

# Advanced Growth Models

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Norwegian University of Science and Technology - A Course in MplusAutomation

May 30, 2021

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## Change starting location to folder 18-advanced-growth

```
source("rep_functions.R")

change_here(glue("{project_location}/18-advanced-growth"))

here()

## [1] "/Users/agarber/github/NTNU-workshop/18-advanced-growth"
```

---

## Data source:

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

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Load packages

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

---

## LSAY data example - Math Scores across 6 timepoints

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Read in data

```
# SKIP (RUNS SLOWLY)

lsay_data <- read_spss("https://garberadamc.github.io/project-site/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

```
lsay_lab7 <- read_csv("https://garberadamc.github.io/project-site/data/lsay_lab7_data.csv")
```

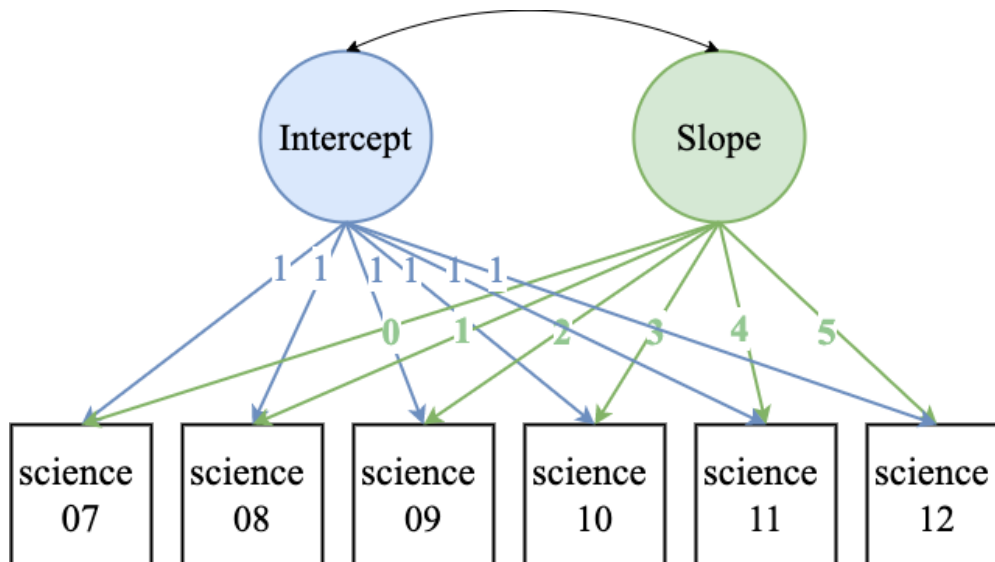
## Let's start modeling

---

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	

### Model 01 - Fixed time effects



