Package 'BeckRPackage'

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Type Package

Title Implement Kmeans using C++

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Description We do unsupervised learning

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Imports data.table, Rcpp (>= 1.0.11)

LinkingTo Rcpp

Suggests testthat (>= 3.0.0)

Config/testthat/edition 3

R topics documented:

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`HCLUST` *HCLUST*

Description

Use hierarchical clustering to create clusters for a given data set and number of clusters.

Usage

```
HCLUST(data.mat, n.clusters)
```

Arguments

`data.mat`	An N x P matrix where N corresponds to the number of observations and P is the number of features.
`n.clusters`	The number of clusters the `HCLUST` function should find.

Examples

```
# get the data from the iris dataset as a matrix
data.mat <- as.matrix(iris[3:4])

# save the number of clusters
n.clusters <- 3

# run the algorithm on the first 20 data points
hclust <- HCLUST(data.mat[1:20,], n.clusters)
```

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kmeans_interface *Kmeans*

Description

Run the kmeans algorithm as implemented in C++ with the function kmeans_interface.

Usage

```
kmeans_interface(n.clusters, data.matrix)
```

Arguments

n.clusters	an integer specifying how many clusters the kmeans algorithm should find.
data.matrix	an N x P matrix, where N is the number of observations and P is the number of features.

Examples

```
# create data matrix from the petal length and width values of the iris data set
data.mat <- as.matrix(iris[3:4])

# save the number of clusters
n.clusters <- 4

# run kmeans
kmeans <- kmeans_interface(n.clusters, data.mat)
```