Package 'gimme'

June 21, 2024

Title Group Iterative Multiple Model Estimation

Version 0.7-18

Date 2024-06-21

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Depends R (>= 3.5.0)

Imports lavaan (>= 0.6-17), igraph (>= 1.0-0), qgraph, data.tree,
MIIVsem(>= 0.5.4), imputeTS(>= 3.0), nloptr, graphics, stats,
MASS, tseries

Description Data-driven approach for arriving at person-specific time series models. The method first identifies which relations replicate across the majority of individuals to detect signal from noise. These group-level relations are then used as a foundation for starting the search for person-specific (or individual-level) relations. See Gates & Molenaar (2012) <doi:10.1016/j.neuroimage.2012.06.026>.

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LazyData true

URL https://github.com/GatesLab/gimme/,
https://tarheels.live/gimme/tutorials/

BugReports https://github.com/GatesLab/gimme/issues

ByteCompile true

RoxygenNote 7.2.3

NeedsCompilation no

Suggests knitr, rmarkdown

VignetteBuilder knitr

Encoding UTF-8

Repository CRAN

Date/Publication 2024-06-21 16:30:02 UTC

Contents

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  gimme-package   *Group iterative multiple model estimation*

Description

This package contains functions to automatically identify the structure of group- and individual-level networks from a range of vector autoregressive models, estimated with structural equation modeling.

Details

Researchers across varied domains gather multivariate data for each individual unit of study across multiple occasions of measurement. Generally referred to as time series (or in the social sciences, intensive longitudinal) data, examples include psychophysiological processes such as neuroimaging and heart rate variability, daily diary studies, ecological momentary assessments, data passively collected from devices such as smartphones, and observational coding of social interactions among dyads.

A primary goal for acquiring these data is to understand dynamic processes. The gimme package contains several functions for use with these data. These functions include [gimmeSEM](#), which provides both group- and individual-level results by looking across individuals for patterns of relations among variables. A function that provides group-level results, [aggSEM](#), is included, as well as a function that provides individual-level results, [indSEM](#). The major functions within the gimme package all require the user to specify the data, although many additional options exist.

Author(s)

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aggSEM   *Group-level structural equation model search.*

Description

Concatenates all individual-level data files and fits a group model to the data.

Usage

```
aggSEM(data   = "",
       out    = "",
       sep    = "",
       header = "",
       ar     = TRUE,
       plot   = TRUE,
       paths  = NULL,
       exogenous = NULL,
       outcome   = NULL,
       conv_vars       = NULL,
       conv_length     = 16,
       conv_interval   = 1,
       mult_vars       = NULL,
       mean_center_mult = FALSE,
       standardize      = FALSE,
```

```
       hybrid = FALSE,
       VAR    = FALSE)
```

