Package ‘ccfindR’

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       Cell clustering and feature gene selection analysis employ Bayesian
       (and maximum likelihood) non-negative matrix factorization (NMF) algorithm.
       Input data set consists of RNA count matrix, gene, and cell bar code
       annotations. Analysis outputs are factor matrices for multiple ranks and
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**assignCelltype**

*Cell type assignment via GSEA*

**Description**

Computes GSEA enrichment score of marker sets in meta gene list

**Usage**

```r
assignCelltype(obj, rank, gset, gene_names = NULL, p = 0,
               remove.na = FALSE, p.value = FALSE, nperm = 1000,
               progress.bar = TRUE, grp.prefix = c("IG"))
```

**Arguments**

- **obj**: Object of class `scNMFSet`.
- **rank**: Rank to examine.
- **gset**: List of gene sets to be used as markers.
- **gene_names**: Names of genes to be used for meta-gene identification.
- **p**: Enrichment score exponent.
basis

remove.na  Remove gene sets with no overlap
p.value  Estimate p values using permutation
nperm  No. of permutation replicates
progress.bar  Display progress bar for p value computation
grp.prefix  Gene name prefix to search for with wildcard matches in query

Details

If obj is of class scNMFSet, it computes meta gene list using meta_gene.cv. Otherwise, obj is expected to be a data frame of the same structure as the output of meta_gene.cv; the number of rows same as the total number of metagenes per cluster, three columns per each cluster (gene name, meta-gene score, and coefficient of variation). The argument gset is a list of gene sets to be checked for enrichment in each cluster meta gene list. The enrichment score is computed using the GSEA algorithm (Subramanian et al. 2005).

Value

Matrix of enrichment score statistics with cell types in rows and clusters in columns

References


Examples

dir <- system.file('extdata', package='ccfindR')
pbmc <- read_10x(dir)
pbmc <- vb_factorize(pbmc, ranks=5)
meta <- meta_gene.cv(pbmc, rank=5, gene_names=rowData(pbmc)[,2])
markers <- list('B cell'=c('CD74','IG','HLA'),
                 'CD8+ T'=c('CD8A','CD8B','GZMK','CCR7','LTB'),
                 'CD4+ T'=c('CD3D','CD3E','IL7R','LEF1'),
                 'NK'=c('GNLY','NKG7','GZMA','GZMH'),
                 'Macrophage'=c('S100A8','S100A9','CD14','LYZ','CFD'))
gsea <- assignCelltype(meta, rank=5, gset=markers, grp.prefix=c('IG','HLA'))
gsea

---

basis

Basis matrices in an Object

Description

Retrieve or set the basis matrices W from factorization in an object
Usage

basis(object)

Arguments

object Object of class scNMFSet

Details

After factorization, basis matrices corresponding to each rank value are stored as elements of a list, which is in slot basis of object of class scNMFSet. basis(object) will return the list of matrices. basis(object) <- value can be used to modify it.

Value

Either NULL or a list of same length as ranks(object), whose elements are basis matrices derived from factorization under each rank value.

Examples

s <- scNMFSet(count=matrix(rpois(n=12,lambda=3),4,3))
s <- vb_factorize(s,ranks=seq(2,4))
basis(s)[[1]]
Generics for basis matrix assignment

**Description**

Access and modify basis matrices

**Usage**

basis(object) <- value

**Arguments**

- **object**: Object of class scNMFSet
- **value**: Basis matrix to be substituted

**Value**

Input object with updated basis matrices

**Examples**

```r
set.seed(1)
s <- scNMFSet(count=matrix(rpois(n=12,lambda=3),4,3))
s <- vb_factorize(s, ranks=3)
basis(s)[[1]] <- apply(basis(s)[[1]],seq(1,2),round,digits=3)
basis(s)
```

Modify basis matrices

**Description**

Access and modify basis matrices

**Usage**

```r
## S4 replacement method for signature 'scNMFSet'
basis(object) <- value
```

**Arguments**

- **object**: Object of class scNMFSet
- **value**: Basis matrix to be substituted
Value

Input object with updated basis matrices

Examples

```r
set.seed(1)
s <- scNMFSet(count=matrix(rpois(n=12,lambda=3),4,3))
s <- vb_factorize(s, ranks=3)
basis(s)[[1]] <- apply(basis(s)[[1]],c(1,2),round,digits=3)
basis(s)
```

---

**build_tree**

Build tree connecting clusters at different ranks

Description

Build tree connecting clusters at different ranks

Usage

```r
build_tree(object, rmax)
```

Arguments

- **object**: Object of class `scNMFSet`
- **rmax**: Maximum rank at which tree branching stops

Value

List containing the tree structure

Examples

```r
set.seed(1)
x <- simulate_whx(nrow=50,ncol=100,rank=5)
s <- scNMFSet(x$x)
s <- vb_factorize(s,ranks=seq(2,8),nrun=5)
tree <- build_tree(s,rmax=5)
tree
```
**ccfindR**

**ccfindR: Cancer Clone FindeR**

**Description**

This package contains tools and utilities for cell-type discovery using single-cell transcriptomic data while evaluating significance of the depth of clustering (Woo et al. 2019).

**References**


---

**cell_map**

**Plot heatmap of clustering coefficient matrix**

**Description**

Retrieve a coefficient matrix $H$ derived from factorization by rank value and generate heatmap of its elements.

**Usage**

```
cell_map(object, rank, main = "Cells", ...)  
```

**Arguments**

- `object` Object of class `scNMFSet`.
- `rank` Rank value for which the cell map is to be displayed. The object must contain the corresponding slot: one element of `coeff(object)[[k]]` for which `ranks(object)[[k]]==rank`.
- `main` Title of plot.
- `...` Other arguments to be passed to `heatmap`, `image`, and `plot`.

**Value**

NULL
cluster_id

Examples

```r
set.seed(1)
x <- simulate_data(nfeatures=10, nsamples=c(20,20,60))
rownames(x) <- seq_len(10)
colnames(x) <- seq_len(100)
s <- scNMFSet(count=x, rowData=seq_len(10), colData=seq_len(100))
s <- vb_factorize(s, ranks=seq(2,5))
plot(s)
cell_map(s, rank=3)
```

---

<table>
<thead>
<tr>
<th>cluster_id</th>
<th>Assign cells into clusters</th>
</tr>
</thead>
</table>

**Description**

Use factorization results in an object to assign cells into clusters.

