Package ‘SPEM’

January 28, 2016

Type Package

Title S-system parameter estimation method

Depends R (>= 2.15.1), Rsolnp, Biobase, methods

Version 1.10.0

Date 2013-1-12

Author Xinyi YANG Developer, Jennifer E. DENT Developer and Christine NARDINI Supervisor

Maintainer Xinyi YANG <yangxinyi@picb.ac.cn>

Description This package can optimize the parameter in S-system models given time series data

License GPL-2

LazyLoad yes

biocViews Network, NetworkInference, Software

NeedsCompilation no

R topics documented:

SPEM-package ................................................................. 2
row_optimize .............................................................. 2
sos ........................................................................... 4
SPEM ................................................................. 5
s_diff ................................................................. 6

Index 8
Description

The function in this package allows for the computation of parameters in the n-gene S-system from time series data.

Details

Package: SPEM
Type: Package
Version: 1.0
Date: 2013-01-13
License: GPL-2
LazyLoad: yes

Author(s)

Yang, X-Y, Dent, J. E. and Nardini, C.
Maintainer: Xinyi Yang <yangxinyi@picb.ac.cn>

Description

This function calculates parameters for a single row in the expression data. If a large-size dataset will be calculated, this function is recommended.

Usage

## S4 method for signature 'ExpressionSet'
row_optimize(TS_eSet, S, beta, sparsity = 0.2, lbH = -3, ubH = 3, lbB = 0, ubB = 10)

Arguments

TS_eSet Time series data in ExpressionSet class assayData: Matrix with n metabolite in row and m time points in column. phenoData: Dataframe includes label "time", which represents the time points.
row_optimize

Slope of the row you want to calculated. You can either input a vector with length equal to the rows of assayData of TS_eSet, or use s_diff function in this package to calculate it.

beta Initial beta.

sparsity A threshold used to control the sparsity of reconstructed matrix. Values whose absolute value smaller than sparsity will be set to zero.

lbh Lower boundary value of h.

ubh Upper boundary value of h.

lbb Lower boundary value of beta.

ubb Upper boundary value of beta.

Details

In this SPEM package, we aim to reconstruct gene networks from time-series expression data using the S-system model. The input dataset should be as an ExpressionSet data container, describing, in assayData, expression data for n genes (rows) and m time points (columns), along with a vector of length m, which records the exact values of time points, thus showing the sample intervals in phenoData. SPEM will calculate the parameters alpha, g, beta and h of the S-system function set that best fits the dataset.

In this function, user can calculate one row at a time. This function offers a parallel calculation option for users.

Value

This function return a vector bind with c(alpha, $g_i$, beta, $h_i$, Initial Beta, error).

Methods

signature(TS_eSet = "ExpressionSet") This method is created for the function row_optimize.

Author(s)

Yang, X-Y, Dent, Jennifer E. and Nardini, C.

Examples

Load the SOS pathway data

data(sos)

Set Slope and Initial Beta

Slope<- s_diff(sos)
S<- Slope[1,] #S is the slope of the row you want to calculate. You can either input a vector yourself.
beta<- runif(n=1,min=1,max=10)

Set parameters

sparsity<- 0.2
lbh<- -3
Description

In this package we offer the SOS data obtained from Uri Alon’s lab (http://www.weizmann.ac.il/mcb/UriAlon/). SOS response is a general DNA repair system in bacteria which allows survival after DNA damage. This SOS dataset is taken from real experiment expression data in *Escherichia coli*. It contains 8 genes under Experiment 3 (UV light intensities, 4:20 Jm^(-2)).

Usage

data(sos)

Format

sos.data is time series gene expression value data in ExpressionSet Class. assayData: Matrix with expression values of 8 genes in SOS pathway of *Escherichia coli*. These expression levels are observed at 50 time points. phenoData: Sample data.frame includes label "time", which represents the value of time points.

References


Examples

data(sos)
Description

This function calculates parameters of S-system from entire time series matrix.

Usage

```r
## S4 method for signature 'ExpressionSet'
SPEM(TS_eSet, n = 3, sparsity = 0.2, lbH = -3, ubH = 3, lbB = 0, ubB = 10)
```

Arguments

- `TS_eSet`: Time series data in ExpressionSet class. assayData: Matrix with n metabolite in row and m time points in column. phenoData: phenoData type. The sample data.frame should include the label "time", which represents the values of time points.
- `n`: Positive integer, SPEM will guess initial beta n times.
- `sparsity`: A positive number. In order to force the interaction matrix to be sparse, interactions with absolute value smaller than "sparsity" will be set to zero.
- `lbH`: Lower boundary value of h.
- `ubH`: Upper boundary value of h.
- `lbB`: Lower boundary value of beta.
- `ubB`: Upper boundary value of beta.

Details

In this SPEM package, we aim to reconstruct gene networks from time-series expression data using the S-system model. The input dataset should be as an ExpressionSet data container, describing, in assayData, expression data for n genes (rows) and m time points (columns), along with a vector of length m, which records the exact values of time points, thus showing the sample intervals in phenoData. SPEM will calculate the parameters alpha, G, beta and H of the S-system function set that best fits the dataset.

Value

- `alpha, G, beta, H`: Parameters of the reconstructed S-system.
- `IniBeta`: Guess of the IniBeta value (Picked randomly by SPEM itself).
- `error`: Regression error.

Methods

- `signature(TS_eSet = "ExpressionSet")`: This method is created for function SPEM.
### s_diff

#### Calculate slopes from time points and time series matrix.

**Description**

This function allows users to calculate slopes from time points and time series data.

**Usage**

```r
## S4 method for signature 'ExpressionSet'
s_diff(TS_eSet)
```

**Arguments**

- `TS_eSet` Time series data in ExpressionSet class. assayData: Matrix with n metabolite in row and m time points in column. phenoData: phenoData type. The sample data.frame should include the label "time", which represents the values of time points.
Value

This function directly return a slope matrix.

Methods

signature(TS_eSet = "ExpressionSet") This method is created for function `s_diff`.

Author(s)

Yang, X-Y, Dent, Jennifer E. and Nardini, C.

Examples

```
# Load the SOS pathway data
data(sos)

# Calculate results
Slope <- s_diff(sos)
```
Index

*Topic **Bioinformatics**, **NetworkAnalysis**, **NetworkInference**, **Software**
  SPEM, 5
*Topic **Datasets**
  sos, 4
*Topic **Package**
  SPEM-package, 2
*Topic **Reconstruction**
  row_optimize, 2
*Topic **Slope**
  s_diff, 6
  row_optimize, 2
  row_optimize, ExpressionSet-method
    (row_optimize), 2
  s_diff, 6
  s_diff, ExpressionSet-method (s_diff), 6
  sos, 4
  SPEM, 5
  SPEM, ExpressionSet-method (SPEM), 5
  SPEM-package, 2