# Package ‘switchde’

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**Type** Package

**Title** Switch-like differential expression across single-cell trajectories

**Version** 1.0.0

**Date** 2016-10-7

**Description** Inference and detection of switch-like differential expression across single-cell RNA-seq trajectories.

**License** GPL (>= 2)

**LazyData** TRUE

**biocViews** Software, Transcriptomics, GeneExpression, RNASeq, Regression, DifferentialExpression

**Depends** R (>= 3.3)

**Imports** Biobase, dplyr, ggplot2, methods, stats

**Suggests** knitr, rmarkdown, BiocStyle, testthat, numDeriv, tidyR, scater

**VignetteBuilder** knitr

**RoxygenNote** 5.0.1

**URL** https://github.com/kieranrcampbell/switchde

**BugReports** https://github.com/kieranrcampbell/switchde

**NeedsCompilation** no

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example_sigmoid

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**

```r
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**

```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 $\mu_0$, $k_0$, $\sigma^2$ 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 $\mu_0$, $k_0$, $\lambda$, $\sigma^2$ 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 = 0.001, 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)

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"))

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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