

# Package ‘scDDboost’

September 4, 2025

**Type** Package

**Title** A compositional model to assess expression changes from  
single-cell rna-seq data

**Version** 1.11.0

**Date** 2018-10-31

## Description

scDDboost is an R package to analyze changes in the distribution of single-cell expression data between two experimental conditions. Compared to other methods that assess differential expression, scDDboost benefits uniquely from information conveyed by the clustering of cells into cellular subtypes. Through a novel empirical Bayesian formulation it calculates gene-specific posterior probabilities that the marginal expression distribution is the same (or different) between the two conditions. The implementation in scDDboost treats gene-level expression data within each condition as a mixture of negative binomial distributions.

**License** GPL (>= 2)

**Imports** Rcpp (>= 0.12.11), RcppEigen (>= 0.3.2.9.0), EBSeq,  
BiocParallel, mclust, SingleCellExperiment, cluster, Oscope,  
SummarizedExperiment, stats, methods

**biocViews** SingleCell, Software, Clustering, Sequencing,  
GeneExpression, DifferentialExpression, Bayesian

**Depends** R (>= 4.2), ggplot2

**LinkingTo** Rcpp, RcppEigen, BH

**Suggests** knitr, rmarkdown, BiocStyle, testthat

**SystemRequirements** c++14

**Roxygen** list(wrap=FALSE)

**RoxygenNote** 7.1.2

**VignetteBuilder** knitr

**BugReports** <https://github.com/wiscstatman/scDDboost/issues>

**URL** <https://github.com/wiscstatman/scDDboost>

**git\_url** <https://git.bioconductor.org/packages/scDDboost>

**git\_branch** devel

**git\_last\_commit** a51e490

**git\_last\_commit\_date** 2025-04-15

**Repository** Bioconductor 3.22

**Date/Publication** 2025-09-03

**Author** Xiuyu Ma [cre, aut],  
Michael A. Newton [ctb]

**Maintainer** Xiuyu Ma <watsonforfun@gmail.com>

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|                   |                                                                                         |
|-------------------|-----------------------------------------------------------------------------------------|
| scDDboost-package | <i>A compositional model to assess expression changes from single-cell rna-seq data</i> |
|-------------------|-----------------------------------------------------------------------------------------|

---

## Description

scDDboost is an R package to analyze changes in the distribution of single-cell expression data between two experimental conditions. Compared to other methods that assess differential expression, scDDboost benefits uniquely from information conveyed by the clustering of cells into cellular subtypes. Through a novel empirical Bayesian formulation it calculates gene-specific posterior probabilities that the marginal expression distribution is the same (or different) between the two conditions. The implementation in scDDboost treats gene-level expression data within each condition as a mixture of negative binomial distributions.

**Details**

The DESCRIPTION file: This package was not yet installed at build time.

Index: This package was not yet installed at build time.

Package used to score evidence of differential distribution in single-cell RNA-seq data

**Author(s)**

Xiuyu Ma [cre, aut], Michael A. Newton [ctb]

Maintainer: Xiuyu Ma <watsonforfun@gmail.com>

**References**

<https://projecteuclid.org/journals/annals-of-applied-statistics/volume-15/issue-2/A-compositional-model-to-assess-expression-changes-from-single-cell/10.1214/20-AOAS1423.short>

**See Also**

<https://github.com/wiscstatman/scDDboost/blob/master/DESCRIPTION>

**Examples**

```
data(sim_dat)
dat = extractInfo(sim_dat)
data_counts = dat$count_matrix
cd = dat$condition
bp <- BiocParallel::MulticoreParam(4)
D_c = calD(data_counts, bp)
pDD = pdd(data_counts, cd, bp, D_c)
```

---

|      |                                  |
|------|----------------------------------|
| calD | <i>calculate distance matrix</i> |
|------|----------------------------------|

---

**Description**

calculate distance matrix

**Usage**

```
calD(data, bp)
```

**Arguments**

|      |                         |
|------|-------------------------|
| data | transcripts             |
| bp   | bioc parallel parameter |

**Value**

distance matrix

**Examples**

```
data(sim_dat)
dat <- extractInfo(sim_dat)
data_counts <- dat$count_matrix
bp <- BiocParallel::MulticoreParam(4)
D_c <- calD(data_counts,bp)
```

---

|            |                                                              |
|------------|--------------------------------------------------------------|
| clusHelper | <i>function to get intra and inter distance for clusters</i> |
|------------|--------------------------------------------------------------|