```
m1_growth <- mplusObject(
  TITLE = "m1 growth model fixed time scores",
  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", "LSAY.dat"),
                             modelout=here("mplus_files", "m1_growth.inp"),
                             check=TRUE, run = TRUE, hashfilename = FALSE)

```

---

Load in the mplus.R functions

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

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

## 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.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])

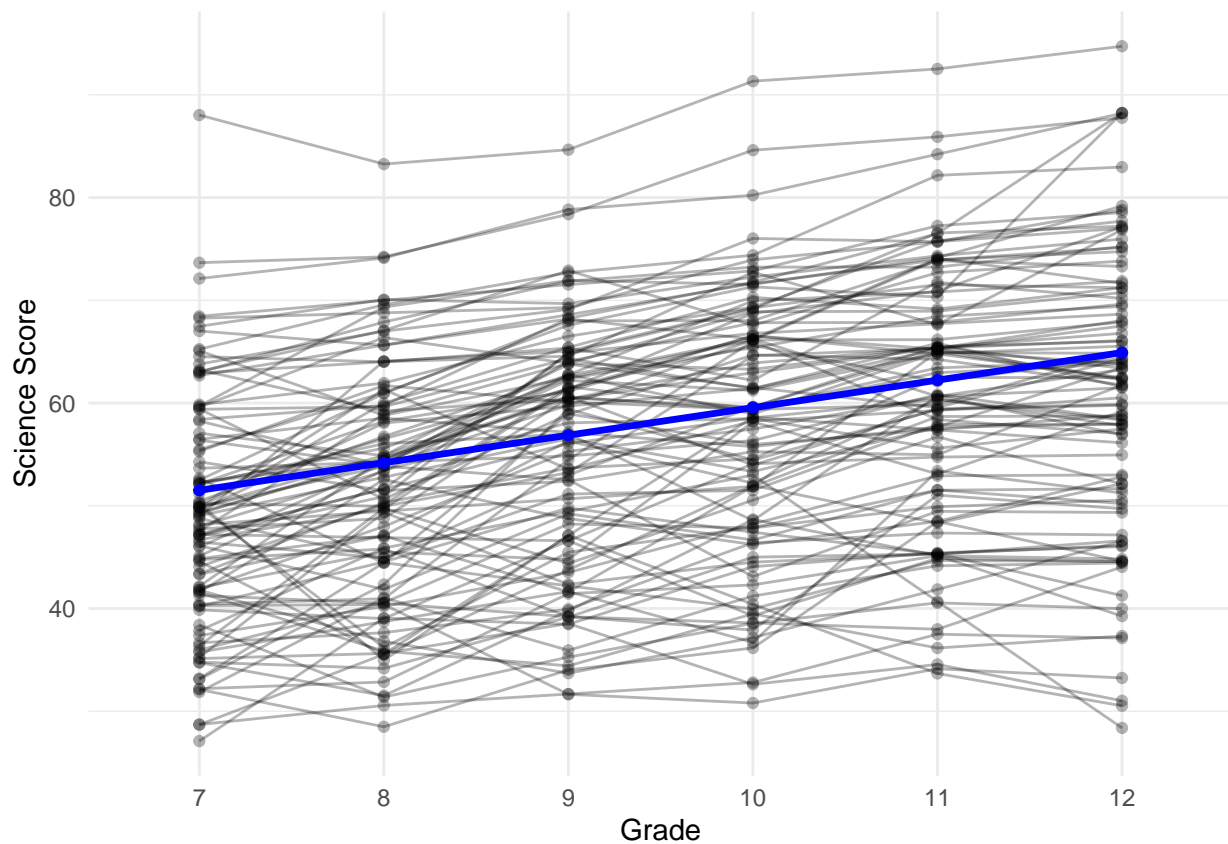
mean_est <- as.data.frame(mplus.get.estimated_means(here(
  "mplus_files", "m1_growth.gh5")) %>%
  mutate(grade = gradelevels))