Arguments

data	The path to the directory where the data files are located, or the name of the list containing each individual's time series. Each file or matrix must contain one matrix for each individual containing a T (time) by p (number of variables) matrix where the columns represent variables and the rows represent time. If in list form, each item in the list (i.e., matrix) must be named.
out	The path to the directory where the results will be stored (optional). If specified, a copy of output files will be replaced in directory. If directory at specified path does not exist, it will be created.
sep	The spacing of the data files when data are in a directory. "" indicates space-delimited, "/t" indicates tab-delimited, "," indicates comma delimited. Only necessary to specify if reading data in from physical directory.
header	Logical. Indicate TRUE for data files with a header, FALSE otherwise. Only necessary to specify if reading data in from physical directory.
ar	Logical. If TRUE, begins search for group model with autoregressive (AR) paths open. Defaults to TRUE.
plot	Logical. If TRUE, figures depicting relations among variables of interest will automatically be created. For aggregate-level plot, red paths represent positive weights and blue paths represent negative weights. Dashed lines denote lagged relations (lag 1) and solid lines are contemporaneous (lag 0). Defaults to TRUE.
paths	lavaan-style syntax containing paths with which to begin model estimation (optional). That is, Y~X indicates that Y is regressed on X, or X predicts Y. Paths can also be set to a specific value for estimation using lavaan-style syntax (e.g., 'V4 ~ 0.5*V3'), or set to 0 so that they will not be estimated (e.g., 'V4 ~ 0*V3'). If no header is used, then variables should be referred to with V followed (with no separation) by the column number. If a header is used, variables should be referred to using variable names. To reference lag variables, "lag" should be added to the end of the variable name with no separation. Defaults to NULL.
exogenous	Vector of variable names to be treated as exogenous (optional). That is, exogenous variable X can predict Y but cannot be predicted by Y. If no header is used, then variables should be referred to with V followed (with no separation) by the column number. If a header is used, variables should be referred to using variable names. Defaults to NULL.
outcome	Vector of variable names to be treated as outcome (optional). This is a variable that can be predicted by others but cannot predict. If no header is used, then variables should be referred to with V followed (with no separation) by the column number. If a header is used, variables should be referred to using variable names.
conv_vars	Vector of variable names to be convolved via smoothed Finite Impulse Response (sFIR). Defaults to NULL.
conv_length	Expected response length in seconds. For functional MRI BOLD, 16 seconds (default) is typical for the hemodynamic response function.

conv_interval	Interval between data acquisition. Currently conv_length/conv_interval must be a constant. For fMRI studies, this is the repetition time. Defaults to 1.
mult_vars	Vector of variable names to be multiplied to explore bilinear/modulatory effects (optional). All multiplied variables will be treated as exogenous (X can predict Y but cannot be predicted by Y). Within the vector, multiplication of two variables should be indicated with an asterik (e.g. V1*V2). If no header is used, variables should be referred to with V followed by the column number (with no separation). If a header is used, each variable should be referred to using variable names. If multiplication with the lag 1 of a variable is desired, the variable name should be followed by "lag" with no separation (e.g. V1*V2lag). Note that if multiplied variables are desired, at least one variable in the dataset must be specified as exogenous. Defaults to NULL.

mean_center_mult

Logical. If TRUE, the variables indicated in mult_vars will be mean-centered before being multiplied together. Defaults to FALSE.

standardize	Logical. If TRUE, all variables will be standardized to have a mean of zero and a standard deviation of one. Defaults to FALSE.
hybrid	Logical. If TRUE, enables hybrid-VAR models where both directed contemporaneous paths and contemporaneous covariances among residuals are candidate relations in the search space. Defaults to FALSE.
VAR	Logical. If true, VAR models where contemporaneous covariances among residuals are candidate relations in the search space. Defaults to FALSE.

Details

Output is a list of results if saved as an object and/or files printed to a directory if the "out" argument is used.

Author(s)

Stephanie Lane

Examples

```
## Not run:
exFit <- aggSEM(data = ts)

## End(Not run)

plot(exFit)
```

---

gimmeSEM *Group iterative multiple model estimation.*

Description

This function identifies structural equation models for each individual that consist of both group-level and individual-level paths.

Usage

```
gimmeSEM(data        = NULL,
         out         = NULL,
         sep         = NULL,
         header      = NULL,
         ar          = TRUE,
         plot        = TRUE,
         subgroup    = FALSE,
         sub_feature = "lag & contemp",
         sub_method  = "Walktrap",
         sub_sim_thresh   = "lowest",
         confirm_subgroup = NULL,
         paths       = NULL,
         exogenous   = NULL,
         outcome     = NULL,
         conv_vars   = NULL,
         conv_length = 16,
         conv_interval = 1,
         mult_vars   = NULL,
         mean_center_mult = FALSE,
         standardize = FALSE,
         groupcutoff = .75,
         subcutoff   = .75,
         diagnos     = FALSE,
         ms_allow        = FALSE,
         ms_tol          = 1e-5,
         lv_model        = NULL,
         lv_estimator    = "miiv",
         lv_scores       = "regression",
         lv_miiv_scaling = "first.indicator",
         lv_final_estimator = "miiv",
         lasso_model_crit   = NULL,
         hybrid = FALSE,
         VAR = FALSE,
         dir_prop_cutoff =0,
         ordered = NULL)
```

