

# Appendix - LTA with MplusAutomation

## Contents

<b>Rationale for MplusAutomation workflow:</b>	<b>1</b>
<b>Preparation</b>	<b>2</b>
Download the R-Project . . . . .	2
Project folder organization: nested structure . . . . .	2
Notation guide . . . . .	2
<b>Step 1: Enumeration</b>	<b>3</b>
Enumerate time point 1 (7th grade) . . . . .	3
Enumerate time point 2 (10th grade) . . . . .	4
Plot LCAs . . . . .	5
<b>Step 2: Create model fit summary table</b>	<b>8</b>
<b>Step 3: Estimate Latent Transition Analysis</b>	<b>10</b>
Estimate non-invariant estimated LTA model . . . . .	10
Estimate invariant LTA model . . . . .	11
<b>END COPY EDITING - ALL PLOTS CURRENTLY INCOMPLETE</b>	<b>15</b>
<b>Plot LTA transitions</b>	<b>15</b>
<b>References: (INCOMPLETE)</b>	<b>16</b>

---

## Rationale for MplusAutomation workflow:

This R-script is intended to provide a template for running LTA and associated tasks in a systematic manner. Using this approach all code for data pre-processing, model estimation, tabulation, and figure processing can be contained within a single script providing clear documentation. It is the authors belief that this dramatically reduces risk of user-error, is conducive to open-science philosophy, and scientific transparency. All models are estimated using **Mplus** (cite) using the wrapping program **MplusAutomation** (cite). This method requires that the user to have the proprietary software **Mplus** installed on their OS.

This approach relies on the utility of **R-Projects**. This provides a structured framework for organizing all associated data files, Mplus text files, scripts, and figures. Given the high output of Mplus files inherent to LTA modeling, creating a system of project sub-folders greatly improves organization (i.e., folders; ‘data’, ‘mplus\_files’ ‘figures’, etc.) Additionally, the communication between R and Mplus requires the specification of file-paths a procedure which is streamlined by use of **R-projects**. Due to the reliance on file-paths the **here** package is utilized for reproducibility, by making all path syntax uniform across operating systems.

---

## Preparation

### Download the R-Project

Download Github repository here: <https://github.com/garberadamc/LTA-FAQ>

For readers unfamiliar with Github and version controlled R-projects:  
Within the repository site, click the green ‘Code’ menu button and choose ‘Download ZIP’

### Project folder organization: nested structure

The following sub-folders will be used to contain files:

1. “data”
2. “enum\_LCA\_time1”
3. “enum\_LCA\_time2”
4. “LTA\_models”

#### Note regarding choice of project location:

If the project folder is located within too many nested folders it may result in a file-path error when estimating models with **MplusAutomation**.

---

## Notation guide

In the following script, three types of comments are included in code blocks in which models are estimated using **MplusAutomation**.

- a. **Annotate in R:** The hashtag symbol # identifies comments written in R-language form.
  - b. **Annotate in Mplus input:** Within the `mplusObject()` function all text used to generate Mplus input files is enclosed within quotation marks (green text). To add comments the Mplus language convention is used (e.g., !!! annotate Mplus input !!!).
  - c. **Annotate context-specific syntax:** To signal to the user areas of the syntax which must be adapted to fit specific modeling contexts the text, **NOTE CHANGE:** is used.
- 

To install package {`rhdf5`}

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

BiocManager::install("rhdf5")
```

Load packages

```
library(MplusAutomation)
library(rhdf5)
library(tidyverse)
library(here)
library(glue)
library(janitor)
library(gt)
library(rhdf5)
library(reshape2)
library(cowplot)
```

Read in LSAY data file

*Note:* The LSAY data file, `lsay_lta_faq_2020.csv`, has been pre-processed.

```
lsay_data <- read_csv(here("data", "lsay_lta_faq_2020.csv"),
  na=c("9999", "9999.00"))
```

---

## Step 1: Enumeration

---

### Enumerate time point 1 (7th grade)

```
# NOTE CHANGE: '6' indicates the number of k-class models to estimate.
# User can change this number it fit research context.
# In this example, the code loops or iterates over values 1 through 6 ( '{k}' ).
t1_enum_k_16 <- lapply(1:6, function(k) {
  enum_t1 <- mplusObject(

# The 'glue' function inserts R code within {---} a string chunk.
  TITLE = glue("Class-{k}_Time1"),

  VARIABLE = glue(
    "!!! NOTE CHANGE: List of the five 7th grade indicators !!!
    categorical = ab39m-ab39x;
    usevar = ab39m-ab39x;

    !!! The value of 'k' is inserted here !!!
    classes = c({k});"),
```

```

ANALYSIS =
  "estimator = mlr;
  type = mixture;
  !!! NOTE CHANGE: The intial and final start values. Reduce to speed up estimation time. !!!
  starts = 500 100;
  processors=10;";

