Package: omada (via r-universe)

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Type Package

Title Machine learning tools for automated transcriptome clustering analysis

Version 1.14.0

Description Symptomatic heterogeneity in complex diseases reveals differences in molecular states that need to be investigated. However, selecting the numerous parameters of an exploratory clustering analysis in RNA profiling studies requires deep understanding of machine learning and extensive computational experimentation. Tools that assist with such decisions without prior field knowledge are nonexistent and further gene association analyses need to be performed independently. We have developed a suite of tools to automate these processes and make robust unsupervised clustering of transcriptomic data more accessible through automated machine learning based functions. The efficiency of each tool was tested with four datasets characterised by different expression signal strengths. Our toolkit's decisions reflected the real number of stable partitions in datasets where the subgroups are discernible. Even in datasets with less clear biological distinctions, stable subgroups with different expression profiles and clinical associations were found.

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`clusteringMethodSelection` *Method Selection through intra-method Consensus Partition Consistency*

Description

Method Selection through intra-method Consensus Partition Consistency

Usage

```
clusteringMethodSelection(data, method.upper.k = 5, number.of.comparisons = 3)
```

Arguments

`data`	A dataframe, where columns are features and rows are data points
`method.upper.k`	The number of clusters, k, up to which the average agreements will be calculated
`number.of.comparisons`	The number of comparisons to average over per k

Value

An object of class "methodSelection" containing a dataframe of partition agreement scores for a set of random parameters clustering runs across different methods and the corresponding plot

Examples

```
clusteringMethodSelection(toy_genes, method.upper.k = 3,
number.of.comparisons = 2)
```

`clusterVoting` *Estimating number of clusters through internal exhaustive ensemble majority voting*

Description

Estimating number of clusters through internal exhaustive ensemble majority voting

Usage

```
clusterVoting(data, min.k, max.k, algorithm)
```

Arguments

`data`	A dataframe, where columns are features and rows are data points
`min.k`	Minimum number of clusters for which we calculate stabilities
`max.k`	Maximum number of clusters for which we calculate stabilities
`algorithm`	The clustering algorithm to use for the multiple clustering runs to be measured

Value

An object of class "clusterVoting" containing a matrix with metric scores for every k and internal index, cluster memberships for every k, a dataframe with the k votes for every index, k vote frequencies and the frequency barplot of the k votes

Examples

```
clusterVoting(toy_genes, 4,14,"sc")
```

`feasibilityAnalysis` *Simulating dataset and calculate stabilities over different number of clusters*

Description

Simulating dataset and calculate stabilities over different number of clusters

Usage

```
feasibilityAnalysis(classes = 3, samples = 320, features = 400)
```

Arguments

classes	The number of classes of samples to be reflected in the simulated dataset. Also determines the ks to be considered (classes-2, classes+2)
samples	The number of samples in the simulated dataset
features	The number of features in the simulated dataset

Value

An object of class "feasibilityAnalysis" containing the average stabilities for all number of clusters(k), the average (over all k) and maximum stabilities observed and the generated dataset

Examples

```
feasibilityAnalysis(classes = 2, samples = 20, features = 30)
```

---

feasibilityAnalysisDataBased

Simulating dataset based on existing dataset's dimensions, mean and standard deviation

---

Description

Simulating dataset based on existing dataset's dimensions, mean and standard deviation

Usage

```
feasibilityAnalysisDataBased(data, classes = 3)
```

Arguments

data	The dataset to base the simulation extracting the number of samples, features and numeric
classes	The number of classes of samples to be reflected in the simulated dataset. Also determines the ks to be considered (classes-2, classes+2)

Value

An object of class "feasibilityAnalysis" containing the average stabilities for all numbers of clusters(k), the average (over all k) and maximum stabilities observed and the generated dataset

Examples

```
feasibilityAnalysisDataBased(data = toy_genes, classes = 2)
```

`featureSelection` *Predictor variable subsampling sets and bootstrapping stability set selection*

Description

Predictor variable subsampling sets and bootstrapping stability set selection

Usage

```
featureSelection(data, min.k = 2, max.k = 4, step = 5)
```

Arguments

`data`	A dataframe, where columns are features and rows are data points
`min.k`	Minimum number of clusters for which we calculate stabilities
`max.k`	Maximum number of clusters for which we calculate stabilities
`step`	The number for additional features each feature set will contain

