Package ‘switchde’

April 11, 2023

Type Package

Title Switch-like differential expression across single-cell trajectories

Version 1.24.0

Date 2017-10-24

Description Inference and detection of switch-like differential expression across single-cell RNA-seq trajectories.

License GPL (>= 2)

LazyData TRUE

biocViews ImmunoOncology, Software, Transcriptomics, GeneExpression, RNASeq, Regression, DifferentialExpression, SingleCell

Depends R (>= 3.4), SingleCellExperiment

Imports SummarizedExperiment, dplyr, ggplot2, methods, stats

Suggests knitr, rmarkdown, BiocStyle, testthat, numDeriv, tidyr

VignetteBuilder knitr

RoxygenNote 6.0.1

URL `https://github.com/kieranrcampbell/switchde`

BugReports `https://github.com/kieranrcampbell/switchde`

git_url https://git.bioconductor.org/packages/switchde

git_branch RELEASE_3_16

git_last_commit e00371e

git_last_commit_date 2022-11-01

Date/Publication 2023-04-10

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R topics documented:

`example_sigmoid` *Example sigmoid plot*

Description

Plot an example sigmoid function. For demonstration and documentation.

Usage

```
example_sigmoid()
```

Value

An object of class `ggplot`

Examples

```
example_sigmoid()
```

`extract_pars` *Extract parameters from fitted model*

Description

Extract maximum likelihood parameter estimates from a call to `switchde`.

Usage

```
extract_pars(sde, gene)
```

Arguments

`sde`	The `data.frame` returned by `switchde`
`gene`	The gene for which to extract parameters

Value

A vector of length 3 corresonding to the parameters μ_0, k and t_0

Examples

```
data(synth_gex)
data(ex_pseudotime)
sde <- switchde(synth_gex, ex_pseudotime)
pars <- extract_pars(sde, "Gene1")
```

`ex_pseudotime` *Synthetic gene pseudotimes*

Description

A vector with example pseudotimes for the synthetic gene expression data in `example_gex`

Usage

```
ex_pseudotime
```

Format

An object of class `array` of length 100.

Value

A vector of length 100

`fit_nzi_model` *Fit a (non-zero-inflated) model for a single gene*

Description

Fits a sigmoidal expression model for a single gene vector, returning MLE model parameters and p-value.

Usage

```
fit_nzi_model(y, pst)
```

Arguments

`y`	Vector of gene expression values
`pst`	Pseudotime vector, of same length as y

Value

A vector with 5 entries: maximum likelihood estimates for μ_0, k $t0$, σ^2 and a p-value

Examples

```
data(synth_gex)
data(ex_pseudotime)
y <- synth_gex[1, ]
fit <- fit_nzi_model(y, ex_pseudotime)
```

`fit_zi_model` *Fit a zero-inflated model for a single gene*

Description

Fits a zero-inflated sigmoidal model for a single gene vector, returning MLE model parameters and p-value.

Usage

```
fit_zi_model(y, pst, maxiter = 10000, log_lik_tol = 0.001,
  verbose = FALSE)
```

Arguments

`y`	Vector of gene expression values
`pst`	Pseudotime vector, of same length as y
`maxiter`	Maximum number of iterations for EM algorithm if zero inflation enabled. Default 100
`log_lik_tol`	If the change in the log-likelihood falls below this for zero inflated EM the algorithm is assumed to have converged
`verbose`	Print convergence update for EM algorithm

Value

A vector with 6 entries: maximum likelihood estimates for μ_0, k $t0$, λ, σ^2 and a p-value

Examples

```
data(synth_gex)
data(ex_pseudotime)
y <- synth_gex[1, ]
fit <- fit_zi_model(y, ex_pseudotime)
```

`switchde` *Switch-like model fitting and differential expression test*

Description

Fit sigmoidal differential expression models to gene expression across pseudotime. Parameter estimates are returned along with a p-value for switch-like differential expression over a null model (constant expression).

Usage

```
switchde(object, pseudotime = NULL, zero_inflated = FALSE,
  lower_threshold = 0.01, maxiter = 1000, log_lik_tol = 0.01,
  verbose = FALSE, sce_assay = "exprs")
```

Arguments

`object`	Gene expression data that is either • A vector of length number of cells for a single gene • A matrix of dimension number of genes x number of cells • An object of class `SingleCellExperiment` from package SingleCellExperiment
`pseudotime`	A pseudotime vector with a pseudotime corresponding to every cell. Can be `NULL` if object is of class `SCESet` and `colData(sce)$pseudotime` is defined.
`zero_inflated`	Logical. Should zero inflation be implemented? Default `FALSE`
`lower_threshold`	The minimum threshold below which to set expression to zero to avoid numerical issues. Default is 0.01
`maxiter`	Maximum number of iterations for EM algorithm if zero inflation enabled. Default 100
`log_lik_tol`	If the change in the log-likelihood falls below this for zero inflated EM the algorithm is assumed to have converged
`verbose`	Print convergence update for EM algorithm
`sce_assay`	The assay from the `SingleCellExperiment` to be used as expression, defaulting to "exprs"

Value

A matrix where each column corresponds to a gene, the first row is the p-value for that gene and subsequent rows are model parameters.

Examples

```
data(synth_gex)
data(ex_pseudotime)
sde <- switchde(synth_gex, ex_pseudotime)
```

`switchplot` *Plot gene behaviour*

Description

Plot gene behaviour and MLE sigmoid as a function of pseudotime.

Usage

```
switchplot(x, pseudotime, pars)
```

Arguments

`x`	Gene expression vector
`pseudotime`	Pseudotime vector (of same length as x)
`pars`	Fitted model parameters

Details

This plots expression of a single gene. Fitted model parameters can either be specified manually or can be extracted from the `data.frame` returned by `switchde` using the function `extract_pars`.

Value

A `ggplot2` plot of gene expression and MLE sigmoid

Examples

```
data(synth_gex)
data(ex_pseudotime)
sde <- switchde(synth_gex, ex_pseudotime)
switchplot(synth_gex[1, ], ex_pseudotime, extract_pars(sde, "Gene1"))
```

`synth_gex` *Synthetic gene expression matrix*

Description

A matrix containing some synthetic gene expression data for 100 cells and 12 genes

Usage

```
synth_gex
```

Format

An object of class `matrix` with 12 rows and 100 columns.

Value

A 12 by 100 matrix

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