

Package ‘mlVAR’

October 25, 2021

Type Package

Title Multi-Level Vector Autoregression

Version 0.5

Depends R (>= 3.3.0)

Imports lme4, arm, qgraph, dplyr (>= 0.5.0), clusterGeneration,
mvtnorm, corpcor, plyr, abind, methods, parallel,
MplusAutomation, graphicalVAR, rlang

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Description Estimates the multi-level vector autoregression model on time-series data.
Three network structures are obtained: temporal networks, contemporaneous
networks and between-subjects networks.

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NeedsCompilation no

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Repository CRAN

Date/Publication 2021-10-25 10:30:02 UTC

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| | |
|--------|---------------------------------|
| getNet | <i>Gets a network structure</i> |
|--------|---------------------------------|

Description

This function is simply a wrapper around the plotting method for mlVAR objects, that extracts the network structure rather than plotting them.

Usage

```
getNet(x, ...)
```

Arguments

| | |
|-----|--|
| x | An 'mlVAR' or 'mlVARsim0' object. |
| ... | Arguments sent to plot.mlVAR |

Author(s)

Sacha Epskamp <mail@sachaepskamp.com>

| | |
|-------------|---------------------------------|
| importMplus | <i>Import output from Mplus</i> |
|-------------|---------------------------------|

Description

This function imports the output from an Mplus model that has been generated by mlVAR. It can be used to make manual changes to the input file.

Usage

```
importMplus(outfile)
```

Arguments

| | |
|---------|--------------------------------|
| outfile | Location of Mplus output file. |
|---------|--------------------------------|

Author(s)

Sacha Epskamp <mail@sachaepskamp.com>

Description

The function `mIVAR` computes estimates of the multivariate vector autoregression model. This model returns three structures: temporal effects (e.g., lag-1 regression weights), contemporaneous relationships (correlations or partial correlations) and between-subject effects (correlations and partial correlations). See details.

Usage

```
mIVAR(data, vars, idvar, lags = 1, dayvar, beepvar,
       estimator = c("default", "lmer", "lm", "Mplus"),
       contemporaneous = c("default", "correlated",
                           "orthogonal", "fixed", "unique"), temporal =
       c("default", "correlated", "orthogonal", "fixed",
         "unique"), nCores = 1, verbose = TRUE, compareToLags,
       scale = TRUE, scaleWithin = FALSE, AR = FALSE,
       MplusSave = TRUE, MplusName = "mIVAR", iterations = "(2000)",
       chains = nCores, signs, orthogonal
)
```

Arguments

| | |
|------------------------------|--|
| <code>data</code> | Data frame |
| <code>vars</code> | Vectors of variables to include in the analysis |
| <code>idvar</code> | String indicating the subject ID |
| <code>lags</code> | Vector indicating the lags to include |
| <code>dayvar</code> | String indicating assessment day. Adding this argument makes sure that the first measurement of a day is not regressed on the last measurement of the previous day. IMPORTANT: only add this if the data has multiple observations per day. |
| <code>beepvar</code> | Optional string indicating assessment beep per day. Adding this argument will cause non-consecutive beeps to be treated as missing! |
| <code>estimator</code> | The estimator to be used. "lmer" for sequential univariate multi-level estimation, "Mplus" for multivariate Bayesian estimation (requires Mplus), and "lm" for fixed effects estimation. |
| <code>contemporaneous</code> | How should the contemporaneous networks be estimated? These networks are always estimated post-hoc by investigating the residuals of the temporal models. "correlated" and "orthogonal" run second multi-level models in which the networks are estimated using node-wise estimation. "fixed" and "unique" simply correlate the residuals, either by computing one network for all subjects (fixed) or a single network per per subject. |

