

# Package ‘switchde’

September 20, 2025

**Type** Package

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

**Version** 1.35.0

**Date** 2017-10-24

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

**License** GPL (>= 2)

**LazyData** TRUE

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

**Depends** R (>= 3.4), SingleCellExperiment

**Imports** SummarizedExperiment, dplyr, ggplot2, methods, stats

**Suggests** knitr, rmarkdown, BiocStyle, testthat, numDeriv, tidyr

**VignetteBuilder** knitr

**RoxygenNote** 6.0.1

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

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

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|                 |                             |
|-----------------|-----------------------------|
| example_sigmoid | <i>Example sigmoid plot</i> |
|-----------------|-----------------------------|

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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 | <i>Extract parameters from fitted model</i> |
|--------------|---------------------------------------------|

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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")
```

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|               |                                   |
|---------------|-----------------------------------|
| ex_pseudotime | <i>Synthetic gene pseudotimes</i> |
|---------------|-----------------------------------|

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**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

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|               |                                                          |
|---------------|----------------------------------------------------------|
| fit_nzi_model | <i>Fit a (non-zero-inflated) model for a single gene</i> |
|---------------|----------------------------------------------------------|

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**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  $\mu_0$ ,  $k$ ,  $t_0$ ,  $\sigma^2$  and a p-value

**Examples**

```
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 = 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**

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

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|                 |                        |
|-----------------|------------------------|
| sanitise_inputs | <i>Sanitise inputs</i> |
|-----------------|------------------------|

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**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  $pst$ .

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|         |                                                                                     |
|---------|-------------------------------------------------------------------------------------|
| sigmoid | <i>Calculate the mean vector given parameters and pseudotimes (mu0 formulation)</i> |
|---------|-------------------------------------------------------------------------------------|

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**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 $\mu_0$ , $k$ , $\tau_0$ |

**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**

```
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 <ul style="list-style-type: none"> <li>• A vector of length number of cells for a single gene</li> <li>• A matrix of dimension number of genes x number of cells</li> <li>• An object of class SingleCellExperiment from package SingleCellExperiment</li> </ul> |
| 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**

```
data(synth_gex)
data(ex_pseudotime)
sde <- switchde(synth_gex, ex_pseudotime)
```

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|            |                            |
|------------|----------------------------|
| switchplot | <i>Plot gene behaviour</i> |
|------------|----------------------------|

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**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 | <i>Synthetic gene expression matrix</i> |
|-----------|-----------------------------------------|

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**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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