Package ‘mbkmeans’

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

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### Description

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

### Usage

```r
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

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

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

Details
This function is deprecated. Please use the clusterRows function in the bluster Bioconductor package.

compute_wcss

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)
c1 <- mini_batch(data, 2, 10, 10)
compute_wcss(c1$Clusters, c1$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**

```r
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
reduceMethod
clusters
batch_size
max_iters
num_init
init_fraction
initializer
compute_labels
calc_wcss
early_stop_iter
verbose
CENTROIDS
tol
BPPARAM

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.

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 and Yuwei Ni

References
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

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, ...)

Arguments
centers 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 mbkmeans function uses the argument clusters argument to represent this argument. However, we use centers to match

... Further arguments to pass to mbkmeans.

Details
This function is deprecated. Please use the MbkmeansParam function in the bluster Bioconductor package.
**mini_batch**

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**mini_batch**  
*Mini_batch*

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**Description**

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

**Usage**

```r
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**

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


Examples

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

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**

```r
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**

```r
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)
```
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