

# Package ‘ClusterR’

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**Type** Package

**Title** Gaussian Mixture Models, K-Means, Mini-Batch-Kmeans, K-Medoids and Affinity Propagation Clustering

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**BugReports** <https://github.com/mlampros/ClusterR/issues>

**URL** <https://github.com/mlampros/ClusterR>

**Description** Gaussian mixture models, k-means, mini-batch-kmeans, k-medoids and affinity propagation clustering with the option to plot, validate, predict (new data) and estimate the optimal number of clusters. The package takes advantage of 'RcppArmadillo' to speed up the computationally intensive parts of the functions. For more information, see (i) "Clustering in an Object-Oriented Environment" by Anja Struyf, Mia Hubert, Peter Rousseeuw (1997), Journal of Statistical Software, <doi:10.18637/jss.v001.i04>; (ii) "Web-scale k-means clustering" by D. Sculley (2010), ACM Digital Library, <doi:10.1145/1772690.1772862>; (iii) "Armadillo: a template-based C++ library for linear algebra" by Sanderson et al (2016), The Journal of Open Source Software, <doi:10.21105/joss.00026>; (iv) "Clustering by Passing Messages Between Data Points" by Brendan J. Frey and Delbert Dueck, Science 16 Feb 2007: Vol. 315, Issue 5814, pp. 972-976, <doi:10.1126/science.1136800>.

**License** GPL-3

**Encoding** UTF-8

**SystemRequirements** libarmadillo: apt-get install -y libarmadillo-dev (deb), libblas: apt-get install -y libblas-dev (deb), liblapack: apt-get install -y liblapack-dev (deb), libarpack++2: apt-get install -y libarpack++2-dev (deb), gfortran: apt-get install -y gfortran (deb), libgmp3: apt-get install -y libgmp3-dev (deb), libfftw3: apt-get install -y libfftw3-dev (deb), libtiff5: apt-get install -y libtiff5-dev (deb)

**LazyData** TRUE

**Depends** R(>= 3.2), gtools

**Imports** Rcpp (>= 0.12.5), graphics, grDevices, utils, stats, gmp, ggplot2

**LinkingTo** Rcpp, RcppArmadillo (>= 0.9.1)

**Suggests** OpenImageR, FD, testthat, covr, knitr, rmarkdown

**VignetteBuilder** knitr

**RoxygenNote** 6.1.0

**NeedsCompilation** yes

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 AP\_affinity\_propagation

*Affinity propagation clustering*


---

**Description**

Affinity propagation clustering

**Usage**

```
AP_affinity_propagation(data, p, maxits = 1000, convits = 100,
  dampfact = 0.9, details = FALSE, nonoise = 0, time = FALSE)
```

**Arguments**

data	a matrix. Either a similarity matrix (where number of rows equal to number of columns) or a 3-dimensional matrix where the 1st, 2nd and 3rd column correspond to (i-index, j-index, value) triplet of a similarity matrix.
p	a numeric vector of size 1 or size equal to the number of rows of the input matrix. See the details section for more information.
maxits	a numeric value specifying the maximum number of iterations (defaults to 1000)
convits	a numeric value. If the estimated exemplars stay fixed for convits iterations, the affinity propagation algorithm terminates early (defaults to 100)
dampfact	a float number specifying the update equation damping level in [0.5, 1). Higher values correspond to heavy damping, which may be needed if oscillations occur (defaults to 0.9)
details	a boolean specifying if details should be printed in the console
nonoise	a float number. The affinity propagation algorithm adds a small amount of noise to <i>data</i> to prevent degenerate cases; this disables that.
time	a boolean. If TRUE then the elapsed time will be printed in the console.

**Details**

The *affinity propagation* algorithm automatically determines the number of clusters based on the input preference  $p$ , a real-valued  $N$ -vector.  $p(i)$  indicates the preference that data point  $i$  be chosen as an exemplar. Often a good choice is to set all preferences to  $\text{median}(\text{data})$ . The number of clusters identified can be adjusted by changing this value accordingly. If  $p$  is a scalar, assumes all preferences are that shared value.

The number of clusters eventually emerges by iteratively passing messages between data points to update two matrices,  $A$  and  $R$  (Frey and Dueck 2007). The "responsibility" matrix  $R$  has values  $r(i, k)$  that quantify how well suited point  $k$  is to serve as the exemplar for point  $i$  relative to other candidate exemplars for point  $i$ . The "availability" matrix  $A$  contains values  $a(i, k)$  representing how "appropriate" point  $k$  would be as an exemplar for point  $i$ , taking into account other points' preferences for point  $k$  as an exemplar. Both matrices  $R$  and  $A$  are initialized with all zeros. The AP

algorithm then performs updates iteratively over the two matrices. First, "Responsibilities"  $r(i, k)$  are sent from data points to candidate exemplars to indicate how strongly each data point favors the candidate exemplar over other candidate exemplars. "Availabilities"  $a(i, k)$  then are sent from candidate exemplars to data points to indicate the degree to which each candidate exemplar is available to be a cluster center for the data point. In this case, the responsibilities and availabilities are messages that provide evidence about whether each data point should be an exemplar and, if not, to what exemplar that data point should be assigned. For each iteration in the message-passing procedure, the sum of  $r(k; k) + a(k; k)$  can be used to identify exemplars. After the messages have converged, two ways exist to identify exemplars. In the first approach, for data point  $i$ , if  $r(i, i) + a(i, i) > 0$ , then data point  $i$  is an exemplar. In the second approach, for data point  $i$ , if  $r(i, i) + a(i, i) > r(i, j) + a(i, j)$  for all  $i$  not equal to  $j$ , then data point  $i$  is an exemplar. The entire procedure terminates after it reaches a predefined number of iterations or if the determined clusters have remained constant for a certain number of iterations... ( <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5650075/> – See chapter 2 )

Excluding the main diagonal of the similarity matrix when calculating the median as preference ('p') value can be considered as another option too.

