, status)
```

learnNNET2

Fit models and make predictions with a multi-level neural network classifier

Description

These functions are used to apply the generic cross-validation mechanism to a classifier using neural networks.

Usage

```
learnNNET2(data, status, params, pfun)
predictNNET2(newdata, details, status, ...)
```

Arguments

<code>data</code>	The data matrix, with rows as features ("genes") and columns as the samples to be classified.
<code>status</code>	A factor, with two levels, classifying the samples. The length must equal the number of data columns.
<code>params</code>	A list of additional parameters used by the classifier; see Details.
<code>pfun</code>	The function used to make predictions on new data, using the cross-validated classifier. Should always be set to <code>predictNNET2</code> .
<code>newdata</code>	Another data matrix, with the same number of rows as <code>data</code> .
<code>details</code>	A list of additional parameters describing details about the particular classifier; see Details.
<code>...</code>	Optional extra parameters required by the generic "predict" method.

Details

The input arguments to both `learnNNET2` and `predictNNET2` are dictated by the requirements of the general cross-validation mechanism provided by the [Modeler-class](#).

The NNET2 classifier is similar in spirit to the "supervised principal components" method implemented in the `superpc` package. We start by performing univariate two-sample t-tests to identify features that are differentially expressed between two groups of training samples. We then set a cutoff to select features using a bound (α) on the false discovery rate (FDR). If the number of selected features is smaller than a prespecified goal (`minNgenes`), then we increase the FDR until we get the desired number of features. Next, we perform PCA on the selected features from the training data. we retain enough principal components (PCs) to explain a prespecified fraction of the variance (`perVar`). We then fit a logistic regression model using these PCs to predict the binary class of the training data. In order to use this model to make binary predictions, you must specify a prior probability that a sample belongs to the first of the two groups (where the ordering is determined by the levels of the classification factor, `status`).

In order to fit the model to data, the `params` argument to the `learnNNET2` function should be a list containing components named `alpha`, `minNgenes`, `perVar`, and `prior`. It may also contain a logical value called `verbose`, which controls the amount of information that is output as the algorithm runs.

The result of fitting the model using `learnNNET2` is a member of the [FittedModel-class](#). In addition to storing the prediction function (`pfun`) and the training data and `status`, the `FittedModel` stores those details about the model that are required in order to make predictions of the outcome on new data. In this case, the details are: the prior probability, the set of selected features (`sel`, a logical vector), the principal component decomposition (`spca`, an object of the [SamplePCA](#) class), the logistic regression model (`mmod`, of class `glm`), the number of PCs used (`nCompUsed`) as well as the number of components available (`nCompAvail`) and the number of gene-features selected (`nGenesSelected`). The `details` object is appropriate for sending as the second argument to the `predictNNET2` function in order to make predictions with the model on new data. Note that the `status` vector here is the one used for the *training* data, since the prediction function only uses the *levels* of this factor to make sure that the direction of the predictions is interpreted correctly.

Value

The `learnNNET2` function returns an object of the [FittedModel-class](#), representing a NNET2 classifier that has been fitted on a training data set.

The `predictNNET2` function returns a factor containing the predictions of the model when applied to the new data set.

Author(s)

Kevin R. Coombes <krc@silicovore.com>

See Also

See [Modeler-class](#) and [Modeler](#) for details about how to perform cross-validation. See [FittedModel-class](#) and [FittedModel](#) for details about the structure of the object returned by `learnNNET2`.

Examples

```
# simulate some data
data <- matrix(rnorm(100*20), ncol=20)
status <- factor(rep(c("A", "B"), each=10))

# set up the parameter list
nnet.params <- list()

# learn the model
#fm <- learnNNET2(data, status, nnet.params, predictNNET2)

# Make predictions on some new simulated data
#newdata <- matrix(rnorm(100*30), ncol=30)
#predictNNET2(newdata, fm@details, status)
```

learnPCALR

Fit models and make predictions with a PCA-LR classifier

Description

These functions are used to apply the generic cross-validation mechanism to a classifier that combines principal component analysis (PCA) with logistic regression (LR).

Usage