**Usage**

```r
cluster_id(object, rank = 2)
```

**Arguments**

- `object`: Object of class `scNMFSet`
- `rank`: Rank value whose factor matrices are to be used for assignment.

**Value**

Vector of length equal to the number of cells containing cluster ID numbers of each cell.

**Examples**

```r
set.seed(1)
x <- simulate_whx(nrow=50, ncol=100, rank=5)
s <- scNMFSet(count=x$x)
s <- vb_factorize(s, ranks=seq(2,8), nrun=5)
cid <- cluster_id(s, rank=5)
table(cid)
```
### Description
Retrieve or set the coefficient matrices from factorization in an object.

### Usage
```r
coeff(object)
```

### Arguments
- **object**: Object of class `scNMFSet`.

### Details
After factorization, coefficient matrices $H$ corresponding to each rank value are stored as elements of a list, which is in slot `coeff` of object of class `scNMFSet`. `coeff(object)` will return the list of matrices. `coeff(object) <- value` can be used to modify it.

### Value
Either `NULL` or a list of same length as `ranks(object)`, whose elements are coefficient matrices derived from factorization under each rank value.

### Examples
```r
s <- scNMFSet(count=matrix(rpois(n=12,lambda=3),4,3))
s <- vb_factorize(s,ranks=seq(2,4))
coeff(s)[[1]]
```

---

### Description
Coefficient matrix accessor

### Usage
```r
## S4 method for signature 'scNMFSet'
coeff(object)
```

### Arguments
- **object**: Object containing coefficient matrix

---
Value

List of coefficient matrices

Description

Access and modify coefficient matrices

Usage

```r
coeff(object) <- value
```

Arguments

- `object`: Object of class `scNMFSet`
- `value`: Coefficient matrix to be substituted

Value

Input object with updated coefficient matrices

Examples

```r
s <- scNMFSet(count=matrix(rpois(n=12,lambda=3),4,3))
s <- vb_factorize(s, ranks=3)
coeff(s)[[1]] <- apply(coeff(s)[[1]],c(1,2),round,digits=2)
coeff(s)
```

Description

Modify coefficient matrices

Usage

```r
## S4 replacement method for signature 'scNMFSet'
coeff(object) <- value
```
**Arguments**

- **object**: Object of class scNMFSet
- **value**: Coefficient matrix to be substituted

**Value**

Input object with updated coefficient matrices

**Examples**

```r
s <- scNMFSet(count=matrix(rpois(n=12,lambda=3),4,3))
s <- vb_factorize(s, ranks=3)
coeff(s)[[1]] <- apply(coeff(s)[[1]],c(1,2),round,digits=2)
coeff(s)
```

---

**colData,scNMFSet-method**

*Sample annotation accessor*

**Description**

Sample annotation accessor

**Usage**

```r
## S4 method for signature 'scNMFSet'
colData(x)
```

**Arguments**

- **x**: Object containing sample annotation

**Value**

Column annotation DataFrame

**Examples**

```r
library(S4Vectors)
x <- matrix(rpois(n=12,lambda=3),4,3)
rownames(x) <- seq_len(4)
colnames(x) <- c('a','b','c')
s <- scNMFSet(count=x,rowData=seq_len(4),colData=c('a','b','c'))
cols <- DataFrame(tissue=c('tissue1','tissue1','tissue2'))
rownames(cols) <- c('a','b','c')
colData(s) <- cols
ts
```
**Description**

Cell annotation assignment

**Usage**

```r
## S4 replacement method for signature 'scNMFSet,ANY'
colData(x) <- value
```

**Arguments**

- `x`: Object containing cell annotation
- `value`: DataFrame to be substituted

**Value**

Updated column annotation

**Examples**

```r
library(S4Vectors)
x <- matrix(rpois(n=12,lambda=3),4,3)
rownames(x) <- seq_len(4)
colnames(x) <- c('a','b','c')
s <- scNMFSet(count=x,rowData=seq_len(4),colData=c('a','b','c'))
cols <- DataFrame(tissue=c('tissue1','tissue1','tissue2'))
rownames(cols) <- c('a','b','c')
colData(s) <- cols
s
```

**Description**

Accessor for count matrix

**Usage**

```r
## S4 method for signature 'scNMFSet'
counts(object)
```
counts<-,scNMFSet-method

**Arguments**

object Object containing count matrix

**Value**

Count matrix

**Examples**

```r
s <- scNMFSet(count = matrix(rpois(n=12,lambda=3),3,4))
counts(s)
```

---

**Assignment of count matrix**

**Description**

Count matrix can be modified

**Usage**

```r
## S4 replacement method for signature 'scNMFSet'
counts(object) <- value
```

**Arguments**

object Object containing count

value Matrix-like object for replacement

**Value**

Object with updated count

**Examples**

```r
mat <- matrix(rpois(n=12,lambda=3),3,4)
s <- scNMFSet(count = mat)
counts(s) <- mat^2
counts(s)
```
**dbasis**

**Basis SD matrix accessor**

### Description

Basis SD matrix accessor

### Usage

```r
dbasis(object)
```

### Arguments

- **object**
  
  Object containing dbasis matrix

### Value

List of dbasis matrices

### dbasis,scNMFSet-method

**Basis SD matrix accessor**

### Description

Basis SD matrix accessor

### Usage

```r
## S4 method for signature 'scNMFSet'
dbasis(object)
```

### Arguments

- **object**
  
  Object containing basis standard deviation (SD) matrix

### Value

List of dbasis matrices
**dbasis<-,scNMFSet-method**

**Description**

Basis SD matrix assignment

**Usage**

```r
dbasis(object) <- value
```

**Arguments**

- `object`: Object containing dbasis matrix
- `value`: List for assignment

**Value**

Updated object

---

**dbasis<-,scNMFSet-method**

Modify dbasis matrices

**Description**

Access and modify dbasis matrices

**Usage**

```r
## S4 replacement method for signature 'scNMFSet'
# S4 replacement method for signature 'scNMFSet'
dbasis(object) <- value
```

