

Package ‘gimme’

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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/>

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gimme-package	<i>Group iterative multiple model estimation</i>
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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.

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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,
```

```

stop_crit      = "model fit",
indiv_correct  = "Bonferroni",
alpha         = .05,
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.
stop_crit	Stopping criterion for the individual-level search. "standard" stops when either fit is adequate or no significant paths remain. "model fit" (default) continues adding the highest-MI path until fit is adequate, even if the path is not significant. "significance" continues adding significant paths even after fit is adequate.
indiv_correct	Indicate how to correct for multiple comparisons at the individual level. "Bonferroni" (Default) applies a Bonferroni correction dividing alpha by the number of eligible paths; "fdr" applies a Benjamini-Hochberg false discovery rate correction.
alpha	The base alpha level used for significance testing. Defaults to .05.
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)

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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,
group_correct = "Bonferroni Group",
indiv_correct = "Bonferroni",
alpha = .05,
stop_crit = "model fit",
  rmsea_cutoff = .05,
  srmr_cutoff = .05,
  nnfi_cutoff = .95,
  cfi_cutoff = .95,
  n_excellent = 2)

```

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 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.

<code>mult_vars</code>	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).
<code>mean_center_mult</code>	Logical. If TRUE, the variables indicated in <code>mult_vars</code> will be mean-centered before being multiplied together. Defaults to FALSE.
<code>standardize</code>	Logical. If TRUE, all variables will be standardized to have a mean of zero and a standard deviation of one. Defaults to FALSE
<code>groupcutoff</code>	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.
<code>subcutoff</code>	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.
<code>diagnos</code>	Logical. If TRUE provides internal output for diagnostic purposes. Defaults to FALSE.
<code>ms_allow</code>	Logical. If TRUE provides multiple solutions when more than one path has identical modification index values. When <code>ms_allow=TRUE</code> , it is recommended to set <code>ar=FALSE</code> . Multiple solutions are unlikely to be found when <code>ar=TRUE</code> . Additionally, <code>subgroup</code> 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.
<code>ms_tol</code>	Precision used when evaluating similarity of modification indices when <code>ms_allow = TRUE</code> . We recommend that <code>ms_tol</code> not be greater than the default, especially when <code>standardize=TRUE</code> . Defaults to 1e-5.
<code>lv_model</code>	Invoke latent variable modeling by providing the measurement model syntax here. lavaan conventions are used for relating observed variables to factors. Defaults to NULL.
<code>lv_estimator</code>	Estimator used for factor analysis. Options are "miiv" (default), "pml" (pseudo-ML) or "svd".
<code>lv_scores</code>	Method used for estimating latent variable scores from parameters obtained from the factor analysis when <code>lv_model</code> is not NULL. Options are: "regression" (Default), "bartlett".
<code>lv_miiv_scaling</code>	Type of scaling indicator to use when "miiv" selected for <code>lv_estimator</code> . 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).
<code>lv_final_estimator</code>	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 individuals.
ordered	A character vector containing the names of all ordered categorical variables in the model.
group_correct	Indicate how to correct for multiple testing at the group level. "Bonferroni Group" (Default) corrects alpha for the number of people (N) in the sample; "Bonferroni Paths" corrects alpha for the number of eligible paths; a numeric value between 0 and 1 sets the alpha level directly; "fdr" applies a Benjamini-Hochberg false discovery rate correction.
indiv_correct	Indicate how to correct for multiple comparisons at the individual level. "Bonferroni" (Default) applies a Bonferroni correction dividing alpha by the number of eligible paths; "fdr" applies a Benjamini-Hochberg false discovery rate correction.
alpha	The base alpha level used for significance testing in all searches (group and individual). Defaults to .05.
stop_crit	Stopping criterion for the individual-level search. "standard" stops when either fit is adequate or no significant paths remain. "model fit" (default) continues adding the paths until fit is adequate regardless of significance of those paths. "significance" continues adding significant paths even after fit is adequate.
rmsea_cutoff	Cutoff for RMSEA for an individual model (default is .05; must be between 0.0 and 1.0).
srmr_cutoff	Cutoff for SRMR for an individual model (default is .05; must be between 0.0 and 1.0).
nnfi_cutoff	Cutoff for NNFI for an individual model (default is .95; must be between 0.0 and 1.0).
cfi_cutoff	Cutoff for CFI for an individual model (default is .95; must be between 0.0 and 1.0).
n_excellent	Number of fit indices needed to surpass their cutoffs for an individual model to be considered excellent. Default is 2. Max is 4.

Details

gimmeSEM is a data-driven method for identifying structural equation models for each individual that consist of both group-level and individual-level paths. The group-level search identifies paths that are significant across a prespecified proportion of individuals in the sample (e.g., 75%). The