---

**Description**

function to get intra and inter distance for clusters

**Usage**

```
clusHelper(D, i)
```

**Arguments**

|   |                    |
|---|--------------------|
| D | distance matrix    |
| i | number of clusters |

**Value**

vector of intra and inter distance

---

|      |                                         |
|------|-----------------------------------------|
| detK | <i>determine the number of clusters</i> |
|------|-----------------------------------------|

---

**Description**

determine the number of clusters

**Usage**

```
detK(D, epi = 1)
```

**Arguments**

|     |                           |
|-----|---------------------------|
| D   | distance matrix           |
| epi | threshold for cutting off |

**Value**

number of clusters

**Examples**

```
data(sim_dat)
dat <- extractInfo(sim_dat)
data_counts <- dat$count_matrix
bp <- BiocParallel::MulticoreParam(4)
D_c <- calD(data_counts,bp)
detK(D_c)
```

EBS

*accelerated empirical bayesian***Description**

accelerated empirical bayesian

**Usage**

```
EBS(data, conditions, gclus, sf, iter = 10, hyper, PP, stp1, stp2)
```

**Arguments**

|            |                                                                        |
|------------|------------------------------------------------------------------------|
| data       | single cell expression matrix, row as genes column as cells            |
| conditions | partition of cells                                                     |
| gclus      | partition of genes                                                     |
| sf         | size factors                                                           |
| iter       | maximum iteration step of EM                                           |
| hyper      | hyper parameters for beta distributions                                |
| PP         | pattern of partitions                                                  |
| stp1       | step size of hyperparameter alpha (shared by all units) in one step EM |
| stp2       | step size of hyperparameter beta (unit specific) in one step EM        |

**Value**

posterior probability of mean expression pattern

extractInfo

*extract count matrix from SingleCellExperiment object***Description**

extract count matrix from SingleCellExperiment object

**Usage**

```
extractInfo(data)
```

**Arguments**

data                      SingleCellExperiment object

**Value**

list of count matrix and condition vector

**Examples**

```
data(sim_dat)
dat <- extractInfo(sim_dat)
```

---

|     |                           |
|-----|---------------------------|
| gCl | <i>gene_level cluster</i> |
|-----|---------------------------|

---

**Description**

gene\_level cluster

**Usage**

```
gCl(data, bp)
```

**Arguments**

data                      transcripts  
bp                        bioc parallel parameter

**Value**

return a matrix whose row represent gene specific cluster

---

|          |                                    |
|----------|------------------------------------|
| genRClus | <i>generate random clusterings</i> |
|----------|------------------------------------|

---

**Description**

generate random clusterings

**Usage**

```
genRClus(D, a, K)
```

**Arguments**

D                        distance matrix of cells  
a                        paramter for weights  
K                        number of subtypes

**Value**

random generated clustering of cells

---

|       |                                            |
|-------|--------------------------------------------|
| getDD | <i>index of DD genes under FDR control</i> |
|-------|--------------------------------------------|

---

**Description**

index of DD genes under FDR control

**Usage**

```
getDD(pDD, FDR = 0.01)
```

**Arguments**

|     |                               |
|-----|-------------------------------|
| pDD | probability of genes being DD |
| FDR | fdr to be controlled          |

**Value**

index of positive genes

**Examples**

```
p_dd <- c(0.01, 0.99, 0.7, 0.5)
getDD(p_dd)
```

---

|             |                                             |
|-------------|---------------------------------------------|
| getSizeofDD | <i>number of DD genes under FDR control</i> |
|-------------|---------------------------------------------|

---

**Description**

number of DD genes under FDR control

**Usage**

```
getSizeofDD(pDD, FDR = 0.01)
```

**Arguments**

|     |                                   |
|-----|-----------------------------------|
| pDD | estimated probability of being DD |
| FDR | fdr to be controlled              |

**Value**

number of positive genes

**Examples**

```
p_dd <- c(0.1, 0.99, 1, 0.05, 0.05)
getSizeofDD(p_dd)
```

---

|         |                                                                  |
|---------|------------------------------------------------------------------|
| getZ1Z2 | <i>function to get counts of cluster sizes at two conditions</i> |
|---------|------------------------------------------------------------------|

---

**Description**

function to get counts of cluster sizes at two conditions

**Usage**

```
getZ1Z2(cc1, cd)
```

**Arguments**

|     |                  |
|-----|------------------|
| cc1 | clustering label |
| cd  | condition label  |

**Value**

return list of counts

---

|      |                                  |
|------|----------------------------------|
| gRef | <i>generate reference matrix</i> |
|------|----------------------------------|

---

**Description**

generate reference matrix

**Usage**

```
gRef(Posp)
```

**Arguments**

|      |                            |
|------|----------------------------|
| Posp | possible partition of data |
|------|----------------------------|

**Value**

return a matrix indicate the refinement relation between different partitions.