## References

<https://www.psi.toronto.edu/index.php?q=affinity>

<https://www.psi.toronto.edu/affinitypropagation/faq.html>

<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5650075/> ( SEE chapter 2 )

## Examples

```
set.seed(1)
dat = matrix(sample(1:255, 2500, replace = TRUE), 100, 25)

smt = 1.0 - distance_matrix(dat, method = 'euclidean', upper = TRUE, diagonal = TRUE)
diag(smt) = 0.0

ap = AP_affinity_propagation(smt, p = median(as.vector(smt)))
```

---

AP\_preferenceRange      *Affinity propagation preference range*

---

## Description

Affinity propagation preference range

## Usage

```
AP_preferenceRange(data, method = "bound", threads = 1)
```

**Arguments**

data	a matrix. Either a similarity matrix (where number of rows equal to number of columns) or a 3-dimensional matrix where the 1st, 2nd and 3rd column correspond to (i-index, j-index, value) triplet of a similarity matrix.
method	a character string specifying the preference range method to use. One of 'exact', 'bound'. See the details section for more information.
threads	an integer specifying the number of cores to run in parallel ( applies only if <i>method</i> is set to 'exact' which is more computationally intensive )

**Details**

Given a set of similarities, *data*, this function computes a lower bound, *pmin*, on the value for the preference where the optimal number of clusters (exemplars) changes from 1 to 2, and the exact value of the preference, *pmax*, where the optimal number of clusters changes from  $n-1$  to  $n$ . For  $N$  data points, there may be as many as  $N^2-N$  pair-wise similarities (note that the similarity of data point  $i$  to  $k$  need not be equal to the similarity of data point  $k$  to  $i$ ). These may be passed in an  $N \times N$  matrix of similarities, *data*, where  $data(i,k)$  is the similarity of point  $i$  to point  $k$ . In fact, only a smaller number of relevant similarities need to be provided, in which case the others are assumed to be  $-\text{Inf}$ .  $M$  similarity values are known, can be passed in an  $M \times 3$  matrix *data*, where each row of *data* contains a pair of data point indices and a corresponding similarity value:  $data(j,3)$  is the similarity of data point  $data(j,1)$  to data point  $data(j,2)$ .

A single-cluster solution may not exist, in which case *pmin* is set to NaN. The *AP\_preferenceRange* uses one of the methods below to compute *pmin* and *pmax*:

*exact* : Computes the exact values for *pmin* and *pmax* (Warning: This can be quite slow) *bound* : Computes the exact value for *pmax*, but estimates *pmin* using a bound (default)

**References**

<https://www.psi.toronto.edu/affinitypropagation/preferenceRange.m>

**Examples**

```
set.seed(1)
dat = matrix(sample(1:255, 2500, replace = TRUE), 100, 25)

smt = 1.0 - distance_matrix(dat, method = 'euclidean', upper = TRUE, diagonal = TRUE)
diag(smt) = 0.0

ap_range = AP_preferenceRange(smt, method = "bound")
```

---

center_scale	<i>Function to scale and/or center the data</i>
--------------	---

---

### Description

Function to scale and/or center the data

### Usage

```
center_scale(data, mean_center = TRUE, sd_scale = TRUE)
```

### Arguments

data	matrix or data frame
mean_center	either TRUE or FALSE. If mean_center is TRUE then the mean of each column will be subtracted
sd_scale	either TRUE or FALSE. See the details section for more information

### Details

If sd\_scale is TRUE and mean\_center is TRUE then each column will be divided by the standard deviation. If sd\_scale is TRUE and mean\_center is FALSE then each column will be divided by  $\sqrt{\text{sum}(x^2) / (n-1)}$ . In case of missing values the function raises an error. In case that the standard deviation equals zero then the standard deviation will be replaced with 1.0, so that NaN's can be avoided by division

### Value

a matrix

### Examples

```
data(dietary_survey_IBS)

dat = dietary_survey_IBS[, -ncol(dietary_survey_IBS)]

dat = center_scale(dat, mean_center = TRUE, sd_scale = TRUE)
```

---

Clara_Medoids	<i>Clustering large applications</i>
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---

**Description**

Clustering large applications

**Usage**

```
Clara_Medoids(data, clusters, samples, sample_size,
              distance_metric = "euclidean", minkowski_p = 1, threads = 1,
              swap_phase = TRUE, fuzzy = FALSE, verbose = FALSE, seed = 1)
```

**Arguments**

<code>data</code>	matrix or data frame
<code>clusters</code>	the number of clusters
<code>samples</code>	number of samples to draw from the data set
<code>sample_size</code>	fraction of data to draw in each sample iteration. It should be a float number greater than 0.0 and less or equal to 1.0
<code>distance_metric</code>	a string specifying the distance method. One of, <i>euclidean</i> , <i>manhattan</i> , <i>chebyshev</i> , <i>canberra</i> , <i>braycurtis</i> , <i>pearson_correlation</i> , <i>simple_matching_coefficient</i> , <i>minkowski</i> , <i>hamming</i> , <i>jaccard_coefficient</i> , <i>Rao_coefficient</i> , <i>mahalanobis</i> , <i>cosine</i>
<code>minkowski_p</code>	a numeric value specifying the minkowski parameter in case that <code>distance_metric = "minkowski"</code>
<code>threads</code>	an integer specifying the number of cores to run in parallel. Openmp will be utilized to parallelize the number of the different sample draws
<code>swap_phase</code>	either TRUE or FALSE. If TRUE then both phases ('build' and 'swap') will take place. The 'swap_phase' is considered more computationally intensive.
<code>fuzzy</code>	either TRUE or FALSE. If TRUE, then probabilities for each cluster will be returned based on the distance between observations and medoids
<code>verbose</code>	either TRUE or FALSE, indicating whether progress is printed during clustering
<code>seed</code>	integer value for random number generator (RNG)

**Details**

The Clara\_Medoids function is implemented in the same way as the 'clara' (clustering large applications) algorithm (Kaufman and Rousseeuw(1990)). In the 'Clara\_Medoids' the 'Cluster\_Medoids' function will be applied to each sample draw.

**Value**

a list with the following attributes : medoids, medoid\_indices, sample\_indices, best\_dissimilarity, clusters, fuzzy\_probs (if fuzzy = TRUE), clustering\_stats, dissimilarity\_matrix, silhouette\_matrix

**Author(s)**

Lampros Mouselimis

**References**

Anja Struyf, Mia Hubert, Peter J. Rousseeuw, (Feb. 1997), Clustering in an Object-Oriented Environment, Journal of Statistical Software, Vol 1, Issue 4

**Examples**

```
data(dietary_survey_IBS)

dat = dietary_survey_IBS[, -ncol(dietary_survey_IBS)]

dat = center_scale(dat)

clm = Clara_Medoids(dat, clusters = 3, samples = 5, sample_size = 0.2, swap_phase = TRUE)
```

Cluster\_Medoids

*Partitioning around medoids***Description**

Partitioning around medoids

**Usage**

```
Cluster_Medoids(data, clusters, distance_metric = "euclidean",
  minkowski_p = 1, threads = 1, swap_phase = TRUE, fuzzy = FALSE,
  verbose = FALSE, seed = 1)
```

**Arguments**

<code>data</code>	matrix or data frame. The data parameter can be also a dissimilarity matrix, where the main diagonal equals 0.0 and the number of rows equals the number of columns
<code>clusters</code>	the number of clusters
<code>distance_metric</code>	a string specifying the distance method. One of, <i>euclidean</i> , <i>manhattan</i> , <i>chebyshev</i> , <i>canberra</i> , <i>braycurtis</i> , <i>pearson_correlation</i> , <i>simple_matching_coefficient</i> , <i>minkowski</i> , <i>hamming</i> , <i>jaccard_coefficient</i> , <i>Rao_coefficient</i> , <i>mahalanobis</i> , <i>cosine</i>
<code>minkowski_p</code>	a numeric value specifying the minkowski parameter in case that <code>distance_metric = "minkowski"</code>
<code>threads</code>	an integer specifying the number of cores to run in parallel



swap_phase	either TRUE or FALSE. If TRUE then both phases ('build' and 'swap') will take place. The 'swap_phase' is considered more computationally intensive.
fuzzy	either TRUE or FALSE. If TRUE, then probabilities for each cluster will be returned based on the distance between observations and medoids
verbose	either TRUE or FALSE, indicating whether progress is printed during clustering
seed	integer value for random number generator (RNG)

### Details

The Cluster\_Medoids function is implemented in the same way as the 'pam' (partitioning around medoids) algorithm (Kaufman and Rousseeuw(1990)). In comparison to k-means clustering, the function Cluster\_Medoids is more robust, because it minimizes the sum of unsquared dissimilarities. Moreover, it doesn't need initial guesses for the cluster centers.

