Appendix - Implement LCA Analyses with MplusAutomation

Motivation for MplusAutomation workflow:

This `R` tutorial is intended to provide a template for estimating latent class analysis (LCA), integrating the unconditional LCA with a larger SEM model, and producing publication ready figures 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` (Muthén & Muthén, 1998 - 2017) using the wrapping package `MplusAutomation` (Hallquist & Wiley, 2018). This method requires the user to have the proprietary software `Mplus` installed on their computer.

This approach also relies on the utility of `R-Projects`. This provides a structured framework for organizing all associated data files, Mplus input/output files, scripts, and figures. Given the large number of Mplus output files inherent to fitting mixture models, 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 ensures that the syntax for file-paths is uniform across operating systems (e.g., Windows or Mac) enabling reproducibility.

0.0 Preparation

Download the `R-Project` (NOTE: The coping example data is not currently available)

Link to Github repository here: Appendix - LCA-COPING-BD

For readers unfamiliar with Github and version controlled R-projects:

1. On the repository page, click the green `Code` button and in the menu choose option `Download ZIP`
2. Place the un-zipped downloaded folder on your desktop
3. Within this folder open the file with the blue cube icon that is file named `LCA-COPING-BD.Rproj`
4. Next open the file containing all analysis code named `rcode-lca-coping-bd.R`.

Project folder organization (nested folders are used to contain files within the project folder):

1. "data"; 2. "enum_mplus"; 3. "3step_mplus"; 4. "figures"

Note regarding project location: If the main project folder is located within too many nested folders it may result in a file-path error when estimating models with `MplusAutomation`.

To install package {rhdf5}

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

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

Load packages

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

Read in data. File-paths are set using R-Projects & the {here} package

```r
ies_data <- read_csv(here("data","ies_bd_data.csv"),
                     na=c("",".", "999"))
```

1.1 Enumeration:

Estimate K-class models with 1 through 6 classes.

Specification details that are specific to applied coping example:

- Within the `lapply()` function `1:6` indicates the number of K-class models to estimate.
- The measurement model item names for the coping strategy example are listed after the `categorical = ...;` & `usevar = ...;` statements.
- Note, that for Latent Profile Analysis (LPA) the `categorical = ...;` statement would be removed so that items are estimated as continuous variables.

```r
lca_k1_6  <- lapply(1:6, function(k) {
  lca_enum  <- mplusObject(

  TITLE = glue("Class-{k} LCA Enumeration - Youth Coping Strategies"),

  VARIABLE = glue(
    "categorical = do1 do2 do3 do5 do6; !!! Coping strategy items for measurement model !!!
     usevar = do1 do2 do3 do5 do6;

     classes = c({k});"),

  ANALYSIS =
    "estimator = mlr;
     type = mixture;
     processors=10;",

  PLOT =
    "type = plot3;
     series = do1 do2 do3 do5 do6(*);",

  OUTPUT = "sampstat tech11 tech14;",

  usevariables = colnames(ies_data),
  rdata = ies_data)

lca_enum_fit <- mplusModeler(lca_enum,
                  dataout=glue(here("enum_mplus", "c_lca_enum_bd.dat")),
                  modelout=glue(here("enum_mplus", "c{k}_lca_enum_bd.inp")) ,
                  check=TRUE, run = TRUE, hashfilename = FALSE)
})
```

1.2 Generate Model Fit Summary Table

- This syntax can be used to compare model fit from the series of LCA models generated during enumeration (*Table 4* in manuscript).
- The code produces a table that is approximately in APA format.

```
output_enum <- readModels(here("enum_mplus"), quiet = TRUE)

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

Calculate relevant fit indices for summary table

```r
allFit <- enum_extract %>%
  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)
```

Create table using {gt}

```r
allFit %>%
  mutate(Title = str_remove(Title, " LCA Enumeration - Youth Coping Strategies")) %>%
  gt() %>%
  tab_header(
    title = md("**Model Fit Summary Table**"), subtitle = md("&nbsp;")) %>%
  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* = 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 = 0) %>%
  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)))
```

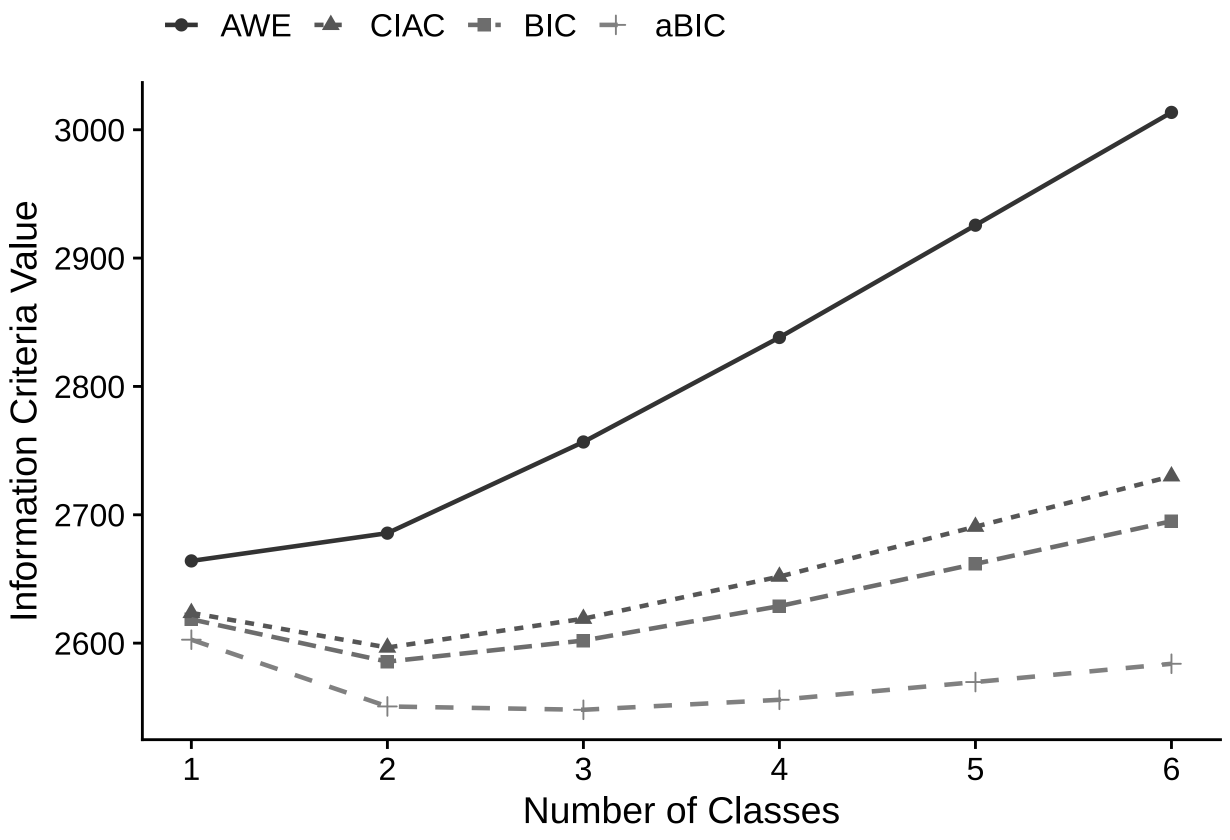
Model Fit Summary Table[1]

Classes	Par	*LL*	BIC	aBIC	CIAC	AWE	BLRT	VLMR	BF	*cmP_k*
Class-1	5	$-1,294$	$2,619$	$2,603$	$2,624$	$2,664$	–	–	>100	<.001
Class-2	11	$-1,259$	$2,586$	$2,551$	$2,597$	$2,686$	<.001	<.001	>100	1.00
Class-3	17	$-1,249$	$2,602$	$2,548$	$2,619$	$2,757$	<.001	0.12	>100	<.001
Class-4	23	$-1,244$	$2,629$	$2,556$	$2,652$	$2,838$	0.27	0.01	>100	<.001
Class-5	29	$-1,242$	$2,662$	$2,570$	$2,691$	$2,926$	0.67	0.46	>100	<.001
Class-6	35	$-1,241$	$2,695$	$2,584$	$2,730$	$3,014$	0.67	0.49	–	<.001

[1]Note. Par = parameters; LL = 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.

1.3 Plot Information Criteria

