

Package ‘MKMeans’

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Type Package

Title A Modern K-Means (MKMeans) Clustering Algorithm

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Depends methods, MASS

Description

It's a Modern K-Means clustering algorithm which works for data of any number of dimensions, has no limit with number of clusters expected, and can start with any initial cluster centers.

Collate AllClasses.R MKMeans.R C.f.R Dist.R

License GPL-2

NeedsCompilation no

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MKMeans-package

Modern K-Means (MKMeans) Clustering.

Description

It's a Modern K-Means clustering algorithm which works for data of any number of dimensions, has no limit with the number of clusters expected, and can start with any initial cluster centers.

Details

Package: MKMeans
Type: Package
Version: 3.3
Date: 2025-08-27
License: GPL-2

Author(s)

Yarong Yang, Nader Ebrahimi, Yoram Rubin, and Jacob Zhang

References

Yarong Yang, Nader Ebrahimi, Yoram Rubin, and Jacob Zhang.(2025) MKMeans: A Modern K-Means Clustering Algorithm. technical report

Examples

```
# Example 1:

# Generate 20 bivariate samples
x<-rnorm(20,0,1)
y<-rnorm(20,1,1)
data.test<-cbind(x,y)

# Conduct MKMeans analysis with K=3 and taking the first 3 samples as initial cluster centers
Res<-MKMeans(data.test,3,1,iteration=1000,type=1)
Res<-Res
names(Res@Classes[[1]])<-rep("red",length(Res@Classes[[1]]))
names(Res@Classes[[2]])<-rep("blue",length(Res@Classes[[2]]))
names(Res@Classes[[3]])<-rep("green",length(Res@Classes[[3]]))
Cols<-names(sort(c(Res@Classes[[1]],Res@Classes[[2]],Res@Classes[[3]])))
plot(x,y,type="p",col=Cols,lwd=2)
points(Res@Centers,pch=15,col=c("red","blue","green"))

# Example 2:
```

```

library(MASS)
# Generate 10 bivariate normal samples
mu1 <- c(0, 0)
sigma1 <- matrix(c(1, 0.5, 0.5, 1), nrow=2)
SP1 <- mvrnorm(n=10, mu=mu1, Sigma=sigma1)

# Generate another 10 bivariate normal samples
mu2<-c(1,1)
sigma2<-matrix(c(1,0,0,1),nrow=2)
SP2<-mvrnorm(n=10,mu=mu2,Sigma=sigma2)

# Generate 10 more new bivariate normal samples
mu3<-c(2,2)
sigma3<-matrix(c(1,0.5,0.5,1),nrow=2)
SP3<-mvrnorm(n=10,mu=mu3,Sigma=sigma3)

# Combine the three groups of bivariate normal samples
data<-rbind(SP1,SP2,SP3)

# Conduct MKMeans analysis with K=4 and randomly picking four samples as initial cluster centers
Res<-MKMeans(data,4,data[sample(1:30,4),,],iteration=1000,type=1)
names(Res@Classes[[1]])<-rep("red",length(Res@Classes[[1]]))
names(Res@Classes[[2]])<-rep("blue",length(Res@Classes[[2]]))
names(Res@Classes[[3]])<-rep("green",length(Res@Classes[[3]]))
names(Res@Classes[[4]])<-rep("black",length(Res@Classes[[4]]))
Cols<-names(sort(c(Res@Classes[[1]],Res@Classes[[2]],Res@Classes[[3]],Res@Classes[[4]])))
plot(data[,1],data[,2],type="p",pch=19,col=Cols,lwd=2,xlab="",ylab="")
points(Res@Centers,pch=5,col=c("red","blue","green","black"))

```

C.f

*Finding the center of a cluster.***Description**

It's a function of finding the center of a cluster.

Usage

```
C.f(dat, type)
```

Arguments

dat	Numeric. A cluster matrix with each row being an observaion.
type	Integer. The type of distance between observations. 1 for Euclidean distance. 2 for Manhattan distance. 3 for maximum deviation along dimensions.

Value

A vector.

Author(s)

Yarong Yang

Examples

```
x<-rnorm(5,0,1)
y<-rnorm(5,1,1)
data<-cbind(x,y)
Res<-C.f(dat=data, type=1)
```

Dist

Finding the distance between two observations.

Description

It's a function of finding the distance between two observations.

Usage

```
Dist(x,y,type)
```

Arguments

x	Numeric. A vector denoting an observation.
y	Numeric. A vector denoting an observation.
type	Integer. The type of distance between observations. 1 for Euclidean distance. 2 for Manhattan distance. 3 for maximum deviation among dimensions.

Value

A numeric number.

Examples

```
x<-rnorm(10,0,1)
y<-rnorm(10,1,1)
z<-rnorm(10,2,1)
data<-cbind(x,y,z)
Res<-Dist(data[1,],data[2,],type=1)
```

MKMean

Class to contain the results from function MKMeans.

Description

The function MKMeans return object of class MKMean that contains the number of clusters, the center of each cluster, and the observations in each cluster.