Arguments

data	The path to the directory where the data files are located, or the name of the list containing each individual's time series. Each file or matrix must contain one matrix for each individual containing a T (time) by p (number of variables) matrix where the columns represent variables and the rows represent time. Individuals must have the same variables (p) but can have different lengths of observations (T).
out	The path to the directory where the results will be stored (optional). If specified, a copy of output files will be replaced in directory. If directory at specified path does not exist, it will be created.
sep	The spacing of the data files. Follows R convention. "" indicates space-delimited, backslash "t" indicates tab-delimited, "," indicates comma delimited. Only necessary to specify if reading data in from physical directory.
header	Logical. Indicate TRUE for data files with a header. Only necessary to specify if reading data in from physical directory.
ar	Logical. If TRUE, begins search for group model with autoregressive (AR) paths freed for estimation. If ms_allow=TRUE, it is recommended to set ar=FALSE. Multiple solutions are unlikely to be found when ar=TRUE. Defaults to TRUE.
plot	Logical. If TRUE, graphs depicting relations among variables of interest will automatically be created. Solid lines represent contemporaneous relations (lag 0) and dashed lines reflect lagged relations (lag 1). For individual-level plots, red paths represent positive weights and blue paths represent negative weights. Width of paths corresponds to estimated path weight. For the group-level plot, black represents group-level paths, grey represents individual-level paths, and (if subgroup = TRUE) green represents subgroup-level paths. For the group-level plot, the width of the edge corresponds to the count. Defaults to TRUE.
subgroup	Logical. If TRUE, subgroups are generated based on similarities in model features using the `walktrap.community` function from the `igraph` package. When ms_allow=TRUE, subgroup should be set to FALSE. Defaults to FALSE.
sub_feature	Option to indicate feature(s) used to subgroup individuals. Defaults to "lag & contemp" for lagged and contemporaneous, which is the original method. Can use "lagged" or "contemp" to subgroup solely on features related to lagged and contemporaneous relations, respectively.
sub_method	Community detection method used to cluster individuals into subgroups. Options align with those available in the igraph package: "Walktrap" (default), "Infomap", "Louvain", "Edge Betweenness", "Label Prop", "Fast Greedy", "Leading Eigen", and "Spinglass".
sub_sim_thresh	Threshold for inducing sparsity in similarity matrix. Options are: the percent of edges in the similarity matrix to set to zero (e.g., .25 would set the lower quartile), "lowest" (default) subtracts the minimum value from all values, and "search" searches across thresholds to arrive at one providing highest modularity.
confirm_subgroup	
	Dataframe. Option only available when subgroup = TRUE. Dataframe should contain two columns. The first column should specify file labels (the name

of the data files without file extension), and the second should contain integer values (beginning at 1) specifying the subgroup membership for each individual. function from the igraph package. Defaults to TRUE.

paths   lavaan-style syntax containing paths with which to begin model estimation (optional). That is, Y~X indicates that Y is regressed on X, or X predicts Y. Paths can also be set to a specific value for estimation using lavaan-style syntax (e.g., 'V4 ~ 0.5*V3'), or set to 0 so that they will not be estimated (e.g., 'V4 ~ 0*V3'). If no header is used, then variables should be referred to with V followed (with no separation) by the column number. If a header is used, variables should be referred to using variable names. To reference lag variables, "lag" should be added to the end of the variable name with no separation. Defaults to NULL.

exogenous   Vector of variable names to be treated as exogenous (optional). That is, exogenous variable X can predict Y but cannot be predicted by Y. If no header is used, then variables should be referred to with V followed (with no separation) by the column number. If a header is used, variables should be referred to using variable names. The default for exogenous variables is that lagged effects of the exogenous variables are not included in the model search. If lagged paths are wanted, "&lag" should be added to the end of the variable name with no separation. Defaults to NULL.