```r
allFit %>% select(2:7) %>%
  rowid_to_column() %>%
  pivot_longer(`BIC`:`AWE`,
    names_to = "Index",
    values_to = "ic_value") %>%
  mutate(Index = factor(Index,
    levels = c("AWE","CIAC","BIC","aBIC"))) %>%
  ggplot(aes(x = rowid, y = ic_value,
    color = Index, shape = Index,
    group = Index, lty = Index)) +
  geom_point(size = 2.0) + geom_line(size = .8) +
  scale_x_continuous(breaks = 1:6) +
  scale_colour_grey(end = .5) +
  theme_cowplot() +
  labs(x = "Number of Classes", y = "Information Criteria Value") +
  theme(legend.title = element_blank(),
        legend.position = "top")
```



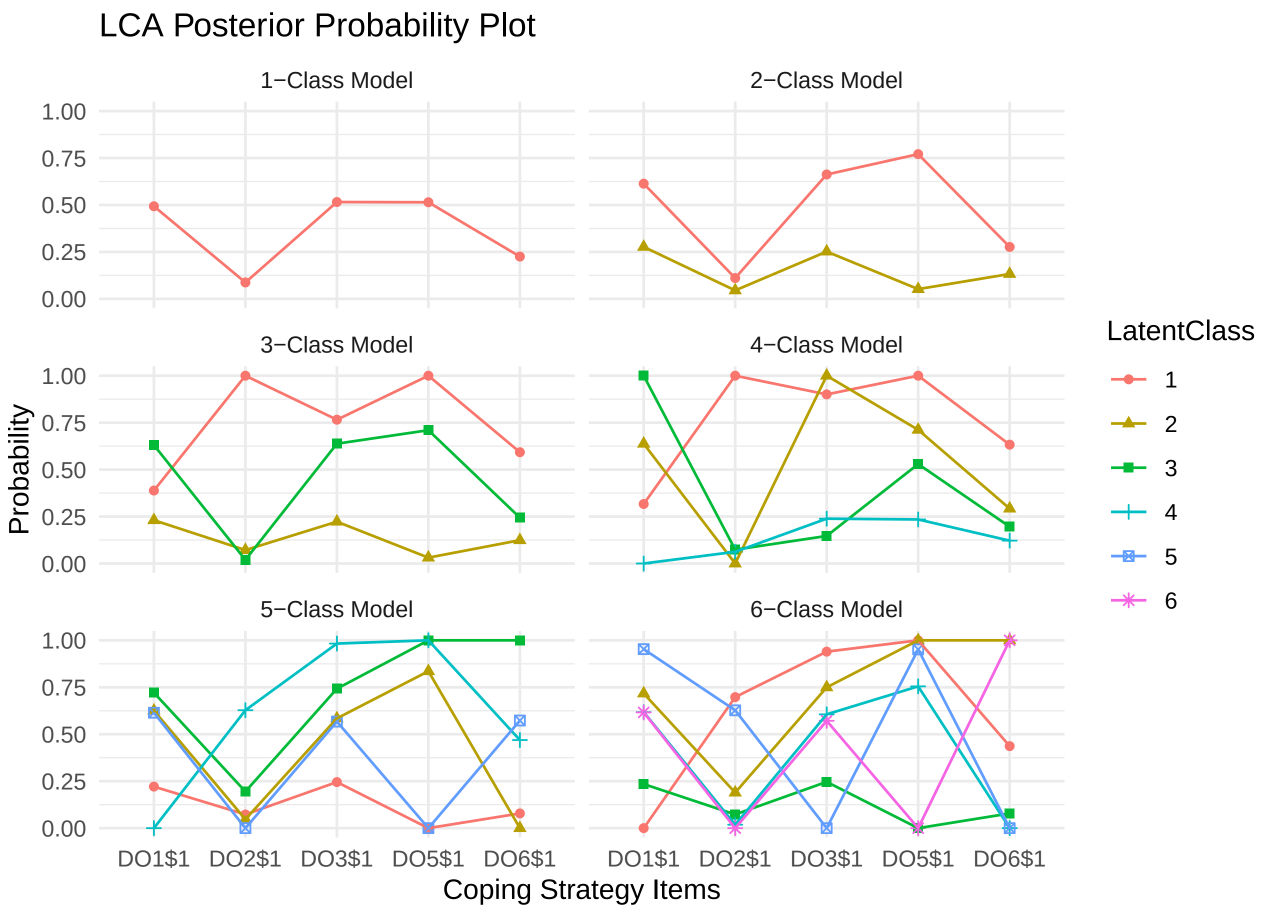
Save plot in the `figures` folder.