```

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)
```

```
#
#
#
#
#
```

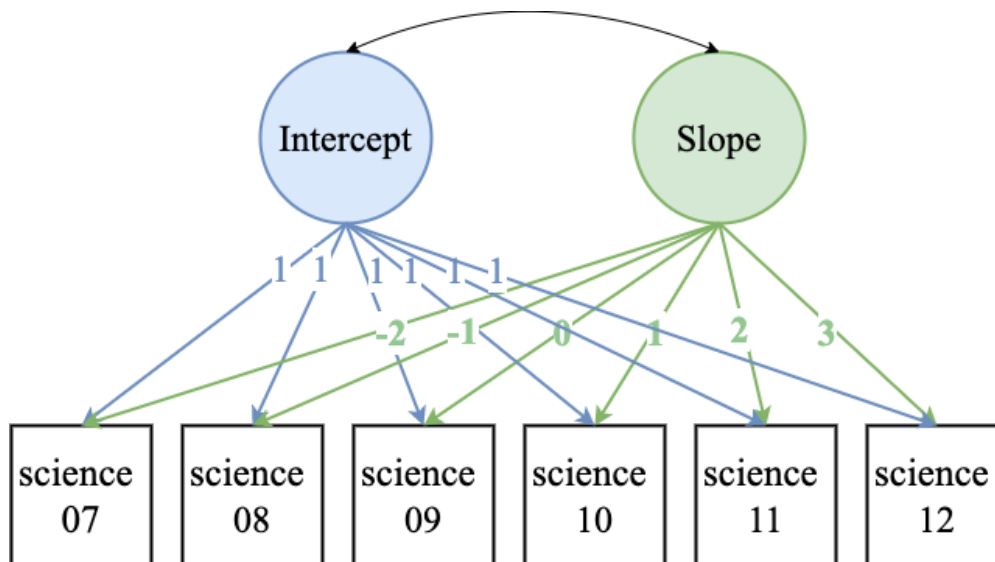
```
anim_save(here("figures", "spaghetti_plot.gif"), height = 6, width = 8, dpi = "retina")
```

---

## 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",
  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,
```

```

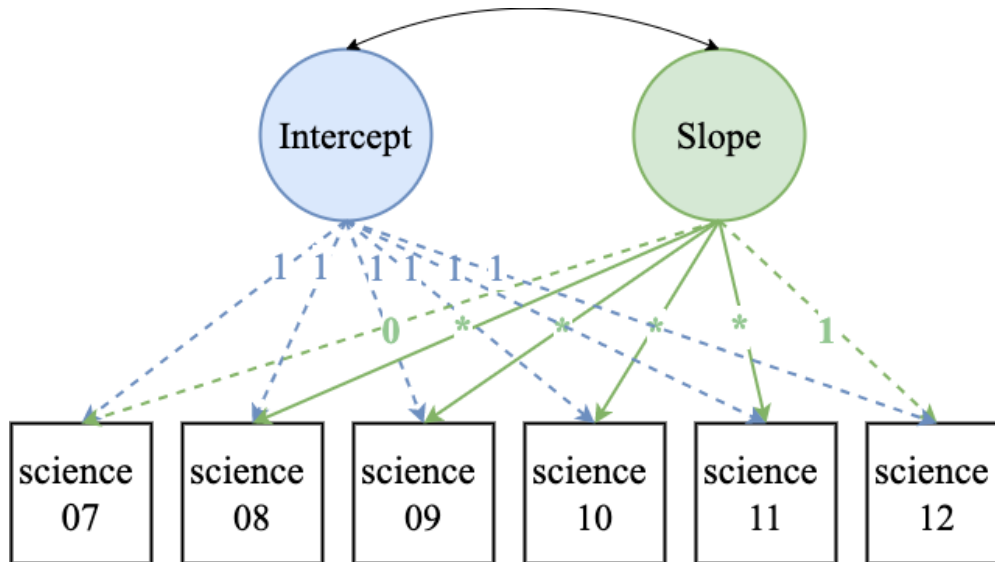
dataout=here("mplus_files", "LSAY.dat"),
modelout=here("mplus_files", "m2_growth.inp"),
check=TRUE, run = TRUE, hashfilename = FALSE)

```

---

## Model 03 - freely estimated time scores

---



```

m3_growth <- mplusObject(
  TITLE = "m3 growth model freely estimated time scores",
  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", "LSAY.dat"),
  modelout=here("mplus_files", "m3_growth.inp"),
  check=TRUE, run = TRUE, hashfilename = FALSE)

