Package: regmed (via r-universe)

October 12, 2026

Type Package

Title Regularized Mediation Analysis

Version 2.1.5

Date 2025-08-28

Description Mediation analysis for multiple mediators by penalized structural equation models with different types of penalties depending on whether there are multiple mediators and only one exposure and one outcome variable (using sparse group lasso) or multiple exposures, multiple mediators, and multiple outcome variables (using lasso, L1, penalties).

License GPL (>= 2)

Suggests testthat, rmarkdown

Depends R (>= 4.2.0), methods, graphics, glasso, igraph

Imports knitr, Rcpp, RcppArmadillo, lavaan, gtools

LinkingTo Rcpp, RcppArmadillo

NeedsCompilation yes

VignetteBuilder knitr

URL https://cran.r-project.org/package=regmed

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

Date/Publication 2025-08-28 20:34:09 UTC

RemoteUrl https://github.com/cran/regmed

RemoteRef HEAD

RemoteSha 97a1753b058d1f0f6294f79bff16a9de43fb78b5

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`regmed-package` *Regularized Mediation Analysis*

Description

Mediation analysis for multiple mediators by penalized structural equation models with different types of penalties depending on whether there are multiple mediators and only one exposure and one outcome variable (using sparse group lasso) or multiple exposures, multiple mediators, and multiple outcome variables (using lasso, L1, penalties).

Details

The DESCRIPTION file:

Package:	regmed
Type:	Package
Title:	Regularized Mediation Analysis
Version:	2.1.5
Date:	2025-08-28
Authors@R:	c(person("Jason", "Sinnwell", email = "sinnwell.jason@mayo.edu", comment=c(ORCID="0000-0003-

Description:	Mediation analysis for multiple mediators by penalized structural equation models with different types o
License:	GPL (>= 2)
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Depends:	R (>= 4.2.0), methods, graphics, glasso, igraph
Imports:	knitr, Rcpp, RcppArmadillo, lavaan, gtools
LinkingTo:	Rcpp, RcppArmadillo
NeedsCompilation:	yes
VignetteBuilder:	knitr
URL:	https://cran.r-project.org/package=regmed
Author:	Jason Sinnwell [aut, cre] (<https://orcid.org/0000-0003-1964-5522>), Daniel Schaid [aut] (<https://orci
Maintainer:	Jason Sinnwell <sinnwell.jason@mayo.edu>

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mvregmed.grid.bestfit	Choose best fit model from a grid search based on minimum Bayesian Information Criterion
mvregmed.grid.data	Helper function to summarize fits of models across a grid of lambda values
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regmed.grid	Regularized mediation models over a vector grid

	of lambda penalty values.
regmed.grid.bestfit	Find best fitting regmed model from regmed.grid object.
regmed.lavaan.dat	Set up data to input to lavaan sem
regmed.lavaan.model	Create a lavaan model
regmed.prefilter	Prefilter to reduce the number of mediators for subsequent analyses
summary.mvregmed	Summary of mvregmed object

Author(s)

Jason Sinnwell [aut, cre] (<https://orcid.org/0000-0003-1964-5522>), Daniel Schaid [aut] (<https://orcid.org/0000-0003-1457-6433>)

Maintainer: Jason Sinnwell <sinnwell.jason@mayo.edu>

References

Schaid, DJ, Sinnwell JP. (2020) Penalized Models for Analysis of Multiple Mediators. Genet Epidemiol 44:408-424.

Schaid DS, Dikilitas O, Sinnwell JP, Kullo I (2022). Penalized mediation models for multivariate data. Genet Epidemiol 46:32-50.

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medsim *Simulated dataset for regmed package*

Description

Example data simulated from 2 response (y) variables, 10 exposure (x) variables, and 200 mediators (med). The all variables are generated from multivariate standard normal, with varying degrees of association between exposure, mediators, and responses.

Usage

```
data("medsim")
```

Format

Three data frames with 100 observsations each:

`x` matrix with 10 columns of continuous exposure variables

`y` matrix with 2 columns of continuous response variables

`med` numeric matrix of 200 columns of simulated mediators between exposures and responses

`mvregmed.dat.check` *Helper function to check x, y, mediator for input to mvregmed functions*

Description

Assure that x, y, mediator are matrices, check column names and fill in if NULL, and reduce x, y, mediator so no missing values among all three matrices.

