Multiple Indicator, Multiple Causes (MIMIC Models)

Adam Garber

Norwegian University of Science and Technology - A Course in `MplusAutomation`

June 01, 2021

Chapter 8 outline

a. Prepare, wrangle, and explore data
b. Run an unconditional CFA baseline model
c. Specify a MIMIC model with a single binary covariate
d. Specify a MIMIC model and probe for DIF
e. Specify a MIMIC model with a DIF parameter
f. Specify a MIMIC model with two binary covariates & an interaction
g. Specify a MIMIC model with three continuous covariates
h. Experiment with path diagram notation & formatting
i. We will keep close track of parameters and their status throughout exercise

---

loading packages:

```
library(tidyverse)
library(here)
library(semPlot)
library(DiagrammeR)
library(MplusAutomation)
library(stargazer)
library(gtsummary)
library(gt)
library(glue)
```

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

Begin

read in data

```
lab_data <- read_csv("https://garberadamc.github.io/project-site/data/els_sub5_data.csv")
```

take a look at the EFA data (same indicators used for lab 4)

```
stargazer(as.data.frame(lab_data), type="text", digits=1)
```

```
##
## ===================================================
## Statistic   N   Mean St. Dev. Min  Pctl(25) Pctl(75) Max
## ---------------------------------------------------
## bysex      758 1.5    0.5    1.0    1.0      2.0    2.0
## bystlang   749 0.8    0.4    0.0    1.0      1.0    1.0
## byincome   794 9.2    2.5     1      8        11     13
## stu_exp    692 5.3    1.4    1.0    5.0      6.0    7.0
## par_asp    794 5.4    1.3     2      5        6      7
## mth_read   785 50.9   10.0   25.1   44.3     57.6   79.9
## mth_test   785 51.1   10.1   24.4   44.6     57.5   84.8
## rd_test    785 50.6   10.0   22.6   43.4     57.2   78.8
## freelnch   726 3.0    1.9    1.0    1.0      5.0    7.0
## stu_tch    718 2.2    0.6    1.0    2.0      2.0    4.0
## putdownt   715 3.1    0.7    1.0    3.0      4.0    4.0
## safe       711 3.3    0.7    1.0    3.0      4.0    4.0
## disrupt    713 2.6    0.9    1.0    2.0      3.0    4.0
## gangs      705 3.0    0.9    1.0    3.0      4.0    4.0
## rac_fght   716 3.0    0.8    1.0    3.0      4.0    4.0
## fair       708 2.5    0.8    1.0    2.0      3.0    4.0
## strict     714 2.3    0.7    1.0    2.0      3.0    4.0
## stolen     718 1.5    0.6    1.0    1.0      2.0    3.0
## drugs      717 1.3    0.6    1.0    1.0      1.0    3.0
## t_hurt     714 1.3    0.6    1.0    1.0      1.0    3.0
## p_fight    715 1.2    0.4    1.0    1.0      1.0    3.0
## hit        711 1.3    0.6    1.0    1.0      1.0    3.0
## damaged    716 1.2    0.4    1.0    1.0      1.0    3.0
## bullied    713 1.3    0.6    1.0    1.0      1.0    3.0
## late       719 2.3    1.2    1.0    1.0      3.0    5.0
## skipped    715 1.5    0.9    1.0    1.0      2.0    5.0
## ---------------------------------------------------
```

alternative way to make summary tables using package {gtsummary}

```
table_data <- lab_data %>%
  dplyr::select(byincome, mth_test, rd_test, freelnch, bystlang)

table2 <- tbl_summary(table_data,
```

```
            by = bystlang,    # split table by group "bystlang" ()
            missing = "no"    # don't list missing data separately
            ) %>%
            add_n() %>%       # add column with total number of non-missing observations
            add_p() %>%       # test if there's difference between groups
            bold_labels()

table2
```

Characteristic	N	**0**, N = 117	**1**, N = 632	p-value
byincome	749	8.00 (6.00, 10.00)	10.00 (8.00, 11.00)	<0.001
mth_test	749	48 (41, 55)	52 (45, 58)	<0.001
rd_test	749	46 (40, 52)	51 (44, 58)	<0.001
freelnch	685			<0.001
1		23 (23%)	222 (38%)	
2		9 (8.9%)	67 (11%)	
3		14 (14%)	82 (14%)	
4		9 (8.9%)	72 (12%)	
5		15 (15%)	89 (15%)	
6		18 (18%)	30 (5.1%)	
7		13 (13%)	22 (3.8%)	

prepare dataframe for analysis (select & reorder columns)

```
mimic_data <-  lab_data %>%
  select(bystlang, freelnch, byincome,                    # covariates
         stolen, t_hurt, p_fight, hit, damaged, bullied,  # factor 1 (indicators)
         safe, disrupt, gangs, rac_fght,                  # factor 2 (indicators)
         late, skipped, mth_read, mth_test, rd_test) %>%
  mutate(
    freelnch = case_when(    # Grade 10, percent free lunch - transform to binary
        freelnch <  5 ~ 0,   # < 50%
        freelnch >= 5 ~ 1))  # > 50%
```

Estimate the Unconditional Confirmatory Factor Analysis (CFA) model

Lab exercise: How many parameters are there in this model?