```

---

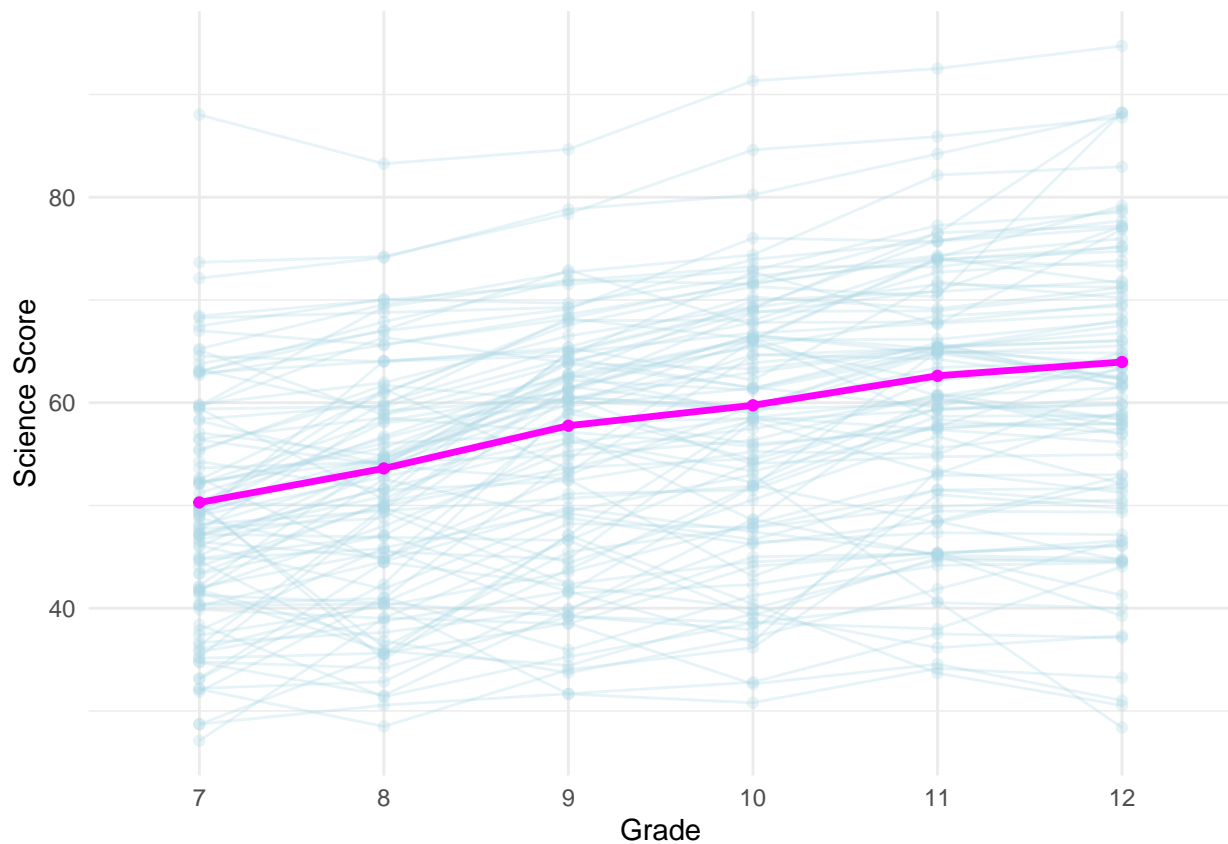
Prepare plot data

```
mean_est2 <- as.data.frame(mplus.get.estimated_means(here(
  "mplus_files", "m3_growth.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
```