```
ggsave(here("figures", "Fig2_IC_plot.png"), dpi=300, height=5, width=7, units="in")
```

1.4 Compare Conditional Item Probability Plots

This syntax produces a plot containing a series of LCA probability plot facets. This can be used to compare solutions across K-class models.

```
model_results <- data.frame()

for (i in 1:length(output_enum)) {
  temp <- output_enum[[i]]$parameters$unstandardized
  temp <- data.frame(unclass(temp)) %>%
    mutate(model = paste0(i, "-Class Model"))
  model_results <- rbind(model_results, temp)
}

model_results <- model_results %>%
  filter(paramHeader == "Thresholds") %>%
  select(est, model, LatentClass, param) %>%
  mutate(prob = (1 / (1 + exp(est))))

ggplot(model_results,
       aes(x = param, y = prob,
           color = LatentClass,
           shape = LatentClass,
           group = LatentClass)) +
  geom_point() + geom_line() +
  facet_wrap(~ model, ncol = 2) +
  labs(title = "LCA Posterior Probability Plot",
       x= "Coping Strategy Items", y = "Probability") +
  theme_minimal()
```



```
ggsave(here("figures","FigA1_compare_kclass_LCAs.png"), dpi=300, height=4, width=6, units="in")
```

1.5 Plot Final Model - Conditional Item Probability Plot

This code generates the figure as presented in the manuscript for the final unconditional LCA model.

This syntax creates a function called `plot_lca_function` that requires 7 arguments (inputs):

- `model_name`: name of Mplus model object (e.g., `model_step1`)
- `item_num`: the number of items in LCA measurement model (e.g., `5`)
- `class_num`: the number of classes (k) in LCA model (e.g., `3`)
- `item_labels`: the item labels for x-axis (e.g., `c("Enjoy","Useful","Logical","Job","Adult")`)
- `class_labels`: the class label names (e.g., `c("Adaptive Coping","Externalizing Behavior","No Coping")`)
- `class_legend_order` = change the order that class names are listed in the plot legend (e.g., `c(2,1,3)`)
- `plot_title`: include the title of the plot here (e.g., `"LCA Posterior Probability Plot"`)

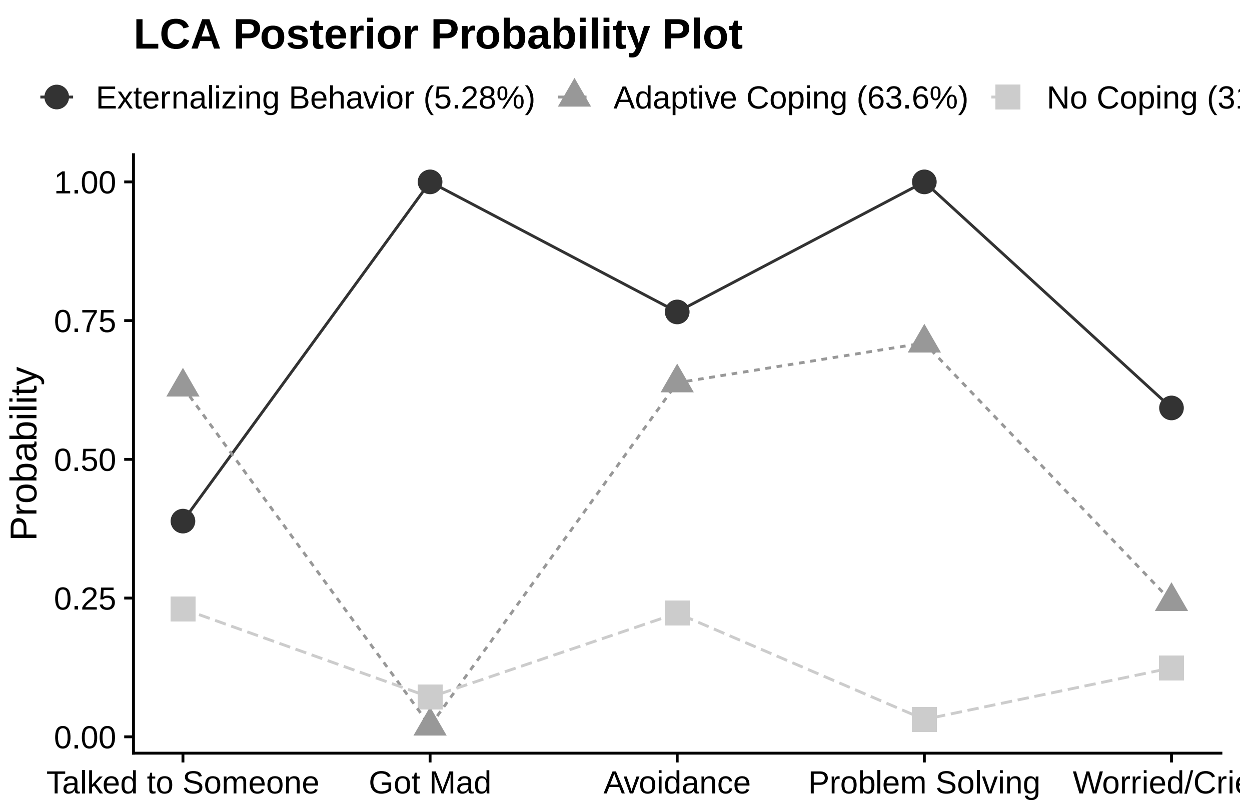
Read in plot data from Mplus output file `Step1_3step_BD.out`

```r
model_step1 <- readModels(here("3step_mplus", "Step1_3step_BD.out"), quiet = TRUE)
```