```
learnPCALR(data, status, params, pfun)
predictPCALR(newdata, details, status, ...)
```

Arguments

<code>data</code>	The data matrix, with rows as features ("genes") and columns as the samples to be classified.
<code>status</code>	A factor, with two levels, classifying the samples. The length must equal the number of data columns.
<code>params</code>	A list of additional parameters used by the classifier; see Details.
<code>pfun</code>	The function used to make predictions on new data, using the cross-validated classifier. Should always be set to <code>predictPCALR</code> .
<code>newdata</code>	Another data matrix, with the same number of rows as <code>data</code> .
<code>details</code>	A list of additional parameters describing details about the particular classifier; see Details.
<code>...</code>	Optional extra parameters required by the generic "predict" method.

Details

The input arguments to both `learnPCALR` and `predictPCALR` are dictated by the requirements of the general cross-validation mechanism provided by the [Modeler-class](#).

The PCALR classifier is similar in spirit to the "supervised principal components" method implemented in the `superpc` package. We start by performing univariate two-sample t-tests to identify features that are differentially expressed between two groups of training samples. We then set a cutoff to select features using a bound (α) on the false discovery rate (FDR). If the number of selected features is smaller than a prespecified goal (`minNgenes`), then we increase the FDR until we get the desired number of features. Next, we perform PCA on the selected features from the training data. we retain enough principal components (PCs) to explain a prespecified fraction of the variance (`perVar`). We then fit a logistic regression model using these PCs to predict the binary class of the training data. In order to use this model to make binary predictions, you must specify a prior probability that a sample belongs to the first of the two groups (where the ordering is determined by the levels of the classification factor, `status`).

In order to fit the model to data, the `params` argument to the `learnPCALR` function should be a list containing components named `alpha`, `minNgenes`, `perVar`, and `prior`. It may also contain a logical value called `verbose`, which controls the amount of information that is output as the algorithm runs.

The result of fitting the model using `learnPCALR` is a member of the [FittedModel-class](#). In addition to storing the prediction function (`pfun`) and the training data and status, the `FittedModel` stores those details about the model that are required in order to make predictions of the outcome on new data. In this case, the details are: the prior probability, the set of selected features (`sel`, a logical vector), the principal component decomposition (`spca`, an object of the [SamplePCA](#) class), the logistic regression model (`mmod`, of class `glm`), the number of PCs used (`nCompUsed`) as well as the number of components available (`nCompAvail`) and the number of gene-features selected (`nGenesSelected`). The `details` object is appropriate for sending as the second argument to the `predictPCALR` function in order to make predictions with the model on new data. Note that the status vector here is the one used for the *training* data, since the prediction function only uses the *levels* of this factor to make sure that the direction of the predictions is interpreted correctly.

Value

The `learnPCALR` function returns an object of the [FittedModel-class](#), representing a PCALR classifier that has been fitted on a training data set.

The `predictPCALR` function returns a factor containing the predictions of the model when applied to the new data set.

Author(s)

Kevin R. Coombes <krc@silicovore.com>

See Also

See [Modeler-class](#) and [Modeler](#) for details about how to perform cross-validation. See [FittedModel-class](#) and [FittedModel](#) for details about the structure of the object returned by `learnPCALR`.

Examples

```
# simulate some data
data <- matrix(rnorm(100*20), ncol=20)
status <- factor(rep(c("A", "B"), each=10))

# set up the parameter list
```

```

pcalr.params <- list(minNgenes=10, alpha=0.10, perVar=0.80, prior=0.5)

# learn the model
fm <- learnPCALR(data, status, pcalr.params, predictPCALR)

# Make predictions on some new simulated data
newdata <- matrix(rnorm(100*30), ncol=30)
predictPCALR(newdata, fm@details, status)

```

learnRF

*Fit models and make predictions with a PCA-LR classifier***Description**

These functions are used to apply the generic cross-validation mechanism to a classifier that combines principal component analysis (PCA) with logistic regression (LR).

Usage

