# Note: This is an older version of the labs for this class. There is a lot of helpful material here, but you do not need to submit anything regarding this document.

# Intro to LCA: Practice 1

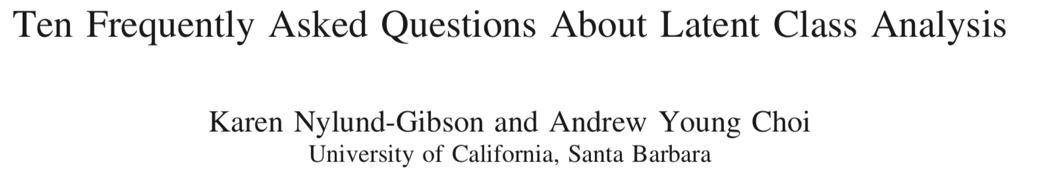
**Outline**

1. Why use **MplusAutomation R package**, is it worth the trouble?
   1. Compared to doing in R
   2. Or entirely in Mplus
2. Demonstrate the enumeration example using MplusAutomation
3. Review the Mplus & R BASICS handouts
4. Use the R script, template file, and PDF handout in the Lab 1 folder to run the example on your own computer.

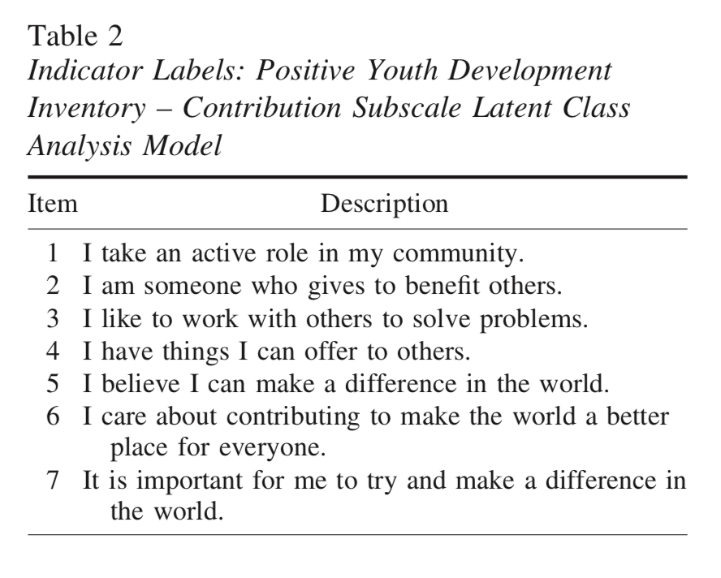
**Practicing LCA enumeration using MplusAutomation in R:**

**Applied Example: Positive Youth Development Inventory Analysis**

We will replicate the LCA illustrated in the following 2018 article published in, Translational Issues in Psychological Science

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The indicators used in the LCA are from the Positive Youth Development Inventory (PYDI) Contribution subscale (Arnold, Nott, & Meinhold, 2012). The data was collected from 1,629 college students in the Santa Barbara by GGSE’s CoVitality lab.



**Step 1 – Organization**

* Create a folder on your computers desktop (e.g. “lab\_1”) with a subfolder inside titled “mplus\_lab1”.
* From GauchoSpace download the Lab 1 template file (.txt), the data file (PYDI.dat), the R script file (.R), and the Lab 1 handout (.pdf).
* Put all the files in the folder you created on your desktop.
* Move the data file, PYDI.dat, into the subfolder “mplus\_lab1”

**Step 2 – Edit the template file [[/init]] section.**

* Add the appropriate **file-path**
* Check that the **iterator** line of code will create the desired set of models.
* Add the iterator command in the following places (as shown in the PDF handout):
  + Specify the iterator name, and values it should iterate
  + Add the iterator command into the **filename** code. This tells Mplus how to name the input files.
  + Add the iterator command into the **title**
  + Add the iterator command into the syntax which specifies the number of classes
* Edit the file-path line of code to reflect the location of the folder you created called **mplus\_lab1**

**Step 3 – run Mplus automation, follow the steps from the PDF Lab 1 handout.**

* Generate the 3-class plot in R using ggplot2
* Try generating the 4-class plot, does it replicate the Nylund-Gibson, & Choi (2018) figure? This will require changing the R code in a couple of places. Ask for help!

**Step 4 – locate the following parameters from the 3-Class Mplus output file**

1. Locate the following in the output file:
   1. Total analysis sample size.
   2. Number of free parameters.
   3. Observed item response counts and proportions.
   4. Final class counts and proportions based on the estimated model.
   5. Model-estimated item thresholds for each class.
   6. Latent class multinomial logit means (class proportion/size).
   7. Class-specific item response probabilities.
2. Thinking of this in terms of a latent variable measurement model, which parameters are “measurement parameters” and which parameters are “structural parameters”?

Mplus gives you a message similar to the following:

IN THE OPTIMIZATION, ONE OR MORE LOGIT THRESHOLDS APPROACHED AND WERE SET

AT THE EXTREME VALUES. EXTREME VALUES ARE -15.000 AND 15.000.

THE FOLLOWING THRESHOLDS WERE SET AT THESE VALUES:

\* THRESHOLD 1 OF CLASS INDICATOR CA28GR FOR CLASS 2 AT ITERATION 69

Locate the message this message in your output file. Any thoughts on what it means?