Package ‘kselection’

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Type Package

Title Selection of K in K-Means Clustering

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Description Selection of k in k-means clustering based on Pham et al. paper
``Selection of k in k-means clustering''.

License GPL-3

URL `https://github.com/drodriguezperez/kselection`

BugReports `https://github.com/drodriguezperez/kselection/issues`

Imports tools

Suggests amap, FactoClass, foreach, testthat

Encoding UTF-8

RoxygenNote 7.2.0

NeedsCompilation no

Repository CRAN

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Contents

`kselection-package` *Selection of K in K-Means Clustering*

Description

Selection of k in k-means clustering based on Pham et al. paper “Selection of k in k-means clustering”

Details

This package implements the method for selecting the number of clusters for the algorithm K-means introduced in the publication of Pham, Dimov and Nguyen of 2004.

Package:	kselection
Version:	0.2.0
License:	GPL-3

Author(s)

Daniel Rodriguez `<daniel.rodriguez.perez@gmail.com>`

References

D T Pham, S S Dimov, and C D Nguyen, "Selection of k in k-means clustering", Mechanical Engineering Science, 2004, pp. 103-119.

`get_f_k` *Get the $f(K)$ vector*

Description

Get the $f(K)$ vector.

Usage

```
get_f_k(obj)
```

Arguments

`obj`	the output of `kselection` function.

Value

the vector of $f(K)$ function.

Author(s)

Daniel Rodriguez

See Also

`num_clusters`, `num_clusters_all`

Examples

```
# Create a data set with two clusters
dat <- matrix(c(rnorm(100, 2, .1), rnorm(100, 3, .1),
                rnorm(100, -2, .1), rnorm(100, -3, .1)), 200, 2)

# Get the f(k) vector
sol <- kselection(dat)
f_k <- get_f_k(sol)
```

`get_k_threshold` *Get the* `k_threshold`

Description

Get the maximum value of $f(K)$ from which can not be considered the existence of more than one cluster.

Usage

```
get_k_threshold(obj)
```

Arguments

`obj`	the output of `kselection` function.

Value

the `k_threshold` value.

Author(s)

Daniel Rodriguez

See Also

`set_k_threshold`

`kselection` *Selection of K in K-means Clustering*

Description

Selection of k in k-means clustering based on Pham et al. paper.

Usage

```
kselection(
  x,
  fun_cluster = stats::kmeans,
  max_centers = 15,
  k_threshold = 0.85,
  progressBar = FALSE,
  trace = FALSE,
  parallel = FALSE,
  ...
)
```

Arguments

`x`	numeric matrix of data, or an object that can be coerced to such a matrix.
`fun_cluster`	function to cluster by (e.g. `kmeans`). The first parameter of the function must a numeric matrix and the second the number of clusters. The function must return an object with a named attribute `withinss` which is a numeric vector with the within.
`max_centers`	maximum number of clusters for evaluation.
`k_threshold`	maximum value of $f(K)$ from which can not be considered the existence of more than one cluster in the data set. The default value is 0.85.
`progressBar`	show a progress bar.
`trace`	display a trace of the progress.
`parallel`	If set to true, use parallel `foreach` to execute the function that implements the kmeans algorithm. Must register parallel before hand, such as `doMC` or others. Selecting this option the progress bar is disabled.
`...`	arguments to be passed to the kmeans method.

Details

This function implements the method proposed by Pham, Dimov and Nguyen for selecting the number of clusters for the K-means algorithm. In this method a function $f(K)$ is used to evaluate the quality of the resulting clustering and help decide on the optimal value of K for each data set. The $f(K)$ function is defined as

$$f(K) = \begin{cases} 1 & \text{if } K = 1 \\ \frac{S_K}{\alpha_K S_{K-1}} & \text{if } S_{K-1} \neq 0, \forall K > 1 \\ 1 & \text{if } S_{K-1} = 0, \forall K > 1 \end{cases}$$

where S_K is the sum of the distortion of all cluster and α_K is a weight factor which is defined as

$$\alpha_K = \begin{cases} 1 - \frac{3}{4N_d} & \text{if } K = 1 \text{ and } N_d > 1 \\ \alpha_{K-1} + \frac{1-\alpha_{K-1}}{6} & \text{if } K > 2 \text{ and } N_d > 1 \end{cases}$$

where N_d is the number of dimensions of the data set.

In this definition $f(K)$ is the ratio of the real distortion to the estimated distortion and decreases when there are areas of concentration in the data distribution.

The values of K that yield $f(K) < 0.85$ can be recommended for clustering. If there is not a value of K which $f(K) < 0.85$, it cannot be considered the existence of clusters in the data set.

Value

an object with the $f(K)$ results.

Author(s)

Daniel Rodriguez

References

D T Pham, S S Dimov, and C D Nguyen, "Selection of k in k-means clustering", Mechanical Engineering Science, 2004, pp. 103-119.

See Also

`num_clusters`, `get_f_k`

Examples

```
# Create a data set with two clusters
dat <- matrix(c(rnorm(100, 2, .1), rnorm(100, 3, .1),
                rnorm(100, -2, .1), rnorm(100, -3, .1)), 200, 2)

# Execute the method
sol <- kselection(dat)

# Get the results
k   <- num_clusters(sol) # optimal number of clustes
f_k <- get_f_k(sol)      # the f(K) vector

# Plot the results
plot(sol)

## Not run:
# Parallel
require(doMC)
registerDoMC(cores = 4)

system.time(kselection(dat, max_centers = 50 , nstart = 25))
system.time(kselection(dat, max_centers = 50 , nstart = 25, parallel = TRUE))
```

```
## End(Not run)
```

`num_clusters` *Get the number of clusters.*

Description

The optimal number of clusters proposed by the method.

Usage

```
num_clusters(obj)
```

Arguments

`obj`	the output of kselection function.

Value

the number of clusters proposed.

Author(s)

Daniel Rodriguez

See Also

`num_clusters_all`, `get_f_k`

Examples

```
# Create a data set with two clusters
dat <- matrix(c(rnorm(100, 2, .1), rnorm(100, 3, .1),
                rnorm(100, -2, .1), rnorm(100, -3, .1)), 200, 2)

# Get the optimal number of clustes
sol <- kselection(dat)
k   <- num_clusters(sol)
```

`num_clusters_all` *Get all recommended numbers of clusters*

Description

The number of cluster which could be recommender according the method threshold.

Usage

```
num_clusters_all(obj)
```

Arguments

`obj`	the output of `kselection` function.

Value

an array of number of clusters that could be recommended.

Author(s)

Daniel Rodriguez

See Also

`num_clusters`, `get_f_k`

Examples

```
# Create a data set with two clusters
dat <- matrix(c(rnorm(100, 2, .1), rnorm(100, 3, .1),
                rnorm(100, -2, .1), rnorm(100, -3, .1)), 200, 2)

# Get the optimal number of clustes
sol <- kselection(dat)
k   <- num_clusters(sol)
```

`set_k_threshold` *Set the* `k_threshold`

Description

Set the maximum value of $f(K)$ from which can not be considered the existence of more than one cluster.

Usage

```
set_k_threshold(obj, k_threshold)
```

Arguments

`obj`	the output of `kselection` function.
`k_threshold`	maximum value of $f(K)$ from which can not be considered the existence of more than one cluster in the data set.

Value

the output of kselection function with new `k_threshold`.

Author(s)

Daniel Rodriguez

See Also

`get_k_threshold`

Index