Group Iterative Multiple Model Estimation (GIMME)

User's Manual

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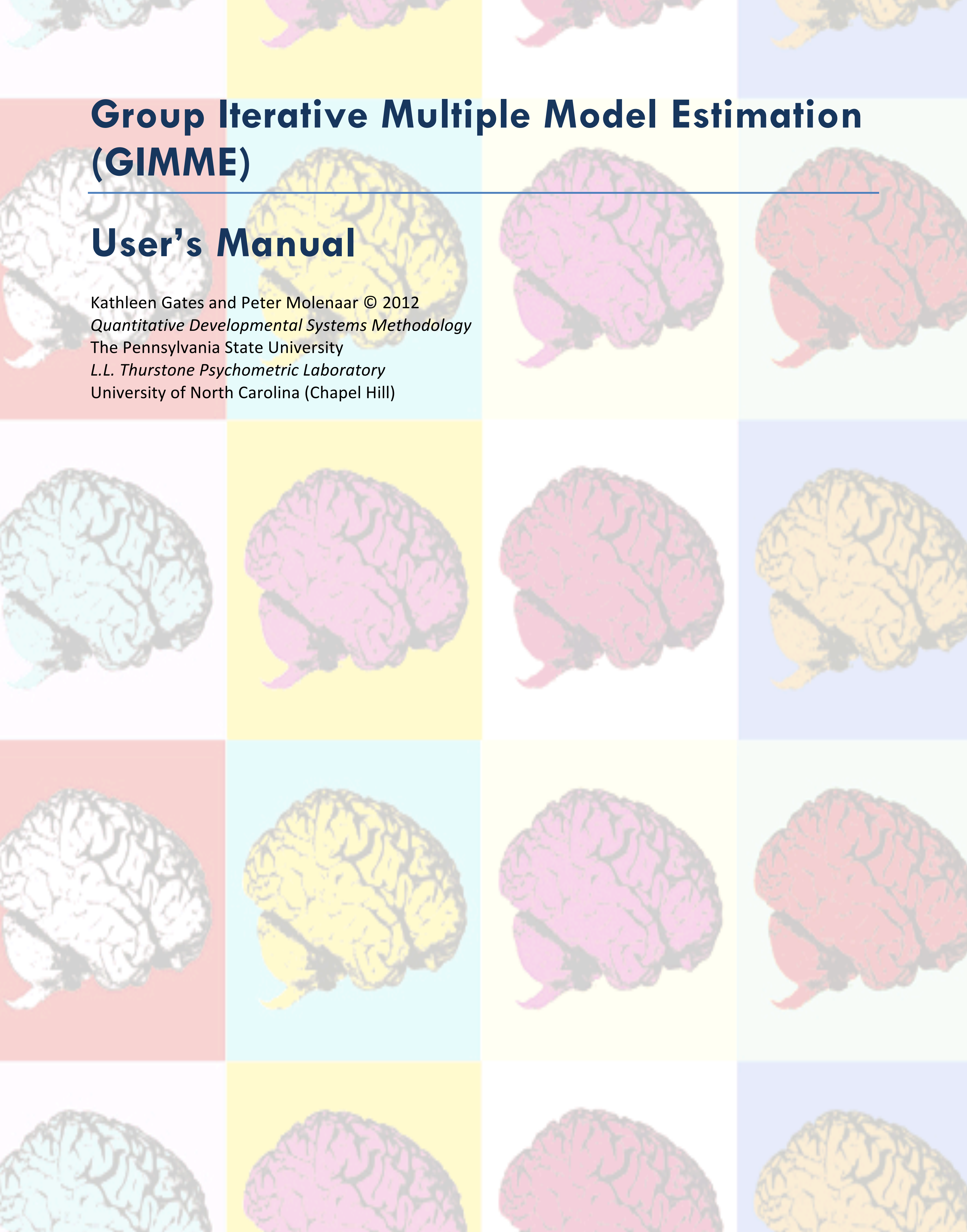

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Group Iterative Multiple Model Estimation (GIMME): The basics.

- GIMME can be used to estimate the unified SEM (uSEM; Kim et al., 2007) for block designs.

- Missing data is not a problem (see directions).

- Heterogeneous data is not a problem:
    - No “group” or “common” structure will be forced unless it truly describes the majority.
    - Individual-level nuances will surface after a group or common structure is fit (provided one exists).

- Works well with as little as 3 or as many as 25 nodes/regions of interest.

