Lab 1 - Path Models, Indirect Effects, and Single Indicator Factors

Structural Equation Modeling ED 216F - Instructor: Karen Nylund-Gibson

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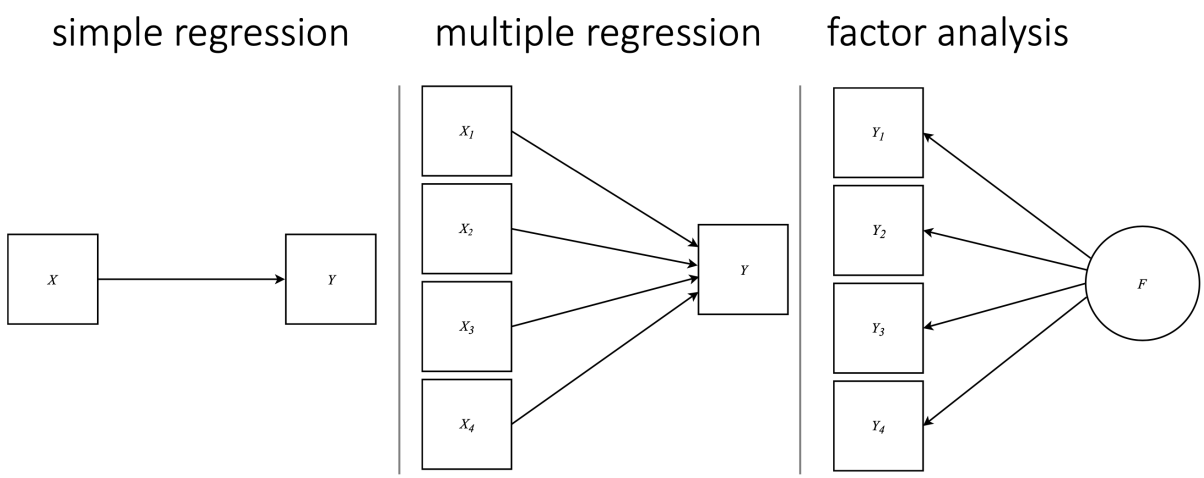

DATA SOURCE: This lab exercise utilizes the NCES public-use dataset: Education Longitudinal Study of 2002 (Lauff & Ingels, 2014) See website: nces.ed.gov

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Tools for reproducibility:

Tool/Package	Purpose/Utility	Advantages
{MplusAutomation} package	Current capabilities supporting full SEM modeling	High flexibility
R Project	Unbreakable file paths & neatness	Reproducibility (kindness to your future self)
{tidyverse} package	Intuitive/descriptive function names	Accessibility to new users
{here} package	Unbreakable/consistent file paths across OS	Reproducibility (for Science's sake!)
{haven} package	View-able metadata in R from SPSS data-files	Getting to know your measures
{ggplot2} package	Clear, customizable, reproducible figures	Publication quality data visualizations
pipe operator (%>%) notation	Ease of reading/writing scripts	e.g., first() %>% and_then() %>% and_finally()

Creating a version-controlled R-Project by downloading repository from Github

Download ropository here: https://github.com/garberadamc/SEM-Lab1

Create a class folder (to save labs and assignments)

a. click "NEW PROJECT" (upper right corner of window)
b. choose option **Version Control**
c. choose option **Git**
d. paste the repository web URL path coppied from the `clone or download` button on the repo page
e. choose location of the R-Project (too many nested folders will result in filepath error)

Create sub-folders within the project folder. In R-studio under the files pane ...

a. click "New Folder" and name folder "data"
b. click "New Folder" and name folder "mplus_files"
c. click "New Folder" and name folder "figures"

Install the "rhdf5" package to read gh5 files

```
if (!requireNamespace("BiocManager", quietly = TRUE))
    install.packages("BiocManager")
 BiocManager::install("rhdf5")
```

Load packages

```
library(MplusAutomation)
library(haven)
library(rhdf5)
library(tidyverse)
library(here)
library(corrplot)
library(kableExtra)
library(reshape2)
library(janitor)
library(ggridges)
library(DiagrammeR)
library(semPlot)
library(sjPlot)
```

Keyboard shortcuts

- ALT + DASH(-) = <-
- SHIFT + CONTROL = %>%

Read in SPSS data

```
spss_data <- read_spss(here("data", "els_sub1_spss.sav")) %>%
  janitor::clean_names() # makes all variable names lowercase
```

