

Lab 7 - Ten Growth Models - Simple to Advanced

Structural Equation Modeling - Instructor: Karen Nylund-Gibson

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1 Lab preparation

1.1 Creating a version-controlled R-Project with Github

Download repository here: <https://github.com/garberadamc/SEM-Lab7>

On the Github repository webpage:

- a. **fork** your own **branch** of the lab repository
- b. copy the repository web URL address from the **clone or download** menu

Within R-Studio:

- c. click “NEW PROJECT”
 - d. choose option **Version Control**
 - e. choose option **Git**
 - f. paste the repository web URL path copied from the **clone or download** menu on Github page
 - g. choose location of the R-Project
-

1.2 Data source:

The first 3 models utilize a public use data subset the *Longitudinal Survey of American Youth (LSAY)*
[See documentation here](#)

Load packages

```
library(transformr)
library(gganimate)
library(hrbrthemes)
library(tidyverse)
library(haven)
library(janitor)
library(MplusAutomation)
library(rhdf5)
library(here)
library(kableExtra)
library(gtsummary)
library(semPlot)
library(naniar)
```

1.3 LSAY data example - Math Scores across 6 timepoints

Read in data

```
lsay_data <- read_spss(here("data", "LSAY_labs.sav")) %>% #
  select(RURAL, GENDER, FATHED, MOTHEd, #
    -starts_with("AB"), #
    ends_with("IMP"), #
    -contains("BIO"), #
    -contains("PHY")) %>% #
  clean_names() %>% #
  rename( math_07 = amthimp , #
    math_08 = cmthimp , #
    math_09 = emthimp , #
    math_10 = gmthimp , #
    math_11 = imthimp , #
    math_12 = kmthimp , #
    sci_07 = asciimp , #
    sci_08 = csciimp , #
    sci_09 = esciimp , #
    sci_10 = gsciimp , #
    sci_11 = isciimp , #
    sci_12 = ksciimp ) %>% #
  replace_with_na_all(condition = ~.x == 9999.00) #
```

View metadata

```
sjPlot::view_df(lsay_data)
```

Write a CSV file

```
write_csv(lsay_data, here("data", "lsay_lab7_data.csv"))
```

Read in the CSV file (SPSS labels removed)

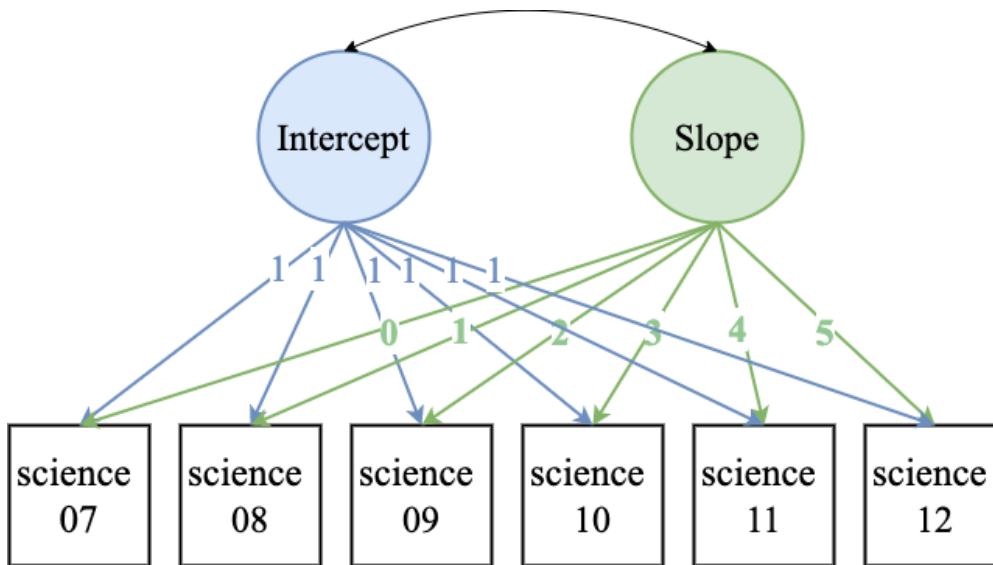
```
lsay_lab7 <- read_csv(here("data", "lsay_lab7_data.csv"))
```

2 Let's start modeling

Table. LSAY repeated measures

Name	Labels	Variable type
math_07	7th grade math score	time varying covariate
math_08	8th grade math score	
math_09	9th grade math score	
math_10	10th grade math score	
math_11	11th grade math score	
math_12	12th grade math score	
sci_07	7th grade science score	model indicators (outcomes)
sci_08	8th grade science score	
sci_09	9th grade science score	
sci_10	10th grade science score	
sci_11	11th grade science score	
sci_12	12th grade science score	

2.1 Model 01 - Fixed time effects



```
m1_growth <- mplusObject(
  TITLE = "m1 growth model fixed time scores - Lab 7",
  VARIABLE =
    "usevar =
      sci_07-sci_12; ",
  ANALYSIS =
    "estimator = MLR" ,
  MODEL =
    "i s | sci_07@0 sci_08@1 sci_09@2 sci_10@3 sci_11@4 sci_12@5; " ,
  OUTPUT = "sampstat standardized;",
```

```

PLOT = "type=plot3;
        series = sci_07-sci_12(*)",

usevariables = colnames(lsay_lab7),
rdata = lsay_lab7)

m1_growth_fit <- mplusModeler(m1_growth,
                             dataout=here("mplus_files", "Lab7.dat"),
                             modelout=here("mplus_files", "m1_growth_Lab7.inp"),
                             check=TRUE, run = TRUE, hashfilename = FALSE)