**Arguments**

- `object`: Object of class scNMFSet
- `value`: Basis SD matrix to be substituted

**Value**

Modified object
Description
Coeff SD matrix accessor

Usage
dcoeff(object)

Arguments
object Object containing dcoeff matrix

Value
List of dcoeff matrices

## S4 method for signature 'scNMFSet'

dcoeff(object)

Arguments
object Object containing coeffient standard deviation (SD) matrix

Value
List of dcoeff matrices
dcoeff<- scNMFSet-method

---

**dcoeff<-**

*Coeff SD matrix assignment*

---

**Description**

Coeff SD matrix assignment

**Usage**

```r
dcoeff(object) <- value
```

**Arguments**

- `object`: Object containing dcoeff matrix
- `value`: List for assignment

**Value**

Updated object

---

**dcoeff<-.scNMFSet-method**

*Modify dcoeff matrices*

---

**Description**

Access and modify dcoeff matrices

**Usage**

```r
## S4 replacement method for signature 'scNMFSet'
dcoeff(object) <- value
```

**Arguments**

- `object`: Object of class scNMFSet
- `value`: Coeff SD matrix to be substituted

**Value**

Updated object
factorize  

Maximum likelihood factorization

Description

Performs single or multiple rank NMF factorization of count matrix using maximum likelihood

Usage

factorize(object, ranks = 2, nrun = 20, randomize = FALSE, 
nsmpl = 1, verbose = 2, progress.bar = TRUE, Itmax = 10000, 
ncnn.step = 40, criterion = "likelihood", linkage = "average", 
Tol = 1e-05, store.connectivity = FALSE)

Arguments

- **object**: scNMFSet object containing count matrix.
- **ranks**: Rank for factorization; can be a vector of multiple values.
- **nrun**: No. of runs with different initial guess.
- **randomize**: Boolean; if TRUE, input matrix is randomized.
- **nsmpl**: No. of randomized samples to average over.
- **verbose**: The verbosity level: 3, each iteration output printed; 2, each run output printed; 1, each randomized sample output printed; 0, silent.
- **progress.bar**: Display progress bar when nrun > 1 and verbose = 1.
- **Itmax**: Maximum no. of iteration.
- **ncnn.step**: Minimum no. of steps with no change in connectivity matrix to achieve convergence.
- **criterion**: If 'likelihood', iteration stops when fractional changes in likelihood is below tolerance Tol. If criterion = 'connectivity', iteration stops when connectivity matrix does not change for at least ncnn.step steps.
- **linkage**: Method to be sent to hclust in calculating cophenetic correlation.
- **Tol**: Tolerance for checking convergence with criterion = 'likelihood'.
- **store.connectivity**: Returns a list also containing connectivity data.

Details

The main input is the scNMFSet object with count matrix. This function performs non-negative factorization and fills in the empty slots basis, coeff, and ranks.

When run with multiple values of ranks, factorization is repeated for each rank and the slot measure contains quality measures of the ranks. The quality measure likelihood is negative the KL distance of the fit to the target. With nrun > 1, the likelihood is the maximum among all runs.
The quality measure dispersion is the scalar measure of how far the connectivity matrix is from 0, 1. With increasing \texttt{nrun}, dispersion decreases from 1. \texttt{nrun} should be chosen such that dispersion does not change appreciably. With randomization, count matrix of \texttt{object} is shuffled. \texttt{nsmpl} can be used to average over multiple permutations. This averaging applies to each quality measure under a given rank.

### Value
Object of class \texttt{scNMFSet} with factorization slots filled.

### Examples
```r
set.seed(1)
x <- simulate_data(nfeatures=10,nsamples=c(20,20,60,40,30))
s <- scNMFSet(count=x)
s <- factorize(s,ranks=seq(2,8),nrun=5)
plot(s)
```

---

### \texttt{feature_map}

#### Plot heatmap of basis matrix

### Description
Generate heatmap of features derived from factorization of count data.

### Usage
```r
feature_map(object, basis.matrix = NULL, rank, markers = NULL,
subtract.mean = TRUE, log = TRUE, max.per.cluster = 10,
feature.names = NULL, perm = NULL, main = "Feature map",
cscale = NULL, cex.cluster = 1, cex.feature = 0.5, mar = NULL,
...)
```

### Arguments
- **object**: Object of class \texttt{scNMFSet}.
- **basis.matrix**: Basis matrix can be supplied instead of \texttt{object}.
- **rank**: Rank value for which the gene map is to be displayed. The object must contain the corresponding slot (one element of \texttt{basis(object)}[[\texttt{k}]] for which \texttt{ranks(object)}[[\texttt{k}]]==\texttt{rank}.
- **markers**: Vector of gene names containing markers to be included in addition to the meta-genes. All entries of \texttt{rowData(object)} matching them will be added to the metagene list.
- **subtract.mean**: Process each rows of basis matrix \textbf{W} by standardization using the mean of elements within the row.
- **log**: If \texttt{TRUE}, \texttt{subtract.mean} uses geometric mean and division. Otherwise, use arithmetic mean and subtraction.
filter_cells

max.per.cluster

feature.names

perm

main

cscale

cex.cluster

cex.feature

mar

...

Details

This function uses image() and is more flexible than gene_map.

If object contains multiple ranks, only the requested rank’s basis matrix \( W \) will be displayed. As in gene_map, the features displayed in rows are selected by "max" scheme.

Value

NULL

Examples

```r
set.seed(1)
x <- simulate_data(nfeatures=10,nsamples=c(20,20,60))rownames(x) <- seq_len(10)

set.seed(1)x <- simulate_data(nfeatures=10,nsamples=c(20,20,60))rownames(x) <- seq_len(10)colnames(x) <- seq_len(100)s <- scNMFSet(count=x,rowData=seq_len(10),colData=seq_len(100))s <- vb_factorize(s,ranks=seq(2,5))plot(s)feature_map(s, rank=3)
```

filter_cells

Filter cells with quality control criteria

Description

Remove low quality cell entries from object

Usage

```
filter_cells(object, umi.min = 0, umi.max = Inf, plot = TRUE, remove.zeros = TRUE)
```
filter_genes

Arguments

object scNMFSet object
umi.min Minimum UMI count for cell filtering
umi.max Maximum UMI count for cell filtering
plot If TRUE, the UMI count distribution of all cells will be displayed. Cells selected are colored red.
remove.zeros Remove rows/columns containing zeros only

Details

Takes as input scNMFSet object and plots histogram of UMI counts for each cell. Optionally, cells are filtered using minimum and maximum UMI counts. The resulting object is returned after removing empty rows and columns, if any.