Preparations: subset, rename, and reorder columns

1. **subset:** select columns in 3 ways, remove columns with (-), select by index number, and select by column name
2. **rename:** change variable names to be descriptive and within the Mplus 8 character limit
3. **reorder:** this makes it easy to choose sequential variables for {MplusAutomation}

```
spss_sub0 <- spss_data %>%
  select(-stu_id,   -sch_id,   -byrace,
         -byparace, -byparlng, -byfcomp,
         -bypared,  -bymothed, -byfathed,
         -bysctrl,  -byurban,  -byregion)
```

Select the first 9 columns (by index) and select the next 17 columns (by name)

```
spss_sub1 <- spss_sub0 %>%
  select(1:9,
         bys20a, bys20h, bys20j, bys20k, bys20m, bys20n,
         bys21b, bys21d, bys22a, bys22b, bys22c, bys22d,
         bys22e, bys22g, bys22h, bys24a, bys24b) %>%
  rename("stu_exp" = "bystexp",    # "NEW_NAME" = "OLD_NAME"
         "par_asp" = "byparasp",
         "mth_read" = "bytxcstd",
         "mth_test" = "bytxmstd",
         "rd_test" = "bytxrstd",
         "freelnch" = "by10flp",
         "stu_tch" = "bys20a",
         "putdownt" = "bys20h",
         "unsafe" = "bys20j",
         "disrupt" = "bys20k",
         "gangs" = "bys20m",
         "rac_fght" = "bys20n",
         "fair" = "bys21b",
         "strict" = "bys21d",
         "stolen" = "bys22a",
         "drugs" = "bys22b",
         "t_hurt" = "bys22c",
         "p_fight" = "bys22d",
         "hit" = "bys22e",
         "damaged" = "bys22g",
         "bullied" = "bys22h",
         "late" = "bys24a",
         "skipped" = "bys24b")
```

More housekeeping: reorder columns

```
spss_sub2 <-  spss_sub1 %>%
  select(
    bystlang,                                          # dichotomous (yes,no)
    freelnch, byincome,                                # ordinal (binned, continuous scale)
    stolen, t_hurt, p_fight, hit, damaged, bullied,    # ordinal frequency (3-point)
    unsafe, disrupt, gangs, rac_fght,                  # ordinal Likert (4-point scale)
    late, skipped,                                     # ordinal frequency (4-point scale)
    mth_test, rd_test)                                 # continuous (standardized test scores)
```

Make a codebook including metadata using 'sjPlot'

```
sjPlot::view_df(spss_sub2)
```

Types of data for different tasks

- SAV (e.g., spss_data.sav): this data format is for SPSS files & contains variable labels (meta-data)
- CSV (e.g., r_ready_data.csv): this is the preferable data format for reading into R (no labels)
- DAT (e.g., mplus_data.dat): this is the data format used to read into Mplus (no column names or strings)

NOTE: Mplus also accepts TXT formatted data (e.g., mplus_data.txt)

Converting data between 3 formats: writing and reading data

Write a CSV datafile (preferable format for reading into R, with SPSS labels removed)

```
write_csv(spss_sub2, here("data", "els_sub6_data.csv"))
```

Write a SPSS datafile (preferable format for reading into SPSS, labels are preserved)

```
write_sav(spss_sub2, here("data", "els_sub6_data.sav"))
```

Read the unlabeled data back into R

```
tidy_data <- read_csv(here("data", "els_sub6_data.csv"))
```

Write a DAT datafile for Mplus (this function removes header row & converts missing values to non-string)

```r
prepareMplusData(tidy_data, here("data", "els_sub6_data.dat"))
```

