

# Rmagpie

October 25, 2011

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classifyNewSamples-methods

*classifyNewSamples Method to classify new samples for a given*

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## Description

This method classify one or several new samples provided in the file 'newSamplesFile' using the final classifier build by 'findFinalClassifier'.

## Arguments

`object` object of class assessment. Object assessment of interest

`newSamplesFile` character. URL of the file containing the gene expressions of the samples to be classified. The first line of the file must corresponds to the sample names and the first column to the names of the genes.

`optionValue` numeric. Size of subset (for RFE-SVM) or threshold (for NSC) to be considered, the option value must be available in the slot `featureSelectionOptions` of the assessment. If not, the smallest value bigger than 'optionValue' is selected. If this argument is missing the best option value according to one-layer cross-validation is used.

## Methods

**object = "assessment"** This method is only applicable on objects of class assessment.

## Examples

```
data('vV70genesDataset')

expeOfInterest <- new("assessment", dataset=vV70genes,
                      noFolds1stLayer=10,
                      noFolds2ndLayer=9,
                      classifierName="svm",
                      typeFoldCreation="original",
                      svmKernel="linear",
                      noOfRepeat=2,
                      featureSelectionOptions=new("geneSubsets", optionValue
```

```

# Build the final classifier
expeOfInterest <- findFinalClassifier(expeOfInterest)

## Not run:
classifyNewSamples(expeOfInterest, "pathToFile/testSamples_geneExpr.txt", 4)

## End(Not run)
expeOfInterest <- runOneLayerExtCV(expeOfInterest)
## Not run:
classifyNewSamples(expeOfInterest, "pathToFile/testSamples_geneExpr.txt")

## End(Not run)

```

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assessment-class     *assessment: A central class to perform one and two layers of external*

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## Description

This class stores the information relevant to a microarray classification assessment: data set, classifier and options are set here and then one-layer and two-layer cross-validation can be applied.

## Creating objects

```

new("assessment", dataset noFolds1stLayer=10, noFolds2ndLayer=9, classifierName=
featureSelectionMethod="rfe", typeFoldCreation="original", svmKernel="linear",
noOfRepeat=2, featureSelectionOptions)

```

Creates an assessment to be performed on the data set `dataset` using the feature selection options defined by `featureSelectionMethod` on the feature selection method `featureSelectionMethod` and with the classifier `classifierName`. Once all the options have been selected one-layer and two-layers of cross-validation can be performed by calling `runOneLayerExtCv` and `runTwoLayerExtCv` respectively.

```

new("assessment", dataset noFolds1stLayer=10, noFolds2ndLayer=9, classifierName=
featureSelectionMethod="rfe", typeFoldCreation="original", svmKernel="linear",
noOfRepeat=2)

```

If `featureSelectionOptions` is not precised in the arguments then the options for the feature selection method are determined according to the `dataset` and the `featureSelectionMethod`. If RFE is selected as feature selection method then an object of class `geneSubsets` is automatically created. It defines sizes of subsets of genes for 1 to the number of features in the `dataset` by power of 2. If the feature selection method is NSC then the thresholds are taken to be the default thresholds generated by the function `pamr.train` from package `pamr` applied on `dataset`.

## Slots

**dataset:** Object of class "dataset". Microarray data set to be used for cross-validation

**noFolds1stLayer:** numeric. Number of folds in the inner layer of cross-validation

**noFolds2ndLayer:** numeric. Number of folds in one-layer cross-validation and in the second layer of cross-validation

**classifierName:** character. Name of the classifier: 'svm' for Support Vector Machines or 'nsc' for Nearest Shrunken Centroid

**featureSelectionMethod:** Object of class "character" ~~  
**typeFoldCreation:** character. Type of fold creation: 'original', 'simple' or 'naive'  
**svmKernel:** Object of class "character" ~~  
**noOfRepeats:** numeric. Number of repeats to be performed for each cross-validation.  
**featureSelectionOptions:** Object of class "featureSelectionOptions". Sizes of subsets to be tried in the RFE or thresholds to be tried with the NSC.  
**resultRepeated1LayerCV:** Object of class "resultRepeated1LayerCVorNULL" NULL is the external one layer CV has not been run yet, resultRepeated1LayerCV containing the results  
**resultRepeated2LayerCV:** Object of class "result2LayerCVorNULL" NULL is the external one layer CV has not been run yet, result2LayerCV containing the results  
**finalClassifier:** Object of class "finalClassifierorNULL" NULL is the final classifier has not been determined yet, finalClassifier containing the final Classifier for each feature selection option.

## Methods

`classifyNewSamples(assessment)` Classify new samples using the final classifier. See related documentation.

`findFinalClassifier(assessment)` Train the final classifier related to an assessment based on each feature selection option. See related documentation

`getClassifierName(assessment)`, `getClassifierName(assessment)<-` Retrieve and Modify the classifier name associated to the current assessment (slot classifierName)

`getDataset(assessment)`, `getDataset(assessment)<-` Retrieve and Modify the dataset associated to the current assessment (slot dataset), see related documentation for more details.

`getFeatureSelectionOptions(assessment)`, `getFeatureSelectionOptions(assessment)<-` Retrieve and Modify the options of feature selection associated to the current assessment (slot featureSelectionOptions)

`getFinalClassifier(assessment)` Retrieve the final classifier associated with an experiment.

`getNoFolds1stLayer(assessment)`, `getNoFolds1stLayer(assessment)<-` Retrieve and Modify the number of folds in the inner layer of cross-validation (slot nbFolds1stLayer)

`getNoFolds2ndLayer(assessment)`, `getNoFolds2ndLayer(assessment)<-` Retrieve and Modify the number of folds in the outer layer of cross-validation (slot nbFolds1stLayer)

`getNoOfRepeats(assessment)`, `getNoOfRepeats(assessment)<-` Retrieve and Modify the number of repeats of each cross-validation (slot nbOfRepeat)

`getResult1LayerCV(assessment)` Retrieve the results of the one-layer cross validation (slot resultRepeated1LayerCV). An easier access to this data is available via the method `getResults()`

`getResult2LayerCV(assessment)` Retrieve the results of the two-layers cross validation (slot result2LayerCV). An easier access to this data is available via the method `getResults()`

**getResults** User-friendly methods to retrieve data in the results of one-layer and two-layers of cross-validation. See related documentation page.

`getSvmKernel(assessment)`, `getSvmKernel(assessment)<-` Retrieve and Modify the svm kernel used as a final classifier if svm is the concerned classifier and during the Recursive Feature Elimination (slot svmKernel)

```

getTypeFoldCreation(assessment), getTypeFoldCreation(assessment)<-
  Retrieve and Modify the type of folds creation to use for each cross-validation (slot typeFold-
  Creation)

runOneLayerExtCV Run one-layer cross-validation, see related documentation for more de-
  tails.

runTwoLayerExtCV Run two-layer cross-validation, see related documentation for more de-
  tails.

