

# Package ‘mbkmeans’

March 30, 2021

**Type** Package

**Title** Mini-batch K-means Clustering for Single-Cell RNA-seq

**Version** 1.6.1

**Description** Implements the mini-batch k-means algorithm for large datasets, including support for on-disk data representation.

**Depends** R (>= 3.6)

**Imports** methods, DelayedArray, Rcpp, S4Vectors, SingleCellExperiment, SummarizedExperiment, bluster, ClusterR, benchmarkme, Matrix, BiocParallel

**Suggests** beachmat, HDF5Array, Rhdf5lib, BiocStyle, TENxPBMCDData, scater, DelayedMatrixStats, knitr, testthat

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**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 7.1.1

**LinkingTo** Rcpp, RcppArmadillo (>= 0.7.2), Rhdf5lib, beachmat, ClusterR

**SystemRequirements** C++11

**VignetteBuilder** knitr

**biocViews** Clustering, GeneExpression, RNASeq, Software, Transcriptomics, Sequencing, SingleCell

**BugReports** <https://github.com/drisso/mbkmeans/issues>

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**R topics documented:**

blocksize . . . . .	2
clusterRows . . . . .	2
compute_wcss . . . . .	3
mbkmeans . . . . .	4
MbkmeansParam-class . . . . .	6
mini_batch . . . . .	7
predict_mini_batch . . . . .	9
predict_mini_batch_r . . . . .	10

<b>Index</b>	<b>11</b>
--------------	-----------

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blocksize	<i>blocksize</i>
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**Description**

Return the maximum number of rows to use based on the amount of ram memory.

**Usage**

```
blocksize(data, ram = get_ram())
```

**Arguments**

data	matrix-like object.
ram	the max amount of ram (in bytes) to use.

**Value**

Numeric value of the maximum number of rows.

**Examples**

```
data <- matrix(NA, nrow = 100, ncol=1000)
blocksize(data, ram=1e6)
```

---

clusterRows	<i>Cluster rows of a matrix</i>
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**Description**

Cluster rows of a matrix-like object with a variety of algorithms.

**Usage**

```
clusterRows(x, BLUSPARAM, full = FALSE)
```

**Arguments**

x	A numeric matrix-like object where rows represent observations and columns represent variables.
BLUSPARAM	A <a href="#">BlusterParam</a> object specifying the algorithm to use.
full	Logical scalar indicating whether the full clustering statistics should be returned for each method.

**Details**

This generic allows users to write agile code that can use a variety of clustering algorithms. By simply changing BLUSPARAM, we can tune the clustering procedure in analysis workflows and package functions.

**Value**

By default, a factor of length equal to `nrow(x)` containing cluster assignments for each row of `x`.

If `full=TRUE`, a list is returned containing `clusters`, a factor as described above; and `objects`, an arbitrary object containing algorithm-specific statistics or intermediate objects.

**Author(s)**

Aaron Lun, Stephanie Hicks

**See Also**

[MbkmeansParam](#) for some examples of values for BLUSPARAM.

**Examples**

```
m <- matrix(runif(10000), ncol=10)
clusterRows(m, MbkmeansParam(2))
```

---

compute\_wcss

*Compute Within-Cluster Sum of Squares*

---

**Description**

Given a vector of cluster labels, a matrix of centroids, and a dataset, it computes the WCSS.

**Usage**

```
compute_wcss(clusters, cent, data)
```

**Arguments**

clusters	numeric vector with the cluster assignments.
cent	numeric matrix with the centroids (clusters in rows, variables in columns).
data	matrix-like object containing the data (numeric or integer).

**Value**

A numeric vector with the value of WCSS per cluster.

**Examples**

```
data = matrix(1:30,nrow = 10)
cl <- mini_batch(data, 2, 10, 10)
compute_wcss(cl$Clusters, cl$centroids, data)
```

---

mbkmeans

*Mini-Batch k-means for large single cell sequencing data*


---

**Description**

This is an implementation of the mini-batch k-means algorithm of Sculley (2010) for large single cell sequencing data with the dimensionality reduction results as input in the reducedDim() slot.