### Value

a list with the following attributes: medoids, medoid\_indices, best\_dissimilarity, dissimilarity\_matrix, clusters, fuzzy\_probs (if fuzzy = TRUE), silhouette\_matrix, clustering\_stats

### Author(s)

Lampros Mouselimis

### References

Anja Struyf, Mia Hubert, Peter J. Rousseeuw, (Feb. 1997), Clustering in an Object-Oriented Environment, Journal of Statistical Software, Vol 1, Issue 4

### Examples

```
data(dietary_survey_IBS)

dat = dietary_survey_IBS[, -ncol(dietary_survey_IBS)]

dat = center_scale(dat)

cm = Cluster_Medoids(dat, clusters = 3, distance_metric = 'euclidean', swap_phase = TRUE)
```

---

dietary\_survey\_IBS      *Synthetic data using a dietary survey of patients with irritable bowel syndrome (IBS)*

---

**Description**

The data are based on the article "A dietary survey of patients with irritable bowel syndrome". The mean and standard deviation of the table 1 (Foods perceived as causing or worsening irritable bowel syndrome symptoms in the IBS group and digestive symptoms in the healthy comparative group) were used to generate the synthetic data.

**Usage**

```
data(dietary_survey_IBS)
```

**Format**

A data frame with 400 Instances and 43 attributes (including the class attribute, "class")

**Details**

The predictors are: bread, wheat, pasta, breakfast\_cereal, yeast, spicy\_food, curry, chinese\_takeaway, chilli, cabbage, onion, garlic, potatoes, pepper, vegetables\_unspecified, tomato, beans\_and\_pulses, mushroom, fatty\_foods\_unspecified, sauces, chocolate, fries, crisps, desserts, eggs, red\_meat, processed\_meat, pork, chicken, fish\_shellfish, dairy\_products\_unspecified, cheese, cream, milk, fruit\_unspecified, nuts\_and\_seeds, orange, apple, banana, grapes, alcohol, caffeine

The response variable ("class") consists of two groups: healthy-group (class == 0) vs. the IBS-patients (class == 1)

**References**

P. Hayes, C. Corish, E. O'Mahony, E. M. M. Quigley (May 2013). A dietary survey of patients with irritable bowel syndrome. Journal of Human Nutrition and Dietetics.

**Examples**

```
data(dietary_survey_IBS)

X = dietary_survey_IBS[, -ncol(dietary_survey_IBS)]

y = dietary_survey_IBS[, ncol(dietary_survey_IBS)]
```

---

distance_matrix	<i>Distance matrix calculation</i>
-----------------	------------------------------------

---

**Description**

Distance matrix calculation

**Usage**

```
distance_matrix(data, method = "euclidean", upper = FALSE,
  diagonal = FALSE, minkowski_p = 1, threads = 1)
```

**Arguments**

data	matrix or data frame
method	a string specifying the distance method. One of, <i>euclidean</i> , <i>manhattan</i> , <i>chebyshev</i> , <i>canberra</i> , <i>braycurtis</i> , <i>pearson_correlation</i> , <i>simple_matching_coefficient</i> , <i>minkowski</i> , <i>hamming</i> , <i>jaccard_coefficient</i> , <i>Rao_coefficient</i> , <i>mahalanobis</i> , <i>cosine</i>
upper	either TRUE or FALSE specifying if the upper triangle of the distance matrix should be returned. If FALSE then the upper triangle will be filled with NA's
diagonal	either TRUE or FALSE specifying if the diagonal of the distance matrix should be returned. If FALSE then the diagonal will be filled with NA's
minkowski_p	a numeric value specifying the minkowski parameter in case that method = "minkowski"
threads	the number of cores to run in parallel (if OpenMP is available)

**Value**

a matrix

**Examples**

```
data(dietary_survey_IBS)
dat = dietary_survey_IBS[, -ncol(dietary_survey_IBS)]
dat = distance_matrix(dat, method = 'euclidean', upper = TRUE, diagonal = TRUE)
```

---

external\_validation    *external clustering validation*

---

**Description**

external clustering validation

**Usage**

```
external_validation(true_labels, clusters,
  method = "adjusted_rand_index", summary_stats = FALSE)
```

**Arguments**

true_labels	a numeric vector of length equal to the length of the clusters vector
clusters	a numeric vector ( the result of a clustering method ) of length equal to the length of the true_labels

method	one of <i>rand_index</i> , <i>adjusted_rand_index</i> , <i>jaccard_index</i> , <i>fowlkes_Mallows_index</i> , <i>mirkin_metric</i> , <i>purity</i> , <i>entropy</i> , <i>nmi</i> (normalized mutual information), <i>var_info</i> (variation of information), and <i>nvi</i> (normalized variation of information)
summary_stats	besides the available methods the <i>summary_stats</i> parameter prints also the specificity, sensitivity, precision, recall and F-measure of the clusters

**Details**

This function uses external validation methods to evaluate the clustering results

**Value**

if *summary\_stats* is FALSE the function returns a float number, otherwise it returns also a summary statistics table

**Author(s)**

Lampros Mouselimis

**Examples**

```
data(dietary_survey_IBS)
dat = dietary_survey_IBS[, -ncol(dietary_survey_IBS)]
X = center_scale(dat)
km = KMeans_rcpp(X, clusters = 2, num_init = 5, max_iters = 100, initializer = 'kmeans++')
res = external_validation(dietary_survey_IBS$class, km$clusters, method = "adjusted_rand_index")
```

---

GMM

*Gaussian Mixture Model clustering*


---

**Description**

Gaussian Mixture Model clustering

**Usage**

```
GMM(data, gaussian_comps = 1, dist_mode = "eucl_dist",
     seed_mode = "random_subset", km_iter = 10, em_iter = 5,
     verbose = FALSE, var_floor = 1e-10, seed = 1)
```

