

# Package ‘LEAP’

October 12, 2022

**Type** Package

**Title** Constructing Gene Co-Expression Networks for Single-Cell  
RNA-Sequencing Data Using Pseudotime Ordering

**Version** 0.2

**Date** 2016-09-09

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**Maintainer** Alicia T. Specht <aspect2@nd.edu>

**Suggests** ggplot2

**Description** Advances in sequencing technology now allow researchers to capture the expression profiles of individual cells. Several algorithms have been developed to attempt to account for these effects by determining a cell's so-called ‘pseudotime’, or relative biological state of transition. By applying these algorithms to single-cell sequencing data, we can sort cells into their pseudotemporal ordering based on gene expression. LEAP (Lag-based Expression Association for Pseudotime-series) then applies a time-series inspired lag-based correlation analysis to reveal linearly dependent genetic associations.

**License** GPL-2

**LazyData** yes

**NeedsCompilation** no

**Repository** CRAN

**Date/Publication** 2016-09-13 21:19:05

## R topics documented:

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|              |   |
|--------------|---|
| LEAP-package | <i>Constructing Gene Co-Expression Networks for Single-Cell RNA-Sequencing Data Using Pseudotime Ordering</i> |
|--------------|---|

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## Description

Advances in sequencing technology now allow researchers to capture the expression profiles of individual cells. Several algorithms have been developed to attempt to account for these effects by determining a cell's so-called 'pseudotime', or relative biological state of transition. By applying these algorithms to single-cell sequencing data, we can sort cells into their pseudotemporal ordering based on gene expression. LEAP (Lag-based Expression Association for Pseudotime-series) then applies a time-series inspired lag-based correlation analysis to reveal linearly dependent genetic associations.

## Details

The DESCRIPTION file:

```
Package:      LEAP
Type:        Package
Title:       Constructing Gene Co-Expression Networks for Single-Cell RNA-Sequencing Data Using Pseudotime Ordering
Version:     0.2
Date:       2016-09-09
Author:      Alicia T. Specht and Jun Li
Maintainer:  Alicia T. Specht <aspect2@nd.edu>
Suggests:   ggplot2
Description: Advances in sequencing technology now allow researchers to capture the expression profiles of individual cells
License:    GPL-2
LazyData:   yes
```

Index of help topics:

|               |  |
|---------------|--|
| LEAP-package  | Constructing Gene Co-Expression Networks for Single-Cell RNA-Sequencing Data Using Pseudotime Ordering   |
| MAC_counter   | Function to perform lag-based correlation analysis of single-cell sequencing data, sorted by pseudotime. |
| MAC_example   | Numerical matrix   |
| MAC_lags      | Internal function used by MAC_counter and MAC_perm   |
| MAC_perm      | Function to perform a permutation analysis to determine a cutoff for significant MAC values.             |
| MAC_symmetric | Numeric data frame   |
| example_data  | Numeric data frame of example data   |

|              |   |
|--------------|---|
| lag_example  | Integer data frame  |
| perm_example | The resulting data output from applying<br>MAC_perm() to example_data |

Further information is available in the following vignettes:

LEAP\_Vignette    LEAP\_Vignette (source, pdf)

~~ An overview of how to use the package, including the most important functions ~~

### Author(s)

Alicia T. Specht and Jun Li

Maintainer: Alicia T. Specht <aspect2@nd.edu>

### References

Shalek AK, Satija R., Shuga J., Trombetta J.J. et al. (2014) Single-cell RNA-seq reveals dynamic paracrine control of cellular variation. *Nature*, 510(7505), 363-369. <http://www.ncbi.nlm.nih.gov/pmc/articles/PMC4193940>.

### Examples

```
## Not run: MAC_results = MAC_counter(data=example_data)

## Not run: MAC_perm(data=example_data, MACs_observ=MAC_example)
```

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|              |   |
|--------------|---|
| example_data | <i>Numeric data frame of example data</i> |
|--------------|---|

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### Description

Contains 20 genes across 564 single-cell sequencing experiments, sorted by pseudotime using the package Monocle.

### Usage

```
data("example_data")
```

### Format

A data frame with 20 observations on 564 variables.

### Details

See vignette for more details.

**Source**

Shalek AK, Satija R., Shuga J., Trombetta J.J. et al. (2014) Single-cell RNA-seq reveals dynamic paracrine control of cellular variation. Nature, 510(7505), 363-369. <http://www.ncbi.nlm.nih.gov/pmc/articles/PMC4193940>.

**Examples**

```
data(example_data)
```

---

|             |                           |
|-------------|---------------------------|
| lag_example | <i>Integer data frame</i> |
|-------------|---------------------------|

---

**Description**

Contains the resulting lag matrix from applying MAC\_counter() to example\_data

**Usage**

```
data("lag_example")
```

**Format**

A data frame with 20 observations on 20 variables.

**Details**

See vignette for more details.

**Examples**

```
data(lag_example)
```

---

|             |   |
|-------------|---|
| MAC_counter | <i>Function to perform lag-based correlation analysis of single-cell sequencing data, sorted by pseudotime.</i> |
|-------------|---|

---

**Description**

See vignette for more details.

