Package ‘switchde’

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Description Inference and detection of switch-like differential expression across single-cell RNA-seq trajectories.
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VignetteBuilder knitr
RoxygenNote 5.0.1
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BugReports https://github.com/kieranrcampbell/switchde
NeedsCompilation no
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**example_sigmoid**  
*Example sigmoid plot*

**Description**
Plot an example sigmoid function. For demonstration and documentation.

**Usage**
```r
example_sigmoid()
```

**Value**
An object of class ggplot

**Examples**
```r
example_sigmoid()
```

---

**extract_pars**  
*Extract parameters from fitted model*

**Description**
Extract maximum likelihood parameter estimates from a call to switchde.

**Usage**
```r
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 corresponding to the parameters $\mu_0$, $k$ and $t_0$

**Examples**
```r
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 $\mu_0$, $k_0$, $\sigma^2$ and a p-value

**Examples**

```r
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 = 1000, log_lik_tol = 0.001, verbose = FALSE)

Arguments

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

Value

A vector with 6 entries: maximum likelihood estimates for $\mu_0$, $k0$, $\lambda$, $\sigma^2$ 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 = 0.001, verbose = FALSE)
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 SCESet from package scater

pseudotime: A pseudotime vector with a pseudotime corresponding to every cell. Can be NULL if object is of class SCESet and pData(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

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(x, pseudotime, pars)

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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