Package ‘scShapes’

May 17, 2024

Type Package

Title A Statistical Framework for Modeling and Identifying Differential Distributions in Single-cell RNA-sequencing Data

Version 1.10.0

Description We present a novel statistical framework for identifying differential distributions in single-cell RNA-sequencing (scRNA-seq) data between treatment conditions by modeling gene expression read counts using generalized linear models (GLMs). We model each gene independently under each treatment condition using error distributions Poisson (P), Negative Binomial (NB), Zero-inflated Poisson (ZIP) and Zero-inflated Negative Binomial (ZINB) with log link function and model based normalization for differences in sequencing depth. Since all four distributions considered in our framework belong to the same family of distributions, we first perform a Kolmogorov-Smirnov (KS) test to select genes belonging to the family of ZINB distributions. Genes passing the KS test will be then modeled using GLMs. Model selection is done by calculating the Bayesian Information Criterion (BIC) and likelihood ratio test (LRT) statistic.

NeedsCompilation yes

Imports Matrix, stats, methods, pscl, VGAM, dgof, BiocParallel, MASS, emdbook, magrittr, utils

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Encoding UTF-8

RoxygenNote 7.1.1

URL https://github.com/Malindrie/scShapes

BugReports https://github.com/Malindrie/scShapes/issues

Suggests knitr, rmarkdown, testthat (>= 3.0.0)

VignetteBuilder knitr

Config/testthat/edition 3

biocViews RNASeq, SingleCell, MultipleComparison, GeneExpression
change_shape

Description

This function returns a list of genes changing shape between conditions and the list of genes changing distribution from a unimodal to distribution to a zero-inflated distribution.

Usage

change_shape(shapes_genes)

Arguments

shapes_genes  A dataframe consisting of distributions followed by each gene passing the KS test. Where rows are genes and each column the treatment condition.
filter_counts

Value

A list of two lists with genes changing distribution shape between conditions. The list "All" contains all the genes changing distribution. The list "Uni2ZI" contains the genes changing distribution form a unimodal distribution in one condition to a zero-inflated distribution in another condition.

Description

This function is used to preprocess matrix of read counts to only keep genes with a certain number of nonzero entries.

Usage

filter_counts(counts, perc.zero = 0.1)

Arguments

counts A non-negative integer matrix of scRNA-seq raw read counts. The rows of the matrix are genes and columns are samples/cells.

perc.zero A numeric value between 0 and 1 that represents the proportion of zeros per gene in the processed dataset.

Value

An object of class Matrix with genes removed if they have more than perc.zero zeros.

Examples

# load toy example data
data(scData)

# apply the filter_counts function to filter out genes if they have # more than 10% zero
scData_filt <- filter_counts(scData$counts, perc.zero = 0.1)
### Description

This function is used to fit genes with GLM.

### Usage

```r
fit_models(counts, cexpr, lib.size, formula = NULL, model = NULL, BPPARAM)
```

### Arguments

- **counts**: A non-negative integer matrix of scRNA-seq filtered read counts containing genes belonging to the family of ZINB distributions selected from `ks_test`.
- **cexpr**: A dataframe that contains the covariate values. The rows of the dataframe are the corresponding samples/cells from the counts matrix from `filter_counts`. The cells of the dataframe are the covariates to be included in the GLM.
- **lib.size**: A numeric vector that contains the total number of counts per cell from the counts matrix from `filter_counts`.
- **formula**: A regression formula to fit the covariates in the ZINB GLM.
- **model**: A specific model to fit (1:P, 2:NB, 3:ZIP, 4:ZINB, NULL:All)
- **BPPARAM**: Configuration parameter related to the method of parallel execution. For further information on how to set-up parallel execution refer to `BiocParallel` vignette.

### Value

A list of models fitted by `glm`.

### Examples

```r
data(scData)

# apply the `fit_models` function to subset genes belonging to the family of ZINB distributions, selected from `ks_test` function.

library(BiocParallel)
scData_models <- fit_models(counts=scData$counts, cexpr=scData$covariates, lib.size=scData$lib_size, BPPARAM=bpparam())
```
Description

This function is used to perform the likelihood ratio test on the models chosen based on the BIC values from best_model to check for model adequacy.

