Package: scCAN (via r-universe)

November 4, 2026

Type Package

Title scCAN: Single-cell clustering using autoencoder and network fusion

Version 1.0.0

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Description A single-cell Clustering method using Autoencoder and Network fusion (scCAN) scCAN can accurately segregate cells from the high-dimensional scRNA-Seq data.

License LGPL

Encoding UTF-8

LazyData true

Depends R (>= 3.4)

Imports scDHA, FNN, purrr, stats, markdown

RoxygenNote 7.1.1

Suggests knitr

VignetteBuilder knitr

Config/pak/sysreqs cmake libglpk-dev libxml2-dev

Repository https://bangtran365.r-universe.dev

Date/Publication 2021-07-07 07:51:16 UTC

RemoteUrl https://github.com/bangtran365/sccan

RemoteRef HEAD

RemoteSha 3db00c017986d994706af75e551820d2448ebeff

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scCAN *scCAN*

Description

This is the main function to perform sc-RNA seq data clustering clustering. scCAN is fully unsupervised scRNA-seq clustering framework that uses deep neural network and network fusion-based clustering algorithm. First, scCAN applies a non-negative autoencoder to filter scRNA-seq data. Second, the filtered data is passed to stacked Bayesian autoencoder to get multiple low-dimensional representations of input data. Subsequently, scCAN converts these compressed data into networks and unify those networks to a single graph. Then, scCAN uses a spectral clustering algorithm to obtain final clusters assignment.

Usage

```
scCAN(
  data,
  sparse = F,
  n.neighbors = 30,
  alpha = 0.5,
  n.iters = 10,
  ncores = 10L,
  r.seed = 1
)
```

Arguments

`data`	Gene expression matrix, with rows represent samples and columns represent genes.
`sparse`	Boolen variable indicating whether data is a sparse matrix. The input must be a non negative sparse matrix.
`n.neighbors`	Number of neighboring cells that are used to caculate the edge's weight. The number of neighbors are set `n.neighbors = 30` by default.
`alpha`	A hyper-parameter that is used to calculate the network kernel. The value is set to `alpha = 0.5` by default.
`n.iters`	A hyper-parameter to set the number of network fusion iterations. It is set to `n.iters = 10` by default.
`ncores`	Number of processor cores to use.
`r.seed`	A parameter to set a seed for reproducibility. This values is set to `r.seed = 1` by default.

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.

`SCE` *SCE*

Description

SCE dataset includes scRNA-seq data and cell type information.

Usage

```
SCE
```

Format

An object of class `list` of length 2.

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