## 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",
  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)

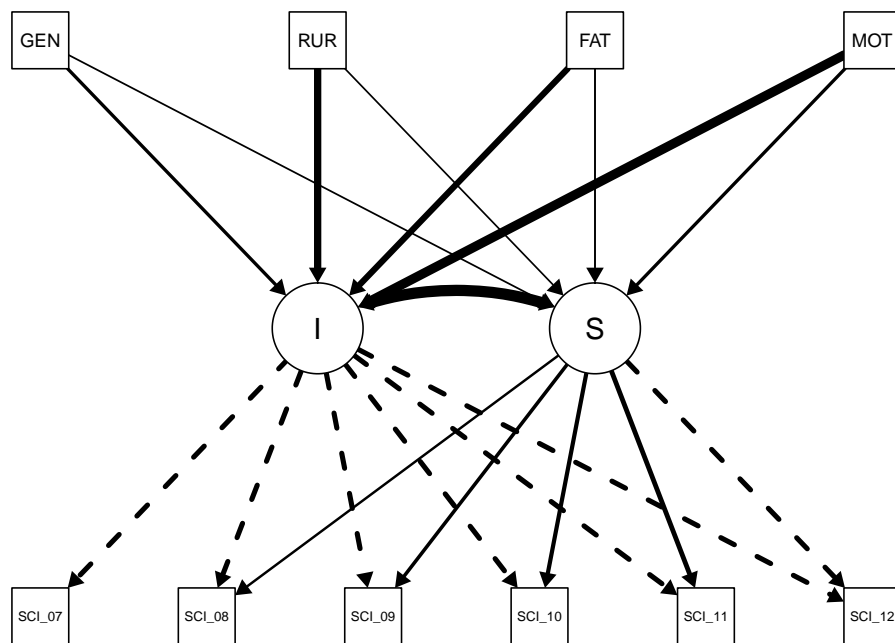
m4_growth_fit <- mplusModeler(m4_growth,
  dataout=here("mplus_files", "LSAY.dat"),
  modelout=here("mplus_files", "m4_growth.inp"),
  check=TRUE, run = TRUE, hashfilename = FALSE)
```

---

Check the path diagram with semPlot

```
m4_output <- readModels(here("mplus_files", "m4_growth.out"), quiet = TRUE)

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




---

## 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",
  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", "LSAY.dat"),
  modelout=here("mplus_files", "m5_growth.inp"),
  check=TRUE, run = TRUE, hashfilename = FALSE)

```

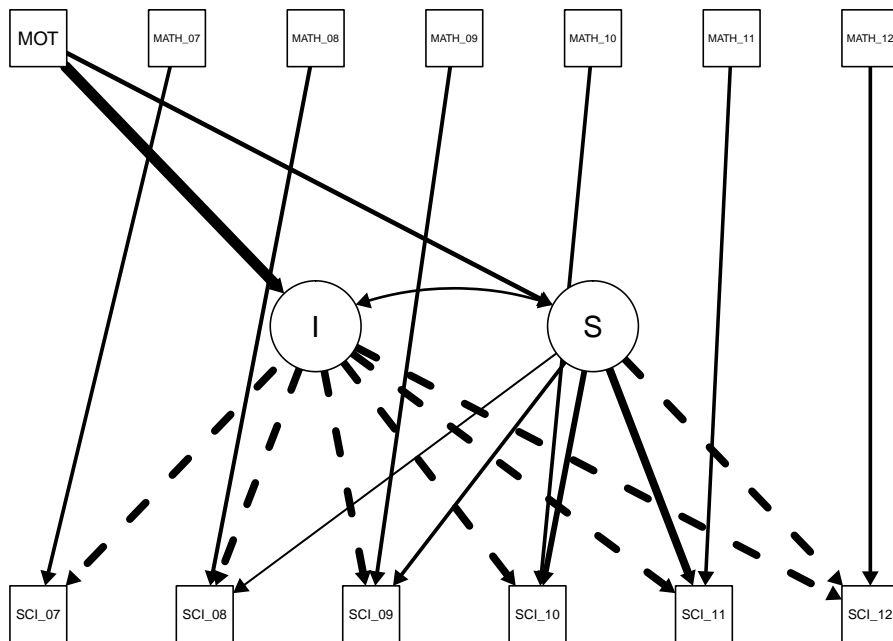
Check the path diagram

```

m5_output <- readModels(here("mplus_files", "m5_growth.out"), quiet = TRUE)

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

```



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

```

m6_growth <- mplusObject(
  TITLE = "m06 time-varying covariates",
  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)

