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Description Classical hierarchical clustering algorithms, agglomerative and divisive clustering. Algorithms are implemented as a theoretical way, step by step. It includes some detailed functions that explain each step. Every function allows options to get different results using different techniques. The package explains non expert users how hierarchical clustering algorithms work.

License Unlimited

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agglomerativeHC	<i>To execute agglomerative hierarchical clusterization algorithm by distance and approach.</i>
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Description

To execute complete agglomerative hierarchical clusterization algorithm choosing distance and approach type.

Usage

```
agglomerativeHC(data, distance, approach)
```

Arguments

data	could be a numeric vector, a matrix or a numeric data frame. It will be transformed into matrix and list to be used.
distance	is a string. It chooses the distance to use.
approach	is a string. It chooses the approach to use.

Details

This function is the main part of the agglomerative hierarchical clusterization method. It executes the theoretical algorithm step by step.

- 1 - The function transforms data in useful object to be used.
- 2 - It creates the clusters.
- 3 - It calculates a matrix distances with the clusters created applying distance and approach given.
- 4 - It chooses the distance value and gets the clusters.
- 5 - It groups the clusters in a new one and updates clusters list.
- 6 - It repeats these steps until an unique cluster exists.

Value

R object with a dendrogram, the grouped clusters and the list with every cluster.

Author(s)

Roberto Alcántara <roberto.alcantara@edu.uah.es>

Juan José Cuadrado <jjcg@uah.es>

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Examples

```
a <- c(1,2,1,3,1,4,1,5,1,6)
matrixA <- matrix(a,ncol=2)
dataFrameA <- data.frame(matrixA)
agglomerativeHC(a,'EUC','MAX')
agglomerativeHC(matrixA,'MAN','AVG')
agglomerativeHC(dataFrameA,'CAN','MIN')
```

agglomerativeHC.details

To explain agglomerative hierarchical clusterization algorithm by distance and approach.

Description

To explain the complete agglomerative hierarchical clusterization algorithm choosing distance and approach type.

Usage

```
agglomerativeHC.details(data, distance, approach)
```

Arguments

data	could be a numeric vector, a matrix or a numeric data frame. It will be transformed into matrix and list to be used.
distance	is a string. It chooses the distance to use.
approach	is a string. It chooses the approach to use.

Details

This function is the main part of the agglomerative hierarchical clusterization method. It explains the theoretical algorithm step by step.

- 1 - The function transforms data into useful object to be used.
- 2 - It creates the clusters.
- 3 - It calculates a matrix distance with the clusters created by applying the distance and the approach given.
- 4 - It chooses the distance value and gets the clusters.
- 5 - It groups the clusters in a new one and updates clusters list.
- 6 - It repeats these steps until an unique cluster exists.

Value

agglomerative algorithm explanation.

Author(s)

Roberto Alcántara <roberto.alcantara@edu.uah.es>

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Examples

```
a <- c(1,2,1,3,1,4,1,5,1,6)
matrixA <- matrix(a,ncol=2)
dataFrameA <- data.frame(matrixA)
agglomerativeHC.details(a,'EUC','MAX')
agglomerativeHC.details(matrixA,'MAN','AVG')
agglomerativeHC.details(dataFrameA,'CAN','MIN')
```

canberradistance

To calculate the Canberra distance.

Description

To calculate the Canberra distance of two clusters.

Usage

```
canberradistance(x, y)
```

Arguments

x is a numeric vector or a matrix. It represents the values of a cluster.
y is a numeric vector or a matrix. It represents the values of a cluster.

Details

This function is part of the hierarchical clusterization method. The function calculates the Canberra distance value from x and y.

Value

canberra distance value.

Author(s)

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Examples

```
x <- c(1,2)
y <- c(1,3)

cluster1 <- matrix(x,ncol=2)
cluster2 <- matrix(y,ncol=2)

canberradistance(x,y)

canberradistance(cluster1,cluster2)
```

canberradistance.details

To show the formula and to return the Canberra distance.

Description

To show the formula and to return the Canberra distance of two clusters.

Usage

```
canberradistance.details(x, y)
```

Arguments

- x is a numeric vector or a matrix. It represents the values of a cluster.
- y is a numeric vector or a matrix. It represents the values of a cluster.

Details

This function is part of the hierarchical clusterization method. The function calculates the Canberra distance value from x and y.

Value

canberra distance value with its formula.

Author(s)

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Examples

```
x <- c(1,2)
y <- c(1,3)

cluster1 <- matrix(x,ncol=2)
cluster2 <- matrix(y,ncol=2)

canberradistance(x,y)

canberradistance(cluster1,cluster2)
```

canberradistanceW *To calculate the Canberra distance applying weights.*

Description

To calculate the Canberra distance between clusters applying weights given.

Usage

```
canberradistanceW(cluster1, cluster2, weight)
```

Arguments

cluster1 is a cluster.
cluster2 is a cluster.
weight is a numeric vector.

Details

The function calculates the Canberra distance value from cluster1 and cluster2, applying weights to the cluster's components.

Value

canberra distance applying weights value.

Author(s)

Roberto Alcántara <roberto.alcantara@edu.uah.es>
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Examples

```
cluster1 <- matrix(c(1,2),ncol=2)
cluster2 <- matrix(c(1,3),ncol=2)

weight1 <- c(0.4,0.6)
weight2 <- c(2,12)

canberradistanceW(cluster1,cluster2,weight1)

canberradistanceW(cluster1,cluster2,weight2)
```

canberradistanceW.details

To calculate the Canberra distance applying weights .

Description

To explain how to calculate the Canberra distance between clusters applying weights given.

Usage

```
canberradistanceW.details(cluster1, cluster2, weight)
```


Arguments

cluster1 is a cluster.
cluster2 is a cluster.
weight is a numeric vector.

Details

The function calculates the Canberra distance value from cluster1 and cluster2, applying weights to the cluster's components.

Value

canberra distance applying weights value. Explanation.

Author(s)

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Examples

```
cluster1 <- matrix(c(1,2),ncol=2)
cluster2 <- matrix(c(1,3),ncol=2)

weight1 <- c(0.4,0.6)
weight2 <- c(2,12)

canberradistanceW.details(cluster1,cluster2,weight1)

canberradistanceW.details(cluster1,cluster2,weight2)
```

chebyshevDistance *To calculate the Chebyshev distance.*

Description

To calculate the Chebyshev distance of two clusters.

Usage

```
chebyshevDistance(x, y)
```

Arguments

`x` is a numeric vector or a matrix. It represents the values of a cluster.
`y` is a numeric vector or a matrix. It represents the values of a cluster.

Details

This function is part of the hierarchical clusterization method. The function calculates the Chebyshev distance value from `x` and `y`.

Value

Chebyshev distance value.

Author(s)

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Examples

```
x <- c(1,2)
y <- c(1,3)

cluster1 <- matrix(x,ncol=2)
cluster2 <- matrix(y,ncol=2)

chebyshevDistance(x,y)

chebyshevDistance(cluster1,cluster2)
```

chebyshevDistance.details

To show the formula of the Chebyshev distance.