outcome   Vector of variable names to be treated as outcome (optional). This is a variable that can be predicted by others but cannot predict. If no header is used, then variables should be referred to with V followed (with no separation) by the column number. If a header is used, variables should be referred to using variable names.

conv_vars   Vector of variable names to be convolved via smoothed Finite Impulse Response (sFIR). Note, conv_vars are not not automatically considered exogenous variables. To treat conv_vars as exogenous use the exogenous argument. Variables listed in conv_vars must be binary variables. You cannot do lagged variables. If there is missing data in the endogenous variables their values will be imputed for the convolution operation only. Defaults to NULL.

conv_length   Expected response length in seconds. For functional MRI BOLD, 16 seconds (default) is typical for the hemodynamic response function.

conv_interval   Interval between data acquisition. Currently conv_length/conv_interval must be an integer. For fMRI studies, this is the repetition time. Defaults to 1.

mult_vars   Vector of variable names to be multiplied to explore bilinear/modulatory effects (optional). All multiplied variables will be treated as exogenous (X can predict Y but cannot be predicted by Y). Within the vector, multiplication of two variables should be indicated with an asterik (e.g. V1*V2). If no header is used, variables should be referred to with V followed by the column number (with no separation). If a header is used, each variable should be referred to using variable names. If multiplication with the lag 1 of a variable is desired, the variable name should be followed by "lag" with no separation (e.g. V1*V2lag).

mean_center_mult
                 Logical. If TRUE, the variables indicated in mult_vars will be mean-centered before being multiplied together. Defaults to FALSE.

standardize   Logical. If TRUE, all variables will be standardized to have a mean of zero and a standard deviation of one. Defaults to FALSE

groupcutoff   Cutoff value for group-level paths. Defaults to .75, indicating that a path must be significant across 75% of individuals to be included as a group-level path.

subcutoff   Cutoff value for subgroup- level paths. Defaults to .75, indicating that a path must be significant across at least 75% of the individuals in a subgroup to be considered a subgroup-level path.

diagnos   Logical. If TRUE provides internal output for diagnostic purposes. Defaults to FALSE.

ms_allow   Logical. If TRUE provides multiple solutions when more than one path has identical modification index values. When ms_allow=TRUE, it is recommended to set ar=FALSE. Multiple solutions are unlikely to be found when ar=TRUE. Additionally, subgroup should be set to FALSE. Output files for individuals with multiple solutions will represent the last solution found for the individual, not necessarily the best solution for the individual.

ms_tol   Precision used when evaluating similarity of modification indices when ms_allow = TRUE. We recommend that ms_tol not be greater than the default, especially when standardize=TRUE. Defaults to 1e-5.

lv_model   Invoke latent variable modeling by providing the measurement model syntax here. lavaan conventions are used for relating observed variables to factors. Defaults to NULL.

lv_estimator   Estimator used for factor analysis. Options are "miiv" (default), "pml" (pseudo-ML) or "svd".

lv_scores   Method used for estimating latent variable scores from parameters obtained from the factor analysis when lv_model is not NULL. Options are: "regression" (Default), "bartlett".

lv_miiv_scaling

     Type of scaling indicator to use when "miiv" selected for lv_estimator. Options are "first.indicator" (Default; the first observed variable in the measurement equation is used), "group" (best one for the group), or "individual" (each individual has the best one for them according to R2).

lv_final_estimator

     Estimator for final estimations. "miiv" (Default) or "pml" (pseudo-ML).

lasso_model_crit

     When not null, invokes multiLASSO approach for the GIMME model search procedure. Arguments indicate the model selection criterion to use for model selection: 'bic' (select on BIC), 'aic', 'aicc', 'hqc', 'cv' (cross-validation).

hybrid   Logical. If TRUE, enables hybrid-VAR models where both directed contemporaneous paths and contemporaneous covariances among residuals are candidate relations in the search space. Defaults to FALSE.