| | |
|---------------|--|
| temporal | How should the temporal effects be estimated? "correlated" estimates correlated random effects, "orthogonal" estimates non-correlated random effects and "fixed" estimates a model in which only the intercept is random. Defaults to "correlated" when the number of variables is less than 6 and "orthogonal" otherwise. "unique" uses lm to estimate an unique model for each subject. |
| nCores | Number of cores to use in computation |
| verbose | Logical indicating if console messages and the progress bar should be shown. |
| scale | Logical, should variables be standardized before estimation? |
| scaleWithin | Logical, should variables be scaled within-person (set to FALSE to only center within-person) |
| compareToLags | A vector indicating which lags to base the data on. If the model is to be compared with a model with multiple lags using <code>mlVARcompare</code> , this argument must be used to make sure the number of observations is the same in both models (e.g., a lag 1 model can model the second observation of a day and a lag-2 model can't, causing different number of observations and incomparable models). It is suggested to not use this argument unless you want to compare models, and always run mlVAR without using this argument afterwards in the selected model. |
| AR | Logical, should an auto-regression only model be fitted? |
| MplusSave | Logical, should the Mplus model file and output be saved? |
| MplusName | Name of the Mplus model file and output (without extensions) |
| iterations | The string used to define the number of iterations in Mplus |
| chains | Number of Mplus chains |
| signs | Optional matrix fixing the signs of contemporaneous correlations. Is estimated by running mlVAR with estimator = "lmer" if missing. |
| orthogonal | Deprecated argument only added for backward compatibility. Ignore. |

Details

This function estimates the multi-level VAR model to obtain temporal, contemporaneous and between-subject effects using nodewise estimation. Temporal and between-subject effects are obtained directly from the models and contemporaneous effects are estimated post-hoc by correlating the residuals. See arxiv.org/abs/1609.04156 for details.

Setting estimator = "Mplus" will generate a Mplus model, run the analysis and read the results into R. Mplus 8 is required for this estimation. It is recommended to set contemporaneous = "fixed", though not required. For the estimation of contemporaneous random effects, the signs of contemporaneous *correlations* (not partial correlations) need be set (or estimated) via the signs argument.

Value

An mlVAR object

Author(s)

Sacha Epskamp (mail@sachaepskamp.com)

References

- Bringmann, L. F., Vissers, N., Wichers, M., Geschwind, N., Kuppens, P., Peeters, F., ... & Tuerlinckx, F. (2013). A network approach to psychopathology: New insights into clinical longitudinal data. *PLoS one*, 8(4), e60188.
- Hamaker, E. L., & Grasman, R. P. (2014). To center or not to center? Investigating inertia with a multilevel autoregressive model. *Frontiers in psychology*, 5.
- Epskamp, S., Waldorp, L. J., Mottus, R., & Borsboom, D. (2017). Discovering Psychological Dynamics: The Gaussian Graphical Model in Cross-sectional and Time-series Data. arxiv.org/abs/1609.04156.

See Also

[mIVARcompare](#), [summary.mIVAR](#), [plot.mIVAR](#)