**Arguments**

<code>data</code>	matrix or data frame
<code>gaussian_comps</code>	the number of gaussian mixture components
<code>dist_mode</code>	the distance used during the seeding of initial means and k-means clustering. One of, <i>eucl_dist</i> , <i>maha_dist</i> .
<code>seed_mode</code>	how the initial means are seeded prior to running k-means and/or EM algorithms. One of, <i>static_subset</i> , <i>random_subset</i> , <i>static_spread</i> , <i>random_spread</i> .
<code>km_iter</code>	the number of iterations of the k-means algorithm
<code>em_iter</code>	the number of iterations of the EM algorithm
<code>verbose</code>	either TRUE or FALSE; enable or disable printing of progress during the k-means and EM algorithms
<code>var_floor</code>	the variance floor (smallest allowed value) for the diagonal covariances
<code>seed</code>	integer value for random number generator (RNG)

**Details**

This function is an R implementation of the 'gmm\_diag' class of the Armadillo library. The only exception is that user defined parameter settings are not supported, such as `seed_mode = 'keep_existing'`. For probabilistic applications, better model parameters are typically learned with `dist_mode` set to `maha_dist`. For vector quantisation applications, model parameters should be learned with `dist_mode` set to `eucl_dist`, and the number of EM iterations set to zero. In general, a sufficient number of k-means and EM iterations is typically about 10. The number of training samples should be much larger than the number of Gaussians. Seeding the initial means with `static_spread` and `random_spread` can be much more time consuming than with `static_subset` and `random_subset`. The k-means and EM algorithms will run faster on multi-core machines when OpenMP is enabled in your compiler (eg. `-fopenmp` in GCC)

**Value**

a list consisting of the centroids, covariance matrix ( where each row of the matrix represents a diagonal covariance matrix), weights and the log-likelihoods for each gaussian component. In case of Error it returns the error message and the possible causes.

**References**

<http://arma.sourceforge.net/docs.html>

**Examples**

```
data(dietary_survey_IBS)

dat = as.matrix(dietary_survey_IBS[, -ncol(dietary_survey_IBS)])

dat = center_scale(dat)

gmm = GMM(dat, 2, "maha_dist", "random_subset", 10, 10)
```

---

`KMeans_arma`*k-means using the Armadillo library*

---

**Description**

k-means using the Armadillo library

**Usage**

```
KMeans_arma(data, clusters, n_iter = 10, seed_mode = "random_subset",  
            verbose = FALSE, CENTROIDS = NULL, seed = 1)
```

**Arguments**

<code>data</code>	matrix or data frame
<code>clusters</code>	the number of clusters
<code>n_iter</code>	the number of clustering iterations (about 10 is typically sufficient)
<code>seed_mode</code>	how the initial centroids are seeded. One of, <i>keep_existing</i> , <i>static_subset</i> , <i>random_subset</i> , <i>static_spread</i> , <i>random_spread</i> .
<code>verbose</code>	either TRUE or FALSE, indicating whether progress is printed during clustering
<code>CENTROIDS</code>	a matrix of initial cluster centroids. The rows of the CENTROIDS matrix should be equal to the number of clusters and the columns should be equal to the columns of the data. CENTROIDS should be used in combination with <code>seed_mode</code> 'keep_existing'.
<code>seed</code>	integer value for random number generator (RNG)

**Details**

This function is an R implementation of the 'kmeans' class of the Armadillo library. It is faster than the `KMeans_rcpp` function but it lacks some features. For more info see the details section of the `KMeans_rcpp` function. The number of columns should be larger than the number of clusters or `CENTROIDS`. If the clustering fails, the means matrix is reset and a bool set to false is returned. The clustering will run faster on multi-core machines when OpenMP is enabled in your compiler (eg. `-fopenmp` in GCC)

**Value**

the centroids as a matrix. In case of Error it returns the error message, whereas in case of an empty centroids-matrix it returns a warning-message.

**References**

<http://arma.sourceforge.net/docs.html>

**Examples**

```

data(dietary_survey_IBS)

dat = dietary_survey_IBS[, -ncol(dietary_survey_IBS)]

dat = center_scale(dat)

km = KMeans_arma(dat, clusters = 2, n_iter = 10, "random_subset")

```

---

KMeans_rcpp	<i>k-means using RcppArmadillo</i>
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---

**Description**

k-means using RcppArmadillo

**Usage**

```

KMeans_rcpp(data, clusters, num_init = 1, max_iters = 100,
  initializer = "kmeans++", fuzzy = FALSE, verbose = FALSE,
  CENTROIDS = NULL, tol = 1e-04, tol_optimal_init = 0.3, seed = 1)

```

**Arguments**

data	matrix or data frame
clusters	the number of clusters
num_init	number of times the algorithm will be run with different centroid seeds
max_iters	the maximum number of clustering iterations
initializer	the method of initialization. One of, <i>optimal_init</i> , <i>quantile_init</i> , <i>kmeans++</i> and <i>random</i> . See details for more information
fuzzy	either TRUE or FALSE. If TRUE, then prediction probabilities will be calculated using the distance between observations and centroids
verbose	either TRUE or FALSE, indicating whether progress is printed during clustering.
CENTROIDS	a matrix of initial cluster centroids. The rows of the CENTROIDS matrix should be equal to the number of clusters and the columns should be equal to the columns of the data.
tol	a float number. If, in case of an iteration ( $\text{iteration} > 1$ and $\text{iteration} < \text{max\_iters}$ ) 'tol' is greater than the squared norm of the centroids, then kmeans has converged
tol_optimal_init	tolerance value for the 'optimal_init' initializer. The higher this value is, the far appart from each other the centroids are.
seed	integer value for random number generator (RNG)

## Details

This function has the following features in comparison to the `KMeans_arma` function:

Besides `optimal_init`, `quantile_init`, `random` and `kmeans++` initializations one can specify the centroids using the `CENTROIDS` parameter.

The running time and convergence of the algorithm can be adjusted using the `num_init`, `max_iters` and `tol` parameters.

If `num_init > 1` then `KMeans_rcpp` returns the attributes of the best initialization using as criterion the within-cluster-sum-of-squared-error.