Usage

```
mvregmed.dat.check(x, y, mediator, max.cor=0.99)
```

Arguments

`x`	matrix with columns representing "exposure" variable (sometimes called instrumental variable)
`y`	matrix with columns representing outcome variables
`mediator`	matrix with columns representing mediator variables
`max.cor`	maximum correlation within y, x, or mediators, so fitting is more robust

Value

list with updated x, y, mediator

Author(s)

Daniel Schaid and Jason Sinnwell

See Also

`mvregmed.fit` `mvregmed.grid`

`mvregmed.edges` *For an object of class mvregmed, create edges for a graph object that can be used for plots, or for creating models input to lavaan function sem*

Description

Using the names of the alpha, beta, and delta matrices in the fitted object, create directed edges

Usage

```
mvregmed.edges(fit, eps = 0.001)
```

Arguments

fit	The fit as an object of class mvregmed. This can be output from either mvregmed.fit or mvregmed.grid.bestfit.
eps	Threshold to determine whether any of alpha, beta, or delta parameters are close to zero to be rounded to zero.

Value

an object of class mvregmed.edges, which is a list with all.edge which is a data.frame with directed edges that are the names of x, mediator, y that are in the fitted model. Also returns data frames for alpha, beta, delta (each data frame containing vertex labels, row/col indices from which parameters were selected, and coefficient values), as well as names of x, mediator, and y.

Author(s)

Daniel Schaid and Jason Sinnwell

References

Schaid DS, Dikilitas O, Sinnwell JP, Kullo I (2022). Penalized mediation models for multivariate data. Genet Epidemiol 46:32-50.

See Also

mvregmed.fit plot.mvregmed.edges

---

mvregmed.fit *Multivariate regularized mediation model*

Description

Fit regularized mediation model for a specified lambda penalty value. Structural equation models for analysis of multiple exposures (x), multiple mediators, and multiple outcome variables (y) are fit with a lasso (L1) penalaty on the model parameters. The model is x-[alpha] -> mediator-[beta] -> outcome, where alpha and beta are the parameters for the indirect effect of x on y, through the mediator. The model also allows a direct effect of x on y: x-[delta]->y.

Usage

```
mvregmed.fit(x, mediator, y, lambda, x.std = TRUE, med.std = TRUE,
y.std = TRUE, max.outer = 5000, max.inner = 2, step.multiplier = 0.5,
print.iter = FALSE, max.cor=0.99)
```

Arguments

x	matrix with columns representing "exposure" variable (sometimes called instrumental variable)
mediator	matrix with columns representing mediator variables
y	matrix with columns representing outcome variables
lambda	lambda penalty parameter
x.std	logical (TRUE/FALSE) whether to standardize x by dividing by standard devation of x. Note that each column of x will be centered on its mean.
med.std	logical (TRUE/FALSE) whether to standardize mediator by dividing by standard devation of mediator. Note that each column of mediator will be centered on its mean.
y.std	logical (TRUE/FALSE) whether to standardize y by dividing by standard devation of y. Note that each column of y will be centered on its mean.
max.outer	maximum number of outer loop iterations. The outer loop cycles over several inner loops.
max.inner	maximum number of iterations for each inner loop. There is an inner loop for each paramemeter in the matrices alpha, beta, delta, and vary.
step.multiplier	In inner loop, the step size is shrunk by the step.multiplier to assure that step size is not too large. Generally, the default of 0.5 works well.
print.iter	print iteration number during fitting routine
max.cor	maximum correlation within y, x, or mediators, so fitting is more robust

Value

An object of class mvregmed

Author(s)

Daniel Schaid and Jason Sinnwell

References

Schaid DJ, Dikilitas O, Sinnwell JP, Kullo I (2022). Penalized Mediation Models for Multivariate Data. Genet Epidemiol 46:32-50.

See Also

mvregmed.grid

Examples

```
data(medsim)
mvfit <- mvregmed.fit(x, med[,1:10], y, lambda=.1)
summary(mvfit)
```

`mvregmed.graph.attributes` *Setup attributes of graph object for plotting*

Description

Setup attributes of graph object for plotting directed acyclic graph with graph attributes

Usage

```
mvregmed.graph.attributes(fit.edges, x.color = "palegreen",
y.color = "palevioletred", med.color = "skyblue", v.size = 30)
```

Arguments

`fit.edges`	A data.frame of edges with 1st column a vertex directed to the vertex in the 2nd column. This is all.edge from the list that is output from mvregmed.edges
`x.color`	Color of vertices for x variables
`y.color`	Color of vertices for y variables
`med.color`	Color of vertices for mediators
`v.size`	Size of vertices for plotting

Details

User can use this as template for taking advantage of more igraph attributes.