```

Load in the mplus.R functions

```
source(here("mplus.R.txt"))
```

```
## [1] "Loaded rhdf5 package"
```

2.2 ~~~~ Plotting using gh5 plot data generated by Mplus

1. View plots available for a given model
2. Generate plots using the `get.plot.---` function
3. Extract data and transform to tidy format
4. Plot with `ggplot`

```
mplus.view.plots(here("mplus_files", "m1_growth_Lab6.gh5"))
```

Prepare plot data

```

observed <- lsay_lab7 %>% select(starts_with("sci")) %>%
  rownames_to_column() %>% drop_na()

obs100 <- observed[1:100,]

plot_obs <- obs100 %>%
  pivot_longer(`sci_07`:`sci_12`, # The columns I'm gathering together
               names_to = "grade", # new column name for existing names
               values_to = "value") # new column name to store values

gradelevels <- colnames(observed[,2:7])

mean_est <- as.data.frame(mplus.get.estimated_means(here(
  "mplus_files", "m1_growth_Lab7.gh5")) %>%
  mutate(grade = gradelevels)

```

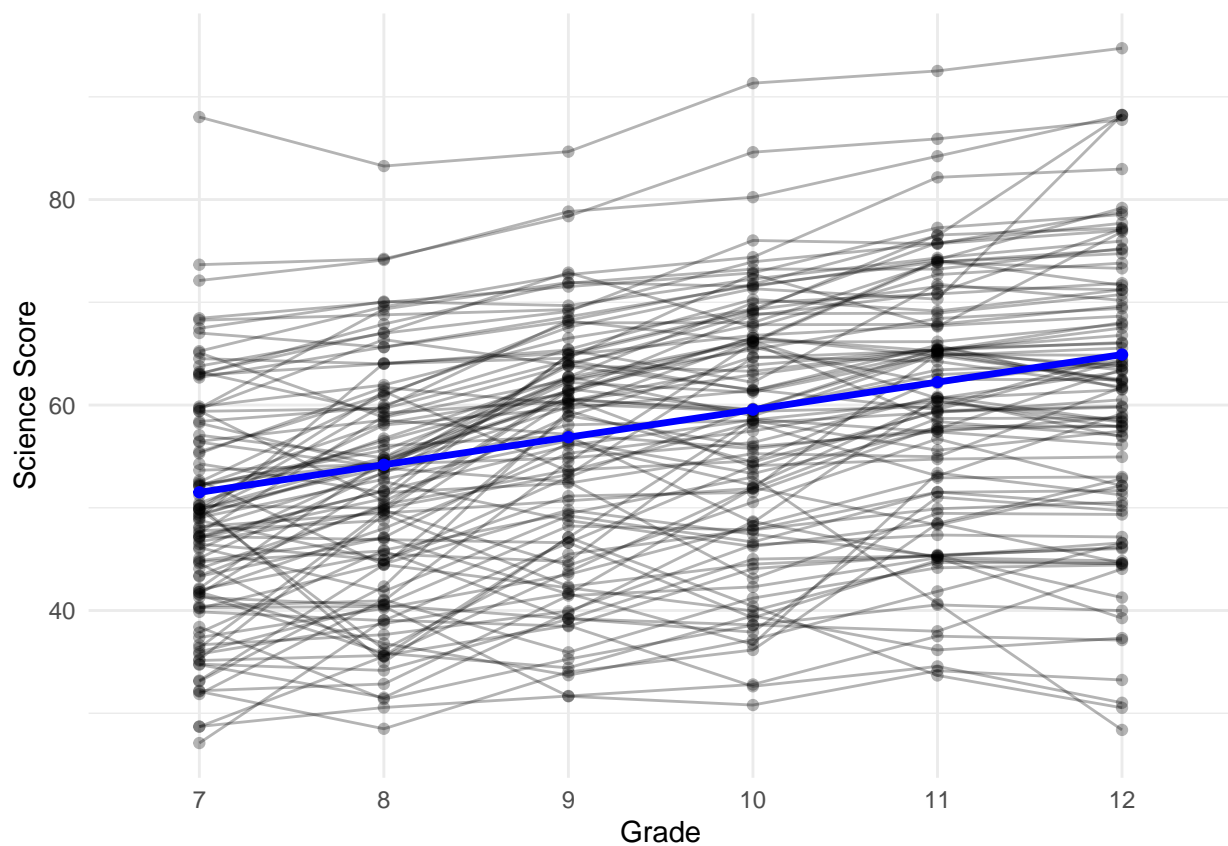
Plot the model estimated means superimposed on the observed individual values

```

growth_plot <- ggplot() +
  geom_point(data = plot_obs,
    aes(x = grade, y = value, group = rowname), alpha = .3) +
  geom_line(data = plot_obs,
    aes(x = grade, y = value, group = rowname), alpha = .3) +
  geom_point(data=mean_est,
    aes(x=grade, y = V1), color = "Blue", size = 1.5) +
  geom_line(data=mean_est,
    aes(x=grade, y = V1, group = 1), color = "Blue", size = 1.2) +
  scale_x_discrete(labels = c("7", "8", "9", "10", "11", "12")) +
  labs(x="Grade", y="Science Score") +
  theme_minimal()

```

growth_plot



```

ggsave(here("figures", "spaghetti_p1.png"), height = 6, width = 8, dpi = "retina")