Description

To show the formula of the Chebyshev distance of two clusters.

Usage

```
chebyshevDistance.details(x, y)
```

Arguments

- x is a numeric vector or a matrix. It represents the values of a cluster.
y is a numeric vector or a matrix. It represents the values of a cluster.

Details

This function is part of the hierarchical clusterization method. The function calculates the Chebyshev distance value from x and y.

Value

Chebyshev distance value and formula.

Author(s)

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Examples

```
x <- c(1,2)
y <- c(1,3)

cluster1 <- matrix(x,ncol=2)
cluster2 <- matrix(y,ncol=2)

chebyshevDistance(x,y)

chebyshevDistance(cluster1,cluster2)
```

chebyshevDistanceW *To calculate the Chebyshev distance applying weights.*

Description

To calculate the Chebyshev distance between clusters applying weights given.

Usage

```
chebyshevDistanceW(cluster1, cluster2, weight)
```

Arguments

cluster1 is a cluster.
cluster2 is a cluster.
weight is a numeric vector.

Details

The function calculates the Chebyshev distance value from cluster1 and cluster2, applying weights to the cluster's components.

Value

Chebyshev distance applying weights value.

Author(s)

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Examples

```
cluster1 <- matrix(c(1,2),ncol=2)
cluster2 <- matrix(c(1,3),ncol=2)

weight1 <- c(0.4,0.6)
weight2 <- c(2,12)

chebyshevDistanceW(cluster1,cluster2,weight1)

chebyshevDistanceW(cluster1,cluster2,weight2)
```

chebyshevDistanceW.details

To calculate the Chebyshev distance applying weights.

Description

To explain how to calculate the Chebyshev distance between clusters applying weights given.

Usage

```
chebyshevDistanceW.details(cluster1, cluster2, weight)
```

Arguments

cluster1 is a cluster.
cluster2 is a cluster.
weight is a numeric vector.

Details

The function calculates the Chebyshev distance value from cluster1 and cluster2, applying weights to the cluster's components.

Value

Chebyshev distance applying weights value. Explanation.

Author(s)

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Examples

```
cluster1 <- matrix(c(1,2),ncol=2)
cluster2 <- matrix(c(1,3),ncol=2)

weight1 <- c(0.4,0.6)
weight2 <- c(2,12)

chebyshevDistanceW.details(cluster1,cluster2,weight1)
chebyshevDistanceW.details(cluster1,cluster2,weight2)
```

clusterDistance *To calculate the distance between clusters.*

Description

To calculate the distance between clusters depending on the approach and distance type.

Usage

```
clusterDistance(cluster1, cluster2, approach, distance)
```

Arguments

cluster1	is a matrix
cluster2	is a matrix
approach	is a string. Type of function to apply.
distance	is a string. Type of distance to use.

Details

This function is part of the hierarchical clusterization method. The function calculates the final distance between cluster1 and cluster2 applying the approach definition, using the distance type given.

approach indicates the algorithm used to get the value. distance indicates the distance used to get the value. Possible values: 'MAX', 'MIN', 'AVG'.

Value

Distance between clusters.

Author(s)

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Examples

```
cluster1 <- matrix(c(1,2),ncol=2)
cluster2 <- matrix(c(1,4),ncol=2)

clusterDistance.details(cluster1,cluster2,'AVG','MAN')

clusterDistance.details(cluster1,cluster2,'MAX','OCT')
```

clusterDistance.details

To explain how to calculate the distance between clusters.

Description

To explain how to calculate the distance between clusters depending on the approach and distance type.

Usage

```
clusterDistance.details(cluster1, cluster2, approach, distance)
```

Arguments

cluster1	is a matrix
cluster2	is a matrix
approach	is a string. Type of function to apply.
distance	is a string. Type of distance to use.

Details

This function is part of the hierarchical clusterization method. The function explains how to calculate the final distance between cluster1 and cluster2 applying the approach definition, using the distance type given.

approach indicates the algorithm used to get the value. distance indicates the distance used to get the value. Possible values: 'MAX', 'MIN', 'AVG'.

Value

Distance between clusters. Explanation.

Author(s)

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Examples

```
cluster1 <- matrix(c(1,2),ncol=2)
cluster2 <- matrix(c(1,4),ncol=2)

clusterDistance.details(cluster1,cluster2,'AVG','MAN')

clusterDistance.details(cluster1,cluster2,'MAX','OCT')
```

clusterDistanceByApproach

To calculate the distance by approach option.

Description

To calculate the distance depending on option given.

Usage

```
clusterDistanceByApproach(distances, approach)
```

Arguments

distances is a numeric vector.
approach is a string. Type of function to apply.

Details

This function is part of the hierarchical clusterization method. The function calculates the distance value from distances.

approach indicates the algorithm used to get the value. Possible values: 'MAX', 'MIN', 'AVG'.

Value

max, min or average from a vector.

Author(s)

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Examples

```
distances1 <- c(4,14,24,34)
distances2 <- c(1:10)
clusterDistanceByApproach(distances1, 'MAX')
clusterDistanceByApproach(distances2, 'MIN')
```

clusterDistanceByApproach.details

To explain how to calculate the distance by approach option.

Description

To explain how to calculate the distance depending on option given.

Usage

```
clusterDistanceByApproach.details(distances, approach)
```

Arguments

distances is a numeric vector.
approach is a string. Type of function to apply.

Details

This function is part of the hierarchical clusterization method. The function explains how to calculate the distance value from distances.

approach indicates the algorithm used to get the value. Possible values: 'MAX', 'MIN', 'AVG'.

Value

max, min or average from a vector.

Author(s)

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Examples

```
distances1 <- c(4,14,24,34)
```

```
distances2 <- c(1:10)
```

```
clusterDistanceByApproach(distances1, 'MAX')
```

```
clusterDistanceByApproach(distances2, 'MIN')
```

complementaryClusters *To check if two clusters are complementary*

Description

To check if two clusters include every element but without repeating anyone.

Usage

```
complementaryClusters(components, cluster1, cluster2)
```

Arguments

components	is an elements list. It contains every component that has to be in one cluster or in the other one. But each element can only be included in one cluster.
cluster1	is a cluster (matrix).
cluster2	is a cluster (matrix).

Details

This function checks if the cluster that will be divided contains the simple elements that they have to include. They have to contain every element, but anyone should be duplicated.

The function will return a boolean value.

Value

Boolean value.

Author(s)

Roberto Alcántara <roberto.alcantara@edu.uah.es>

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Examples

```
data <- c(1,2,1,3,1,4,1,5)

components <- toListDivisive(data)

cluster1 <- matrix(c(1,2,1,3),ncol=2)
cluster2 <- matrix(c(1,4,1,5),ncol=2)
cluster3 <- matrix(c(1,6,1,7),ncol=2)

complementaryClusters(components,cluster1,cluster2) #TRUE

complementaryClusters(components,cluster3,cluster2) #FALSE
```

complementaryClusters.details

To explain how and why two clusters are complementary.

Description

To explain how and why two clusters include every element but without repeating anyone.

