Package ‘switchde’

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```r
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Description

A vector with example pseudotimes for the synthetic gene expression data in example_gex

Usage

```r
ex_pseudotime
```

Format

An object of class `array` of length 100.

Value

A vector of length 100

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Description

Plot an example sigmoid function. For demonstration and documentation.

Usage

```r
example_sigmoid()
```

Value

An object of class `ggplot`
**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")
```

**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**  
```r
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 $\mu_0$, $k t0$, $\sigma^2$ and a p-value

Examples

data(synth_gex)
data(ex_pseudotime)
y <- synth_gex[1,]
fit <- fit_zi_model(y, ex_pseudotime)

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 $\mu_0$, $k t0$, $\lambda$, $\sigma^2$ and a p-value

Examples

data(synth_gex)
data(ex_pseudotime)
y <- synth_gex[1,]
fit <- fit_zi_model(y, ex_pseudotime)
**sanitise_inputs**

**Sanitise inputs**

**Description**
Sanitise inputs

**Usage**
`sanitise_inputs(object, pseudotime, lower_threshold, zero_inflated, sce_assay)`

**Arguments**
- **object**
  The object passed at the entry point (either a SCESet or gene expression matrix)
- **pseudotime**
  A pseudotime vector
- **lower_threshold**
  The minimum threshold below which to set expression to zero to avoid numerical issues. Default is 0.01
- **zero_inflated**
  Logical. Should zero inflation be implemented? Default FALSE
- **sce_assay**
  The assay from the SingleCellExperiment to be used as expression, defaulting to "exprs"

**Value**
A list with two entries: a gene expression matrix $X$ and a pseudotime vector $\text{pst}$.

---

**sigmoid**

*Calculate the mean vector given parameters and pseudotimes (mu0 formulation)*

**Description**
This function (common to all models) calculates the sigmoidal mean vector given the parameters and factor of pseudotimes

**Usage**
`sigmoid(pst, params)`

**Arguments**
- **pst**
  Vector of pseudotimes
- **params**
  Vector of length 3 with entries mu_0, k, t0

**Value**
Mean sigmoidal vector
**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, 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**

```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
switchplot(x, pseudotime, pars)

Arguments
xGene 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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