Examples

```
## Not run:
### Small example ###
# Simulate data:
Model <- mIVARsim(nPerson = 50, nNode = 3, nTime = 50, lag=1)

# Estimate using correlated random effects:
fit1 <- mIVAR(Model$Data, vars = Model$vars, idvar = Model$idvar, lags = 1, temporal = "correlated")

# Print some pointers:
print(fit1)

# Summary of all parameter estimates:
summary(fit1)

# Compare temporal relationships:
layout(t(1:2))
plot(Model, "temporal", title = "True temporal relationships", layout = "circle")
plot(fit1, "temporal", title = "Estimated temporal relationships", layout = "circle")

# Compare contemporaneous partial correlations:
layout(t(1:2))
plot(Model, "contemporaneous", title = "True contemporaneous relationships",
      layout = "circle")
plot(fit1, "contemporaneous", title = "Estimated contemporaneous relationships",
      layout = "circle")

# Compare between-subjects partial correlations:
layout(t(1:2))
plot(Model, "between", title = "True between-subjects relationships", layout = "circle")
plot(fit1, "between", title = "Estimated between-subjects relationships",
      layout = "circle")

# Run same model with non-correlated temporal relationships and fixed-effect model:
fit2 <- mIVAR(Model$Data, vars = Model$vars, idvar = Model$idvar, lags = 1,
              temporal = "orthogonal")
fit3 <- mIVAR(Model$Data, vars = Model$vars, idvar = Model$idvar, lags = 1,
```

```

    temporal = "fixed")

# Compare models:
mlVARcompare(fit1,fit2,fit3)

# Inspect true parameter correlation matrix:
Model$Model$Omega$cor$mean
# Even though correlations are high, orthogonal model works well often!

### Large example ###
Model <- mlVARsim(nPerson = 100, nNode = 10, nTime = 100,lag=1)

# Correlated random effects no longer practical. Use orthogonal or fixed:
fit4 <- mlVAR(Model$Data, vars = Model$vars, idvar = Model$idvar, lags = 1,
  temporal = "orthogonal")
fit5 <- mlVAR(Model$Data, vars = Model$vars, idvar = Model$idvar, lags = 1,
  temporal = "fixed")

# Compare models:
mlVARcompare(fit4, fit5)

# Compare temporal relationships:
layout(t(1:2))
plot(Model, "temporal", title = "True temporal relationships", layout = "circle")
plot(fit4, "temporal", title = "Estimated temporal relationships", layout = "circle")

# Compare contemporaneous partial correlations:
layout(t(1:2))
plot(Model, "contemporaneous", title = "True contemporaneous relationships",
  layout = "circle")
plot(fit4, "contemporaneous", title = "Estimated contemporaneous relationships",
  layout = "circle")

# Compare between-subjects partial correlations:
layout(t(1:2))
plot(Model, "between", title = "True between-subjects relationships", layout = "circle")
plot(fit4, "between", title = "Estimated between-subjects relationships",
  layout = "circle")

## End(Not run)

```

Description

These functions return a table of the fixed and random effects.

FUNCTIONS ARE DEPRECATED AND WILL BE REMOVED SOON.

Usage

```
fixedEffects(object, digits = 5)
randomEffects(object, digits = 5)
```

Arguments

| | |
|--------|----------------------------|
| object | A mIVAR object |
| digits | Number of digits to output |

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mIVAR0

Multilevel VAR Estimation for Multiple Time Series

Description

The function mIVAR0 computes estimates of the multivariate vector autoregression model as introduced by Bringmann et al. (2013) which can be extended through treatment effects, covariates and pre- and post assessment effects.

FUNCTION IS DEPRECATED AND WILL BE REMOVED SOON.

Usage

```
mIVAR0(data, vars, idvar, lags = 1, dayvar, beepvar,
        periodvar, treatmentvar, covariates, timevar,
        maxTimeDiff, control = list(optimizer = "bobyqa"),
        verbose = TRUE, orthogonal, estimator = c("lmer",
        "lmmlasso"), method = c("default", "stepwise",
        "movingWindow"), laginteractions = c("none", "mains",
        "interactions"), critFun = BIC, lambda = 0,
        center = c("inSubject", "general", "none"))
```

Arguments

| | |
|-----------|---|
| data | Data frame |
| vars | Vectors of variables to include in the analysis |
| idvar | String indicating the subject ID |
| lags | Vector indicating the lags to include |
| dayvar | String indicating assessment day (if missing, every assessment is set to one day) |
| beepvar | String indicating assessment beep per day (if missing, is added) |
| periodvar | String indicating the period (baseline, treatment period, etc.) of assessment (if missing, every assessment is set to one period) |