Value

scNMFSet object with cells filtered.

Examples

```r
set.seed(1)
s <- scNMFSet(matrix(stats::rpois(n=1200,lambda=3),40,30))
s <- filter_cells(s,umi.min=10^2.0,umi.max=10^2.1)
```

filter_genes Filter genes with quality control criteria

Description

Select genes with high relative variance in count data for further analysis.

Usage

```r
filter_genes(object, markers = NULL, vmr.min = 0, min.cells.expressed = 0, max.cells.expressed = Inf, rescue.genes = FALSE, progress.bar = TRUE, save.memory = FALSE, plot = TRUE, log = "xy", cex = 0.5)
```

Arguments

object scNMFSet object.
markers A vector containing marker genes to be selected. All rows in rowData that contain columns matching this set will be selected.
vmr.min Minimum variance-to-mean ratio for gene filtering.
min.cells.expressed Minimum no. of cells expressed for gene filtering.
max.cells.expressed

Maximum no. of cells expressed for gene filtering.

rescue.genes

Selected additional genes whose (non-zero) count distributions have at least one mode.

progress.bar

Display progress of mode-gene scan or VMR calculation with save.memory = TRUE.

save.memory

For a very large number of cells, calculate VMR row by row while avoiding calls to as.matrix(). Progress bar will be displayed unless progress.bar=FALSE.

plot

Plot the distribution of no. of cells expressed vs. VMR.

log

Axis in log-scale, c('x','y','xy').

cex

Symbol size for each gene in the plot.

Details

Takes as input scNMFSet object and scatterplot no. of cells expressed versus VMR (variance-to-mean ratio) for each gene. Optionally, genes are filtered using minimum VMR together with a range of no. of cells expressed.

Value

Object of class scNMFSet.

Examples

set.seed(1)
s <- scNMFSet(matrix(stats::rpois(n=1200,lambda=3),40,30))
s <- filter_genes(s, vmr.min=1.0, min.cells.expressed=28,
rescue.genes=FALSE)

gene_map

Plot heatmap of metagene matrix

description

Generate heatmap of metagenes derived from factorization of count data.

Usage

gene_map(object, rank, markers = NULL, subtract.mean = TRUE,
log = TRUE, max.per.cluster = 10, Colv = NA, gene.names = NULL,
main = "Genes", col = NULL, ...)
Arguments

object Object of class scNMFSet.
rank Rank value for which the gene map is to be displayed. The object must contain the corresponding slot (one element of basis(object)[[k]] for which ranks(object)[[k]]==rank.
markers Vector of gene names containing markers to be included in addition to the metagenes. All entries of rowData(object) matching them will be added to the metagene list.
subtract.mean Process each rows of basis matrix \( W \) by standardization using the mean of elements within the row.
log If TRUE, subtract.mean uses geometric mean and division. Otherwise, use arithmetic mean and subtraction.
max.per.cluster Maximum number of metagenes per cluster.
Colv NA suppresses reordering and dendrogram of clusters along the column. See heatmap.
gene.names Names to be used in the plot for genes.
main Title of plot.
col Colors for the cluster panels on the left and top.
... Other arguments to be passed to heatmap, image, and plot.

Details

Wrapper for heatmap to display metagenes and associated basis matrix element magnitudes. Factorization results inside an object specified by its rank value will be retrieved, and metagene sets identified from clusters.

If object contains multiple ranks, only the requested rank's basis matrix \( W \) will be displayed. The genes displayed in rows are selected by "max" scheme [Carmona-Saez, BMC Bioinformatics (2006), https://doi.org/10.1186/1471-2105-7-54]: for each cluster \( (k \in 1:ncol) \), rows of \( W \) are sorted by decreasing order of \( W[,k] \). Marker genes for \( k \) are those among the top nmarker for which \( W[,k] \) is maximum within each row.

Value

NULL

Examples

set.seed(1)
x <- simulate_data(nfeatures=10,nsamples=c(20,20,60))rownames(x) <- seq_len(10)colnames(x) <- seq_len(100)
s <- scNMFSet(count=x,rowData=seq_len(10),colData=seq_len(100))s <- vb_factorize(s,ranks=seq(2,5))plot(s)gene_map(s, rank=3)
**measure**

**Factorization measures in an Object**

Description
Retrieve or set factorization measures in an object

Usage
measure(object)

Arguments
object Object of class scNMFSet.

Details
Factorization under multiple rank values lead to measures stored in a data frame inside a slot measure. In maximum likelihood using factorize, this set of quality measures include dispersion and cophenetic coefficients for each rank. In Bayesian factorization using vb_factorize, log evidence for each rank is stored. measure(object) will return the data frame. measure(object) <- value can be used to modify it.

Value
Either NULL or a data frame containing measures.

Examples
s <- scNMFSet(count=matrix(rpois(n=12,lambda=3),4,3))
s <- vb_factorize(s,ranks=seq(2,4))
measure(s)

**measure,scNMFSet-method**

**Rank measure accessor**

Description
Rank measure accessor

Usage
## S4 method for signature 'scNMFSet'
measure(object)
Arguments

object       Object containing measure

Value

Data frame of measure

measure<-  

Generics for factorization measure assignment

Description

Can be used to access and modify factorization measure

Usage

measure(object) <- value

Arguments

object       Object of class scNMFS

value       Measure to be substituted

Value

Input object with updated measure

Examples

s <- scNMFS(count=matrix(rpois(n=12,lambda=3),4,3))
s <- vb_factorize(s, ranks=3)
measure(s)[,-1] <- apply(measure(s)[,-1], c(1,2), round,digits=3)
measure(s)

measure<-,scNMFS-method

Modify factorization measure

Description

Can be used to access and modify factorization measure

Usage

## S4 replacement method for signature 'scNMFS'
measure(object) <- value
**Arguments**

- **object**: Object of class `scNMFSet`
- **value**: Measure to be substituted

**Value**

Input object with updated measure

**Examples**

```r
s <- scNMFSet(count=matrix(rpois(n=12,lambda=3),4,3))
s <- vb_factorize(s, ranks=3)
measure(s)[,-1] <- apply(measure(s)[,-1], c(1,2), round,digits=3)
measure(s)
```