Make a 'tribble' table

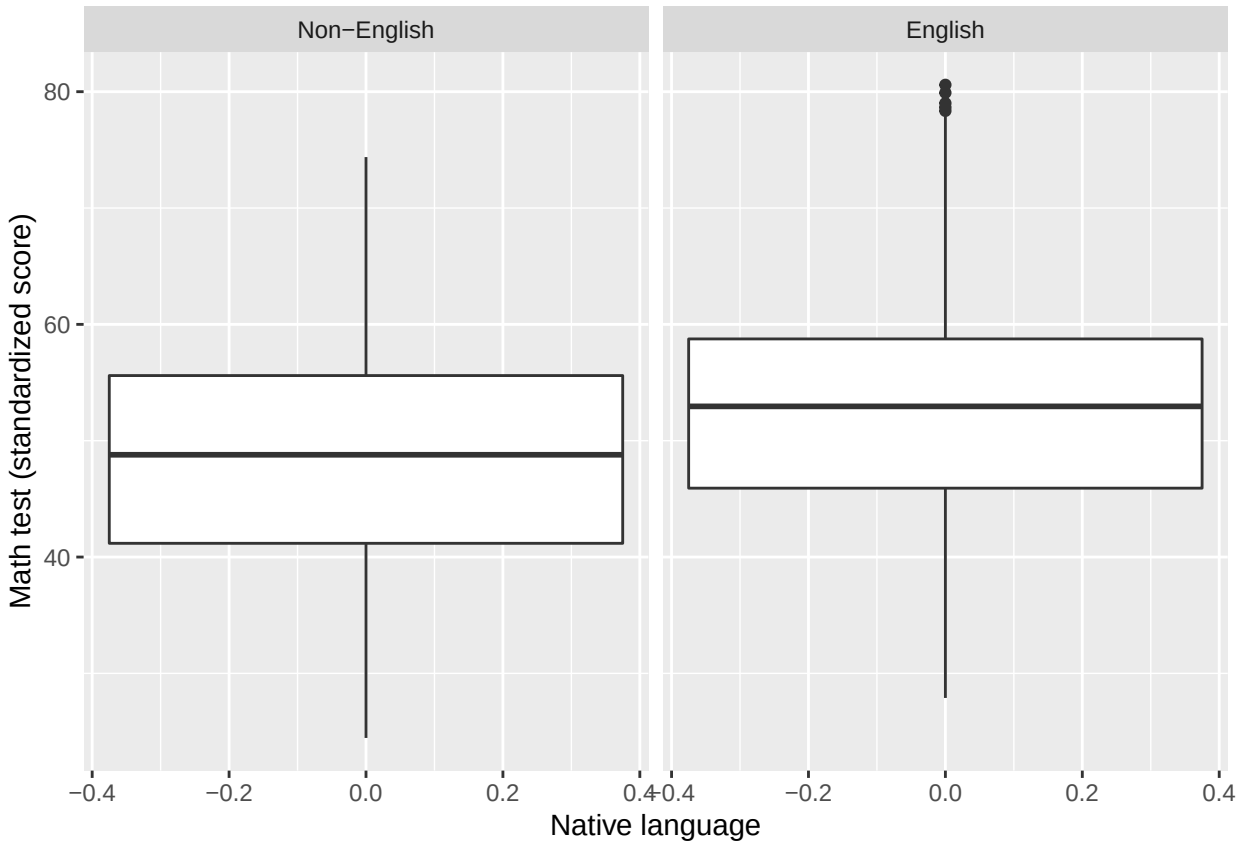
```r
var_table <- tribble(
   ~"Name",    ~"Labels",                                          ~"Value Labels (limit)",
 #-----------/-------------------------------------------------/-------------------------------------/,
  "bystlang" , "Whether English is students native language" ,"0=No, 1=Yes",
  "freelnch" , "Grade 10 percent free lunch-categorical"     ,"0=0-5%, 7=76-100%",
  "byincome" , "Total family income from all sources 2001"   ,"1=None, 13=$200,001 or more",
  "stolen"   , "Had something stolen at school"              ,"1=Never, 3=More than twice",
  "t_hurt"   , "Someone threatened to hurt 10th grader at school","1=Never, 3=More than twice",
  "p_fight"  , "Got into a physical fight at school"         ,"1=Never, 3=More than twice"  ,
  "hit"      , "Someone hit 10th grader"                     ,"1=Never, 3=More than twice"  ,
  "damaged"  , "Someone damaged belongings"                  ,"1=Never, 3=More than twice"  ,
  "bullied"  , "Someone bullied or picked on 10th grader"    ,"1=Never, 3=More than twice"  ,
  "unsafe"   , "Does not feel safe at this school"           ,"1=Strongly agree, 4=Strongly disagree"
  "disrupt"  , "Disruptions get in way of learning"          ,"1=Strongly agree, 4=Strongly disagree"
  "gangs"    , "There are gangs in school"                   ,"1=Strongly agree, 4=Strongly disagree"
  "rac_fght" , "Racial-ethnic groups often fight"            ,"1=Strongly agree, 4=Strongly disagree"
  "late"     , "How many times late for school"              ,"1=Never, 4=10 or more times"  ,
  "skipped"  , "How many times cut-skip classes"             ,"1=Never, 4=10 or more times"  ,
  "mth_test" , "Math test standardized score"                ,"0-100"  ,
  "rd_test"  , "Reading test standardized score"             ,"0-100"  ,
)

var_table %>%
  kable("latex", booktabs = T, linesep = "") %>%
  kable_styling(latex_options = c("striped"),
                full_width = F,
                position = "left")
```