Value

An object of class "featureSelection" containing the dataframe of average bootstrap stabilities, where rows represent feature sets and columns number of clusters, the corresponding line plot, the number and the names of the selected features

Examples

```
featureSelection(toy_genes, min.k = 2, max.k = 4, step = 10)
```

`get_agreement_scores` *Get a dataframe of partition agreement scores for a set of random parameters clustering runs across different methods*

Description

Get a dataframe of partition agreement scores for a set of random parameters clustering runs across different methods

Usage

```
get_agreement_scores(object)
```

Arguments

`object`	An object of class "partitionAgreement"

Value

A dataframe of partition agreement scores for a set of random parameters clustering runs across different methods

Examples

```
pa.object <- partitionAgreement(toy_genes, algorithm.1 = "spectral",
measure.1 = "rbfdot", algorithm.2 = "kmeans",measure.2 = "Lloyd",
number.of.clusters = 3)
get_agreement_scores(pa.object)
```

---

get_average_feature_k_stabilities

Get a dataframe of average bootstrap stabilities

Description

Get a dataframe of average bootstrap stabilities

Usage

```
get_average_feature_k_stabilities(object)
```

Arguments

object	An object of class "featureSelection"

Value

A dataframe of average bootstrap stabilities

Examples

```
fs.object <- featureSelection(toy_genes, min.k = 3, max.k = 4, step = 10)
get_average_feature_k_stabilities(fs.object)
```

get_average_stabilities_per_k *Get average stabilities for all numbers of clusters(k)*

Description

Get average stabilities for all numbers of clusters(k)

Usage

```
get_average_stabilities_per_k(object)
```

Arguments

object	An object of class "feasibilityAnalysis"

Value

Average stabilities for all numbers of clusters(k)

Examples

```
fa.object <- feasibilityAnalysis(classes = 2, samples = 10, features = 15)
average.sts.k <- get_average_stabilities_per_k(fa.object)
```

get_average_stability *Get the average stability(over all k)*

Description

Get the average stability(over all k)

Usage

```
get_average_stability(object)
```

Arguments

object	An object of class "feasibilityAnalysis"

Value

The average stability(over all k)

Examples

```
fa.object <- feasibilityAnalysis(classes = 2, samples = 10, features = 15)
average.st <- get_average_stability(fa.object)
```

get_cluster_memberships_k

Get cluster memberships for every k

Description

Get cluster memberships for every k

Usage

```
get_cluster_memberships_k(object)
```

Arguments

object	An object of class "clusterVoting"

Value

Cluster memberships for every k

Examples

```
cv.object <- clusterVoting(toy_genes, 4,6,"sc")
get_cluster_memberships_k(cv.object)
```

get_cluster_voting_k_votes

Get k vote frequencies

Description

Get k vote frequencies

Usage

```
get_cluster_voting_k_votes(object)
```

Arguments

object	An object of class "clusterAnalysis"

Value

Matrix with k vote frequencies

Examples

```
oa.object <- omada(toy_genes, method.upper.k = 4)
get_cluster_voting_k_votes(oa.object)
```

`get_cluster_voting_memberships`

Get cluster memberships for every k

Description

Get cluster memberships for every k

Usage

```
get_cluster_voting_memberships(object)
```

Arguments

`object`	An object of class "clusterAnalysis"

Value

Cluster memberships for every k

Examples

```
oa.object <- omada(toy_genes, method.upper.k = 4)
get_cluster_voting_memberships(oa.object)
```

`get_cluster_voting_metric_votes`

Get a dataframe with the k votes for every index

Description

Get a dataframe with the k votes for every index

Usage

```
get_cluster_voting_metric_votes(object)
```

Arguments

`object`	An object of class "clusterAnalysis"

Value

Dataframe with the k votes for every index

Examples

```
oa.object <- omada(toy_genes, method.upper.k = 4)
get_cluster_voting_metric_votes(oa.object)
```

---

get_cluster_voting_scores

Get a matrix with metric scores for every k and internal index

---

Description

Get a matrix with metric scores for every k and internal index

Usage

```
get_cluster_voting_scores(object)
```

Arguments

object	An object of class "clusterAnalysis"

Value

A matrix with metric scores for every k and internal index

Examples

```
oa.object <- omada(toy_genes, method.upper.k = 4)
get_cluster_voting_scores(oa.object)
```