Value

List with items 1) output from graph_from_edgelist (see igraph); 2) vertex names; 3)vertex size; 4) vertex colors

Author(s)

Daniel Schaid and Jason Sinnwell

References

Schaid DS, Dikilitas O, Sinnwell JP, Kullo I (2022). Penalized mediation models for multivariate data. Genet Epidemiol 46:32-50.

See Also

`mvregmed.edges` `graph_from_edgelist`

`mvregmed.grid` *Fit a grid of mvregmed models over a vector of lambda penalty parameters*

Description

For each lambda in an input vector of values, fit a penalized mvregmed model

Usage

```
mvregmed.grid(x, mediator, y, lambda.vec, max.outer = 5000,
max.inner = 2, x.std = TRUE, med.std = TRUE, y.std = TRUE,
step.multiplier = 0.5, print.iter = FALSE, max.cor=0.99)
```

Arguments

`x`	matrix with columns representing "exposure" variable (sometimes called instrumental variable)
`mediator`	matrix with columns representing mediator variables
`y`	matrix with columns representing outcome variables
`lambda.vec`	Vector of values of penalty parameter lambda's
`max.outer`	maximum number of outer loop iterations. The outer loop cycles over several inner loops.
`max.inner`	maximum number of iterations for each inner loop. There is an inner loop for each paramemeter in the matrices alpha, beta, delta, and vary.
`x.std`	logical (TRUE/FALSE) whether to standardize x by dividing by standard devation of x. Note that each column of x will be centered on its mean.
`med.std`	logical (TRUE/FALSE) whether to standardize mediator by dividing by standard devation of mediator. Note that each column of mediator will be centered on its mean.
`y.std`	logical (TRUE/FALSE) whether to standardize y by dividing by standard devation of y. Note that each column of y will be centered on its mean.
`step.multiplier`	In inner loop, the step size is shrunk by the step.multiplier to assure that step size is not too large. Generally, the default of 0.5 works well.
`print.iter`	print iteration number during fitting routine
`max.cor`	maximum correlation within y, x, or mediators, so fitting is more robust

Value

An object of class mvregmed.grid

Author(s)

Daniel Schaid and Jason Sinnwell

References

Schaid DS, Dikilitas O, Sinnwell JP, Kullo I (2022). Penalized mediation models for multivariate data. Genet Epidemiol 46:32-50.

See Also

mvregmed.fit

Examples

```
data(medsim)
mvfit.grid <- mvregmed.grid(x, med[,1:10], y, lambda.vec=seq(.3, .04, by=-.01))
summary(mvfit.grid)
## plot(mvfit.grid)
```

---

mvregmed.grid.bestfit *Choose best fit model from a grid search based on minimum Bayesian Information Criterion*

Description

Search over all models fit in a grid and choose model with min BIC as best model.

Usage

```
mvregmed.grid.bestfit(fit.grid)
```

Arguments

fit.grid	An object of class mvregmed.grid, output from function mvregmed.grid

Value

An object of class mvregmed, a single best fitting model.

Author(s)

Daniel Schaid and Jason Sinnwell

References

Schaid DS, Dikilitas O, Sinnwell JP, Kullo I (2022). Penalized mediation models for multivariate data. Genet Epidemiol 46:32-50.

See Also

mvregmed.grid

`mvregmed.grid.data` *Helper function to summarize fits of models across a grid of lambda values*

Description

elper function to summarize fits of models across a grid of lambda values

Usage

```
mvregmed.grid.data(fit.lst, lambda.vec)
```

Arguments

`fit.lst`	A list of model fits over a grid of lambda values; length of list is length of vector of lambdas.
`lambda.vec`	A vector of penalty lambda values/

Details

Create a data.frame of summmary information for each model fit in a grid.

Value

data.frame of summary information

Author(s)

Daniel Schaid and Jason Sinnwell

References

Schaid DS, Dikilitas O, Sinnwell JP, Kullo I (2022). Penalized mediation models for multivariate data. Genet Epidemiol 46:32-50.

See Also

`mvregmed.grid`

mvregmed.grid.update *Helper function to update parameters in a grid search*

Description

After a model is fit with a specific lambda, use the output of the fitted parameters as initial values for the next lambda value, thus using warm starts at each successive lambda value.

