

Package ‘MajMinKmeans’

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Type Package

Title k-Means Algorithm with a Majorization-Minimization Method

Version 0.1.0

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Description A hybrid of the K-means algorithm and a Majorization-Minimization method to introduce a robust clustering. The reference paper is: Julien Mairal, (2015) <[doi:10.1137/140957639](https://doi.org/10.1137/140957639)>. The two most important functions in package 'MajMinKmeans' are `cluster_km()` and `cluster_MajKm()`. `cluster_km()` clusters data without Majorization-Minimization and `cluster_MajKm()` clusters data with Majorization-Minimization method. Both of these functions calculate the sum of squares (SS) of clustering. Another useful function is `MajMinOptim()`, which helps to find the optimum values of the Majorization-Minimization estimator.

Imports MASS

License GPL-3

Encoding UTF-8

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NeedsCompilation no

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clusters_km *clustering results of the k-mean algorithm*

Description

clusters data into two clusters. This function uses the kmeans function to cluster the data and exports the clustering results as well as the sum of square (SS) of clustering using the Euclidian distance.

Usage

```
clusters_km(x, k = 2)
```

Arguments

x matrix of data (dim 1: samples (must be equal to dim 1 of X), dim 2: attributes (must be equal to dim 2 of X))

k number of clusters (this version considers 2 clusters)

Value

sum of square (SS) of clustering

Examples

```
{
X=rbind(matrix(rnorm(1000*2),4,.1),1000,2),matrix(rnorm(1000*2),3,0.2),1000,2)
M<- X[sample(nrow(X), 2),]
clusters_km(X,2)
}
```

clusters_MajKm *clustering results of the majorized k-mean algorithm*

Description

clusters data into two clusters with a majorization k-means This function uses a hybrid of the k-means and the majorization-minimization method to cluster the data and exports the clustering results as well as the sum of square (SS) of clustering

Usage

```
clusters_MajKm(X, k = 2, La)
```

Arguments

X	matrix of data (dim 1: samples (must be equal to dim 1 of X), dim 2: attributes (must be equal to dim 2 of X))
k	number of clusters (this version considers 2 clusters)
La	the tunning parameter

Value

sum of square (SS) of clustering and the 'delta' (difference of two successive majorization function).

Examples

```
{
X=rbind(matrix(rnorm(1000*2 ,4,.1),1000,2),matrix(rnorm(1000*2, 3, 0.2),1000,2))
M <- X[sample(nrow(X), 2),]
clusters_MajKm(X,2, 0.5)
}
```

Euclid	<i>Euclidian distance</i>
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Description

Calculates the Euclidian distance between points. This function can use in kmeans function to do the clustering procedure using the Euclidian distance.

Usage

```
Euclid(x, mu)
```

Arguments

x	matrix of data (dim 1: samples (must be equal to dim 1 of X), dim 2: attributes (must be equal to dim 2 of X))
mu	initial seleted centroids (randomly or another method).

Value

Euclidian distance between two points.

Examples

```
{
X=rbind(matrix(rnorm(1000*2 ,4,.1),1000,2),matrix(rnorm(1000*2, 3, 0.2),1000,2))
M <- X[sample(nrow(X), 2),]
Euclid(X,M)
}
```

kmeans	<i>k-means function</i>
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Description

k-means algorithm in clustering. This function export the clustered results based on one replication of the k-means method

Usage

```
kmeans(x, centers, nItter = 4)
```

Arguments

x	matrix of data (dim 1: samples (must be equal to dim 1 of X), dim 2: attributes (must be equal to dim 2 of X))
centers	initial seleted centroids (randomly or another method)
nItter	Number of itteration function

Value

clustered results based on k-means methods.

Examples

```
{
X=rbind(matrix(rnorm(1000*2 ,4,.1),1000,2),matrix(rnorm(1000*2, 3, 0.2),1000,2))
M <- X[sample(nrow(X), 2),]
kmeans(X,M, 4)
}
```

MajMinOptim	<i>majorization-minimization optimization</i>
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Description

Finding the optimized majorization-minimization centers

Usage

```
MajMinOptim(X, Z, M, eps, lambda)
```

Arguments

X	matrix of data (dim 1: samples (must be equal to dim 1 of X), dim 2: attributes (must be equal to dim 2 of X))
Z	is a n by k matrix where for all i and j, $z_{i,j}$ is abinary variable that is equal to 1 if the case i is assigned to cluster j and zero otherwise. (dim 1: samples (must be equal to dim 1 of X), dim 2: attributes (must be equal to dim 2 of X))
M	initial seleted centroids (randomly or another method)
eps	a threshold value assumed as 0.0001
lambda	a threshold value assumed as 0.5

Value

The optimized majorization-minimization centers.

Examples

```
{
X=rbind(matrix(rnorm(1000*2) ,4,.1),1000,2),matrix(rnorm(1000*2, 3, 0.2),1000,2))
M <- X[sample(nrow(X), 2),]
distsToCenters <- Euclid(X, M)
clusters <- apply(distsToCenters, 1, which.min)
Z <- matrix(0, nrow = NROW(X), ncol = 1)
for(i in 1:NROW(X))
  if (clusters[[i]] == 1)
    Z[i,]=clusters[[i]]
Z=cbind(Z, 1-Z)
MajMinOptim(X,Z,M ,eps=1e-4, lambda=.5)
}
```

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