```

learnRF(data, status, params, pfun)
predictRF(newdata, details, status, ...)

```

Arguments

data	The data matrix, with rows as features ("genes") and columns as the samples to be classified.
status	A factor, with two levels, classifying the samples. The length must equal the number of data columns.
params	A list of additional parameters used by the classifier; see Details.
pfun	The function used to make predictions on new data, using the cross-validated classifier. Should always be set to predictRF.
newdata	Another data matrix, with the same number of rows as data.
details	A list of additional parameters describing details about the particular classifier; see Details.
...	Optional extra parameters required by the generic "predict" method.

Details

The input arguments to both learnRF and predictRF are dictated by the requirements of the general cross-validation mechanism provided by the [Modeler-class](#).

The RF classifier is similar in spirit to the "supervised principal components" method implemented in the superpc package. We start by performing univariate two-sample t-tests to identify features that are differentially expressed between two groups of training samples. We then set a cutoff to select features using a bound (alpha) on the false discovery rate (FDR). If the number of selected features is smaller than a prespecified goal (minNgenes), then we increase the FDR until we get the desired number of features. Next, we perform PCA on the selected features from the training data. We retain enough principal components (PCs) to explain a prespecified fraction of the variance (perVar). We then fit a logistic regression model using these PCs to predict the binary class of the training data. In order to use this model to make binary predictions, you must specify a prior

probability that a sample belongs to the first of the two groups (where the ordering is determined by the levels of the classification factor, *status*).

In order to fit the model to data, the `params` argument to the `learnRF` function should be a list containing components named `alpha`, `minNgenes`, `perVar`, and `prior`. It may also contain a logical value called `verbose`, which controls the amount of information that is output as the algorithm runs.

The result of fitting the model using `learnRF` is a member of the `FittedModel-class`. In addition to storing the prediction function (`pfun`) and the training data and status, the `FittedModel` stores those details about the model that are required in order to make predictions of the outcome on new data. In this case, the details are: the prior probability, the set of selected features (`sel`, a logical vector), the principal component decomposition (`spca`, an object of the `SamplePCA` class), the logistic regression model (`mmod`, of class `glm`), the number of PCs used (`nCompUsed`) as well as the number of components available (`nCompAvail`) and the number of gene-features selected (`nGenesSelected`). The details object is appropriate for sending as the second argument to the `predictRF` function in order to make predictions with the model on new data. Note that the status vector here is the one used for the *training* data, since the prediction function only uses the *levels* of this factor to make sure that the direction of the predictions is interpreted correctly.

Value

The `learnRF` function returns an object of the `FittedModel-class`, representing a RF classifier that has been fitted on a training data set.

The `predictRF` function returns a factor containing the predictions of the model when applied to the new data set.

Author(s)

Kevin R. Coombes <krc@silicovore.com>

See Also

See `Modeler-class` and `Modeler` for details about how to perform cross-validation. See `FittedModel-class` and `FittedModel` for details about the structure of the object returned by `learnRF`.

Examples

```
# simulate some data
data <- matrix(rnorm(100*20), ncol=20)
status <- factor(rep(c("A", "B"), each=10))

# set up the parameter list
svm.params <- list(minNgenes=10, alpha=0.10, perVar=0.80, prior=0.5)

# learn the model
#fm <- learnRF(data, status, svm.params, predictRF)

# Make predictions on some new simulated data
#newdata <- matrix(rnorm(100*30), ncol=30)
#predictRF(newdata, fm@details, status)
```

learnRPART

Fit models and make predictions with a PCA-LR classifier

Description

These functions are used to apply the generic cross-validation mechanism to a classifier that combines principal component analysis (PCA) with logistic regression (LR).

Usage