```

**Author(s)**

Camille Maumet

**See Also**

[geneSubsets](#), [getResults-methods](#), [runOneLayerExtCV-methods](#), [runTwoLayerExtCV-methods](#)

**Examples**

```

#dataPath <- file.path("C:", "Documents and Settings", "c.maumet", "My Documents", "Progr
#myDataset <- new("dataset", dataId="vantVeer_70", dataPath=file.path(dataPath, "vantVeer
# myDataset<-loadData(myDataset)

data('vV70genesDataset')

# assessment with RFE and SVM
myExpe <- new("assessment", dataset=vV70genes,
             noFolds1stLayer=10,
             noFolds2ndLayer=9,
             classifierName="svm",
             typeFoldCreation="original",
             svmKernel="linear",
             noOfRepeat=2,
             featureSelectionOptions=new("geneSubsets", optionValues=c(1,2,3,4,5,6))

# Another assessment where the subsets are computed automatically
anotherExpe <- new("assessment", dataset=vV70genes,
                 noFolds1stLayer=10,
                 noFolds2ndLayer=9,
                 classifierName="svm",
                 typeFoldCreation="original",
                 svmKernel="linear",
                 noOfRepeat=2)

getFeatureSelectionOptions(anotherExpe, topic='maxSubsetSize')
getFeatureSelectionOptions(anotherExpe, topic='subsetsSizes')

# assessment with NSC
expeWithNSC <- new("assessment", dataset=vV70genes,
                  noFolds1stLayer=10,
                  noFolds2ndLayer=9,
                  classifierName="nsc",
                  featureSelectionMethod='nsc',
                  typeFoldCreation="original",
                  svmKernel="linear",
                  noOfRepeat=2)

getFeatureSelectionOptions(expeWithNSC, topic='thresholds')

```

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`featureSelectionOptions-class`*"featureSelectionOptions": A virtual class to store the options of a*

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**Description**

This virtual class has two descendants: `geneSubsets` and `thresholds`. As a virtual class, you can't create an object of class `featureSelectionOptions`.

**Slots**

`optionValues`: numeric (vector). Value of the possible options

`noOfOptions`: numeric. Total number of options

**Methods**

`getOptionValues(featureSelectionOptions)` Retrieve the value of options (slot `optionValues`)

`getNoOfOptions(featureSelectionOptions)` Retrieve the number of options (slot `featureSelectionOptions`)

**Author(s)**

Camille Maumet

**See Also**

[geneSubsets](#), [thresholds](#)

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`finalClassifier-class`*finalClassifier: A class to store the final classifier corresponding to*

---

**Description**

This class stores the properties of the final classifiers associated to a given assessment. A classifier is usually available for each option value defined in the slot `featureSelectionOptions`. This final classifier is obtained by running the feature selection method on the whole dataset to find the relevant genes and then train the classifier on the whole data considering only the relevant genes.

**Creating objects**

To generate the final classifier, call the method `'findFinalClassifier'` on an object of class `assessment` ([findFinalClassifier-methods](#)).

**Slots**

**genesFromBestToWorst:** character. If the feature selection method is RFE: the genes ordered by the weights obtained with the smallest subset size during RFE. If the method of feature selection is the Nearest Shrunken Centroid, this slot is empty.

**models:** list of object of class svm. If the feature selection method is RFE: svm models trained on the whole dataset for each size of subset (2 attributes: 'model', the classifier model and 'modelFeatures' the features selected for each subset). If the feature selection method is NSC: the object created by pamr.train on the whole dataset.

**Methods**

`getGenesFromBestToWorst(finalClassifier)` Retrieve the genes ordered by their weights obtained with the smallest subset during RFE (slot `genesFromBestToWorst`)

`getModels(finalClassifier)` Retrieve the svm models for each size of subset (slot `models`)

**Author(s)**

Camille Maumet

**See Also**

[finalClassifier, assessment, getFinalClassifier-methods](#)

**Examples**

```
#dataPath <- file.path("C:", "Documents and Settings", "c.maumet", "My Documents", "Programs")
#aDataset <- new("dataset", dataId="vantVeer_70", dataPath=dataPath)
#aDataset <- loadData(aDataset)
data('vV70genesDataset')

mySubsets <- new("geneSubsets", optionValues=c(1,2,4,8,16,32,64,70))
expeOfInterest <- new("assessment", dataset=vV70genes,
                     noFolds1stLayer=10,
                     noFolds2ndLayer=9,
                     classifierName="svm",
                     typeFoldCreation="original",
                     svmKernel="linear",
                     noOfRepeat=2,
                     featureSelectionOptions=mySubsets)

expeOfInterest <- findFinalClassifier(expeOfInterest)

# Return the whole object of class finalClassifier
finalClassifier <- getFinalClassifier(expeOfInterest)

# Svm model corresponding to a subset of size 4 (3rd size of subset)
getModels(finalClassifier)[[3]]$model
# Relevant genes for a subset of size 4 (3rd size of subset)
getModels(finalClassifier)[[3]]$modelFeatures

# Genes ordered according to their weight after performing the RFE up to 1 gene
getGenesFromBestToWorst(finalClassifier)
```

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`findFinalClassifier-methods`*findFinalClassifier Method to train and build the final classifier*

---

## Description

This method generates and stores the final classifier corresponding to an assessment. This classifier can then be used to classify new samples by calling `classifyNewSamples`. The final classifier is build according to the classifier selected for a given assessment, applied on the whole data considering only the genes selected by the feature selction method selected.

## Value

The methods returns an object of class `assessment` which `finalClassifier` has been build.

## Methods

**object = "assessment"** This method is only applicable on objects of class `assessment`.

## See Also

[finalClassifier](#), [assessment](#)

## Examples

```
#dataPath <- file.path("C:", "Documents and Settings", "c.maumet", "My Documents", "Progr
#aDataset <- new("dataset", dataId="vantVeer_70", dataPath=dataPath)
#aDataset <- loadData(aDataset)
data('vV70genesDataset')

# With the RFE-SVM as feature selection method
expeOfInterest <- new("assessment", dataset=vV70genes,
                      noFolds1stLayer=10,
                      noFolds2ndLayer=9,
                      classifierName="svm",
                      typeFoldCreation="original",
                      svmKernel="linear",
                      noOfRepeat=2,
                      featureSelectionOptions=new("geneSubsets", optionValue

# Build the final classifier
expeOfInterest <- findFinalClassifier(expeOfInterest)

# With the NSC as feature selection method
expeOfInterest <- new("assessment", dataset=vV70genes,
                      noFolds1stLayer=10,
                      noFolds2ndLayer=9,
                      featureSelectionMethod="nsc",
                      classifierName="nsc",
                      typeFoldCreation="original",
                      svmKernel="linear",
                      noOfRepeat=2,
                      featureSelectionOptions=new("thresholds"))
```

```
# Build the final classifier
expeOfInterest <- findFinalClassifier(expeOfInterest)
```

---

geneSubsets-class *geneSubsets: A class to handle the sizes of gene subsets to be tested*

---

## Description

Forward gene selection is usually a computationally expensive task. To reduce the computation expense one may want to do not consider one gene at a time but chunks of genes. This class store the sizes of gene subsets to be tested during forward gene selection.

## Creating objects

```
new("geneSubsets", optionValues)
```

Create a `geneSubsets`, the sizes of the different subsets are determined by `optionValues`. The size of the biggest subset `maxSubsetSize` and the number of subsets to be tried `noOfOptions` are automatically deducted. The speed is set to `high` if there are less models than the size of the biggest subset and `slow` if not.

```
new("geneSubsets", maxSubsetSize, speed="high")
```

Create a `geneSubsets`, with a biggest subset of size `maxSubsetSize`. If the speed is `high` the sizes of the subsets are increased by a power of 2 from 1 to the biggest power of 2 smaller than `maxSubsetSize`. If the speed is `slow` the sizes of the subsets are increased by 1 from 1 to the `maxSubsetSize`.

## Slots

`maxSubsetSize`: numeric. Size of the biggest subset

`optionValues`: numeric (vector). Sizes of the subsets in ascending order

`noOfOptions`: numeric. Total number of subsets to be tried during backward gene selection

`speed`: character. Speed of the backward feature selection. `high` if the number of models is smaller than the size of the biggest subset, `slow` if not.