| | |
|-----------------|--|
| treatmentvar | Character vector indicating treatment |
| covariates | Character indicating covariates independent of assessment. |
| timevar | Character indicating the time variable |
| maxTimeDiff | Maximum time difference to include observation pairs |
| control | A list of arguments sent to <code>lmerControl</code> |
| verbose | Logical to print progress to the console |
| orthogonal | Logical to indicate if orthogonal estimation (no correlated random effects) should be used. Defaults to FALSE if the number of nodes is less than 6 and TRUE otherwise |
| estimator | Estimator to use. Note: <code>lmmlasso</code> implementation is very experimental |
| method | Method to use. Experimental |
| laginteractions | Experimental, do not use. |
| critFun | Experimental, do not use. |
| lambda | <code>lmmlasso</code> lambda parameter |
| center | Centering to be used. "inSubject" uses within-person centering, "general" uses grand-mean centering and "none" does not use centering. IMPORTANT NOTE: "inSubject" leads to coefficients to resemble within-person slopes, the other centering option leads to coefficients to be a blend of within and between person slopes. |

Details

mIVARO has been built to extract individual network dynamics by estimating a multilevel vector autoregression model that models the time dynamics of selected variables both within an individual and on group level. For example, in a lag-1-model each variable at time point t is regressed to a lagged version of itself at time point $t-1$ and all other variables at time point $t-1$. In psychological research, for example, this analysis can be used to relate the dynamics of symptoms on one day (as assessed by experience sampling methods) to the dynamics of these symptoms on the consecutive day.

Value

mIVARO returns a 'mIVARO' object containing

| | |
|-----------------------|---|
| fixedEffects | A matrix that contains all fixed effects coefficients with dependent variables as rows and the lagged independent variables as columns. |
| se.fixedEffects | A matrix that contains all standard errors of the fixed effects. |
| randomEffects | A list of matrices that contain the random effects coefficients. |
| randomEffectsVariance | A matrix containing the estimated variances between the random-effects terms |
| pvals | A matrix that contains p-values for all fixed effects. |
| pseudologlik | The pseudo log-likelihood. |
| BIC | Bayesian Information Criterion, i.e. the sum of all univariate models' BICs |
| input | List containing the names of variables used in the analysis |

Author(s)

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References

Bringmann, L. F., Vissers, N., Wichers, M., Geschwind, N., Kuppens, P., Peeters, F., ... & Tuerlinckx, F. (2013). A network approach to psychopathology: New insights into clinical longitudinal data. *PloS one*, 8(4), e60188.

See Also

[fixedEffects](#), [fixedEffects](#)

Examples

```
## Not run:
### Small network ###
nVar <- 3
nPerson <- 25
nTime <- 25

# Simulate model and data:
Model <- mlVARsim0(nPerson,nVar,nTime,sparsity = 0.5)

# Run mlVAR0:
Res <- mlVAR0(Model)

# Compare true fixed model with significant edges of estimated fixed model:
layout(t(1:2))
plot(Model,"fixed", title = "True model",layout="circle", edge.labels = TRUE)
plot(Res,"fixed", title = "Estimated model", layout = "circle", onlySig = TRUE,
     alpha = 0.05, edge.labels = TRUE)

# Compare true and estimated individual differences in parameters:
layout(t(1:2))
plot(Model,"fixed", title = "True model",layout="circle", edge.color = "blue",
     edge.labels = TRUE)
plot(Res,"fixed", title = "Estimated model", layout = "circle", edge.color = "blue",
     edge.labels = TRUE)

# Compare networks of subject 1:
layout(t(1:2))
plot(Model,"subject",subject = 1, title = "True model",layout="circle",
     edge.labels = TRUE)
plot(Res,"subject",subject = 1,title = "Estimated model", layout = "circle",
     edge.labels = TRUE)

### Large network ###
nVar <- 10
```

```

nPerson <- 50
nTime <- 50

# Simulate model and data:
Model <- mlVARsim0(nPerson,nVar,nTime, sparsity = 0.5)

# Run orthogonal mlVAR:
Res <- mlVAR0(Model, orthogonal = TRUE)

# Compare true fixed model with significant edges of estimated fixed model:
layout(t(1:2))
plot(Model,"fixed", title = "True model",layout="circle")
plot(Res,"fixed", title = "Estimated model", layout = "circle", onlySig = TRUE,
      alpha = 0.05)

# Compare true and estimated individual differences in parameters:
layout(t(1:2))
plot(Model,"fixed", title = "True model",layout="circle", edge.color = "blue")
plot(Res,"fixed", title = "Estimated model", layout = "circle", edge.color = "blue")

# Compare networks of subject 1:
layout(t(1:2))
plot(Model,"subject",subject = 1, title = "True model",layout="circle")
plot(Res,"subject",subject = 1,title = "Estimated model", layout = "circle")

## End(Not run)

