

Package ‘scDHA’

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Type Package

Title Single-Cell Decomposition using Hierarchical Autoencoder

Version 1.1.2

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Description Provides a fast and accurate pipeline for single-cell analyses.

The 'scDHA' software package can perform clustering, dimension reduction and visualization, classification, and time-trajectory inference on single-cell data (Tran et.al. (2021) <[DOI:10.1038/s41467-021-21312-2](https://doi.org/10.1038/s41467-021-21312-2)>).

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Encoding UTF-8

LazyData true

Depends R (>= 3.4)

Imports matrixStats, foreach, doParallel, igraph, Matrix, uwot, cluster, clusterCrit, Rcpp, RcppParallel, RcppAnnoy, methods, torch (>= 0.3.0), RhpcBLASctl

LinkingTo Rcpp, RcppArmadillo, RcppParallel, RcppAnnoy

RoxygenNote 7.1.0

Suggests testthat, knitr, mclust

NeedsCompilation yes

VignetteBuilder knitr

URL <https://github.com/duct317/scDHA>

BugReports <https://github.com/duct317/scDHA/issues>

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Goolam	<i>Goolam</i>
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Description

Goolam dataset in list format, include scRNA-seq data and cell type information.

Usage

Goolam

Format

An object of class `list` of length 2.

Goolam_result	<i>Goolam_result</i>
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Description

Result of processing Goolam dataset using 'scDHA' function.

Usage

Goolam_result

Format

An object of class `list` of length 4.

`scDHA``scDHA`

Description

The main function to perform dimension deduction and clustering.

Usage

```
scDHA(  
  data = data,  
  k = NULL,  
  method = "scDHA",  
  sparse = FALSE,  
  n = 5000,  
  ncores = 10L,  
  gen_fil = TRUE,  
  do.clus = TRUE,  
  sample.prob = NULL,  
  seed = NULL  
)
```

Arguments

<code>data</code>	Gene expression matrix, with rows represent samples and columns represent genes.
<code>k</code>	Number of clusters, leave as default for auto detection. Has no effect when <code>do.clus = False</code> .
<code>method</code>	Method used for clustering. It can be "scDHA" or "louvain". The default setting is "scDHA".
<code>sparse</code>	Boolean variable indicating whether data is a sparse matrix. The input must be a non negative sparse matrix.
<code>n</code>	Number of genes to keep after feature selection step.
<code>ncores</code>	Number of processor cores to use.
<code>gen_fil</code>	Boolean variable indicating whether to perform scDHA gene filtering before performing dimension deduction and clustering.
<code>do.clus</code>	Boolean variable indicating whether to perform scDHA clustering. If <code>do.clus = False</code> , only dimension deduction is performed.
<code>sample.prob</code>	Probability used for classification application only. Leave this parameter as default, no user input is required.
<code>seed</code>	Seed for reproducibility.

Value

List with the following keys:

- cluster - A numeric vector containing cluster assignment for each sample. If `do.clus = False`, this values is always NULL.
- latent - A matrix representing compressed data from the input data, with rows represent samples and columns represent latent variables.

Examples

```
library(scDHA)
#Load example data (Goolam dataset)
data('Goolam'); data <- t(Goolam$data); label <- as.character(Goolam$label)
#Log transform the data
data <- log2(data + 1)
if(torch::torch_is_installed()) #scDHA need libtorch installed
{
  #Generate clustering result, the input matrix has rows as samples and columns as genes
  result <- scDHA(data, ncores = 2, seed = 1)
  #The clustering result can be found here
  cluster <- result$cluster
}
```

scDHA.class

scDHA classification

Description

Perform classification of new data based on available data.

Usage

```
scDHA.class(
  train = train,
  train.label = train.label,
  test = test,
  ncores = 10L,
  seed = NULL
)
```

Arguments

train	Expression matrix of available data, with rows represent samples and columns represent genes.
train.label	A vector containing label for each sample in training data.

test	Expression matrix new data for classification, with rows represent samples and columns represent genes.
ncores	Number of processor cores to use.
seed	Seed for reproducibility.

Value

A vector contain classified labels for new data.