Usage

```
complementaryClusters.details(components, cluster1, cluster2)
```

Arguments

components	is an elements list. It contains every component that has to be in one cluster or in the other one. But each element can only be included in one cluster.
cluster1	is a cluster (matrix).
cluster2	is a cluster (matrix).

Details

This function checks if the cluster that will be divided contains the simple elements that they have to include. They have to contain every element, but anyone should be duplicated.

The function will return a boolean value.

Value

Boolean value. Explanation.

Author(s)

Roberto Alcántara <roberto.alcantara@edu.uah.es>

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Examples

```
data <- c(1,2,1,3,1,4,1,5)

components <- toListDivisive(data)

cluster1 <- matrix(c(1,2,1,3),ncol=2)
cluster2 <- matrix(c(1,4,1,5),ncol=2)
cluster3 <- matrix(c(1,6,1,7),ncol=2)

complementaryClusters.details(components,cluster1,cluster2) #TRUE

complementaryClusters.details(components,cluster3,cluster2) #FALSE
```

correlationHC *To execute hierarchical correlation algorithm.*

Description

To execute hierarchical correlation algorithm applying weights, distance types, ...

Usage

```
correlationHC(
  data,
  target = NULL,
  weight = c(),
  distance = "EUC",
  normalize = TRUE,
  labels = NULL
)
```

Arguments

data	is a data frame with the main data.
target	is a data frame , a numeric vector or a matrix. Default value = NULL.
weight	is a numeric vector. Default value = empty vector.
distance	is a string. The distance type. Default value = Euclidean distance.
normalize	is a boolean parameter. If the user wants to normalize weights. Default value = TRUE.
labels	is a string vector. For the graphical solution. Default value = NULL.

Details

This function execute the complete hierarchical correlation method.

- 1 - The function transforms data in useful object to be used.
- 2 - It creates the clusters.
- 3 - It calculates the distance from the target to every cluster applying distance type given.
- 4 - It orders the distance in increasing way.
- 5 - It orders the clusters according to their distance from the previous step
- 6 - It shows the clusters sorted and the distance used.

Value

R object with a dendrogram, the sorted distances and the list with every cluster.

Author(s)

Roberto Alcántara <roberto.alcantara@edu.uah.es>

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Examples

```
data <- matrix(c(1,2,1,4,5,1,8,2,9,6,3,5,8,5,4),ncol= 3)

dataFrame <- data.frame(data)

target1 <- c(1,2,3)

target2 <- dataFrame[1,]

weight1 <- c(1,6,3)

weight2 <- c(0.1,0.6,0.3)

correlationHC(dataFrame, target1)
```

```
correlationHC(dataFrame, target1, weight1)
correlationHC(dataFrame, target1, weight1, normalize = FALSE)
correlationHC(dataFrame, target1, weight2, 'CAN', FALSE)
```

correlationHC.details *To explain how hierarchical correlation algorithm works.*

Description

To explain how the hierarchical correlation algorithm works.

Usage

```
correlationHC.details(
  data,
  target = NULL,
  weight = c(),
  distance = "EUC",
  normalize = TRUE,
  labels = NULL
)
```

Arguments

data	is a data frame with the main data.
target	is a data frame , a numeric vector or a matrix. Default value = NULL.
weight	is a numeric vector. Default value = empty vector.
distance	is a string. The distance type. Default value = Euclidean distance.
normalize	is a boolean parameter. If the user wants to normalize weights. Default value = TRUE.
labels	is a string vector. For the graphical solution. Default value = NULL.

Details

This function explains the complete hierarchical correlation method. It explains the theoretical algorithm step by step.

- 1 - The function transforms data in useful object to be used.
- 2 - It creates the clusters.
- 3 - It calculates the distance from the target to every cluster applying the distance type given.
- 4 - It orders the distance in an increasing way.
- 5 - It orders the clusters according to their distance from the previous step
- 6 - It shows the clusters sorted and the distance used.

Value

R object with a dendrogram, the sorted distances and the list with every cluster. Explanation.

Author(s)

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Examples

```
data <- matrix(c(1,2,1,4,5,1,8,2,9,6,3,5,8,5,4),ncol= 3)
dataFrame <- data.frame(data)
target1 <- c(1,2,3)
target2 <- dataFrame[1,]
weight1 <- c(1,6,3)
weight2 <- c(0.1,0.6,0.3)
correlationHC.details(dataFrame, target1)
correlationHC.details(dataFrame, target1, weight1)
correlationHC.details(dataFrame, target1, weight1, normalize = FALSE)
correlationHC.details(dataFrame, target1, weight2, 'CAN', FALSE)
```

distances

To calculate distances applying weights.

Description

To calculate distances between two clusters applying weights depending on the distance type.

Usage

```
distances(cluster1, cluster2, distance, weight)
```

Arguments

cluster1 is a matrix.
cluster2 is a matrix.
distance is a string. The distance type to apply.
weight is a numeric vector.

Details

This function calculates distance applying distance type and applying each weight to its characteristic.

Distance type could be EUC, MAN, CAN, CHE or OCT.

Value

Distance value applying weights.

Author(s)

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Examples

```
cluster1 <- matrix(c(2,3))
cluster2 <- matrix(c(4,5))

weight1 <- c(0.6,0.4)
weight2 <- c(2,4)

distances(cluster1, cluster2, 'MAN', weight1)

distances(cluster1, cluster2, 'CHE', weight2)
```

distances.details *To calculate distances applying weights.*

Description

To explain how to calculate distances between two clusters applying weights depending on the distance type.

Usage

```
distances.details(cluster1, cluster2, distance, weight)
```

Arguments

cluster1 is a matrix.
cluster2 is a matrix.
distance is a string. The distance type to apply.
weight is a numeric vector.

Details

This function calculates distance applying distance type and applying each weight to its characteristic.

Distance type could be EUC, MAN, CAN, CHE or OCT.

Value

Distance value applying weights. Explanation.

Author(s)

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Examples

```
cluster1 <- matrix(c(2,3))
cluster2 <- matrix(c(4,5))

weight1 <- c(0.6,0.4)
weight2 <- c(2,4)

distances.details(cluster1, cluster2, 'MAN', weight1)

distances.details(cluster1, cluster2, 'CHE', weight2)
```

divisiveHC

To execute divisive hierarchical clusterization algorithm by distance and approach.

Description

To execute complete divisive hierarchical clusterization algorithm by choosing distance and approach types.

Usage

```
divisiveHC(data, distance, approach)
```

Arguments

data	could be a numeric vector, a matrix or a numeric data frame. It will be transformed into matrix and list to be used.
distance	is a string. It chooses the distance to use.
approach	is a string. It chooses the approach to use.

Details

This function is the main part of the divisive hierarchical clusterization method. It executes the theoretical algorithm step by step.

- 1 - The function transforms data in useful object to be used.
- 2 - It creates a cluster that includes every simple elements.
- 3 - It initializes possible clusters using the initial elements.
- 4 - It calculates a matrix distance with the clusters created in the 3rd step.
- 5 - It chooses the maximal distance value and gets the clusters to be divided.
- 6 - It divides the cluster into two new complementary clusters and updates the clusters list.
- 6 - It repeats these steps until every cluster can't be divided again. The solution includes every simple cluster.