**Usage**

```
mbkmeans(x, ...)

## S4 method for signature 'SummarizedExperiment'
mbkmeans(x, whichAssay = 1, ...)

## S4 method for signature 'SingleCellExperiment'
mbkmeans(x, reduceMethod = "PCA", whichAssay = 1, ...)

## S4 method for signature 'LinearEmbeddingMatrix'
mbkmeans(x, ...)

## S4 method for signature 'ANY'
mbkmeans(
  x,
  clusters,
  batch_size = min(500, NCOL(x)),
  max_iters = 100,
  num_init = 1,
  init_fraction = batch_size/NCOL(x),
  initializer = "kmeans++",
  compute_labels = TRUE,
  calc_wcss = FALSE,
  early_stop_iter = 10,
  verbose = FALSE,
  CENTROIDS = NULL,
  tol = 1e-04,
  BPPARAM = BiocParallel::SerialParam(),
  ...
)
```

**Arguments**

x	The object on which to run mini-batch k-means. It can be a matrix-like object (e.g., matrix, Matrix, DelayedMatrix, HDF5Matrix) with genes in the rows and samples in the columns. Specialized methods are defined for SummarizedExperiment and SingleCellExperiment.
...	passed to 'blockApply'.
whichAssay	The assay to use as input to mini-batch k-means. If x is a SingleCellExperiment, this is ignored unless reduceMethod = NA.
reduceMethod	Name of dimensionality reduction results to use as input to mini-batch k-means. Set to NA to use the full matrix.
clusters	the number of clusters
batch_size	the size of the mini batches. By default, it equals the minimum between the number of observations and 500.
max_iters	the maximum number of clustering iterations
num_init	number of times the algorithm will be run with different centroid seeds
init_fraction	proportion of data to use for the initialization centroids (applies if initializer is <i>kmeans++</i> ). Should be a float number between 0.0 and 1.0. By default, it uses the relative batch size.
initializer	the method of initialization. One of <i>kmeans++</i> and <i>random</i> . See details for more information
compute_labels	logical indicating whether to compute the final cluster labels.
calc_wcss	logical indicating whether the per-cluster WCSS is computed. Ignored if 'compute_labels = FALSE'.
early_stop_iter	continue that many iterations after calculation of the best within-cluster-sum-of-squared-error
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 (iteration > 1 and iteration < max_iters) 'tol' is greater than the squared norm of the centroids, then kmeans has converged
BPPARAM	See the 'BiocParallel' package. Only the label assignment is done in parallel.

**Details**

The implementation is largely based on the [MiniBatchKmeans](#) function of the ClusterR package. The contribution of this package is to provide support for on-disk data representations such as HDF5, through the use of DelayedMatrix and HDF5Matrix objects, as well as for sparse data representation through the classes of the Matrix package. We also provide high-level methods for objects of class SummarizedExperiment, SingleCellExperiment, and LinearEmbeddingMatrix.

This function performs k-means clustering using mini batches.

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

**Author(s)**

Lampros Mouselimis and Yuwei Ni

**References**

Sculley. Web-Scale K-Means Clustering. WWW 2010, April 26–30, 2010, Raleigh, North Carolina, USA. ACM 978-1-60558-799-8/10/04.  
<https://github.com/mlampros/ClusterR>

**Examples**

```
library(SummarizedExperiment)
se <- SummarizedExperiment(matrix(rnorm(100), ncol=10))
mbkmeans(se, clusters = 2)
library(SingleCellExperiment)
sce <- SingleCellExperiment(matrix(rnorm(100), ncol=10))
mbkmeans(sce, clusters = 2, reduceMethod = NA)
x<-matrix(rnorm(100), ncol=10)
mbkmeans(x,clusters = 3)
```

---

MbkmeansParam-class    *Mini-batch k-means clustering*

---

**Description**

Run the mini-batch k-means `mbkmeans` function with the specified number of centers within `clusterRows` from the `bluster` Bioconductor package.