```

mlVAR0-methods

print and summary functions for mlVAR0 objects

Description

Create a short summary of an object created by [mlVAR0](#).

FUNCTION IS DEPRECATED AND WILL BE REMOVED SOON.

Usage

```

## S3 method for class 'mlVAR0'
print(x, ...)
## S3 method for class 'mlVAR0'
summary(object, ...)

```

Arguments

| | |
|--------|-------------------|
| object | A "mlVAR0" object |
| x | A "mlVAR0" object |
| ... | Not used |

Author(s)

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mIVARcompare

Compare mIVAR model fit

Description

This function compares the fit of several mIVAR models. Since an mIVAR model is a combination of univariate models this function will compare the fits for each univariate model.

Usage

```
mIVARcompare(...)
```

Arguments

... Any number of objects obtained from [mIVAR](#)

Details

Important to note is that the number of observations must be equal to make models comparable. If the lags are different and compareToLags was not used in mIVAR this function will stop with an informative error message.

Author(s)

Sacha Epskamp (mail@sachaepskamp.com)

Examples

```
## Not run:
### Small example ###
# Simulate data:
Model <- mIVARsim(nPerson = 50, nNode = 3, nTime = 50, lag=1)

# Estimate using different methods:
fit1 <- mIVAR(Model$Data, vars = Model$vars, idvar = Model$idvar, lags = 1,
  temporal = "correlated")
fit2 <- mIVAR(Model$Data, vars = Model$vars, idvar = Model$idvar, lags = 1,
  temporal = "orthogonal")
fit3 <- mIVAR(Model$Data, vars = Model$vars, idvar = Model$idvar, lags = 1,
  temporal = "fixed")

# Compare models:
mIVARcompare(fit1,fit2,fit3)

## End(Not run)
```

mlVARsample

Simulator function given an mlVAR object

Description

Simulates data based on an mlVAR object, estimates the mlVAR network model based on the simulated data and compares the estimated network to the mlVAR object network.

Usage

```
mlVARsample(object, nTime = c(25,50,100,200), nSample = 100, pMissing = 0,
  nReps = 100, nCores = 1, ...)
```

```
## S3 method for class 'mlVARsample'
summary(object, ...)
```

Arguments

| | |
|----------|--|
| object | mlVAR object, or mlVARsample object in the summary method |
| nTime | Vector with number of time points to test. |
| nSample | Number of individuals in the dataset. It is possible to decrease the number of individuals compared to the individuals in the mlVAR object. However, it is not possible to have more individuals than there are in the mlVAR object. |
| pMissing | Percentage of missing data to be simulated. |
| nReps | Number of repetitions for each condition. |
| nCores | Number of cores to use. |
| ... | Arguments sent to mlVAR. |

Details

This function simulates data based on the mlVAR object. The individual networks (random effects) are used to simulate data using the `graphicalVARsim` function from the `graphicalVAR` package (Epskamp, 2020). The individual data is combined into one dataset. This dataset is used to estimate the mlVAR network.

For every condition, the function returns four values per network comparison measure (correlation, sensitivity, specificity, bias, and precision): one for the fixed temporal effects, one for the fixed contemporaneous effects, the mean comparison value of the random temporal effects, and the mean comparison value of the random contemporaneous effects.