Value

A list with the divided clusters.

Author(s)

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Examples

```
a <- c(1,2,1,3,1,4,1,5,1,6)
matrixA <- matrix(a,ncol=2)
dataFrameA <- data.frame(matrixA)
divisiveHC(a, 'EUC', 'MAX')
divisiveHC(matrixA, 'MAN', 'AVG')
```

```
divisiveHC(dataFrameA, 'CHE', 'MIN')
```

divisiveHC.details *To explain the divisive hierarchical clusterization algorithm by distance and approach.*

Description

To explain the complete divisive hierarchical clusterization algorithm by choosing distance and approach types.

Usage

```
divisiveHC.details(data, distance, approach)
```

Arguments

data	could be a numeric vector, a matrix or a numeric data frame. It will be transformed into matrix and list to be used.
distance	is a string. It chooses the distance to use.
approach	is a string. It chooses the approach to use.

Details

This function is the main part of the divisive hierarchical clusterization method. It explains the theoretical algorithm step by step.

- 1 - The function transforms data in useful object to be used.
- 2 - It creates a cluster that includes every simple elements.
- 3 - It initializes possible clusters using the initial elements.
- 4 - It calculates a matrix distance with the clusters created in the 3rd step.
- 5 - It chooses the maximal distance value and gets the clusters to be divided.
- 6 - It divides the cluster into two new complementary clusters and updates the clusters list.
- 6 - It repeats these steps until every cluster can't be divided again. The solution includes every simple cluster.

Value

A list with the divided clusters. Explanation

Author(s)

Roberto Alcántara <roberto.alcantara@edu.uah.es>
Juan José Cuadrado <jjcg@uah.es>
Universidad de Alcalá de Henares

Examples

```
a <- c(1,2,1,3,1,4,1,5,1,6)
matrixA <- matrix(a,ncol=2)
dataFrameA <- data.frame(matrixA)
divisiveHC.details(a, 'EUC', 'MAX')
divisiveHC.details(matrixA, 'MAN', 'AVG')
divisiveHC.details(dataFrameA, 'CHE', 'MIN')
```

edistance	<i>To calculate the Euclidean distance.</i>
-----------	---

Description

To calculate the Euclidean distance of two clusters.

Usage

```
edistance(x, y)
```

Arguments

x	is a numeric vector or a matrix. It represents the values of a cluster.
y	is a numeric vector or a matrix. It represents the values of a cluster.

Details

This function is part of the hierarchical clusterization method. The function calculates the Euclidean distance value from x and y.

Value

Euclidean distance value.

Author(s)

Roberto Alcántara <roberto.alcantara@edu.uah.es>
Juan José Cuadrado <jjcg@uah.es>
Universidad de Alcalá de Henares

Examples

```
x <- c(1,2)
y <- c(1,3)

cluster1 <- matrix(x,ncol=2)
cluster2 <- matrix(y,ncol=2)

edistance(x,y)

edistance(cluster1,cluster2)
```

edistance.details *To show the Euclidean distance formula.*

Description

To show the Euclidean distance formula and to calculate the Euclidean distance of two clusters.

Usage

```
edistance.details(x, y)
```

Arguments

x is a numeric vector or a matrix. It represents the values of a cluster.
y is a numeric vector or a matrix. It represents the values of a cluster.

Details

This function is part of the hierarchical clusterization method. The function calculates the Euclidean distance value from **x** and **y**.

Value

Euclidean distance value and formula.

Author(s)

Roberto Alcántara <roberto.alcantara@edu.uah.es>
Juan José Cuadrado <jjcg@uah.es>
Universidad de Alcalá de Henares

Examples

```
x <- c(1,2)
y <- c(1,3)

cluster1 <- matrix(x,ncol=2)
cluster2 <- matrix(y,ncol=2)

edistance(x,y)

edistance(cluster1,cluster2)
```

edistanceW

To calculate the Euclidean distance applying weights.

Description

To calculate the Euclidean distance between clusters applying weights given.

Usage

```
edistanceW(cluster1, cluster2, weight)
```

Arguments

cluster1	is a cluster.
cluster2	is a cluster.
weight	is a numeric vector.

Details

The function calculates the Euclidean distance value from cluster1 and cluster2, applying weights to the cluster's components.

Value

Euclidean distance applying weights value.

Author(s)

Roberto Alcántara <roberto.alcantara@edu.uah.es>
Juan José Cuadrado <jjcg@uah.es>
Universidad de Alcalá de Henares

Examples

```
cluster1 <- matrix(c(1,2),ncol=2)
cluster2 <- matrix(c(1,3),ncol=2)

weight1 <- c(0.4,0.6)
weight2 <- c(2,12)

edistanceW(cluster1,cluster2,weight1)

edistanceW(cluster1,cluster2,weight2)
```

edistanceW.details *To calculate the Euclidean distance applying weights.*

Description

To explain how to calculate the Euclidean distance between clusters applying weights given.

Usage

```
edistanceW.details(cluster1, cluster2, weight)
```

Arguments

cluster1	is a cluster.
cluster2	is a cluster.
weight	is a numeric vector.

Details

The function calculates the Euclidean distance value from cluster1 and cluster2, applying weights to the cluster's components.

Value

Euclidean distance applying weights value. Explanation.

Author(s)

Roberto Alcántara <roberto.alcantara@edu.uah.es>
Juan José Cuadrado <jjcg@uah.es>
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Examples

```
cluster1 <- matrix(c(1,2),ncol=2)
cluster2 <- matrix(c(1,3),ncol=2)

weight1 <- c(0.4,0.6)
weight2 <- c(2,12)

edistanceW.details(cluster1,cluster2,weight1)

edistanceW.details(cluster1,cluster2,weight2)
```

getCluster *To get the clusters with minimal distance.*

Description

To get the clusters with the minimal distance value. By using the given distance, it gets the matrix index.

Usage

```
getCluster(distance, matrix)
```

Arguments

distance is a number. It should be in the matrix.
matrix is a numeric matrix.

Details

This function is part of the hierarchical clusterization method. The function uses the distance value and gets the clustersId with the minimal distance.

For the divisive algorithm, it chooses the distances from a distances list.

Value

numeric vector with two cluster indexes.

Author(s)

Roberto Alcántara <roberto.alcantara@edu.uah.es>
Juan José Cuadrado <jjcg@uah.es>
Universidad de Alcalá de Henares

Examples

```
matrixExample <- matrix(c(1:10), ncol=2)

getCluster(2,matrixExample)
```

getCluster.details *To explain how to get the clusters with minimal distance.*

Description

To explain how to get the clusters with the minimal distance value. By using the given distance, it gets the matrix index.

Usage

```
getCluster.details(distance, matrix)
```

Arguments

distance	is a number. It should be in the matrix.
matrix	is a numeric matrix.

Details

This function is part of the hierarchical clusterization method. The function uses the distance value and gets the clustersId with the minimal distance.

For the divisive algorithm, it chooses the distances from a distances list.

Value

Numeric vector with two clusters indexes.