---

**Description**

Generates meta gene table with coefficient of variation

**Usage**

```r
meta_gene.cv(object = NULL, rank, basis.matrix = NULL, dbasis = NULL,
      max.per.cluster = 100, gene_names = NULL, subtract.mean = TRUE,
      log = TRUE, cv.max = Inf)
```

**Arguments**

- **object**: Main object containing factorization outcome
- **rank**: Rank for which meta gene is to be found
- **basis.matrix**: Basis matrix to work with. Only necessary when `object` is `NULL`.
- **dbasis**: Variance of basis matrix. Only necessary when `object` is `NULL`.
- **max.per.cluster**: Maximum meta genes per cluster.
- **gene_names**: Name of genes. If `NULL`, will be taken from row names.
- **subtract.mean**: Standardize magnitudes of basis elements by subtracting mean
- **log**: Use geometric mean.
- **cv.max**: Upper bound for CV in selecting meta genes.

**Value**

Data frame with meta genes and their CV in each column.
Examples

```r
set.seed(1)
x <- simulate_whx(nrow=50, ncol=100, rank=5)
s <- scNMFSet(x$x)
s <- vb_factorize(s, ranks=seq(2,8), nrun=5)
plot(s)
meta_gene.cv(s, rank=5)
```

---

**meta_genes**

*Find metagenes from basis matrix*

**Description**

Retrieve a basis matrix from an object and find metagenes.

**Usage**

```r
meta_genes(object, rank, basis.matrix = NULL, max.per.cluster = 10,
gene_names = NULL, subtract.mean = TRUE, log = TRUE)
```

**Arguments**

- **object**: Object of class `scNMFSet`.
- **rank**: Rank value for which metagenes are to be found.
- **basis.matrix**: Instead of an object containing basis matrices, the matrix itself can be provided.
- **max.per.cluster**: Maximum number of metagenes per cluster.
- **gene_names**: Names of genes to replace row names of basis matrix.
- **subtract.mean**: Standardize the matrix elements with means within each row.
- **log**: Use geometric mean and division instead of arithmetic mean and subtraction with `subtract.mean`.

**Value**

List of vectors each containing metagene names of clusters.

**Examples**

```r
set.seed(1)
x <- simulate_data(nfeatures=10, nsamples=c(20,20,60))
rownames(x) <- seq_len(10)
colnames(x) <- seq_len(100)
s <- scNMFSet(count=x, rowData=seq_len(10), colData=seq_len(100))
s <- vb_factorize(s, ranks=seq(2,5))
meta_genes(s, rank=4)
```
newick

Generate Newick format tree string from tree list object

Description

Generate Newick format tree string from tree list object

Usage

`newick(tree, parent = "1.1", string = "")`

Arguments

- `tree`: Tree list object from `build_tree`
- `parent`: Parent ID
- `string`: Newick string of parent tree

Value

String of newick tree

Examples

```r
set.seed(1)
x <- simulate_whx(nrow=50, ncol=100, rank=5)
s <- scNMFSet(x$x)
s <- vb_factorize(s, ranks=seq(2,8), nrun=5)
tree <- build_tree(s, rmax=5)
nw <- newick(tree=tree)
nw
```

normalize_count

Normalize count data

Description

Rescale count matrix entries such that all cells have the same library size.

Usage

`normalize_count(object)`

Arguments

- `object`: scNMFSet object.
Details

For analysis purposes, it is sometimes useful to rescale integer count data into floats such that all
cells have the same median counts. This function will calculate the median of all UMI counts of
cells (total number of RNAs derived from each cell). All count data are then rescaled such that cells
have uniform UMI count equal to the median.

Value

scNMFSet object with normalized count data.

Examples

library(Matrix)
set.seed(1)
s <- scNMFSet(count=matrix(rpois(n=1200,lambda=3),40,30))
colMeans(counts(s))
s <- normalize_count(s)
colMeans(counts(s))

optimal_rank

Determine optimal rank

Description

Takes as main argument scNMFSet object containing factorized output and estimate the optimal
rank.

Usage

optimal_rank(object, df = 10, BF.threshold = 3, type = NULL,
m = NULL)

Arguments

object scNMFSet object containing factorization output, or data frame containing the
rank-evidence profile.
df Degrees of freedom for split fit. Upper bound is the total number of data points
(number of rank values scanned).
BF.threshold Bayes factor threshold for statistical threshold.
type c(1,2). Type 1 is where there is a clear maximum. Type 2 is where marginal
likelihood reaches a maximal level and stays constant. If omitted, the type will
be inferred from data.
m Number of features (e.g., genes) in the count matrix. Only necessary when
object is of type data.frame.
Details

The input object is used along with Bayes factor threshold to determine the heterogeneity type (1 or 2) and the optimal rank. If evidence(rank 1)/evidence(rank2) > BF.threshold, rank 1 is favorable than rank 2.

Value

List containing type and ropt (optimal rank).

Examples

```r
set.seed(1)
x <- simulate.whx(nrow=50, ncol=100, rank=5)
s <- scNMFSet(x$x)
s <- vb_factorize(s, ranks=seq(2,8), nrun=5)
plot(s)
optimal_rank(s)
```

Description

Gene variance to mean ratio and the number of expressing cells are plotted.