```

Animate the plot with {gganimate}

```

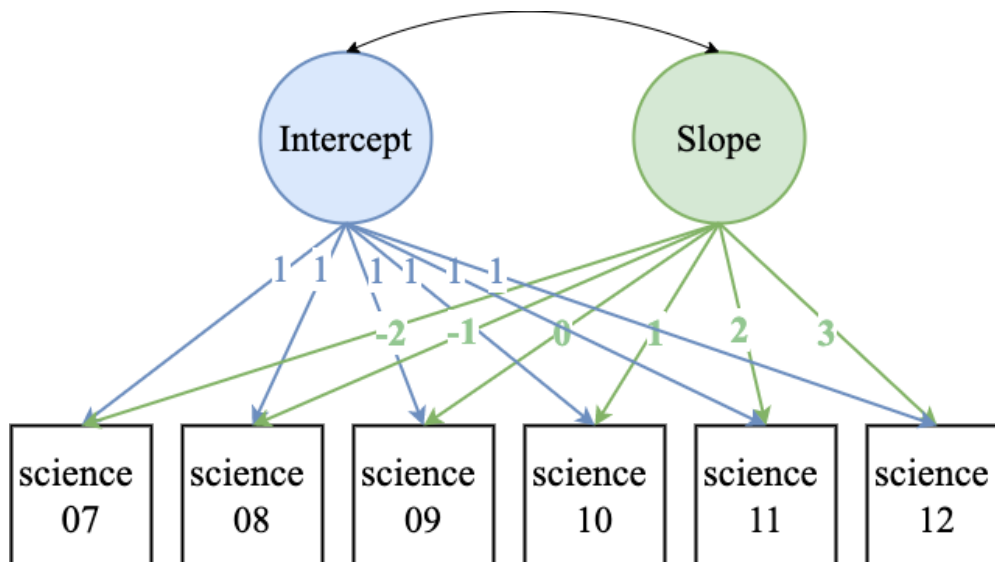
growth_plot +
  transition_states(rowname,
    transition_length = 1,
    state_length = 1) +
  shadow_mark(color = "Magenta", alpha = .3)

```

```
anim_save(here("figures", "spaghetti_plot.gif"), height = 6, width = 8, dpi = "retina")
```

2.3 Model 02 - Centering the Intercept

- Centering determines the interpretation of the intercept growth factor
- The centering point is the timepoint at which the time score is zero
- A model can be estimated for different centering points depending on which interpretation is of interest



```
m2_growth <- mplusObject(
  TITLE = "m2 growth model centering time scores - Lab 7",
  VARIABLE =
    "usevar =
      sci_07-sci_12; ",

  ANALYSIS =
    "estimator = MLR" ,

  MODEL =
    "i s | sci_07@-2 sci_08@-1 sci_09@0 sci_10@1 sci_11@2 sci_12@3; " ,

  OUTPUT = "sampstat standardized;",

  PLOT = "type=plot3;
          series = sci_07-sci_12(*)",

  usevariables = colnames(lsay_lab7),
  rdata = lsay_lab7)

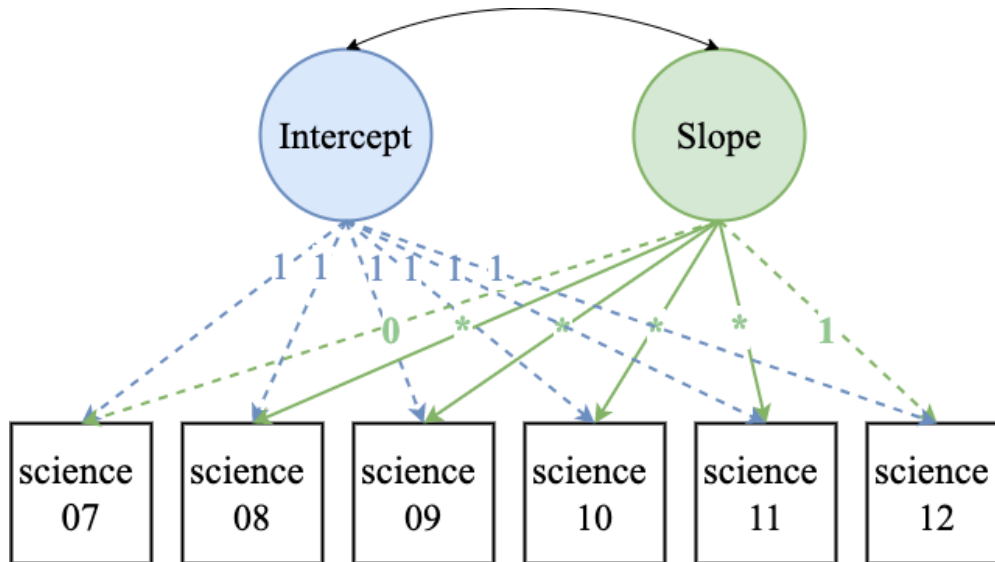
m2_growth_fit <- mplusModeler(m2_growth,
```

```

dataout=here("mplus_files", "Lab7.dat"),
modelout=here("mplus_files", "m2_growth_Lab7.inp"),
check=TRUE, run = TRUE, hashfilename = FALSE)