Objects from the Class

```
new("MKMean",K=new("numeric"),Centers=new("matrix"),Classes=new("list"),Clusters=new("list"),SSE=new("numeric"))
```

Slots

K: An integer being the number of clusters.

Centers: A numeric matrix with each row being center of a cluster.

Classes: An integer list showing the original indexes of the observations in each cluster.

Clusters: A numeric list showing the observations in each cluster.

SSE: A numeric vector composed of SSE of each cluster and the total SSE of all the clusters.

Author(s)

Yarong Yang

References

Yarong Yang, Nader Ebrahimi, Yoram Rubin, and Jacob Zhang.(2025) MKMeans: A Modern K-Means Clustering Algorithm. technical report

Examples

```
showClass("MKMean")
```

MKMeans

Modern K-Means clustering.

Description

It's a Modern K-Means clustering algorithm which works for data of any number of dimensions, has no limit with the number of clusters expected, and can start with any initial cluster centers.

Usage

```
MKMeans(data, K, initial, iteration, type)
```

Arguments

<code>data</code>	Numeric. An observation matrix with each row being an observation.
<code>K</code>	Integer. The number of clusters expected.
<code>initial</code>	Numeric. Either the selected initial center matrix with each row being an observation, or 1 for the first K rows of the data matrix being the initial center.
<code>iteration</code>	Integer. The number of the most iterations wanted for the clustering process.
<code>type</code>	Integer. The type of distance between observations. 1 for Euclidean distance. 2 for Manhattan distance. 3 for maximum deviation among dimensions.

Value

An object of class MKMean.

Author(s)

Yarong Yang

References

Yarong Yang, Nader Ebrahimi, Yoram Rubin, and Jacob Zhang.(2025) MKMeans: A Modern K-Means Clustering Algorithm. technical report

Examples

```
library(MASS)
# Generate 10 bivariate normal samples
mu1 <- c(0, 0)
sigma1 <- matrix(c(1, 0.5, 0.5, 1), nrow=2)
SP1 <- mvrnorm(n=10, mu=mu1, Sigma=sigma1)

# Generate another 10 bivariate normal samples
mu2<-c(1,1)
sigma2<-matrix(c(1,0,0,1),nrow=2)
SP2<-mvrnorm(n=10,mu=mu2,Sigma=sigma2)

# Generate 10 more new bivariate normal samples
mu3<-c(2,2)
sigma3<-matrix(c(1,0.5,0.5,1),nrow=2)
SP3<-mvrnorm(n=10,mu=mu3,Sigma=sigma3)

# Combine the three groups of bivariate normal samples
data<-rbind(SP1,SP2,SP3)

# Conduct MKMeans analysis with K=3 and randomly picking three samples as initial cluster centers
Res<-MKMeans(data,3,data[sample(1:30,3),],iteration=1000,type=1)
names(Res@Classes[[1]])<-rep("red",length(Res@Classes[[1]]))
names(Res@Classes[[2]])<-rep("blue",length(Res@Classes[[2]]))
names(Res@Classes[[3]])<-rep("green",length(Res@Classes[[3]]))
Cols<-names(sort(c(Res@Classes[[1]],Res@Classes[[2]],Res@Classes[[3]])))
plot(data[,1],data[,2],type="p",pch=19,col=Cols,lwd=2,xlab="",ylab="")
```

```

points(Res@Centers,pch=5,col=c("red","blue","green"))

# Compare the clustering results with the original samples
par(mfrow=c(1,2))
plot(data[,1],data[,2],type="p",pch=19,col=rep(c("sky blue","orange","purple"),rep(10,3)),
      lwd=2,xlab="",ylab="",main="Original Data")
plot(data[,1],data[,2],type="p",pch=19,col=Cols,lwd=2,xlab="",ylab="",
      main="MKMeans Clustering Results")
points(Res@Centers,pch=5,col=c("red","blue","green"))

# conduct MKMeans analysis with K=4 and randomly picking four samples as initial cluster centers
Res<-MKMeans(data,4,data[sample(1:30,4),],iteration=1000,type=1)
names(Res@Classes[[1]])<-rep("red",length(Res@Classes[[1]]))
names(Res@Classes[[2]])<-rep("blue",length(Res@Classes[[2]]))
names(Res@Classes[[3]])<-rep("green",length(Res@Classes[[3]]))
names(Res@Classes[[4]])<-rep("black",length(Res@Classes[[4]]))
Cols<-names(sort(c(Res@Classes[[1]],Res@Classes[[2]],Res@Classes[[3]],Res@Classes[[4]])))
plot(data[,1],data[,2],type="p",pch=19,col=Cols,lwd=2,xlab="",ylab="")
points(Res@Centers,pch=5,col=c("red","blue","green","black"))

# Compare the clustering results with the original data
par(mfrow=c(1,2))
plot(data[,1],data[,2],type="p",pch=19,col=rep(c("sky blue","orange","purple"),rep(10,3)),
      lwd=2,xlab="",ylab="",main="Original Data")
plot(data[,1],data[,2],type="p",pch=19,col=Cols,lwd=2,xlab="",ylab="",
      main="MKMeans Clustering Results")
points(Res@Centers,pch=5,col=c("red","blue","green","black"))

```

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