

# Package ‘scImpute’

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**Type** Package

**Title** Accurate and robust imputation of single-cell RNA sequencing data

**Version** 0.0.2

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**Author** Wei Vivian Li, Jingyi Jessica Li

**Maintainer** Wei Vivian Li <liw@ucla.edu>

**Description** scRNA-seq analysis is complicated by the excess of zero or near zero counts in the data, which are the so-called dropouts due to low amounts of mRNA within each individual cell. scImpute is developed to simultaneously determine which expression values are affected by dropout events in scRNA-seq data and perform imputation only on dropout entries.

**Depends** R (>= 3.3.2), glmnet, parallel, stats, utils

**License** GPL

**RoxygenNote** 6.0.1

**Suggests** knitr,  
rmarkdown

**VignetteBuilder** knitr

## R topics documented:

scimpute . . . . .	1
scimpute_quick . . . . .	2

<b>Index</b>	4
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scimpute	<i>use SCimpute to impute dropout values in scRNA-seq data</i>
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## Description

use SCimpute to impute dropout values in scRNA-seq data

## Usage

```
scimpute(count_path, infile = "csv", outfile = "csv", out_dir,  
drop_thre = 0.5, celltype = FALSE, labels = NULL, ncores = 5)
```

**Arguments**

count_path	A character specifying the full path of the raw count matrix;
infile	A character specifying the type of file storing the raw count matrix; can be either "csv" or "txt". The input file should have rows representing genes and columns representing cells, with its first row as cell names and first column as gene names.
outfile	A character specifying the type of file storing the imputed count matrix; can be either "csv" or "txt".
out_dir	A character specifying the full path of the output directory, which is used to store all intermediate and final outputs.
drop_thre	A number between 0 and 1, specifying the threshold to determine dropout values.
celltype	A logical value indicating whether cell type information is available. labels must be specified if celltype = TRUE.
labels	A character vector specifying the cell type of each column in the raw count matrix. Only needed when celltype = TRUE. Each cell type should have at least two cells for imputation.
ncores	A integer specifying the number of cores used for parallel computation.

**Value**

Save the imputed count matrix to SCimpute.csv or SCimpute.txt (depending on outfile) to out\_dir.

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scimpute_quick	<i>quick re-run of SCimpute with a different drop_thre</i>
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**Description**

quick re-run of SCimpute with a different drop\_thre

**Usage**

```
scimpute_quick(count_path, infile = "csv", outfile = "csv", out_dir,
  drop_thre = 0.5, celltype = FALSE, labels = NULL, ncores = 5)
```

**Arguments**

count_path	A character specifying the full path of the raw count matrix;
infile	A character specifying the type of file storing the raw count matrix; can be either "csv" or "txt". The input file should have rows representing genes and columns representing cells, with its first row as cell names and first column as gene names.
outfile	A character specifying the type of file storing the imputed count matrix; can be either "csv" or "txt".
out_dir	A character specifying the full path of the output directory, which is used to store all intermediate and final outputs.
drop_thre	A number between 0 and 1, specifying the threshold to determine dropout values.

celltype	A logical value indicating whether cell type information is available. labels must be specified if celltype = TRUE.
labels	A character vector specifying the cell type of each column in the raw count matrix. Only needed when celltype = TRUE. Each cell type should have at least two cells for imputation.
ncores	A integer specifying the number of cores used for parallel computation.

**Value**

Save the imputed count matrix to SCimpute.csv or SCimpute.txt (depending on outfile) to out\_dir.

# Index

scimpute, [1](#)  
scimpute\_quick, [2](#)