—————initializers—————

**optimal\_init** : this initializer adds rows of the data incrementally, while checking that they do not already exist in the centroid-matrix [ experimental ]

**quantile\_init** : initialization of centroids by using the cumulative distance between observations and by removing potential duplicates [ experimental ]

**kmeans++** : kmeans++ initialization. Reference : <http://theory.stanford.edu/~sergei/papers/kMeansPP-soda.pdf> AND <http://stackoverflow.com/questions/5466323/how-exactly-does-k-means-work>

**random** : random selection of data rows as initial centroids

## Value

a list with the following attributes: `clusters`, `fuzzy_clusters` (if `fuzzy = TRUE`), `centroids`, `total_SSE`, `best_initialization`, `WCSS_per_cluster`, `obs_per_cluster`, `between.SS_DIV_total.SS`

## Author(s)

Lampros Mouselimis

## Examples

```
data(dietary_survey_IBS)
dat = dietary_survey_IBS[, -ncol(dietary_survey_IBS)]
dat = center_scale(dat)
km = KMeans_rcpp(dat, clusters = 2, num_init = 5, max_iters = 100, initializer = 'kmeans++')
```

---

MiniBatchKmeans

*Mini-batch-k-means using RcppArmadillo*

---

## Description

Mini-batch-k-means using RcppArmadillo



**Usage**

```
MiniBatchKmeans(data, clusters, batch_size = 10, num_init = 1,
  max_iters = 100, init_fraction = 1, initializer = "kmeans++",
  early_stop_iter = 10, verbose = FALSE, CENTROIDS = NULL,
  tol = 1e-04, tol_optimal_init = 0.3, seed = 1)
```

**Arguments**

<code>data</code>	matrix or data frame
<code>clusters</code>	the number of clusters
<code>batch_size</code>	the size of the mini batches
<code>num_init</code>	number of times the algorithm will be run with different centroid seeds
<code>max_iters</code>	the maximum number of clustering iterations
<code>init_fraction</code>	percentage of data to use for the initialization centroids (applies if initializer is <i>kmeans++</i> or <i>optimal_init</i> ). Should be a float number between 0.0 and 1.0.
<code>initializer</code>	the method of initialization. One of, <i>optimal_init</i> , <i>quantile_init</i> , <i>kmeans++</i> and <i>random</i> . See details for more information
<code>early_stop_iter</code>	continue that many iterations after calculation of the best within-cluster-sum-of-squared-error
<code>verbose</code>	either TRUE or FALSE, indicating whether progress is printed during clustering
<code>CENTROIDS</code>	a matrix of initial cluster centroids. The rows of the CENTROIDS matrix should be equal to the number of clusters and the columns should be equal to the columns of the data
<code>tol</code>	a float number. If, in case of an iteration ( $\text{iteration} > 1$ and $\text{iteration} < \text{max\_iters}$ ) 'tol' is greater than the squared norm of the centroids, then kmeans has converged
<code>tol_optimal_init</code>	tolerance value for the 'optimal_init' initializer. The higher this value is, the far apart from each other the centroids are.
<code>seed</code>	integer value for random number generator (RNG)

**Details**

This function performs k-means clustering using mini batches.

—————initializers—————

**optimal\_init** : this initializer adds rows of the data incrementally, while checking that they do not already exist in the centroid-matrix [ experimental ]

**quantile\_init** : initialization of centroids by using the cumulative distance between observations and by removing potential duplicates [ experimental ]

**kmeans++** : kmeans++ initialization. Reference : <http://theory.stanford.edu/~sergei/papers/kMeansPP-soda.pdf> AND <http://stackoverflow.com/questions/5466323/how-exactly-does-k-means-work>

**random** : random selection of data rows as initial centroids

**Value**

a list with the following attributes: centroids, WCSS\_per\_cluster, best\_initialization, iters\_per\_initialization

**Author(s)**

Lampros Mouselimis

**References**

<http://www.eecs.tufts.edu/~dsculley/papers/fastkmeans.pdf>, <https://github.com/siddharth-agrawal/Mini-Batch-K-Means>

**Examples**

```
data(dietary_survey_IBS)

dat = dietary_survey_IBS[, -ncol(dietary_survey_IBS)]

dat = center_scale(dat)

MbatchKm = MiniBatchKmeans(dat, clusters = 2, batch_size = 20, num_init = 5, early_stop_iter = 10)
```

---

mushroom

*The mushroom data*

---

**Description**

This data set includes descriptions of hypothetical samples corresponding to 23 species of gilled mushrooms in the Agaricus and Lepiota Family (pp. 500-525). Each species is identified as definitely edible, definitely poisonous, or of unknown edibility and not recommended. This latter class was combined with the poisonous one. The Guide clearly states that there is no simple rule for determining the edibility of a mushroom; no rule like 'leaflets three, let it be' for Poisonous Oak and Ivy.

**Usage**

```
data(mushroom)
```

**Format**

A data frame with 8124 Instances and 23 attributes (including the class attribute, "class")

## Details

The column names of the data (including the class) appear in the following order:

1. class: edible=e, poisonous=p
2. cap-shape: bell=b, conical=c, convex=x, flat=f, knobbed=k, sunken=s
3. cap-surface: fibrous=f, grooves=g, scaly=y, smooth=s
4. cap-color: brown=n, buff=b, cinnamon=c, gray=g, green=r, pink=p, purple=u, red=e, white=w, yellow=y
5. bruises: bruises=t, no=f
6. odor: almond=a, anise=l, creosote=c, fishy=y, foul=f, musty=m, none=n, pungent=p, spicy=s
7. gill-attachment: attached=a, descending=d, free=f, notched=n
8. gill-spacing: close=c, crowded=w, distant=d
9. gill-size: broad=b, narrow=n
10. gill-color: black=k, brown=n, buff=b, chocolate=h, gray=g, green=r, orange=o, pink=p, purple=u, red=e, white=w, yellow=y
11. stalk-shape: enlarging=e, tapering=t
12. stalk-root: bulbous=b, club=c, cup=u, equal=e, rhizomorphs=z, rooted=r, missing=?
13. stalk-surface-above-ring: fibrous=f, scaly=y, silky=k, smooth=s
14. stalk-surface-below-ring: fibrous=f, scaly=y, silky=k, smooth=s
15. stalk-color-above-ring: brown=n, buff=b, cinnamon=c, gray=g, orange=o, pink=p, red=e, white=w, yellow=y
16. stalk-color-below-ring: brown=n, buff=b, cinnamon=c, gray=g, orange=o, pink=p, red=e, white=w, yellow=y
17. veil-type: partial=p, universal=u
18. veil-color: brown=n, orange=o, white=w, yellow=y
19. ring-number: none=n, one=o, two=t
20. ring-type: cobwebby=c, evanescent=e, flaring=f, large=l, none=n, pendant=p, sheathing=s, zone=z
21. spore-print-color: black=k, brown=n, buff=b, chocolate=h, green=r, orange=o, purple=u, white=w, yellow=y
22. population: abundant=a, clustered=c, numerous=n, scattered=s, several=v, solitary=y
23. habitat: grasses=g, leaves=l, meadows=m, paths=p, urban=u, waste=w, woods=d

## References

Mushroom records drawn from The Audubon Society Field Guide to North American Mushrooms (1981). G. H. Lincoff (Pres.), New York: Alfred A. Knopf

Donor: Jeff Schlimmer (Jeffrey.Schlimmer@a.gp.cs.cmu.edu)

download source: <https://archive.ics.uci.edu/ml/datasets/Mushroom>

**Examples**

```

data(mushroom)

X = mushroom[, -1]

y = mushroom[, 1]

```

---

Optimal\_Clusters\_GMM *Optimal number of Clusters for the gaussian mixture models*