Author(s)

Roberto Alcántara <roberto.alcantara@edu.uah.es>
Juan José Cuadrado <jjcg@uah.es>
Universidad de Alcalá de Henares

Examples

```
matrixExample <- matrix(c(1:10), ncol=2)

getCluster.details(2,matrixExample)
```

getClusterDivisive *To get the clusters with maximal distance.*

Description

To get the clusters with the maximal distance value. By using the given distance, it gets the matrix index.

Usage

```
getClusterDivisive(distance, vector)
```

Arguments

distance is a number. It should be in the matrix.
vector is a numeric vector

Details

This function is part of the hierarchical clusterization method. The function uses the distance value and gets the clustersId with the minimal distance.

For the divisive algorithm, it chooses the distances from a distances list.

Value

A cluster.

Author(s)

Roberto Alcántara <roberto.alcantara@edu.uah.es>

Juan José Cuadrado <jjcg@uah.es>

Universidad de Alcalá de Henares

Examples

```
getClusterDivisive(2,c(1:10))
```

```
getClusterDivisive(6,c(2,4,6,8,10,12))
```

getClusterDivisive.details

To explain how to get the clusters with maximal distance.

Description

To explain how to get the clusters with the maximal distance value. By using the given distance, it gets the matrix index.

Usage

```
getClusterDivisive.details(distance, vector)
```

Arguments

distance	is a number. It should be in the matrix.
vector	is a numeric vector.

Details

This function is part of the hierarchical clusterization method. The function uses the distance value and gets the clustersId with the minimal distance.

For the divisive algorithm, it chooses the distances from a distances list.

Value

A cluster. Explanation.

Author(s)

Roberto Alcántara <roberto.alcantara@edu.uah.es>

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Examples

```
getClusterDivisive.details(2,c(1:10))
```

```
getClusterDivisive(6,c(2,4,6,8,10,12))
```

initClusters	<i>To initialize clusters for the divisive algorithm.</i>
--------------	---

Description

To initialize clusters for the divisive algorithm.

Usage

```
initClusters(initList)
```

Arguments

`initList` is a clusters list. It will contain clusters with one element.

Details

This function will calculate every cluster that can be created by joining initial clusters with each other. It creates clusters from length = 1 until a cluster with every element is created.

These clusters will be used to find the most different clusters that we can create by dividing the initial cluster.

Value

A cluster list.

Author(s)

Roberto Alcántara <roberto.alcantara@edu.uah.es>

Juan José Cuadrado <jjcg@uah.es>

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Examples

```
data <- c(1:8)
matrix <- matrix(data,ncol=2)
listData <- toListDivisive(data)
listMatrix <- toListDivisive(matrix)
initClusters(listData)
initClusters(listMatrix)
```

`initClusters.details` *To explain how to initialize clusters for the divisive algorithm.*

Description

To explain how to initialize clusters for the divisive algorithm.

Usage

```
initClusters.details(initList)
```

Arguments

`initList` is a clusters list. It will contain clusters with one element.

Details

This function will explain how to calculate every cluster that can be created by joining initial clusters with each other. It creates clusters from length = 1 until a cluster with every element is created.

These clusters will be used to find the most different clusters that we can create by dividing the initial cluster.

Value

A cluster list. Explanation.

Author(s)

Roberto Alcántara <roberto.alcantara@edu.uah.es>

Juan José Cuadrado <jjcg@uah.es>

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Examples

```
data <- c(1:8)

matrix <- matrix(data, ncol=2)

listData <- toListDivisive(data)

listMatrix <- toListDivisive(matrix)

initClusters.details(listData)

initClusters.details(listMatrix)
```

initData	<i>To initialize data, hierarchical correlation algorithm.</i>
----------	--

Description

To initialize data, hierarchical correlation algorithm.

Usage

```
initData(data)
```

Arguments

data is a data frame with the main data.

Details

This function is part of the hierarchical correlation method. The function initializes data transforming each row from the data frame into a matrix with every row elements.

Value

A cluster list. Initializing data.

Author(s)

Roberto Alcántara <roberto.alcantara@edu.uah.es>

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Examples

```
data <- matrix(c(1,2,1,4,5,1,8,2,9,6,3,5,8,5,4), ncol= 3)
```

```
dataFrame <- data.frame(data)
```

```
initData(dataFrame)
```

initData.details *To initialize data, hierarchical correlation algorithm.*

Description

To explain how to initialize data, hierarchical correlation algorithm.

Usage

```
initData.details(data)
```

Arguments

data is a data frame with the main data.

Details

This function is part of the hierarchical correlation method. The function initializes data transforming each row from the data frame into a matrix with every row elements.

Value

A cluster list. Initializing data. Explanation.

Author(s)

Roberto Alcántara <roberto.alcantara@edu.uah.es>

Juan José Cuadrado <jjcg@uah.es>

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Examples

```
data <- matrix(c(1,2,1,4,5,1,8,2,9,6,3,5,8,5,4), ncol= 3)
```

```
dataFrame <- data.frame(data)
```

```
initData.details(dataFrame)
```

initImages	<i>To display an image.</i>
------------	-----------------------------

Description

An auxiliar function to display a picture.

Usage

```
initImages(path)
```

Arguments

path is a file path.

initTarget	<i>To initialize target, hierarchical correlation algorithm.</i>
------------	--

Description

To initialize target, hierarchical correlation algorithm. It checks if target is valid, if not, it initializes the target

Usage

```
initTarget(target, data)
```

Arguments

target is a numeric vector, a matrix or a data frame.
data is a data frame with the main data.

Details

This function is part of the hierarchical correlation method. The function initializes target and checks if it is a valid target.

The function transforms the target into a matrix. Then, it checks if the target has only one row and the same columns has the main data.

If it is not a valid target, the function will notice the problem and will initialized a new target with every column with value 0.

Value

A cluster.

Author(s)

Roberto Alcántara <roberto.alcantara@edu.uah.es>

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Examples

```
data <- matrix(c(1,2,1,4,5,1,8,2,9,6,3,5,8,5,4), ncol= 3)
dataFrame <- data.frame(data)
target1 <- matrix(c(2,3))
target2 <- matrix(c(2,3,6))
initTarget(target1, dataFrame)
initTarget(target2, dataFrame)
```

initTarget.details *To initialize target, hierarchical correlation algorithm.*

Description

To initialize target, hierarchical correlation algorithm. It checks if target is valid, if not, it initializes the target

Usage

```
initTarget.details(target, data)
```

Arguments

target	is a numeric vector, a matrix or a data frame.
data	is a data frame with the main data.

Details

This function is part of the hierarchical correlation method. The function initializes target and checks if it is an acceptable target.

The function transforms the target into a matrix. Then, it checks if the target has only one row and the same columns have the main data.

If it is not an acceptable target, the function will notice the problem and will initialize a new target with every column with value 0.

Value

A cluster. Explanation.

Author(s)

Roberto Alcántara <roberto.alcantara@edu.uah.es>

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Examples

```
data <- matrix(c(1,2,1,4,5,1,8,2,9,6,3,5,8,5,4), ncol= 3)
dataFrame <- data.frame(data)
target1 <- matrix(c(2,3))
target2 <- matrix(c(2,3,6))
initTarget.details(target1,dataFrame)
initTarget.details(target2,dataFrame)
```

matrixDistance	<i>Matrix distance by distance type</i>
----------------	---

Description

To calculate the matrix distance by using distance type.

