Package ‘GeneScape’

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Type Package

Title Simulation of Single Cell RNA-Seq Data with Complex Structure

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Description Simulating single cell RNA-seq data with complicated structure. This package is developed based on the Splat method (Zappia, Phipson and Oshlack (2017) <doi:10.1186/s13059-017-1305-0>). ‘GeneScape’ incorporates additional features to simulate single cell RNA-seq data with complicated differential expression and correlation structures, such as sub-cell-types, correlated genes (pathway genes) and hub genes.

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Imports MASS (>= 7.3-53.1), corpcor (>= 1.6.10), stats

RoxygenNote 7.2.3

NeedsCompilation no

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### Description

This function similate differential expression fold change level

### Usage

```r
fcsim(n.gene, de.id, fc.loc, fc.scale)
```

### Arguments

- **n.gene**: total number of genes
- **de.id**: index of differentially expressed genes
- **fc.loc**: location parameter for fold change (log-normal distribution)
- **fc.scale**: scale parameter for fold change (log-normal distribution)

### References


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### Description

This function simulate single cell RNAseq data with complicated differential expression and correlation structure.

### Usage

```r
GeneScape(
  nCells = 6000,
  nGroups = NULL,
  groups = NULL,
  lib.size.loc = 9.3,
  lib.size.scale = 0.25,
  de.fc.mat = NULL,
  nGenes = 5000,
  gene.mean.shape = 0.3,
  gene.mean.rate = 0.15,
  gene.means = NULL,
  de.n = 50,
)```
de.share = NULL,
de.id = NULL,
de.fc.loc = 0.7,
de.fc.scale = 0.2,
add.sub = FALSE,
sub.major = NULL,
sub.prop = 0.1,
sub.group = NULL,
sub.de.n = 20,
sub.de.id = NULL,
sub.de.common = FALSE,
sub.de.fc.loc = 0.7,
sub.de.fc.scale = 0.2,
add.cor = FALSE,
cor.n = 4,
cor.size = 20,
cor.cor = 0.7,
cor.id = NULL,
band.width = 10,
add.hub = FALSE,
hub.n = 10,
hub.size = 20,
hub.cor = 0.4,
hub.id = NULL,
hub.fix = NULL,
drop = FALSE,
dropout.location = -2,
dropout.slope = -1
)

Arguments

nCells  number of cells
nGroups  number of cell groups
groups  group information for cells
lib.size.loc  location parameter for library size (log-normal distribution)
lib.size.scale  scale parameter for library size (log-normal distribution)
de.fc.mat  differential expression fold change matrix, could be generated by this function
nGenes  number of genes
gene.mean.shape  shape parameter for mean expression level (Gamma distribution)
gene.mean.rate  rate parameter for mean expression level (Gamma distribution)
gene.means  mean gene expression levels
de.n  number of differentially expressed genes in each cell type. Should be a integer
or a vector of length nGroups
GeneScape de.share number of shared DE genes between neighbor cell types. Should be a vector of length \((nGroups - 1)\)

de.id the index of genes that are DE across cell types. Should be a list of vectors. Each vector corresponds to a cell type. With non-null value of de.id, de.n and de.share would be ignored.

de.fc.loc the location parameter for the fold change of DE genes. Should be a number, a vector of length \(nGroups\)

de.fc.scale the scale parameter for fold change (log-normal distribution). Should be a number or a vector of length \(nGroups\)

add.sub whether to add sub-cell-types

sub.major the major cell types correspond to the sub-cell-types

sub.prop proportion of sub-cell-types in the corresponding major cell type

sub.group cell index for sub-cell-types. With non-null sub.group specified, sub.prop would be ignored.

sub.de.n number of differentially expressed genes in each sub-cell-type compared to the corresponding major cell type. Should be a integer or a vector of length sub.major

sub.de.id the index of additional differentially expressed genes between sub-cell-types and the corresponding major cell types

sub.de.common whether the additional differential expression structure should be same for all sub-cell-types

sub.de.fc.loc similar to de.fc.loc, but for additional differentially expressed genes in sub-cell-types

sub.de.fc.scale similar to de.fc.scale, but for additional differentially expressed genes in sub-cell-types

add.cor whether to add pathways (correlated genes)

cor.n number of pathways included. Should be a integer.

cor.size number of correlated genes (length of pathway). Should be a number or a vector of length cor.n

cor.cor correlation parameters between hub genes and their correlated genes

cor.id gene index of correlated (pathway) genes. Should be a list of vectors, with each vector represents a pathway. With non-null value of cor.id, cor.n would be ignored.

band.width No correlation exists if distance of 2 genes are further than band_width in a pathway

add.hub whether to add hub genes

hub.n number of hub genes included. Should be a integer.

hub.size number of genes correlated to the hub gene. Should be a number or a vector of length hub.n

hub.cor correlation parameters between hub genes and their correlated genes
**GeneScape**

- **hub.id**: gene index of hub genes. Should be a list of vectors. With non-null value of hub.id, hub.n would be ignored.
- **hub.fix**: user defined genes correlated to hub genes (others are randomly selected). Should be a list of vectors of length hub.n or same as hub.id.
- **drop**: whether to add dropout
- **dropout.location**: dropout mid point (the mean expression level at which the probability is equal to 0.5, same as splat. Could be negative)
- **dropout.slope**: how dropout proportion changes with increasing expression

**Details**

Compared to splat method in Splatter R package, this function can fix the number and position of differentially expressed genes, have more complicated differential expression structure, add sub-cell-types, correlated genes (AR(1) correlation structure with bound, mimicking pathways) and hub genes.

**Value**

A list of observed data, true data (without dropout), differential expression rate and hub gene indices.

**References**


**Examples**

```r
set.seed(1)
data <- GeneScape()
```
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