---

|       |                                                       |
|-------|-------------------------------------------------------|
| isRef | <i>check refinement relation between two clusters</i> |
|-------|-------------------------------------------------------|

---

**Description**

check refinement relation between two clusters

**Usage**

```
isRef(x, y)
```

**Arguments**

|   |           |
|---|-----------|
| x | a cluster |
| y | a cluster |

**Value**

whether x refines y

---

|    |                                                           |
|----|-----------------------------------------------------------|
| LL | <i>likelihood function for hyperparameters estimation</i> |
|----|-----------------------------------------------------------|

---

**Description**

likelihood function for hyperparameters estimation

**Usage**

```
LL(param, x, d0)
```

**Arguments**

|       |                                              |
|-------|----------------------------------------------|
| param | parameters to be determined by MLE           |
| x     | distance matrix of cells                     |
| d0    | rate parameter of prior of 1 / true distance |

**Value**

return hyperparameters a.

---

|        |                                                                            |
|--------|----------------------------------------------------------------------------|
| lpt1t2 | <i>log likelihood of <math>z_1, z_2</math> given <math>t_1, t_2</math></i> |
|--------|----------------------------------------------------------------------------|

---

**Description**

log likelihood of  $z_1, z_2$  given  $t_1, t_2$

**Usage**

lpt1t2( $z_1$ ,  $z_2$ , pp, alpha1, alpha2)

**Arguments**

|        |                                     |
|--------|-------------------------------------|
| $z_1$  | counts of each group in condition 1 |
| $z_2$  | counts of each group in condition 2 |
| pp     | a partition                         |
| alpha1 | parameter of double dirichlet prior |
| alpha2 | parameter of double dirichlet prior |

**Value**

log likelihood of  $z_1, z_2$  given  $t_1, t_2$

---

|       |                                                                                                                   |
|-------|-------------------------------------------------------------------------------------------------------------------|
| lpzgt | <i>log likelihood of aggregated multinomial counts <math>z</math> given aggregated proportions <math>t</math></i> |
|-------|-------------------------------------------------------------------------------------------------------------------|

---

**Description**

log likelihood of aggregated multinomial counts  $z$  given aggregated proportions  $t$

**Usage**

lpzgt( $z$ , pp, alpha)

**Arguments**

|       |                                       |
|-------|---------------------------------------|
| $z$   | counts of each group in one condition |
| pp    | a partition                           |
| alpha | parameter of double dirichlet prior   |

**Value**

log likelihood of aggregated multinomial counts  $z$  given aggregated proportions  $t$

---

|     |                                                                            |
|-----|----------------------------------------------------------------------------|
| mdd | <i>posterior of proportion change given mixture double dirichlet prior</i> |
|-----|----------------------------------------------------------------------------|

---

**Description**

posterior of proportion change given mixture double dirichlet prior

**Usage**

```
mdd(z1, z2, pat, alpha1, alpha2)
```

**Arguments**

|        |                                     |
|--------|-------------------------------------|
| z1     | counts of each group in condition 1 |
| z2     | counts of each group in condition 2 |
| pat    | partition patterns                  |
| alpha1 | parameter of double dirichlet prior |
| alpha2 | parameter of double dirichlet prior |

**Value**

posterior of proportion change

---

|     |                                      |
|-----|--------------------------------------|
| pat | <i>generating partition patterns</i> |
|-----|--------------------------------------|

---

**Description**

generating partition patterns

**Usage**

```
pat(K)
```

**Arguments**

|   |                    |
|---|--------------------|
| K | number of elements |
|---|--------------------|

**Value**

all possible partition of K elements

**Examples**

```
pat(3)
```

---

|     |                                                                                   |
|-----|-----------------------------------------------------------------------------------|
| pdd | <i>calculate posterior probabilities of a gene to be differential distributed</i> |
|-----|-----------------------------------------------------------------------------------|

