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()

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 $\mu_0$, $k0$, $\sigma^2$ 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 = 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 $\mu_0, k t 0, \lambda, \sigma^2$ 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 = 0.01, 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**

```r
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**

```r
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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