Package ‘switchde’

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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()

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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 corresponding to the parameters $\mu_0$, $k$ 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 $\mu_0$, $k_0$, $\sigma^2$ 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

```r
fit_zi_model(y, pst, maxiter = 1000, 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 $\mu_0$, $k0$, $\lambda$, $\sigma^2$ and a p-value

#### Examples

```r
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

```r
switchde(object, pseudotime = NULL, zero_inflated = FALSE, lower_threshold = 0.01, maxiter = 1000, log_lik_tol = 0.001, verbose = FALSE)
```
switchplot

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)

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"))

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**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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