Usage

```r
plot_genes(object, vmr = NULL, ncexpr = NULL, selected_genes = NULL,
variable_genes = NULL, mode_genes = NULL, marker_genes = NULL,
save.memory = FALSE, progress.bar = TRUE, log = "xy", cex = 0.5)
```

Arguments

- **object**: Object containing count data
- **vmr**: Variance to mean ratio (VMR)
- **ncexpr**: Number of cells expressing each gene
- **selected_genes**: Logical vector specifying genes selected
- **variable_genes**: Logical vector specifying genes with high VMR
- **mode_genes**: Logical vector specifying genes with nonzero modes
- **marker_genes**: Logical vector specifying marker genes
- **save.memory**: If TRUE, calculate VMR using slower method to save memory. Not used when gene lists are supplied.
- **progress.bar**: Display progress bar for VMR calculation. Not used when gene lists are supplied.
- **log**: Axis in log-scale, c("x", "y", "xy").
- **cex**: Symbol size for genes (supplied to plot()).
plot_tree

Details
This function can be called separately or is also called within filter_genes by default. In the latter case, parameters other than object will have been already filled. If called separately with NULL gene lists, VMR is recalculated but gene selection is not done.

Value
NULL

Examples

```r
set.seed(1)
s <- scNMFSet(matrix(stats::rpois(n=1200,lambda=3),40,30))
plot_genes(s)
```

plot_tree
Plot cluster tree

Description
Visualize the output of build_tree as a dendrogram.

Usage

```r
plot_tree(tree, direction = "rightwards", cex = 0.7, ...)
```

Arguments

- `tree`: List containing tree structure. Output from build_tree
- `direction`: c('rightwards', 'downwards'); the direction of dendrogram
- `cex`: Font size of edge/tip labels
- `...`: Other parameters to plot.phylo

Details
Uses plot.phylo to visualize cluster tree.

Value
NULL

Examples

```r
set.seed(1)
x <- simulate_whx(nrow=50,ncol=100,rank=5)
s <- scNMFSet(x$x)
s <- vb_factorize(s,ranks=seq(2,8),nrun=5)
tree <- build_tree(s,rmax=5)
plot_tree(tree)
```
ranks

---

**ranks**

*Rank values in an Object*

---

**Description**

Retrieve or set the rank values in an object

**Usage**

`ranks(object)`

**Arguments**

- `object` Object of class `scNMFSet`.

**Details**

Ranks for which factorization has been performed are stored in slot `ranks` of `scNMFSet` object. `ranks(object)` will return the rank vector. `ranks(object) <- value` can be used to modify it.

**Value**

Either `NULL` or vector.

**Examples**

```r
s <- scNMFSet(matrix(rpois(n=12,lambda=3),4,3))
s <- vb_factorize(s,ranks=seq(2,4))
ranks(s)
```

**ranks,scNMFSet-method**

*Rank accessor*

---

**Description**

Rank accessor

**Usage**

```r
## S4 method for signature 'scNMFSet'
ranks(object)
```

**Arguments**

- `object` Object containing rank values

**Value**

Vector of rank values
ranks<-,scNMFSet-method

Generics for ranks assignment

Description

Replace ranks slot of scNMFSet object

Usage

ranks(object) <- value

Arguments

object Object of class scNMFSet
value Rank values (vector) to be substituted

Value

Input object with updated ranks

Examples

s <- scNMFSet(count=matrix(rpois(n=12,lambda=3),4,3))
s <- vb_factorize(s, ranks=seq(2,3))
ranks(s) <- c('two','three')
ranks(s)

ranks<-,scNMFSet-method

Modify ranks

Description

Replace ranks slot of scNMFSet object

Usage

## S4 replacement method for signature 'scNMFSet'
ranks(object) <- value

Arguments

object Object of class scNMFSet
value Rank values (vector) to be substituted
Value

Input object with updated ranks

Examples

```r
s <- scNMFSet(count=matrix(rpois(n=12, lambda=3), 4, 3))
s <- vb_factorize(s, ranks=seq(2, 3))
ranks(s) <- c('two', 'three')
ranks(s)
```

Description

Read count, gene, and barcode annotation data in 10x format and create an object of class `scNMFSet`.

Usage

```r
read_10x(dir, count = "matrix.mtx", genes = "genes.tsv",
          barcodes = "barcodes.tsv", remove.zeros = TRUE)
```

Arguments

- `dir` Name of directory containing data files.
- `count` Name of count matrix file.
- `genes` Name of gene annotation file.
- `barcodes` Name of cell annotation file.
- `remove.zeros` If TRUE, empty rows/columns are removed.

Details

Files for `count`, `genes`, and `barcodes` are assumed to be present in `dir`. Count data are in sparse "Matrix Market" format (https://math.nist.gov/MatrixMarket/formats.html).

Value

Object of class `scNMFSet`

Examples

```r
library(S4Vectors)
s <- scNMFSet(count=matrix(rpois(n=12, lambda=3), 4, 3))
rowData(s) <- DataFrame(seq_len(4))
colData(s) <- DataFrame(seq_len(3))
write_10x(s, dir='.')
s <- read_10x(dir='.')
s
```
**remove_zeros**  
*Remove rows or columns that are empty from an object*

**Description**  
Remove rows or columns that are empty from an object

**Usage**  
`remove_zeros(object)`

**Arguments**
- **object**: Object containing data

**Value**  
Object with empty rows/columns removed

**Examples**
```r
s2 <- remove_zeros(s)
s2
```

---

**rename_tips**  
*Rename tips of trees with cell types*

**Description**  
Rename tips of trees with cell types

**Usage**  
`rename_tips(tree, rank, tip.labels)`

**Arguments**
- **tree**: List containing tree
- **rank**: Rank value of which tip names are to be replaced
- **tip.labels**: Vector of new names for tips

**Value**  
List containing tree with updated tip labels

```r
tip <- rename_tips(tree, rank, tip.labels)
tip
```
Examples

```r
set.seed(1)
x <- simulate_whx(nrow=50,ncol=100,rank=5)
s <- scNMFSet(x$x)
s <- vb_factorize(s,ranks=seq(2,8),nrun=5)
tree <- build_tree(s,rmax=5)
tree <- rename_tips(tree,rank=5,tip.labels=letters[seq_len(5)])
tree
```

rowData,scNMFS-set-method

Feature annotation accessor

Description

Feature annotation accessor

Usage

```r
## S4 method for signature 'scNMFSet'
rowData(x)
```

Arguments

- `x`: Object containing data

Value

DataFrame of feature annotation

Examples

```r
x <- matrix(rpois(n=12,lambda=3),4,3)
rownames(x) <- seq_len(4)
colnames(x) <- seq_len(3)
s <- scNMFS(count=x,rowData=seq_len(4),colData=seq_len(3))
rowData(s)
```
rowData<-,scNMFSet-method

**Gene annotation assignment**

### Description

Gene annotation assignment

### Usage

```r
## S4 replacement method for signature 'scNMFSet'
rowData(x) <- value
```

### Arguments

- `x` Object containing data
- `value` DataFrame of row annotation to be substituted

### Value

Row annotation DataFrame

---

**scNMFSet**

Create scNMFSet object

### Description

Object derived from `SingleCellExperiment`

### Usage

```r
scNMFSet(count = NULL, ..., remove.zeros = TRUE)
```

### Arguments

- `count` Count matrix
- `...` Other parameters of `SingleCellExperiment`
- `remove.zeros` Remove empty rows and columns

### Value

Object of class scNMFSet.