```
learnRPART(data, status, params, pfun)
predictRPART(newdata, details, status, ...)
```

Arguments

data	The data matrix, with rows as features ("genes") and columns as the samples to be classified.
status	A factor, with two levels, classifying the samples. The length must equal the number of data columns.
params	A list of additional parameters used by the classifier; see Details.
pfun	The function used to make predictions on new data, using the cross-validated classifier. Should always be set to predictRPART.
newdata	Another data matrix, with the same number of rows as data.
details	A list of additional parameters describing details about the particular classifier; see Details.
...	Optional extra parameters required by the generic "predict" method.

Details

The input arguments to both learnRPART and predictRPART are dictated by the requirements of the general cross-validation mechanism provided by the [Modeler-class](#).

The RPART classifier is similar in spirit to the "supervised principal components" method implemented in the superpc package. We start by performing univariate two-sample t-tests to identify features that are differentially expressed between two groups of training samples. We then set a cutoff to select features using a bound (alpha) on the false discovery rate (FDR). If the number of selected features is smaller than a prespecified goal (minNgenes), then we increase the FDR until we get the desired number of features. Next, we perform PCA on the selected features from the training data. we retain enough principal components (PCs) to explain a prespecified fraction of the variance (perVar). We then fit a logistic regression model using these PCs to predict the binary class of the training data. In order to use this model to make binary predictions, you must specify a prior probability that a sample belongs to the first of the two groups (where the ordering is determined by the levels of the classification factor, status).

In order to fit the model to data, the params argument to the learnRPART function should be a list containing components named alpha, minNgenes, perVar, and prior. It may also contain a logical value called verbose, which controls the amount of information that is output as the algorithm runs.

The result of fitting the model using learnRPART is a member of the [FittedModel-class](#). In addition to storing the prediction function (pfun) and the training data and status, the FittedModel stores those details about the model that are required in order to make predictions of the outcome

on new data. In this case, the details are: the prior probability, the set of selected features (`sel`, a logical vector), the principal component decomposition (`spca`, an object of the [SamplePCA](#) class), the logistic regression model (`mmod`, of class [glm](#)), the number of PCs used (`nCompUsed`) as well as the number of components available (`nCompAvail`) and the number of gene-features selected (`nGenesSelected`). The `details` object is appropriate for sending as the second argument to the `predictRPART` function in order to make predictions with the model on new data. Note that the status vector here is the one used for the *training* data, since the prediction function only uses the *levels* of this factor to make sure that the direction of the predictions is interpreted correctly.

Value

The `learnRPART` function returns an object of the [FittedModel-class](#), representing a RPART classifier that has been fitted on a training data set.

The `predictRPART` function returns a factor containing the predictions of the model when applied to the new data set.

Author(s)

Kevin R. Coombes <krc@silicovore.com>

See Also

See [Modeler-class](#) and [Modeler](#) for details about how to perform cross-validation. See [FittedModel-class](#) and [FittedModel](#) for details about the structure of the object returned by `learnRPART`.

Examples

```
# simulate some data
data <- matrix(rnorm(100*20), ncol=20)
status <- factor(rep(c("A", "B"), each=10))

# set up the parameter list
rpart.params <- list(minNgenes=10, alpha=0.10, perVar=0.80, prior=0.5)

# learn the model
fm <- learnRPART(data, status, rpart.params, predictRPART)

# Make predictions on some new simulated data
newdata <- matrix(rnorm(100*30), ncol=30)
predictRPART(newdata, fm@details, status)
```

learnSelectedLR

Fit models and make predictions with a PCA-LR classifier

Description

These functions are used to apply the generic cross-validation mechanism to a classifier that combines principal component analysis (PCA) with logistic regression (LR).

Usage