Usage

```
matrixDistance(list, distance)
```

Arguments

list	is a clusters list.
distance	is a literal.

Details

This function is part of the hierarchical clusterization method. The function calculates the matrix distance by using the distance type given.

The list parameter will be a list with the clusters as rows and columns.

The function avoids distances equal 0 and undefined clusters.

Examples

```
data <- c(1:10)
clusters <- toList(data)
matrixDistance(clusters, 'EUC')
```

maxDistance	<i>Maximal distance</i>
-------------	-------------------------

Description

Get the matrix maximal value.

Usage

```
maxDistance(matrix)
```

Arguments

`matrix` is a numeric matrix. It could be a numeric vector.

Details

This function is part of the hierarchical clusterization method. The function uses the numeric vector or matrix `matrix` given and return the maximal value. The function avoids distances equal 0, and initialize maximal value with an auxiliar function `ini tMax`, which gets the first matrix element with a valid distance.

Value

numeric value. Max value from a matrix

Author(s)

Roberto Alcántara <roberto.alcantara@edu.uah.es>
Juan José Cuadrado <jjcg@uah.es>
Universidad de Alcalá de Henares

Examples

```
matrixExample <- matrix(c(1:10), nrow=2)
maxDistance(1:10)
maxDistance(matrixExample)
```

maxDistance.details *Maximal distance*

Description

To explain how to get the matrix maximal value.

Usage

```
maxDistance.details(matrix)
```

Arguments

`matrix` is a numeric matrix. It could be a numeric vector.

Details

This function is part of the hierarchical clusterization method. The function uses the numeric vector or matrix `matrix` given and return the maximal value. The function avoids distances equal 0, and initialize maximal value with an auxiliar function `ini tMax`, which gets the first matrix element with a valid distance.

Value

Numeric value. Max value from a matrix. Explanation.

Author(s)

Roberto Alcántara <roberto.alcantara@edu.uah.es>

Juan José Cuadrado <jjcg@uah.es>

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Examples

```
matrixExample <- matrix(c(1:10), nrow=2)
```

```
maxDistance.details(1:10)
```

```
maxDistance.details(matrixExample)
```

mdAgglomerative *Matrix distance by distance and approach type.*

Description

To calculate the matrix distance by using distance and approach type.

Usage

```
mdAgglomerative(list, distance, approach)
```

Arguments

list	is a clusters list.
distance	is a literal. The distance type to be used.
approach	is a literal. The approach type to be used.

Details

This function is part of the hierarchical clusterization method. The function calculates the matrix distance by using the distance and approach type given.

The `list` parameter will be a list with the clusters as rows and columns.

The function avoids distances equal 0 and undefined clusters.

Value

A matrix distance.

Author(s)

Roberto Alcántara <roberto.alcantara@edu.uah.es>

Juan José Cuadrado <jjcg@uah.es>

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Examples

```
data <- c(1,2,1,3,1,4,1,5,1,6)
clusters <- toList(data)
mdAgglomerative(clusters, 'EUC', 'MAX')
mdAgglomerative(clusters, 'CHE', 'AVG')
```

`mdAgglomerative.details`*Matrix distance by distance and approach type.*

Description

To explain how to calculate the matrix distance by using distance and approach type.

Usage

```
mdAgglomerative.details(list, distance, approach)
```

Arguments

<code>list</code>	is a clusters list.
<code>distance</code>	is a literal. The distance type to be used.
<code>approach</code>	is a literal. The approach type to be used.

Details

This function is part of the hierarchical clusterization method. The function calculates the matrix distance by using the distance and approach type given.

The `list` parameter will be a list with the clusters as rows and columns.

The function avoids distances equal 0 and undefined clusters.

Value

A matrix distance. Explanation.

Author(s)

Roberto Alcántara <roberto.alcantara@edu.uah.es>

Juan José Cuadrado <jjcg@uah.es>

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Examples

```
data <- c(1,2,1,3,1,4,1,5,1,6)

clusters <- toList(data)

mdAgglomerative.details(clusters, 'EUC', 'MAX')

mdAgglomerative.details(clusters, 'CHE', 'AVG')
```

`mdDivisive`*Matrix distance by distance and approach type.*

Description

To calculate the matrix distance by using distance and approach types.

Usage

```
mdDivisive(list, distance, approach, components)
```

Arguments

<code>list</code>	is a clusters list.
<code>distance</code>	is a string. The distance type to be used.
<code>approach</code>	is a string. The approach type to be used.
<code>components</code>	is a clusters list. It contains every clusters with only one element. It is used to check if complementary condition is 'TRUE'.

Details

This function is part of the divisive hierarchical clusterization method. The function calculates the matrix distance by using the distance and approach types given.

The `list` parameter will be a list with the clusters as rows and columns.

The function avoids distances equal 0 and undefined clusters.

It also avoids distances between clusters that are not complementary because they can't be chosen to divide all the clusters.

Value

Matrix distance.

Author(s)

Roberto Alcántara <roberto.alcantara@edu.uah.es>

Juan José Cuadrado <jjcg@uah.es>

Universidad de Alcalá de Henares

Examples

```
data <- c(1,2,1,3,1,4,1,5,1,6)
```

```
clusters <- toList(data)
```

```
components <- toList(data)
```

```
mdDivisive(clusters, 'EUC', 'MAX', components)
```

```
mdDivisive(clusters, 'MAN', 'MIN', components)
```

mdDivisive.details *Matrix distance by distance and approach type.*

Description

To explain how to calculate the matrix distance by using distance and approach types.

Usage

```
mdDivisive.details(list, distance, approach, components)
```

Arguments

list	is a clusters list.
distance	is a string. The distance type to be used.
approach	is a string. The approach type to be used.
components	is a clusters list. It contains every clusters with only one element. It is used to check if complementary condition is 'TRUE'.

Details

This function is part of the divisive hierarchical clusterization method. The function calculates the matrix distance by using the distance and approach types given.

The list parameter will be a list with the clusters as rows and columns.

The function avoids distances equal 0 and undefined clusters.

It also avoids distances between clusters that are not complementary because they can't be chosen to divide all the clusters.

Value

Matrix distance. Explanation.

Author(s)

Roberto Alcántara <roberto.alcantara@edu.uah.es>

Juan José Cuadrado <jjcg@uah.es>

Universidad de Alcalá de Henares

Examples

```
data <- c(1,2,1,3,1,4,1,5,1,6)
clusters <- toList(data)
components <- toList(data)
mdDivisive.details(clusters, 'EUC', 'MAX', components)
mdDivisive.details(clusters, 'MAN', 'MIN', components)
```

mdistance	<i>To calculate the Manhattan distance.</i>
-----------	---

Description

To calculate the Manhattan distance of two clusters.

Usage

```
mdistance(x, y)
```

Arguments

x is a numeric vector or a matrix. It represents the values of a cluster.
y is a numeric vector or a matrix. It represents the values of a cluster.

