# Package 'GBClust'

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**Type** Package

**Title** Generalized Bayes clustering

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**Description** This panckage is an implementation of several generalized Bayes clustering methods.

**Encoding** UTF-8

**License** MIT + file LICENSE

**LazyData** TRUE

**Depends** R (>= 4.0.0)

**Imports** Rcpp (>= 1.0.5), RcppArmadillo(>= 0.10.1.2.0), ggplot2, cluster

**LinkingTo** Rcpp, RcppArmadillo

**RoxygenNote** 7.1.1

**Suggests** knitr,
rmarkdown

**VignetteBuilder** knitr

## R topics documented:

## comp_medoids *Compute the medoids*

### Description

Compute the medoids of a given clustering solution based on the corresponding dissimilarity matrix.

### Usage

```
comp_medoids(D, cluster)
```

### Arguments

| | |
|---|---|
| D | A n x n numeric matrix containing the dissimilarities, i.e. the output of the functions dist or daisy. |
| cluster | A clustering solution, i.e. the output of kdiss. |

### Value

medoids Indexes of the medoids.

## kbinary *K-binary clustering*

### Description

Perform the so-called k-binary clustering algorithm, for obtaining groups when the data are binary observations.

### Usage

```
kbinary(x, k, nstart = 1, trace = FALSE)
```

### Arguments

| | |
|---|---|
| x | binary matrix of data, or an object that can be coerced to such a matrix (such as a numeric vector or a data frame with all numeric columns). |
| k | The number of clusters to be considered. A random set of (distinct) rows in x is chosen as the initial centers. |
| nstart | Number of random sets that has been chosen. |
| trace | logical: if true, tracing information on the progress of the algorithm is produced. |

### Value

cluster Labels of the clusters at convergence.

centers The value of the centroids at convergence.

loss Numeric value of the loss function at convergence.

## kbinary_gibbs *K-binary Gibbs sampling*

### Description

Perform the Gibbs-sampling for the k-binary algorithm. This function is complementary to `kbinary`, which is used instead to get a point estimate.

### Usage

```
kbinary_gibbs(
  x,
  k,
  lambda = 1,
  R = 1000,
  burn_in = 1000,
  nstart = 10,
  trace = FALSE
)
```

### Arguments

| | |
|---|---|
| `x` | binary matrix of the data |
| `k` | The number of clusters to be considered |
| `lambda` | Gibbs posterior tuning parameter |
| `R` | Number of MCMC samples after burn-in |
| `burn_in` | Number of MCMC samples to be discarded as burn-in period |
| `nstart` | Number of random initializations for the k-means algorithm |
| `trace` | logical: if true, tracing information on the progress of the algorithm is produced. |

### Value

`G` A `R` x `n` matrix including the cluster labels for each MCMC iteration.

`loss` A `R`-dimensional vector including the values of the loss function for each MCMC iteration.

`G_map` Labels of the clusters at the lowest value of the posterior that has been computed.

`loss_map` Lowest value of the loss that has been computed.

## kbinary_select *Selection of the number of cluster for the k-binary algorithm*

### Description

It displays the value of the loss function for various choices of k.

### Usage

```
kbinary_select(x, k_max, nstart = 1)
```

### Arguments

| | |
|---|---|
| x | numeric matrix of data, or an object that can be coerced to such a matrix (such as a numeric vector or a data frame with all numeric columns). |
| k_max | The maximum number of clusters to be considered. A random set of (distinct) rows in x is chosen as the initial centers. |
| nstart | Number of random sets that has been chosen. |

### Value

It plots the loss function for different clustering solutions.

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## kdiss *K-dissimilarities algorithm*

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### Description

Perform the so-called k-dissimilarities algorithm.

### Usage

```
kdiss(D, k, nstart = 1, trace = FALSE)
```

### Arguments

| | |
|---|---|
| D | A n x n numeric matrix containing the dissimilarities, typically the output of dist or daisy. |
| k | The number of clusters to be considered. See kdiss_select for selection criteria. |
| nstart | Number of random initializations. |
| trace | logical: if true, tracing information on the progress of the algorithm is produced. |

### Value

`cluster` Labels of the clusters at convergence

`loss` Numeric value of the loss function at convergence

## kdiss_select *Selection of the number of cluster for the k-dissimilarities algorithm*

### Description

It displays the value of the loss function / average silhouette width, for different values of k

### Usage

```
kdiss_select(D, k_max, nstart = 1, method = "elbow")
```

### Arguments

| | |
|---|---|
| D | A n x n numeric matrix containing the dissimilarities, typically the output of dist or daisy. |
| k_max | Maximum number of clusters to be considered. |
| nstart | Number of random initializations. |
| method | The graph that will be displayed. Supported options are method="elbow", which displays the loss function, or method="silhouette". See silhouette for details about the latter. |

### Value

It return a ggplot2 graph of the loss function / average silhouette width, for k=1,...,k_max.