## Methods

`getMaxSubsetSize(geneSubsets)`, `getMaxSubsetSize(geneSubsets) <-` Retrieve and modify the size of the biggest subset (slot `maxSubsetSize`)

`getOptionValues(geneSubsets)`, `getOptionValues(geneSubsets) <-` Retrieve and modify the sizes of the subsets of features (slot `optionValues`)

`getNoOfOptions(geneSubsets)` Retrieve the total number of subsets to be tried during backward gene selection (slot `noModels`)

`getSpeed(geneSubsets)`, `getSpeed(geneSubsets) <-` Retrieve and modify the speed of the backward feature selection. (slot `speed`)

## Author(s)

Camille Maumet



**See Also**

[thresholds,assessment](#)

**Examples**

```
geneSubset235 <- new("geneSubsets", optionValues=c(2,3,5))
geneSubset235
getSubsetsSizes(geneSubset235)
getSpeed(geneSubset235)
getMaxSubsetSize(geneSubset235)

geneSubsetMax60 <- new("geneSubsets", maxSubsetSize=60, speed="slow")
geneSubsetMax60

geneSubsetSlow <- new("geneSubsets", maxSubsetSize=70, speed="slow")
geneSubsetSlow

getMaxSubsetSize(geneSubsetMax60) <- 70
geneSubsetMax60

newSizes <- c(1,2,3,4,5)
getSubsetsSizes(geneSubsetMax60) <- newSizes
geneSubsetMax60

getSpeed(geneSubset235) <- 'slow'
geneSubset235
```

---

getDataset-methods *getDataset Method to access the attributes of a dataset from an*

---

**Description**

This method provides an easy interface to access the attributes of a dataset directly from an object assessment. The argument `topic` specifies which part of the dataset is of interest.

**Arguments**

|                     |  |
|---------------------|--|
| <code>object</code> | Object of class <code>assessment</code> . Object assessment of interest  |
| <code>topic</code>  | character. Optional argument that specifies which attribute of the dataset is requested, the possible values are <code>"dataId"</code> (slot <code>dataId</code> of the dataset), <code>"dataPath"</code> (slot <code>dataPath</code> of the dataset), <code>"geneExprFile"</code> (slot <code>geneExprFile</code> of the dataset), <code>"classesFile"</code> (slot <code>classesFile</code> of the dataset), <code>"eset"</code> (slot <code>eset</code> of the dataset) if the <code>"topic"</code> is missing then the whole dataset object is returned. |

**Value**

The value returned by the method changes accordingly to the `"topic"` argument.

If `"topic"` is missing object of class `dataset` the dataset corresponding to the assessment of interest

If `"topic"` is `"dataId"` object of class `character` corresponding to the `dataId` of the dataset

If "topic" is "dataPath" object of class character corresponding to the dataPath of the dataset

If "topic" is "geneExprFile" object of class character corresponding to the geneExprFile of the dataset

If "topic" is "classesFile" object of class character corresponding to the classesFile of the dataset

If "topic" is "eset" object of class ExpressionSetOrNull corresponding to the eset of the dataset

## Methods

**object = "assessment"** The method is only applicable on objects of class assessment.

## Author(s)

Camille Maumet

## See Also

[assessment](#)

## Examples

```
#dataPath <- file.path("C:", "Documents and Settings", "c.maumet", "My Documents", "Progr
#aDataset <- new("dataset", dataId="vantVeer_70", dataPath=dataPath)
#aDataset <- loadData(aDataset)

data('vV70genesDataset')

expeOfInterest <- new("assessment", dataset=vV70genes,
                      noFolds1stLayer=10,
                      noFolds2ndLayer=9,
                      classifierName="svm",
                      typeFoldCreation="original",
                      svmKernel="linear",
                      noOfRepeat=2,
                      featureSelectionOptions=new("geneSubsets", optionValue

getDataset(expeOfInterest)
```

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getFeatureSelectionOptions-methods

*getFeatureSelectionOptions Method to access the attributes of a*

---

## Description

This method provides an easy interface to access the attributes of the object of class featureSelectionOptions related to a particular assessment, directly from this object assessment. The argument topic specifies which part of the featureSelectionOptions is of interest.

**Arguments**

|        |   |
|--------|---|
| object | Object of class assessment. Object assessment of interest   |
| topic  | character. Optional argument that specifies which attribute of the featureSelectionOptions is requested, the possible values are: "optionValues" (Access the slot optionValues of the featureSelectionOptions), "noOfOptions" (Access the slot noOfOptions of the featureSelectionOptions), if the featureSelectionOptions object is an object of class geneSubsets, then the following values are also available for the argument topic "subsetsSizes" (Access the slot optionValues of the geneSubsets), "noModels" (Access the slot noOfOptions of the geneSubsets), "maxSubsetSize" (Access the slot maxSelectedFeatures of the geneSubsets), "speed" (Access the slot speed of the featureSelectionOptions), if the featureSelectionOptions object is an object of class thresholds, then the following values are also available for the argument topic "thresholds" (Access the slot optionValues of the object thresholds), "noThresholds" (Access the slot noOfOptions of the object thresholds)<br>if the topic is missing then the whole featureSelectionOptions object is returned. |

**Value**

The value returned by the method changes accordingly to the 'topic' argument.

If topic is missing object of class featureSelectionOptions the featureSelectionOptions corresponding to the assessment of interest

If topic is "optionValues" numeric corresponding to the optionValues of the featureSelectionOptions

If topic is "noOfOptions" numeric corresponding to the noOfOptions of the featureSelectionOptions

If object is of class geneSubsets and topic is "maxSubsetSize" numeric corresponding to the maxSubsetSize of the geneSubsets

If object is of class geneSubsets and topic is "subsetsSizes" numeric corresponding to the optionValues of the geneSubsets

If object is of class geneSubsets and topic is "noModels" numeric corresponding to the noOfOptions of the geneSubsets

If object is of class geneSubsets and topic is "speed" numeric corresponding to the speed of the geneSubsets

If object is of class thresholds and topic is "thresholds" numeric corresponding to the optionValues of the object of class thresholds

If object is of class thresholds and topic is "noThresholds" numeric corresponding to the noOfOptions of the object of class thresholds

**Methods**

**object = "assessment"** The method is only applicable on objects of class assessment.

**Author(s)**

Camille Maumet

**See Also**

[featureSelectionOptions](#), [assessment](#)

**Examples**

```
# With an assessment using RFE
#dataPath <- file.path("C:", "Documents and Settings", "c.maumet", "My Documents", "Programs")
#aDataset <- new("dataset", dataId="vantVeer_70", dataPath=dataPath)
#aDataset <- loadData(aDataset)

data('vV70genesDataset')

mySubsets <- new("geneSubsets", optionValues=c(1,2,3,4,5,6))
myExpe <- new("assessment", dataset=vV70genes,
             noFolds1stLayer=10,
             noFolds2ndLayer=9,
             classifierName="svm",
             typeFoldCreation="original",
             svmKernel="linear",
             noOfRepeat=2,
             featureSelectionOptions=mySubsets)

# Return the whole object 'featureSelectionOptions' (an object of class geneSubsets)
getFeatureSelectionOptions(myExpe)
# Size of the biggest subset
getFeatureSelectionOptions(myExpe, topic='maxSubsetSize')
# All sizes of subsets
getFeatureSelectionOptions(myExpe, topic='subsetsSizes')
# Speed
getFeatureSelectionOptions(myExpe, topic='speed')
# Number of subsets
getFeatureSelectionOptions(myExpe, topic='noModels') == getNoModels(mySubsets)

# With an assessment using NSC as a feature selection method
myThresholds <- new("thresholds", optionValues=c(0.1,0.2,0.3))
myExpe2 <- new("assessment", dataset=vV70genes,
             noFolds1stLayer=10,
             noFolds2ndLayer=9,
             classifierName="nsc",
             featureSelectionMethod='nsc',
             typeFoldCreation="original",
             svmKernel="linear",
             noOfRepeat=2,
             featureSelectionOptions=myThresholds)

# Return the whole object 'featureSelectionOptions' (an object of class geneSubsets)
getFeatureSelectionOptions(myExpe2)
# vector of thresholds
getFeatureSelectionOptions(myExpe2, topic='thresholds')
# Number of thresholds
getFeatureSelectionOptions(myExpe2, topic='noThresholds')
```