```

2.4 Model 03 - freely estimated time scores



```

m3_growth <- mplusObject(
  TITLE = "m3 growth model freely estimated time scores - Lab 7",
  VARIABLE =
    "usevar =
      sci_07-sci_12; ",

  ANALYSIS =
    "estimator = MLR" ,

  MODEL =
    "i s | sci_07@0 sci_08* sci_09* sci_10* sci_11* sci_12@1; " ,

  OUTPUT = "sampstat standardized;",

  PLOT = "type=plot3;
          series = sci_07-sci_12(*)",

  usevariables = colnames(lsay_lab7),
  rdata = lsay_lab7)

m3_growth_fit <- mplusModeler(m3_growth,
  dataout=here("mplus_files", "Lab7.dat"),
  modelout=here("mplus_files", "m3_growth_Lab7.inp"),
  check=TRUE, run = TRUE, hashfilename = FALSE)

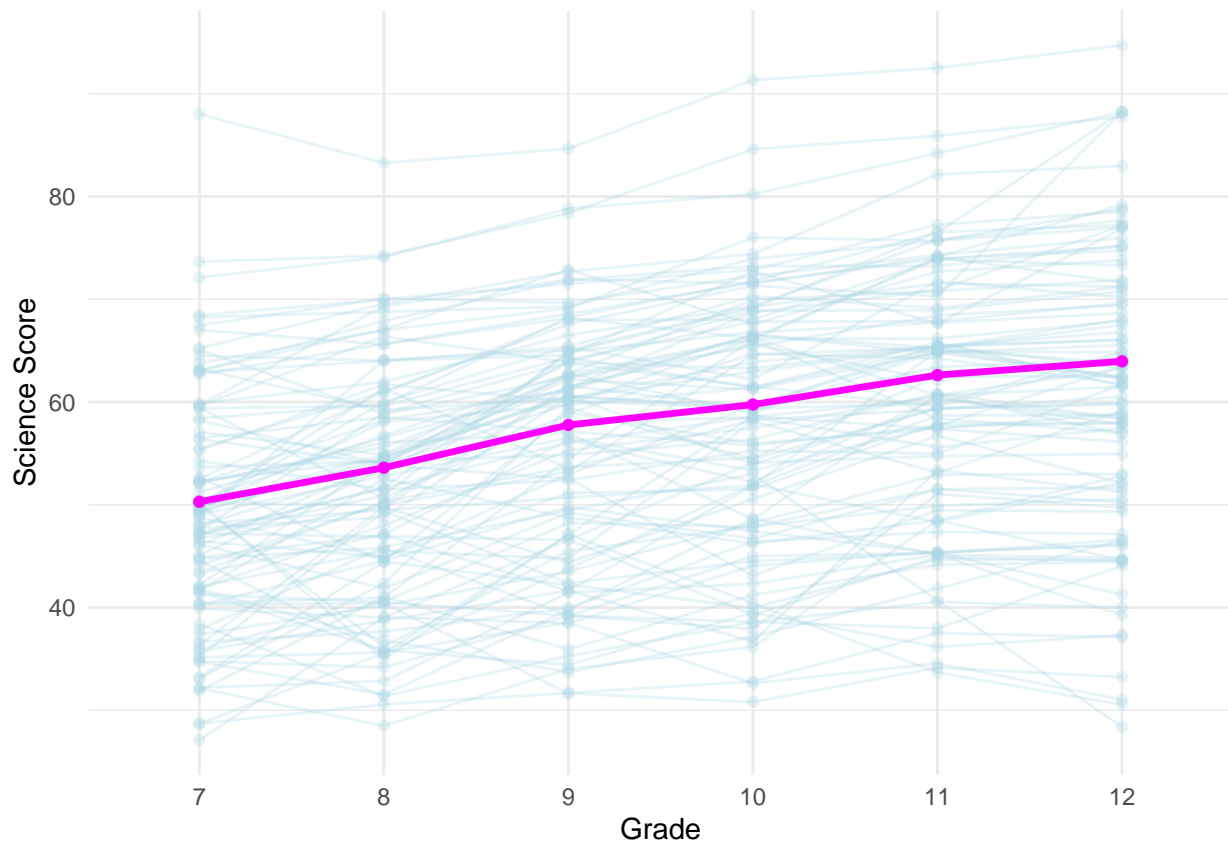
```

Prepare plot data

```
mean_est2 <- as.data.frame(mplus.get.estimated_means(here("mplus_files", "m3_growth_Lab7.gh5"))) %>%  
  mutate(grade = gradelevels)
```

Plot the model estimated means superimposed on the observed individual values

```
growth_plot <- ggplot() +  
  geom_point(data = plot_obs,  
            aes(x = grade, y = value, group = rowname), color = "lightblue", alpha = .3) +  
  geom_line(data = plot_obs,  
           aes(x = grade, y = value, group = rowname), color = "lightblue", alpha = .3) +  
  geom_point(data=mean_est2,  
            aes(x=grade, y = V1), color = "magenta", size = 1.5) +  
  geom_line(data=mean_est2,  
           aes(x=grade, y = V1, group = 1), color = "magenta", size = 1.2) +  
  scale_x_discrete(labels = c("7", "8", "9", "10", "11", "12")) +  
  labs(x="Grade", y="Science Score") +  
  theme_minimal()  
  
growth_plot
```



2.5 Model 04 - time-invariant covariates and freely estimated time scores

covariates:

- gender: 1 = female
- rural: 1 = rural
- fathed: Father's reported education
- mothed: Mother's reported education

```
m4_growth <- mplusObject(
  TITLE = "m4 time-invariant covariates and freely estimated time scores - Lab 7",
  VARIABLE =
    "usevar =
      sci_07-sci_12
      gender rural fathed mothed; ",

  ANALYSIS =
    "estimator = MLR" ,

  MODEL =
    "i s | sci_07@0 sci_08* sci_09* sci_10* sci_11* sci_12@1;
      i s on gender rural fathed mothed;" ,

  OUTPUT = "sampstat standardized;",

  PLOT = "type=plot3;
          series = sci_07-sci_12(*)",

  usevariables = colnames(lsay_lab7),
  rdata = lsay_lab7)

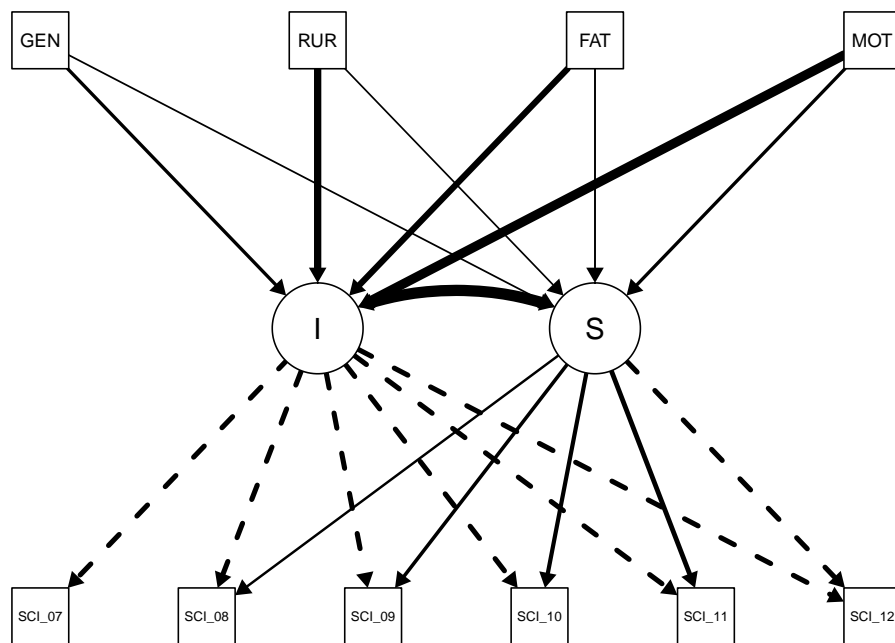
m4_growth_fit <- mplusModeler(m4_growth,
  dataout=here("mplus_files", "Lab7.dat"),
  modelout=here("mplus_files", "m4_growth_Lab7.inp"),
  check=TRUE, run = TRUE, hashfilename = FALSE)
```

Check the path diagram with `semPlot`

```
m4_output <- readModels(here("mplus_files", "m4_growth_Lab7.out"))

## Reading model: /Users/agarber/Desktop/SEM_S20/Lab7_SEM/mplus_files/m4_growth_Lab7.out

semPaths(m4_output, "est",
  intercepts=FALSE, residuals = FALSE, fade = FALSE,
  edge.color = "black", edgeLabels = "")
```



2.6 Model 05 - time-varying covariates

repeated measure covariate: math scores: grades 7 to 12 time-invariant covariate: mothed

```
m5_growth <- mplusObject(
  TITLE = "m05 time-varying covariates - Lab 7",
  VARIABLE =
    "usevar =
      sci_07-sci_12
      math_07-math_12 mothed; ",
  ANALYSIS =
    "estimator = MLR" ,
  MODEL =
    "i s | sci_07@0 sci_08* sci_09* sci_10* sci_11* sci_12@1;
     i s on mothed;
     sci_07 on math_07;
     sci_08 on math_08;
     sci_09 on math_09;
     sci_10 on math_10;
     sci_11 on math_11;
     sci_12 on math_12; ",
  OUTPUT = "sampstat standardized;",
  PLOT = "type=plot3;
```

```

series = sci_07-sci_12(*)",

usevariables = colnames(lsay_lab7),
rdata = lsay_lab7)

m5_growth_fit <- mplusModeler(m5_growth,
  dataout=here("mplus_files", "Lab7.dat"),
  modelout=here("mplus_files", "m5_growth_Lab7.inp"),
  check=TRUE, run = TRUE, hashfilename = FALSE)

```

Check the path diagram

```

m5_output <- readModels(here("mplus_files", "m5_growth_Lab7.out"))

```

```

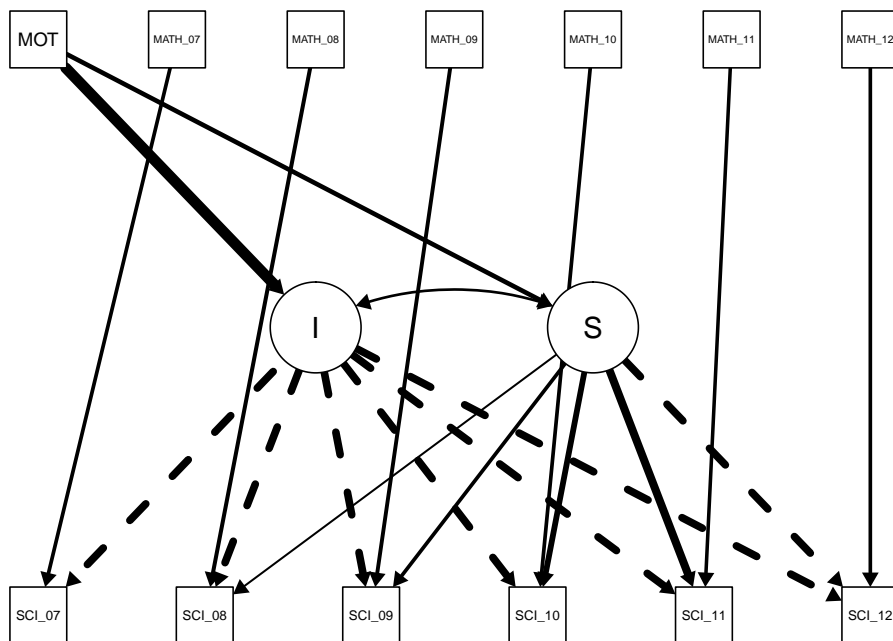
## Reading model: /Users/agarber/Desktop/SEM_S20/Lab7_SEM/mplus_files/m5_growth_Lab7.out