OUTPUT = "sampstat residual tech11 tech14;";

PLOT =
  "type = plot3;
  series = ab39m-ab39x(*)";

usevariables = colnames(lsay_data),
rdata = lsay_data)

# NOTE CHANGE: Fix to match appropriate sub-folder name
# See after `here` function (e.g., "enum_LCA_time1")
enum_t1_fit <- mplusModeler(enum_t1,
  dataout=here("enum_LCA_time1", "t1.dat"),
  modelout=glue(here("enum_LCA_time1", "c{k}_lca_enum_time1.inp")),
  check=TRUE, run = TRUE, hashfilename = FALSE)
})

```

---

## Enumerate time point 2 (10th grade)

```

t2_enum_k_16 <- lapply(1:6, function(k) {
  enum_t2 <- mplusObject(

    TITLE = glue("Class-{k}_Time2"),

    VARIABLE =
  glue(
    "!!! CHANGE: List of the five 10th grade indicators !!!
    categorical = ga33a-ga33l;
    usevar = ga33a-ga33l;

    classes = c({k}); !!! Loop value 'k' inserted here !!!"),

    ANALYSIS =
    "estimator = mlr;
    type = mixture;
    starts = 500 100;
    processors=10;";

    OUTPUT = "sampstat residual tech11 tech14;";

    PLOT =
    "type = plot3;

```

```

    series = ga33a-ga33l(*)";

usevariables = colnames(lsay_data),
rdata = lsay_data)

enum_t2_fit <- mplusModeler(enum_t2,
  dataout=here("enum_LCA_time2", "t2.dat"),
  modelout=glue(here("enum_LCA_time2", "c{k}_lca_enum_time2.inp")),
  check=TRUE, run = TRUE, hashfilename = FALSE)
})

```

---

## Plot LCAs

---

Read models

```

# timepoint 1
output_enum_t1 <- readModels(here("enum_LCA_time1"), quiet = TRUE)
# timepoint 2
output_enum_t2 <- readModels(here("enum_LCA_time2"), quiet = TRUE)

```

Plot time 1 LCA

```

# extract posterior probabilities
plot_t1 <- as.data.frame(output_enum_t1[["c4_lca_enum_time1.out"]][
  ["gh5"]][["means_and_variances_data"]][
  ["estimated_probs"]][["values"]][
  [seq(2, 10, 2),]) #seq("from", "to", "by")

# extract class size proportions
c_size <- as.data.frame(output_enum_t1[["c4_lca_enum_time1.out"]][
  ["class_counts"]][["modelEstimated"]][["proportion"]])
colnames(c_size) <- paste0("cs")
c_size <- c_size %>% mutate(cs = round(cs*100, 2))

#rename class and indicator names
colnames(plot_t1) <- paste0("C", 1:4, glue(" ({c_size[1:4,]}%)"))
plot_t1 <- cbind(Var = paste0("U", 1:5), plot_t1)

plot_t1$Var <- factor(plot_t1$Var,
  levels = c("U1", "U2", "U3", "U4", "U5"),
  labels = c("Enjoy", "Useful", "Logical", "Job", "Adult"))

#change data-frame from wide to long format
pd_long_t1 <- melt(plot_t1, id.vars = "Var")

