

# Package ‘Cepo’

November 7, 2025

**Title** Cepo for the identification of differentially stable genes

**Version** 1.17.0

## 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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|           |                  |
|-----------|------------------|
| cellbench | <i>cellbench</i> |
|-----------|------------------|

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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](https://github.com/LuyiTian/sc_mixology)

## 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 = 0.05,
  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.             |
| prefilter_pzero | Numeric value indicating threshold relating to the percentage of zero expression of genes. Used with prefilter_sd. |
| 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. |
| block             | Vector of batch labels                                                                                                                                                                           |
| ...               | Additional arguments passed to BiocParallel::MulticoreParam and BiocParallel::SnowParam.                                                                                                         |

Value

Returns a list of key genes.

Examples

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

---

|               |                       |
|---------------|-----------------------|
| plotDensities | <i>Plot densities</i> |
|---------------|-----------------------|

---

Description

Plot densities

Usage

```
plotDensities(
  x,
  cepoOutput,
  nGenes = 2,
  assay = "logcounts",
  celltypeColumn,
```

```

    celltype = NULL,
    genes = NULL,
    plotType = c("histogram", "density"),
    color = NULL
  )

```

### Arguments

|                             |                                                                                                                                                                                                                                                                        |
|-----------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>x</code>              | a <a href="#">SummarizedExperiment</a> or a <a href="#">SingleCellExperiment</a> object.                                                                                                                                                                               |
| <code>cepoOutput</code>     | an output from <code>Cepo</code> or <code>doLimma/doVoom/doTtest/doWilcoxon</code> functions                                                                                                                                                                           |
| <code>nGenes</code>         | number of top genes from each celltype to plot. Default to 2.                                                                                                                                                                                                          |
| <code>assay</code>          | a character ('logcounts' by default), indicating the name of the assays(x) element which stores the expression data (i.e., <code>assays(x)\$name_assays_expression</code> ). We strongly encourage using normalized data, such as counts per million (CPM) or log-CPM. |
| <code>celltypeColumn</code> | a character, indicating the name of the name of the cell type column in the <code>colData(x)</code> .                                                                                                                                                                  |
| <code>celltype</code>       | a character, indicating the name of the cell type to plot. Default is <code>NULL</code> which selects all celltypes in the <code>cepoOutput</code> .                                                                                                                   |
| <code>genes</code>          | a character vector, indicating the name of the genes to plot. Default to <code>NULL</code> , so that 2 top genes from each celltype will be plotted.                                                                                                                   |
| <code>plotType</code>       | Either 'histogram' or 'density'                                                                                                                                                                                                                                        |
| <code>color</code>          | a named color vector. The names should correspond to the <code>celltype</code> 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,

```

```
genes = c('PLTP', 'CPT1C', 'MEG3', 'SYCE1', 'MICOS10P3', 'HOXB7'),
assay = 'logcounts',
plotType = 'histogram',
celltypeColumn = 'celltype'
)
```

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|              |                     |
|--------------|---------------------|
| sce_pancreas | <i>sce_pancreas</i> |
|--------------|---------------------|

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**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 | <i>Setting parallel params based on operating platform</i> |
|----------------|------------------------------------------------------------|

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**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**

```
# 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 | <i>Extract the top genes from the Cepo output</i> |
|----------|---------------------------------------------------|

---

**Description**

Extract the top genes from the Cepo output

**Usage**

```
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**

```
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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