Author(s)

Sacha Epskamp <mail@sachaepskamp.com>

References

Sacha Epskamp (2020). graphicalVAR: Graphical VAR for Experience Sampling Data. R package version 0.2.3. <https://CRAN.R-project.org/package=graphicalVAR>

See Also

[mIVARsim](#), [mIVAR](#)

Examples

```
## Not run:
### Small example ###
# Simulate data:
Model <- mIVARsim(nPerson = 100, nNode = 3, nTime = 50, lag=1)

# Estimate using correlated random effects:
fit <- mIVAR(Model$Data, vars = Model$vars,
             idvar = Model$idvar, lags = 1,
             temporal = "correlated")

# Sample from fitted model:
samples <- mIVARsample(fit, nTime = 50, nSample = 50, pMissing = 0.1,
                      nReps = 5, nCores = 1)

# Summarize results:
summary(samples)

## End(Not run)
```

mIVARsim

Simulates an mIVAR model and data

Description

Simulates an mIVAR model and data with a random variance-covariance matrix for the random effects.

Usage

```
mIVARsim(nPerson = 10, nNode = 5, nTime = 100, lag = 1, thetaVar = rep(1,nNode),
         DF_theta = nNode * 2, mu_SD = c(1, 1), init_beta_SD = c(0.1, 1), fixedMuSD = 1,
         shrink_fixed = 0.9, shrink_deviation = 0.9)
```

Arguments

| | |
|---------|-----------------------------------|
| nPerson | Number of subjects |
| nNode | Number of variables |
| nTime | Number of observations per person |

| | |
|------------------|--|
| lag | The maximum lag to be used |
| thetaVar | Contemporaneous fixed effect variances |
| DF_theta | Degrees of freedom in simulating person-specific contemporaneous covariances (e.g., the individual differences in contemporaneous effects) |
| mu_SD | Range of standard deviation for the means |
| init_beta_SD | Initial range of standard deviations for the temporal effects |
| fixedMuSD | Standard deviation used in sampling the fixed effects |
| shrink_fixed | Shrinkage factor for shrinking the fixed effects if the VAR model is not stationary |
| shrink_deviation | Shrinkage factor for shrinking the random effects variance if the VAR model is not stationary |

Author(s)

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mlVARsim0

Old mlVAR simulation function

Description

FUNCTION IS DEPRECATED AND WILL BE REMOVED SOON.

Usage

```
mlVARsim0(nPerson = 10, nNode = 5, nTime = 100, sparsity = 0, parRange = c(0.22, 0.4),
propPositive = 0.5, diagPositive = TRUE, diagIncluded = TRUE, sdRange = c(0.01, 0.2),
shrinkFactor = 0.95, residualStyle = c("full", "diag"), residualShared = TRUE,
residualSDrange = c(0.05, 0.1), verbose = TRUE)
```

Arguments

nPerson
nNode
nTime
sparsity
parRange
propPositive
diagPositive
diagIncluded
sdRange
shrinkFactor

```

residualStyle
residualShared
residualSDrange

```

```

verbose

```

```

plot.mlVAR

```

Plot Method for mlVAR

Description

The function `plot.mlVAR` plots estimated model coefficients as networks using `qgraph`. These can be three networks: temporal, contemporaneous and between-subjects effects, of which the latter two can be plotted as a correlation or a partial correlation network.

Usage

```

## S3 method for class 'mlVAR'
plot(x, type = c("temporal", "contemporaneous", "between"),
      lag = 1, partial = TRUE, SD = FALSE, subject, order,
      nonsig = c("default", "show", "hide", "dashed"), rule
      = c("or", "and"), alpha = 0.05, onlySig = FALSE,
      layout = "spring", verbose = TRUE, ...)
## S3 method for class 'mlVARsim'
plot(x, ...)