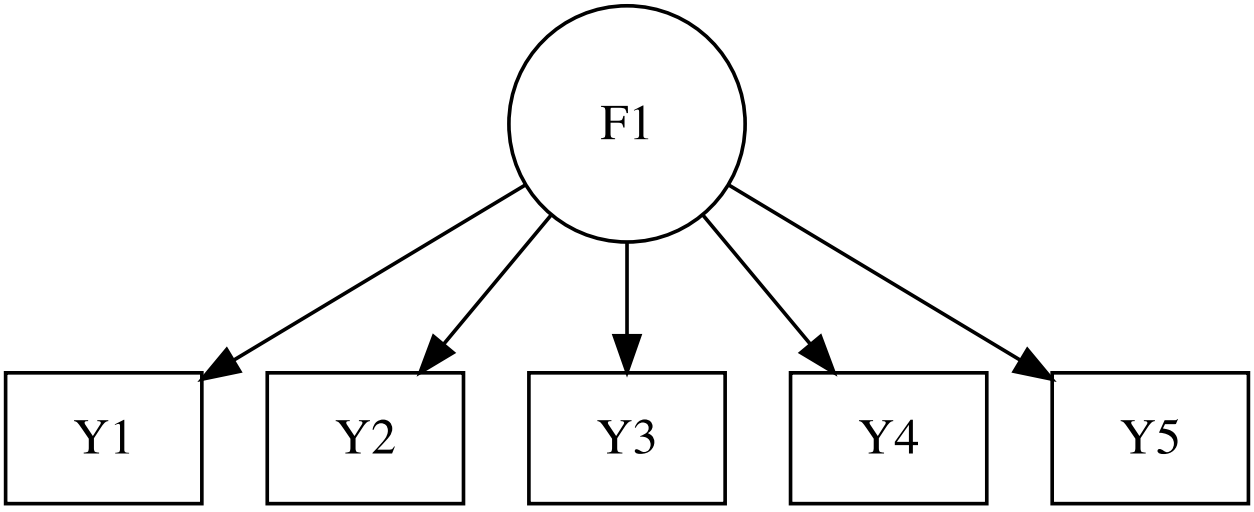
(no cheating - i.e., jumping ahead)

Number of parameters for the Unconditional CFA model:

- ?? item loadings
- ?? intercepts
- ?? residual variances
- ?? factor variances
- ?? factor co-variance

Make a simple CFA path diagram using package {DiagrammeR}

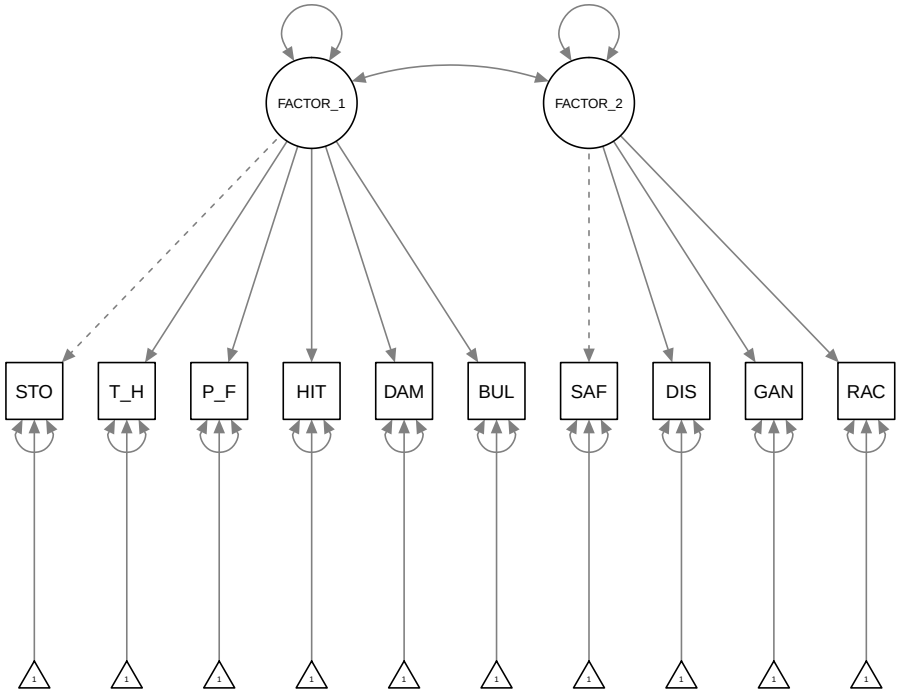
```
# starting simple...

grViz(" digraph CFA_basic {

 node [shape=box]
 Y1; Y2; Y3; Y4; Y5;

 node [shape=circle, width = 0.9]
 F1;

 edge []
 F1->{Y1 Y2 Y3 Y4 Y5}

}")
```




```
cfa_m0  <- mplusObject(
  TITLE = "CFA model0 - LAB 8 mimic models",
  VARIABLE =
    "usevar = stolen-rac_fght;",

  ANALYSIS =
    "estimator = mlr;",

  MODEL =
    "FACTOR_1 by stolen t_hurt p_fight hit damaged bullied;

     FACTOR_2 BY safe disrupt gangs rac_fght;" ,

  PLOT = "type = plot3;",
  OUTPUT = "sampstat standardized residual modindices (3.84);",

  usevariables = colnames(mimic_data),
  rdata = mimic_data)
```

```
cfa_m0_fit <- mplusModeler(cfa_m0,
              dataout=here("08-MIMIC", "mimic_mplus", "mimic_data.dat"),
              modelout=here("08-MIMIC", "mimic_mplus", "cfa_model0.inp"),
              check=TRUE, run = TRUE, hashfilename = FALSE)
```

```
# Read in the model to R within the "mimic_mplus" folder
mimic_output1 <- readModels(here("08-MIMIC", "mimic_mplus", "cfa_model0.out"), quiet = TRUE)

# Plot model:
semPaths(mimic_output1,
         # intercepts=FALSE,
         # fixedStyle = c(1)
         )
```




```
# comment out the arguments "intercepts" & "fixedStyle" to make all parameters explicit
```