---

**Description**

Optimal number of Clusters for the gaussian mixture models

**Usage**

```

Optimal_Clusters_GMM(data, max_clusters, criterion = "AIC",
  dist_mode = "eucl_dist", seed_mode = "random_subset", km_iter = 10,
  em_iter = 5, verbose = FALSE, var_floor = 1e-10,
  plot_data = TRUE, seed = 1)

```

**Arguments**

data	matrix or data frame
max_clusters	either a numeric value, a contiguous or non-contiguous numeric vector specifying the cluster search space
criterion	one of 'AIC' or 'BIC'
dist_mode	the distance used during the seeding of initial means and k-means clustering. One of, <i>eucl_dist</i> , <i>maha_dist</i> .
seed_mode	how the initial means are seeded prior to running k-means and/or EM algorithms. One of, <i>static_subset</i> , <i>random_subset</i> , <i>static_spread</i> , <i>random_spread</i> .
km_iter	the number of iterations of the k-means algorithm
em_iter	the number of iterations of the EM algorithm
verbose	either TRUE or FALSE; enable or disable printing of progress during the k-means and EM algorithms
var_floor	the variance floor (smallest allowed value) for the diagonal covariances
plot_data	either TRUE or FALSE indicating whether the results of the function should be plotted
seed	integer value for random number generator (RNG)

**Details**

**AIC** : the Akaike information criterion

**BIC** : the Bayesian information criterion

In case that the *max\_clusters* parameter is a contiguous or non-contiguous vector then plotting is disabled. Therefore, plotting is enabled only if the *max\_clusters* parameter is of length 1.

**Value**

a vector with either the AIC or BIC for each iteration. In case of Error it returns the error message and the possible causes.

**Author(s)**

Lampros Mouselimis

**Examples**

```
data(dietary_survey_IBS)

dat = dietary_survey_IBS[, -ncol(dietary_survey_IBS)]

dat = center_scale(dat)

opt_gmm = Optimal_Clusters_GMM(dat, 10, criterion = "AIC", plot_data = FALSE)

#-----
# non-contiguous search space
#-----

search_space = c(2,5)

opt_gmm = Optimal_Clusters_GMM(dat, search_space, criterion = "AIC", plot_data = FALSE)
```

---

Optimal\_Clusters\_KMeans

*Optimal number of Clusters for Kmeans or Mini-Batch-Kmeans*

---

**Description**

Optimal number of Clusters for Kmeans or Mini-Batch-Kmeans

**Usage**

```
Optimal_Clusters_KMeans(data, max_clusters,
    criterion = "variance_explained", fK_threshold = 0.85,
    num_init = 1, max_iters = 200, initializer = "kmeans++",
    tol = 1e-04, plot_clusters = TRUE, verbose = FALSE,
    tol_optimal_init = 0.3, seed = 1, mini_batch_params = NULL)
```

**Arguments**

<code>data</code>	matrix or data frame
<code>max_clusters</code>	either a numeric value, a contiguous or non-contiguous numeric vector specifying the cluster search space
<code>criterion</code>	one of <i>variance_explained</i> , <i>WCSSE</i> , <i>dissimilarity</i> , <i>silhouette</i> , <i>distortion_fK</i> , <i>AIC</i> , <i>BIC</i> and <i>Adjusted_Rsquared</i> . See details for more information.
<code>fK_threshold</code>	a float number used in the 'distortion_fK' criterion
<code>num_init</code>	number of times the algorithm will be run with different centroid seeds
<code>max_iters</code>	the maximum number of clustering iterations
<code>initializer</code>	the method of initialization. One of, <i>optimal_init</i> , <i>quantile_init</i> , <i>kmeans++</i> and <i>random</i> . See details for more information
<code>tol</code>	a float number. If, in case of an iteration ( $\text{iteration} > 1$ and $\text{iteration} < \text{max\_iters}$ ) 'tol' is greater than the squared norm of the centroids, then kmeans has converged
<code>plot_clusters</code>	either TRUE or FALSE, indicating whether the results of the <i>Optimal_Clusters_KMeans</i> function should be plotted
<code>verbose</code>	either TRUE or FALSE, indicating whether progress is printed during clustering
<code>tol_optimal_init</code>	tolerance value for the 'optimal_init' initializer. The higher this value is, the far apart from each other the centroids are.
<code>seed</code>	integer value for random number generator (RNG)
<code>mini_batch_params</code>	either NULL or a list of the following parameters : <i>batch_size</i> , <i>init_fraction</i> , <i>early_stop_iter</i> . If not NULL then the optimal number of clusters will be found based on the Mini-Batch-Kmeans. See the details and examples sections for more information.

**Details**

—————criteria—————

**variance\_explained** : the sum of the within-cluster-sum-of-squares-of-all-clusters divided by the total sum of squares

**WCSSE** : the sum of the within-cluster-sum-of-squares-of-all-clusters

**dissimilarity** : the average intra-cluster-dissimilarity of all clusters (the distance metric defaults to euclidean)

**silhouette** : the average silhouette width of all clusters (the distance metric defaults to euclidean)

**distortion\_fK** : this criterion is based on the following paper, 'Selection of K in K-means clustering' (<https://www.ee.columbia.edu/~dpwe/papers/PhamDN05-kmeans.pdf>)

**AIC** : the Akaike information criterion

**BIC** : the Bayesian information criterion

**Adjusted\_Rsquared** : the adjusted R<sup>2</sup> statistic

—————initializers—————

**optimal\_init** : this initializer adds rows of the data incrementally, while checking that they do not already exist in the centroid-matrix [ experimental ]

**quantile\_init** : initialization of centroids by using the cumulative distance between observations and by removing potential duplicates [ experimental ]

**kmeans++** : kmeans++ initialization. Reference : <http://theory.stanford.edu/~sergei/papers/kMeansPP-soda.pdf> AND <http://stackoverflow.com/questions/5466323/how-exactly-does-k-means-work>

**random** : random selection of data rows as initial centroids

If the *mini\_batch\_params* parameter is not NULL then the optimal number of clusters will be found based on the Mini-batch-Kmeans algorithm, otherwise based on the Kmeans. The higher the *init\_fraction* parameter is the more close the results between Mini-Batch-Kmeans and Kmeans will be.

In case that the *max\_clusters* parameter is a contiguous or non-contiguous vector then plotting is disabled. Therefore, plotting is enabled only if the *max\_clusters* parameter is of length 1. Moreover, the *distortion\_fK* criterion can't be computed if the *max\_clusters* parameter is a contiguous or non-contiguous vector ( the *distortion\_fK* criterion requires consecutive clusters ). The same applies also to the *Adjusted\_Rsquared* criterion which returns incorrect output.

## Value

a vector with the results for the specified criterion. If *plot\_clusters* is TRUE then it plots also the results.

