

# Package: lglasso (via r-universe)

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**Type** Package

**Title** Longitudinal Graphical Lasso

**Version** 0.1.0

**Description** For high-dimensional correlated observations, this package carries out the L<sub>1</sub> penalized maximum likelihood estimation of the precision matrix (network) and the correlation parameters. The correlated data can be longitudinal data (may be irregularly spaced) with dampening correlation or clustered data with uniform correlation. For the details of the algorithms, please see the paper Jie Zhou et al. Identifying Microbial Interaction Networks Based on Irregularly Spaced Longitudinal 16S rRNA sequence data  
[<doi:10.1101/2021.11.26.470159>](https://doi.org/10.1101/2021.11.26.470159).

**License** GPL-3

**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 7.3.1

**URL** <https://github.com/jiezhou-2/lglasso>

**Suggests** knitr, rmarkdown

**Imports** stats, glasso

**Depends** R (>= 2.10)

**NeedsCompilation** no

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**Repository** <https://jiezou-2.r-universe.dev>

**RemoteUrl** <https://github.com/jiezhou-2/lglasso>

**RemoteRef** HEAD

**RemoteSha** 321ca35d14d751d5ecef3bf2421538c68bd178da

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lglasso                    *Graphical Lasso for Longitudinal Data*

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### Description

This function implements the L<sub>1</sub> penalized maximum likelihood estimation for precision matrix (network) based on correlated data, e.g., irregularly spaced longitudinal data. It can be regarded as an extension of the package **glasso** (Friedman,Hastie and Tibshirani, 2008) which aims to find the sparse estimate of the network from independent continuous data.

### Usage

```
lglasso(
  data,
  x = NULL,
  rho,
  heter = TRUE,
  type = 1,
  tol = 0.01,
  lower = 0.01,
  upper = 10
)
```

### Arguments

<b>data</b>	Data matrix in which the first column is subject id, the second column is time points of observations for temporal data or site id for spatial data. Columns 3 to (p+2) is the observations for p variables.
<b>rho</b>	Tuning parameter used in L <sub>1</sub> penalty
<b>heter</b>	Binary variable TRUE or FALSE, indicating heterogeneous model or homogeneous model is fitted. In heterogeneous model, subjects are allowed to have his/her own temporal correlation parameter <b>tau_i</b> ; while in homogeneous model, all the subjects are assumed to share the same temporal correlation parameter,i.e., <b>tau_1=tau_2=...tau_m</b> .
<b>type</b>	A positive number which specify the correlation function. The general form of correlation function is given by <b>exp(tau t_i-t_j ^type)</b> . in which <b>type=0</b> can be used for spatial correlation while <b>type&gt;0</b> are used for temporal correlation. For latter, the default value is set to be <b>type=1</b> .

<b>tolerance</b>	Threshold for convergence. Default value is <code>1e-2</code> . Iterations stop when maximum absolute difference between consecutive estimates of parameter change is less than <code>tolerance</code> .
<b>lower</b>	Lower bound for predicts of correlation parameter <code>tau</code> . Default value is <code>1e-2</code> . The estimate of <code>tau(alpha)</code> will be searched in the interval <code>[lower,upper]</code> , where parameter <code>upper</code> is explained in the following.
<b>upper</b>	Upper bound for predicts of correlation parameter <code>tau</code> .

**Value**

If `heter=TRUE`, then a list with three components is returned which are respectively the estimate of parameter `alpha` in exponent distribution, correlation parameter `tau` and precision matrix `omega`. If `heter=FALSE`, then a list with two components is returned which are respectively the estimate of correlation parameter `tau` and precision matrix `omega`.

**Author(s)**

Jie Zhou

**References**

Jie Zhou, Jiang Gui, Weston D.Viles, Anne G.Hoen Identifying Microbial Interaction Networks Based on Irregularly Spaced Longitudinal 16S rRNA sequence data. bioRxiv 2021.11.26.470159; doi: <https://doi.org/10.1101/2021.11.26.470159>

Friedman J, Tibshirani TH and R. Glasso: Graphical Lasso: Estimation of Gaussian Graphical Models.; 2019. Accessed November 28, 2021. <https://CRAN.R-project.org/package=glasso>

Friedman J, Hastie T, Tibshirani TH, Sparse inverse covariance estimation with the graphical lasso, Biostatistics, Volume 9, Issue 3, July 2008, Pages 432â 441, <https://doi.org/10.1093/biostatistics/kxm045>

**mle**

*Maximum Likelihood Estimate of Precision Matrix and Correlation Parameters for Given Network*

**Description**

Maximum Likelihood Estimate of Precision Matrix and Correlation Parameters for Given Network

**Usage**

```
mle(
  data,
  x = NULL,
  network,
  heter = TRUE,
  type = 1,
  tol = 0.01,
```

```

lower = 0.01,
upper = 10
)

```

### Arguments

<b>data</b>	Data matrix in which the first column is subject id, the second column is time points of observations for temporal data or site id for spatial data. Columns 3 to (p+2) is the observations for p variables.
<b>network</b>	The network selected by function lglasso
<b>heter</b>	Binary variable TRUE or FALSE, indicating heterogeneous model or homogeneous model is fitted. In heterogeneous model, subjects are allowed to have his/her own temporal correlation parameter <b>tau_i</b> ; while in homogeneous model, all the subjects are assumed to share the same temporal correlation parameter,i.e., <b>tau_1=tau_2=...tau_m</b> .
<b>type</b>	A positive number which specify the correlation function. The general form of correlation function is given by <b>exp(tau t_i-t_j ^type)</b> . in which <b>type=0</b> can be used for spatial correlation while <b>type&gt;0</b> are used for temporal correlation. For latter, the default value is set to be <b>type=1</b> .
<b>tol</b>	Threshold for convergence. Default value is <b>1e-2</b> . Iterations stop when maximum absolute difference between consecutive estimates of parameter change is less than <b>tol</b> .
<b>lower</b>	Lower bound for predicts of correlation parameter <b>tau</b> . Default value is <b>1e-2</b> . The estimate of <b>tau(alpha)</b> will be searched in the interval <b>[lower,upper]</b> , where parameter <b>upper</b> is explained in the following.
<b>upper</b>	Upper bound for predicts of correlation parameter <b>tau</b> .

### Value

A list which include the maximum likelihood estimate of precision matrix, correlation parameter **tau**. If **heter=TRUE**, the output also include the estimate of alpha where **tau~exp(alpha)**

### Author(s)

Jie Zhou

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