Usage

gof_model(lbic, cexpr, lib.size, formula = NULL, BPPARAM)

Arguments

- **lbic**: A list of genes together with filtered read counts based on the selected distribution from best_model. Output from best_model.
- **cexpr**: A dataframe that contains the covariate values. The rows of the dataframe are the corresponding samples/cells from the counts matrix from filter_counts. The cells of the dataframe are the covariates to be included in the GLM.
- **lib.size**: A numeric vector that contains the total number of counts per cell from the counts matrix from filter_counts.
- **formula**: A regression formula to fit the covariates in the ZINB GLM.
- **BPPARAM**: configuration parameter related to the method of parallel execution. For further information on how to set-up parallel execution refer to BiocParallel vignette.

Value

A list of genes with the p-values from performing the GOF tests.

Examples

data(scData)

# apply the gof_model function to perform the likelihood ratio test on the models selected by using the lbic_model function

library(BiocParallel)
scData_models <- fit_models(counts=scData$counts, cexpr=scData$covariates, lib.size=scData$lib_size, BPPARAM=bpparam())
scData_bicvals <- model_bic(scData_models)
scData_least.bic <- lbic_model(scData_bicvals, scData$counts)
s
scData_gof <- gof_model(scData_least.bic, cexpr=scData$covariates, lib.size=scData$lib_size, BPPARAM=bpparam())
ks_sig

Description
This function is used to select genes significant from the ks_test.

Usage
ks_sig(ks.pval.unadj)

Arguments
ks.pval.unadj The output from ks_test which is a list of p-values from the KS test with gene names.

Value
List object containing the significant gene indices from the KS test, their adjusted p-values

Examples
data(scData)

# apply the ks_test function to subset genes belonging to the
# family of ZINB distributions.
library(BiocParallel)
scData_KS <- ks_test(counts=scData$counts, cexpr=scData$covariates, lib.size=scData$lib_size, BPPARAM=bpparam())

# apply the ks_sig function to select genes significant from
# the Kolmogorov Smirnov test.
scData_KS_sig <- ks_sig(scData_KS)

ks_test

Description
This function is used to perform Kolmogorov-Smirnov test on the filtered sparse counts matrix from filter_counts to select genes belonging to the family of ZINB distributions

Usage
ks_test(counts, cexpr, lib.size, formula = NULL, BPPARAM)
**Arguments**

- **counts**: A non-negative integer matrix of scRNA-seq filtered read counts from `filter_counts`. The rows of the matrix are genes and columns are samples/cells.
- **cexpr**: A dataframe that contains the covariate values. The rows of the dataframe are the corresponding samples/cells from the counts matrix from `filter_counts`. The cells of the dataframe are the covariates to be included in the GLM.
- **lib.size**: A numeric vector that contains the total number of counts per cell from the counts matrix from `filter_counts`.
- **formula**: A regression formula to fit the covariates in the ZINB GLM.
- **BPPARAM**: configuration parameter related to the method of parallel execution. For further information on how to set-up parallel execution refer to `BiocParallel` vignette.

**Value**

List object containing the p-values from the KS test.

**Examples**

```r
# load toy example data
data(scData)

# apply the ks_test function to subset genes belonging to the
# family of ZINB distributions.
library(BiocParallel)
scData_KS <- ks_test(counts = scData$counts, cexpr = scData$covariates, lib.size = scData$lib_size, BPPARAM = bpparam())
```

**Description**

This function is used to select the best fit model for each gene based on the least BIC value.