```r
plot_lca_function <- function(model_name,item_num,class_num,item_labels,
                              class_labels,class_legend_order,plot_title){

mplus_model <- as.data.frame(model_name$gh5$means_and_variances_data$estimated_probs$values)
plot_data <- mplus_model[seq(2, 2*item_num, 2),]

c_size <- as.data.frame(model_name$class_counts$modelEstimated$proportion)
colnames(c_size) <- paste0("cs")
c_size <- c_size %>% mutate(cs = round(cs*100, 2))
colnames(plot_data) <- paste0(class_labels, glue(" ({c_size[1:class_num,]}%)"))
plot_data <- plot_data %>% relocate(class_legend_order)

plot_data <- cbind(Var = paste0("U", 1:item_num), plot_data)
plot_data$Var <- factor(plot_data$Var,
               labels = item_labels)
plot_data$Var <- fct_inorder(plot_data$Var)

pd_long_data <- melt(plot_data, id.vars = "Var")

# This syntax uses the date-frame created above to produce the plot with `ggplot()`

p <- pd_long_data %>%
  ggplot(aes(x = as.integer(Var), y = value,
  shape = variable, colour = variable, lty = variable)) +
  geom_point(size = 4) + geom_line() +
  scale_x_continuous("", breaks = 1:5, labels = plot_data$Var) +
  scale_colour_grey() +
  labs(title = plot_title, y = "Probability") +
  theme_cowplot() +
  theme(legend.title = element_blank(),
        legend.position = "top")

p
return(p)
}
```

Run the `plot_lca_function` by specifying each input (*Figure 1*)

```r
plot_lca_function(
  model_name = model_step1,
  item_num = 5,
  class_num = 3,
  item_labels = c("Talked to Someone","Got Mad", "Avoidance","Problem Solving", "Worried/Cried"),
  class_labels = c("Adaptive Coping","Externalizing Behavior","No Coping"),
  class_legend_order = c(2,1,3),
  plot_title = "LCA Posterior Probability Plot"
  )
```



```r
ggsave(here("figures", "Fig1_LCA_3-Class.png"), dpi=300, height=5, width=7, units="in")
```

1.6 Manual "3-Step" ML Auxiliary Variable Integration Method

Step 1 - Estimate the unconditional model with all covariate & distal outcome variables mentioned in the auxiliary statement.

```
m_step1  <- mplusObject(
  TITLE = "Step1_3step_automation Behavioral Disorder",
  VARIABLE =
   "categorical = do1 do2 do3 do5 do6;

    usevar = do1 do2 do3 do5 do6;

    classes = c(3);

    !!! NOTE: All auxiliary variables to be considered in the final model should be listed here !!!
    auxiliary =
    FEMALE ETHN_CMP SOC_STRS
    BOTHR_U negmood1 posmood1;",

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

  SAVEDATA =
   "!!! NOTE: This saved dataset will contain class probabilities and modal assignment columns !!!
    File=3step_BD_savedata_012020.dat;
    Save=cprob;
    Missflag= 999;",

  MODEL = "",
  OUTPUT = "",

  PLOT =
    "type = plot3;
    series = do1 do2 do3 do5 do6(*);",

  usevariables = colnames(ies_data),
  rdata = ies_data)

m_step1_fit <- mplusModeler(m_step1,
                 dataout=here("3step_mplus", "Step1_3step_BD.dat"),
                 modelout=here("3step_mplus", "Step1_3step_BD.inp") ,
                 check=TRUE, run = TRUE, hashfilename = FALSE)
```

Step 2 - Extract logits & saved data from the step 1 unconditional model.

Extract logits for the classification probabilities for the most likely latent class

```
logit_cprobs <- as.data.frame(m_step1_fit[["results"]]
                                         [["class_counts"]]
                                         [["logitProbs.mostLikely"]])
```

Extract saved data from the step 1 model `mplusObject` named "m_step1_fit"

```
savedata <- as.data.frame(m_step1_fit[["results"]]
                                     [["savedata"]])
```

Rename the column in `savedata` for "C" and change to "N"

```
colnames(savedata)[colnames(savedata)=="C"] <- "N"
```

Step 3 (part 1) - Estimate the unconditional model with logits from step 2.

This model is estimated to check that the class proportions are approximately the same as in step 1.

```
m_step2  <- mplusObject(
  TITLE = "Step2_3step_automation Behavioral Disorder",

  VARIABLE =
 "nominal=N;
  USEVAR = n;
  missing are all (999);
  classes = c(3); ",

  ANALYSIS =
 "estimator = mlr;
  type = mixture;
  starts = 0;",

  MODEL =
    glue(
 "%C#1%
  [n#1@{logit_cprobs[1,1]}];
  [n#2@{logit_cprobs[1,2]}];

  %C#2%
  [n#1@{logit_cprobs[2,1]}];
  [n#2@{logit_cprobs[2,2]}];

  %C#3%
  [n#1@{logit_cprobs[3,1]}];
  [n#2@{logit_cprobs[3,2]}];"),

  OUTPUT = "!tech11  tech14 res;",
  PLOT =
 "!type = plot3;
  !series = do1 do2 do3 do5 do6(*);",

  usevariables = colnames(savedata),
  rdata = savedata)

m_step2_fit <- mplusModeler(m_step2,
                dataout=here("3step_mplus", "Step2_3step_BD.dat"),
                modelout=here("3step_mplus", "Step2_3step_BD.inp"),
                check=TRUE, run = TRUE, hashfilename = FALSE)
```

Step 3 (part 2) - Add covariates & distal outcomes to the model.

1.7 Moderation - Estimate the final SEM Model

Specification details:

- This example contains two distal outcomes (`POSMOOD1` & `NEGMOOD1`) and one binary covariate (`SOC_STRS`).
- Under each class-specific statement (e.g., `%C#1%`) the distal outcomes are mentioned to estimate the intercept parameters.
- Moderation is specified by mentioning the `"outcome ON covariate;"` syntax under each of the class-specific statements.
- Note that the binary covariate is centered so that reported distal means (intercepts) are estimated at the weighted average of Social Stress.