## kmeans2 *K-means clustering*

### Description

Perform the k-means clustering on a data matrix.

### Usage

```
kmeans2(x, k, nstart = 1, algorithm = "kmeans", trace = FALSE)
```

### Arguments

| | |
|---|---|
| x | numeric matrix of data, or an object that can be coerced to such a matrix (such as a numeric vector or a data frame with all numeric columns). |
| k | The number of clusters to be considered. A random set of (distinct) rows in x is chosen as the initial centres. |
| nstart | Number of random sets that has been chosen |
| algorithm | The algorithm to be used |
| trace | logical: if true, tracing information on the progress of the algorithm is produced. |

### Value

`cluster` Labels of the clusters at convergence

`centers` The value of the centroids at convergence

`loss` Numeric value of the loss function at convergence

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## kmeans2_select *Selection of the number of cluster for the k-means algorithm*

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### Description

It displays the value of the loss function for various choices of k

### Usage

```
kmeans2_select(x, k_max, nstart = 1, algorithm = "kmeans")
```

### Arguments

| | |
|---|---|
| `x` | numeric matrix of data, or an object that can be coerced to such a matrix (such as a numeric vector or a data frame with all numeric columns). |
| `k_max` | The maximum number of clusters to be considered. A random set of (distinct) rows in x is chosen as the initial centres. |
| `nstart` | Number of random sets that has been chosen |
| `algorithm` | The algorithm to be used, either `kmeans` or `kmeans2` |

### Value

It plots the loss function for different clustering solutions

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## kmeans_gibbs *K-means Gibbs sampling*

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### Description

Perform the Gibbs-sampling for the k-means algorithm. This function is complementary to `kmeans2`, which is used instead to get a point estimate.

### Usage

```
kmeans_gibbs(
  x,
  k,
  a_lambda,
  b_lambda,
  R = 1000,
  burn_in = 1000,
  nstart = 10,
  trace = FALSE
)
```

### Arguments

| | |
|---|---|
| x | A n x d numeric matrix of the data. |
| k | The number of clusters to be considered. |
| a_lambda | Hyperparameter of the Gamma prior on the scale parameter. |
| b_lambda | Hyperparameter of the Gamma prior on on the scale parameter. |
| R | Number of MCMC samples after burn-in. |
| burn_in | Number of MCMC samples to be discarded as burn-in period. |
| nstart | Number of random initializations for the k-means algorithm. |
| trace | logical: if true, tracing information on the progress of the algorithm is produced. |

### Value

`G` A R x n matrix including the cluster labels for each MCMC iteration.

`lambda` A R-dimensional vector including the values of lambda for each MCMC iteration.

`loss` A R-dimensional vector including the values of the loss function for each MCMC iteration.

`G_map` Labels of the clusters at the lowest value of the posterior that has been computed.

`loss_map` Lowest value of the loss that has been computed.

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## `Minkowski_gibbs` *K-dissimilarities (Minkowski) Gibbs sampling*

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### Description

Perform the Gibbs-sampling for the k-dissimilarities algorithm using the Minkowski distance. This function is complementary to `kdiss`, which is used instead to get a point estimate.

### Usage

```
Minkowski_gibbs(
  x,
  k,
  p,
  a_lambda = 0,
  b_lambda = 0,
  R = 1000,
  burn_in = 1000,
  nstart = 10,
  trace = FALSE
)
```

### Arguments

| | |
|---|---|
| x | numeric matrix of of the data. |
| k | The number of clusters to be considered. |
| p | Power of the Minkowski distance. |
| a_lambda | Hyperparameter of the Gamma prior on the scale parameter. The default `a_lambda = 0` leads to an improper prior. |

| | |
|---|---|
| b_lambda | Hyperparameter of the Gamma prior on on the scale parameter. The default a_lambda = 0 leads to an improper prior. |
| R | Number of MCMC samples after burn-in. |
| burn_in | Number of MCMC samples to be discarded as burn-in period. |
| nstart | Number of random initializations for the kdiss algorithm, used to initialize the MCMC chain. |
| trace | logical: if true, tracing information on the progress of the algorithm is produced. |

## Value

G Labels of the clusters at each MCMC iteration.

lambda Numeric vector of the values of lambda at each MCMC iteration.

loss Numeric vector of the loss function at each MCMC iteration.

G_map Labels of the clusters obtained using kdiss, representing the maximum a posteriori.

loss_map Numeric value of the loss function obtained using kdiss, representing the maximized loss.

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