```

Arguments

| | |
|----------------------|--|
| <code>x</code> | An <code>mlVAR</code> object. |
| <code>type</code> | What network to plot? |
| <code>lag</code> | The lag to use when <code>type = "temporal"</code> |
| <code>partial</code> | Logical, should partial correlation matrices be plotted instead of correlation methods? Only used if <code>type</code> is <code>"contemporaneous"</code> or <code>"between"</code> . Defaults to <code>TRUE</code> . |
| <code>SD</code> | Logical. Plot the standard-deviation of random effects instead of the fixed effect estimate? |
| <code>subject</code> | Subject number. If not missing, will plot the network of a specific subject instead. |
| <code>order</code> | An optional character vector used to set the order of nodes in the network. |
| <code>nonsig</code> | How to handle non-significant edges? Default will hide non-significant edges when p-values are available (fixed effects, partial correlations and temporal effects). |

| | |
|---------|--|
| rule | How to choose significance in node-wise estimated GGMs (contemporaneous and between-subjects). "or" selects an edge as being significant if one node predicting the other is significant, and "and" requires both predictions to be significant. |
| alpha | Alpha level to test for significance |
| onlySig | Deprecated argument only used for backward compatibility. |
| layout | The layout argument used by qgraph |
| verbose | Logical, should message be printed to the console? |
| ... | Arguments sent to qgraph |

Author(s)

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plot.mlVAR0

Plot Method for mlVAR0

Description

The function `plot.mlVAR0` plots estimated model coefficients as a network using `qgraph`.
 FUNCTION IS DEPRECATED AND WILL BE REMOVED SOON.

Usage

```
## S3 method for class 'mlVAR0'
plot(x, type = c("fixed", "SD", "subject"), lag = 1,
      subject, order, onlySig = FALSE, alpha, ...)
## S3 method for class 'mlVARsim0'
plot(x, type = c("fixed", "SD", "subject"), lag = 1,
      subject, order, ...)
```

Arguments

| | |
|---------|---|
| x | A mlVAR0 object obtained through the <code>mlVAR0</code> -function |
| type | Indicates whether to plot a network of fixed effects coefficients ("fixed"), the standard deviations of the random effect terms ("SD") or an individual subject's random effects network ("subject"). |
| lag | Vector indicating the lags to include |
| subject | If type="subject", vector indicating the ID subject number |
| order | Order of nodes |
| onlySig | Logical. Set to TRUE to only plot significant fixed effects. |
| alpha | Significance level to test edges at if onlySig == TRUE. Defaults to Bonferonni corrected alpha level of 0.05 divided by the number of fixed effects. |
| ... | Arguments sent to qgraph |

Author(s)

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simulateVAR

Simulate data from VAR model

Description

Simulates a timeseries using VAR parameters

Usage

```
simulateVAR(pars, means = 0, lags = 1, Nt = 100, init, residuals = 0.1,
            burnin)
```

Arguments

| | |
|------------------------|---|
| <code>pars</code> | A square matrix or a list of square matrices indicating the VAR parameters |
| <code>means</code> | A vector of means. |
| <code>lags</code> | The lags to which the 'pars' argument parameters correspond. If 'pars' is a list then this argument should be a vector indicating which lags are represented by each element of the 'pars' list. |
| <code>Nt</code> | Number of time points |
| <code>init</code> | Initial setup. Must be a matrix of the first lags with rows corresponding to time points and columns corresponding to variables (e.g., if only two lags are used then the matrix must have two rows indicating the first two times points.) |
| <code>residuals</code> | Standard deviation of the residuals or a residual covariance matrix |
| <code>burnin</code> | Initial simulations not returned. Defaults to $\min(\text{round}(Nt/2), 100)$. |

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`summary.mIVAR`*Summary of mIVAR results*

Description

Prints tables with fit indices and parameter estimates.

Usage

```
## S3 method for class 'mIVAR'  
summary(object, show = c("fit", "temporal", "contemporaneous", "between"),  
        round = 3, ...)  
## S3 method for class 'mIVAR'  
print(x, ...)
```

Arguments

| | |
|---------------------|-----------------------|
| <code>object</code> | An mIVAR object. |
| <code>show</code> | Which tables to show? |
| <code>round</code> | Number of digits. |
| <code>x</code> | An mIVAR object. |
| <code>...</code> | Not used |

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