Package: switchde (via r-universe)

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Type Package

Title Switch-like differential expression across single-cell trajectories

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

License GPL (>= 2)

LazyData TRUE

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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

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Contents

ex_pseudotime 2
example_sigmoid 2
extract_pars 3
fit_nzi_model 3
fit_zi_model 4
switchde 5
switchplot 6
synth_gex 6

Index **8**

`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

`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")
```

`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

Index

∗ **datasets**
ex_pseudotime, 2
synth_gex, 6

ex_pseudotime, 2
example_sigmoid, 2
extract_pars, 3

fit_nzi_model, 3
fit_zi_model, 4

switchde, 5
switchplot, 6
synth_gex, 6