Lab exercise: Count model parameters from the path diagram

(i.e., count number of arrows)

MIMIC model 1 - single bivariate covariate Number of parameters for the MIMIC model 1 = 33

- 8 item loadings (10 items - 2 fixed loadings)
- 10 intercepts
- 10 residual variances
- 2 factor variances

- 1 factor co-variance
- 1 covariate mean
- 1 covariate variance

```
grViz(" digraph mimic_path_diagram {

graph [overlap = true, fontsize = 10,   # this is the 'graph' statement
       fontname = Times,
       label=
       'Figure 1: MIMIC model with single covariate.']

  node [shape = box]                   # this is the 'node' statement

  A; B; C; D; E;

  node [shape = box,
        label = 'Covariate']

  X;

  node [shape = circle, fixedsize = true,
        width = 0.9, label = 'Factor 1']

  F;

  edge [color = black]                   # this is the 'edge' statement

  F->{A B C D E}
  X->F

}")
```

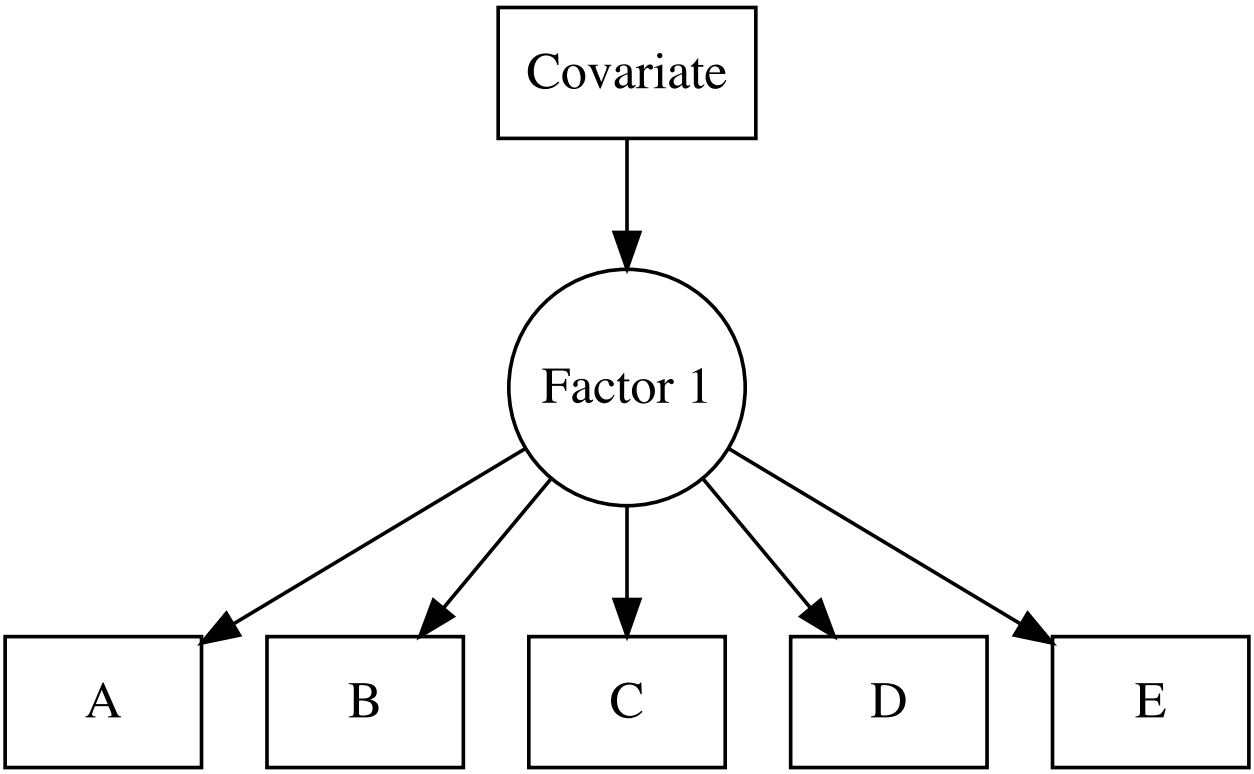
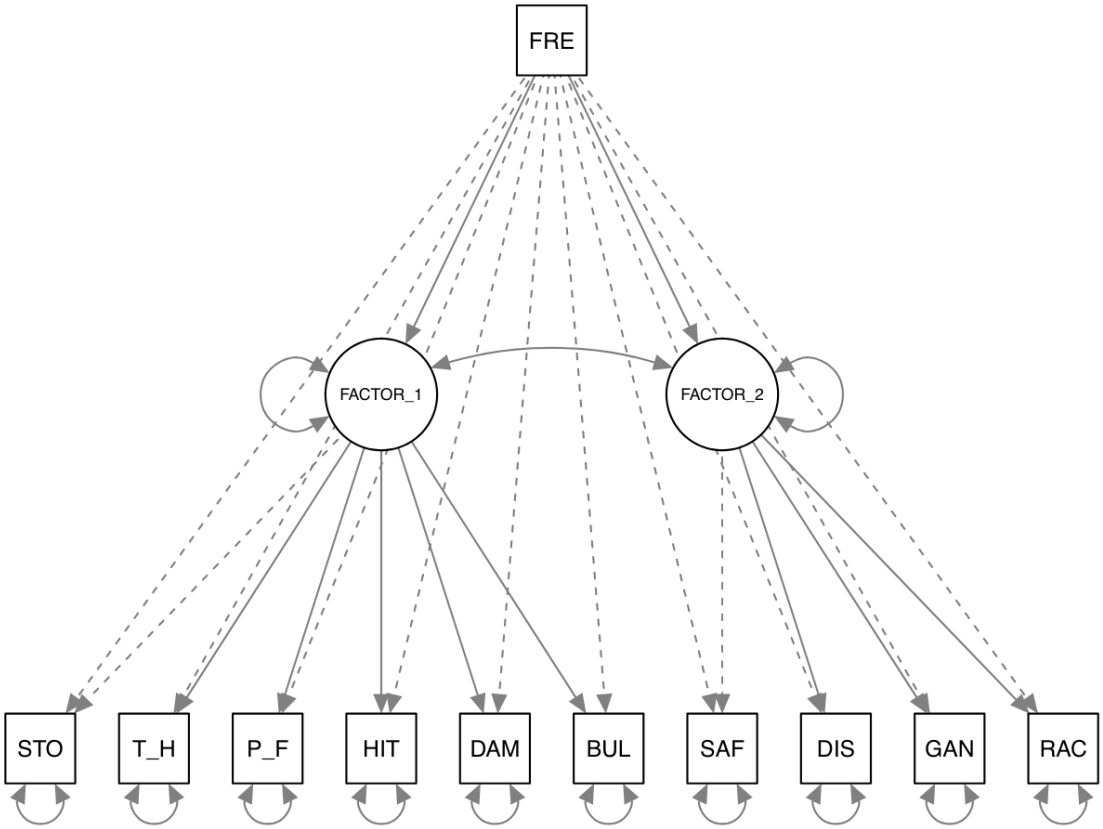