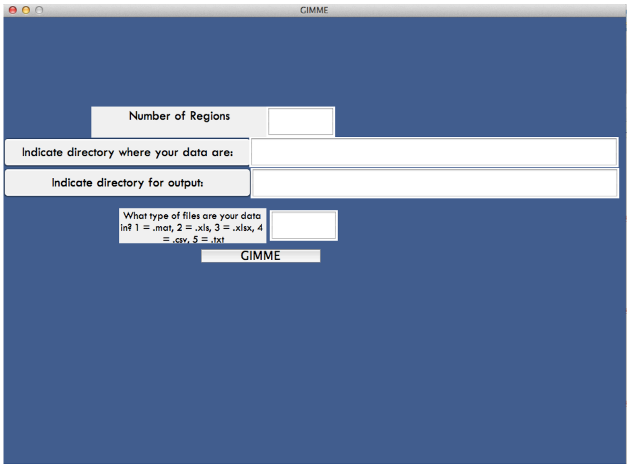
- Requires the “Statistics Toolbox” in Matlab.

    - Also requires the “Finance Toolbox” if you have missing data.

- Requires Lisrel. A student version is available for free, but then you have to have 5 or fewer regions of interest (and no experimental manipulation can be included). Some licenses for the full Lisrel program are quite affordable: a renter’s license for 6 months is only $75! http://www.ssicentral.com/ordering/index.html

Using GIMME (Group Iterative Mixed Model Estimation) with the GUI

1. **Create two new folders (i.e., directories):**
    a. Create **source** folder for where you put your ROI time series (for example, “\source”). This can be anywhere that you have permission to read and write. This folder must be empty except for the ROI files created in step 2 below.
    b. Create an **output** folder for your output (for example, “\output”). This must be different from the above folder.
2. **Extract the time series for your ROIs** using the method of your choice.
    a. Have each ROI be a column, with the rows being the observations (i.e., TR or scan).
    b. For missing values, do NOT assign it ‘0’ or use text:
        i. In excel, have the cell remain empty
        ii. In Matlab, assign NaN to the cell
    c. Have a separate file for each individual / session.
    d. If it is a Matlab file, name the variable containing the ROI series, “series”.
    e. Put these files in the “source” folder you created I step 1a. *Nothing else can be in this folder.*
3. **Ensure that GIMME is in a directory that Matlab searches.** You can add the path by typing addpath(‘C:\<*insert location of GIMME folder*>\GIMME12’) into the command window, or clicking “Set Path…” from the Matlab file menu.
4. Go to: C:\Program Files (x86)\LISREL9 . Right click the file “LisWin32.exe” and select “run as administrator”.
5. **Type “GIMME” into the command window.** A figure looking like this will come up:



6. Type in the number of ROIs.
7. Indicate the directory where your time series are located (“Source” from step 1A).
8. Indicate the directory where you would like the results to go (“Output” from step 1B).

9. The program will generate the following **output files**:
    a. finalALL.mat = file containing:
        i. MeanBeta = a beta matrix of the averaged beta matrices across all individuals and
        ii. Percent = the percent of individuals that have each possible beta in the beta matrix of connections
        iii. Signif = the percent of individuals for whom each possible beta element is significant
        iv. FIT = the percent of individuals for whom the final model is excellent according to the fit indices used to evaluate models.
    b. gbeta.mat
        i. beta = the pattern of relations common to the group.
        ii. ordermi = the order in which the paths were selected.
    c. ibeta.mat = the pattern of relations for each individual (this is rewritten for each one and can be ignored by the user)
    d. final##.mat = final results for each individual (## indicates the individual number). Contains the following:
        i. Betas.Contemporary = estimated contemporary directed effects (the A matrix)
        ii. Betas.Lagged = estimated lagged directed effects (the phi matrix)
        iii. se = estimated standard errors associated with beta values
        iv. fit = contains fit indices
    e. convergence.mat = file containing a list of participants whose models did not converge; oftentimes the program is able to fix this, but these individuals should be examined.
    f. trackparts.mat = a list of the participant files in order.

Visual explanation of matrices.