Examples

```
library(scDHA)
#Load example data (Goolam dataset)
data('Goolam'); data <- t(Goolam$data); label <- as.character(Goolam$label)
#Log transform the data
data <- log2(data + 1)
#Split data into training and testing sets
set.seed(1)
idx <- sample.int(nrow(data), size = round(nrow(data)*0.75))
train.x <- data[idx, ]; train.y <- label[idx]
test.x <- data[-idx, ]; test.y <- label[-idx]
if(torch::torch_is_installed()) #scDHA need libtorch installed
{
  #Predict the labels of cells in testing set
  prediction <- scDHA.class(train = train.x, train.label = train.y, test = test.x,
                           ncores = 2, seed = 1)
  #Calculate accuracy of the predictions
  acc <- round(sum(test.y == prediction)/length(test.y), 2)
  print(paste0("Accuracy = ", acc))
}
```

scDHA.pt

scDHA pseudo time inference

Description

Inferring pseudo-time data.

Usage

```
scDHA.pt(sc = sc, start.point = 1, ncores = 10L, seed = NULL)
```

Arguments

sc	Embedding object, produced by scDHA function.
start.point	Starting point of the trajectory.
ncores	Number of processor cores to use.
seed	Seed for reproducibility.

Value

List with the following keys:

- pt - Pseudo-time values for each sample.

Examples

```
library(scDHA)
#Load example data (Goolam dataset)
data('Goolam'); data <- t(Goolam$data); label <- as.character(Goolam$label)
#Log transform the data
data <- log2(data + 1)
if(torch::torch_is_installed()) #scDHA need libtorch installed
{
  #Generate clustering result, the input matrix has rows as samples and columns as genes
  result <- scDHA(data, ncores = 2, seed = 1)
  #Cell stage order in Goolam dataset
  cell.stages <- c("2cell", "4cell", "8cell", "16cell", "blast")
  #Generate pseudo-time for each cell, the input is the output from scDHA function
  result <- scDHA.pt(result, start.point = 1, ncores = 2, seed = 1)
  #Calculate R-squared value
  r2 <- round(cor(result$pt, as.numeric(factor(label, levels = cell.stages)))^2, digits = 2)
}
```

scDHA.vis

scDHA visualization

Description

Generating 2D embeded data for visulation.

Usage

```
scDHA.vis(sc = sc, method = "UMAP", ncores = 10L, seed = NULL)
```

Arguments

sc	Embedding object produced by the scDHA function.
method	Visualization method to use. It can be "UMAP" or "scDHA". The default setting is "UMAP".
ncores	Number of processor cores to use.
seed	Seed for reproducibility.

Value

a list with the following keys:

- `pred` - A matrix representing the 2D projection of single-cell data, where rows represent samples and columns represent latent components.

Examples

```
library(scDHA)
#Load example data (Goolam dataset)
data('Goolam'); data <- t(Goolam$data); label <- as.character(Goolam$label)
#Log transform the data
data <- log2(data + 1)
if(torch::torch_is_installed()) #scDHA need libtorch installed
{
  #Generate clustering result, the input matrix has rows as samples and columns as genes
  result <- scDHA(data, ncores = 2, seed = 1)
  #Generate 2D representation, the input is the output from scDHA function
  result <- scDHA.vis(result, ncores = 2, seed = 1)
  #Plot the representation of the dataset, different colors represent different cell types
  plot(result$pred, col=factor(label), xlab = "scDHA1", ylab = "scDHA2")
}
```

scDHA.w

scDHA.w

Description

This function will plot a graph with normalized weights of all genes so user can select the appropriate number of genes to keep.

Usage

```
scDHA.w(data = data, sparse = FALSE, ncores = 10L, seed = NULL)
```

Arguments

<code>data</code>	Gene expression matrix, with rows represent samples and columns represent genes.
<code>sparse</code>	Boolean variable indicating whether data is a sparse matrix. The input must be a non negative sparse matrix.
<code>ncores</code>	Number of processor cores to use.
<code>seed</code>	Seed for reproducibility.

Value

A plot with normalized weights of all genes.

Examples

```
library(scDHA)
#Load example data (Goolam dataset)
data('Goolam'); data <- t(Goolam$data); label <- as.character(Goolam$label)
#Log transform the data
data <- log2(data + 1)
if(torch::torch_is_installed()) #scDHA need libtorch installed
{
  #Generate weight variances for each genes
  weight_variance <- scDHA.w(data, ncores = 2, seed = 1)
  #Plot weight variances for top 5,000 genes
  #plot(weight_variance, xlab = "Genes", ylab = "Normalized Weight Variance", xlim=c(1, 5000))
  #Plot the change of weight variances for top 5,000 genes
  #weight_variance_change <- weight_variance[-length(weight_variance)] - weight_variance[-1]
  #plot(weight_variance_change, xlab = "Genes", ylab = "Weight Variance Change", xlim=c(1, 5000))
}
```


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