Figure 1: MIMIC model with single covariate.

```
mimic_m1  <- mplusObject(
  TITLE = "MIMIC model1 ",
  VARIABLE =
    "usevar = freelnch stolen-rac_fght;",

  ANALYSIS =
    "estimator = mlr;",

  MODEL =
    "FACTOR_1 by stolen t_hurt p_fight hit damaged bullied;

     FACTOR_2 by safe disrupt gangs rac_fght;

     FACTOR_1 on freelnch;

     FACTOR_2 on freelnch;" ,

  PLOT = "type = plot3;",
  OUTPUT = "sampstat standardized residual modindices (3.84);",

  usevariables = colnames(mimic_data),
  rdata = mimic_data)

mimic_m1_fit <- mplusModeler(mimic_m1,
                dataout=here("08-MIMIC", "mimic_mplus", "mimic_data.dat"),
```

```
                modelout=here("08-MIMIC", "mimic_mplus", "mimic_model1.inp"),
                check=TRUE, run = TRUE, hashfilename = FALSE)
```

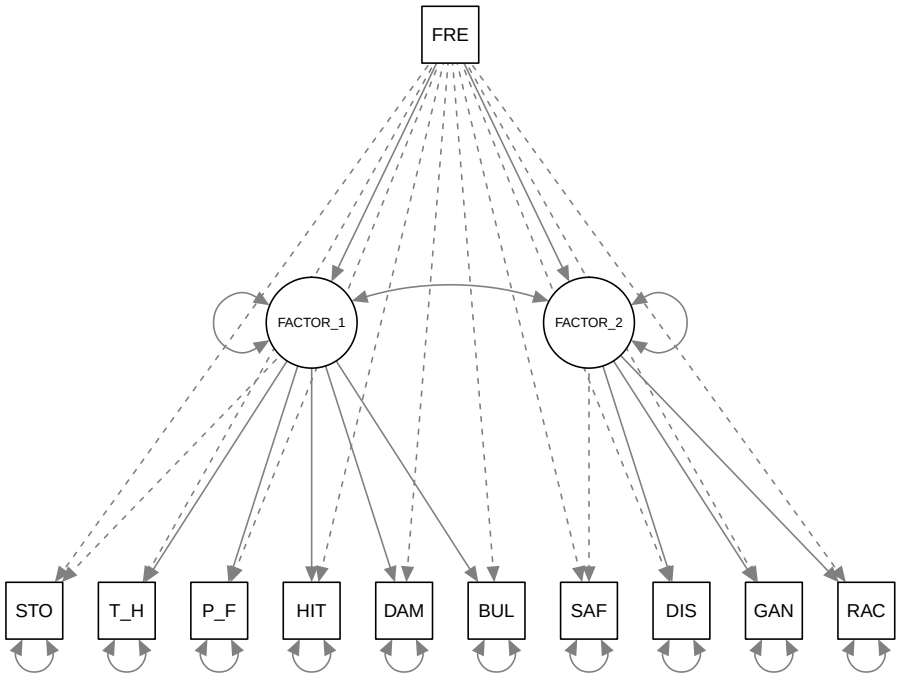
MIMIC model 2 - probe for covariate -> indicator DIFF




```
mimic_m2  <- mplusObject(
  TITLE = "MIMIC model2",
  VARIABLE =
    "usevar = freelnch stolen-rac_fght;",

  ANALYSIS =
    "estimator = mlr;",

  MODEL =
    "FACTOR_1 by stolen t_hurt p_fight hit damaged bullied;

     FACTOR_2 by safe disrupt gangs rac_fght;

     FACTOR_1 on freelnch;
```

```
    FACTOR_2 on freelnch;

    stolen-rac_fght on freelnch@0; ! to check DIFF see modification indices ",

  PLOT = "type = plot3;",
  OUTPUT = "sampstat standardized residual modindices (.1);",

  usevariables = colnames(mimic_data),
  rdata = mimic_data)

mimic_m2_fit <- mplusModeler(mimic_m2,
                dataout=here("08-MIMIC", "mimic_mplus", "mimic_data.dat"),
                modelout=here("08-MIMIC", "mimic_mplus", "mimic_model2.inp"),
                check=TRUE, run = TRUE, hashfilename = FALSE)
```

```
mimic_output2 <- readModels(here("08-MIMIC", "mimic_mplus", "mimic_model2.out"), quiet = TRUE)

# Plot model:
semPaths(mimic_output2,
          intercepts=FALSE,
          #fixedStyle = c(1)
         )
```



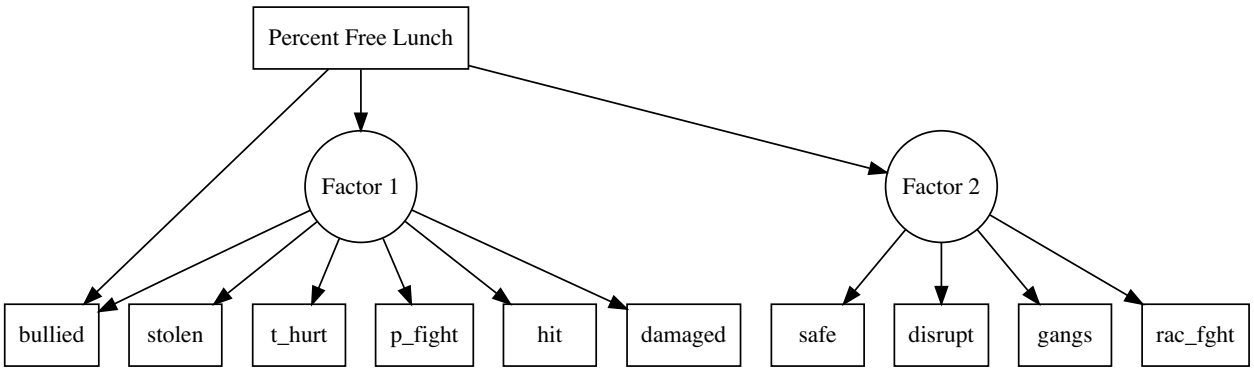
MIMIC model 3 - specify covariate -> indicator DIFF

Number of parameters for MIMIC model 3 = 34

- 8 indicator loadings (10 items - 2 fixed loadings)

- 10 intercepts
- 10 residual variances
- 2 factor variances
- 1 factor co-variance
- 1 covariate mean
- 1 covariate variance
- 1 DIF (covariate -> indicator)