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getFinalClassifier-methods

*getFinalClassifier Method to access the attributes of a finalClassifier*

---



```

expeOfInterest <- findFinalClassifier(expeOfInterest)

# Return the whole object of class finalClassifier
getFinalClassifier(expeOfInterest)
getFinalClassifier(expeOfInterest, 'genesFromBestToWorst')
getFinalClassifier(expeOfInterest, 'models')

# assessment with NSC
expeOfInterest <- new("assessment", dataset=vV70genes,
                     noFolds1stLayer=10,
                     noFolds2ndLayer=9,
                     featureSelectionMethod='nsc',
                     classifierName="nsc",
                     typeFoldCreation="original",
                     svmKernel="linear",
                     noOfRepeat=2,
                     featureSelectionOptions=new("thresholds"))

expeOfInterest <- findFinalClassifier(expeOfInterest)

# Return the whole object of class finalClassifier
getFinalClassifier(expeOfInterest)
getFinalClassifier(expeOfInterest, 'genesFromBestToWorst')
getFinalClassifier(expeOfInterest, 'models')

```

---

getResults-methods *getResults Method to access the result of one-layer and two-layers*

---

## Description

This method provides an easy interface to access the results of one-layer and two-layers of cross-validation directly from an object assessment.

## Arguments

|        |  |
|--------|--|
| object | Object of class assessment. Object assessment of interest  |
| layer  | numeric. Indice that states which layer of cross-validation must be accessed. Set to 1 to acces the one-layer cross-validation, Set to $c(1, i)$ to acces the $i$ th repeat of the one-layer cross-validation, Set to 2 to acces to the two-layers cross-validation, Set to $c(2, i)$ to access the $i$ th repeat of the two-layers cross-validation, Set to $c(2, i, j)$ to access the $j$ th inner layer of $i$ th repeat of the two-layers cross-validation, Set to $c(2, i, j, k)$ to access the $k$ th repeat of the $j$ th inner layer of $i$ th repeat of the two-layers cross-validation   |
| topic  | character. Argument that specifies which kind of result is requested, the possible values are "errorRate": Access to cross-validation error rate, standard error on cross-validated error rate, error rate per fold, number of samples per fold and error rate per class, "selectedGenes": Access to the genes selected for each fold or their frequency of selection among the folds and the repeats, "bestOptionValue": For one-layer of cross-validation, access to the best option value (size of gene subset for SVM-RFE or thresholds for NSC) corresponding to the best value of the cross-validated error rate. For the two-layers |

|           |  |
|-----------|--|
|           | of cross-validation, access the average best option value (over the repeats and folds). "executionTime": Time used to run the selected layer in seconds.   |
| errorType | character. Optional, ignored if topic is not "errorRate". Specify the type of error rate requested, the possible values are: missing or "all" to access all the following error rates "cv" to access the cross-validated error rate, "se" to access the standard error on the cross validated error rate, "fold" to access the error rate per fold (not available in certain cases see section value for more details), "noSamplesPerFold" to access the number of samples in each folds (not available in certain cases see section value for more details), "class" to access the error rate per class |
| genesType | character. Optional, ignored if topic is not "selectedGenes". Specify the type of display of genes selected, the possible values are: missing "fold" to access the genes selected for each fold (not available in certain case see section value for more details), "frequ" to access the genes order by their frequency among the folds(not available in certain case see section value for more details)   |

### Value

if there is no error, the value returned by the method depends on the arguments namely, layer, topic, errorType and genesType.

If layer is 1

General           Get the results of the repeated one-layer cross-validation corresponding to the object of class assessment. If the one-layer cross-validation has not been performed and the user try to access it then the function return an error indicating that he must call runOneLayerExtCV first.

if topic is "errorRate"

If errorType="all" or is missing

All the following error rates

If errorType="cv"

numeric. Cross-validated error-rate for each value of option tried obtained by one-layer of cross-validation (1 value per value of option).

If errorType="se"

numeric. Standard error on cross-validated error-rate for each value of option tried obtained by one-layer of cross-validation (1 value per value of option).

If errorType="class"

numeric. Class cross-validated error rate error for each value of option tried obtained by one-layer of cross-validation (1 value per class and value of option).

Else               Error signaling that the topic is not appropriate.

if topic is "genesSelected"

If genesType="freq" or is missing

list. Each element of the list corresponds to the genes selected for each model ordered by frequency.

Else               Error signaling that the topic is not appropriate.

if topic is "bestOptionValue"

Size of subset (for RFE-SVM) or threshold (for NSC) corresponding to the minimum cross-validated error rate.

if topic is "executionTime"

Time in second to perform this one-layer cross-validation.

If layer is c(1,i)

General           Get the results of the ith repeat of the one-layer cross-validation corresponding to the object of class assessment. If the one-layer cross-validation has not been performed and the user try to access it then the function return an error indicating that he must call `runOneLayerExtCV` first.

if topic is "errorRate"

If errorType="all" or is missing

    All the following error rates

If errorType="cv"

    numeric. Cross-validated error-rate for each value of option tried obtained by one-layer of cross-validation on the ith repeat(1 value per subset).

If errorType="se"

    numeric. Standard error on cross-validated error-rate for each value of option tried obtained by one-layer of cross-validation on the ith repeat (1 value per value of option).

If errorType="class"

    numeric. Class cross-validated error rate error for each value of option tried obtained by one-layer of cross-validation on the ith repeat (1 value per class and value of option).

If errorType="fold"

    numeric. Class cross-validated error rate error for each fold and each value of option tried obtained by one-layer of cross-validation on the ith repeat (1 value per class and value of option).

Else               Error signaling that the topic is not appropriate.

if topic is "genesSelected"

If genesType="freq" or is missing

    list. Each element of the list corresponds to the genes selected for each model ordered by frequency.

If genesType="fold"

    list. Each element of the list corresponds to a model and contains a list of which one element correspond to the genes selected in a particular fold.

Else               Error signaling that the topic is not appropriate.

if topic is "bestOptionValue"

    numeric. Size of subset (for RFE) or threshold (for NSC) corresponding to the minimum cross-validated error rate in the ith repeat of the one-layer cross-validation.

if topic is "executionTime"

    Time in second to perform this repeat of one-layer cross-validation.

If layer is 2

General           Get the results of the repeated two-layers cross-validation corresponding to the object of class assessment. If the two-layer cross-validation has not been performed and the user try to access it then the function return an error indicating that he must call `runTwoLayerExtCV` first.

if topic is 'errorRate'