```
m_step3  <- mplusObject(
  TITLE = "Step3_3step_automation Behavioral Disorder",

  VARIABLE =
 "nominal = N;
  usevar = n;
  missing are all (999);

  usevar = SOC_STRS POSMOOD1 NEGMOOD1;
  classes = c(3); ",

  DEFINE =
 "Center SOC_STRS (Grandmean);",

  ANALYSIS =
 "estimator = mlr;
  type = mixture;
  starts = 0;",

  MODEL =
  glue(
 "!DISTAL = POSMOOD1 NEGMOOD1
  !MODERATOR = SOC_STRS

  %OVERALL%
  POSMOOD1 on SOC_STRS;
  POSMOOD1;

  NEGMOOD1 on SOC_STRS;
  NEGMOOD1;

  %C#1%
  [n#1@{logit_cprobs[1,1]}];
  [n#2@{logit_cprobs[1,2]}];

  [NEGMOOD1](m01);
  NEGMOOD1;                        !!! estimate conditional intercept !!!
  NEGMOOD1 on SOC_STRS (s01);     !!! estimate conditional regression !!!

  [POSMOOD1] (m1);
  POSMOOD1;
  POSMOOD1 on SOC_STRS (s1);

  %C#2%
  [n#1@{logit_cprobs[2,1]}];
  [n#2@{logit_cprobs[2,2]}];

  [NEGMOOD1](m02);
  NEGMOOD1;
  NEGMOOD1 on SOC_STRS (s02);

  [POSMOOD1] (m2);
  POSMOOD1;
  POSMOOD1 on SOC_STRS (s2);

  %C#3%
  [n#1@{logit_cprobs[3,1]}];
  [n#2@{logit_cprobs[3,2]}];

  [NEGMOOD1](m03);
  NEGMOOD1;
  NEGMOOD1 on SOC_STRS (s03);

  [POSMOOD1] (m3);
  POSMOOD1;
  POSMOOD1 on SOC_STRS (s3);"),

  MODELCONSTRAINT =
 "New (diff12 diff13
  diff23 slope12 slope13
  slope23 ndiff12 ndiff13
  ndiff23 nslope12 nslope13
  nslope23);
```

```
  diff12 = m1-m2;   ndiff12 = m01-m02;
  diff13 = m1-m3;   ndiff13 = m01-m03;
  diff23 = m2-m3;   ndiff23 = m02-m03;
  slope12 = s1-s2;  nslope12 = s01-s02;
  slope13 = s1-s3;  nslope13 = s01-s03;
  slope23 = s2-s3;  nslope23 = s02-s03;",

  MODELTEST =
  ## NOTE: Only a single Wald test can be conducted per model run. Therefore,
  ## this example requires running separate models for each omnibus test (e.g.,
  ## 4 models; 2 outcomes and 2 slope coefficients). This can be done by
  ## commenting out all but one test and then making multiple input/output files.

 "m1=m2;       !!! Distal outcome omnibus Wald test for `POSMOOD1` !!!
  m2=m3;

  !s1=s2;      !!! Slope difference omnibus Wald test `POSMOOD1 on SOC_STRS` !!!
  !s2=s3;

  !m01=m02;    !!! Distal outcome omnibus Wald test for `NEGMOOD1` !!!
  !m02=m03;

  !s01=s02;   !!! Slope difference omnibus Wald test for `POSMOOD1 on SOC_STRS` !!!
  !s02=s03;",

  usevariables = colnames(savedata),
  rdata = savedata)

m_step3_fit <- mplusModeler(m_step3,
                 dataout=here("3step_mplus", "Step3_3step_BD.dat"),
                 modelout=here("3step_mplus", "Step3_3step_BD.inp"),
                 check=TRUE, run = TRUE, hashfilename = FALSE)
```

End of 3-step procedure

Estimate step 3 model with covariate un-centered for simple-slopes plots. This puts the intercepts fixed at the first level of the covariate (`SOC_STRS`). These values are needed to produce the simple slope plots.

Note: Here the `update()` function is used to take the previous model and remove the Mplus syntax within the `DEFINE` statement that was used to center the covariate `Social Stress`. Next, the updated model input syntax is used to estimate a new model. To learn more about the `update` function see the `MplusAutomation` tutorial article (https://www.tandfonline.com/doi/pdf/10.1080/10705511.2017.1402334).

```
m_uncen <- update(m_step3,
  DEFINE = ~" ") # This update removes the centering syntax from the model object `m_step3`