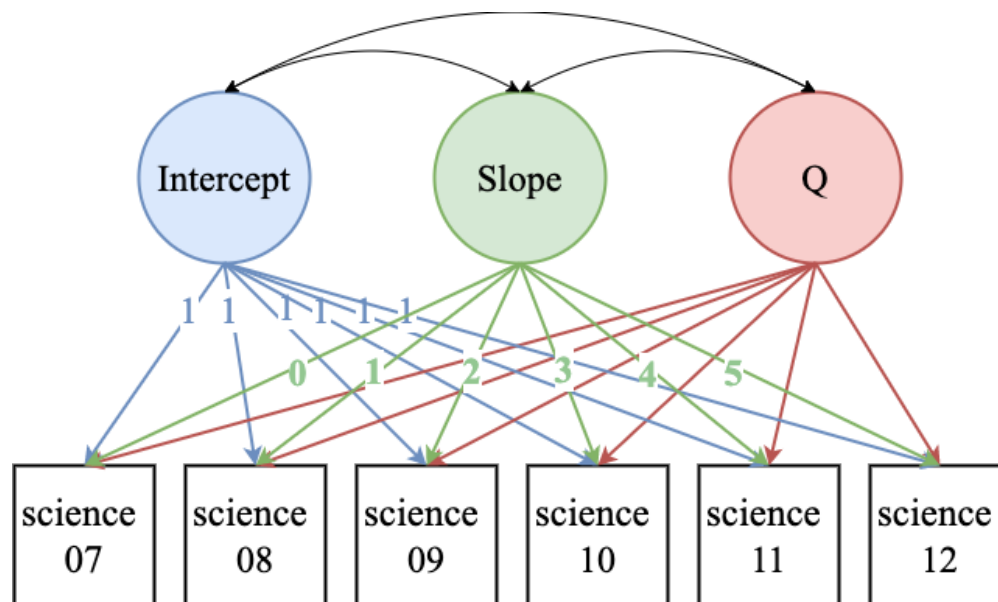
m6_growth_fit <- mplusModeler(m6_growth,
                             dataout=here("mplus_files", "LSAY.dat"),
                             modelout=here("mplus_files", "m6_growth.inp"),
                             check=TRUE, run = TRUE, hashfilename = FALSE)

```

---

## Model 07 - Quadratic Growth

---



```

m7_growth <- mplusObject(
  TITLE = "m07 Quadratic Growth (i s q)",
  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)