VAR   Logical. If true, VAR models where contemporaneous covariances among residuals are candidate relations in the search space. Defaults to FALSE.

dir_prop_cutoff

     Option to require that the directionality of a relation has to be higher than the reverse direction for a prespecified proportion of indivdiuals.

ordered   A character vector containing the names of all ordered categorical variables in the model.

Details

Output is a list of results if saved as an object and/or files printed to a directory if the "out" argument is used.

Author(s)

Zachary Fisher, Kathleen Gates, & Stephanie Lane

References

Gates, K.M. & Molenaar, P.C.M. (2012). Group search algorithm recovers effective connectivity maps for individuals in homogeneous and heterogeneous samples. NeuroImage, 63, 310-319.

Lane, S.T. & Gates, K.M. (2017). Automated selection of robust individual-level structural equation models for time series data. Structural Equation Modeling.

Adriene M. Beltz & Peter C. M. Molenaar (2016) Dealing with Multiple Solutions in Structural Vector Autoregressive Models, Multivariate Behavioral Research, 51:2-3, 357-373.

Examples

```
 ## Not run:
paths <- 'V2 ~ V1
          V3 ~ V4lag'

fit <- gimmeSEM(data     = simData,
                out      = "C:/simData_out",
                subgroup = TRUE,
                paths    = paths)

print(fit, mean = TRUE)
print(fit, subgroup = 1, mean = TRUE)
print(fit, file = "group_1_1", estimates = TRUE)
print(fit, subgroup = 2, fitMeasures = TRUE)
plot(fit, file = "group_1_1")

## End(Not run)
```

HRFsim   *Hemodynamic Response Function (HRF) GIMME example.*

Description

This object contains a list of simulated time series data for twenty-five individuals. Each data set has 500 time points and five variables. The fifth variable represents an onset vector for stimulation.

Usage

```
HRFsim
```

Format

A list of data frames with 25 individuals, who each have 500 observations on 5 variables.

---

indSEM *Individual-level structural equation model search.*

Description

This function identifies structural equation models for each individual. It does not utilize any shared information from the sample.

Usage

```
indSEM(data   = NULL,
       out    = NULL,
       sep    = NULL,
       header = NULL,
       ar     = TRUE,
       plot   = TRUE,
       paths  = NULL,
       exogenous       = NULL,
       outcome         = NULL,
       conv_vars       = NULL,
       conv_length     = 16,
       conv_interval   = 1,
       mult_vars       = NULL,
       mean_center_mult = FALSE,
       standardize     = FALSE,
       hybrid = FALSE,
       VAR    = FALSE)
```

Arguments

data   The path to the directory where the data files are located, or the name of the list containing each individual's time series. Each file or matrix must contain one matrix for each individual containing a T (time) by p (number of variables) matrix where the columns represent variables and the rows represent time.

out   The path to the directory where the results will be stored (optional). If specified, a copy of output files will be replaced in directory. If directory at specified path does not exist, it will be created.

sep   The spacing of the data files. "" indicates space-delimited, "/t" indicates tab-delimited, "," indicates comma delimited. Only necessary to specify if reading data in from physical directory.

header   Logical. Indicate TRUE for data files with a header. Only necessary to specify if reading data in from physical directory.