```

```

semPaths(m5_output, "est", intercepts = FALSE, residuals = FALSE, fade = FALSE, edge.color = "black",
  edgeLabels = "")

```



2.7 Model 06 - Time-varying covariate with time-invariant effect

```

m6_growth <- mplusObject(
  TITLE = "m06 time-varying covariates - Lab 7",
  VARIABLE =
    "usevar =
      sci_07-sci_12
      math_07-math_12 methoded; ",

```

```

ANALYSIS =
  "estimator = MLR" ,

MODEL =
  "i s | sci_07@0 sci_08* sci_09* sci_10* sci_11* sci_12@1;
  i s on mothed;
  sci_07 on math_07(1); ! TIME-INVARIANT: Fixed to equality
  sci_08 on math_08(1);
  sci_09 on math_09(1);
  sci_10 on math_10(1);
  sci_11 on math_11(1);
  sci_12 on math_12(1); ",

OUTPUT = "sampstat standardized;",

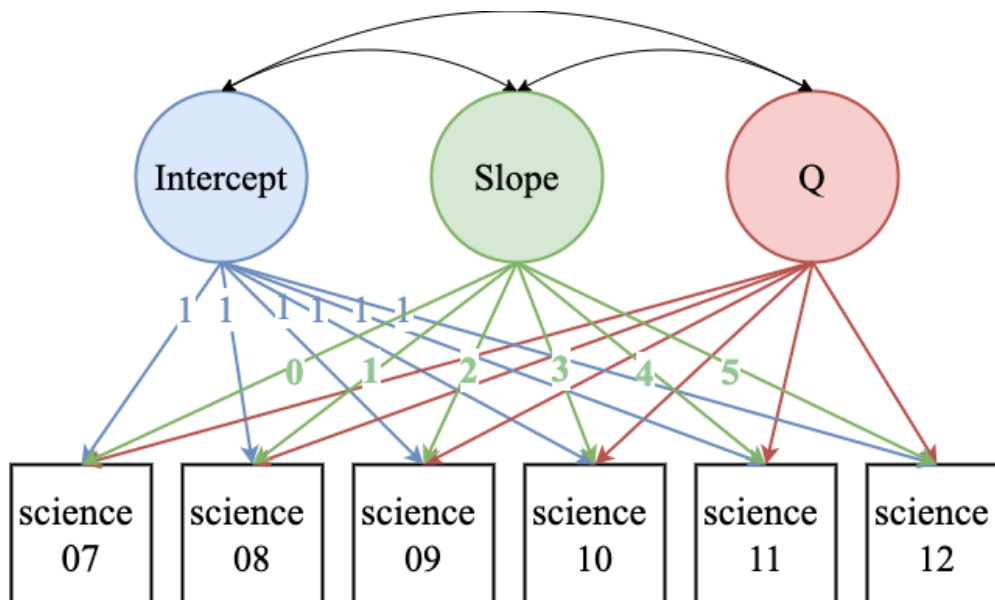
PLOT = "type=plot3;
        series = sci_07-sci_12(*)",

usevariables = colnames(lsay_lab7),
rdata = lsay_lab7)

m6_growth_fit <- mplusModeler(m6_growth,
                             dataout=here("mplus_files", "Lab7.dat"),
                             modelout=here("mplus_files", "m6_growth_Lab7.inp"),
                             check=TRUE, run = TRUE, hashfilename = FALSE)

