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 $\mu_0$, $k_0$, $\sigma^2$ 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

- **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 $\mu_0$, $k_0$, $\lambda$, $\sigma^2$ 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)
**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(pseudotime, pars)
```

**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"))

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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