

# Package ‘switchde’

May 26, 2026

**Type** Package

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

**Version** 1.39.0

**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, tidy

**VignetteBuilder** knitr

**RoxygenNote** 6.0.1

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

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

**git\_url** <https://git.bioconductor.org/packages/switchde>

**git\_branch** devel

**git\_last\_commit** 8527700

**git\_last\_commit\_date** 2026-04-28

**Repository** Bioconductor 3.24

**Date/Publication** 2026-05-25

**Author** Kieran Campbell [aut, cre]

**Maintainer** Kieran Campbell <kieranrcampbell@gmail.com>

## Contents

|                           |   |
|---------------------------|---|
| example_sigmoid . . . . . | 2 |
| extract_pars . . . . .    | 2 |
| ex_pseudotime . . . . .   | 3 |
| fit_nzi_model . . . . .   | 3 |
| fit_zi_model . . . . .    | 4 |
| sanitise_inputs . . . . . | 5 |
| sigmoid . . . . .         | 5 |
| switchde . . . . .        | 6 |
| switchplot . . . . .      | 7 |
| synth_gex . . . . .       | 7 |

|              |          |
|--------------|----------|
| <b>Index</b> | <b>8</b> |
|--------------|----------|

---

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

---

### Description

Plot an example sigmoid function. For demonstration and documentation.

### Usage

```
example_sigmoid()
```

### Value

An object of class `ggplot`

### Examples

```
example_sigmoid()
```

---

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

---

### Description

Extract maximum likelihood parameter estimates from a call to `switchde`.

### Usage

```
extract_pars(sde, gene)
```

### Arguments

|      |  |
|------|--|
| sde  | The data.frame returned by <code>switchde</code> |
| 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 | <i>Synthetic gene pseudotimes</i> |
|---------------|-----------------------------------|

---

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

---

**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**

|                  |   |
|------------------|---|
| <code>y</code>   | Vector of gene expression values                    |
| <code>pst</code> | Pseudotime vector, of same length as <code>y</code> |

**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 | <i>Fit a zero-inflated model for a single gene</i> |
|--------------|--|

---

**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)
```

---

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

---

**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  $pst$ .

---

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

---

**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 $\mu_0$ , $k$ , $t_0$ |

**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)
```

---

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

---

**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"))
```

---

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

---

**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

# Index

## \* datasets

ex\_pseudotime, 3

synth\_gex, 7

## \* internal

sanitise\_inputs, 5

sigmoid, 5

ex\_pseudotime, 3

example\_sigmoid, 2

extract\_pars, 2

fit\_nzi\_model, 3

fit\_zi\_model, 4

sanitise\_inputs, 5

sigmoid, 5

switchde, 6

switchplot, 7

synth\_gex, 7