Package ‘pdglasso’

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Type Package

Title What the Package Does (Title Case)

Version 0.1.0

Author Who wrote it

Maintainer The package maintainer `<yourself@somewhere.net>`

Description More about what it does (maybe more than one line)
Use four spaces when indenting paragraphs within the Description.

License What license is it under?

Encoding UTF-8

LazyData true

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R topics documented:

`admm.pdglasso` *Estimate a concentration matrix under the pdColG model using adaptive ADMM graphical lasso algorithm.*

Description

Description here.

Usage

```
admm.pdglasso(
  S,
  lambda1 = 1,
  lambda2 = 1e-04,
  type = c("vertex", "inside.block.edge", "across.block.edge"),
  force.symm = NULL,
  X.init = NULL,
  rho1 = 1,
  rho2 = 1,
  varying.rho1 = TRUE,
  varying.rho2 = TRUE,
  max_iter = 1000,
  eps.abs = 1e-12,
  eps.rel = 1e-12,
  verbose = FALSE
)
```

Arguments

`S`	A $p \times p$ covariance (or correlation) matrix.
`lambda1`	A non-negative scalar (or vector) penalty that encourages sparsity in the concentration matrix. If a vector is provided, it should match the appropriate length, i.e.
`lambda2`	A non-negative scalar (or vector) penalty that encourages equality constraints in the concentration matrix. If a vector is provided, it should match the appropriate length, i.e.
`type`	A string or vector of strings for the type of equality constraints to be imposed; zero, one or more available options can be selected among: * "vertex", symmetries are imposed on the diagonal entries of the concentration matrix. * "inside.block.edge", symmetries are imposed between elements of the LL and RR block the concentration matrix. * "across.block.edge", symmetries are imposed between elements of the LR and RL block the concentration matrix. Shortened forms are accepted too, i.e. "V" or "vert" for "vertex".
`force.symm`	A string or vector of strings to impose forced symmetry on the corresponding block of the concentration matrix. Same options as "type".
`X.init`	(optional) A $p \times p$ initial guess for the concentration matrix and/or starting solution for the ADMM algorithm.
`rho1`	A scalar; tuning parameter of the ADMM algorithm to be used for the outer loop. It must be strictly positive.
`rho2`	A scalar; tuning parameter of the ADMM algorithm to be used for the inner loop. It must be strictly positive.
`varying.rho1`	A boolean value; if `TRUE` the parameter rho1 is updated iteratively to speed-up convergence.
`varying.rho2`	A boolean value; if `TRUE` the parameter rho2 is updated iteratively to speed-up convergence.
`max_iter`	An integer; maximum number of iterations to be run in case the algorithm does not converge.

`eps.abs`	A scalar; the absolute precision required for the computation of primal and dual residuals of the ADMM algorithm.
`eps.rel`	A scalar; the relative precision required for the computation of primal and dual residuals of the ADMM algorithm.
`verbose`	A boolean value; if `TRUE` the progress (and internal convergence of inner loop) is shown in the console while the algorithm is running.

Value

A list, whose element are: * `X`, the estimated concentration matrix under the pdglasso model; the model is identified by the values of lambda1 and lambda 2, together with the type of penalization imposed. * `acronims`, a vector of strings for the type of penalties and forced symmetries imposed when calling the function. * `internal.par`, a list of internal parameters passed to the function at the call, as well as convergence information.

Examples

```
!!! Create fake dataset
S <- cov(toy.data)
admm.pdglasso(S)
```

`G.merge` *Conversion from the multiple matrix representation of the model to the single matrix representation.*

Description

This is the inverse of the function G.split, i.e. X is equal to `G.split(G.merge(X))`.

Usage

```
G.merge(X)
```

Arguments

`X`	list with three upper triangular matrices with entries 0 and 1: G, G.sym and G.across, any of G.sym and G.across may be NULL

Value

a pXp symmetric matrix with entries 0, 1, and 2

Examples

```
# random generation of a list(G=G, G.sym=G.sym, G.across=G.across)

q <- 5 # this can be any integer
p <- q*2

g.p <- matrix(sample(c(0,1), size=p^2, replace=TRUE), nrow=p, ncol=p)
g.p[lower.tri(g.p, diag=TRUE)] <- 0
```

```
g.q1 <- matrix(sample(c(0,1), size=q^2, replace=TRUE), nrow=q, ncol=q)
g.q1[lower.tri(g.q1, diag = FALSE)] <- 0

g.q2 <- matrix(sample(c(0,1), size=q^2, replace=TRUE), nrow=q, ncol=q)
g.q2[lower.tri(g.q2, diag = TRUE)] <- 0
g.q2sym <- g.q2+t(g.q2)

g.p[1:q, 1:q] <- g.p[1:q, 1:q] *(1-g.q1)
g.p[(q+1):p, (q+1):p] <- g.p[(q+1):p, (q+1):p] *(1-g.q1)
g.p[1:q, (q+1):p] <- g.p[1:q, (q+1):p] * (1-g.q2sym)

# list obtained

X <- list(G=g.p, G.sym=g.q1, G.across=g.q2)

g  <- G.merge(X)
gs <- G.split(g)

identical(X, gs)

X <- list(G=g.p, G.sym=NULL, G.across=NULL)

g  <- G.merge(X)
gs <- G.split(g)

identical(X, gs)
```

G.split — *Conversion from the single matrix representation of the model to the multiple matrix representation.*

Description

This is the inverse of the function `G.merge()`, i.e. g is equal to `G.merge(G.split(g))`.

Usage

```
G.split(g)
```

Arguments

g	is a pXp symmetric matrix with entries 0, 1, and 2

Value

a list with three upper triangular matrices: G, G.sym and G.across with entries 0 and 1, any of G.sym and G.across may be NULL

Examples

```
# see example in function [G.merge()].
```

`get.pdColG` *Build a graph from the output of a call to* `admm.pdglasso`.

Description

Description here.

Usage

```
get.pdColG(admm.out, th1 = NULL, th2 = NULL, verbose = FALSE)
```

Arguments

`admm.out`	An object of list type, that is the output of a call to the `admm-pdglasso` function.
`th1`	(optional) A scalar, the threshold to identify edges in the graph; it must be non-negative.
`th2`	(optional) A scalar, the threshold to identify coloured edges in the graph; it must be non-negative.
`verbose`	(optional) if `TRUE` provides summary statistics of the graph.

Value

a list, containing:

- g, the graph in matrix form.
- dof, the degrees of freedom corresponding to the graph build under the pdglasso model provided.

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