```

2.8 Model 07 - Quadratic Growth



```

m7_growth <- mplusObject(
  TITLE = "m07 Quadratic Growth (i s q) - Lab 7",
  VARIABLE =
    "usevar =
      sci_07-sci_12
      math_07-math_12; ",

  ANALYSIS =
    "estimator = MLR" ,

  MODEL =
    "i s q | sci_07@0 sci_08@1 sci_09@2 sci_10@3 sci_11@4 sci_12@5; ",

  OUTPUT = "sampstat standardized;",

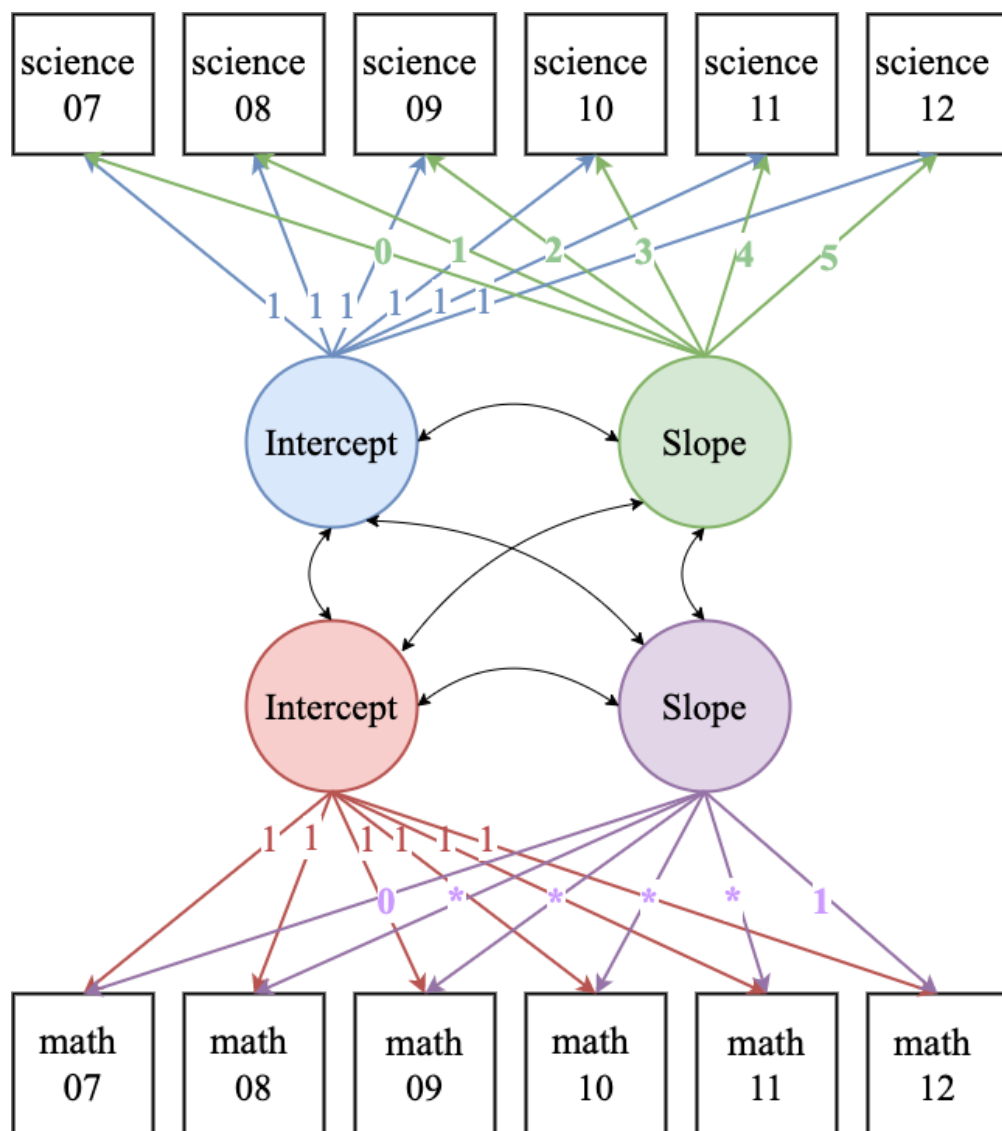
  PLOT = "type=plot3;
          series = sci_07-sci_12(*)",

  usevariables = colnames(lsay_lab7),
  rdata = lsay_lab7)

m7_growth_fit <- mplusModeler(m7_growth,
  dataout=here("mplus_files", "Lab7.dat"),
  modelout=here("mplus_files", "m7_growth_Lab7.inp"),
  check=TRUE, run = TRUE, hashfilename = FALSE)

```

2.9 Model 08 - Parallel Process Growth Model



```
m8_growth <- mplusObject(
  TITLE = "m08 Parallel Process - Lab 7",
  VARIABLE =
    "usevar =
      sci_07-sci_12
      math_07-math_12 mothed;",
  ANALYSIS =
    "estimator = MLR" ,
  MODEL =
    "is ss | sci_07@0 sci_08@1 sci_09@2 sci_10@3 sci_11@4 sci_12@5;
     im sm | math_07@0 math_08@1 math_09@2 math_10@3 math_11@4 math_12@5;

     is ss im sm on mothed; ! time-invariant covariate ",
  OUTPUT = "sampstat standardized;",
```

```

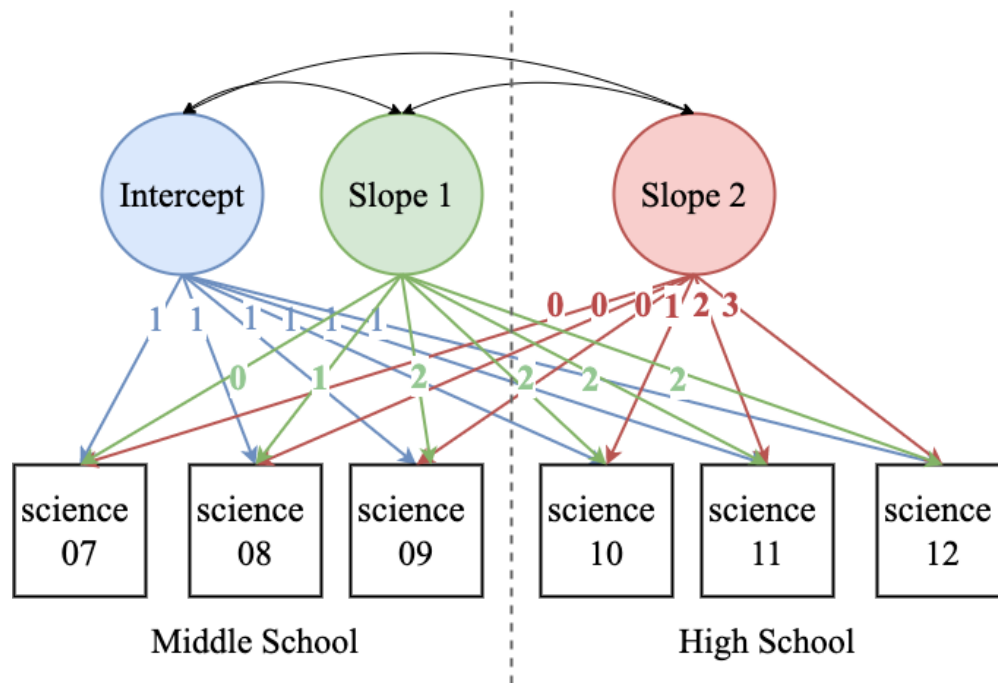
PLOT = "type=plot3;
       series = sci_07-sci_12(*)",

usevariables = colnames(lsay_lab7),
rdata = lsay_lab7)

m8_growth_fit <- mplusModeler(m8_growth,
                             dataout=here("mplus_files", "Lab7.dat"),
                             modelout=here("mplus_files", "m8_growth_Lab7.inp"),
                             check=TRUE, run = TRUE, hashfilename = FALSE)