### Examples

```r
count <- matrix(rpois(n=12,lambda=2),4,3)
s <- scNMFSet(count=count)
s <- scNMFSet(count=count)
```
scNMFSets-class

Class scNMFSets for storing input data and results

Description

S4 class derived from SingleCellExperiment that can store single-cell count matrix, gene and cell annotation data frames, and factorization factors as well as quality measures for rank determination.

Usage

```r
## S4 method for signature 'scNMFSets,ANY'
plot(x)
```

Arguments

- `x` Object containing measure

Value

Object of class scNMFSets

NULL

Methods (by generic)

- `plot`: Plot measures of an object. For quality measures derived from maximum likelihood inference, dispersion and cophenetic will be plotted separately.
  For measure derived from Bayesian inference, log evidence as a function of rank values will be plotted.

Slots

- `assays` Named list for count matrix counts.
- `rowData` DataFrame for gene (feature) names and annotations in columns.
- `colData` DataFrame for cell IDs and other annotations in columns (e.g., barcodes, cell types).
- `ranks` Vector for rank values for which factorization has been performed.
- `basis` List (of length equal to that of ranks) of basis matrices \( W \) from factorization; dimension \( \text{nr} \times \text{rank} \), where \( \text{nr} \) is no. of rows in count.
- `coeff` List (of length equal to that of ranks) of coefficient matrices \( H \) from factorization; dimension \( \text{rank} \times \text{ncol} \), where \( \text{ncol} \) is no. of columns in count.
- `measure` Data frame of factorization quality measures for each rank (likelihood and dispersion).
  Other slots inherited from SingleCellExperiment class are not explicitly used.
Examples

library(S4Vectors)
# toy matrix
ngenes <- 8
ncells <- 5
mat <- matrix(rpois(n=ngenes*ncells,lambda=3),ngenes,ncells)

abc <- letters[seq_len(ngenes)]
ABC <- LETTERS[seq_len(ncells)]
gen <- DataFrame(gene_id=abc)
cell <- DataFrame(cell_id=ABC)
rownames(mat) <- rownames(gen) <- abc
colnames(mat) <- rownames(cell) <- ABC

# create scNMFSet object
s <- scNMFSet(count=mat,rowData=gen,colData=cell)
# alternative ways
s2 <- scNMFSet(count=mat)
s2 <- scNMFSet(assays=list(counts=mat))

# show dimensions
dim(s)

# show slots
rowData(s)

# modify slots
colData(s) <- DataFrame(cell_id=seq_len(ncells),
cell_type=c(rep('tissue1',2),
rep('tissue2',ncells-2)))
colData(s)

show,scNMFSet-method  Display object

Description

Display the class and dimension of an object
Object name itself on command line or (show(object)) will display class and dimensionality

Usage

## S4 method for signature 'scNMFSet'
show(object)

Arguments

object  Object of class scNMFSet
## simulate_data

Generate simulated data for factorization

### Description

Use one of two schemes to generate simulated data suitable for testing factorization.

### Usage

```r
simulate_data(nfeatures, nsamples, generate.factors = FALSE,
              nfactor = 10, alpha0 = 0.5, shuffle = TRUE)
```

### Arguments

- **nfeatures**: Number of features \( m \) (e.g., genes).
- **nsamples**: Vector of sample sizes in each cluster. Rank \( r \) is equal to the length of this vector. Sum of elements is the total sample size \( n \).
- **generate.factors**: Generate factor matrices \( W \) and \( H \), each with dimension \( n \times r \) and \( r \times n \). If `FALSE`, factor matrices are not used and count data are generated directly from \( r \) multinomials for \( m \) genes.
- **nfactor**: Total RNA count of multinomials for each cluster with `generate.factors = FALSE`. Small `nfactor` will yield sparse count matrix.
- **alpha0**: Variance parameter of Dirichlet distribution from which multinomial probabilities are sampled with `generate.factors = FALSE`.
- **shuffle**: Randomly permute rows and columns of count matrix.

### Details

In one scheme (`generate.factors = TRUE`), simulated factor matrices \( W \) and \( H \) are used to build count data \( X = WH \). In the second scheme, factor matrices are not used and \( X \) is sampled directly from \( r \) (rank requested) sets of multinomial distributions.

### Value

If `generate.factors = TRUE`, list of components `w` (basis matrix, \( nfeatures \times \text{rank} \)), `h` (coefficient matrix, \( \text{rank} \times \text{ncells} \), where `ncells` is equal to \( n \), the sum of `nsamples`), and `x`, a matrix of Poisson deviates with mean \( W \times H \). If `generate.factors = FALSE`, only the count matrix `x` is in the list.
simulate_whx

Simulate factor matrices and data using priors

Description

Under Bayesian formulation, use prior distributions of factor matrices and generate simulated data

Usage

simulate_whx(nrow, ncol, rank, aw = 0.1, bw = 1, ah = 0.1, bh = 1)

Arguments

nrow Number of features (genes).
ncol Number of cells (samples).
rank Rank (ncol of W, nrow of H).
aw Shape parameter of basis prior.
bw Mean of basis prior. Scale parameter is equal to \( \frac{aw}{bw} \).
ah Shape parameter of coefficient prior.
bh Mean of coefficient prior. Scale parameter is equal to \( \frac{ah}{bh} \).

Details

Basis \( W \) and coefficient matrices \( H \) are sampled from gamma distributions (priors) with shape \((aw, ah)\) and mean \((bw, bh)\) parameters. Count data \( X \) are sampled from Poisson distribution with mean values given by \( WH \).

