

Package ‘FeatureImpCluster’

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Title Feature Importance for Partitional Clustering

Version 0.1.5

Description Implements a novel approach for measuring feature importance in k-means clustering. Importance of a feature is measured by the misclassification rate relative to the baseline cluster assignment due to a random permutation of feature values. An explanation of permutation feature importance in general can be found here: <https://christophm.github.io/interpretable-ml-book/feature-importance.html>.

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Encoding UTF-8

Suggests flexclust, clustMixType, knitr, rmarkdown, testthat, attempt, ClustImpute, covr

Imports ggplot2

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Depends data.table

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Contents

create_random_data	2
FeatureImpCluster	2
PermMisClassRate	3
plot.featImpCluster	5
Index	6

create_random_data *Create random data set with 4 clusters*

Description

Create random data set with 4 clusters in a 2 dimensional subspace of a nr_other_vars+2 dimensional space

Usage

```
create_random_data(n = 10000, nr_other_vars = 4)
```

Arguments

n number of points
nr_other_vars number of other variables / "noise" dimensions

Value

list containing the random data.table and a vector with the true underlying cluster assignments

Examples

```
create_random_data(n=1e3)
```

FeatureImpCluster *Feature importance for k-means clustering*

Description

This function loops through [PermMisClassRate](#) for each variable of the data. The mean misclassification rate over all iterations is interpreted as variable importance.

Usage

```
FeatureImpCluster(  
  clusterObj,  
  data,  
  basePred = NULL,  
  predFUN = NULL,  
  sub = 1,  
  biter = 10  
)
```

Arguments

<code>clusterObj</code>	a "typical" cluster object. The only requirement is that there must be a prediction function which maps the data to an integer
<code>data</code>	<code>data.table</code> with the same features as the data set used for clustering (or the simply the same data)
<code>basePred</code>	should be equal to results of <code>predFUN(clusterObj,newdata=data)</code> ; this option saves time when data is a very large data set
<code>predFUN</code>	<code>predFUN(clusterObj,newdata=data)</code> should provide the cluster assignment as a numeric vector; typically this is a wrapper around a build-in prediction function
<code>sub</code>	integer between 0 and 1(=default), indicates that only a subset of the data should be used if <1
<code>biter</code>	the permutation is iterated <code>biter</code> (=5, default) times

Value

A list of

misClassRate A matrix of the permutation misclassification rate for each variable and each iteration

featureImp For each row of `complete_data`, the associated cluster

Examples

```
set.seed(123)
dat <- create_random_data(n=1e3)$data # random data

library(flexclust)
res <- kcca(dat,k=4)
f <- FeatureImpCluster(res,dat)
plot(f)
```

PermMisClassRate

Permutation misclassification rate for single variable

Description

Answers the following question: Using the current partition as a baseline, what is the misclassification rate if a given feature is permuted?

Usage

```
PermMisClassRate(
  clusterObj,
  data,
  varName,
  basePred = NULL,
  predFUN = NULL,
  sub = 1,
  biter = 5,
  seed = 123
)
```

Arguments

clusterObj	a "typical" cluster object. The only requirement is that there must be a prediction function which maps the data to an integer
data	data.table with the same features as the data set used for clustering (or the simply the same data)
varName	character; variable name
basePred	should be equal to results of predFUN(clusterObj,newdata=data); this option saves time when data is a very large data set
predFUN	predFUN(clusterObj,newdata=data) should provide the cluster assignment as a numeric vector; typically this is a wrapper around a build-in prediction function
sub	integer between 0 and 1(=default), indicates that only a subset of the data should be used if <1
biter	the permutation is iterated biter(=5, default) times
seed	value for random seed

Value

vector of length biter with the misclassification rate

Examples

```
set.seed(123)
dat <- create_random_data(n=1e3)$data # random data

library(flexclust)
res <- kcca(dat,k=4)
PermMisClassRate(res,dat,varName="x")
```

`plot.featImpCluster` *Feature importance box plot*

Description

Feature importance box plot

Usage

```
## S3 method for class 'featImpCluster'  
plot(x, dat = NULL, color = "none", showPoints = FALSE, ...)
```

Arguments

<code>x</code>	an object returned from <code>FeatureImpCluster</code>
<code>dat</code>	same data as used for the computation of the feature importance (only relevant for colored plots)
<code>color</code>	If set to "type", the plot will show different variable types with a different color.
<code>showPoints</code>	Show points (default is <code>False</code>)
<code>...</code>	arguments to be passed to base plot method

Value

Returns a `ggplot2` object

Index

`create_random_data`, [2](#)

`FeatureImpCluster`, [2](#)

`PermMisClassRate`, [2](#), [3](#)

`plot_featImpCluster`, [5](#)