## Author(s)

Lampros Mouselimis

## Examples

```
data(dietary_survey_IBS)

dat = dietary_survey_IBS[, -ncol(dietary_survey_IBS)]

dat = center_scale(dat)

#-----
# kmeans
#-----

opt_km = Optimal_Clusters_KMeans(dat, max_clusters = 10, criterion = "distortion_fK",
```

```

                                plot_clusters = FALSE)

#-----
# mini-batch-kmeans
#-----

params_mbkm = list(batch_size = 10, init_fraction = 0.3, early_stop_iter = 10)

opt_mbkm = Optimal_Clusters_KMeans(dat, max_clusters = 10, criterion = "distortion_fK",
                                plot_clusters = FALSE, mini_batch_params = params_mbkm)

#-----
# non-contiguous search space
#-----

search_space = c(2,5)

opt_km = Optimal_Clusters_KMeans(dat, max_clusters = search_space,
                                criterion = "variance_explained",
                                plot_clusters = FALSE)

```

---

Optimal\_Clusters\_Medoids

*Optimal number of Clusters for the partitioning around Medoids functions*

---

### Description

Optimal number of Clusters for the partitioning around Medoids functions

### Usage

```

Optimal_Clusters_Medoids(data, max_clusters, distance_metric,
  criterion = "dissimilarity", clara_samples = 0,
  clara_sample_size = 0, minkowski_p = 1, swap_phase = TRUE,
  threads = 1, verbose = FALSE, plot_clusters = TRUE, seed = 1)

```

### Arguments

data	matrix or data.frame. If both clara_samples and clara_sample_size equal 0, then the data parameter can be also a dissimilarity matrix, where the main diagonal equals 0.0 and the number of rows equals the number of columns
------	---



<code>max_clusters</code>	either a numeric value, a contiguous or non-contiguous numeric vector specifying the cluster search space
<code>distance_metric</code>	a string specifying the distance method. One of, <i>euclidean</i> , <i>manhattan</i> , <i>chebyshev</i> , <i>canberra</i> , <i>braycurtis</i> , <i>pearson_correlation</i> , <i>simple_matching_coefficient</i> , <i>minkowski</i> , <i>hamming</i> , <i>jaccard_coefficient</i> , <i>Rao_coefficient</i> , <i>mahalanobis</i> , <i>cosine</i>
<code>criterion</code>	one of 'dissimilarity' or 'silhouette'
<code>clara_samples</code>	number of samples to draw from the data set in case of clustering large applications (clara)
<code>clara_sample_size</code>	fraction of data to draw in each sample iteration in case of clustering large applications (clara). It should be a float number greater than 0.0 and less or equal to 1.0
<code>minkowski_p</code>	a numeric value specifying the minkowski parameter in case that <code>distance_metric = "minkowski"</code>
<code>swap_phase</code>	either TRUE or FALSE. If TRUE then both phases ('build' and 'swap') will take place. The 'swap_phase' is considered more computationally intensive.
<code>threads</code>	an integer specifying the number of cores to run in parallel. Openmp will be utilized to parallelize the number of sample draws
<code>verbose</code>	either TRUE or FALSE, indicating whether progress is printed during clustering
<code>plot_clusters</code>	TRUE or FALSE, indicating whether the iterative results should be plotted. See the details section for more information
<code>seed</code>	integer value for random number generator (RNG)

### Details

In case of `plot_clusters = TRUE`, the first plot will be either a plot of dissimilarities or both dissimilarities and silhouette widths giving an indication of the optimal number of the clusters. Then, the user will be asked to give an optimal value for the number of the clusters and after that the second plot will appear with either the dissimilarities or the silhouette widths belonging to each cluster.

In case that the `max_clusters` parameter is a contiguous or non-contiguous vector then plotting is disabled. Therefore, plotting is enabled only if the `max_clusters` parameter is of length 1.

### Value

a list of length equal to the `max_clusters` parameter (the first sublist equals NULL, as dissimilarities and silhouette widths can be calculated if the number of clusters > 1). If `plot_clusters` is TRUE then the function plots also the results.

### Author(s)

Lampros Mouselimis

## Examples

```
## Not run:
data(soybean)

dat = soybean[, -ncol(soybean)]

opt_md = Optimal_Clusters_Medoids(dat, 10, 'jaccard_coefficient', plot_clusters = FALSE)

#-----
# non-contiguous search space
#-----

search_space = c(2,5)

opt_md = Optimal_Clusters_Medoids(dat, search_space, 'jaccard_coefficient', plot_clusters = FALSE)

## End(Not run)
```

---

plot\_2d

*2-dimensional plots*

---

## Description

2-dimensional plots

## Usage

```
plot_2d(data, clusters, centroids_medoids)
```

## Arguments

data	a 2-dimensional matrix or data frame
clusters	numeric vector of length equal to the number of rows of the data, which is the result of a clustering method
centroids_medoids	a matrix of centroids or medoids. The rows of the centroids_medoids should be equal to the length of the unique values of the clusters and the columns should be equal to the columns of the data.

## Details

This function plots the clusters using 2-dimensional data and medoids or centroids.

## Value

a plot

**Author(s)**

Lampros Mouselimis

**Examples**

```
# data(dietary_survey_IBS)
# dat = dietary_survey_IBS[, -ncol(dietary_survey_IBS)]
# dat = center_scale(dat)
# pca_dat = stats::princomp(dat)$scores[, 1:2]
# km = KMeans_rcpp(pca_dat, clusters = 2, num_init = 5, max_iters = 100)
# plot_2d(pca_dat, km$clusters, km$centroids)
```

---

predict\_GMM

*Prediction function for a Gaussian Mixture Model object*

---

**Description**

Prediction function for a Gaussian Mixture Model object

**Usage**

```
predict_GMM(data, CENTROIDS, COVARIANCE, WEIGHTS)
```

**Arguments**

data	matrix or data frame
CENTROIDS	matrix or data frame containing the centroids (means), stored as row vectors
COVARIANCE	matrix or data frame containing the diagonal covariance matrices, stored as row vectors
WEIGHTS	vector containing the weights

**Details**

This function takes the centroids, covariance matrix and weights from a trained model and returns the log-likelihoods, cluster probabilities and cluster labels for new data.

**Value**

a list consisting of the log-likelihoods, cluster probabilities and cluster labels.

**Author(s)**

Lampros Mouselimis

**Examples**

```
data(dietary_survey_IBS)

dat = as.matrix(dietary_survey_IBS[, -ncol(dietary_survey_IBS)])

dat = center_scale(dat)

gmm = GMM(dat, 2, "maha_dist", "random_subset", 10, 10)

# pr = predict_GMM(dat, gmm$centroids, gmm$covariance_matrices, gmm$weights)
```

---

predict\_KMeans

*Prediction function for the k-means*

---

**Description**

Prediction function for the k-means

**Usage**

```
predict_KMeans(data, CENTROIDS)
```

**Arguments**

data	matrix or data frame
CENTROIDS	a matrix of initial cluster centroids. The rows of the CENTROIDS matrix should be equal to the number of clusters and the columns should be equal to the columns of the data.