**Usage**

```r
lbic_model(bic.value, counts)
```

**Arguments**

- **bic.value**: A dataframe of BIC values from fitting GLM using error distributions P, NB, ZIP, ZINB; the output from `model_bic`.
- **counts**: A non-negative integer matrix of scRNA-seq filtered read counts containing genes belonging to the family of ZINB distributions selected from `ks_test`. The rows of the matrix are genes and columns are samples/cells.
Value
A list of genes chosen to be following one of the 4 distributions P, NB, ZIP, ZINB based on the least BIC value and the corresponding subset of counts from filter_counts

Examples

data(scData)
# apply the lbic_model function to select the model with the least
# BIC value on the matrix of BIC values obtained after running
# model_bic function.

library(BiocParallel)
scData_models <- fit_models(counts=scData$counts, cexpr=scData$covariates, lib.size=scData$lib_size, BPPARAM=bpparam())

scData_bicvals <- model_bic(scData_models)
scData_least.bic <- lbic_model(scData_bicvals, scData$counts)

Description

Usage

Value
... Reports the logo of the package:scShapes.

Description
This function is used to calculate the Bayesian information criterion of the models fitted in fit_models.

Usage

model_bic
**model_param**

**Arguments**

| fit_list | A list of models fitted from fit_models |

Value

A dataframe containing the BIC values for each distribution type (P, NB, ZIP, ZINB).

**Examples**

```r
data(scData)

# apply the model_bic function to calculate the BIC values on the models
# obtained after running fit_models function.

library(BiocParallel)
scData_models <- fit_models(counts=scData$counts, cexpr=scData$covariates, lib.size=scData$lib_size, BPPARAM=bpparam())
scData_bicvals <- model_bic(scData_models)
```

**Description**

This function returns model parameters based on the best fit distribution as selected by distr_fit and models fitted by fit_models.

**Usage**

```r
model_param(fit.model, gof.res, model = NULL)
```

**Arguments**

| fit.model | A list of models fitted by 'glm' from fit_models. |
| gof.res   | A list of selected model distributions for genes select_model. |
| model     | A specific model to fit (1:P, 2:NB, 3:ZIP, 4:ZINB, NULL:All) |

**Value**

A list of model parameters estimated. Estimated model parameters include mean (for all 4 models), theta (over-dispersion parameter for NB & ZINB models), pi (zero-inflation parameter for ZIP & ZINB models).
Examples

```r
data(scData)

# apply the model_param function to extract the parameters of the best fit
# model obtained by running the select_model function

library(BiocParallel)
sData_models <- fit_models(counts=scData$counts, cexpr=scData$covariates, lib.size=scData$lib_size, 
BPPARAM=bpparam())
sData_bicvals <- model_bic(scData_models)
sData_least.bic <- lbic_model(scData_bicvals, scData$counts)
sData_gof <- gof_model(scData_least.bic, cexpr=scData$covariates, lib.size=scData$lib_size, 
BPPARAM=bpparam())
sData_fit <- select_model(scData_gof)

scData_params <- model_param(scData_models, scData_fit, model=NA)
```

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**scData**  
*Sample data for analysis*

**Description**

Toy example data list of scRNA-seq counts, information on covariates, and library sizes for randomly generated 20 genes to illustrate how to use the functions of the package scShapes

**Usage**

```r
data(scData)
```

**Format**

A list of three lists labeled 'counts', 'covariates', 'lib_size'. 'counts' an RNA-seq counts matrix of 20 genes and 500 cells; 'covariates' a dataframe of covariates corresponding to the RNA-seq counts where rows are cells of the counts matrix; 'lib_size' a numeric vector of library sizes corresponding to the columns of the RNA-seq counts matrix.

**Value**

An RData object

**Examples**

```r
# load toy example data
data(scData)
```
Description

This function is used to select the distribution of best fit for scRNA-seq count data.

Usage

`select_model(lrt.value)`

Arguments

- `lrt.value` A list of genes with the p-values from performing the GOF tests from `gof_model`.

Value

A list of selected model distributions for genes scShapes selects.

Examples

```r
data(scData)

# apply the select_model function to the best fit model from the results of
# the gof_model function

library(BiocParallel)
scData_models <- fit_models(counts=scData$counts, cexpr=scData$covariates, lib.size=scData$lib_size, BPPARAM=bpparam())
scData_bicvals <- model_bic(scData_models)
scData_least.bic <- lbic_model(scData_bicvals, scData$counts)
scData_gof <- gof_model(scData_least.bic, cexpr=scData$covariates, lib.size=scData$lib_size, BPPARAM=bpparam())
scData_fit <- select_model(scData_gof)
```
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