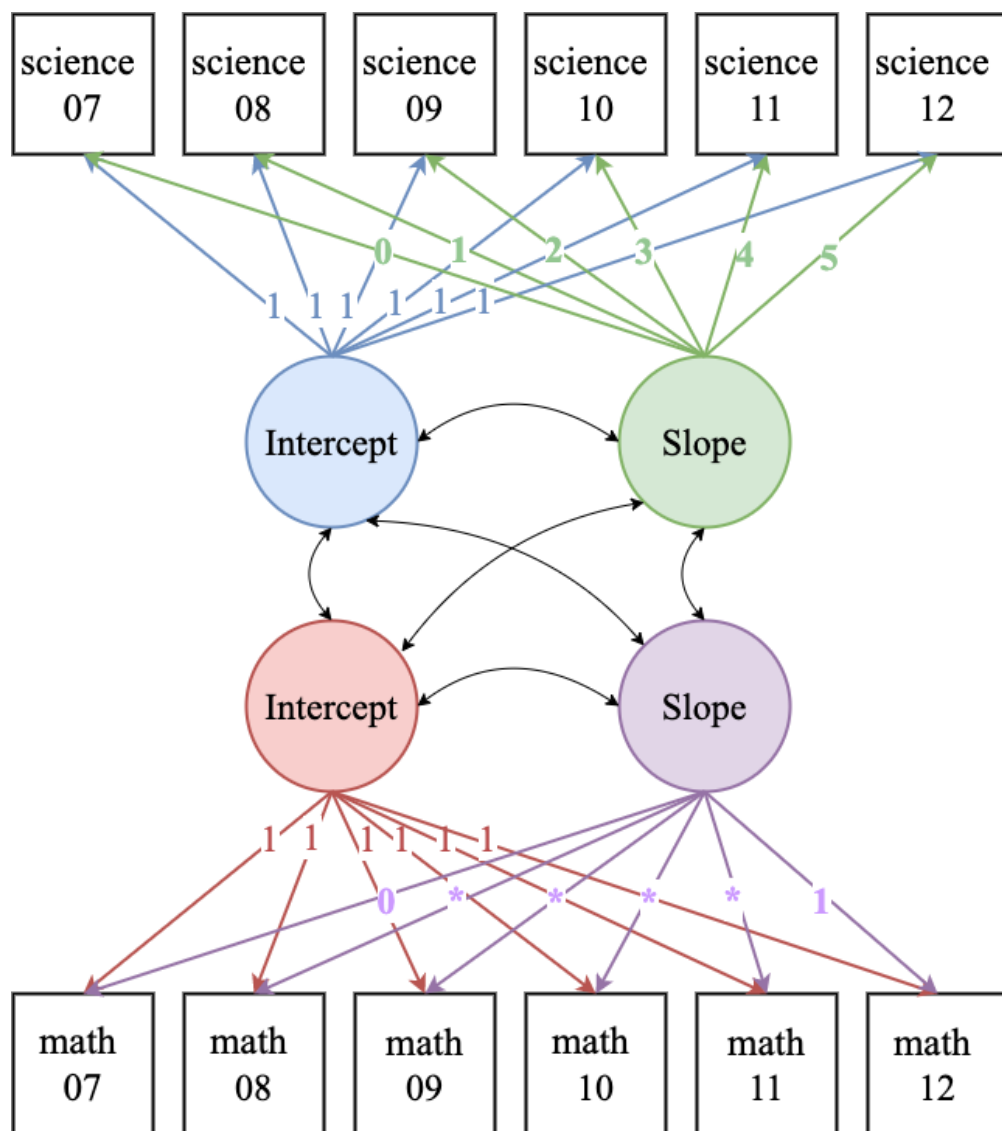
m7_growth_fit <- mplusModeler(m7_growth,
                             dataout=here("mplus_files", "LSAY.dat"),
                             modelout=here("mplus_files", "m7_growth.inp"),
                             check=TRUE, run = TRUE, hashfilename = FALSE)

```

---

## Model 08 - Parallel Process Growth Model

---



```
m8_growth <- mplusObject(
  TITLE = "m08 Parallel Process",
  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)