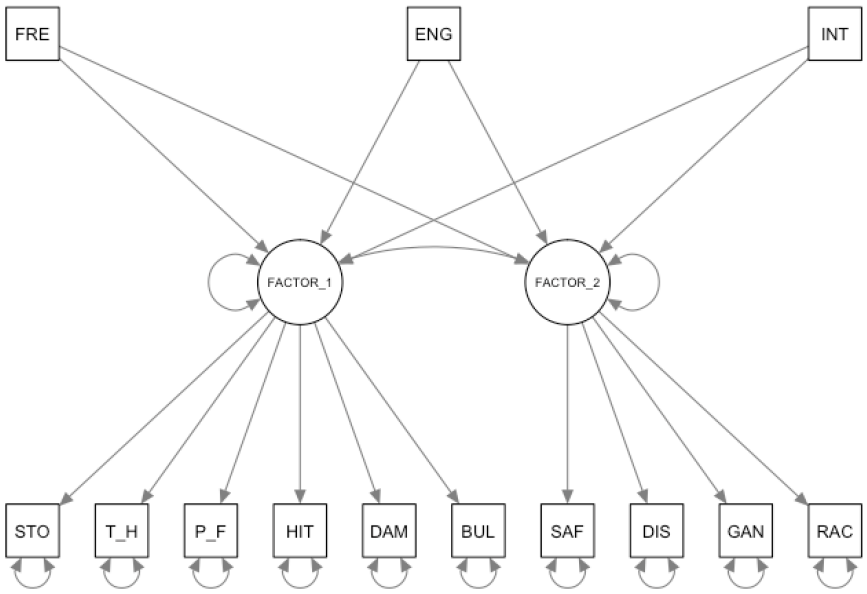
```
grViz(" digraph mimic_mode_3 {

graph [overlap = true, fontsize = 12, fontname = Times]

  node [shape = box]
  stolen; t_hurt; p_fight; hit; damaged; bullied; safe; disrupt; gangs; rac_fght;

  node [shape = box, label = 'Percent Free Lunch']
  X;

  node [shape = circle, fixedsize = true, width = 0.9, label = 'Factor 1']
  F1;

  node [shape = circle, fixedsize = true, width = 0.9, label = 'Factor 2']
  F2;

  edge [color = black]

  F1->{stolen t_hurt p_fight hit damaged bullied}
  F2->{safe disrupt gangs rac_fght}
  X->F1 X->F2 X->bullied
}")
```



```
mimic_m3  <- mplusObject(
  TITLE = "MIMIC model3",
  VARIABLE =
    "usevar = freelnch stolen-rac_fght;",
```

```
  ANALYSIS =
    "estimator = mlr;",

  MODEL =
    "FACTOR_1 by stolen t_hurt p_fight hit damaged bullied;

     FACTOR_2 by safe disrupt gangs rac_fght;

     FACTOR_1 FACTOR_2 on freelnch;

     bullied on freelnch; ",

  PLOT = "type = plot3;",
  OUTPUT = "sampstat standardized residual modindices (3.84);",

  usevariables = colnames(mimic_data),
  rdata = mimic_data)

mimic_m3_fit <- mplusModeler(mimic_m3,
                dataout=here("08-MIMIC", "mimic_mplus", "mimic_data.dat"),
                modelout=here("08-MIMIC", "mimic_mplus", "mimic_model3.inp"),
                check=TRUE, run = TRUE, hashfilename = FALSE)
```

MIMIC model 4 - two covariates & an interaction term

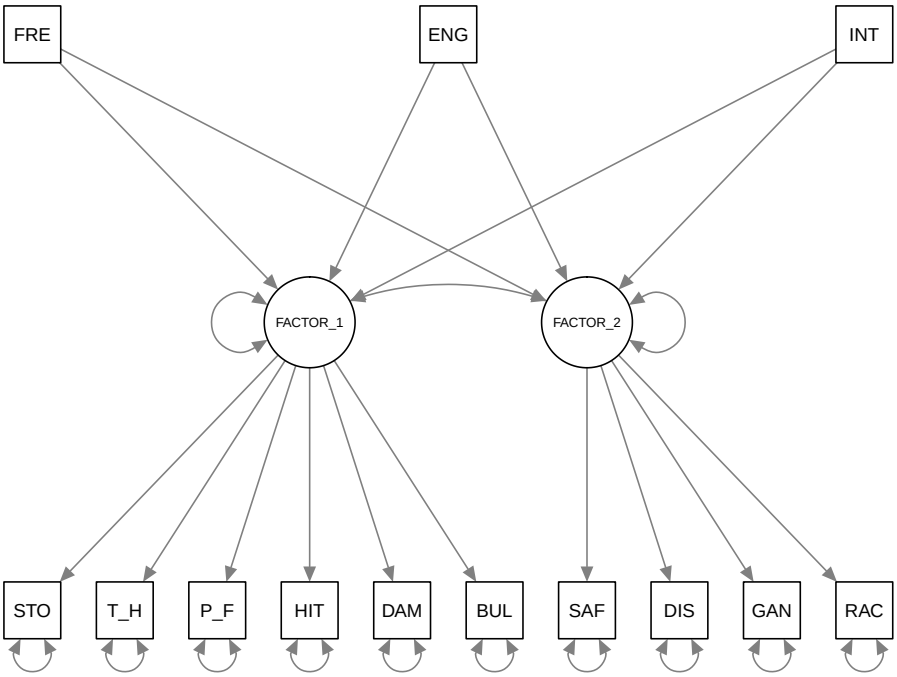


```
mimic_m4  <- mplusObject(
  TITLE = "MIMIC model4",
  VARIABLE =
    "usevar = freelnch stolen-rac_fght eng_2nd int;",

  ANALYSIS =
    "estimator = mlr;",

  DEFINE =
  "if bystlang == 1 THEN eng_2nd=0;
   if bystlang == 0 THEN eng_2nd=1;
  int = eng_2nd*freelnch;",

  MODEL =
    "FACTOR_1 by stolen t_hurt p_fight hit damaged bullied;

     FACTOR_2 by safe disrupt gangs rac_fght;

     FACTOR_1 FACTOR_2 on freelnch eng_2nd int; ",

  PLOT = "type = plot3;",
  OUTPUT = "sampstat standardized residual modindices (3.84);",

  usevariables = colnames(mimic_data),
  rdata = mimic_data)

mimic_m4_fit <- mplusModeler(mimic_m4,
                dataout=here("08-MIMIC", "mimic_mplus", "mimic_data.dat"),
                modelout=here("08-MIMIC", "mimic_mplus", "mimic_model4.inp"),
                check=TRUE, run = TRUE, hashfilename = FALSE)
```