**Details**

This function takes the data and the output centroids and returns the clusters.

**Value**

a vector (clusters)

**Author(s)**

Lampros Mouselimis

## Examples

```
data(dietary_survey_IBS)

dat = dietary_survey_IBS[, -ncol(dietary_survey_IBS)]

dat = center_scale(dat)

km = KMeans_rcpp(dat, clusters = 2, num_init = 5, max_iters = 100, initializer = 'kmeans++')

pr = predict_KMeans(dat, km$centroids)
```

---

predict\_MBatchKMeans *Prediction function for Mini-Batch-k-means*

---

## Description

Prediction function for Mini-Batch-k-means

## Usage

```
predict_MBatchKMeans(data, CENTROIDS, fuzzy = FALSE)
```

## Arguments

data	matrix or data frame
CENTROIDS	a matrix of initial cluster centroids. The rows of the CENTROIDS matrix should be equal to the number of clusters and the columns should equal the columns of the data.
fuzzy	either TRUE or FALSE. If TRUE then prediction probabilities will be calculated using the distance between observations and centroids.

## Details

This function takes the data and the output centroids and returns the clusters.

## Value

if fuzzy = TRUE the function returns a list with two attributes: a vector with the clusters and a matrix with cluster probabilities. Otherwise, it returns a vector with the clusters.

## Author(s)

Lampros Mouselimis

**Examples**

```

data(dietary_survey_IBS)

dat = dietary_survey_IBS[, -ncol(dietary_survey_IBS)]

dat = center_scale(dat)

MbatchKm = MiniBatchKmeans(dat, clusters = 2, batch_size = 20, num_init = 5, early_stop_iter = 10)

pr = predict_MBatchKMeans(dat, MbatchKm$centroids, fuzzy = FALSE)

```

---

predict_Medoids	<i>Predictions for the Medoid functions</i>
-----------------	---

---

**Description**

Predictions for the Medoid functions

**Usage**

```

predict_Medoids(data, MEDOIDS = NULL, distance_metric = "euclidean",
  fuzzy = FALSE, minkowski_p = 1, threads = 1)

```

**Arguments**

<code>data</code>	matrix or data frame
<code>MEDOIDS</code>	a matrix of initial cluster medoids (data observations). The rows of the MEDOIDS matrix should be equal to the number of clusters and the columns of the MEDOIDS matrix should be equal to the columns of the data.
<code>distance_metric</code>	a string specifying the distance method. One of, <i>euclidean, manhattan, chebyshev, canberra, braycurtis, pearson_correlation, simple_matching_coefficient, minkowski, hamming, jaccard_coefficient, Rao_coefficient, mahalanobis, cosine</i>
<code>fuzzy</code>	either TRUE or FALSE. If TRUE, then probabilities for each cluster will be returned based on the distance between observations and medoids.
<code>minkowski_p</code>	a numeric value specifying the minkowski parameter in case that <code>distance_metric = "minkowski"</code>
<code>threads</code>	an integer specifying the number of cores to run in parallel. Openmp will be utilized to parallelize the number of initializations ( <code>num_init</code> )

**Value**

a list with the following attributes will be returned : `clusters`, `fuzzy_clusters` (if `fuzzy = TRUE`), `dissimilarity`.

**Author(s)**

Lampros Mouselimis

**Examples**

```
data(dietary_survey_IBS)

dat = dietary_survey_IBS[, -ncol(dietary_survey_IBS)]

dat = center_scale(dat)

cm = Cluster_Medoids(dat, clusters = 3, distance_metric = 'euclidean', swap_phase = TRUE)

pm = predict_Medoids(dat, MEDOIDS = cm$medoids, 'euclidean', fuzzy = TRUE)
```

---

Silhouette\_Dissimilarity\_Plot

*Plot of silhouette widths or dissimilarities*

---

**Description**

Plot of silhouette widths or dissimilarities

**Usage**

```
Silhouette_Dissimilarity_Plot(evaluation_object, silhouette = TRUE)
```

**Arguments**

evaluation_object	the output of either a <i>Cluster_Medoids</i> or <i>Clara_Medoids</i> function
silhouette	either TRUE or FALSE, indicating whether the silhouette widths or the dissimilarities should be plotted

**Details**

This function takes the result-object of the *Cluster\_Medoids* or *Clara\_Medoids* function and depending on the argument *silhouette* it plots either the dissimilarities or the silhouette widths of the observations belonging to each cluster.

**Value**

TRUE if either the silhouette widths or the dissimilarities are plotted successfully, otherwise FALSE

**Author(s)**

Lampros Mouselimis

## Examples

```
# data(soybean)

# dat = soybean[, -ncol(soybean)]

# cm = Cluster_Medoids(dat, clusters = 5, distance_metric = 'jaccard_coefficient')

# plt_sd = Silhouette_Dissimilarity_Plot(cm, silhouette = TRUE)
```

---

soybean

*The soybean (large) data set from the UCI repository*

---

## Description

There are 19 classes, only the first 15 of which have been used in prior work. The folklore seems to be that the last four classes are unjustified by the data since they have so few examples. There are 35 categorical attributes, some nominal and some ordered. The value 'dna' means does not apply. The values for attributes are encoded numerically, with the first value encoded as '0', the second as '1', and so forth. Unknown values were imputed using the mice package.

## Usage

```
data(soybean)
```

## Format

A data frame with 307 Instances and 36 attributes (including the class attribute, "class")

## Details

The column names of the data (including the class) appear in the following order:

date, plant-stand, precip, temp, hail, crop-hist, area-damaged, severity, seed-tmt, germination, plant-growth, leaves, leafspots-halo, leafspots-marg, leafspot-size, leaf-shread, leaf-malf, leaf-mild, stem, lodging, stem-cankers, canker-lesion, fruiting-bodies, external decay, mycelium, int-discolor, sclerotia, fruit-pods, fruit spots, seed, mold-growth, seed-discolor, seed-size, shriveling, roots, class

## References

R.S. Michalski and R.L. Chilausky, Learning by Being Told and Learning from Examples: An Experimental Comparison of the Two Methods of Knowledge Acquisition in the Context of Developing an Expert System for Soybean Disease Diagnosis, International Journal of Policy Analysis and Information Systems, Vol. 4, No. 2, 1980.

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download source: [https://archive.ics.uci.edu/ml/datasets/Soybean+\(Large\)](https://archive.ics.uci.edu/ml/datasets/Soybean+(Large))



**Examples**

```
data(soybean)
```

```
X = soybean[, -ncol(soybean)]
```

```
y = soybean[, ncol(soybean)]
```

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