

# Package ‘SiPSiC’

December 17, 2025

**Type** Package

**Title** Calculate Pathway Scores for Each Cell in scRNA-Seq Data

**Version** 1.11.0

**Date** 2022-12-29

**Description** Infer biological pathway activity of cells from single-cell RNA-sequencing data by calculating a pathway score for each cell (pathway genes are specified by the user). It is recommended to have the data in Transcripts-Per-Million (TPM) or Counts-Per-Million (CPM) units for best results. Scores may change when adding cells to or removing cells off the data. SiPSiC stands for Single Pathway analysis in Single Cells.

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**URL** <https://www.genome.org/cgi/doi/10.1101/gr.278431.123>

**biocViews** Software, DifferentialExpression, GeneSetEnrichment, BiomedicalInformatics, CellBiology, Transcriptomics, RNASeq, SingleCell, Transcription, Sequencing, ImmunoOncology, DataImport

**Depends** Matrix, SingleCellExperiment

**Suggests** knitr, rmarkdown, BiocStyle

**VignetteBuilder** knitr

**BugReports** <https://github.com/DanielDavis12/SiPSiC/issues>

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SiPSiC-package

*Calculate Pathway Scores for Each Cell in scRNA-Seq Data***Description**

Infer biological pathway activity of cells from single-cell RNA-sequencing data by calculating a pathway score for each cell (pathway genes are specified by the user). It is recommended to have the data in Transcripts-Per-Million (TPM) or Counts-Per-Million (CPM) units for best results. Scores may change when adding cells to or removing cells off the data. SiPSiC stands for Single Pathway analysis in Single Cells.

**Details**

Use this package to calculate per-cell scores for a biological pathway of your choice, from single-cell RNA-seq data. Transcripts-Per-Million (TPM) or Counts-Per-Million (CPM) units of the data are recommended for best results.

**Author(s)**

Daniel Davis, Yotam Drier. Maintainer: Daniel Davis

**References**

<https://medicine.ekmd.huji.ac.il/en/research/yotamd/Pages/default.aspx>

**See Also**

[getPathwayScores](#)

getPathwayScores

*Calculate Pathway Scores for all Cells in a scRNA-Seq Data***Description**

Calculate a pathway score for each cell included in the input scRNA-seq data, using the cell's transcription level of the pathway's genes.

**Usage**

```
getPathwayScores(dataMatrix, pathwayGenes, percentForNormalization)
```

**Arguments**

a list of three items:

- `dataMatrix` a matrix whose rows and columns represent genes and cells, respectively, containing the scRNA-seq data; Counts-Per-Million (CPM) or Transcripts-Per-Million (TPM) units should be used for best results. The matrix should be of type sparse matrix (`dgCMatrx`), otherwise errors might be raised.
- `pathwayGenes` a character vector of the gene names of which the relevant biological pathway consists.
- `percentForNormalization` The percent of top cells for each gene whose median is used to normalize the gene's expression values (5 by default).

**Value**

- `pathwayScores` an array (type double) of the pathway score of each cell in the input `dataMatrix`, less than two of the pathway genes are found in the data, in which case NA is returned.
- `index` a numeric array of the row indices in the `dataMatrix` where genes of the pathway were found.

**Author(s)**

Daniel Davis, Yotam Drier

**References**

<https://medicine.ekmd.huji.ac.il/en/research/yotamd/Pages/default.aspx>

**Examples**

```
library(SiPSiC)
geneCountsMatrix <- matrix(rpois(16, lambda = 10), ncol = 4, nrow = 4)
geneCountsMatrix <- as(geneCountsMatrix, "dgCMatrx")
rownames(geneCountsMatrix) <- c("Gene1", "Gene2", "Gene3", "Gene4")
colnames(geneCountsMatrix) <- c("Cell1", "Cell2", "Cell3", "Cell4")
assayData <- SingleCellExperiment(assays = list(counts = geneCountsMatrix))
pathwayGenesList <- c("Gene1", "Gene2", "Gene4")
percentForNormalization <- 7
scoresAndIndices <- getPathwayScores(counts(assayData), pathwayGenesList, percentForNormalization)
pathwayScoresOfCells <- scoresAndIndices$pathwayScores
pathwayGeneIndices <- scoresAndIndices$index
```

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normalizeCountsForGene

*Gene counts normalization*

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**Description**

Get the counts of a single gene normalized by the median of the top 5 percent cells, unless it's zero; In this case, the counts are all divided by the maximum value across all cells. If all counts are zeros, they are returned untouched.

**Usage**

```
normalizeCountsForGene(expressionValues, percentForNormalization)
```

**Arguments**

`expressionValues`

An array of type double, containing the counts (in any units, e.g. CPM or TPM) of a single gene across different cells.

`percentForNormalization`

The percent of top cells for each gene whose median is used to normalized the gene's expression values.

**Value**

An array (type double) of the normalized input counts.

**Author(s)**

Daniel Davis, Yotam Drier

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