

September 18, 2007

Computer Lab for calculating Cronbach's alpha and Installing Mplus

Goals for today's lab

1. To run an analysis of Cronbach's alpha in SAS (or in SPSS if you prefer), which includes the steps of: downloading data from the web, reading it into SAS, then running the program.
2. To get Mplus Demo version installed onto your laptop.

Step 0: Create a "pubh7435" folder on the desktop where you can keep work that is done throughout the semester.

Calculating Cronbach's alpha

1. Download 2 datasets from the class Data website at <http://www.biostat.umn.edu/~melanie/PH7435/DATA/index.html>. Get the Concerns with genetic testing data "genetictestingrawdata.xls", and get the "raw data for USA q29a-q29h" which is also an Excel file. (the .xls extension indicates it is an Excel file). Also download the "genetictesting.sas" and "mplusgenetictesting.inp" programs by right-clicking on them and saving to your folder.
2. Open SAS and import the genetic testing data. To import the dataset "genetictestingrawdata.xls", click on the **File** button then on **Import Data...** A wizard pops up asking you what type of file it is, usually by default it is on "Microsoft Excel", if so click **Next**, then it will pop-up a window with a **Browse** button which you can use to find the genetictestingrawdata.xls data on your computer (remember you put it in the pubh7435 folder on your desktop). Find the file, click on it and say Ok. Then SAS will ask you which table you want to import (this is because there are actually 3 sheets in the .xls file, but only the first one has any data on it), so we want Sheet1\$. If you click on **Options...** you'll see what SAS is doing by default, make sure that the "Use data in the first row as SAS variable name" has a checkmark next to it. Then say OK, and Next. The next panel asks you to "Choose the SAS destination" and the cursor is located in the "Member" fill-in. In the member slot is where you type in a name for the dataset you are importing. You should give it a simple name that can be used to call it from within SAS. I like to call my datasets very simply, e.g. "a". But you can call it anything, like "mygenetictestingdata", you just can't put blanks in the name. This will be the name SAS uses to call the data when running procedures. Once you've typed in a name, click **Finish**. In the log window, if all went well, it should say "NOTE: WORK.A was successfully created."

3. Run the “geneticesting.sas” program downloaded from the class data website. Scroll through the results in the output Window, these are results we have seen in class. Proc Corr with the alpha option gives us Cronbach’s alpha analysis and Proc Factor gives us eigenvalues (along with a lot of other output we will examine later). To run the program in the program Editor click on Run then Submit, or simply click on the running man icon.
 4. **If you have time after installing the Demo version of Mplus below**, try running a similar Cronbach’s alpha analysis of the “raw data for USA q29a-q29h” data.
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Installing Demo version of Mplus onto the computer

1. Go to www.statmodel.com and click on Mplus Demo Version on the left hand side. Go about halfway down the page and click on mpdzip.exe and follow the steps to install it.
2. **If you have time**, try running an Mplus program to do EFA on the genetic testing data. **MPLUS CANNOT READ EXCEL FILES!!!!** It is necessary to put the data into a comma delimited format in order to read it into Mplus. It is also necessary to delete the first line of the dataset which contains the variable names. Mplus can only read in numeric quantities and you must specify the column variable names in the program itself, not in the dataset. So, open the “geneticestingrawdata.xls” in Excel, delete the first row and then us **Save As...** to save the file as a .csv (Comma Delimited) format.
3. Run the “mplusgeneticesting.inp” program downloaded from the class website. Open Mplus, read the program in, change the **file is** line so that it appropriately references the location of your newly created .csv file. NOTE: Mplus only allows each line of the program to be 80 characters wide, if the program line is very long, get rid of spaces, and or use a carriage return to put it on the next line. In the lower right hand corner of Mplus it says which line and column your cursor is on. Once you have the program ready, try running it by clicking **Run** in the menu bar.