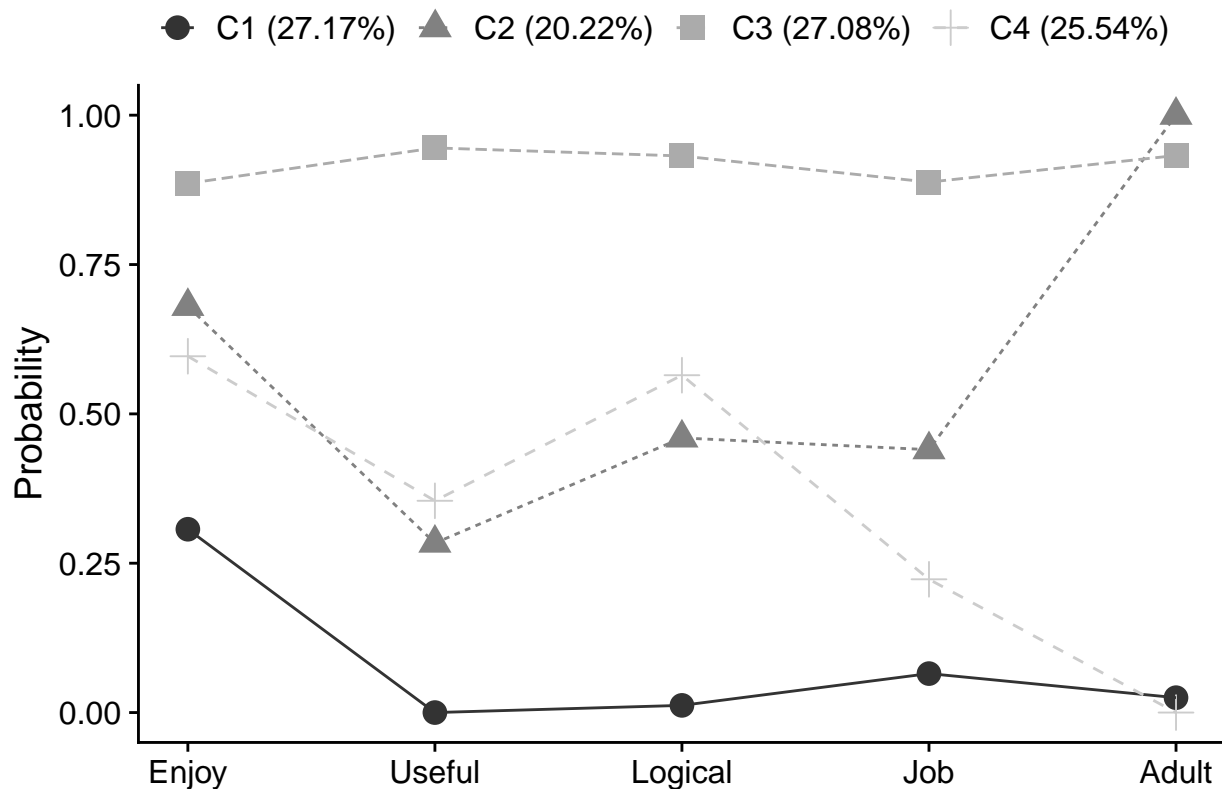
# plot data
ggplot(pd_long_t1, aes(as.integer(Var), value, shape = variable,

```

```

    colour = variable, lty = variable)) +
  geom_point(size = 4) + geom_line() +
  scale_x_continuous("", breaks = 1:5, labels = plot_t1$Var) +
  scale_y_continuous("Probability") +
  scale_colour_grey() +
  theme_cowplot() +
  theme(legend.title = element_blank(),
        legend.position = "top")

```



```

ggsave(here("figures", "T1_C4_LCA_plot.png"), dpi="retina", height=5, width=7, units="in")

```

Plot time 2 LCA

```

# extract posterior probabilities
plot_t2 <- as.data.frame(output_enum_t2[["c4_lca_enum_time2.out"]][
  ["gh5"]][["means_and_variances_data"]][
  ["estimated_probs"]][["values"]][
  [seq(2, 10, 2),]) #seq("from", "to", "by")

# extract class size proportions
c_size <- as.data.frame(output_enum_t2[["c4_lca_enum_time2.out"]][
  ["class_counts"]][["modelEstimated"]][["proportion"]])
colnames(c_size) <- paste0("cs")
c_size <- c_size %>% mutate(cs = round(cs*100, 2))

#rename class and indicator names
colnames(plot_t2) <- paste0("C", 1:4, glue(" ({c_size[1:4,]}%)"))

```

```

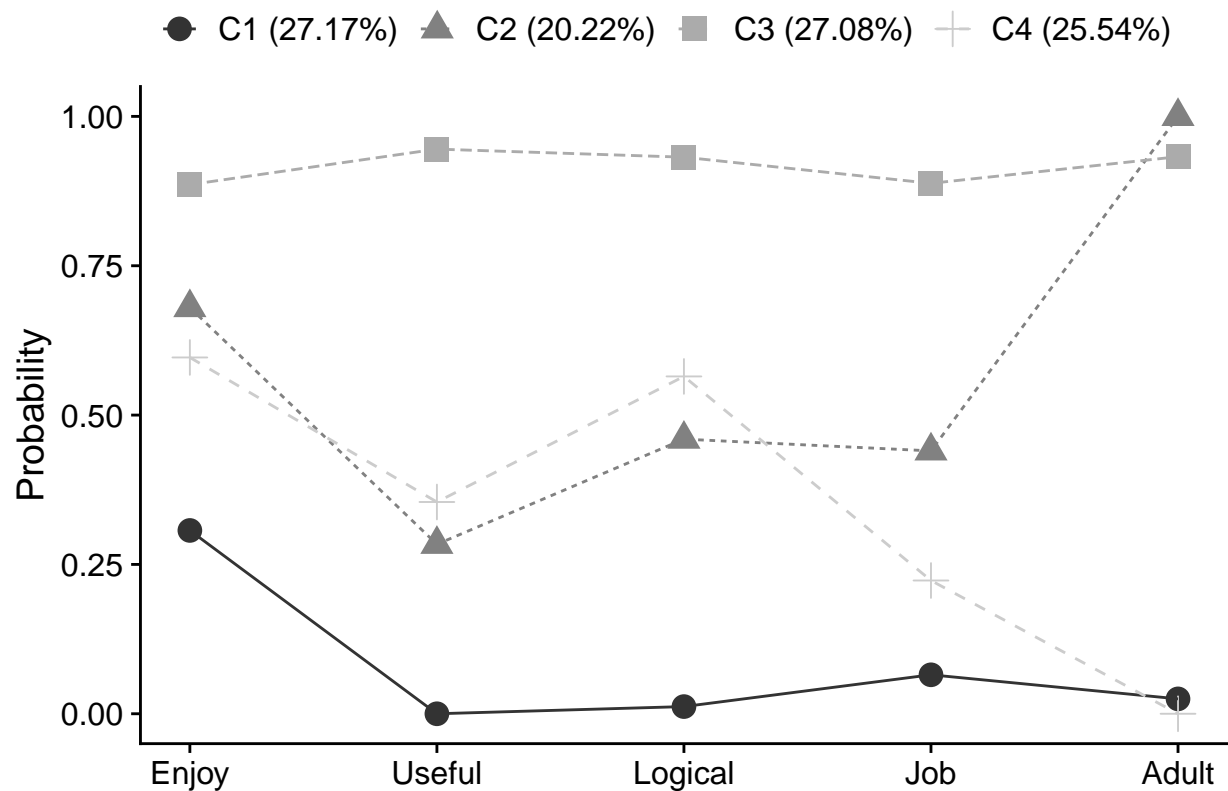
plot_t2 <- cbind(Var = paste0("U", 1:5), plot_t1)