Usage

```
mvregmed.grid.update(fit.obj, inits)
```

Arguments

fit.obj	A fitted model of class mvregmed.
inits	Initial values from mvregmed.init that are subsequently updated with new values from fit.obj

Value

A list with the same components as output from mvregmed.init

Author(s)

Daniel Schaid and Jason Sinnwell

References

Schaid DS, Dikilitas O, Sinnwell JP, Kullo I (2022). Penalized mediation models for multivariate data. Genet Epidemiol 46:32-50.

See Also

mvregmed.init

mvregmed.init *Helper function to setup data and parameters for input to mvregmed.fit and mvregmed.grid*

Description

Helper function to setup data and parameters for input to mvregmed.fit and mvregmed.grid

Usage

```
mvregmed.init(dat.obj, x.std = TRUE, med.std = TRUE, y.std = TRUE)
```

Arguments

dat.obj	A list that is output from mvregmed.dat.check that contains x, mediator, and y.
x.std	logical (TRUE/FALSE) whether to standardize x by dividing by standard deviation of x. Note that each column of x will be centered on its mean.
med.std	logical (TRUE/FALSE) whether to standardize mediator by dividing by standard devation of mediator. Note that each column of mediator will be centered on its mean.
y.std	logical (TRUE/FALSE) whether to standardize y by dividing by standard deviation of y. Note that each column of y will be centered on its mean.

Details

Center and scale (if declared) x, mediator and y. Then regress each mediator on all x to create residuals that are used to create the residual variance matrix for mediators. This variance matrix is penalized by glasso to obtain a matrix of full rank. Variance matrices for x and y variables are also created. Initial values of paramemeter matrices alpha, beta, and delta are created (all intital values = 0).

Value

A list of items used as input to model fitting.

Author(s)

Daniel Schaid and Jason Sinnwell

References

Schaid DS, Dikilitas O, Sinnwell JP, Kullo I (2022). Penalized mediation models for multivariate data. Genet Epidemiol 46:32-50.

See Also

mvregmed.fit mvregmed.grid

---

mvregmed.lavaan.dat *Set up data to input to lavaan sem*

Description

Set up data to input to lavaan structural equation model (sem)

Usage

```
mvregmed.lavaan.dat(x, mediator, y, max.cor=0.99)
```

Arguments

x	matrix of exposure variables
mediator	matrix of mediators
y	matrix of outcome variables
max.cor	maximum correlation within mediators, so that fitting is more robust

Details

Use the function regmed.dat.check to standardize all variables and subset to subjects without missing data

Value

A dataframe with updated x, mediator, and y

Author(s)

Daniel Schaid and Jason Sinnwell

References

Schaid DS, Dikilitas O, Sinnwell JP, Kullo I (2022). Penalized mediation models for multivariate data. Genet Epidemiol 46:32-50.

---

mvregmed.lavaan.model *Setup a model for input to lavaan*

Description

Set up a model statement (string formula) from mvregmed object for input to lavaan

Usage

```
mvregmed.lavaan.model(fit.edge, fit.mvregmed)
```

Arguments

fit.edge	Output from mvregmed.edges
fit.mvregmed	A mvregmed object, either from mvregmed.fit or from mvregmed.grid.bestfit

Details

Loop through all relationships determined important from mrregmed edges object, and create model statement for lavaan, while also specifying covariances pre-estimated by mvregmed. See vignette for examples. The summary method for lavaan supersedes the summary from the lavaan package by simplifying the output to only return the coefficient table, as the covariance estimates were fixd from mvregmed.

Value

Text string to define a model as input to sem

Author(s)

Daniel Schaid and Jason Sinnwell

References

Schaid DS, Dikilitas O, Sinnwell JP, Kullo I (2022). Penalized mediation models for multivariate data. Genet Epidemiol 46:32-50.

---

plot.mvregmed.grid *Plot penalty parameter lambda versus BIC for model fits*

Description

Plot penalty parameter lambda versus BIC for model fits

Usage

```
## S3 method for class 'mvregmed.grid'
plot(x, xlab="lambda", ylab="BIC", pch="*", ...)
```

Arguments

x	An object created by mvregmed.grid
xlab	x axis label, by default set to 'lambda'
ylab	y axis label, by default set to 'BIC' for this plot
pch	plot character, by default set to a star (*)
...	optional plot arguments

Author(s)

Daniel Schaid and Jason Sinnwell

References

Schaid DS, Dikilitas O, Sinnwell JP, Kullo I (2022). Penalized mediation models for multivariate data. Genet Epidemiol 46:32-50.