m_uncen_fit <- mplusModeler(m_uncen,
   dataout=here("3step_mplus", "Step3_3step_BD.dat"),
   modelout=here("3step_mplus", "Step3_uncentered_BD.inp"),
   check=TRUE, run = TRUE, hashfilename = FALSE)UCSB_Navy_mark.png
```

1.8 Distal Outcome Plot

Note: The distal outcome means are estimated with the binary covariate (`SOC_STRS`) at the weighted average. This is specified by centering social stress as shown in the `Step-3` model syntax.

This syntax reads in the `Step3` model & extract model parameter estimates.

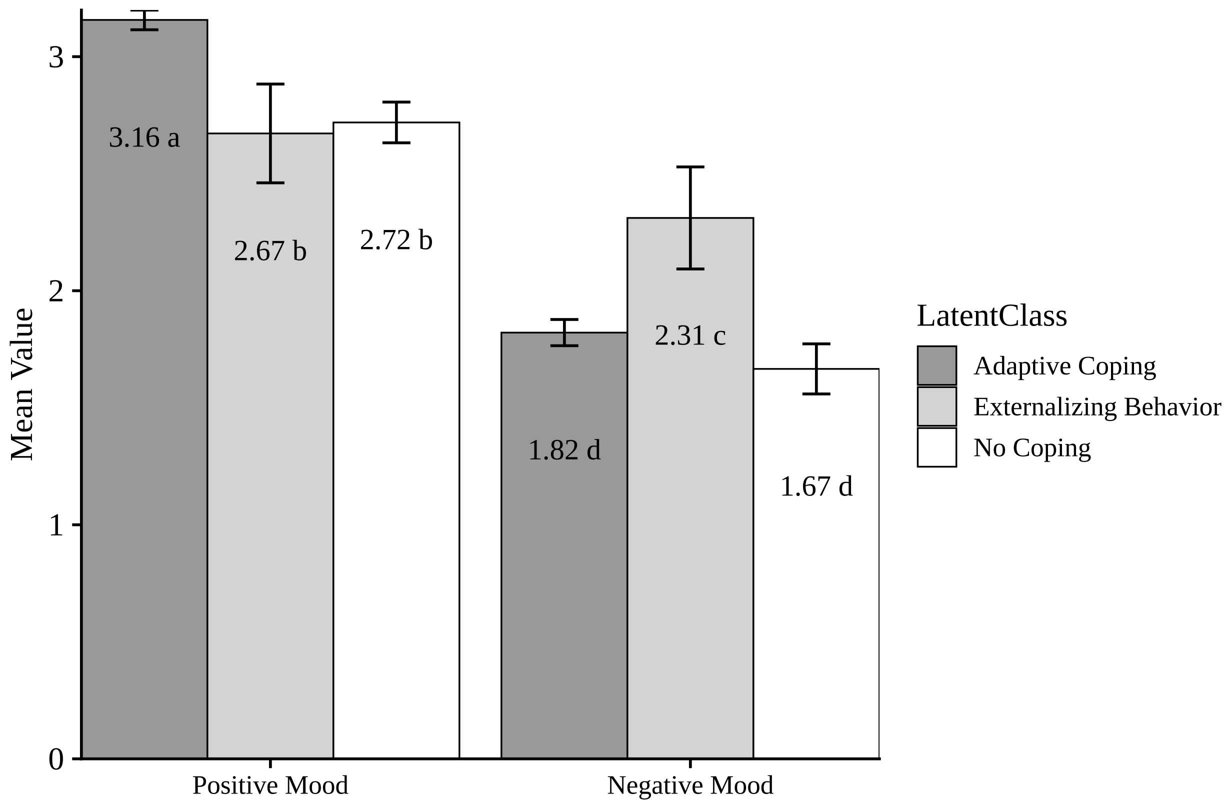
```
model_step3 <- readModels(here("3step_mplus", "Step3_3step_BD.out"), quiet = TRUE)

model_step3 <- data.frame(model_step3$parameters$unstandardized)
```

This syntax is used to create the `data-frame` that produces the distal outcome bar plot.

```
distal_data <- model_step3 %>%
  filter(paramHeader == "Intercepts") %>%
  mutate(param = case_when(
      param == "POSMOOD1" ~ "Positive Mood",
      param == "NEGMOOD1" ~ "Negative Mood")) %>%
  mutate(LatentClass = factor(LatentClass,
      labels = c("Adaptive Coping", "Externalizing Behavior","No Coping"))) %>%
  mutate(value_labels = c("3.16 a", "1.82 d", "2.67 b", "2.31 c", "2.72 b", "1.67 d"))
```

Plot distal outcomes grouped by class (*Figure 3*)

```
ggplot(distal_data,
       aes(fill=LatentClass, y=est, x=fct_rev(param))) +
  geom_bar(position="dodge", stat="identity", color="black", size=.3) +
  geom_errorbar( aes(ymin=est-se, ymax=est+se),
                 width=.2, position=position_dodge(.9)) +
  geom_text(aes(y = est -.5, label = value_labels),
            family="Times New Roman", size=4,
            position=position_dodge(.9)) +
  scale_fill_grey(start = 0.6, end = 1.0) +
  theme_cowplot() +
  xlab("") + ylab("Mean Value") +
  theme(text=element_text(family="Times New Roman", size=12),
        axis.text.x=element_text(size=10)) +
        coord_cartesian(expand = FALSE)
```



```
ggsave(here("figures","Fig3_distal_barplot.png"), dpi=300, height=4, width=6, units="in")
```

1.9 Simple Slope Plots

Note: The un-centered distal intercepts represent the conditional means when the binary covariate is at its first level `SOC_STRS = 0` (i.e., no social stress). Therefore, the conditional mean for `SOC_STRS = 1` (i.e., social stress) can be calculated by adding the associated slope coefficient to the intercept.

Read in the un-centered model & extract relevant parameters

```
model_uncen <- readModels(here("3step_mplus", "Step3_uncentered_BD.out"), quiet = TRUE)

model_uncen <- data.frame(model_uncen$parameters$unstandardized)

slope_data <- model_uncen %>%
  filter(str_detect(paramHeader, 'ON|Inter')) %>%
  unite("param", paramHeader:param, remove = TRUE) %>%
  mutate(param = str_replace(param, "MOOD1.ON_SOC_STRS", "_COEF")) %>%
  mutate(param = str_remove_all(param, "Intercepts_|MOOD1")) %>%
  mutate(LatentClass = factor(LatentClass,
    labels = c("Adaptive Coping (63.6%)", "Externalizing Behavior (5.3%)","No Coping (31.1%)")))
```

Positive mood simple slope graph

Prepare `data-frame` for plotting

```r
pos_data <- slope_data %>%
  filter(str_detect(param, 'POS'))

pos_wide <- pos_data %>%
  select(param,est, LatentClass) %>%
  pivot_wider(names_from = param, values_from = est) %>%
  rename("No.Social.Stress" = 'POS') %>%
  mutate(Social.Stress = No.Social.Stress + POS_COEF) %>% # calc. condit. means `SOC_STRS = 1`
  select(-POS_COEF)

plot_pos <- melt(pos_wide, id.vars = "LatentClass") %>%
  mutate(variable = factor(variable,
                      levels = c("No.Social.Stress","Social.Stress"),
                      labels = c("No Social Stress","Social Stress")))
```

Plot positive mood simple slope graph

```r
p_plot <- ggplot(plot_pos,
            aes(y=value, x=variable,
                color=LatentClass,
                group=LatentClass,
                shape=LatentClass,
                lty=LatentClass)) +
  geom_point(size = 4) + geom_line() +
  xlab("") + ylab("Positive Mood")  + ylim(2.5,3.5)+
  scale_colour_grey() +
  theme_classic() +
  theme(text=element_text(family="Times New Roman", size=12),
        axis.text.x=element_text(size=12),
        legend.text = element_text(family="Times New Roman", size=10),
        legend.position = "top", legend.title = element_blank()) +
      annotate(geom = "text",
           x = 1.8, y = 2.77,
           label = "N.S.", color = "black") +
      annotate(geom = "text",
           x = 1.8, y = 2.60,
           label = "N.S.", color = "black")
```

Negative mood simple slope graph

Prepare data-frame for plotting