ar	Logical. If TRUE, begins search for individual models with autoregressive (AR) paths open. Defaults to TRUE.
plot	Logical. If TRUE, graphs depicting relations among variables of interest will automatically be created. Defaults to TRUE. For individual- level plots, red paths represent positive weights and blue paths represent negative weights.
paths	lavaan-style syntax containing paths with which to begin model estimation. That is, Y~X indicates that Y is regressed on X, or X predicts Y. Paths can also be set to a specific value for estimation using lavaan-style syntax (e.g., 'V4 ~ 0.5*V3'), or set to 0 so that they will not be estimated (e.g., 'V4 ~ 0*V3'). If no header is used, then variables should be referred to with V followed (with no separation) by the column number. If a header is used, variables should be referred to using variable names. To reference lag variables, "lag" should be added to the end of the variable name with no separation. Defaults to NULL.
exogenous	Vector of variable names to be treated as exogenous. That is, exogenous variable X can predict Y but cannot be predicted by Y. If no header is used, then variables should be referred to with V followed (with no separation) by the column number. If a header is used, variables should be referred to using variable names. Defaults to NULL.
outcome	Vector of variable names to be treated as outcome (optional). This is a variable that can be predicted by others but cannot predict. If no header is used, then variables should be referred to with V followed (with no separation) by the column number. If a header is used, variables should be referred to using variable names.
conv_vars	Vector of variable names to be convolved via smoothed Finite Impulse Response (sFIR). Defaults to NULL.
conv_length	Expected response length in seconds. For functional MRI BOLD, 16 seconds (default) is typical for the hemodynamic response function.
conv_interval	Interval between data acquisition. Currently conv_length/conv_interval must be a constant. For fMRI studies, this is the repetition time. Defaults to 1.
mult_vars	Vector of variable names to be multiplied to explore bilinear/modulatory effects (optional). All multiplied variables will be treated as exogenous (X can predict Y but cannot be predicted by Y). Within the vector, multiplication of two variables should be indicated with an asterik (e.g. V1*V2). If no header is used, variables should be referred to with V followed by the column number (with no separation). If a header is used, each variable should be referred to using variable names. If multiplication with the lag 1 of a variable is desired, the variable name should be followed by "lag" with no separation (e.g. V1*V2lag). Note that if multiplied variables are desired, at least one variable in the dataset must be specified as exogenous. Defaults to NULL.
mean_center_mult	
	Logical. If TRUE, the variables indicated in mult_vars will be mean-centered before being multiplied together. Defaults to FALSE.
standardize	Logical. If TRUE, all variables will be standardized to have a mean of zero and a standard deviation of one. Defaults to FALSE.
hybrid	Logical. If TRUE, enables hybrid-VAR models where both directed contemporaneous paths and contemporaneous covariances among residuals are candidate relations in the search space. Defaults to FALSE.

VAR	Logical. If true, VAR models where contemporaneous covariances among residuals are candidate relations in the search space. Defaults to FALSE.

Details

Output is a list of results if saved as an object and/or files printed to a directory if the "out" argument is used.

Author(s)

Stephanie Lane

Examples

```
 ## Not run:
fit <- indSEM(data  = "C:/data100",
              out    = "C:/data100_indSEM_out",
              sep    = ",",
              header = FALSE)
print(fit, file = "group1.1", estimates = TRUE)
plot(fit, file = "group1.1")

## End(Not run)
```

---

ms.fit	*Fitted gimme object with multiple solutions*

Description

This object contains a fitted gimme object where multiple solutions gimme was used. The simulated data had 25 individuals, each with 100 time points.

Usage

```
ms.fit
```

Format

A fitted gimme object, where multiple solutions gimme was used.

---

setupConvolve   *Group iterative multiple model estimation.*

Description

This function estimates the basis vectors related to responses following a binary impulse and convolves that binary impulse vector.

Usage

```
convolveFIR(ts_list = NULL,
    varLabels = NULL,
    conv_length = 16,
    conv_interval = 1)
```

Arguments

ts_list	a list of dataframes.
varLabels	a list of variable sets. Contains varLabels$coln, all column names, varLabels$conv, the names of variables to convolve, and varLabels$exog, a list of exogenous variables (if any).
conv_length	Expected response length in seconds. For functional MRI BOLD, 16 seconds (default) is typical for the hemodynamic response function.
conv_interval	Interval between data acquisition. Currently must be a scalar For fMRI studies, this is the repetition time. Defaults to 1.