If errorType="all" or is missing

    All the following error rates



```

If errorType="cv"
    numeric. Cross-validated error-rate obtained by two-layers of cross-validation
    (1 value).
If errorType="se"
    numeric. Standard error on cross-validated error-rate obtained by two-layers of
    cross-validation (1 value).
If errorType="class"
    numeric. Class cross-validated error rate obtained by two-layers (1 value per
    class)
Else
    Error signaling that the topic is not appropriate.
if topic is "bestOptionValue"
    numeric. Average best number of genes for SVM-RFE of threshold for NSc
    obtained among the folds.
if topic is "executionTime"
    Time in second to perform this two-layers cross-validation.

If layer is c(2,i)

General
    Get the results of the ith repeated of the two-layers cross-validation correspond-
    ing to the object of class assessment. If the two-layer cross-validation has
    not been performed and the user try to access it then the function return an error
    indicating that he must call runTwoLayerExtCV first.
if topic is 'errorRate'

If errorType="all" or is missing
    All the following error rates
If errorType="cv"
    numeric. Cross-validated error-rate obtained by two-layers of cross-validation
    in this repeat. (1 value).
If errorType="se"
    numeric. Standard error on cross-validated error-rate obtained by two-layers of
    cross-validation in this repeat (1 value).
If errorType="class"
    numeric. Class cross-validated error rate obtained by two-layers in this repeat
If errorType="fold"
    numeric. Error rate obtained on each of the folds in the second layer in this
    repeat(1 value per fold). of cross-validation (value per class).
Else
    Error signaling that the topic is not appropriate.
if topic is "genesSelected"

If genesType="fold" or is missing
    list. Each element of the list corresponds to a fold and contains a list of the
    genes selected in this particular fold.
Else
    Error signaling that the topic is not appropriate.
if topic is "bestOptionValue"
    numeric. Average best number of genes obtained among the folds in this repeat.
if topic is "executionTime"
    Time in second to perform this repeat of two-layers cross-validation.

If layer is c(2, i, j)
    This layer corresponds to the jth inner layer of one-layer cross-validation per-
    formed inside the ith repeat of the two-layers cross-validation. The returned
    values are similar to the one returned by a repeated one-layer cross-validation.

```

If layer is `c(2, i, j, k)`

This layer corresponds to the *k*th repeat of the *j*th inner layer of one-layer cross-validation performed inside the *i*th repeat. The returned values are similar to the one returned by a repeat of one-layer cross-validation.

## Methods

**object = "assessment"** The method is only applicable on objects of class `assessment`.

## Author(s)

Camille Maumet

## See Also

[assessment](#)

## Examples

```
#dataPath <- file.path("C:", "Documents and Settings", "c.maumet", "My Documents", "Progr
#aDataset <- new("dataset", dataId="vantVeer_70", dataPath=dataPath)
#aDataset <- loadData(aDataset)
data('vV70genesDataset')

mySubsets <- new("geneSubsets", optionValues=c(1,2,4,8,16,32,64,70))
myassessment <- new("assessment", dataset=vV70genes,
                    noFolds1stLayer=5,
                    noFolds2ndLayer=4,
                    classifierName="svm",
                    typeFoldCreation="original",
                    svmKernel="linear",
                    noOfRepeat=2,
                    featureSelectionOptions=mySubsets)

myassessment <- runOneLayerExtCV(myassessment)
myassessment <- runTwoLayerExtCV(myassessment)

# --- Access to one-layer CV ---
# errorRate
# 1-layer CV: error Rates
getResults(myassessment, 1, 'errorRate')
# 1-layer CV: error Rates - all")
getResults(myassessment, 1, 'errorRate', errorType='all')
# 1-layer CV: error Rates - cv
getResults(myassessment, 1, 'errorRate', errorType='cv')
# 1-layer CV: error Rates - se
getResults(myassessment, 1, 'errorRate', errorType='se')
# 1-layer CV: error Rates - class
getResults(myassessment, 1, 'errorRate', errorType='class')

# genesSelected
# 1-layer CV: genes Selected
getResults(myassessment, 1, 'genesSelected')
# 1-layer CV: genes Selected - frequ
getResults(myassessment, 1, 'genesSelected', genesType='frequ')
# 1-layer CV: genes Selected - model 7
getResults(myassessment, 1, 'genesSelected', genesType='frequ')[[7]]
```

```

getResults(myassessment, 1, 'genesSelected')[[7]]

# bestOptionValue
# 1-layer CV: best number of genes
getResults(myassessment, 1, 'bestOptionValue')

# executionTime
# 1-layer CV: execution time
getResults(myassessment, 1, 'executionTime')

# --- Access to 2nd repeat of one-layer CV ---
# Error rates
# 1-layer CV repeat 2: error Rates
getResults(myassessment, c(1,2), 'errorRate')
# 1-layer CV repeat 2: error Rates - all
getResults(myassessment, c(1,2), 'errorRate', errorType='all')
# 1-layer CV repeat 2: error Rates - cv
getResults(myassessment, c(1,2), 'errorRate', errorType='cv')
# 1-layer CV repeat 2: error Rates - se
getResults(myassessment, c(1,2), 'errorRate', errorType='se')
# 1-layer CV repeat 2: error Rates - fold
getResults(myassessment, c(1,2), 'errorRate', errorType='fold')
# 1-layer CV repeat 2: error Rates - noSamplesPerFold
getResults(myassessment, c(1,2), 'errorRate', errorType='noSamplesPerFold')
# 1-layer CV repeat 2: error Rates - class
getResults(myassessment, c(1,2), 'errorRate', errorType='class')

# genesSelected
# 1-layer CV repeat 2: genes Selected
getResults(myassessment, c(1,2), 'genesSelected')
# 1-layer CV repeat 2: genes Selected - frequ
getResults(myassessment, c(1,2), 'genesSelected', genesType='frequ')
# 1-layer CV repeat 2: genes Selected - model 7 (twice)
getResults(myassessment, c(1,2), 'genesSelected', genesType='frequ')[[7]]
getResults(myassessment, c(1,2), 'genesSelected')[[7]]
# 1-layer CV repeat 2: genes Selected - fold
getResults(myassessment, c(1,2), 'genesSelected', genesType='fold')

# 1-layer CV repeat 2: best number of genes
getResults(myassessment, c(1,2), 'bestOptionValue')

# 1-layer CV repeat 2: execution time
getResults(myassessment, c(1,2), 'executionTime')

# --- Access to two-layers CV ---
# Error rates
# 2-layer CV: error Rates
getResults(myassessment, 2, 'errorRate')
# 2-layer CV: error Rates - all
getResults(myassessment, 2, 'errorRate', errorType='all')
# 2-layer CV: error Rates - cv
getResults(myassessment, 2, 'errorRate', errorType='cv')
# 2-layer CV: error Rates - se
getResults(myassessment, 2, 'errorRate', errorType='se')
# 2-layer CV: error Rates - class
getResults(myassessment, 2, 'errorRate', errorType='class')

```

```

# bestOptionValue
# 2-layer CV: best number of genes (avg)
getResults(myassessment, 2, 'bestOptionValue')

# executionTime
# 2-layer CV: execution time
getResults(myassessment, 2, 'executionTime')

# --- Access to two-layers CV access to repeats ---
# Error rates
# 2-layer CV repeat 1: error Rates
getResults(myassessment, c(2,1), 'errorRate')
# 2-layer CV repeat 1: error Rates - all
getResults(myassessment, c(2,1), 'errorRate', errorType='all')
# 2-layer CV repeat 1: error Rates - cv
getResults(myassessment, c(2,1), 'errorRate', errorType='cv')
# 2-layer CV repeat 1: error Rates - se
getResults(myassessment, c(2,1), 'errorRate', errorType='se')
# 2-layer CV repeat 1: error Rates - fold
getResults(myassessment, c(2,1), 'errorRate', errorType='fold')
# 2-layer CV repeat 1: error Rates - noSamplesPerFold
getResults(myassessment, c(2,1), 'errorRate', errorType='noSamplesPerFold')
# 2-layer CV repeat 1: error Rates - class
getResults(myassessment, c(2,1), 'errorRate', errorType='class')

# genesSelected
# 2-layer CV repeat 1: genes Selected
getResults(myassessment, c(2,1), 'genesSelected')
# 2-layer CV repeat 1: genes Selected - fold
getResults(myassessment, c(2,1), 'genesSelected', genesType='fold')

# 2-layer CV repeat 1: best number of genes
getResults(myassessment, c(2,1), 'bestOptionValue')

# 2-layer CV repeat 1: execution time
getResults(myassessment, c(2,1), 'executionTime')

# --- Access to one-layer CV inside two-layers CV ---
# errorRate
# 2-layer CV repeat 1 inner layer 3: error Rates
getResults(myassessment, c(2,1,3), 'errorRate')
# 2-layer CV repeat 1 inner layer 3: error Rates - all
getResults(myassessment, c(2,1,3), 'errorRate', errorType='all')
# 2-layer CV repeat 1 inner layer 3: error Rates - cv
getResults(myassessment, c(2,1,3), 'errorRate', errorType='cv')
# 2-layer CV repeat 1 inner layer 3: error Rates - se
getResults(myassessment, c(2,1,3), 'errorRate', errorType='se')
# 2-layer CV repeat 1 inner layer 3: error Rates - class
getResults(myassessment, c(2,1,3), 'errorRate', errorType='class')

# genesSelected
# 2-layer CV repeat 1 inner layer 3: genes Selected
getResults(myassessment, c(2,1,3), 'genesSelected')
# 2-layer CV repeat 1 inner layer 3: genes Selected - frequ
getResults(myassessment, c(2,1,3), 'genesSelected', genesType='frequ')
# 2-layer CV repeat 1 inner layer 3: genes Selected - model 7
getResults(myassessment, c(2,1,3), 'genesSelected', genesType='frequ')[[7]]