`plot.regmed.grid` *Plots for regmed.grid object.*

Description

Creates 2 plots: (1) BIC vs. lambda, and (2) Coefficients Alpha and Beta of mediator vs. lambda.

Usage

```
## S3 method for class 'regmed.grid'
plot(x, as.log=FALSE, ...)
```

Arguments

`x`	regmed.grid object, returned by the `regmed.grid()` function
`as.log`	Logical; if TRUE, plot lambda on the log scale
`...`	optional arguments for plot method

Value

nothing is returned

Author(s)

Dan Schaid, Greg Jenkins, Jason Sinnwell

See Also

`regmed.grid`,

Examples

```
data(medsim)
fit.grid <- regmed.grid(x[,1], med[,1:10], y[,1],
  lambda.vec= c(seq(from=1, to=0, by = -.1)), frac.lasso=.8)
summary(fit.grid)
```

`regmed.edges` *For an object of class regmed, create edges for a graph object that can be used for plots, or for creating models input to lavaan function sem*

Description

Using the names of the alpha, beta, and delta matrices in the fitted object, create directed edges

Usage

```
regmed.edges(fit, type="mediators", eps = 0.001)
```

Arguments

`fit`	The fit as an object of class mvregmed. This can be output from either mvregmed.fit or mvregmed.grid.bestfit.
`type`	Character string specifying whether to only keep edges for mediators that have a non-zero coefficient with exposure and response variables ("mediator") or all edges ("all").
`eps`	Threshold to determine whether any of alpha, beta, or delta parameters are close to zero to be rounded to zero.

Value

a list with class "regmed.edges" containing all.edge which is a data.framewith directed edges that are the names of x, mediator, y that are in the fitted model, with the coefficient for that edge. The plot method will plot the edges using igraph plotting options.

Author(s)

Daniel Schaid and Jason Sinnwell

References

Schaid DS, Dikilitas O, Sinnwell JP, Kullo I (2022). Penalized mediation models for multivariate data. Genet Epidemiol 46:32-50.

See Also

`regmed.fit` `plot.regmed.edges`

`regmed.fit` *Regularized Mediation model for a specified lambda penalty value.*

Description

Fit regularized mediation model for a specified lambda penalty value. Structural equation models for analysis of multiple mediators are extended by creating a sparse group lasso penalized model such that the penalty considers the natural groupings of the pair of parameters that determine mediation, as well as encourages sparseness of the model parameters. The model is x-[alpha] -> mediator-[beta] -> outcome, where alpha and beta are the parameters for the indirect effect of x on y, through the mediator. The model also allows a direct effect of x on y: x-[delta] -> y.

Usage

```
regmed.fit(x, mediator, y, lambda, frac.lasso=0.8, x.std=TRUE, med.std=TRUE,
max.outer=5000, max.inner=100, step.multiplier = 0.5, wt.delta = .5,
print.iter=FALSE, max.cor=0.99)
```

Arguments

`x`	vector representing "exposure" variable (sometimes called instrumental variable)
`mediator`	matrix of mediators, rows are observations, columns are different mediators
`y`	vector representing outcome
`lambda`	lambda penalty parameter
`frac.lasso`	fraction of penalty (lambda) that is allocated to L1 penalty (lasso). The remaining fraction, (1-frac.lasso) is allocated to group-lasso penalty, where the group is the pair of parameters alpha and beta that determine mediation (x [alpha] -> mediator -> [beta] y).
`x.std`	logical (TRUE/FALSE) whether to standardize x by dividing by standard deviation of x. Note that x will be centered on its mean.
`med.std`	logical (TRUE/FALSE) whether to standardize mediators by dividing each mediator by its standard deviation. Note that mediators will be centered on their means.
`max.outer`	maximum number of outer loop iterations. The outer loop cycles over several inner loops.
`max.inner`	maximum number of iterations for each inner loop. There is an inner loop for each pair of alpha-beta parameters for each mediator, an inner loop for direct effect (delta), and inner loops for residual variances for x and for y.
`step.multiplier`	a value between 0 and 1 for backtracking, to shrink step size. Value of 0.5 is typical default.
`wt.delta`	a weight >=0 for how much weight should be given to shrinking delta parameter, by penalaty lambda*wt.delta.
`print.iter`	print iteration history during fitting routine
`max.cor`	maximum correlation within mediators, so that fitting is more robust

Value

regmed object, with S3 methods available: plot, print, summary

Author(s)

Dan Schaid, Greg Jenkins, Jason Sinnwell

References

Schaid, DJ, Sinnwell JP. (2020) Penalized Models for Analysis of Multiple Mediators. Genet Epidemiol 44:408-424.