**Usage**

```
MbkmeansParam(centers, ...)

## S4 method for signature 'ANY,MbkmeansParam'
clusterRows(x, BLUSPARAM, full = FALSE)
```

**Arguments**

<code>centers</code>	An integer scalar specifying the number of centers. Alternatively, a function that takes the number of observations and returns the number of centers. Note, the <code>mbkmeans</code> function uses the argument <code>clusters</code> argument to represent this argument. However, we use <code>centers</code> to match
<code>...</code>	Further arguments to pass to <code>mbkmeans</code> .
<code>x</code>	A numeric matrix-like object where rows represent observations and columns represent variables.

BLUSPARAM	A <a href="#">MbkmeansParam</a> object.
full	Logical scalar indicating whether the full mini-batch k-means statistics should be returned.

## Details

The `clusterRows` function from the [bluster](#) Bioconductor package is a generic that controls dispatch to different clustering algorithms. Here we add the option to use the `mbkmeans` clustering algorithm with `clusterRows`. This class usually requires the user to specify the number of clusters beforehand. However, we can also allow the number of clusters to vary as a function of the number of observations. The latter is occasionally useful, e.g., to allow the clustering to automatically become more granular for large datasets.

To modify an existing `MbkmeansParam` object `x`, users can simply call `x[[i]]` or `x[[i]] <-value` where `i` is any argument used in the constructor.

## Value

The `MbkmeansParam` constructor will return a [MbkmeansParam](#) object with the specified parameters.

The `clusterRows` method will return a factor of length equal to `nrow(x)` containing the cluster assignments. If `full=TRUE`, a list is returned with `clusters` (the factor, as above) and `objects`; the latter will contain the direct output of [mbkmeans](#).

## Author(s)

Stephanie Hicks

## See Also

[mbkmeans](#), which actually does all the heavy lifting.

## Examples

```
clusterRows(iris[,1:4], MbkmeansParam(centers=3))
clusterRows(iris[,1:4], MbkmeansParam(centers=3, batch_size=10))
clusterRows(iris[,1:4], MbkmeansParam(centers=3, batch_size=10,
  compute_labels=TRUE, calc_wcss=TRUE))
```

---

mini\_batch

*Mini\_batch*

---

## Description

Mini-batch-k-means for matrix-like objects

## Usage

```

mini_batch(
  data,
  clusters,
  batch_size,
  max_iters,
  num_init = 1L,
  init_fraction = 1,
  initializer = "kmeans++",
  compute_labels = TRUE,
  calc_wcss = FALSE,
  early_stop_iter = 10L,
  verbose = FALSE,
  CENTROIDS = NULL,
  tol = 1e-04
)

```

## Arguments

<code>data</code>	numeric or integer matrix-like object.
<code>clusters</code>	the number of clusters.
<code>batch_size</code>	the size of the mini batches.
<code>max_iters</code>	the maximum number of clustering iterations.
<code>num_init</code>	number of times the algorithm will be run with different centroid seeds.
<code>init_fraction</code>	percentage of data to use for the initialization centroids (applies if <code>initializer</code> is <code>kmeans++</code> ). Should be a float number between 0.0 and 1.0.
<code>initializer</code>	the method of initialization. One of <code>kmeans++</code> and <code>random</code> . See details for more information.
<code>compute_labels</code>	logical indicating whether to compute the final cluster labels.
<code>calc_wcss</code>	logical indicating whether the within-cluster sum of squares should be computed and returned (ignored if <code>compute_labels = FALSE</code> ).
<code>early_stop_iter</code>	continue that many iterations after calculation of the best within-cluster-sum-of-squared-error.
<code>verbose</code>	logical indicating whether progress is printed on screen.
<code>CENTROIDS</code>	an optional matrix of initial cluster centroids. The rows of the <code>CENTROIDS</code> matrix should be equal to the number of clusters and the columns should be equal to the columns of the data.
<code>tol</code>	convergence tolerance.

## Details

This function performs k-means clustering using mini batches. It was inspired by the implementation in <https://github.com/mlampros/ClusterR>.