```
learnSelectedLR(data, status, params, pfun)
predictSelectedLR(newdata, details, status, ...)
```

Arguments

data	The data matrix, with rows as features ("genes") and columns as the samples to be classified.
status	A factor, with two levels, classifying the samples. The length must equal the number of data columns.
params	A list of additional parameters used by the classifier; see Details.
pfun	The function used to make predictions on new data, using the cross-validated classifier. Should always be set to predictSelectedLR.
newdata	Another data matrix, with the same number of rows as data.
details	A list of additional parameters describing details about the particular classifier; see Details.
...	Optional extra parameters required by the generic "predict" method.

Details

The input arguments to both learnSelectedLR and predictSelectedLR are dictated by the requirements of the general cross-validation mechanism provided by the [Modeler-class](#).

The SelectedLR classifier is similar in spirit to the "supervised principal components" method implemented in the superpc package. We start by performing univariate two-sample t-tests to identify features that are differentially expressed between two groups of training samples. We then set a cut-off to select features using a bound (alpha) on the false discovery rate (FDR). If the number of selected features is smaller than a prespecified goal (minNgenes), then we increase the FDR until we get the desired number of features. Next, we perform PCA on the selected features from the training data. We retain enough principal components (PCs) to explain a prespecified fraction of the variance (perVar). We then fit a logistic regression model using these PCs to predict the binary class of the training data. In order to use this model to make binary predictions, you must specify a prior probability that a sample belongs to the first of the two groups (where the ordering is determined by the levels of the classification factor, status).

In order to fit the model to data, the params argument to the learnSelectedLR function should be a list containing components named alpha, minNgenes, perVar, and prior. It may also contain a logical value called verbose, which controls the amount of information that is output as the algorithm runs.

The result of fitting the model using learnSelectedLR is a member of the [FittedModel-class](#). In addition to storing the prediction function (pfun) and the training data and status, the FittedModel stores those details about the model that are required in order to make predictions of the outcome on new data. In this case, the details are: the prior probability, the set of selected features (sel, a logical vector), the principal component decomposition (spca, an object of the [SamplePCA](#) class), the logistic regression model (mmod, of class [glm](#)), the number of PCs used (nCompUsed) as well as the number of components available (nCompAvail) and the number of gene-features selected (nGenesSelected). The details object is appropriate for sending as the second argument to the predictSelectedLR function in order to make predictions with the model on new data. Note that the status vector here is the one used for the *training* data, since the prediction function only uses the *levels* of this factor to make sure that the direction of the predictions is interpreted correctly.

Value

The learnSelectedLR function returns an object of the [FittedModel-class](#), representing a SelectedLR classifier that has been fitted on a training data set.

The predictSelectedLR function returns a factor containing the predictions of the model when applied to the new data set.

Author(s)

Kevin R. Coombes <krc@silicovore.com>

See Also

See [Modeler-class](#) and [Modeler](#) for details about how to perform cross-validation. See [FittedModel-class](#) and [FittedModel](#) for details about the structure of the object returned by `learnSelectedLR`.

Examples

```
# simulate some data
data <- matrix(rnorm(100*20), ncol=20)
status <- factor(rep(c("A", "B"), each=10))

# set up the parameter list
slr.params <- list(minNgenes=10, alpha=0.10, perVar=0.80, prior=0.5)

# learn the model
fm <- learnSelectedLR(data, status, slr.params, predictSelectedLR)

# Make predictions on some new simulated data
newdata <- matrix(rnorm(100*30), ncol=30)
predictSelectedLR(newdata, fm@details, status)
```

learnSVM

Fit models and make predictions with a PCA-LR classifier

Description

These functions are used to apply the generic cross-validation mechanism to a classifier that combines principal component analysis (PCA) with logistic regression (LR).

Usage

```
learnSVM(data, status, params, pfun)
predictSVM(newdata, details, status, ...)
```

Arguments

<code>data</code>	The data matrix, with rows as features ("genes") and columns as the samples to be classified.
<code>status</code>	A factor, with two levels, classifying the samples. The length must equal the number of data columns.
<code>params</code>	A list of additional parameters used by the classifier; see Details.
<code>pfun</code>	The function used to make predictions on new data, using the cross-validated classifier. Should always be set to <code>predictSVM</code> .
<code>newdata</code>	Another data matrix, with the same number of rows as <code>data</code> .
<code>details</code>	A list of additional parameters describing details about the particular classifier; see Details.
<code>...</code>	Optional extra parameters required by the generic "predict" method.

Details

The input arguments to both `learnSVM` and `predictSVM` are dictated by the requirements of the general cross-validation mechanism provided by the [Modeler-class](#).

The SVM classifier is similar in spirit to the "supervised principal components" method implemented in the `superpc` package. We start by performing univariate two-sample t-tests to identify features that are differentially expressed between two groups of training samples. We then set a cutoff to select features using a bound (α) on the false discovery rate (FDR). If the number of selected features is smaller than a prespecified goal (`minNgenes`), then we increase the FDR until we get the desired number of features. Next, we perform PCA on the selected features from the training data. we retain enough principal components (PCs) to explain a prespecified fraction of the variance (`perVar`). We then fit a logistic regression model using these PCs to predict the binary class of the training data. In order to use this model to make binary predictions, you must specify a prior probability that a sample belongs to the first of the two groups (where the ordering is determined by the levels of the classification factor, `status`).

In order to fit the model to data, the `params` argument to the `learnSVM` function should be a list containing components named `alpha`, `minNgenes`, `perVar`, and `prior`. It may also contain a logical value called `verbose`, which controls the amount of information that is output as the algorithm runs.

The result of fitting the model using `learnSVM` is a member of the [FittedModel-class](#). In addition to storing the prediction function (`pfun`) and the training data and status, the `FittedModel` stores those details about the model that are required in order to make predictions of the outcome on new data. In this case, the details are: the prior probability, the set of selected features (`sel`, a logical vector), the principal component decomposition (`spca`, an object of the [SamplePCA](#) class), the logistic regression model (`mmod`, of class `glm`), the number of PCs used (`nCompUsed`) as well as the number of components available (`nCompAvail`) and the number of gene-features selected (`nGenesSelected`). The details object is appropriate for sending as the second argument to the `predictSVM` function in order to make predictions with the model on new data. Note that the status vector here is the one used for the *training* data, since the prediction function only uses the *levels* of this factor to make sure that the direction of the predictions is interpreted correctly.

Value

The `learnSVM` function returns an object of the [FittedModel-class](#), representing a SVM classifier that has been fitted on a training data set.

The `predictSVM` function returns a factor containing the predictions of the model when applied to the new data set.

Author(s)

Kevin R. Coombes <krc@silicovore.com>

See Also

See [Modeler-class](#) and [Modeler](#) for details about how to perform cross-validation. See [FittedModel-class](#) and [FittedModel](#) for details about the structure of the object returned by `learnSVM`.

Examples