See Also

regmed.edges summary.regmed

Examples

```
data(medsim)
filter5 <- regmed.prefilter(x[,1], med, y[,1], k=5)
fit.regmed <- regmed.fit(x[,1], med[,1:5], y[,1], lambda = 0.2, frac.lasso=.8)
summary(fit.regmed)
```

---

regmed.grid *Regularized mediation models over a vector grid of lambda penalty values.*

Description

Fit regularized mediation models over a vector grid of lambda penalty values. Structural equation models for analysis of multiple mediators are extended by creating a sparse group lasso penalized model such that the penalty considers the natural groupings of the pair of parameters that determine mediation, as well as encourages sparseness of the model parameters. The model is x-[alpha] -> mediator-[beta] -> outcome, where alpha and beta are the parameters for the indirect effect of x on y, through the mediator. The model also allows a direct effect of x on y: x-[delta] -> y.

Usage

```
regmed.grid(x, mediator, y, lambda.vec, frac.lasso=0.8, max.outer=5000,
max.inner=100, x.std=TRUE, med.std=TRUE, step.multiplier = 0.5,
wt.delta = .5, print.iter=FALSE, max.cor=0.99)
```

Arguments

x	vector representing "exposure" variable (sometimes called instrumental variable)
mediator	matrix of mediators, rows are observations, columns are different mediators
y	vector representing outcome
lambda.vec	vector of lambda penalty parameters
frac.lasso	fraction of penalty (lambda) that is allocated to L1 penalty (lasso). The remaining fraction, (1-frac.lasso) is allocated to group-lasso penalty, where the group is the pair of parameters alpha and beta that determine mediation (x [alpha] -> mediator -> [beta] y).
max.outer	maximum number of outer loop iterations. The outer loop cycles over several inner loops.
max.inner	maximum number of iterations for each inner loop. There is an inner loop for each pair of alpha-beta parameters for each mediator, an inner loop for direct effect (delta), and inner loops for residual variances for x and for y.
x.std	logical (TRUE/FALSE) whether to standardize x by dividing by standard deviation of x. Note that x will be centered on its mean.
med.std	logical (TRUE/FALSE) whether to standardize mediators by dividing each mediator by its standard deviation. Note that mediators will be centered on their means.
step.multiplier	a value between 0 and 1 for backtracking, to shrink step size. Value of 0.5 is typical default.
wt.delta	a weight >=0 for how much weight should be given to shrinking delta parameter, by penalaty lambda*wt.delta.
print.iter	print iteration history during fitting routine
max.cor	maximum correlation within mediators, so fitting is more robust

Details

Altough outcome y is not required to be scaled by its standard deviation, it can be beneficial to scale y. This helps with setting range of lambda penalty parameters, because when all x, y, and mediators are scaled, it is reasonable to consider lambda values within the range of 0 to 1. See reference for details of algorithm.

Value

regmed.grid object

Author(s)

Dan Schaid, Jason Sinnwell

References

Schaid, DJ, Sinnwell JP. (2020) Penalized Models for Analysis of Multiple Mediators. Genet Epidemiol 44:408-424.

See Also

plot.regmed.grid regmed.fit

Examples

```
data(medsim)
fit.grid <- regmed.grid(x[,1], med[,1:5], y[,1],
lambda.vec= c(seq(from=1, to=0, by = -.1)),
frac.lasso=.8)
print(fit.grid)
```

---

regmed.grid.bestfit *Find best fitting regmed model from regmed.grid object.*

Description

Find best fitting regmed model from regmed.grid object using minimum BIC to select model.

Usage

```
regmed.grid.bestfit(fit.grid)
```

Arguments

fit.grid	a regmed.grid object

Value

fit	best fit regmed object based on minimum BIC
grid	row out of grid.data of regmed.grid object corresponding to best fit

Author(s)

Dan Schaid, Greg Jenkins, Jason Sinnwell

References

Schaid, DJ, Sinnwell JP. (2020) Penalized Models for Analysis of Multiple Mediators. Genet Epidemiol 44:408-424.