The input matrix can be in any format supported by the `'DelayedArray'` / `'beachmat'` framework, including the matrix classes defined in the `'Matrix'` package and the `'HDFMatrix'` class.

There are two possible initializations.

**kmeans++:** kmeans++ initialization.

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



**Value**

a list with the following attributes:

centroids: the final centroids;

WCSS\_per\_cluster (optional): the final per-cluster WCSS.

best\_initialization: which initialization value led to the best WCSS solution;

iters\_per\_initialization: number of iterations per each initialization;

Clusters (optional): the final cluster labels.

**References**

Sculley, D., 2010, April. Web-scale k-means clustering. In Proceedings of the 19th international conference on World wide web (pp. 1177-1178). ACM.

Arthur, D. and Vassilvitskii, S., 2007, January. k-means++: The advantages of careful seeding. In Proceedings of the eighteenth annual ACM-SIAM symposium on Discrete algorithms (pp. 1027-1035). Society for Industrial and Applied Mathematics.

**Examples**

```
data = matrix(1:30,nrow = 10)
mini_batch(data, 2, 10, 10)
```

---

predict_mini_batch	<i>Predict_mini_batch</i>
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---

**Description**

Prediction function for mini-batch k-means applied to matrix-like objects.

**Usage**

```
predict_mini_batch(data, CENTROIDS)
```

**Arguments**

data	matrix-like object containing numeric or integer data (observations in rows, variables in columns).
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.

**Details**

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

This implementation relies very heavily on the [MiniBatchKmeans](#) implementation. We provide the ability to work with other matrix-like objects other than base matrices (e.g. DelayedMatrix and HDF5Matrix) through the beachmat library.

**Value**

it returns a vector with the clusters.

**Author(s)**

Yuwei Ni

**Examples**

```
data(iris)
km = mini_batch(as.matrix(iris[,1:4]), clusters = 3,
               batch_size = 10, max_iters = 10)
clusters = predict_mini_batch(as.matrix(iris[,1:4]),
                             CENTROIDS = km$centroids)
```

---

predict\_mini\_batch\_r *Compute labels for mini-batch k-means*

---

**Description**

Given a data matrix and a centroid matrix, it assigns each data point to the closest centroid, using block processing.

**Usage**

```
predict_mini_batch_r(
  data,
  centroids,
  BPPARAM = BiocParallel::SerialParam(),
  ...
)
```

**Arguments**

data	a matrix-like object with features in row and samples in columns.
centroids	a matrix with the coordinates of the centroids.
BPPARAM	for parallel computations. See the 'BiocParallel' package.
...	passed to 'blockApply'.

**Value**

a vector of cluster labels for each observation.

**Examples**

```
data(iris)
km <- mini_batch(as.matrix(iris[,1:4]), clusters = 3,
                batch_size = 10, max_iters = 100)
predict_mini_batch_r(t(as.matrix(iris[,1:4])), km$centroids)
```

# Index

blocksize, [2](#)  
bluster, [6](#), [7](#)  
BlusterParam, [3](#)

clusterRows, [2](#), [6](#), [7](#)  
clusterRows, ANY, MbkmeansParam-method  
(MbkmeansParam-class), [6](#)  
compute\_wcss, [3](#)

mbkmeans, [4](#), [6](#), [7](#)  
mbkmeans, ANY-method (mbkmeans), [4](#)  
mbkmeans, LinearEmbeddingMatrix-method  
(mbkmeans), [4](#)  
mbkmeans, SingleCellExperiment-method  
(mbkmeans), [4](#)  
mbkmeans, SummarizedExperiment-method  
(mbkmeans), [4](#)  
MbkmeansParam, [3](#), [7](#)  
MbkmeansParam (MbkmeansParam-class), [6](#)  
MbkmeansParam-class, [6](#)  
mini\_batch, [7](#)  
MiniBatchKmeans, [5](#), [9](#)

predict\_mini\_batch, [9](#)  
predict\_mini\_batch\_r, [10](#)

show, MbkmeansParam-method  
(MbkmeansParam-class), [6](#)