Name	Labels	Value Labels (limit)
bystlang	Whether English is students native language	0=No, 1=Yes
freelnch	Grade 10 percent free lunch-categorical	0=0-5%, 7=76-100%
byincome	Total family income from all sources 2001	1=None, 13=$200,001 or more
stolen	Had something stolen at school	1=Never, 3=More than twice
t_hurt	Someone threatened to hurt 10th grader at school	1=Never, 3=More than twice
p_fight	Got into a physical fight at school	1=Never, 3=More than twice
hit	Someone hit 10th grader	1=Never, 3=More than twice
damaged	Someone damaged belongings	1=Never, 3=More than twice
bullied	Someone bullied or picked on 10th grader	1=Never, 3=More than twice
unsafe	Does not feel safe at this school	1=Strongly agree, 4=Strongly disagree
disrupt	Disruptions get in way of learning	1=Strongly agree, 4=Strongly disagree
gangs	There are gangs in school	1=Strongly agree, 4=Strongly disagree
rac_fght	Racial-ethnic groups often fight	1=Strongly agree, 4=Strongly disagree
late	How many times late for school	1=Never, 4=10 or more times
skipped	How many times cut-skip classes	1=Never, 4=10 or more times
mth_test	Math test standardized score	0-100
rd_test	Reading test standardized score	0-100

Take a look at the data - some practice with 'ggplot2'

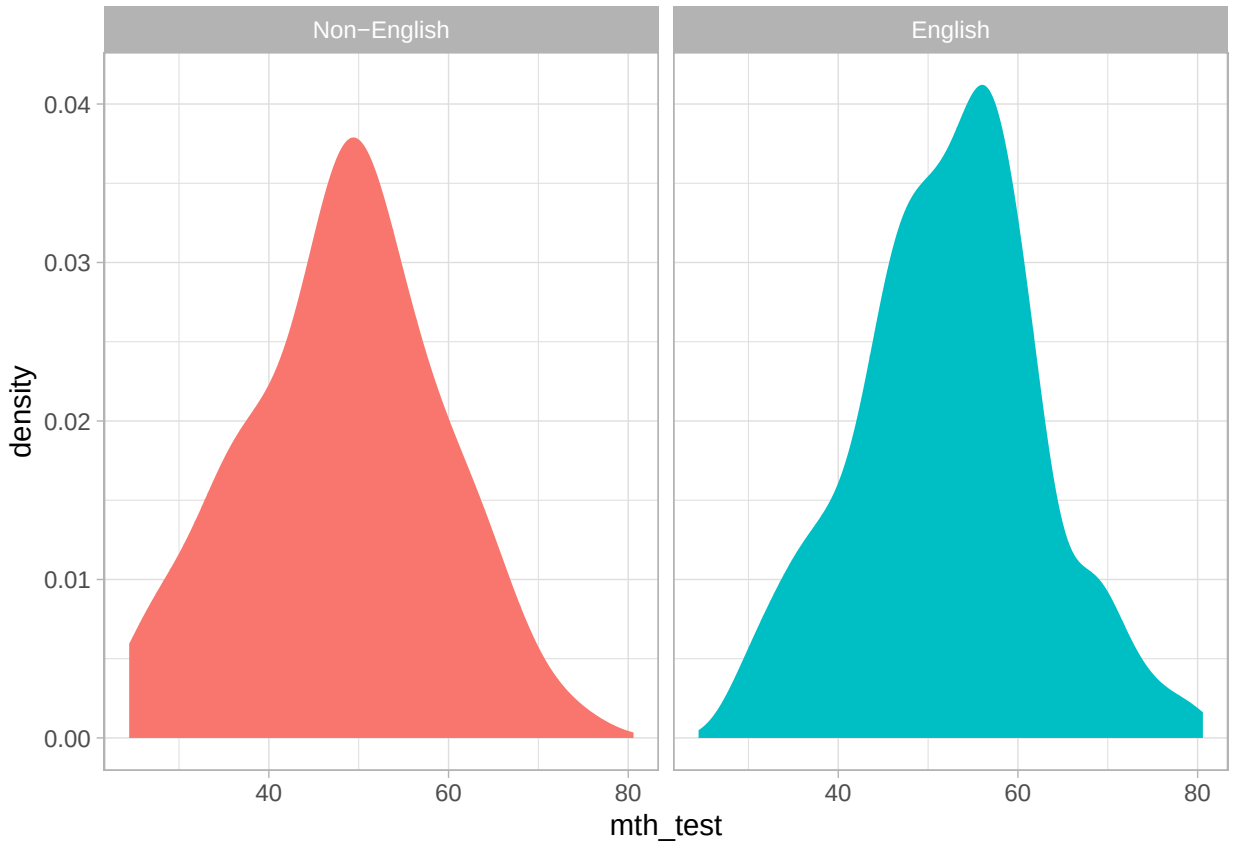
Make a facetted box plot

```
# some formatting, add labels to `bystlang` for plot
tidy_data <- tidy_data %>%
  mutate(
    bystlang = factor(bystlang,
    labels = c(`0` = "Non-English", `1` = "English")))


  ggplot(data=drop_na(tidy_data), aes(y=mth_test)) +
    geom_boxplot() +
    facet_wrap(~bystlang) +
    labs(x = "Native language",
         y = "Math test (standardized score)")
```