Value

List with elements \( w \), \( h \), and \( x \), each containing basis, coefficient, and count matrices.

Examples

```r
set.seed(1)
x <- simulate_data(nfeatures=10,nsamples=c(20,20,60,40,30))
s <- scNMFSet(x)
s
```

```r
set.seed(1)
x <- simulate_whx(nrow=50,ncol=100,rank=5)
s <- scNMFSet(count=x$x)
s <- vb_factorize(s,ranks=seq(2,8),nrun=5)
plot(s)
```
vb_factorize

Bayesian NMF inference of count matrix

Description
Perform variational Bayes NMF and store factor matrices in object

Usage

vb_factorize(object, ranks = 2, nrun = 1, verbose = 2,
progress.bar = TRUE, initializer = "random", Itmax = 10000,
hyper.update = rep(TRUE, 4), gamma.a = 1, gamma.b = 1,
Tol = 1e-05, hyper.update.n0 = 10, hyper.update.dn = 1,
connectivity = TRUE, fudge = NULL, ncores = 1, useC = TRUE,
unif.stop = TRUE)

Arguments

object scNMFSect object containing count matrix.
ranks Rank for factorization; can be a vector of multiple values.
nrun No. of runs with different initial guesses.
verbose The verbosity level: 3, each iteration output printed; 2, each run output printed; 1, each randomized sample output printed; 0, silent.
progress.bar Display progress bar with verbose = 1 for multiple runs.
initializer If 'random', randomized initial conditions; 'svd2' for singular value decomposed initial condition.
Itmax Maximum no. of iteration.
hyper.update Vector of four logicals, each indicating whether hyperparameters (aw, bw, ah, bh) should be optimized.
gamma.a Gamma distribution shape parameter.
gamma.b Gamma distribution mean. These two parameters are used for fixed hyperparameters with hyper.update elements FALSE.
Tol Tolerance for terminating iteration.
hyper.update.n0 Initial number of steps in which hyperparameters are fixed.
hyper.update.dn Step intervals for hyperparameter updates.
connectivity If TRUE, connectivity and dispersion will be calculated after each run. Can be turned off to save memory.
fudge Small positive number used as lower bound for factor matrix elements to avoid singularity. If fudge = NULL (default), it will be replaced by .Machine$double.eps. Can be set to 0 to skip regularization.
ncores Number of processors (cores) to run. If ncores > 1, parallelization is attempted.
useC Use C++ version of updates for speed.
unif.stop Terminate if any of columns in basis matrix is uniform.
Details

The main input is the scNMFSet object with count matrix. This function performs non-negative factorization using Bayesian algorithm and gamma priors. Slots basis, coeff, and ranks are filled.

When run with multiple values of ranks, factorization is repeated for each rank and the slot measure contains log evidence and optimal hyperparameters for each rank. With nrun > 1, the solution with the maximum log evidence is stored for a given rank.

Value

Object of class scNMFSet with factorization slots filled.

Examples

```r
set.seed(1)
x <- simulate_whx(nrow=50,ncol=100,rank=5)
s <- scNMFSet(x$x)
s <- vb_factorize(s,ranks=seq(2,8),nrun=5)
plot(s)
```

visualize_clusters

Visualize clusters

Description

Use tSNE to generate two-dimensional map of coefficient matrix.

Usage

```r
visualize_clusters(object, rank, verbose = FALSE, cex = 1,
cex.names = 0.7, ...)
```

Arguments

- **object**: scNMF object.
- **rank**: Rank value to extract from object.
- **verbose**: Print tSNE messages.
- **cex**: Symbol size in tSNE plot.
- **cex.names**: Font size of labels in count barplot.
- **...**: Other parameters to send to Rtsne.

Details

It retrieves a coefficient matrix H from an object and use its elements to assign each cell into clusters. t-Distributed Stochastic Neighbor Embedding (t-SNE; https://lvdmaaten.github.io/tsne/) is used to visualize the clustering in 2D. Also plotted is the distribution of cell counts for all clusters.
Value

NULL

Examples

```r
set.seed(1)
x <- simulate_data(nfeatures=10,nsamples=c(20,20,60,40,30))
rownames(x) <- seq_len(10)
colnames(x) <- seq_len(170)
s <- scNMFSet(count=x,rowData=seq_len(10),colData=seq_len(170))
s <- vb_factorize(s,ranks=seq(2,5))
visualize_clusters(s,rank=5)
```

---

**Description**

Use an object and write count and annotation files in 10x format.

**Usage**

```r
write_10x(object, dir, count = "matrix.mtx", genes = "genes.tsv",
barcodes = "barcodes.tsv", quote = FALSE)
```

**Arguments**

- `object`: Object of class `scNMFSet` containing count data
- `dir`: Directory where files are to be written.
- `count`: File name for count matrix.
- `genes`: File name for gene annotation.
- `barcodes`: File name for cell annotation.
- `quote`: Suppress quotation marks in output files.

**Value**

NULL

**Examples**

```r
set.seed(1)
x <- matrix(rpois(n=12,lambda=3),4,3)
rownames(x) <- seq_len(4)
colnames(x) <- seq_len(3)
s <- scNMFSet(count=x,rowData=seq_len(4),colData=seq_len(3))
write_10x(s,dir='.')
```
write_meta

Write meta genes to a file

Description
Write a csv file of meta gene lists from input list

Usage
write_meta(meta, file)

Arguments
meta List of meta genes output from meta_genes
file Output file name

Value
NULL

Examples
set.seed(1)
x <- simulate_whx(nrow=50, ncol=100, rank=5)
s <- scNMFSets(x$x)
s <- vb_factorize(s, ranks=seq(2,8), nrun=5)
plot(s)
m <- meta_genes(s, rank=5)
write_meta(m, file='meta.csv')

[scNMFSets,ANY,ANY,ANY-method

Subsetting scNMFSets object

Description
Subsetting scNMFSets object

Usage
## S4 method for signature 'scNMFSets,ANY,ANY,ANY'
x[i, j]
Arguments

- **x**: Object to be subsetted
- **i**: row index
- **j**: column index

Value

- Subsetted object
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