```

```

getResults(myassessment, c(2,1,3), 'genesSelected')[[7]]

# bestOptionValue
# 2-layer CV repeat 1 inner layer 3: best number of genes
getResults(myassessment, c(2,1,3), 'bestOptionValue')

# executionTime
# 2-layer CV repeat 1 inner layer 3: execution time
getResults(myassessment, c(2,1,3), 'executionTime')

# --- two-layers CV access to repeat 1, inner layer 2 repeat 2 ---
# Error rates
# 2-layer CV inner layer 3 repeat 2: error Rates
getResults(myassessment, c(2,1,3,1), 'errorRate')
# 2-layer CV repeat 1 inner layer 3 repeat 1: error Rates - all
getResults(myassessment, c(2,1,3,1), 'errorRate', errorType='all')
# 2-layer CV repeat 1 inner layer 3 repeat 1: error Rates - cv
getResults(myassessment, c(2,1,3,1), 'errorRate', errorType='cv')
# 2-layer CV repeat 1 inner layer 3 repeat 1: error Rates - se
getResults(myassessment, c(2,1,3,1), 'errorRate', errorType='se')
# 2-layer CV repeat 1 inner layer 3 repeat 1: error Rates - class
getResults(myassessment, c(2,1,3,1), 'errorRate', errorType='class')
# 2-layer CV repeat 1 inner layer 3 repeat 1: error Rates - fold
getResults(myassessment, c(2,1,3,1), 'errorRate', errorType='fold')
# 2-layer CV repeat 1 inner layer 3 repeat 1: error Rates - noSamplesPerFold
getResults(myassessment, c(2,1,3,1), 'errorRate', errorType='noSamplesPerFold')

# genesSelected
# 2-layer CV repeat 1 inner layer 3 repeat 1: genes Selected
getResults(myassessment, c(2,1,3,1), 'genesSelected')
# 2-layer CV repeat 1 inner layer 3 repeat 1: genes Selected - fold
getResults(myassessment, c(2,1,3,1), 'genesSelected', genesType='fold')
# 2-layer CV repeat 1 inner layer 3 repeat 1: genes Selected - model 3 fold 1 (twice)
getResults(myassessment, c(2,1,3,1), 'genesSelected', genesType='fold')[[3]][[1]]
# 2-layer CV repeat 1 inner layer 3 repeat 1: genes Selected frequ - model 3
getResults(myassessment, c(2,1,3,1), 'genesSelected')[[3]]

# 2-layer CV repeat 1 inner layer 3 repeat 1: best number of genes
getResults(myassessment, c(2,1,3,1), 'bestOptionValue')

# 2-layer CV repeat 1 inner layer 3 repeat 1: execution time
getResults(myassessment, c(2,1,3,1), 'executionTime')

```

---

initialize-methods *Initialize objects of class from Rmagpie*

---

## Description

Initialize method for Rmagpie classes.

## Author(s)

Camille Maumet

---

```
plotErrorsFoldTwoLayerCV-methods
```

*plotErrorsFoldTwoLayerCV Method to plot the error rate of a two-layer*

---

### Description

This method creates a plot that represent the error rate in each fold of each repeat of the second layer of cross-validation of the two-layer cross-validation of the assessment at stake. The plot represents the error rate versus the size of gene subsets (for SVM-RFE) or the threshold values (for NSC).

### Methods

**object = "assessment"** The method is only applicable on objects of class assessment.

### See Also

[plotErrorsSummaryOneLayerCV-methods](#), [plotErrorsRepeatedOneLayerCV-methods](#)

### Examples

```
data('vV70genesDataset')

expeOfInterest <- new("assessment", dataset=vV70genes,
                      noFolds1stLayer=3,
                      noFolds2ndLayer=2,
                      classifierName="svm",
                      typeFoldCreation="original",
                      svmKernel="linear",
                      noOfRepeat=10,
                      featureSelectionOptions=new("geneSubsets", optionValue

expeOfInterest <- runTwoLayerExtCV(expeOfInterest)

plotErrorsFoldTwoLayerCV(expeOfInterest)
```

---

```
plotErrorsRepeatedOneLayerCV-methods
```

*plotErrorsRepeatedOneLayerCV Method to plot the estimated error rates*

---

### Description

This method creates a plot that represent the summary estimated error rate and the cross-validated error rate in each repeat of the one-layer cross-validation of the assessment at stake. The plot represents the summary estimate of the error rate (averaged over the repeats) and the cross-validated error rate obtained in each repeat versus the size of gene subsets (for SVM-RFE) or the threshold values (for NSC).

**Methods**

**object = "assessment"** The method is only applicable on objects of class assessment.

**See Also**

[plotErrorsFoldTwoLayerCV-methods](#), [plotErrorsSummaryOneLayerCV-methods](#)

**Examples**

```
data('vV70genesDataset')

expeOfInterest <- new("assessment", dataset=vV70genes,
                      noFolds1stLayer=3,
                      noFolds2ndLayer=2,
                      classifierName="svm",
                      typeFoldCreation="original",
                      svmKernel="linear",
                      noOfRepeat=10,
                      featureSelectionOptions=new("geneSubsets", optionValue

expeOfInterest <- runOneLayerExtCV(expeOfInterest)

plotErrorsRepeatedOneLayerCV(expeOfInterest)
```

---

plotErrorsSummaryOneLayerCV-methods

*plotErrorsSummaryOneLayerCV Method to plot the summary estimated error*

---

**Description**

This method creates a plot that represent the summary estimated error rate of the one-layer cross-validation of the assessment at stake. The plot represents the summary estimate of the error rate (averaged over the repeats) versus the size of gene subsets (for SVM-RFE) or the threshold values (for NSC).

**Methods**

**object = "assessment"** The method is only applicable on objects of class assessment.

**See Also**

[plotErrorsFoldTwoLayerCV-methods](#), [plotErrorsRepeatedOneLayerCV-methods](#)

**Examples**

```
data('vV70genesDataset')

expeOfInterest <- new("assessment", dataset=vV70genes,
                      noFolds1stLayer=3,
                      noFolds2ndLayer=2,
                      classifierName="svm",
```

```

typeFoldCreation="original",
svmKernel="linear",
noOfRepeat=10,
featureSelectionOptions=new("geneSubsets", optionValue

expeOfInterest <- runOneLayerExtCV(expeOfInterest)

plotErrorsSummaryOneLayerCV(expeOfInterest)

```

---

rankedGenesImg-methods

*rankedGenesImg Method to plot the genes according to their frequency in*

---

### Description

Generate an image per value of option representing the features (on dot per feature). The color of the dot depends on the frequency of the feature in for the given value of option (number of genes or threshold).