```r
neg_data <- slope_data %>%
  filter(str_detect(param, 'NEG'))

neg_wide <- neg_data %>%
  select(param,est, LatentClass) %>%
  pivot_wider(names_from = param, values_from = est) %>%
  rename("No.Social.Stress" = 'NEG') %>%
  mutate(Social.Stress = No.Social.Stress + NEG_COEF) %>%   # calculate means for `SOC_STRS = 1`
  select(-NEG_COEF)

plot_neg <- melt(neg_wide, id.vars = "LatentClass") %>%
  mutate(variable = factor(variable,
                      levels = c("No.Social.Stress","Social.Stress"),
                      labels = c("No Social Stress","Social Stress")))
```

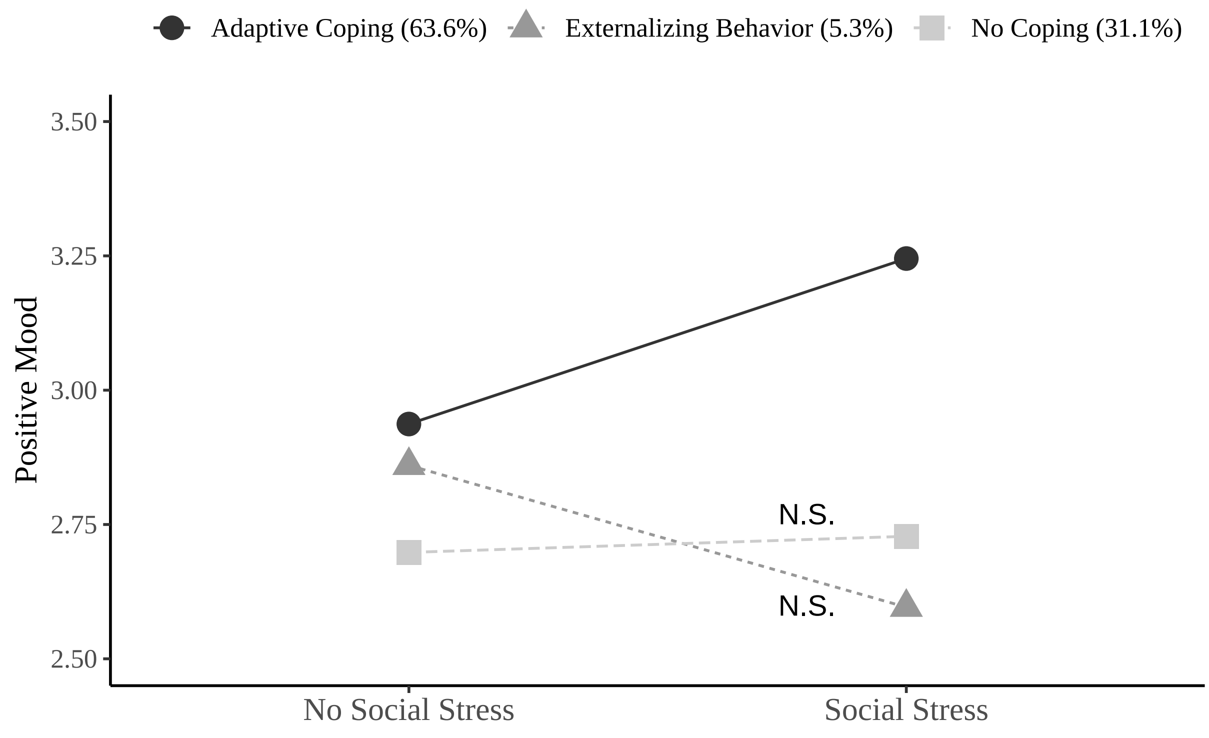
Plot negative mood simple slope graph

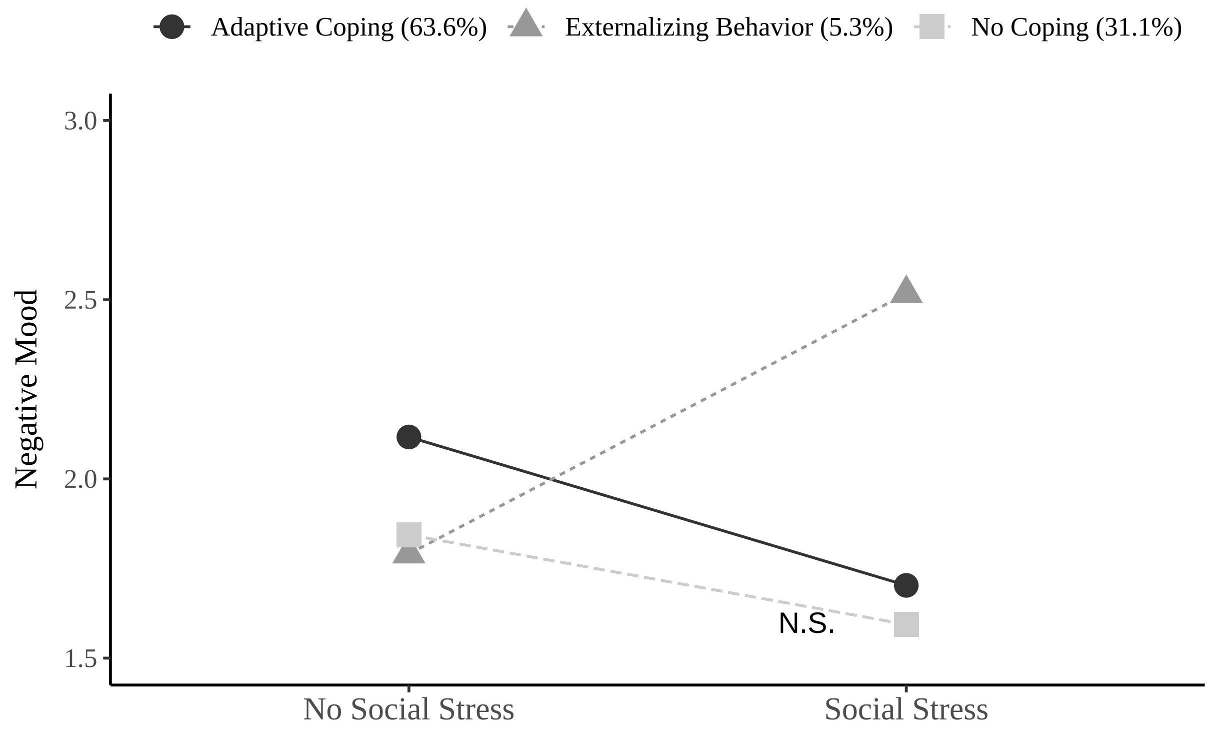
```r
n_plot <- ggplot(plot_neg,
            aes(y=value, x=variable,
            color=LatentClass,
            group=LatentClass,
            shape=LatentClass,
            lty=LatentClass)) +
  geom_point(size=4) + geom_line() +
  xlab("") + ylab("Negative Mood") + ylim(1.5,3)+
  scale_colour_grey() + theme_classic() +
  theme(text=element_text(family="Times New Roman", color = "black", size=12),
        axis.text.x=element_text(size=12),
        legend.text = element_text(family="Times New Roman", size=10),
        legend.position = "top", legend.title = element_blank()) +
    annotate(geom = "text",
      x = 1.8, y = 1.6,
      label = "N.S.", color = "black")
```

Combine the two simple slopes graphs for distal outcomes positive & negative mood (*Figure 5*)

Note: This code combines 2 ggplot objects using the {patchwork} package.