---

simData   *Large example, heterogeneous data, group, subgroup, and individual level effects.*

Description

This object contains a list of simulated time series data for twenty-five individuals with 200 time points and 10 variables, or regions of interest.

Usage

```
simData
```

Format

A list of data frames with 25 individuals, who each have 200 observations on 10 variables.

---

simDataLV	*Latent variable example, heterogeneous data, group, subgroup level effects.*

Description

This object contains a list of simulated time series data for twenty individuals with 500 time points and 9 variables, or regions of interest.

Usage

```
simDataLV
```

Format

A list of data frames with 20 individuals, who each have 500 observations on 9 variables.

---

simulateVAR	*Simulate data from Vector AutoRegression (VAR) models.*

Description

This function simulates data. It allows for structural VAR and VAR data generating models.

Usage

```
simulateVAR(A   = NULL,
            Phi      = NULL,
            Psi      = NULL,
            subAssign = NULL,
            N        = NULL,
            ASign    = "random",
            PhiSign  = "random",
            Obs      = NULL,
            indA     = 0.01,
            indPhi   = 0.01,
            indPsi   = 0.00)
```

Arguments

A	A matrix (for no subgroups) or list of A matrices, with slice # = # of subgroups.
Phi	Phi matrix (for no subgroups) or list of Phi matrices, with slice # = # of subgroups.
Psi	matrix (for no subgroups) or list of Psi matrices, with slice # = # of subgroups.
subAssign	Optional vector of length N that indicates which subgroup each individual is in.

N	Number of indvidiuals.
ASign	Defaults to "random" for ind level paths, with 50 percent chance of positive and 50 percent negative, other option is either "neg" or "pos" which provides all negative or all positive relations, respectively.
PhiSign	Defaults to "random" for ind level paths, with 50 percent chance of positive and 50 percent negative, other option is either "neg" or "pos" which provides all negative or all positive relations, respectively.
Obs	Number of observations (T) per individual. Burn in of 400 is used to generate then discarded.
indA	Sparsity of individual-level A paths. 0 indicates no individual-level. Use decimals. Default is 0.01, meaning that each path that is not in the group-level A matrix has a 0.01 chance of being added.
indPhi	Sparsity of individual-level Phi paths. 0 indicates no individual-level. Use decimals. Default is 0.01, meaning that each path that is not in the group-level Phi matrix has a 0.01 chance of being added.
indPsi	Sparsity of individual-level Psi paths. 0 indicates no individual-level. Use decimals. Default is 0, meaning that each path that is not in the group-level Psi matrix has a 0 chance of being added at the ind. level. Individual- level paths added at this rate per individual.

Author(s)

KM Gates, Ai Ye, Ethan McCormick, & Zachary Fisher

---

solution.tree	*Solution trees for multiple solutions gimme.*

Description

This function allows for the exploration of divergences in multiple solutions gimme for both the group and individuals.

Usage

```
solution.tree(x,
              level    = c("group", "individual"),
              cols     = NULL,
              ids      = "all",
              plot.tree = FALSE)
```

Arguments

x	A fitted gimme object.
level	A character vector indicating what levels of the solution tree you would like returned. Options are "group", "individual", or c("group", "individual"). Defaults to c("group", "individual").

cols	A character vector indicating additional information to include in tree plot. Options include "stage", "pruned", "rmsea", "nnfi", "cfi","srmr", "grp_sol", "bic", "aic", "modularity." Defaults to NULL.
ids	A character vector indicating the names of subjects to print. Defaults to "all."
plot.tree	Logical. If TRUE, plot of tree is produced. Defaults to FALSE.

Details

solution.tree

---

ts	*Small example, heterogeneous data, group and individual level effects*

Description

This object contains a list of simulated time series data for five individuals with 50 time points and 3 variables, or regions of interest.

Usage

```
ts
```

Format

A list of data frames with 5 individuals, who each have 50 observations on 3 variables.

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