### Arguments

`object` Object of class assessment. Object assessment of interest.  
`storagePath` character. URL where the image must be stored.

### Methods

**object = "assessment"** The method is only applicable on objects of class assessment.

### Examples

```

## Not run:
data('vV70genesDataset')

expeOfInterest <- new("assessment", dataset=vV70genes,
                    noFolds1stLayer=3,
                    noFolds2ndLayer=2,
                    classifierName="svm",
                    typeFoldCreation="original",
                    svmKernel="linear",
                    noOfRepeat=10,
                    featureSelectionOptions=new("geneSubsets", optionValue

expeOfInterest <- runOneLayerExtCV(expeOfInterest)

rankedGenesImg(expeOfInterest, storagePath='myPath')

## End(Not run)

```



---

runOneLayerExtCV-methods

*runOneLayerExtCV: Method to run an external one-layer cross-validation*

---

## Description

This method run an external one-layer cross-validation according to the options stored in an object of class `assessment`. The concept of external cross-validation has been introduced by G.J. McLachlan and C. Ambroise in 'Selection bias in gene extraction on the basis of microarray gene-expression data' (cf. section References). This technique of cross-validation is used to determine an unbiased estimate of the error rate when feature selection is involved.

## Arguments

`object`            Object of class `assessment`. Object assessment of interest

## Value

object of class `assessment` in which the one-layer external cross-validation has been computed, therefore, the slot `resultRepeatedLayerCV` is no more NULL. This methods print out the key results of the assessment, to access the full detail of the results, the user must call the method `getResults`.

## Methods

**object = "assessment"** This method is only applicable on objects of class `assessment`.

## References

C. Amboise and G.J. McLachlan 2002. selection bias in gene extraction on the basis of microarray gene-expression data. PNAS, 99(10):6562-6566

## See Also

[assessment](#), [getResults](#), [runTwoLayerExtCV-methods](#)

## Examples

```
data('vV70genesDataset')

# assessment with RFE and SVM
myExpe <- new("assessment", dataset=vV70genes,
             noFolds1stLayer=9,
             noFolds2ndLayer=10,
             classifierName="svm",
             typeFoldCreation="original",
             svmKernel="linear",
             noOfRepeat=2,
             featureSelectionOptions=new("geneSubsets", optionValues=c(1,2,3,4,5,6))

myExpe <- runOneLayerExtCV(myExpe)
```

---

```
runTwoLayerExtCV-methods
```

```
runTwoLayerExtCV: Method to run an external two-layers cross-validation
```

---

## Description

This method run an external two-layers cross-validation according to the options stored in an object of class `assessment`. The concept of two-layers cross-validation has been introduced by J.X. Zhu, G.J. McLachlan, L. Ben-Tovim Jonesa, I.A. Wood in 'On selection biases with prediction rules formed from gene expression data' and by I. A. Wood, P. M. Visscher, and K. L. Mengersen in 'Classification based upon gene expression data: bias and precision of error rates' (cf. section References). This technique of cross-validation is used to determine an unbiased estimate of the best error rate (using the best size of subset for RFE-SVM, of the best threshold for NSC) when feature selection is involved.

## Arguments

`object`            Object of class `assessment`. Object assessment of interest

## Value

object of class `assessment` in which the one-layer external cross-validation has been computed, therefore, the slot `resultRepeated2LayerCV` is no more NULL. This methods print out the key results of the assessment, to access the full detail of the results, the user must call the method `getResults`.

## Methods

**object = "assessment"** This method is only applicable on objects of class `assessment`.

## References

J.X. Zhu, G.J. McLachlan, L. Ben-Tovim, I.A. Wood (2008), "On selection biases with prediction rules formed from gene expression data", *Journal of Statistical Planning and Inference*, 38:374-386.

I.A. Wood, P.M. Visscher, and K.L. Mengersen "Classification based upon gene expression data: bias and precision of error rates" *Bioinformatics*, June 1, 2007; 23(11): 1363 - 1370.

## See Also

[assessment](#), [getResults](#), [runOneLayerExtCV-methods](#)

## Examples

```
data('vV70genesDataset')

# assessment with RFE and SVM
myExpe <- new("assessment", dataset=vV70genes,
             noFolds1stLayer=9,
             noFolds2ndLayer=10,
             classifierName="svm",
             typeFoldCreation="original",
```

```

svmKernel="linear",
noOfRepeat=2,
featureSelectionOptions=new("geneSubsets", optionValues=c(1,2,3,4,5,6))

myExpe <- runTwoLayerExtCV(myExpe)

```

---

setDataset-methods *getDataset<- Method to modify the attributes of a dataset from an*

---

## Description

This method provides an easy interface to modify the attributes of a dataset directly from an object assessment. The argument `topic` specifies which part of the dataset should be modified. This method is only available none of the one-layer CV or two-layers CV have been performed and the final classifier has not been determined yet.

## Arguments

|                     |   |
|---------------------|---|
| <code>object</code> | class assessment. Object assessment of interest   |
| <code>topic</code>  | character. Optional argument that specifies which attribute of the dataset must be changed, the possible values are <code>dataId</code> (slot <code>dataId</code> of the dataset), <code>dataPath</code> (slot <code>dataPath</code> of the dataset), <code>geneExprFile</code> (slot <code>geneExprFile</code> of the dataset), <code>classesFile</code> (slot <code>classesFile</code> of the dataset), if the <code>topic</code> is missing then the whole dataset object is replaced. |
| <code>value</code>  | The replacement value.  |

## Value

The methods modifies the object of class assessment and returned the slot modified accordingly to the request provided by `topic`.

If `'topic'` is missing `object` of class `dataset` the dataset corresponding to the assessment is replaced by `'value'`.

If `'topic'` is `"dataId"` `object` of class `character` the `'dataId'` of the dataset is replaced by `'value'`

If `'topic'` is `"dataPath"` `object` of class `character` the `'dataPath'` of the dataset is replaced by `'value'`

If `'topic'` is `"geneExprFile"` `object` of class `character` the `'geneExprFile'` of the dataset is replaced by `'value'`

If `'topic'` is `"classesFile"` `object` of class `character` the `'classesFile'` of the dataset is replaced by `'value'`

## Methods

**object = "assessment"** This method is only applicable on objects of class `assessment`.

## Author(s)

Camille Maumet

**See Also**

[assessment](#), [getDataset-methods](#)

**Examples**

```
## Not run:
aDataset <- new("dataset", dataId="vantVeer_70", dataPath="pathToFile")
aDataset <- loadData(aDataset)

expeOfInterest <- new("assessment", dataset=aDataset,
                      noFolds1stLayer=10,
                      noFolds2ndLayer=9,
                      classifierName="svm",
                      typeFoldCreation="original",
                      svmKernel="linear",
                      noOfRepeat=2,
                      featureSelectionOptions=new("geneSubsets", optionValue

# Modify the dataId
getDataset(expeOfInterest, topic='dataId') <- "khan"
getDataset(expeOfInterest, 'dataId')

# Replace the dataset
getDataset(expeOfInterest) <- aDataset
getDataset(expeOfInterest, 'dataId')

## End(Not run)
```

---

setFeatureSelectionOptions-methods

*getFeatureSelectionOptions* <- Method to modify the attributes of a

---

**Description**

This method provides an easy interface to modify the attributes of the object of class `featureSelectionOptions` related to a particular assessment, directly from this object `assessment`. The argument `topic` specifies which part of the `featureSelectionOptions` is of interest. This method is only available none of the one-layer CV or two-layers CV have been performed and the final classifier has not been determined yet.