---

get_feature_selection_optimal_features

Get the optimal features

Description

Get the optimal features

Usage

```
get_feature_selection_optimal_features(object)
```

Arguments

object	An object of class "clusterAnalysis"

Value

The list of optimal features

Examples

```
oa.object <- omada(toy_genes, method.upper.k = 4)
get_feature_selection_optimal_features(oa.object)
```

---

get_feature_selection_optimal_number_of_features

Get the optimal number of features

Description

Get the optimal number of features

Usage

```
get_feature_selection_optimal_number_of_features(object)
```

Arguments

object	An object of class "clusterAnalysis"

Value

The optimal number of features

Examples

```
oa.object <- omada(toy_genes, method.upper.k = 6)
get_feature_selection_optimal_number_of_features(oa.object)
```

get_feature_selection_scores *Get a dataframe of average bootstrap stabilities*

Description

Get a dataframe of average bootstrap stabilities

Usage

```
get_feature_selection_scores(object)
```

Arguments

object	An object of class "clusterAnalysis"

Value

A dataframe of average bootstrap stabilities

Examples

```
oa.object <- omada(toy_genes, method.upper.k = 6)
get_feature_selection_scores(oa.object)
```

get_generated_dataset *Get the simulated dataset*

Description

Get the simulated dataset

Usage

```
get_generated_dataset(object)
```

Arguments

object	An object of class "feasibilityAnalysis"

Value

Simulated dataset

Examples

```
fa.object <- feasibilityAnalysis(classes = 4, samples = 50, features = 15)
generated.ds <- get_generated_dataset(fa.object)
```

get_internal_metric_scores *Get a matrix with metric scores for every k and internal index*

Description

Get a matrix with metric scores for every k and internal index

Usage

```
get_internal_metric_scores(object)
```

Arguments

object	An object of class "clusterVoting"

Value

A matrix with metric scores for every k and internal index

Examples

```
cv.object <- clusterVoting(toy_genes, 4,6,"sc")
get_internal_metric_scores(cv.object)
```

get_max_stability *Get the maximum stability*

Description

Get the maximum stability

Usage

```
get_max_stability(object)
```

Arguments

object	An object of class "feasibilityAnalysis"

Value

The maximum stability

Examples

```
fa.object <- feasibilityAnalysis(classes = 2, samples = 10, features = 15)
maximum.st <- get_max_stability(fa.object)
```

get_metric_votes_k *Get a dataframe with the k votes for every index*

Description

Get a dataframe with the k votes for every index

Usage

```
get_metric_votes_k(object)
```

Arguments

object	An object of class "clusterVoting"

Value

Dataframe with the k votes for every index

Examples

```
cv.object <- clusterVoting(toy_genes, 4,6,"sc")
get_metric_votes_k(cv.object)
```

get_optimal_features *Get the optimal features*

Description

Get the optimal features

Usage

```
get_optimal_features(object)
```

Arguments

object	An object of class "featureSelection"

Value

The list of optimal features

Examples

```
fs.object <- featureSelection(toy_genes, min.k = 3, max.k = 6, step = 10)
get_optimal_features(fs.object)
```

`get_optimal_memberships` *Get a dataframe with the memberships of the samples found in the input data*

Description

Get a dataframe with the memberships of the samples found in the input data

Usage

```
get_optimal_memberships(object)
```

Arguments

`object`	An object of class "optimalClustering"

Value

A dataframe with the memberships of the samples found in the input data

Examples

```
oc.object <- optimalClustering(toy_genes, 4, "spectral")
get_optimal_memberships(oc.object)
```

`get_optimal_number_of_features` *Get the optimal number of features*

Description

Get the optimal number of features

Usage

```
get_optimal_number_of_features(object)
```

Arguments

`object`	An object of class "featureSelection"

Value

The optimal number of features

Examples

```
fs.object <- featureSelection(toy_genes, min.k = 3, max.k = 6, step = 10)
get_optimal_number_of_features(fs.object)
```

---

get_optimal_parameter_used

Get the optimal parameter used

Description

Get the optimal parameter used

Usage

```
get_optimal_parameter_used(object)
```

Arguments

object	An object of class "optimalClustering"

Value

The optimal parameter used

Examples

```
oc.object <- optimalClustering(toy_genes, 4, "spectral")
get_optimal_parameter_used(oc.object)
```