The beta matrices are in the following format:

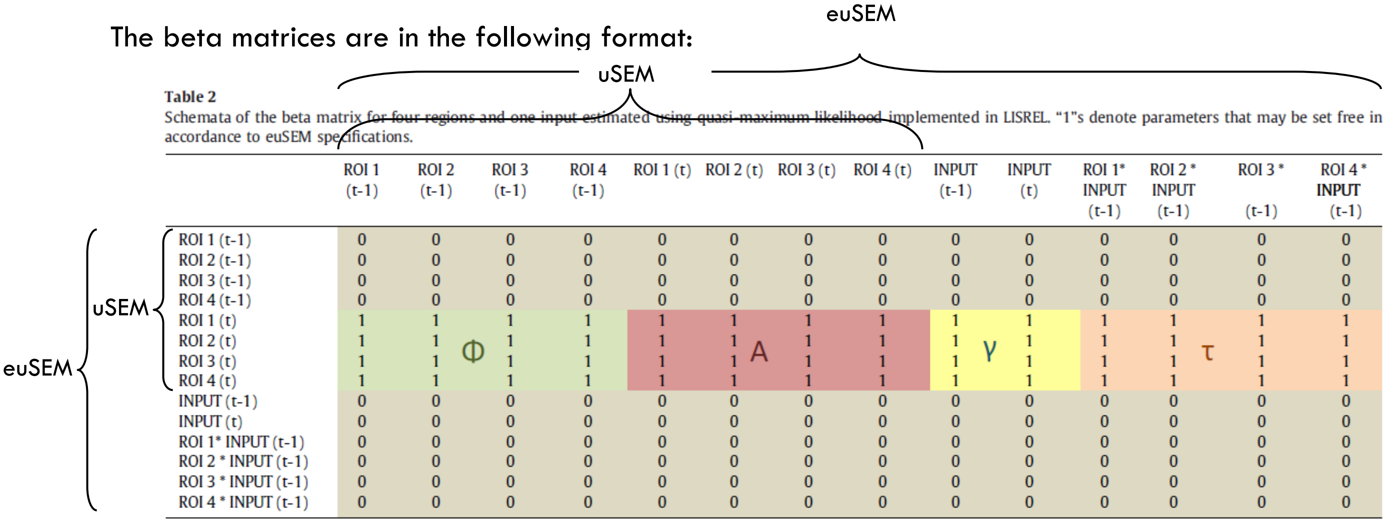


Table 2
Schemata of the beta matrix for four regions and one input estimated using quasi-maximum likelihood implemented in LISREL. "1"s denote parameters that may be set free in accordance to euSEM specifications.

	ROI 1 (t-1)	ROI 2 (t-1)	ROI 3 (t-1)	ROI 4 (t-1)	ROI 1 (t)	ROI 2 (t)	ROI 3 (t)	ROI 4 (t)	INPUT (t-1)	INPUT (t)	ROI 1* INPUT (t-1)	ROI 2 * INPUT (t-1)	ROI 3 * (t-1)	ROI 4 * **INPUT** (t-1)
ROI 1 (t-1)	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ROI 2 (t-1)	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ROI 3 (t-1)	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ROI 4 (t-1)	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ROI 1 (t)	1	1	1	1	1	1	1	1	1	1	1	1	1	1
ROI 2 (t)	1	1	1	1	1	1	1	1	1	1	1	1	1	1
ROI 3 (t)	1	1	1	1	1	1	1	1	1	1	1	1	1	1
ROI 4 (t)	1	1	1	1	1	1	1	1	1	1	1	1	1	1
INPUT (t-1)	0	0	0	0	0	0	0	0	0	0	0	0	0	0
INPUT (t)	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ROI 1* INPUT (t-1)	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ROI 2 * INPUT (t-1)	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ROI 3 * INPUT (t-1)	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ROI 4 * INPUT (t-1)	0	0	0	0	0	0	0	0	0	0	0	0	0	0

where ϕ are the lagged effects, A the contemporaneous effects, γ the input (e.g., experimental manipulation) effects, and τ the bilinear effects. Bilinear effects indicate the influence the ROI has in the presence of the experimental manipulation. The columns are the predictor or independent variables, and the rows are the dependent variables.

FAQ

1. What if the individual models are not excellent for a lot of people?

   If the fit indices are not excellent for a large proportion of individuals (as shown in the "FIT" variable found in "finalALL.mat"), then that means that the model has as many paths as possible without being over-fit. Unfortunately, in this is as good as it can get – if we added just one more path, the degrees of freedom would be 0.

2. What if no paths are opened at the group level (i.e., none of the paths have "1" in the "Percent" variable).

   Then you have no effects that were common to the majority of individuals. You have a very heterogeneous sample.

3. What if the only paths opened were those found for the group?

   Then your sample is very homogeneous. This is probably not going to happen.