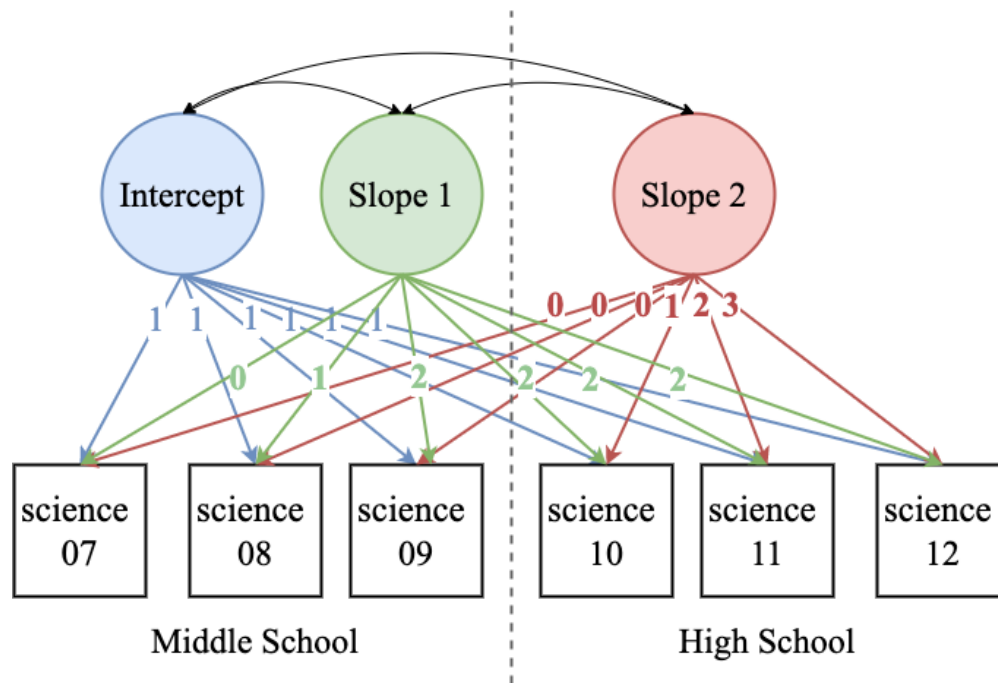
m8_growth_fit <- mplusModeler(m8_growth,
                             dataout=here("mplus_files", "LSAY.dat"),
                             modelout=here("mplus_files", "m8_growth.inp"),
                             check=TRUE, run = TRUE, hashfilename = FALSE)

```

---

## Model 09 - Piecewise Process Growth Model

---



```

m9_growth <- mplusObject(
  TITLE = "m09 piecewise growth",
  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", "LSAY.dat"),
                             modelout=here("mplus_files", "m9_growth.inp"),
                             check=TRUE, run = TRUE, hashfilename = FALSE)

```

---

## Model 10 - Piecewise Process Growth Model

---

```

m10_growth <- mplusObject(
  TITLE = "m10 piecewise growth",
  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", "LSAY.dat"),
                              modelout=here("mplus_files", "m10_growth.inp"),
                              check=TRUE, run = TRUE, hashfilename = FALSE)

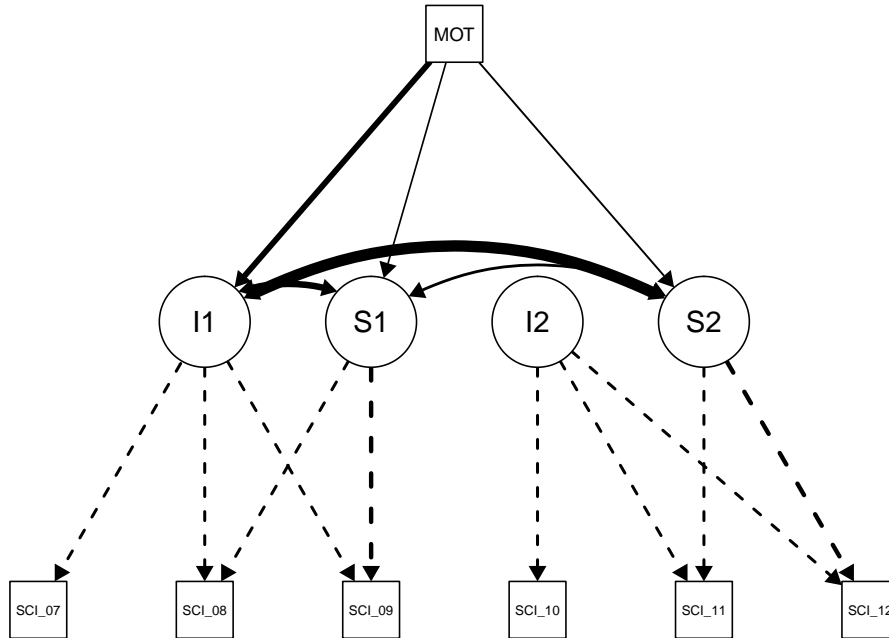
```



Check the path diagram

```
m10_output <- readModels(here("mplus_files", "m10_growth.out"), quiet = TRUE)

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



---

## 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>