

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 (one record for each dyad), conduct analyses using lavaan, and allow for only indistinguishable dyads with no covariates. They can be accessed at

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

and

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

Both programs are highly experimental and results should be carefully checked for their accuracy.

Before running the mediation program, it would help most users to read Ledermann, Macho, and Kenny (2011. Assessing mediation in dyadic data using the Actor-Partner Interdependence Model. *Structural Equation Modeling*, 18, 595-612) or to read Garcia, Ledermann, and Kenny (2015). Moderation in the actor-partner interdependence model. *Personal Relationships*, 22, 8-29) before running the moderation program.

Below is a description for both programs. In some cases, only the APIMeM screen is shown, but the APIMoM screen is essentially the same. Note there may be some changes in these programs and screens may appear a bit different from below. Also with different browsers, the appearance can be a bit different.

The opening screen for APIMeM is 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.”

The upper “Help & Contact” provides some documentation, links to documentation, and a way to give feedback.

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. The first 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 Information” 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 a web interface for data analysis. At the top, there are three tabs: 'Select Data', 'Basic Information' (which is highlighted with a dashed blue border), and 'Miscellaneous'. Below these tabs, there are two more tabs: 'Variables' and 'Miscellaneous'. A purple link 'Download Output' is located below the tabs. The main content area contains several input fields and checkboxes:

- Name for the X Variable:** Input field containing 'X'.
- Name for the Y Variable:** Input field containing 'Y'.
- Name for the M Variable:** Input field containing 'M'.
- Label for Person 1:** Input field containing 'Person 1'.
- Label for Person 2:** Input field containing 'Person 2'.
- Equal Means for the Two Members for Each Variable (uncheck if unequal)
- Equal Variances for the Two Members for Each Variable (uncheck 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 or not to include the mean difference in the computation of the variances. It is generally advisable not to include the mean difference.

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 between variables are going to be the same for both members.

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 Information

Variables Miscellaneous

Download Output

X for Person 1 in Data:
Anxiety_M ▼

X for Person 2 in Data:
Anxiety_W ▼

Y for Person 1 in Data:
Sat_M ▼

Y for Person 2 in Data:
Sat_W ▼

M for Person 1 in Data:
Avoid_M ▼

M for Person 2 in Data:
Avoid_W ▼

Check To View Variable List

This screen is the same in both programs. For each of the six variables in the analysis, the user finds the relevant variable in the dataset. 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:

Begin APIM Mediation Analysis!

Select Data Basic Information

Variables Miscellaneous

Download Output

Bootstrapping Method:

Parametric

Non-Parametric

Number of Trials:

40000

Enter Test k Values

Alpha Equal to .05

Besides changing alpha, the user can choose the type of bootstrapping. If the non-parametric option is chosen, the program defaults to 500 trials and the runs very slowly. T. Lastly the user can estimate a model where the k value (ratio of the partner to the actor effect) 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

Estimate a Model with Constraints on Interaction Effects:

No

Use Main Effect k Values

Enter User k Values

Estimate k Values

From X to Y:

1

From M to Y:

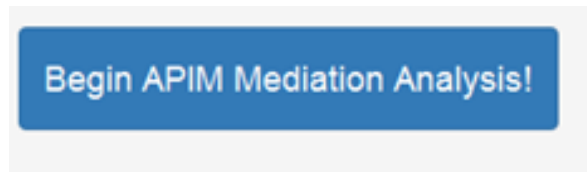
1

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 and interaction terms have the same k values) 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 top blue tab "Begin APIM Mediation (or Moderation) Analysis!" to run the analysis.