See Also

regmed.grid

regmed.lavaan.dat *Set up data to input to lavaan sem*

Description

Set up data to input to lavaan structural equation model (sem)

Usage

```
regmed.lavaan.dat(x, mediator, y)
```

Arguments

x	vector of exposure variables
mediator	matrix of mediator variables
y	vector of outcome variable

Details

Use the function regmed.dat.check to standardize all variables and subset to subjects without missing data

Value

A dataframe with updated x, mediator, and y

Author(s)

Dan Schaid, Jason Sinnwell

References

Schaid, DJ, Sinnwell JP. (2020) Penalized Models for Analysis of Multiple Mediators. Genet Epidemiol 44:408-424.

regmed.lavaan.model *Create a lavaan model*

Description

Create a lavaan model for input to lavan::sem()

Usage

```
regmed.lavaan.model(fit.edge, fit.regmed)
```

Arguments

fit.edge	object created by regmed.edges function
fit.regmed	object created by regmed.fit from which the fit.edge object was made

Details

The fit.regmed object is needed for the fixed covariance estimates to be put into the model statement. The summary method supersedes the default summary from the lavaan package to only return the table of coefficients, as the covariances are fixed from regmed.fit.

Value

a character string that descibes the mediation model in format of lavaan model

Author(s)

Dan Schaid, Greg Jenkins, Jason Sinnwell

---

regmed.prefilter *Prefilter to reduce the number of mediators for subsequent analyses*

Description

Use sure independence screening (Fan & Lv, 2008)to reduce the number of potential mediators when the number of potential mediators is large. This is based on ranking marginal correlations and then selecting the highest ranked values such that the number of parameters is less than the sample size. Because mediation depends on the two correlations, cor(x,med) and cor(med, y) we rank the absolute values of their products, |cor(x, med) * cor(med, y)|, and choose the highest k ranked values to determine which potential mediators to include in penalized mediation models. If k is not specified, the default value of k is n/2, where n is the sample size, because each mediator results in two parameters alpha and beta.

Usage

```
regmed.prefilter(x, mediator, y, k = NULL, x.std = TRUE,
med.std = TRUE, y.std=TRUE, max.cor=0.99)
```

Arguments

x	vector representing "exposure" variable (sometimes called instrumental variable)
mediator	matrix of mediators, rows are observations, columns are different mediators
y	vector representing outcome
k	Number of potential mediators to select. Default is n/2, where n is sample size.
x.std	logical (TRUE/FALSE) whether to standardize x by dividing by standard deviation of x. Note that x will be centered on its mean.

med.std	logical (TRUE/FALSE) whether to standardize mediators by dividing each mediator by its standard deviation. Note that mediators will be centered on their means.
y.std	logical (TRUE/FALSE) whether to standardize y by dividing by standard devation of y. Note that y will be centered on its mean.
max.cor	maximum correlation within mediators, so that fitting is more robust

Value

list with x, mediator, and y, after subsetting to no missing values, applying x.std and med.std, and subsetting mediators to k top choices.

Author(s)

Dan Schaid, Jason Sinnwell

References

Fan, J., & Lv, J. (2008). Sure independence screening for ultrahigh dimensional feature space. J. R. Statist. Soc.B, 70, 849-911. Schaid, DJ, Sinnwell JP. (2020) Penalized Models for Analysis of Multiple Mediators. Genet Epidemiol 44:408-424.

See Also

regmed

Examples

```
data(medsim)
dim(med)
filtered <- regmed.prefilter(x[,1], med, y[,1], k=10)
dim(filtered$med)
```

---

summary.mvregmed *Summary of mvregmed object*

Description

Summary of non-zero parameter estimates. Optional epsilon (eps) parameter controls rounding to 0.

Usage

```
## S3 method for class 'mvregmed'
summary(object, eps=1e-3, ...)
```

Arguments

`object`	mvregmed object returned from mvregmed.fit or mvregmed.grid.bestfit
`eps`	parameters smaller than epsilon (eps) are rounded to zero.
`...`	optional arguments

Value

Nothing is returned

Author(s)

Daniel Schaid and Jason Sinnwell

References

Schaid DS, Dikilitas O, Sinnwell JP, Kullo I (2022). Penalized mediation models for multivariate data. Genet Epidemiol 46:32-50.

See Also

`mvregmed.fit` `mvregmed.grid.bestfit`

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