Package: hclustTeach (via r-universe)

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Type Package

Title Hierarchical Cluster Analysis (Learning Didactically)

Version 0.1.0

Description Implements hierarchical clustering methods (single linkage, complete linkage, average linkage, and centroid linkage) with stepwise printing and dendrograms for didactic purposes.

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Contents

`hclust_average` *Hierarchical Clustering - Average linkage*

Description

A function that performs hierarchical clustering with average linkage. It can also print the clustering steps and display a dendrogram

Usage

```
hclust_average(
  data,
  metric = "euclidean",
  print.steps = TRUE,
  plot = TRUE,
  label.names = TRUE
)
```

Arguments

`data`	Numerical matrix or data frame of observations (rows = observations, columns = variables).
`metric`	Distance metric to be used (default: "euclidean").
`print.steps`	If TRUE, the algorithm's steps are printed.
`plot`	If TRUE, a dendrogram is plotted.
`label.names`	If TRUE, uses the row names as labels in the dendrogram.

Value

object of class "hclust".

Examples

```
y1 <- c(1, 2, 1, 0); y2 <- c(2, 1, 0, 2)
y3 <- c(8, 8, 9, 7); y4 <- c(6, 9, 8, 9)
Data <- rbind(y1, y2, y3, y4)
hc <- hclust_average(Data, metric = "euclidean",
                     print.steps = TRUE,
                     plot = TRUE,
                     label.names = TRUE)
```

`hclust_centroid` *Hierarchical Clustering - Centroid*

Description

A function that performs hierarchical clustering with centroid linkage. It can also print the clustering steps and display a dendrogram

Usage

```
hclust_centroid(
  data,
  metric = "euclidean",
  print.steps = TRUE,
  plot = TRUE,
  label.names = TRUE
)
```

Arguments

`data`	Numerical matrix or data frame of observations (rows = observations, columns = variables).
`metric`	Distance metric to be used (default: "euclidean").
`print.steps`	If TRUE, the algorithm's steps are printed.
`plot`	If TRUE, a dendrogram is plotted.
`label.names`	If TRUE, uses the row names as labels in the dendrogram.

Value

object of class "hclust".

Examples

```
y1 <- c(1, 2, 1, 0); y2 <- c(2, 1, 0, 2)
y3 <- c(8, 8, 9, 7); y4 <- c(6, 9, 8, 9)
Data <- rbind(y1, y2, y3, y4)
hc <- hclust_centroid(Data, metric = "euclidean",
                      print.steps = TRUE,
                      plot = TRUE,
                      label.names = TRUE)
```

`hclust_complete` *Hierarchical Clustering - Complete linkage*

Description

A function that performs hierarchical clustering with complete linkage. It can also print the clustering steps and display a dendrogram

Usage

```
hclust_complete(
  data,
  metric = "euclidean",
  print.steps = TRUE,
  plot = TRUE,
  label.names = TRUE
)
```

Arguments

`data`	Numerical matrix or data frame of observations (rows = observations, columns = variables).
`metric`	Distance metric to be used (default: "euclidean").
`print.steps`	If TRUE, the algorithm's steps are printed.
`plot`	If TRUE, a dendrogram is plotted.
`label.names`	If TRUE, uses the row names as labels in the dendrogram.

Value

object of class "hclust".

Examples

```
y1 <- c(1, 2, 1, 0); y2 <- c(2, 1, 0, 2)
y3 <- c(8, 8, 9, 7); y4 <- c(6, 9, 8, 9)
Data <- rbind(y1, y2, y3, y4)
hc <- hclust_complete(Data, metric = "euclidean",
                      print.steps = TRUE,
                      plot = TRUE,
                      label.names = TRUE)
```

`hclust_single` *Hierarchical Clustering - Single linkage*

Description

A function that performs hierarchical clustering with single linkage. It can also print the clustering steps and display a dendrogram

Usage

```
hclust_single(
  data,
  metric = "euclidean",
  print.steps = TRUE,
  plot = TRUE,
  label.names = TRUE
)
```

Arguments

`data`	Numerical matrix or data frame of observations (rows = observations, columns = variables).
`metric`	Distance metric to be used (default: "euclidean").
`print.steps`	If TRUE, the algorithm's steps are printed.
`plot`	If TRUE, a dendrogram is plotted.
`label.names`	If TRUE, uses the row names as labels in the dendrogram.

Value

object of class "hclust".

Examples

```
y1 <- c(1, 2, 1, 0); y2 <- c(2, 1, 0, 2)
y3 <- c(8, 8, 9, 7); y4 <- c(6, 9, 8, 9)
Data <- rbind(y1, y2, y3, y4)
hc <- hclust_single(Data, metric = "euclidean",
                    print.steps = TRUE,
                    plot = TRUE,
                    label.names = TRUE)
```

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