```

2.10 Model 09 - Piecewise Process Growth Model



```

m9_growth <- mplusObject(
  TITLE = "m09 piecewise growth - Lab 7",
  VARIABLE =
    "usevar =
     sci_07-sci_12 mothed;",

  ANALYSIS =
    "estimator = MLR" ,

  MODEL =
    "i1 s1 | sci_07@0 sci_08@1 sci_09@2 sci_10@2 sci_11@2 sci_12@2;
     s2 by sci_07@0 sci_08@0 sci_09@0 sci_10@1 sci_11@2 sci_12@3;

```



```

    i1 s1 s2 on mothed; ",

OUTPUT = "sampstat standardized;",

PLOT = "type=plot3;
        series = sci_07-sci_12(*)",

usevariables = colnames(lsay_lab7),
rdata = lsay_lab7)

m9_growth_fit <- mplusModeler(m9_growth,
                             dataout=here("mplus_files", "Lab7.dat"),
                             modelout=here("mplus_files", "m9_growth_Lab7.inp"),
                             check=TRUE, run = TRUE, hashfilename = FALSE)

```

2.11 Model 10 - Piecewise Process Growth Model

```

m10_growth <- mplusObject(
  TITLE = "m10 piecewise growth - Lab 7",
  VARIABLE =
    "usevar =
      sci_07-sci_12 mothed;",

  ANALYSIS =
    "estimator = MLR;" ,

  MODEL =
    "i1 s1 | sci_07@0 sci_08@1 sci_09@2;
     i2 s2 | sci_10@0 sci_11@1 sci_12@2;

     [s1] (p1);
     [s2] (p2);

     i1 s1 s2 on mothed; ",

  MODELTEST = "p1=p2; !testing if the two slopes are the same",

  OUTPUT = "sampstat standardized;",

  PLOT = "type=plot3;
          series = sci_07-sci_12(*)",

  usevariables = colnames(lsay_lab7),
  rdata = lsay_lab7)

m10_growth_fit <- mplusModeler(m10_growth,
                              dataout=here("mplus_files", "Lab7.dat"),
                              modelout=here("mplus_files", "m10_growth_Lab7.inp"),
                              check=TRUE, run = TRUE, hashfilename = FALSE)

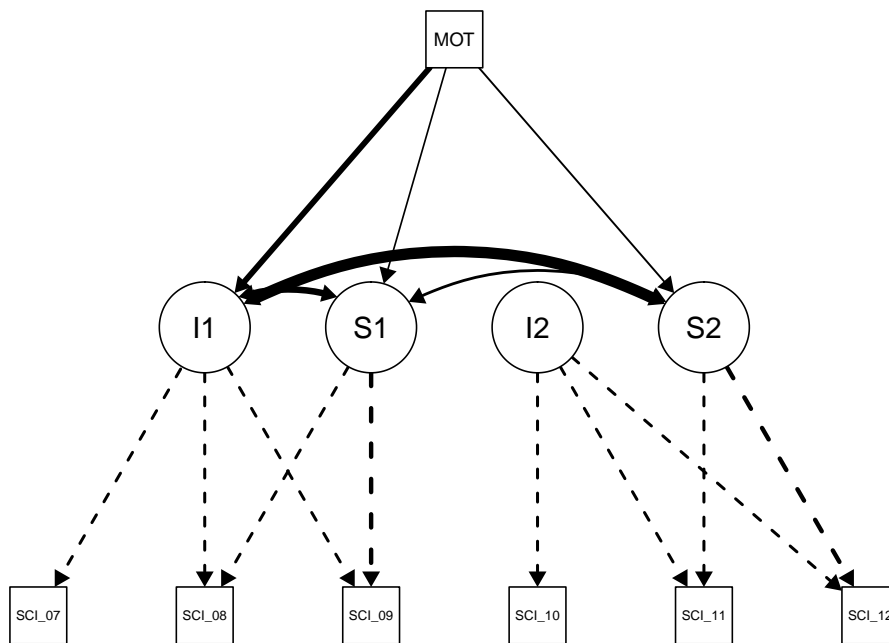
```

Check the path diagram

```
m10_output <- suppressWarnings(readModels(here("mplus_files", "m10_growth_Lab7.out")))
```

```
## Reading model: /Users/agarber/Desktop/SEM_S20/Lab7_SEM/mplus_files/m10_growth_Lab7.out
```

```
semPaths(m10_output, "est", intercepts = FALSE, residuals = FALSE, fade = FALSE,  
         edge.color = "black", edgeLabels = "")
```



3 References

Hallquist, M. N., & Wiley, J. F. (2018). MplusAutomation: An R Package for Facilitating Large-Scale Latent Variable Analyses in Mplus. *Structural equation modeling: a multidisciplinary journal*, 25(4), 621-638.

Miller, J. D., Hoffer, T., Suchner, R., Brown, K., & Nelson, C. (1992). LSAY codebook. Northern Illinois University.

Muthén, B. O., Muthén, L. K., & Asparouhov, T. (2017). Regression and mediation analysis using Mplus. Los Angeles, CA: Muthén & Muthén.

Muthén, L.K. and Muthén, B.O. (1998-2017). Mplus User's Guide. Eighth Edition. Los Angeles, CA: Muthén & Muthén

R Core Team (2017). R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. URL <http://www.R-project.org/>

Wickham et al., (2019). Welcome to the tidyverse. *Journal of Open Source Software*, 4(43), 1686, <https://doi.org/10.21105/joss.01686>

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