```
# simulate some data
data <- matrix(rnorm(100*20), ncol=20)
status <- factor(rep(c("A", "B"), each=10))

# set up the parameter list
```

```
svm.params <- list(minNgenes=10, alpha=0.10, perVar=0.80, prior=0.5)

# learn the model
fm <- learnSVM(data, status, svm.params, predictSVM)

# Make predictions on some new simulated data
newdata <- matrix(rnorm(100*30), ncol=30)
predictSVM(newdata, fm@details, status)
```

learnTailRank

Fit models and make predictions with a PCA-LR classifier

Description

These functions are used to apply the generic cross-validation mechanism to a classifier that combines principal component analysis (PCA) with logistic regression (LR).

Usage

```
learnTailRank(data, status, params, pfun)
predictTailRank(newdata, details, status, ...)
```

Arguments

data	The data matrix, with rows as features ("genes") and columns as the samples to be classified.
status	A factor, with two levels, classifying the samples. The length must equal the number of data columns.
params	A list of additional parameters used by the classifier; see Details.
pfun	The function used to make predictions on new data, using the cross-validated classifier. Should always be set to predictTailRank.
newdata	Another data matrix, with the same number of rows as data.
details	A list of additional parameters describing details about the particular classifier; see Details.
...	Optional extra parameters required by the generic "predict" method.

Details

The input arguments to both learnTailRank and predictTailRank are dictated by the requirements of the general cross-validation mechanism provided by the [Modeler-class](#).

The TailRank classifier is similar in spirit to the "supervised principal components" method implemented in the superpc package. We start by performing univariate two-sample t-tests to identify features that are differentially expressed between two groups of training samples. We then set a cutoff to select features using a bound (alpha) on the false discovery rate (FDR). If the number of selected features is smaller than a prespecified goal (minNgenes), then we increase the FDR until we get the desired number of features. Next, we perform PCA on the selected features from the training data. We retain enough principal components (PCs) to explain a prespecified fraction of the variance (perVar). We then fit a logistic regression model using these PCs to predict the binary

class of the training data. In order to use this model to make binary predictions, you must specify a prior probability that a sample belongs to the first of the two groups (where the ordering is determined by the levels of the classification factor, status).

In order to fit the model to data, the `params` argument to the `learnTailRank` function should be a list containing components named `alpha`, `minNGenes`, `perVar`, and `prior`. It may also contain a logical value called `verbose`, which controls the amount of information that is output as the algorithm runs.

The result of fitting the model using `learnTailRank` is a member of the [FittedModel-class](#). In addition to storing the prediction function (`pfun`) and the training data and status, the `FittedModel` stores those details about the model that are required in order to make predictions of the outcome on new data. In this case, the details are: the prior probability, the set of selected features (`sel`, a logical vector), the principal component decomposition (`spca`, an object of the [SamplePCA](#) class), the logistic regression model (`mmod`, of class [glm](#)), the number of PCs used (`nCompUsed`) as well as the number of components available (`nCompAvail`) and the number of gene-features selected (`nGenesSelected`). The details object is appropriate for sending as the second argument to the `predictTailRank` function in order to make predictions with the model on new data. Note that the status vector here is the one used for the *training* data, since the prediction function only uses the *levels* of this factor to make sure that the direction of the predictions is interpreted correctly.

Value

The `learnTailRank` function returns an object of the [FittedModel-class](#), representing a TailRank classifier that has been fitted on a training data set.

The `predictTailRank` function returns a factor containing the predictions of the model when applied to the new data set.

Author(s)

Kevin R. Coombes <krc@silicovore.com>

See Also

See [Modeler-class](#) and [Modeler](#) for details about how to perform cross-validation. See [FittedModel-class](#) and [FittedModel](#) for details about the structure of the object returned by `learnTailRank`.

Examples

