Package ‘Cepo’

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Title Cepo for the identification of differentially stable genes

Version 1.8.0

Description
Defining the identity of a cell is fundamental to understand the heterogeneity of cells to various environmental signals and perturbations. We present Cepo, a new method to explore cell identities from single-cell RNA-sequencing data using differential stability as a new metric to define cell identity genes. Cepo computes cell-type specific gene statistics pertaining to differential stable gene expression.

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Encoding UTF-8

LazyData false

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Imports DelayedMatrixStats, DelayedArray, HDF5Array, S4Vectors, methods, SingleCellExperiment, SummarizedExperiment, ggplot2, rlang, grDevices, patchwork, reshape2, BiocParallel, stats, dplyr

biocViews Classification, GeneExpression, SingleCell, Software, Sequencing, DifferentialExpression

Suggests knitr, rmarkdown, BiocStyle, testthat, covr, UpSetR, scater, scMerge, fgsea, escape, pheatmap, patchwork

VignetteBuilder knitr

Depends GSEABase, R (>= 4.1)

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| cellbench | cellbench |

Description

A single-cell RNA-seq dataset adapted from sc_mixology

Usage

data(cellbench)

Format

An object of SingleCellExperiment class with 895 cells and 2001 genes.

Source

https://github.com/LuyiTian/sc_mixology

Cepo Computing Cepo cell identity genes

Description

ExprsMat accepts various matrix objects, including DelayedArray and HDF5Array for out-of-memory computations. See vignette.
Usage

Cepo(
  exprsMat,
  cellTypes,
  minCells = 20,
  minCelltype = 3,
  exprsPct = NULL,
  prefilter_sd = NULL,
  prefilter_pzero = NULL,
  logfc = NULL,
  computePvalue = NULL,
  computeFastPvalue = TRUE,
  variability = "CV",
  method = "weightedMean",
  weight = c(0.5, 0.5),
  workers = 1L,
  block = NULL,
  ...
)

Arguments

- **exprsMat**: Expression matrix where columns denote cells and rows denote genes.
- **cellTypes**: Vector of cell type labels.
- **minCells**: Integer indicating the minimum number of cells required within a cell type.
- **minCelltype**: Integer indicating the minimum number of cell types required in each batch.
- **exprsPct**: Percentage of lowly expressed genes to remove. Default to NULL to not remove any genes.
- **prefilter_sd**: Numeric value indicating threshold relating to standard deviation of genes. Used with prefilter_zeros.
- **logfc**: Numeric value indicating the threshold of log fold-change to use to filter genes.
- **computePvalue**: Whether to compute p-values using bootstrap test. Default to NULL to not make computations. Set this to an integer to set the number of bootstraps needed (recommend to be at least 100).
- **computeFastPvalue**: Logical vector indicating whether to perform a faster version of p-value calculation. Set to TRUE by default.
- **variability**: A character indicating the stability measure (CV, IQR, MAD, SD). Default is set to CV.
- **method**: Character indicating the method for integration the two stability measures. By default this is set to 'weightedMean' with equal weights.
- **weight**: Vector of two values indicating the weights for each stability measure. By default this value is c(0.5, 0.5).
- **workers**: Number of cores to use. Default to 1, which invokes BiocParallel::SerialParam. For workers greater than 1, see the workers argument in BiocParallel::MulticoreParam and BiocParallel::SnowParam.
plotDensities

Block

Vector of batch labels

... Additional arguments passed to BiocParallel::MulticoreParam and BiocParallel::SnowParam.

prefilter_pzeros

Numeric value indicating threshold relating to the percentage of zero expression of genes. Used with prefilter_sd.

Value

Returns a list of key genes.

Examples

library(SingleCellExperiment)
data('cellbench', package = 'Cepo')
cellbench
cepoOutput <- Cepo(logcounts(cellbench), cellbench$celltype)
cepoOutput

Arguments

x a SummarizedExperiment or a SingleCellExperiment object.

cepoOutput an output from Cepo or doLimma/doVoom/doTtest/doWilcoxon functions

nGenes number of top genes from each celltype to plot. Default to 2.
plotDensities

assay a character (‘logcounts’ by default), indicating the name of the assays(x) element which stores the expression data (i.e., assays(x)$name_assays_expression). We strongly encourage using normalized data, such as counts per million (CPM) or log-CPM.

celltypeColumn a character, indicating the name of the name of the cell type column in the colData(x).

celltype a character, indicating the name of the cell type to plot. Default is NULL which selects all celltypes in the cepoOutput.

genes a character vector, indicating the name of the genes to plot. Default to NULL, so that 2 top genes from each celltype will be plotted.

plotType Either ‘histogram’ or ‘density’

color a named color vector. The names should correspond to the celltype argument above

Value

A ggplot object with cell-type specific densities for a gene.

A ggplot object.

Examples

library(SingleCellExperiment)
data(‘cellbench’, package = ‘Cepo’)cellbench
cepoOutput <- Cepo(logcounts(cellbench), cellbench$celltype)

plotDensities(
  x = cellbench,
  cepoOutput = cepoOutput,
  assay = ‘logcounts’,
  plotType = ‘histogram’,
  celltypeColumn = ‘celltype’
)

plotDensities(
  x = cellbench,
  cepoOutput = cepoOutput,
  assay = ‘logcounts’,
  plotType = ‘histogram’,
  celltypeColumn = ‘celltype’
)
**Description**

A subsampled single-cell RNA-seq dataset

**Usage**

data(sce_pancreas)

**Format**

An object of SingleCellExperiment class with 528 cells and 1358 genes.

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**setCepoBPPARAM**

Setting parallel params based on operating platform

**Description**

Setting parallel params based on operating platform

**Usage**

setCepoBPPARAM(workers = 1L, ...)

**Arguments**

- **workers**
  - Number of cores to use. Default to 1, which invokes BiocParallel::SerialParam.
  - For workers greater than 1, see the workers argument in BiocParallel::MulticoreParam and BiocParallel::SnowParam.

- **...**
  - Additional arguments passed to BiocParallel::MulticoreParam and BiocParallel::SnowParam.

**Value**

Parameters for parallel computing depending on OS

**Examples**

```r
# system.time(BiocParallel::bplapply(1:3, FUN = function(i){Sys.sleep(i)},
# BPPARAM = setCepoBPPARAM(workers = 1))
# system.time(BiocParallel::bplapply(1:3, FUN = function(i){Sys.sleep(i)},
# BPPARAM = setCepoBPPARAM(workers = 3)))
```
**topGenes**

*Extract the top genes from the Cepo output*

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**Description**

Extract the top genes from the Cepo output

**Usage**

```r
topGenes(object, n = 5, returnValues = FALSE)
```

**Arguments**

- `object`: Output from the Cepo function
- `n`: Number of top genes to extract
- `returnValues`: Whether to return the numeric value associated with the top selected genes

**Value**

Returns a list of key genes.

**Examples**

```r
set.seed(1234)
n <- 50  ## genes, rows
p <- 100  ## cells, cols
exprsMat <- matrix(rpois(n * p, lambda = 5), nrow = n)
rownames(exprsMat) <- paste0('gene', 1:n)
colnames(exprsMat) <- paste0('cell', 1:p)
cellTypes <- sample(letters[1:3], size = p, replace = TRUE)
cepo_output <- Cepo(exprsMat = exprsMat, cellTypes = cellTypes)
cepo_output
topGenes(cepo_output, n = 2)
topGenes(cepo_output, n = 2, returnValues = TRUE)
```
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