Package ‘switchde’

February 3, 2024

Type Package

Title Switch-like differential expression across single-cell trajectories

Version 1.28.0

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

git_url https://git.bioconductor.org/packages/switchde

git_branch RELEASE_3_18

git_last_commit 61db86f

git_last_commit_date 2023-10-24

Repository Bioconductor 3.18

Date/Publication 2024-02-02

Author Kieran Campbell [aut, cre]

Maintainer Kieran Campbell <kieranrcampbell@gmail.com>
R topics documented:

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

Index

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)
**ex_pseudotime**

**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")
```

---

**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

data(synth_gex)
data(ex_pseudotime)
y <- synth_gex[1, ]
fit <- fit_zi_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 $\mu_0$, $k_0$, $\lambda$, $\sigma^2$ and a p-value

Examples

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

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
ces assays
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

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**
- `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
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