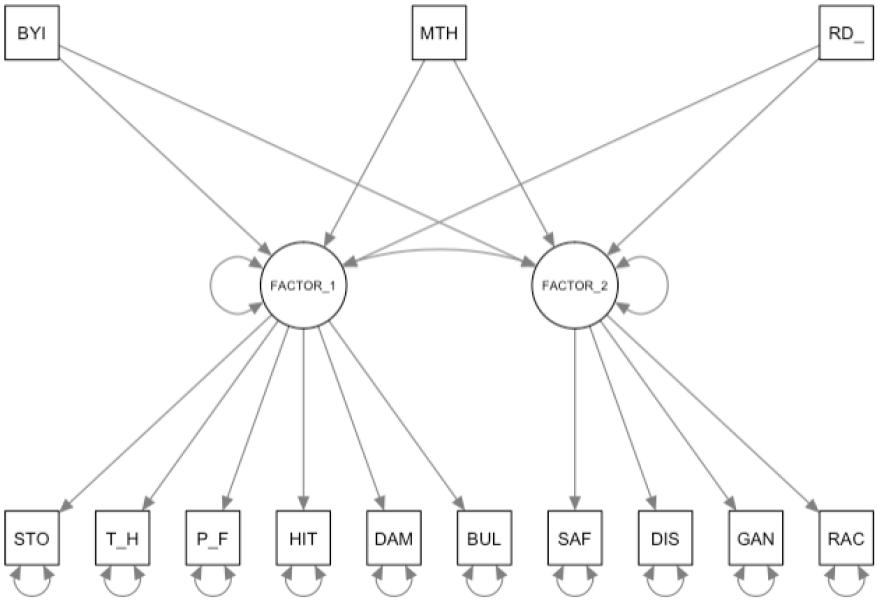
---

create a path diagram of MIMIC model 4

```
# Read in the model to R within the "cfa_mplus" folder
mimic_output4 <- readModels(here("08-MIMIC", "mimic_mplus", "mimic_model4.out"), quiet = TRUE)

# Plot model:
semPaths(mimic_output4,
         intercepts=FALSE,
         fixedStyle = c(1))
```



MIMIC model 5 - three continuous covariates



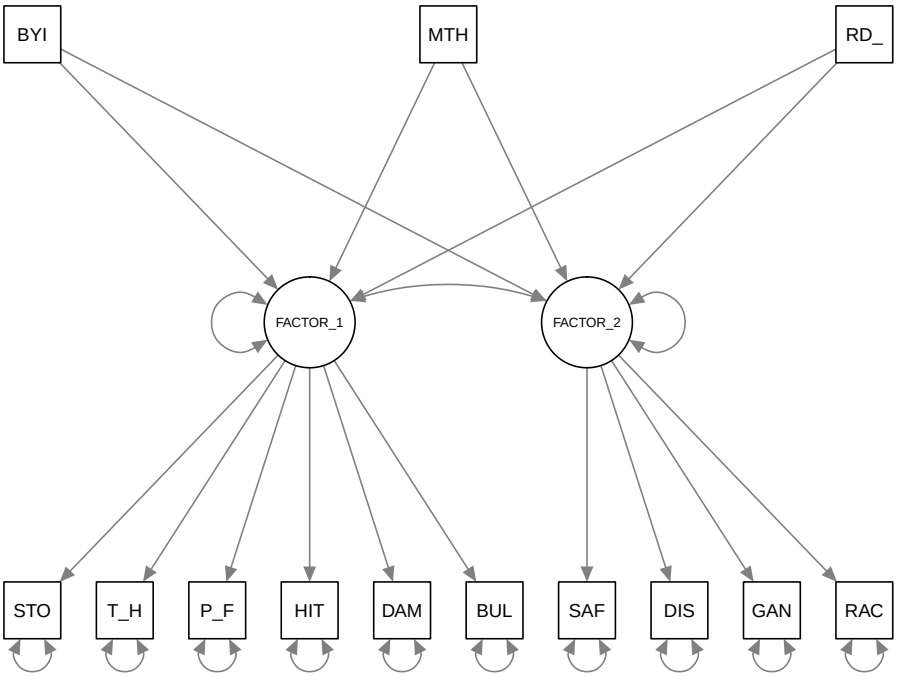
```
mimic_m5  <- mplusObject(
  TITLE = "MIMIC model5",
  VARIABLE =
    "usevar = byincome mth_test rd_test stolen-rac_fght;",

  ANALYSIS =
    "estimator = mlr;",

  MODEL =
    "FACTOR_1 by stolen t_hurt p_fight hit damaged bullied;

     FACTOR_2 by safe disrupt gangs rac_fght;

     FACTOR_1 FACTOR_2 on byincome mth_test rd_test; ",

  PLOT = "type = plot3;",
  OUTPUT = "sampstat standardized residual modindices (3.84);",

  usevariables = colnames(mimic_data),
  rdata = mimic_data)

mimic_m5_fit <- mplusModeler(mimic_m5,
                dataout=here("08-MIMIC", "mimic_mplus", "mimic_data.dat"),
                modelout=here("08-MIMIC", "mimic_mplus", "mimic_model5.inp"),
                check=TRUE, run = TRUE, hashfilename = FALSE)
```