---

get_optimal_stability_score

Get the optimal stability score

Description

Get the optimal stability score

Usage

```
get_optimal_stability_score(object)
```

Arguments

object	An object of class "optimalClustering"

Value

The optimal stability score

Examples

```
oc.object <- optimalClustering(toy_genes, 4, "spectral")
get_optimal_stability_score(oc.object)
```

---

get_partition_agreement_scores

Get a dataframe of partition agreement scores for a set of random parameters clustering runs across different methods

---

Description

Get a dataframe of partition agreement scores for a set of random parameters clustering runs across different methods

Get a dataframe of partition agreement scores

Usage

```
get_partition_agreement_scores(object)

get_partition_agreement_scores(object)
```

Arguments

object	An object of class "clusterAnalysis"

Value

A dataframe of partition agreement scores for a set of random parameters clustering runs across different methods

A dataframe of partition agreement scores parameters clustering runs across different methods

Examples

```
ms.object <- clusteringMethodSelection(toy_genes, method.upper.k = 3,
number.of.comparisons = 2)
get_partition_agreement_scores(ms.object)
oa.object <- omada(toy_genes, method.upper.k = 4)
get_partition_agreement_scores(oa.object)
```

get_sample_memberships

Get a dataframe with the memberships of the samples found in the input data

Description

Get a dataframe with the memberships of the samples found in the input data

Usage

```
get_sample_memberships(object)
```

Arguments

object	An object of class "clusterAnalysis"

Value

A dataframe with the memberships of the samples found in the input data

Examples

```
oa.object <- omada(toy_genes, method.upper.k = 4)
get_sample_memberships(oa.object)
```

get_vote_frequencies_k

Get k vote frequencies

Description

Get k vote frequencies

Usage

```
get_vote_frequencies_k(object)
```

Arguments

object	An object of class "clusterVoting"

Value

Matrix with k vote frequencies

Examples

```
cv.object <- clusterVoting(toy_genes, 4,6,"sc")
get_vote_frequencies_k(cv.object)
```

`omada` *A wrapper function that utilizes all tools to produce the optimal sample memberships*

Description

A wrapper function that utilizes all tools to produce the optimal sample memberships

Usage

```
omada(data, method.upper.k = 5)
```

Arguments

`data`	A dataframe, where columns are features and rows are data points
`method.upper.k`	The upper limit of clusters, k, to be considered. Must be more than 2

Value

An object of class "clusterAnalysis" containing partition.agreement.scores,partition.agreement.plot,feature.selection.scores, feature.selection.plot, feature.selection.optimal.features, feature.selection.optimal.number.of.features, cluster.voting.scores, cluster.voting.cluster.memberships,cluster.voting.metric.votes,

Examples

```
omada(toy_genes, method.upper.k = 3)
```

`optimalClustering` *Clustering with the optimal parameters estimated by these tools*

Description

Clustering with the optimal parameters estimated by these tools

Usage

```
optimalClustering(data, clusters, algorithm)
```

Arguments

`data`	A dataframe, where columns are features and rows are data points
`clusters`	Number of clusters to be generated by this clustering
`algorithm`	The clustering algorithm to be used

Value

An object of class "optimalClustering" containing a dataframe with the memberships of the samples found in the input data, the optimal stability score and parameter used

Examples

```
optimalClustering(toy_genes, 2,"kmeans")
```

`partitionAgreement` *Partition Agreement calculation between two clustering runs*

Description

Calculate the agreement (0,1) between two partitioning generated by two clustering runs using the adjust Rand Index. We can use three clustering algorithms (spectral, kmeans and hierarchical) along with the following parameters for each:

Usage

```
partitionAgreement(
  data,
  algorithm.1 = "hierarchical",
  measure.1 = "canberra",
  hier.agglo.algorithm.1 = "average",
  algorithm.2 = "hierarchical",
  measure.2 = "manhattan",
  hier.agglo.algorithm.2 = "average",
  number.of.clusters = 5
)
```