plot_t2$Var <- factor(plot_t2$Var,
  levels = c("U1", "U2", "U3", "U4", "U5"),
  labels = c("Enjoy", "Useful", "Logical", "Job", "Adult"))

#change data-frame from wide to long format
pd_long_t2 <- melt(plot_t2, id.vars = "Var")

# plot data
ggplot(pd_long_t2, aes(as.integer(Var), value, shape = variable,
  colour = variable, lty = variable)) +
  geom_point(size = 4) + geom_line() +
  scale_x_continuous("", breaks = 1:5, labels = plot_t2$Var) +
  scale_y_continuous("Probability") +
  # labs(title = "LCA Probability Plot") +
  scale_colour_grey() +
  theme_cowplot() +
  theme(legend.title = element_blank(),
    legend.position = "top")

```



```

ggsave(here("figures", "T2_C4_LCA_plot.png"), dpi="retina", height=5, width=7, units="in")

```

## Step 2: Create model fit summary table

---

Extract model fit data

```
# timepoint 1
output_enum_t1 <- readModels(here("enum_LCA_time1"), quiet = TRUE)
# timepoint 2
output_enum_t2 <- readModels(here("enum_LCA_time2"), quiet = TRUE)

enum_extract1 <- LatexSummaryTable(output_enum_t1,
  keepCols=c("Title", "Parameters", "LL", "BIC", "aBIC",
    "BLRT_PValue", "T11_VLMR_PValue", "Observations"))

enum_extract2 <- LatexSummaryTable(output_enum_t2,
  keepCols=c("Title", "Parameters", "LL", "BIC", "aBIC",
    "BLRT_PValue", "T11_VLMR_PValue", "Observations"))
```

---

Calculate indices derived from the Log Likelihood (LL)

```
allFit1 <- enum_extract1 %>%
  mutate(aBIC = -2*LL+Parameters*log((Observations+2)/24)) %>%
  mutate(CIAC = -2*LL+Parameters*(log(Observations)+1)) %>%
  mutate(AWE = -2*LL+2*Parameters*(log(Observations)+1.5)) %>%
  mutate(SIC = -.5*BIC) %>%
  mutate(expSIC = exp(SIC - max(SIC))) %>%
  mutate(BF = exp(SIC-lead(SIC))) %>%
  mutate(cmPk = expSIC/sum(expSIC)) %>%
  select(1:5,9:10,6:7,13,14) %>%
  arrange(Parameters)

allFit2 <- enum_extract2 %>%
  mutate(aBIC = -2*LL+Parameters*log((Observations+2)/24)) %>%
  mutate(CIAC = -2*LL+Parameters*(log(Observations)+1)) %>%
  mutate(AWE = -2*LL+2*Parameters*(log(Observations)+1.5)) %>%
  mutate(SIC = -.5*BIC) %>%
  mutate(expSIC = exp(SIC - max(SIC))) %>%
  mutate(BF = exp(SIC-lead(SIC))) %>%
  mutate(cmPk = expSIC/sum(expSIC)) %>%
  select(1:5,9:10,6:7,13,14) %>%
  arrange(Parameters)

