Package: IsingFit (via r-universe)

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Type Package

Title Fitting Ising Models Using the ELasso Method

Version 0.4.1

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Depends R (>= 3.0.0)

Imports qgraph, Matrix, glmnet

Suggests IsingSampler

Description This network estimation procedure eLasso, which is based on the Ising model, combines l1-regularized logistic regression with model selection based on the Extended Bayesian Information Criterion (EBIC). EBIC is a fit measure that identifies relevant relationships between variables. The resulting network consists of variables as nodes and relevant relationships as edges. Can deal with binary data.

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Repository https://cvborkulo.r-universe.dev

RemoteUrl https://github.com/cvborkulo/isingfit

RemoteRef HEAD

RemoteSha d3977032ac85418c2bf8da5326fbc984672d9112

Contents

`IsingFit-package` *Network estimation using the eLasso method*

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Details

Package:	IsingFit
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Author(s)

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References

Chen, J., & Chen, Z. (2008). Extended bayesian information criteria for model selection with large model spaces. Biometrika, 95(3), 759-771.

Foygel, R., & Drton, M. (2011). Bayesian model choice and information criteria in sparse generalized linear models. arXiv preprint arXiv:1112.5635.

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`Ising-methods` *Methods for IsingFit objects*

Description

Print method prints the IsingFit output , plot method plots the estimated network (with the `qgraph` package), and summary method returns density of the network, the value of gamma used, the rule used, and the time the analysis took.

Usage

```
## S3 method for class 'IsingFit'
print(x, ...)
## S3 method for class 'IsingFit'
summary(object, ...)
## S3 method for class 'IsingFit'
plot(x, ...)
```

Arguments

`x`	output of `IsingFit`
`object`	output of `IsingFit`
`...`	Arguments sent to qgraph. Only used in plot method.

Author(s)

Claudia van Borkulo

`IsingFit` *Network estimation using the eLasso method*

Description

This network estimation procedure eLasso, which is based on the Ising model, combines l1-regularized logistic regression with model selection based on the Extended Bayesian Information Criterion (EBIC). EBIC is a fit measure that identifies relevant relationships between variables. The resulting network consists of variables as nodes and relevant relationships as edges. Can deal with binary data.

Usage

```
IsingFit(x, family = "binomial", AND = TRUE, gamma = 0.25, plot
                 = TRUE, progressbar = TRUE, min_sum = -Inf,
                 lowerbound.lambda = NA, ...)
```

Arguments

`x`	Input matrix. The dimension of the matrix is nobs x nvars; each row is a vector of observations of the variables. Must be cross-sectional data.
`family`	The default is 'binomial', treating the data as binary. Currently, this procedure is only supported for binary data.
`AND`	Logical. Can be TRUE of FALSE to indicate whether the AND-rule or the OR-rule should be used to define the edges in the network. Defaults to TRUE.
`gamma`	A value of hyperparameter gamma in the extended BIC. Can be anything between 0 and 1. Defaults to .25.
`plot`	Logical. Should the resulting network be plotted?
`progressbar`	Logical. Should the pbar be plotted in order to see the progress of the estimation procedure?
`min_sum`	The minimum sum score that is artifically possible in the dataset. Defaults to -Inf. Set this only if you know a lower sum score is not possible in the data, for example due to selection bias.
`lowerbound.lambda`	The minimum value of tuning parameter lambda (regularization parameter). Can be used to compare networks that are based on different sample sizes. The lowerbound.lambda is based on the number of observations in the smallest group n: sqrt(log(p)/n). p is the number of variables, that should be the same in both groups. When both networks are estimated with the same lowerbound for lambda (based on the smallest group), the two networks can be directly compared.
`...`	Arguments sent to `qgraph`.

Value

IsingFit returns (invisibly) a 'IsingFit' object that contains the following items:

`weiadj`	The weighted adjacency matrix.
`thresholds`	Thresholds of the variables.
`q`	The object that is returned by qgraph (class 'qgraph').
`gamma`	The value of hyperparameter gamma.
`AND`	A logical indicating whether the AND-rule is used or not. If not, the OR-rule is used.
`time`	The time it took to estimate the network.
`asymm.weights`	The (asymmetrical) weighted adjacency matrix before applying the AND/OR rule.
`lambda.values`	The values of the tuning parameter per node that ensured the best fitting set of neighbors.

Note

See also my website: http://cvborkulo.com

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Examples

```
library("IsingSampler")

### Simulate dataset ###
# Input:
N <- 6 # Number of nodes
nSample <- 1000 # Number of samples

# Ising parameters:
Graph <- matrix(sample(0:1,N^2,TRUE,prob = c(0.8, 0.2)),N,N) * runif(N^2,0.5,2)
Graph <- pmax(Graph,t(Graph))
diag(Graph) <- 0
Thresh <- -rowSums(Graph) / 2

# Simulate:
Data <- IsingSampler(nSample, Graph, Thresh)

### Fit using IsingFit ###
Res <- IsingFit(Data, family='binomial', plot=FALSE)

# Plot results:
library("qgraph")
layout(t(1:2))
qgraph(Res$weiadj,fade = FALSE)
title("Estimated network")
qgraph(Graph,fade = FALSE)
title("Original network")
```

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