

APIMeM and APIMoM Apps



APIMeM and APIMoM are shiny apps written by David A. Kenny. They can be directly accessed from the web without having to install R. The APIMeM app conducts a mediation analysis of an Actor-Partner Interdependence Model (APIM) with a mixed mediator, and the APIMoM app conducts a moderation analysis of the APIM with a mixed moderator. Both read a dyad dataset, conduct analyses using lavaan, and allow for only indistinguishable dyads. They can be accessed at

<https://davidakenny.shinyapps.io/APIMeM/>

and

<https://davidakenny.shinyapps.io/APIMoM/>.

The initial screen for APIMeM looks as follows:

Actor-Partner Interdependence Mediation Model Estimated Using Structural Equation Modeling

The screen for APIMoM is the same but “Mediation” is replaced with “Moderation.”

To run both apps, the user begins by completing in order the first three green tabs on the left. All three of these tabs must be clicked in order before the program can be run. At the top is the green "Select Data" tab which reads a dyad dataset in either SPSS or csv format. The csv (comma separated variables) file requires the variable names as the first line of the file.

The next tab to click is the green "Basic Info" tab which names the X, Y, and M (mediator or moderator) variables. Even though dyad members are to be treated as distinguishable, the program asks for names for the two members, e.g., "Supervisor" and "Employee." where it says "Label." If members are truly indistinguishable, one can just keep the default names of "Person 1" and "Person 2."

The screenshot shows the 'Basic Information' tab selected in the left sidebar. The main panel contains the following fields and options:

- Name for the X Variable:** Text input field with 'X' entered.
- Name for the Y Variable:** Text input field with 'Y' entered.
- Name for the M Variable:** Text input field with 'M' entered.
- Label for Person 1:** Text input field with 'Person 1' entered.
- Label for Person 2:** Text input field with 'Person 2' entered.
- ☒ Equal Means for the Two Members for Each Variable (unchecked if unequal)
- ☒ Equal Variances for the Two Members for Each Variable (unchecked if unequal)

If dyad members are distinguishable, the user can allow for mean or variances to be unequal across members with the APIMeM app. Nonetheless all actor and partner effects are going to be set equal across members. If means are unequal, the user is asked whether to not include the mean difference between groups in the standardization. It is generally advisable not to include the mean.

For APIMoM, the option is a little different. The user is asked whether or not to treat the means, variances, and covariances as being different for the two members. As with APIMeM, all effects are going to be the same for both members.

The screenshot shows the 'Basic Info' tab selected in the left sidebar. The main panel contains the following fields and options:

- ☒ Grand Mean Center X and M Variables:
- Name for the X Variable:** Text input field with 'X' entered.
- Name for the Y Variable:** Text input field with 'Y' entered.
- Name for the M Variable:** Text input field with 'M' entered.
- Label for Person 1:** Text input field with 'Person 1' entered.
- Label for Person 2:** Text input field with 'Person 2' entered.
- ☒ Equal Means and Variances for the Two Members for Each Variable and Equal Covariances for Every Pair of Variables (unchecked if unequal)

The last green tab is the "Variables" tab and selects at the six variables from the dyad dataset for the analysis. The user needs to select the each of the six variables (X, Y, and M by the two members) for the analysis.

Select Data

Basic Info

Variables

Miscellaneous

Run Analysis

Download Output

X for Person 1 in Data:
OtherPos_W

X for Person 2 in Data:
OtherPos_H

Y for Person 1 in Data:
Satisfaction_W

Y for Person 2 in Data:
Satisfaction_H

M for Person 1 in Data:
Tension_W

M for Person 2 in Data:
Tension_H

☐ Check To View Variable List

This screen is the same in both programs. Sometimes one needs to click on "Check To View Variable List" to be able to check on each of the six appropriate variables. This page uses the labels provided in the previous screen.

After these three Green tabs are completed, but there is an optional Black tab called "Miscellaneous" for both programs. This tab allows the user to change the alpha which defaults to .05. For APIMeM, this page is:

Select Data

Basic Information

Variables

Miscellaneous

Run Analysis

Download Output

Bootstrapping Method:
☒ Parametric
☐ Non-Parametric

Number of Trials:
40000

☒ Enter Test k Values

From X to M:
1

From M to Y:
1

☒ Alpha Equal to .05

Besides changing alpha, the user can choose the type of bootstrapping. If the non-parametric option is chosen, the program runs very slowly. The program defaults to 500 trials. Lastly the user can estimate a model where the k value (ratio of partner to actor) is fixed for the X to M paths and the M to Y paths. The program provides a statistical test of validity of such an assumption.

For APIMoM, the page is

The screenshot shows the APIMoM software interface. On the left is a vertical sidebar with five tabs: 'Select Data' (green), 'Basic Info' (green), 'Variables' (green), 'Miscellaneous' (white with a grey border), and 'Run Analysis' (blue). Below these is a purple tab labeled 'Download Output'. The main area on the right is titled 'Estimate a Model with Constraints on Interaction Effects:'. It contains four radio button options: 'No', 'Use Main Effect k Values', 'Enter User k Values' (which is selected), and 'Estimate k Values'. Below these are two input fields: 'From X to Y:' with the value '1' and 'From M to Y:' with the value '1'. At the bottom, there is a checked checkbox labeled 'Alpha Equal to .05'.

Again, the user can change alpha, and three options are given for k. One is the same as APIMeM which is to enter a priori k values. The other two empirically estimate k, one uses main effect values (i.e., the actor and partner effects without interaction terms included) and the other uses interaction values. All three of these are statistically evaluated in terms of how well they explain the four interaction effects.

Once the run is set up, the user clicks on the left blue tab "Run Analysis" and then clicks on the blue tab "Click Here to Begin APIM Mediation (or Moderation) Analysis Now" to run the analysis. The results appear on the left side of screen and the user can select Text, Tables, Computer Output, or Figures in the purple vertical tabs:

The screenshot shows a horizontal row of four purple tabs: 'Text', 'Tables', 'Computer Output', and 'Figures'. The 'Text' tab is currently selected and has a white background, while the others have a solid purple background.

Finally if the user wants to save the text output, tables, and computer output to a file (docx, html, or pdf formats), the user clicks on the bottom purple tab on the left labelled "Download Output" and selects the options on the left. The downloaded report contains all of the information that the user sees on the right.

Begin the Analysis of Distinguishability Now!

Select Data

Distinguishing Variable

Mixed Variables

Between-Dyads Variables

Within-Dyads Variables

Miscellaneous

Download Output

Title of the Report:
Tests of Distinguishability and N

File Name:
Dingy_Output

Download Output after Running -- pick a format

☒ Word ☐ HTML ☐ PDF

[Download Text, Tables, & Output](#)

The program is reactive. Thus, if the user wants to make a change in the analysis, the user can make that change (e.g., change the variables or the alpha level) and then click the blue tab “Begin the Analysis of Distinguishability Now!” tab and a new set of results will appear on the right which can be downloaded. There is no need to start all over.

An example of pdf output for APIMeM is at davidakenny.net/doc/APIMeM_Output.pdf and for APIMoM is at davidakenny.net/doc/APIMoM_Output.pdf.