allFit <- full_join(allFit1,allFit2)
```

---

Format table



```

allFit %>%
  mutate(Title = str_remove(Title, "_Time*")) %>%
  gt() %>%
  tab_header(
    title = md("**Model Fit Summary Table**"), subtitle = md("&nbsp;")) %>%
    tab_source_note(
      source_note = md("Data Source: **Longitudinal Study of American Youth.**") %>%
    cols_label(
      Title = "Classes",
      Parameters = md("Par"),
      LL = md("*LL*"),
      T11_VLMR_PValue = "VLMR",
      BLRT_PValue = "BLRT",
      BF = md("BF"),
      cmPk = md("*cmP_k*")) %>%
  tab_footnote(
    footnote = md(
      "*Note.* Par = Parameters; *LL* = model log likelihood; BIC = Bayesian information criterion;
      aBIC = sample size adjusted BIC; CAIC = consistent Akaike information criterion;
      AWE = approximate weight of evidence criterion; BLRT = bootstrapped likelihood ratio test p-value;
      VLMR = Vuong-Lo-Mendell-Rubin adjusted likelihood ratio test p-value;
      cmPk = approximate correct model probability."),
    locations = cells_title()) %>%
  tab_options(column_labels.font.weight = "bold") %>%
  fmt_number(10, decimals = 2,
    drop_trailing_zeros=TRUE,
    suffixing = TRUE) %>%
  fmt_number(c(3:9,11), decimals = 2) %>%
  fmt_missing(1:11, missing_text = "---") %>%
  fmt(c(8:9,11),
    fns = function(x)
      ifelse(x<0.001, "<.001", scales::number(x, accuracy = 0.01))) %>%
  fmt(10, fns = function(x)
    ifelse(x>100, ">100", scales::number(x, accuracy = .1))) %>%
  tab_row_group(
    group = "Time-1",
    rows = 1:6) %>%
  tab_row_group(
    group = "Time-2",
    rows = 7:12) %>%
  row_group_order(
    groups = c("Time-1", "Time-2"))

```

Model Fit Summary Table<sup>1</sup>

Classes	Par	<i>LL</i>	BIC	aBIC	CIAC	AWE	BLRT	VLMR	BF	<i>cmP_k</i>
Time-1										
C1_LCA1	5	-10,250.60	20,541.34	20,525.45	20,546.34	20,596.47	–	–	–	<.001
C2_LCA1	11	-8,785.32	17,658.92	17,623.97	17,669.93	17,780.22	<.001	<.001	>100	<.001
C3_LCA1	17	-8,693.57	17,523.59	17,469.57	17,540.59	17,711.04	<.001	<.001	>100	0.00
C4_LCA1	23	-8,664.09	17,512.79	17,439.71	17,535.79	17,766.40	<.001	<.001	>100	1.00
C5_LCA1	29	-8,662.39	17,557.54	17,465.39	17,586.54	17,877.31	1.00	0.66	>100	<.001

C6_LCA1	35	-8,661.54	17,604.01	17,492.80	17,639.01	17,989.94	1.00	0.75	>100	<.001
Time-2										
C1_LCA2	5	-7,658.79	15,356.19	15,340.30	15,361.19	15,409.80	-	-	-	<.001
C2_LCA2	11	-6,073.81	12,232.56	12,197.61	12,243.56	12,350.50	<.001	<.001	>100	<.001
C3_LCA2	17	-5,988.36	12,107.99	12,053.98	12,124.99	12,290.27	<.001	<.001	>100	0.32
C4_LCA2	23	-5,964.45	12,106.50	12,033.43	12,129.51	12,353.12	<.001	0.00	2.1	0.68
C5_LCA2	29	-5,961.68	12,147.30	12,055.16	12,176.30	12,458.25	0.31	0.36	>100	<.001
C6_LCA2	35	-5,961.26	12,192.79	12,081.59	12,227.79	12,568.07	1.00	0.50	>100	<.001

<sup>1</sup>Note. Par = Parameters; LL = model log likelihood; BIC = Bayesian information criterion; aBIC = sample size adjusted BIC; CAIC = consistent Akaike information criterion; AWE = approximate weight of evidence criterion; BLRT = bootstrapped likelihood ratio test p-value; VLMR = Vuong-Lo-Mendell-Rubin adjusted likelihood ratio test p-value; cmPk = approximate correct model probability.

Data Source: **Longitudinal Study of American Youth.**

### Step 3: Estimate Latent Transition Analysis

#### Estimate non-invariant estimated LTA model

```
lta_non_inv <- mplusObject(

  TITLE =
    "4-Class-Non-Invariant",

  VARIABLE =
    "usev = ab39m ab39t ab39u ab39w ab39x ! 7th grade indicators
      ga33a ga33h ga33i ga33k ga33l; ! 10th grade indicators

    categorical = ab39m-ab39x ga33a-ga33l;

    classes = c1(4) c2(4);",

  ANALYSIS =
    "estimator = mlr;
    type = mixture;
    starts = 500 100;
    processors=10;",

  MODEL =
    "%overall%
    c2 on c1; !!! estimate all multinomial logistic regressions !!!