---

create a path diagram of MIMIC model 5

```
# Read in the model to R
mimic_output5 <- readModels(here("08-MIMIC", "mimic_mplus", "mimic_model5.out"), quiet = TRUE)
```

```
# Plot model:
semPaths(mimic_output5,
         intercepts=FALSE,
         fixedStyle = c(1)
         )
```

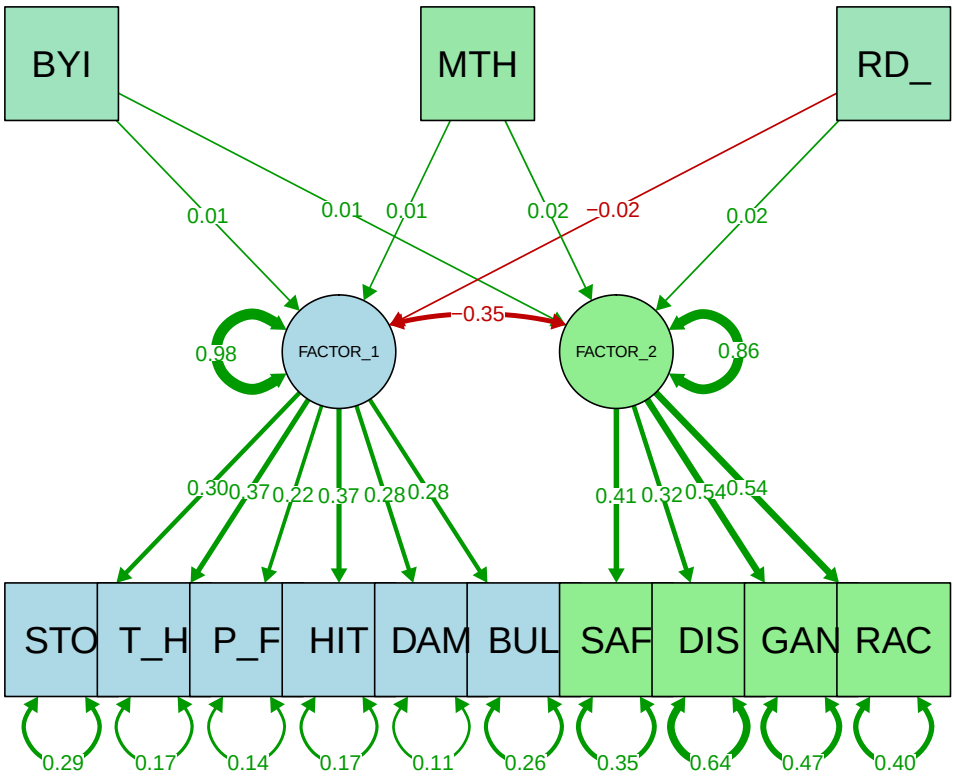



```
# ** Lab exercise: comment out the "intercepts" & "fixedStyle" arguments and then count model parameter
```

---

practice some formatting with `semPlot::semPaths()`

```
semPaths(mimic_output5,
         "stdyx",  # plot the standardized parameter estimates (see output section: STDYX)
         intercepts=FALSE,
         fixedStyle = c(1),
         color= list(lat = c("light blue"," light green")),
         sizeMan = 10, sizeInt = 10, sizeLat = 10,
         edge.label.cex=.8,
         fade=FALSE
         )
```



---

read all models and create table

```
all_models <- readModels(here("08-MIMIC", "mimic_mplus"), quiet = TRUE)

table <- LatexSummaryTable(all_models,
                           keepCols=c(
                           "Filename", "Parameters","ChiSqM_Value",
                           "CFI", "TLI", "SRMR", "RMSEA_Estimate",
                           "RMSEA_90CI_LB", "RMSEA_90CI_UB"),
                       sortBy = "Filename")

table %>%
  mutate(Filename = str_remove(Filename, ".out")) %>%
  gt() %>%
  cols_label(
    Filename = "Model",
    Parameters = "Par",
    ChiSqM_Value = "ChiSq",
    CFI = "CFI", TLI = "TLI", SRMR = "SRMR",
    RMSEA_Estimate = "RMSEA",
    RMSEA_90CI_LB = "Lower CI",
    RMSEA_90CI_UB = "Upper CI")
```

Model	Par	ChiSq	CFI	TLI	SRMR	RMSEA	Lower CI	Upper CI
cfa_model0	31	121.460	0.898	0.865	0.043	0.060	0.048	0.071
mimic_model1	33	133.455	0.894	0.862	0.044	0.057	0.047	0.069
mimic_model2	33	133.455	0.894	0.862	0.044	0.057	0.047	0.069
mimic_model3	34	130.058	0.897	0.862	0.043	0.057	0.046	0.069
mimic_model4	37	153.527	0.899	0.869	0.041	0.050	0.040	0.060
mimic_model5	37	169.116	0.894	0.863	0.042	0.052	0.043	0.061

End

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.

Horst, A. (2020). Course & Workshop Materials. GitHub Repositories, https://https://allisonhorst.github.io/

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