optional subgrouping stage identifies subgroups of individuals with similar model features (e.g., similar patterns of lagged and contemporaneous relations among variables). The individual-level search then adds paths to each individual's model until fit is adequate or no significant paths remain. Output is a list of results if saved as an object and/or files printed to a directory if the "out" argument is used.

Value

A list with the following components:

- data: list of data used in analyses. Contains lagged variables and any data manipulations done within gimme.
- path_est_mats: N matrices of individual-level coefficient estimates for directed paths.
- varnames: Variable names in order of data.
- n_vars_total: total number of variables.
- n_lagged: total number of lagged variables.
- n_endog: total number of endogenous variables.
- fit: Final fit indices, R-squared for each variable, convergence status, subgroup membership (if applicable), and modularity (if applicable).
- path_se_est: Matrix of all individuals' unstandardized & standardized coefficient estimates, standard errors, level of each relation (e.g., "group"), and subgroup membership.
- plots: If number of variables >3, N individual-level plots of directed lagged and contemporaneous relations among variables. Red = high / hot / positive values; Blue = low / cold / negative values. Line width corresponds with absolute value of beta estimate. Use plot() function.
- plots_cov: If number of variables >3 and hybrid = TRUE or VAR = TRUE, N plots of contemporaneous covariances among residuals.
- group_plot_paths: If number of variables >3, aggregated plot of directed relations. Black = group-level, Green = subgroup level, Grey = individual level. Line width corresponds with percent of individuals who have that path estimated.
- group_plot_cov: If number of variables >3 and hybrid = TRUE or VAR = TRUE, aggregated plot of covariances among residuals.
- sub_plots_paths: Aggregated directed subgroup plots for K subgroups if applicable.
- sub_plots_cov: Aggregated covariance subgroup plots for K subgroups if applicable.
- path_counts: Matrix containing counts of the number of people for whom a given directed relation is estimated.
- path_counts_sub: K matrices containing counts of the number of people within that subgroup for whom a given directed relation is estimated.
- cov_counts: Matrix containing counts of the number of people for whom a given covariance relation is estimated.
- cov_counts_sub: K matrices containing counts of the number of people within that subgroup for whom a given covariance relation is estimated.
- vcov: N matrices containing the estimated covariance matrix of parameters of interest in gimme.

- `vcovfull`: N matrices of the full estimated covariance matrix of parameters.
- `psi`: N standardized residual covariance matrices.
- `ps_unstd`: N unstandardied residual covariance matrices.
- `sim_matrix`: If `subgroup = TRUE`, similarity count matrix of how many edges are in common among each pair of individuals after the group-level search (also considers individual-level paths that may be added later via the EPC).
- `syntax`: N individual slices containing lavaan-style syntax.
- `lvgimme`: If provided, the latent variable model syntax (also included in the above).
- `rf_est`: If variables to convolve are provided in `conv_vars`, the N response function estimates for individuals.
- `arguments`: List of arguments provided by the user.

Author(s)

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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	<i>Hemodynamic Response Function (HRF) GIMME example.</i>
--------	---

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	<i>Individual-level structural equation model search.</i>
--------	---

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,
        stop_crit = "model fit",
        indiv_correct = "Bonferroni",
        alpha = .05,
        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, $Y \sim X$ 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., ' $V4 \sim 0.5 * V3$ '), or set to 0 so that they will not be estimated (e.g., ' $V4 \sim 0 * V3$ '). 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.

<code>mean_center_mult</code>	Logical. If TRUE, the variables indicated in <code>mult_vars</code> will be mean-centered before being multiplied together. Defaults to FALSE.
<code>standardize</code>	Logical. If TRUE, all variables will be standardized to have a mean of zero and a standard deviation of one. Defaults to FALSE.
<code>stop_crit</code>	Stopping criterion for the individual-level search. "standard" stops when either fit is adequate or no significant paths remain. "model fit" (default) continues adding the highest-MI path until fit is adequate, even if the path is not significant. "significance" continues adding significant paths even after fit is adequate.
<code>indiv_correct</code>	Indicate how to correct for multiple comparisons at the individual level. "Bonferroni" (Default) applies a Bonferroni correction dividing alpha by the number of eligible paths; "fdr" applies a Benjamini-Hochberg false discovery rate correction.
<code>alpha</code>	The base alpha level used for significance testing. Defaults to .05.
<code>hybrid</code>	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.
<code>VAR</code>	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	<i>Large example, heterogeneous data, group, subgroup, and individual level effects.</i>
---------	--

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	<i>Latent variable example, heterogeneous data, group, subgroup level effects.</i>
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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 individuals.
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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