    !!! The above syntax can also be written as: !!!
    ! c2#1 on c1#1 c1#2 c1#3; !
```

```

! c2#2 on c1#1 c1#2 c1#3; !
! c2#3 on c1#1 c1#2 c1#3; !

MODEL c1:
%c1#1%
[AB39M$1-AB39X$1];
%c1#2%
[AB39M$1-AB39X$1];
%c1#3%
[AB39M$1-AB39X$1];
%c1#4%
[AB39M$1-AB39X$1];

MODEL c2:
%c2#1%
[GA33A$1-GA33L$1];
%c2#2%
[GA33A$1-GA33L$1];
%c2#3%
[GA33A$1-GA33L$1];
%c2#4%
[GA33A$1-GA33L$1];",

OUTPUT = "tech1 tech15 svalues;",

usevariables = colnames(lsay_data),
rdata = lsay_data)

lta_non_inv_fit <- mplusModeler(lta_non_inv,
                               dataout=here("enum_LCA_time2", "lta.dat"),
                               modelout=here("LTA_models", "4-Class-Non-Invariant.inp"),
                               check=TRUE, run = TRUE, hashfilename = FALSE)

```

---

## Estimate invariant LTA model

---

```

lta_inv <- mplusObject(

  TITLE =
    "4-Class-Invariant",

  VARIABLE =
    "usev = ab39m ab39t ab39u ab39w ab39x ! 7th grade indicators
      ga33a ga33h ga33i ga33k ga33l; ! 10th grade indicators

    categorical = ab39m-ab39x ga33a-ga33l;

    classes = c1(4) c2(4);",

```

```

ANALYSIS =
  "estimator = mlr;
  type = mixture;
  starts = 500 100;
  processors=10;";

MODEL =
  "%overall%
  c2 on c1;

  MODEL c1:
  %c1#1%
  [AB39M$1-AB39X$1] (1-5);
  %c1#2%
  [AB39M$1-AB39X$1] (6-10);
  %c1#3%
  [AB39M$1-AB39X$1] (11-15);
  %c1#4%
  [AB39M$1-AB39X$1] (16-20);

  MODEL c2:
  %c2#1%
  [GA33A$1-GA33L$1] (1-5);
  %c2#2%
  [GA33A$1-GA33L$1] (6-10);
  %c2#3%
  [GA33A$1-GA33L$1] (11-15);
  %c2#4%
  [GA33A$1-GA33L$1] (16-20);";

SAVEDATA =
  "file = LTA_Inv_CPROBS.dat;
  save = cprob;
  missflag = 9999;";

OUTPUT = "tech1 tech15 svalues;";

usevariables = colnames(lsay_data),
rdata = lsay_data)

lta_inv_fit <- mplusModeler(lta_inv,
  dataout=here("enum_LCA_time2", "lta.dat"),
  modelout=here("LTA_models", "4-Class-Invariant.inp"),
  check=TRUE, run = TRUE, hashfilename = FALSE)

```

Conduct Satorra-Bentler  $\chi^2$  difference testing

```

# one with more parameters is parent (non-invariant), one with fewer parameters is the nested model (invariant)
# *0 (null or nested model) & *1 (comparison model)

lta_models <- readModels(here("LTA_models"), quiet = TRUE)

```

```

T1 <- lta_models[["X4.Class.Non.Invariant.out"]][["summaries"]][["ChiSqCategoricalLRT_Value"]]
T0 <- lta_models[["X4.Class.Invariant.out"]][["summaries"]][["ChiSqCategoricalLRT_Value"]]
c1 <- lta_models[["X4.Class.Non.Invariant.out"]][["summaries"]][["LLCorrectionFactor"]]
c0 <- lta_models[["X4.Class.Invariant.out"]][["summaries"]][["LLCorrectionFactor"]]
d1 <- lta_models[["X4.Class.Non.Invariant.out"]][["summaries"]][["ChiSqCategoricalLRT_DF"]]
d0 <- lta_models[["X4.Class.Invariant.out"]][["summaries"]][["ChiSqCategoricalLRT_DF"]]
df <- abs(d0-d1)

# Satorra-Bentler scaled Difference test equations
cd <- (((d0*c0)-(d1*c1))/(d0-d1))
t <- (((T0*c0)-(T1*c1))/(cd))

# Chi-square and degrees of freedom
t
df

# Significance test
p_diff <- pchisq(t, df, lower.tail=FALSE)

```

**RESULT:** The Satorra-Bentler scaled  $\chi^2$  difference test comparing the invariant and non-invariant LTA models was,  $T(19) = 20.58, p = 1.0$ .

---

Alternate, less verbose way to run LTA with the `createMixtures` function.