```
# simulate some data
data <- matrix(rnorm(100*20), ncol=20)
status <- factor(rep(c("A", "B"), each=10))

# set up the parameter list
tr.params <- list(minNGenes=10, alpha=0.10, perVar=0.80, prior=0.5)

# learn the model
fm <- learnTailRank(data, status, tr.params, predictTailRank)

# Make predictions on some new simulated data
newdata <- matrix(rnorm(100*30), ncol=30)
predictTailRank(newdata, fm@details, status)
```

Modeler

Constructor for "Modeler" objects

Description

The [Modeler-class](#) represents (parametrized but not yet fit) statistical models that can predict binary outcomes. The `Modeler` function is used to construct objects of this class.

Usage

```
Modeler(learn, predict, ...)
```

Arguments

<code>learn</code>	Object of class "function" that will be used to fit the model to a data set. See learn for details.
<code>predict</code>	Object of class "function" that will be used to make predictions on new data from a fitted model. See predict for details.
<code>...</code>	Additional parameters required for the specific kind of classification model that will be constructed. See Details.

Details

Objects of the [Modeler-class](#) provide a general abstraction for classification models that can be learned from one data set and then applied to a new data set. Each type of classifier is likely to have its own specific parameters. For instance, a K-nearest neighbors classifier requires you to specify `k`. The more complex classifier, PCA-LR has many more parameters, including the false discovery rate (`alpha`) used to select features and the percentage of variance (`perVar`) that should be explained by the number of principal components created from those features. All additional parameters should be supplied as named arguments to the `Modeler` constructor; these additional parameters will be bundled into a list and inserted into the `params` slot of the resulting object of the [Modeler-class](#). The examples illustrate how to do this for three different kinds of classifiers.

Value

Returns an object of the [Modeler-class](#).

Author(s)

Kevin R. Coombes <krc@silicovore.com>

See Also

See the descriptions of the [learn](#) function and the [predict](#) method for details on how to fit models on training data and make predictions on new test data.

See the description of the [FittedModel-class](#) for details about the kinds of objects produced by [learn](#).

See [Modeler-package](#) for a list of the kinds of classifiers that have been adapted for use in this generic framework.

Examples

```
# not yet
```

Modeler-class	<i>Class "Modeler"</i>
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Description

The Modeler class represents (parametrized but not yet fit) statistical models that can predict binary outcomes.

Objects from the Class

Objects can be created by calls to the constructor function, [Modeler](#).

Slots

learnFunction: Object of class "function" that is used to fit the model to a data set. See [learn](#) for details.

predictFunction: Object of class "function" that is used to make predictions on new data from a fitted model. See [predict](#) for details.

paramList: Object of class "list" that contains parameters that are specific for one type of classifier.

Methods

No methods are defined with class "Modeler" in the signature. The only function that can be applied to a Modeler object is [learn](#), which has not been made into a generic function.

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See Also

See the description of the [FittedModel-class](#) for details about the kinds of objects produced by [learn](#).

Examples

```
showClass("Modeler")
```

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