Details

This function is part of the hierarchical clusterization method. The function calculates the Manhattan distance value from **x** and **y**.

Value

Manhattan distance value.

Author(s)

Roberto Alcántara <roberto.alcantara@edu.uah.es>

Juan José Cuadrado <jjcg@uah.es>

Universidad de Alcalá de Henares

Examples

```
x <- c(1,2)
y <- c(1,3)

cluster1 <- matrix(x,ncol=2)
cluster2 <- matrix(y,ncol=2)

mdistance(x,y)

mdistance(cluster1,cluster2)
```

mdistance.details *To explain how to calculate the Manhattan distance.*

Description

To explain how to calculate the Manhattan distance of two clusters.

Usage

```
mdistance.details(x, y)
```

Arguments

x is a numeric vector or a matrix. It represents the values of a cluster.
y is a numeric vector or a matrix. It represents the values of a cluster.

Details

This function is part of the hierarchical clusterization method. The function calculates the Manhattan distance value from **x** and **y**.

Value

Manhattan distance value and formula.

Author(s)

Roberto Alcántara <roberto.alcantara@edu.uah.es>
Juan José Cuadrado <jjcg@uah.es>
Universidad de Alcalá de Henares

Examples

```
x <- c(1,2)
y <- c(1,3)

cluster1 <- matrix(x,ncol=2)
cluster2 <- matrix(y,ncol=2)

mdistance(x,y)

mdistance(cluster1,cluster2)
```

mdistanceW*To calculate the Manhattan distance applying weights.*

Description

To calculate the Manhattan distance between clusters applying weights given.

Usage

```
mdistanceW(cluster1, cluster2, weight)
```

Arguments

cluster1	is a cluster.
cluster2	is a cluster.
weight	is a numeric vector.

Details

The function calculates the Manhattan distance value from cluster1 and cluster2, applying weights to the cluster's components.

Value

Manhattan distance applying weights value.

Author(s)

Roberto Alcántara <roberto.alcantara@edu.uah.es>
Juan José Cuadrado <jjcg@uah.es>
Universidad de Alcalá de Henares

Examples

```
cluster1 <- matrix(c(1,2),ncol=2)
cluster2 <- matrix(c(1,3),ncol=2)

weight1 <- c(0.4,0.6)
weight2 <- c(2,12)

mdistanceW(cluster1,cluster2,weight1)

mdistanceW(cluster1,cluster2,weight2)
```

mdistanceW.details *To calculate the Manhattan distance applying weights.*

Description

To explain how to calculate the Manhattan distance between clusters applying weights given.

Usage

```
mdistanceW.details(cluster1, cluster2, weight)
```

Arguments

cluster1	is a cluster.
cluster2	is a cluster.
weight	is a numeric vector.

Details

The function calculates the Manhattan distance value from cluster1 and cluster2, applying weights to the cluster's components.

Value

Manhattan distance applying weights value. Explanation.

Author(s)

Roberto Alcántara <roberto.alcantara@edu.uah.es>
Juan José Cuadrado <jjcg@uah.es>
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Examples

```
cluster1 <- matrix(c(1,2),ncol=2)
cluster2 <- matrix(c(1,3),ncol=2)

weight1 <- c(0.4,0.6)
weight2 <- c(2,12)

mdistanceW.details(cluster1,cluster2,weight1)

mdistanceW.details(cluster1,cluster2,weight2)
```

minDistance	<i>Minimal distance</i>
-------------	-------------------------

Description

Get the matrix minimal value.

Usage

```
minDistance(matrix)
```

Arguments

`matrix` is a numeric matrix. It could be a numeric vector.

Details

This function is part of the hierarchical clusterization method. The function uses the numeric vector or matrix `matrix` given and return the minimal value. The function avoids distances equal 0, and initialize minimum value with an auxiliar function `initMin`, which gets the first matrix element with a valid distance.

Value

Numeric value. Min value from a matrix.

Author(s)

Roberto Alcántara <roberto.alcantara@edu.uah.es>

Juan José Cuadrado <jjcg@uah.es>

Universidad de Alcalá de Henares

Examples

```
matrixExample <- matrix(c(1:10), nrow=2)

minDistance(1:10)

minDistance(matrixExample)
```

minDistance.details *Minimal distance*

Description

To explain how to get the matrix minimal value.

Usage

```
minDistance.details(matrix)
```

Arguments

`matrix` is a numeric matrix. It could be a numeric vector.

Details

This function is part of the hierarchical clusterization method. The function uses the numeric vector or matrix `matrix` given and return the minimal value. The function avoids distances equal 0, and initialize minimum value with an auxiliar function `initMin`, which gets the first matrix element with a valid distance.

Value

Numeric value. Min value from a matrix. Explanation.

Author(s)

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Examples

```
matrixExample <- matrix(c(1:10), nrow=2)

minDistance(1:10)

minDistance.details(matrixExample)
```

newCluster	<i>To create a new cluster.</i>
------------	---------------------------------

Description

To create the cluster formed by the two clusters given. Add the new cluster to list.

Usage

```
newCluster(list, clusters)
```

Arguments

`list` is the generic cluster list.
`clusters` is a vector with the matrix index clusters.

Details

This function is part of the hierarchical clusterization method.

- 1 - The function maps clusters in list.
- 2 - It creates a new cluster from them.
- 3 - It adds the new cluster to list.
- 4 - It disables the clusters used in the second step.

Value

A list with clusters.

Author(s)

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Examples

```
data <- c(1:10)
list <- toList(data)
clusters <- c(1,2)
newCluster(list,clusters)
```

newCluster.details *To explain how to create a new cluster.*

Description

To explain how to create the cluster formed by the two clusters given. Add the new cluster to list.

Usage

```
newCluster.details(list, clusters)
```

Arguments

list is the generic cluster list.
clusters is a vector with the matrix index clusters.

Details

This function is part of the hierarchical clusterization method.

- 1 - The function maps clusters in list.
- 2 - It creates a new cluster from them.
- 3 - It adds the new cluster to list.
- 4 - It disables the clusters used in the second step.

Value

A list with clusters. Explanation.

Author(s)

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Examples

```
data <- c(1:10)
list <- toList(data)
clusters <- c(1,2)
newCluster.details(list,clusters)
```

normalizeWeight	<i>To normalize weight values.</i>
-----------------	------------------------------------

Description

To normalize weight values if `normalize = TRUE`.

Usage

```
normalizeWeight(normalize, weight, data)
```

Arguments

<code>normalize</code>	is a boolean value.
<code>weight</code>	is a numeric vector.
<code>data</code>	is a data.frame.

Details

This function allows users to normalize weights.

If there is not any weight, the function will create a numeric vector of "1".

If `normalize = TRUE`, the function will make every weight value as a "[0:1]" value.

If `normalize = FALSE`, the function will not make any changes, weights will be the same.

Value

Numeric vector with updated weights.