```

data <- lsay_data %>% select(5:14) # select only the indicator variables

createMixtures(
  classes = 4,
  filename_stem = "sci_attitude",
  model_overall = "c2 ON c1;",
  model_class_specific = c(
    "[ab39m$1] (a{C}); [ab39t$1] (b{C}); [ab39u$1] (c{C}); [ab39w$1] (d{C}); [ab39x$1] (e{C});",
    "[ga33a$1] (a{C}); [ga33h$1] (b{C}); [ga33i$1] (c{C}); [ga33k$1] (d{C}); [ga33l$1] (e{C});"),
  rdata = data,
  ANALYSIS = "PROCESSORS IS 10; STARTS = 500 100; PARAMETERIZATION = PROBABILITY;",
  VARIABLE = "CATEGORICAL = ab39m-ab39x ga33a-ga33l;")

runModels(filefilter = "sci_attitude")

results <- readModels(filefilter = "sci_attitude")

```

Read invariance model and extract parameters (intercepts and multinomial regression coefficients)

```

lta_inv1 <- readModels(here("LTA_models", "4-Class-Invariant.out" ), quiet = TRUE)

par <- as_tibble(lta_inv1[["parameters"]][["unstandardized"]]) %>%
  select(1:3) %>%
  filter(grepl('ON|Means', paramHeader)) %>%
  mutate(est = as.numeric(est))

```

Manual method to calculate transition probabilities. Although possible to extract transition probabilities directly from the output this exercise shows how the parameters are used to calculate each transition. This is useful for conducting advanced LTA model specifications such as making specific constraints to the transitions.

```
# Name each parameter individually to make the subsequent calculations more readable
a1 <- unlist(par[13,3]); a2 <- unlist(par[14,3]); a3 <- unlist(par[15,3]); b11 <- unlist(par[1,3]);
b21 <- unlist(par[4,3]); b31 <- unlist(par[7,3]); b12 <- unlist(par[2,3]); b22 <- unlist(par[5,3]);
b32 <- unlist(par[8,3]); b13 <- unlist(par[3,3]); b23 <- unlist(par[6,3]); b33 <- unlist(par[9,3])

# Calculate transition probabilities from the logit parameters
t11 <- exp(a1+b11)/(exp(a1+b11)+exp(a2+b21)+exp(a3+b31)+exp(0))
t12 <- exp(a2+b21)/(exp(a1+b11)+exp(a2+b21)+exp(a3+b31)+exp(0))
t13 <- exp(a3+b31)/(exp(a1+b11)+exp(a2+b21)+exp(a3+b31)+exp(0))
t14 <- 1 - (t11 + t12 + t13)

t21 <- exp(a1+b12)/(exp(a1+b12)+exp(a2+b22)+exp(a3+b32)+exp(0))
t22 <- exp(a2+b22)/(exp(a1+b12)+exp(a2+b22)+exp(a3+b32)+exp(0))
t23 <- exp(a3+b32)/(exp(a1+b12)+exp(a2+b22)+exp(a3+b32)+exp(0))
t24 <- 1 - (t21 + t22 + t23)

t31 <- exp(a1+b13)/(exp(a1+b13)+exp(a2+b23)+exp(a3+b33)+exp(0))
t32 <- exp(a2+b23)/(exp(a1+b13)+exp(a2+b23)+exp(a3+b33)+exp(0))
t33 <- exp(a3+b33)/(exp(a1+b13)+exp(a2+b23)+exp(a3+b33)+exp(0))
t34 <- 1 - (t31 + t32 + t33)

t41 <- exp(a1)/(exp(a1)+exp(a2)+exp(a3)+exp(0))
t42 <- exp(a2)/(exp(a1)+exp(a2)+exp(a3)+exp(0))
t43 <- exp(a3)/(exp(a1)+exp(a2)+exp(a3)+exp(0))
t44 <- 1 - (t41 + t42 + t43)
```

Create transition table

```
t_matrix <- tibble(
  "Time1" = c("C1=1", "C1=2", "C1=3", "C1=4"),
  "C2=1" = c(t11, t21, t31, t41),
  "C2=2" = c(t12, t22, t32, t42),
  "C2=3" = c(t13, t23, t33, t43),
  "C2=4" = c(t14, t24, t34, t44))