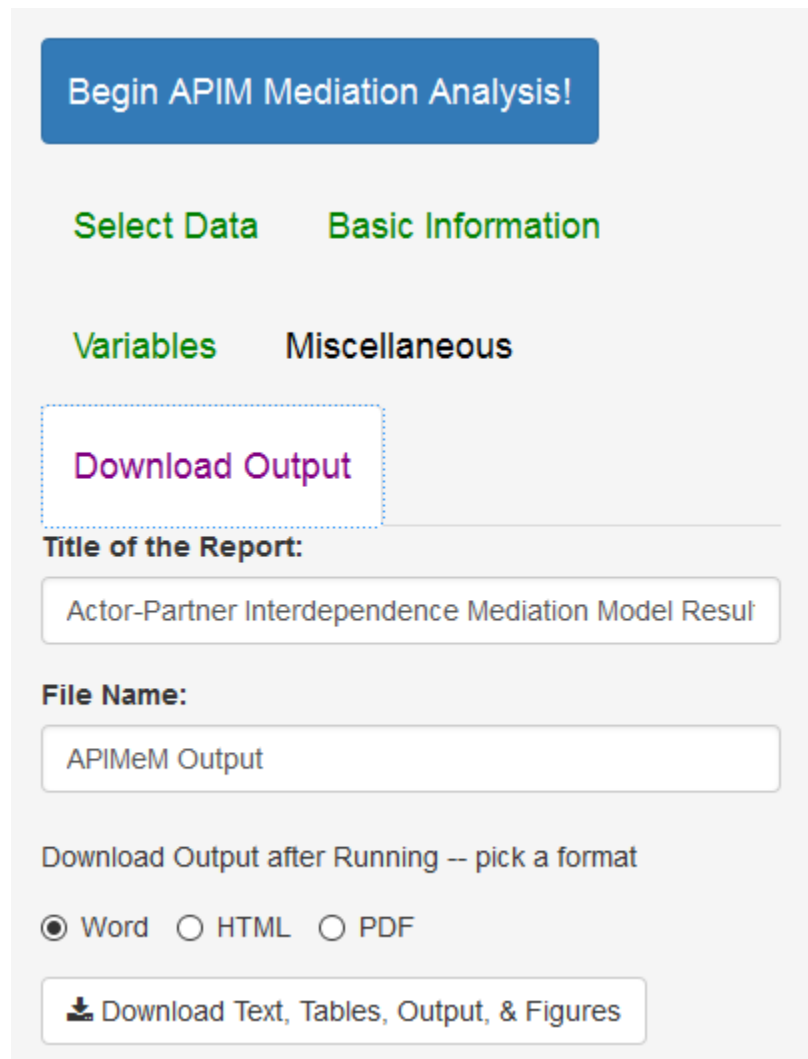


The results appear, perhaps after a few seconds, on the right side of screen and the user can select Text, Tables, Computer Output, or Figures in the purple horizontal tabs:



For APIMeM, the figure is path model with all the APIMeM paths. For APIMoM, a series of graphs are presented. The X-axis is the actor or partner variable for X and the Y-axis it the Y variables. Different curves are drawn for different values of the moderator variable for one standard deviation above the mean and one below for actor and/or partner values of the moderator, M.

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. Note that the user can change the name of this file as well as the title of the report on the document itself.



The screenshot shows a web interface for APIMeM/Mod. At the top is a blue button labeled "Begin APIM Mediation Analysis!". Below it are two tabs: "Select Data" and "Basic Information", both in green. Under "Basic Information" are two sub-tabs: "Variables" and "Miscellaneous", also in green. A purple button labeled "Download Output" is highlighted with a dashed blue border. Below this are two text input fields: "Title of the Report:" with the text "Actor-Partner Interdependence Mediation Model Result" and "File Name:" with the text "APIMeM Output". Below the input fields is a section titled "Download Output after Running -- pick a format" with three radio buttons: "Word" (selected), "HTML", and "PDF". At the bottom is a button with a download icon and the text "Download Text, Tables, Output, & Figures".

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 APIM Mediation (or Moderation) Analysis!” tab and a new set of results will appear on the right which can be downloaded. There is no need to start all over. Though not fully “idiot proofed,” the programs do not always crash when the user makes an error; on the right-side of the screen a message should appear telling the user what the problem is. Hopefully, it alerts the user what needs to be changed, alleviating the need to start the run all over.

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