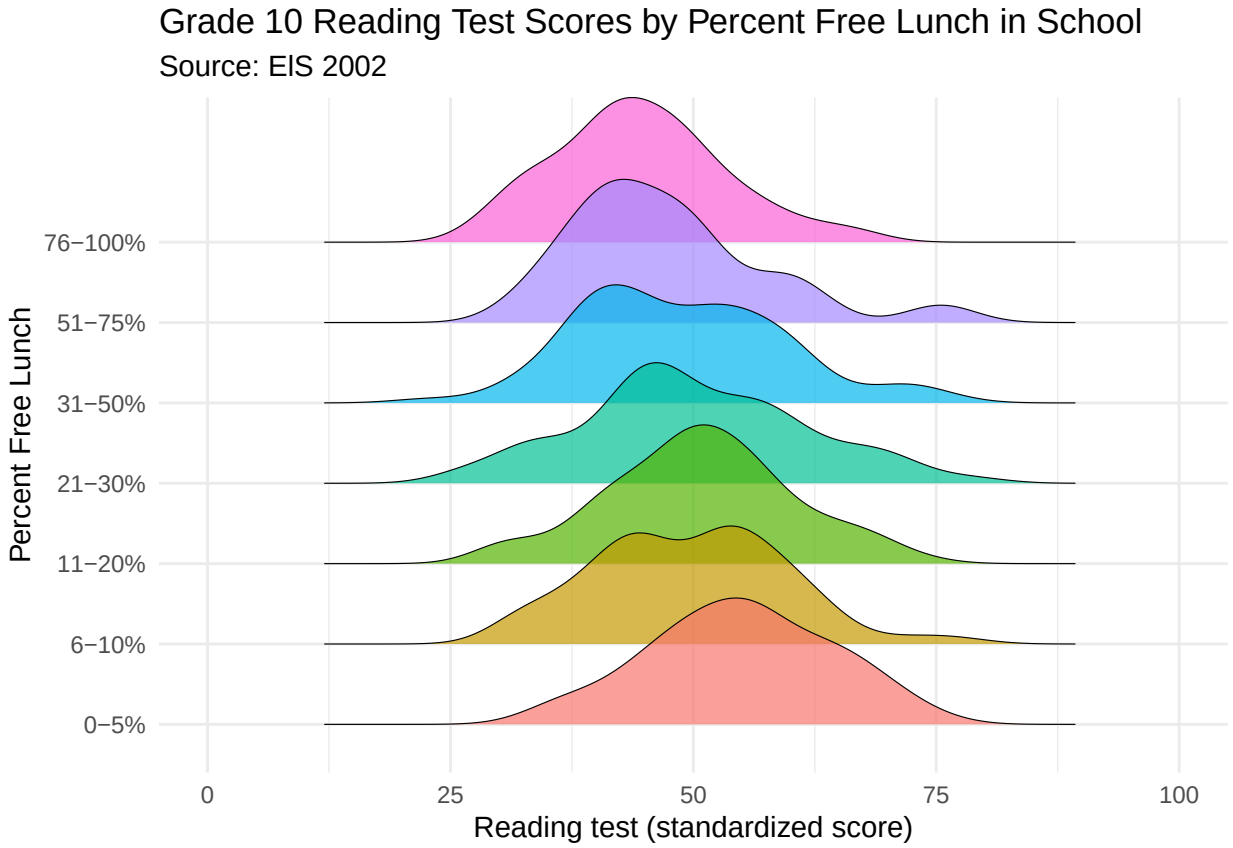
Make a density plot

```
ggplot(data=drop_na(tidy_data), aes(x=mth_test)) +
  geom_density(aes(fill = bystlang),
               color = NA,
               show.legend = FALSE) +
  facet_wrap(~bystlang) +
  theme_light()
```