t_matrix %>%
  gt(rowname_col = "Time1") %>%
  tab_header(
    title = md("**Student transitions from 7th grade (rows) to 10th grade (columns)**"),
    subtitle = md("&nbsp;") %>%
  fmt_number(2:5, decimals = 2) %>%
  tab_spanner(label = "10th grade", columns = 2:5)
```

Student transitions from 7th grade (rows) to 10th grade (columns)

	10th grade			
	C2=1	C2=2	C2=3	C2=4
C1=1	0.27	0.27	0.32	0.15

C1=2	0.09	0.56	0.19	0.16
C1=3	0.15	0.21	0.52	0.12
C1=4	0.08	0.35	0.27	0.30

---

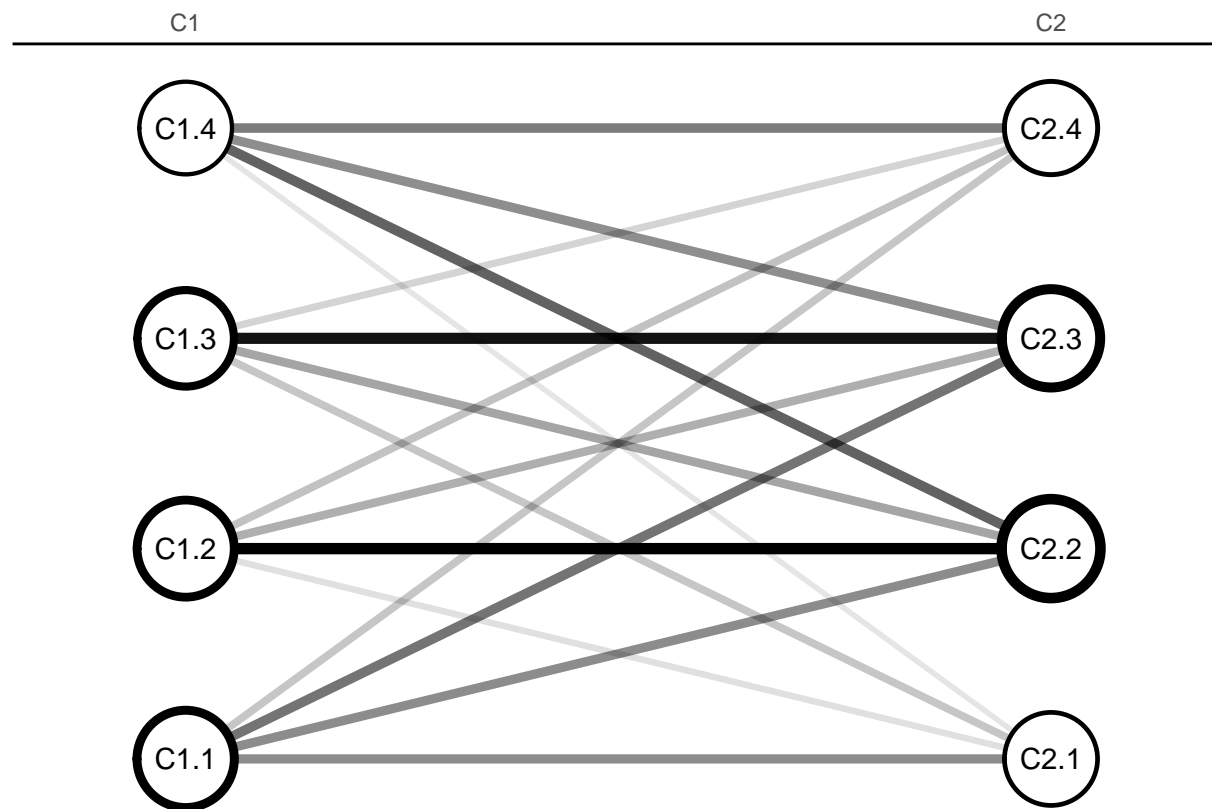
END COPY EDITING - ALL PLOTS CURRENTLY INCOMPLETE

---

Plot LTA transitions

---

```
MplusAutomation::plotLTA(lta_inv1)
```



## References: (INCOMPLETE)

Hallquist, Michael N., and Joshua F. Wiley. 2018. "MplusAutomation: An R Package for Facilitating Large-Scale Latent Variable Analyses in Mplus." *Structural Equation Modeling*, 1–18. <https://doi.org/10.1080/10705511.2017.1402334>.

Müller, Kirill. 2017. *Here: A Simpler Way to Find Your Files*. <https://CRAN.R-project.org/package=here>.

R Core Team. 2019. *R: A Language and Environment for Statistical Computing*. Vienna, Austria: R Foundation for Statistical Computing. <https://www.R-project.org/>.

Wickham, Hadley, Romain François, Lionel Henry, and Kirill Müller. 2020. *Dplyr: A Grammar of Data Manipulation*. <https://CRAN.R-project.org/package=dplyr>.

Wickham, Hadley, Jim Hester, and Winston Chang. 2020. *Devtools: Tools to Make Developing R Packages Easier*. <https://CRAN.R-project.org/package=devtools>.

Wickham, Hadley, Jim Hester, and Romain François. 2018. *Readr: Read Rectangular Text Data*. <https://CRAN.R-project.org/package=readr>.1

---