**Usage**

```
MAC_counter(data, max_lag_prop = 1/3, MAC_cutoff = 0.2,
file_name = F, lag_matrix = T, symmetric = F)
```

**Arguments**

|                           |  |
|---------------------------|--|
| <code>data</code>         | A data matrix for which the rows are genes and the columns are experiments, sorted by their pseudotime.  |
| <code>max_lag_prop</code> | The largest proportion of your experiments that you want the size of the lag to be. Recommended not to go beyond 1/3. Default value is 1/3.  |
| <code>MAC_cutoff</code>   | The lowest MAC desired to be shown in results. Default value is 0.2.   |
| <code>file_name</code>    | The name to be used for resulting .csv files. I.e., using <code>file_name="mine"</code> would create the file "MAC_mine.csv" and "lag_mine.csv"                                    |
| <code>lag_matrix</code>   | Logical. TRUE indicates that the resulting matrix of lags should be saved to a csv. Default value is TRUE.   |
| <code>symmetric</code>    | Logical. TRUE indicates that a symmetric matrix is required for output MAC .csv file. Results in the absolute maximum value for each pair (i,j) and (j,i). Default value is FALSE. |

**Details**

See vignette for more details.

**Value**

Returns a dataset with four columns: Row gene index and Column gene index correspond to the indices for the gene pair (i,j), Correlation is the maximum absolute correlation (MAC) achieved for the pair, and Lag is the lag at which the MAC occurred.

**Examples**

```
x <- matrix(rnorm(6),2,3)
y <- MAC_counter(x)

## Not run: MAC_results = MAC_counter(data=example_data)
```

---

MAC\_example

*Numerical matrix*

---

**Description**

Contains the matrix of MACs that result from applying `MAC_counter()` to `example_data`

**Usage**

```
data("MAC_example")
```

**Format**

The format is: num [1:20, 1:20] NA 0.141 0.418 0.253 0.164 ...

**Details**

See vignette for more details.

**Examples**

```
data(MAC_example)
```

---

MAC\_lags

*Internal function used by MAC\_counter and MAC\_perm*

---

**Description**

Performs the lag-based correlation analysis

**Usage**

```
MAC_lags(data, max_lag_prop = 1/3, symmetric = F)
```

**Arguments**

|                           |  |
|---------------------------|--|
| <code>data</code>         | Data being passed to the function  |
| <code>max_lag_prop</code> | The largest proportion of your experiments that you want the size of the lag to be. Recommended not to go beyond 1/3. Default value is 1/3.  |
| <code>symmetric</code>    | Logical. TRUE indicates that a symmetric matrix is required for output MAC .csv file. Results in the absolute maximum value for each pair (i,j) and (j,i). Default value is FALSE. |

**Details**

See vignette for more details.

**Value**

Returns MAC and associated lag matrices.

**Examples**

```
x <- matrix(rnorm(6),2,3)
y <- MAC_lags(x)

## Not run: MAC_results = MAC_lags(data=example_data, max_lag_prop=1/3, symmetric=F)
```

---

|          |   |
|----------|---|
| MAC_perm | <i>Function to perform a permutation analysis to determine a cutoff for significant MAC values.</i> |
|----------|---|

---

## Description

See vignette for more details.

## Usage

```
MAC_perm(data, MACs_observ, num_perms = 100, max_lag_prop = 1/3,  
FDR_cutoffs = 101, perm_file_name = F)
```

## Arguments

|                |   |
|----------------|---|
| data           | A data matrix for which the rows are genes and the columns are experiments, sorted by their pseudotime.                                     |
| MACs_observ    | The resulting matrix of MACs from running MAC_counter on the dataset  |
| num_perms      | The number of permutations to be performed. Default is 100.   |
| max_lag_prop   | The largest proportion of your experiments that you want the size of the lag to be. Recommended not to go beyond 1/3. Default value is 1/3. |
| FDR_cutoffs    | The number of cutoffs between 0 and 1 to use for FDR analysis. Default value is 101, resulting in 0,0.01,0.02,....,0.98,0.99,1.             |
| perm_file_name | The name to be used for resulting .csv file. I.e., using perm_file_name="mine" would create the file "perm_mine.csv"                        |

## Details

See vignette for more details.

## Value

Returns a dataset with four columns: cors are the correlation cutoffs, MACs\_observ are the number of observed correlations at that cutoff, MACs\_ave\_perm are the average number observed in the permuted datasets at that cutoff, and fdr is the false discovery rate (FDR) observed at that cutoff.

## Examples

```
x <- matrix(rnorm(6),2,3)  
cor <- cor(x)  
y <- MAC_perm(x, cor)  
  
## Not run: MAC_perm(data=example_data, MACs_observ=MAC_example)
```

---

|               |                           |
|---------------|---------------------------|
| MAC_symmetric | <i>Numeric data frame</i> |
|---------------|---------------------------|

---

**Description**

Contains the results of applying `MAC_counter(symmetric=T)` to `example_data`

**Usage**

```
data("MAC_symmetric")
```

**Format**

A data frame with 20 observations on 20 variables.

**Examples**

```
data(MAC_symmetric)
```

---

|              |   |
|--------------|---|
| perm_example | <i>The resulting data output from applying <code>MAC_perm()</code> to <code>example_data</code></i> |
|--------------|---|

---

**Description**

101 observations at correlation cutoffs, from 0 to 1, of the four variables `Cors`, `MACs_observed`, `MACs_ave_perm`, and `fdr`.

**Usage**

```
data("perm_example")
```

**Format**

A data frame with 101 observations on 4 variables.

**Details**

See vignette for more details

**Examples**

```
data(perm_example)
```



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