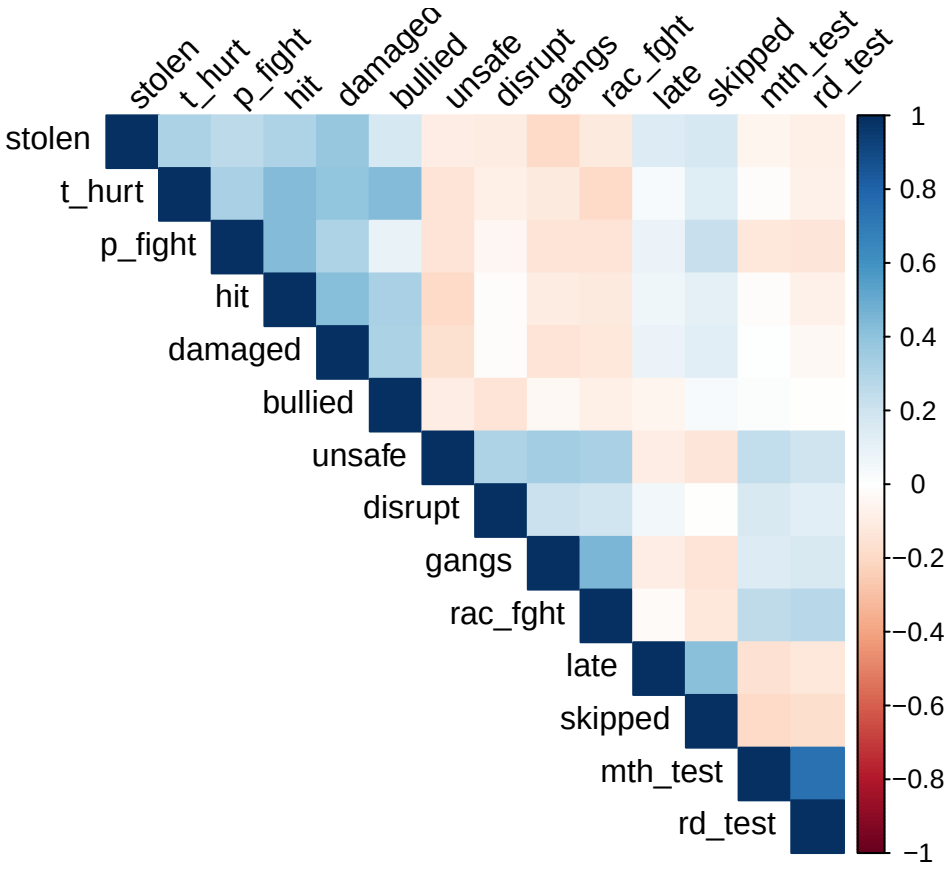
Ridgeline plot {ggridges}

```
# A ridgeline plot is good way to compare distributions across groups.
# In the plot below the distribution of reading test scores is grouped
# by level of the freelunch variable.

ridge_graph <- ggplot(data = drop_na(tidy_data),
                      aes(x = rd_test, y = factor(freelnch))) +
  geom_density_ridges(aes(fill = factor(freelnch)),
                      size = 0.2,
                      alpha = 0.7,
                      show.legend = FALSE) +
  scale_x_continuous(lim = c(0,100)) +
    scale_y_discrete(lim = levels(tidy_data$freelnch),
                     labels = c("0-5%", "6-10%", "11-20%","21-30%",
                                "31-50%", "51-75%", "76-100%")) +
    labs(x = "Reading test (standardized score)",
         y = "Percent Free Lunch",
     title = "Grade 10 Reading Test Scores by Percent Free Lunch in School",
  subtitle = "Source: ElS 2002") +
  theme_minimal()

ridge_graph
```



Look at all bivariate relations

```
t_cor <- cor(tidy_data[,4:17], use = "pairwise.complete.obs")

corrplot(t_cor,
         method = "color",
         type = "upper",
         tl.col="black",
         tl.srt=45)
```



Run some path models with MplusAutomation

Practice run, use `type=basic` to get descriptives

```
m_basic  <- mplusObject(
  TITLE = "RUN TYPE = BASIC ANALYSIS - LAB 1",
  VARIABLE =
    " ! an mplusObject() will always need a 'usevar' statement
      ! ONLY specify variables that will be used in analysis
      ! lines of code in MPLUS ALWAYS end with a semicolon ';'
    usevar =
    bystlang freelnch byincome stolen t_hurt p_fight
    hit damaged bullie, unsafe disrupt gangs rac_fght
    late skipped mth_test rd_test;",

  ANALYSIS =
    "type = basic" ,

  MODEL = "" ,

  PLOT = "",
```

```
  OUTPUT = "",

  usevariables = colnames(tidy_data),    # tell MplusAutomation the column names to use
  rdata = tidy_data)                     # this is the data object used (must be un-label)

m_basic_fit <- mplusModeler(m_basic,
                    dataout=here("mplus_files", "Lab1.dat"),
                    modelout=here("mplus_files", "m0_basic_Lab1.inp"),
                    check=TRUE, run = TRUE, hashfilename = FALSE)
```

Run a path model with model indirect (to estimate the indirect effect)