```r
p_plot / n_plot
```

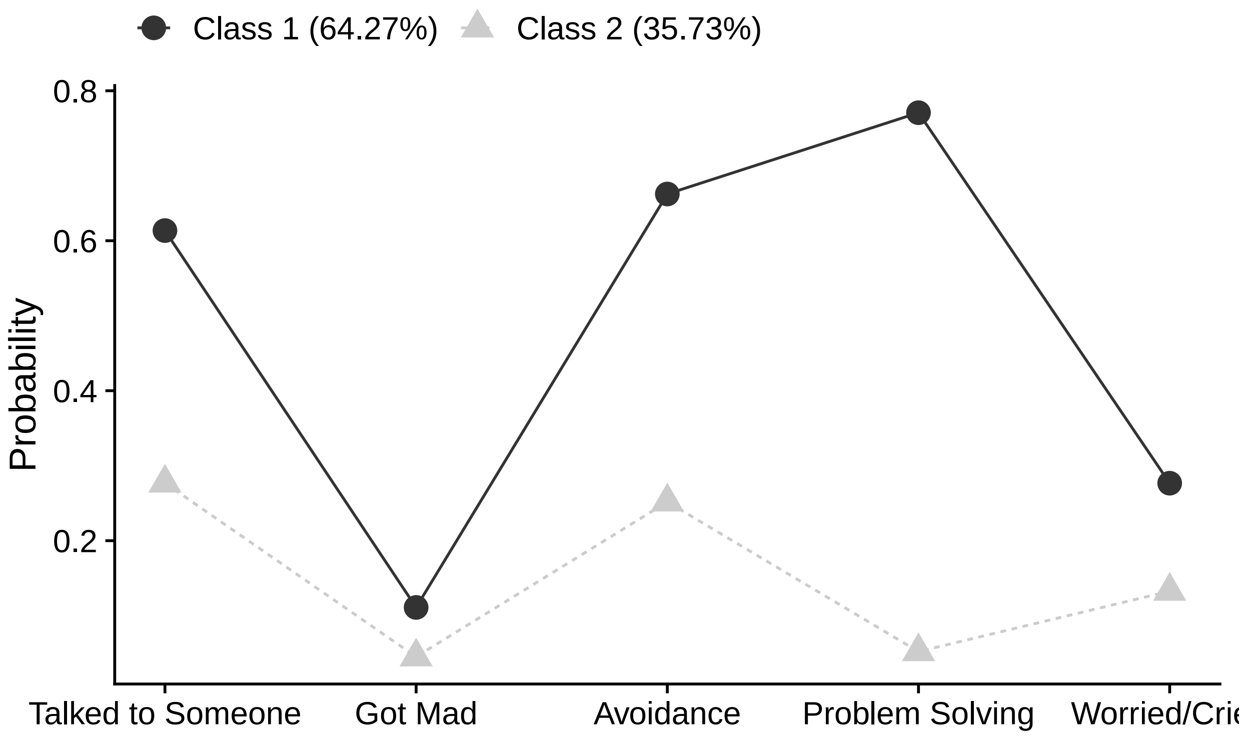




```r
ggsave(here("figures", "Fig5_simple_slopes.png"), dpi=300, height=8.5, width=6.5, units="in")
```

2.0 Plot of the 2-Class Conditional Item Plot for Comparison

```
plot_lca_function(
  model_name = output_enum[[2]],
  item_num = 5,
  class_num = 2,
  item_labels = c("Talked to Someone","Got Mad", "Avoidance","Problem Solving", "Worried/Cried"),
  class_labels = c("Class 1","Class 2"),
  class_legend_order = c(1,2),
  plot_title = ""
  )
```



2.1 Response Pattern Table

To replicate the response pattern table produced in this study (*Table 3*) see the associated `R/MplusAutomation` code example here:

LCA-Response-Ratterns

Additional examples using `R/MplusAutomation` for a range of analyses can be found here:

References:

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Miller, Jon D. Longitudinal Study of American Youth (LSAY), Seventh Grade Data, 1987-1988; 2015-2016. Ann Arbor, MI: Inter-university Consortium for Political and Social Research [distributor], 2019-04-23. https://doi.org/10.3886/ICPSR37287.v1

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

Muthen L.K., & Muthen B.O. (1998-2017) Mplus User’s Guide. Eight Edition. Los Angelos, CA: Muthen & Muthen.

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Wickham H, et al. (2019). “Welcome to the tidyverse.” Journal of Open Source Software, 4(43), 1686. doi: 10.21105/joss.01686.