---

### Description

calculate posterior probabilities of a gene to be differential distributed

### Usage

```
pdd(
  data,
  cd,
  bp,
  D,
  random = TRUE,
  norm = TRUE,
  epi = 1,
  Upper = 1000,
  nrandom = 50,
  iter = 20,
  reltol = 0.001,
  stp1 = 1e-06,
  stp2 = 0.01,
  K = 0
)
```

### Arguments

|         |                                                                                   |
|---------|-----------------------------------------------------------------------------------|
| data    | normalized preprocessed transcripts                                               |
| cd      | conditions label                                                                  |
| bp      | bioc parallel parameter                                                           |
| D       | distance matrix of cells or cluster of cells or a given clustering                |
| random  | boolean indicator of whether randomzation has been implemented on distance matrix |
| norm    | boolean indicator of whether the input expression data is normalized              |
| epi     | tol for change of validity score in determining number of clusters                |
| Upper   | bound for hyper parameters optimization                                           |
| nrandom | number of random generated distance matrix                                        |
| iter    | max number of iterations for EM                                                   |
| reltol  | relative tolerance for optim on weighting paramters                               |
| stp1    | step size of hyperparameter alpha (shared by all units) in one step EM            |
| stp2    | step size of hyperparameter beta (unit specific) in one step EM                   |
| K       | number of subtypes, could be user specified or determined internally(set to 0)    |

### Value

posterior probabilities of a gene to be differential distributed

**Examples**

```

data(sim_dat)
dat <- extractInfo(sim_dat)
data_counts <- dat$count_matrix
cd <- dat$condition
bp <- BiocParallel::MulticoreParam(4)
D_c <- calD(data_counts,bp)
pDD <- pdd(data_counts,cd,bp,D_c)

```

---

|              |                                                                      |
|--------------|----------------------------------------------------------------------|
| pddAggregate | <i>function to aggregate intermediate results and get prob of DD</i> |
|--------------|----------------------------------------------------------------------|

---

**Description**

function to aggregate intermediate results and get prob of DD

**Usage**

```
pddAggregate(z1, z2, Posp, DE, K, REF)
```

**Arguments**

|      |                                                           |
|------|-----------------------------------------------------------|
| z1   | counts of cluster sizes in condition 1                    |
| z2   | counts of cluster sizes in condition 2                    |
| Posp | partition of cells                                        |
| DE   | posterior probabilities of DE patterns                    |
| K    | number of clusters                                        |
| REF  | reference matrix indicating relation of nested partitions |

**Value**

return vector of prob of DD

---

|           |                                                               |
|-----------|---------------------------------------------------------------|
| pddRandom | <i>calculate PDD when add random noise in distance matrix</i> |
|-----------|---------------------------------------------------------------|

---

**Description**

calculate PDD when add random noise in distance matrix

**Usage**

```
pddRandom(data, cd, K, D, a, sz, hp, Posp, iter, REF, stp1, stp2)
```

**Arguments**

|      |                                                                        |
|------|------------------------------------------------------------------------|
| data | normalized preprocessed transcripts                                    |
| cd   | condition label                                                        |
| K    | number of subgroups                                                    |
| D    | distance matrix of cells                                               |
| a    | shape param for weights                                                |
| sz   | size factors                                                           |
| hp   | hyper parameters for EBSeq                                             |
| Posp | partition patterns                                                     |
| iter | max number of iterations for EM in EBSeq                               |
| REF  | refinement relation matrix                                             |
| stp1 | step size of hyperparameter alpha (shared by all units) in one step EM |
| stp2 | step size of hyperparameter beta (unit specific) in one step EM        |

**Value**

posterior probabilities under random distance matrix

---

|       |                                           |
|-------|-------------------------------------------|
| rwMle | <i>MLE for random weighting parameter</i> |
|-------|-------------------------------------------|

---

**Description**

MLE for random weighting parameter

**Usage**

```
rwMle(D, reltol)
```

**Arguments**

|        |                          |
|--------|--------------------------|
| D      | distance matrix of cells |
| reltol | tolerance of convergence |

**Value**

MLE of random weighting parameter

---

`sim_dat`*scDDboost*

---

**Description**

simulated data for demonstration, data are mixture negative binomial distributed

**Usage**

```
data(sim_dat)
```

**Format**

An object of class "list".

**Examples**

```
data(sim_dat)
```

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