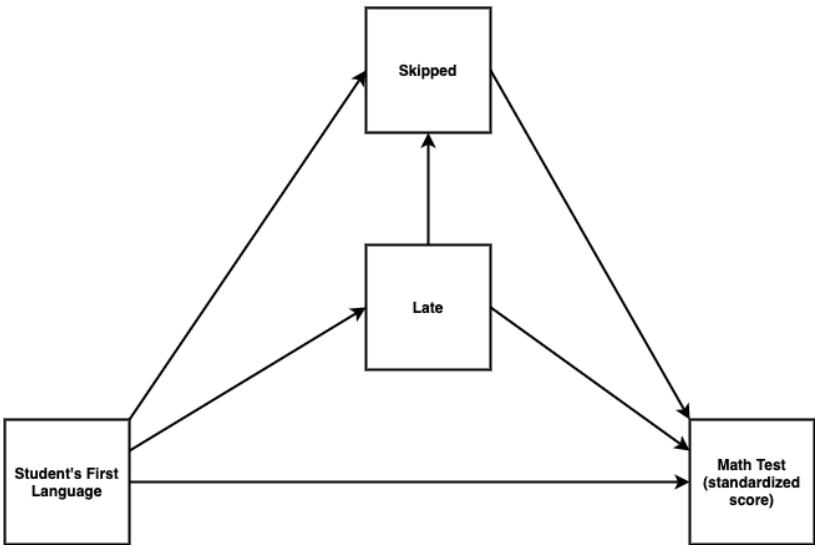


Figure 1. Path Diagram of Multiple Indirect Paths Model

Visualize the path diagram using the {`DiagrammeR`} package

```
mermaid("
graph LR
  bystlang-->late
  bystlang-->skipped
  bystlang-->mth_test
  late-->skipped
  late-->mth_test
  skipped-->mth_test
")
```

Run model depicted above with multiple indirect paths

```
m1_ind  <- mplusObject(
  TITLE = "m1 model indirect - Lab 1",
  VARIABLE =
   "usevar =
    bystlang       ! covariate
    late skipped   ! mediators
    mth_test;      ! outcome   ",

  ANALYSIS =
    "estimator = MLR" ,

  MODEL =
   "late on bystlang ;
    skipped on late bystlang ;
    mth_test on late skipped bystlang;

    Model indirect:
    mth_test ind bystlang;
    mth_test via late skipped bystlang; " ,

  OUTPUT = "sampstat standardized",

  usevariables = colnames(tidy_data),
  rdata = tidy_data)

m1_ind_fit <- mplusModeler(m1_ind,
                     dataout=here("mplus_files", "Lab1.dat"),
                    modelout=here("mplus_files", "m1_indirect_Lab1.inp"),
                    check=TRUE, run = TRUE, hashfilename = FALSE)
```

Generate a path diagram from Mplus output with {`semPlot`}

```
order2_model <- readModels(here("mplus_files",
                                "m1_indirect_Lab1.out"))

# plot model:
semPaths(order2_model,
          intercepts=FALSE)
```

Single indicator factors

Model specifications:

- Fix the loading to 1

- Then fix the residual variance to a specific value (you are not estimating a measurement parameter)

Using reliability you fix the residual variance at:

$(1 - reliabilty) * variance$

Lab example of single indicator factor model:

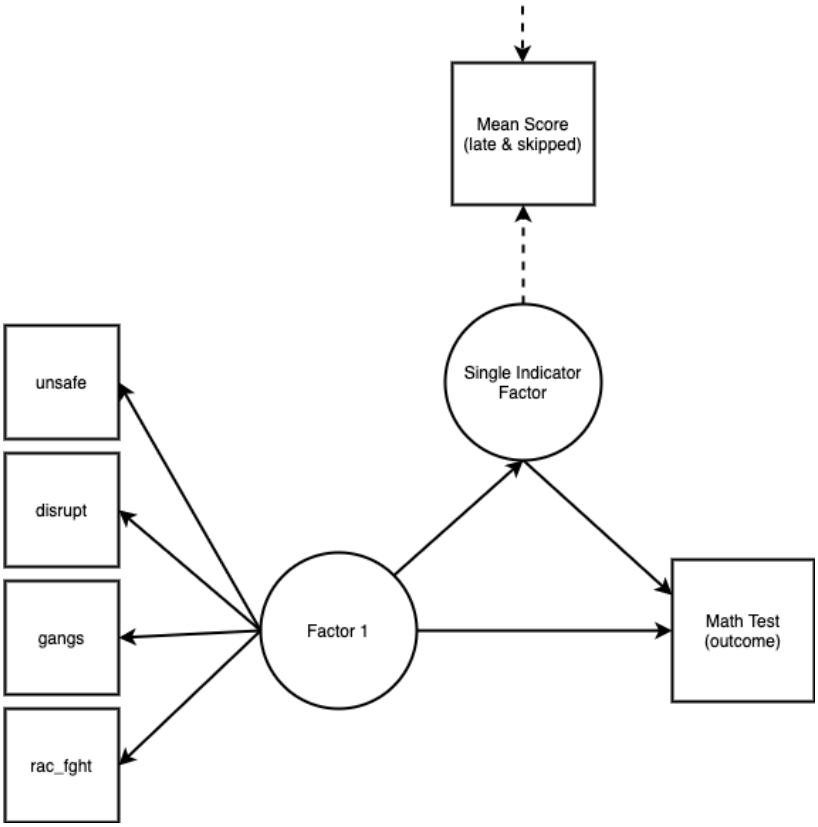


Figure 2. Path Diagram of Single Indicator Factor Model

---

create a mean score variable called `mean_score`

```
tidy_data2 <- tidy_data %>%
  mutate(mean_scr = rowSums(select(., late:skipped))/2)
```

```
- Reliability = .8 (set to)
- Variance = .77 (mean_score)
```

Function to fix the residual variance

```r
# r = reliability, v = variance

resid_var <- function(r,v) {

 y <- ((1-r)*v)
    return(y)
}

y01 <- resid_var(.8,.77)

print(y01)
```

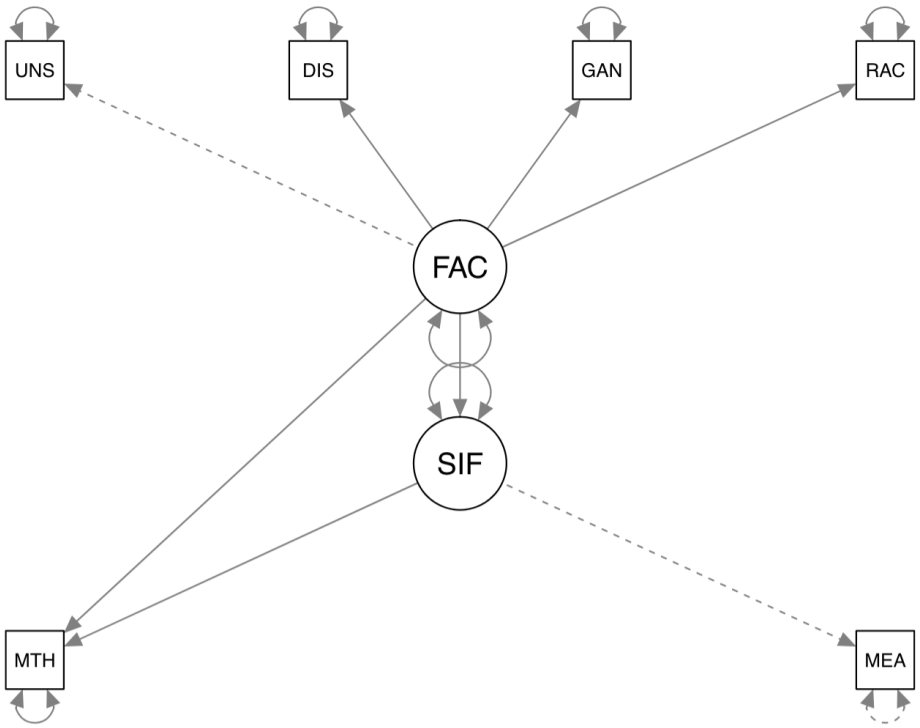
```
## [1] 0.154
```

Run model with single indicator factor

```r
m2_sif  <- mplusObject(
  TITLE = "m2 single indicator factor - Lab 1",
  VARIABLE =
   "usevar =
    unsafe disrupt gangs rac_fght  ! factor 1
    mth_test                       ! outcome
    mean_scr;                      ! mediator ",

  ANALYSIS =
    "estimator = MLR" ,

  MODEL =
   "! measurement model
    factor1 by unsafe, disrupt, gangs, rac_fght;

    SIF by mean_scr@1; ! fix factor loading to 1

    mean_scr@.154;     ! fix residual variance

    ! structural model
    mth_test on factor1 SIF;
    SIF on factor1; ",

  OUTPUT = "sampstat standardized",

  usevariables = colnames(tidy_data2),
  rdata = tidy_data2)

m2_sif_fit <- mplusModeler(m2_sif,
                      dataout=here("mplus_files", "Lab1.dat"),
                     modelout=here("mplus_files", "m2_sif_Lab1.inp"),
                     check=TRUE, run = TRUE, hashfilename = FALSE)
```

Generate a path diagram from Mplus output with {semPlot}

```
order2_model <- readModels(here("mplus_files",
                                "m2_sif_Lab1.out"))

# plot model:
semPaths(order2_model,
         intercepts=FALSE)
```



References

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