**Arguments**

|                     |   |
|---------------------|---|
| <code>object</code> | Object of class <code>assessment</code> . Object assessment of interest   |
| <code>topic</code>  | character. Optional argument that specifies which attribute of the <code>featureSelectionOptions</code> must be replaced, the possible values are: <code>"optionValues"</code> (slot <code>optionValues</code> of the <code>featureSelectionOptions</code> ), <code>"noOfOptions"</code> (slot <code>noOfOptions</code> of the <code>featureSelectionOptions</code> ), if the <code>featureSelectionOptions</code> object is an object of class <code>geneSubsets</code> , then the following values are also available for the argument <code>topic</code> <code>"subsetsSizes"</code> (slot <code>optionValues</code> of the <code>geneSubsets</code> ), <code>"noModels"</code> (slot <code>noOfOptions</code> of the <code>geneSubsets</code> ), <code>"maxSubsetSize"</code> (slot <code>maxSelectedFeatures</code> of the <code>geneSubsets</code> ), |

"speed" (slot speed of the featureSelectionOptions), if the featureSelectionOptions object is an object of class thresholds, then the following values are also available for the argument topic "thresholds" (slot optionValues of the object thresholds), "noThresholds" (slot noOfOptions of the object thresholds)

if the topic is missing then the whole featureSelectionOptions object is replaced.

## Value

The methods modifies the object of class assessment and returned the slot modified accordingly to the request provided by topic.

If topic is missing object of class featureSelectionOptions featureSelectionOptions corresponding to the assessment is replaced by value.

If topic is "optionValues" numeric Slot optionValues of the featureSelectionOptions is replaced by value.

If topic is "noOfOptions" numeric Slot noOfOptions of the featureSelectionOptions is replaced by value.

If object is of class geneSubsets and topic is "maxSubsetSize" numeric Slot maxSubsetSize of the geneSubsets is replaced by value.

If object is of class geneSubsets and topic is "subsetsSizes" numeric Slot optionValues of the geneSubsets is replaced by value.

If object is of class geneSubsets and topic is "noModels" numericSlot noOfOptions of the geneSubsets is replaced by value.

If object is of class geneSubsets and topic is "speed" numeric Slot speed of the geneSubsets is replaced by value.

If object is of class thresholds and topic is "thresholds" numeric Slot optionValues of the object of class thresholds is replaced by value.

If object is of class thresholds and topic is "noThresholds" numeric Slot noOfOptions of the object of class thresholds is replaced by value.

## Methods

**object = "assessment"** The method is only applicable on objects of class assessment.

## Author(s)

Camille Maumet

## See Also

[featureSelectionOptions](#), [assessment](#)

## Examples

```
# With an assessment using RFE
data('vV70genesDataset')

mySubsets <- new("geneSubsets", optionValues=c(1,2,3,4,5,6))
myExpe <- new("assessment", dataset=vV70genes,
```

```

noFolds1stLayer=10,
noFolds2ndLayer=9,
classifierName="svm",
typeFoldCreation="original",
svmKernel="linear",
noOfRepeat=2,
featureSelectionOptions=mySubsets)

# Modify the size of the biggest subset
getFeatureSelectionOptions(myExpe, topic='maxSubsetSize') <- 70
getFeatureSelectionOptions(myExpe, topic='maxSubsetSize')
# Modify all the sizes of subsets
getFeatureSelectionOptions(myExpe, topic='subsetsSizes') <- c(1,5,10,25,30)
getFeatureSelectionOptions(myExpe, topic='subsetsSizes')
# Modify the speed
getFeatureSelectionOptions(myExpe, topic='speed') <- 'slow'
getFeatureSelectionOptions(myExpe, topic='speed')
# Modify the entire geneSubsets
getFeatureSelectionOptions(myExpe) <- mySubsets
getFeatureSelectionOptions(myExpe, topic='maxSubsetSize')
getFeatureSelectionOptions(myExpe, topic='subsetsSizes')
getFeatureSelectionOptions(myExpe, topic='speed')
getFeatureSelectionOptions(myExpe, topic='noModels')

# With an assessment using NSC as a feature selection method
myThresholds <- new("thresholds", optionValues=c(0.1,0.2,0.3))
myExpe2 <- new("assessment", dataset=vV70genes,
              noFolds1stLayer=10,
              noFolds2ndLayer=9,
              classifierName="nsc",
              featureSelectionMethod='nsc',
              typeFoldCreation="original",
              svmKernel="linear",
              noOfRepeat=2,
              featureSelectionOptions=myThresholds)

otherThresholds <- new("thresholds", optionValues=c(0,0.5,1,1.5,2,2.5,3))
# Modify the whole object 'featureSelectionOptions' (an object of class thresholds)
getFeatureSelectionOptions(myExpe2) <- otherThresholds
getFeatureSelectionOptions(myExpe2, topic='thresholds')
getFeatureSelectionOptions(myExpe2, topic='noThresholds')

```

---

show-methods

*show Display the object, by printing, plotting or whatever suits its*


---

### Description

Implementation of R method show to display object from package Rmagpie.

### Author(s)

Camille Maumet

---

thresholds-class    *thresholds: A class to handle the thresholds to be tested during*

---

### Description

The Nearest Shrunken Centroid is computed using a threshold. This threshold is usually determined by finding the best threshold value over a set of values by finding the threshold leading to the best error rate assessed by cross-validation. This class stores the values of thresholds to be tried. If the user wants to use default values it's also possible.

### Creating objects

```
new("thresholds")
```

Create an empty thresholds. The default thresholds values will be computed and this object updated as soon as it is linked in an assessment.

```
new("thresholds", optionValues)
```

Create a thresholds, containing the thresholds values defined by `optionValues`. The slot `noOfOptions` is automatically updated.

### Slots

**optionValues:** numeric Values of the thresholds, if `optionValues` has length zero then the default thresholds values must be used.

**noOfOptions:** numeric Number of thresholds.

### Extends

Class "[featureSelectionOptions](#)", directly.

### Methods

`getNoThresholds(thresholds)` Retrieve the number of the thresholds (slot `noOfOptions`)

`getOptionValues(thresholds)`, `getOptionValues(thresholds) <-` Retrieve and modify the values of the thresholds (slot `optionValues`)

### Author(s)

Camille Maumet

### See Also

[geneSubsets](#), [assessment](#)

### Examples

```
# Empty thresholds, the default values will be used when added to an assessment
emptThresholds <- new("thresholds")
getOptionValues(emptThresholds)
getNoThresholds(emptThresholds)
```

```
# Another thresholds
```

```
thresholds <- new("thresholds", optionValues=c(0,0.1,0.2,1,2))
getOptionValues(thresholds)
getNoThresholds(thresholds)

# Set the thresholds
newThresholds <- c(0.1,0.2,0.5,0.6,1)
getOptionValues(thresholds) <- newThresholds
getOptionValues(thresholds)
getNoThresholds(thresholds)
```

---

vV70genes

*vV70genes: van't Veer et al. 70 best genes in an object of class*

---

### Description

Gene Expression values and output classes of the 70 best genes selected by van't Veer et al. (cf. references) on 78 patients in 'Gene expression profiling predicts clinical outcome of breast cancer'.

### Usage

```
data('vV70genesDataset')
```

### Format

lkdsjsh

### References

L.J. van 't Veer LJ, H. Dai, M.J. van de Vijver, Y.D. He, A.A. Hart, M. Mao, H.L. Peterse, K. van der Kooy, M.J. Marton, A.T. Witteveen, G.J. Schreiber, R.M. Kerkhoven, C. Roberts, P.S. Linsley, R. Bernards, S.H. Friend, 'Gene expression profiling predicts clinical outcome of breast cancer', in Nature. 2002 Jan 31;415(6871):484-5.

### Examples

```
data('vV70genesDataset')
vV70genes
```



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