Arguments

`data`	A dataframe, where columns are features and rows are data points
`algorithm.1`	Second algorithm to be used (spectral/kmeans/hierarchical)
`measure.1`	Concerns the first algorithm to be used and represents a kernel for Spectral/kmeans or a distance measure for hierarchical clustering
`hier.agglo.algorithm.1`	Concerns the first algorithm to be used and represents the agglomerative method for hierarchical clustering (not used in spectral/kmeans clustering)
`algorithm.2`	First algorithm to be used (spectral/kmeans/hierarchical)
`measure.2`	Concerns the second algorithm to be used and represents a kernel for Spectral/kmeans or a distance measure for hierarchical clustering
`hier.agglo.algorithm.2`	Concerns the second algorithm to be used and represents the agglomerative method for hierarchical clustering (not used in spectral/kmeans clustering)

number.of.clusters
: The upper limit of clusters to form starting from 2

Details

Spectral kernels: rbfdot, polydot, vanilladot, tanhdot, laplacedot, besseldot, anovadot, splinedot

K-means kernels: "Hartigan-Wong", Lloyd, Forgy, MacQueen

Hierarchical Agglomeration methods: average, ward.D, ward.D2, single, complete, mcquitty, median, centroid

Distance measures: euclidean, manhattan, canberra, minkowski, maximum

Value

An object of class "partitionAgreement" containing agreements (Rand Indexes) from 1 cluster (ARI=0) up to the number of clusters requested

Examples

```
partitionAgreement(toy_genes, algorithm.1 = "hierarchical",
measure.1 = "canberra",hier.agglo.algorithm.1 = "average",
algorithm.2 = "hierarchical",measure.2 = "manhattan",
hier.agglo.algorithm.2 = "average",number.of.clusters = 3)

partitionAgreement(toy_genes, algorithm.1 = "spectral", measure.1 = "rbfdot",
algorithm.2 = "kmeans",measure.2 = "Lloyd", number.of.clusters = 5)
```

---

plot_average_stabilities

Plot the average bootstrap stabilities

Description

Plot the average bootstrap stabilities

Usage

```
plot_average_stabilities(object)
```

Arguments

object
: An object of class "featureSelection"

Value

Line plot of average bootstrap stabilities

Examples

```
fs.object <- featureSelection(toy_genes, min.k = 3, max.k = 6, step = 10)
plot_average_stabilities(fs.object)
```

plot_cluster_voting *Plot k vote frequencies*

Description

Plot k vote frequencies

Usage

```
plot_cluster_voting(object)
```

Arguments

object	An object of class "clusterAnalysis"

Value

Plot k vote frequencies

Examples

```
oa.object <- omada(toy_genes, method.upper.k = 3)
plot_cluster_voting(oa.object)
```

plot_feature_selection *Plot the average bootstrap stabilities*

Description

Plot the average bootstrap stabilities

Usage

```
plot_feature_selection(object)
```

Arguments

object	An object of class "clusterAnalysis"

Value

Line plot of average bootstrap stabilities

Examples

```
oa.object <- omada(toy_genes, method.upper.k = 4)
plot_feature_selection(oa.object)
```

plot_partition_agreement *Plot of partition agreement scores*

Description

Plot of partition agreement scores

Plot of partition agreement scores

Usage

```
plot_partition_agreement(object)

plot_partition_agreement(object)
```

Arguments

object	An object of class "clusterAnalysis"

Value

Plot of partition agreement scores

Plot of partition agreement scores

Examples

```
ms.object <- clusteringMethodSelection(toy_genes, method.upper.k = 3,
number.of.comparisons = 2)
plot_partition_agreement(ms.object)
oa.object <- omada(toy_genes, method.upper.k = 4)
plot_partition_agreement(oa.object)
```

plot_vote_frequencies *Plot k vote frequencies*

Description

Plot k vote frequencies

Usage

```
plot_vote_frequencies(object)
```

Arguments

object	An object of class "clusterVoting"

Value

Plot k vote frequencies

Examples

```
cv.object <- clusterVoting(toy_genes, 4,6,"sc")
plot_vote_frequencies(cv.object)
```

---

toy_gene_memberships *Cluster memberships for toy gene data for package examples*

Description

Column "id" represents genes and column "memberships" represents their respective clusters. Rows are samples

Usage

```
data(toy_gene_memberships)
```

Format

An object of class '"cross"'; see [qtl::read.cross()].

Source

nope

References

nothing

Examples

```
data(toy_gene_memberships)
```

toy_genes *Toy gene data for package examples*

Description

Columns are genes and rows are samples

Usage

```
data(toy_genes)
```

Format

An object of class ‘"cross"‘; see [qtl::read.cross()].

Source

nope

References

nothing

Examples

```
data(toy_genes)
```

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