Author(s)

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Examples

```
data <- data.frame(matrix(c(1:10),ncol = 2))

weight1 <- c(0.6,0.4)
weight2 <- c(2,4)

normalizeWeight(FALSE, weight1, data)

normalizeWeight(TRUE, weight2, data)

normalizeWeight(FALSE, weight2, data)
```

normalizeWeight.details

To normalize weight values.

Description

To explain how to normalize weight values if `normalize = TRUE`.

Usage

```
normalizeWeight.details(normalize, weight, data)
```

Arguments

<code>normalize</code>	is a boolean value.
<code>weight</code>	is a numeric vector.
<code>data</code>	is a data.frame.

Details

This function allows users to normalize weights.

If there is not any weight, the function will create a numeric vector of "1".

If `normalize = TRUE`, the function will make every weight value as a "[0:1]" value.

If `normalize = FALSE`, the function will not make any changes, weights will be the same.

Value

Numeric vector with updated weights. Explanation.

Author(s)

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Examples

```
data <- data.frame(matrix(c(1:10),ncol = 2))

weight1 <- c(0.6,0.4)
weight2 <- c(2,4)

normalizeWeight.details(FALSE, weight1, data)

normalizeWeight.details(TRUE, weight2, data)

normalizeWeight.details(FALSE, weight2, data)
```

octileDistance	<i>To calculate the Octile distance.</i>
----------------	--

Description

To calculate the octile distance of two clusters.

Usage

```
octileDistance(x, y)
```

Arguments

x	is a numeric vector or a matrix. It represents the values of a cluster.
y	is a numeric vector or a matrix. It represents the values of a cluster.

Details

This function is part of the hierarchical clusterization method. The function calculates the octile distance value from x and y.

Value

Octile distance value.

Author(s)

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Examples

```
x <- c(1,2)
y <- c(1,3)

cluster1 <- matrix(x,ncol=2)
cluster2 <- matrix(y,ncol=2)

octileDistance(x,y)

octileDistance(cluster1,cluster2)
```

octileDistance.details

To explain how to calculate the Octile distance.

Description

To explain how to calculate the octile distance of two clusters.

Usage

```
octileDistance.details(x, y)
```

Arguments

x is a numeric vector or a matrix. It represents the values of a cluster.
y is a numeric vector or a matrix. It represents the values of a cluster.

Details

This function is part of the hierarchical clusterization method. The function calculates the octile distance value from **x** and **y**.

Value

Octile distance value.

Author(s)

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Juan José Cuadrado <jjcg@uah.es>

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Examples

```
x <- c(1,2)
y <- c(1,3)

cluster1 <- matrix(x,ncol=2)
cluster2 <- matrix(y,ncol=2)

octileDistance.details(x,y)

octileDistance.details(cluster1,cluster2)
```

octileDistanceW *To calculate the Octile distance applying weights.*

Description

To calculate the Octile distance between clusters applying weights given.

Usage

```
octileDistanceW(cluster1, cluster2, weight)
```

Arguments

cluster1	is a cluster.
cluster2	is a cluster.
weight	is a numeric vector.

Details

The function calculates the Octile distance value from cluster1 and cluster2, applying weights to the cluster's components.

Value

Octile distance applying weights value.

Author(s)

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Examples

```
cluster1 <- matrix(c(1,2),ncol=2)
cluster2 <- matrix(c(1,3),ncol=2)

weight1 <- c(0.4,0.6)
weight2 <- c(2,12)

octileDistanceW(cluster1,cluster2,weight1)

octileDistanceW(cluster1,cluster2,weight2)
```

octileDistanceW.details

To calculate the Octile distance applying weights.

Description

To explain how to calculate the Octile distance between clusters applying weights given.

Usage

```
octileDistanceW.details(cluster1, cluster2, weight)
```

Arguments

cluster1	is a cluster.
cluster2	is a cluster.
weight	is a numeric vector.

Details

The function calculates the Octile distance value from cluster1 and cluster2, applying weights to the cluster's components.

Value

Octile distance applying weights value. Explanation.

Author(s)

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Examples

```
cluster1 <- matrix(c(1,2),ncol=2)
cluster2 <- matrix(c(1,3),ncol=2)

weight1 <- c(0.4,0.6)
weight2 <- c(2,12)

octileDistanceW.details(cluster1,cluster2,weight1)

octileDistanceW.details(cluster1,cluster2,weight2)
```

toList

To transform data into list

Description

To transform data into list.

Usage

```
toList(data)
```

Arguments

data could be a numeric vector, a matrix or a numeric data frame.

Details

This function is part of the agglomerative hierarchical clusterization method. The function initializes data content as a list.

In agglomerative algorithm, it adds a TRUE flag to each element, which indicates that the cluster is not grouped.

Value

A list with clusters.

Author(s)

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Examples

```
data <- c(1:10)
matrix <- matrix(data,ncol=2)
dataFrame <- data.frame(matrix)
toList(data)
toList(matrix)
toList(dataFrame)
```

toList.details	<i>To explain how to transform data into list</i>
----------------	---

Description

To explain how to transform data into list.

Usage

```
toList.details(data)
```

Arguments

data could be a numeric vector, a matrix or a numeric data frame.

Details

This function is part of the agglomerative hierarchical clusterization method. The function initializes data content as a list.

In agglomerative algorithm, it adds a TRUE flag to each element, which indicates that the cluster is not grouped.

Value

A list with cñusters. Explanation.

Author(s)

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Examples

```
data <- c(1:10)
matrix <- matrix(data,ncol=2)
dataFrame <- data.frame(matrix)
toList(data)
toList(matrix)
toList(dataFrame)
```

toListDivisive	<i>To transform data into list</i>
----------------	------------------------------------

Description

To transform data into list.

Usage

```
toListDivisive(data)
```

Arguments

data could be a numeric vector, a matrix or a numeric data frame.

Details

This function is part of the divisive hierarchical clusterization method. The function initializes data content as a list.

Value

a list with clusters.

Author(s)

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Examples

```
data <- c(1:10)
matrix <- matrix(data,ncol=2)
dataFrame <- data.frame(matrix)
toListDivisive(data)
toListDivisive(matrix)
toListDivisive(dataFrame)
```

```
toListDivisive.details
```

To explain how to transform data into list

Description

To explain how to transform data into list.

Usage

```
toListDivisive.details(data)
```

Arguments

`data` could be a numeric vector, a matrix or a numeric data frame.

Details

This function is part of the divisive hierarchical clusterization method. The function initializes data content as a list.

Value

A list with clusters. Explanation.

Author(s)

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Examples

```
data <- c(1:10)
matrix <- matrix(data,ncol=2)
dataFrame <- data.frame(matrix)
toListDivisive.details(data)
toListDivisive.details(matrix)
toListDivisive.details(dataFrame)
```

usefulClusters	<i>To delete clusters grouped.</i>
----------------	------------------------------------

Description

To delete the clusters already used to create a new one.

Usage

```
usefulClusters(list)
```

Arguments

`list` is a list of clusters.

Details

This function is part of the hierarchical clusterization method. The function updates the cluster list with the clusters used after to calculate de matrix distance.

Value

A list of clusters.

Author(s)

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Examples

```
data <- c(1:10)
list <- toList(data)
usefulClusters(list)
```

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