

Table S1.

Modeling Phases Diagram

Modeling Phase	Analysis tasks	How it shows up in a manuscript
0: Model design	<ul style="list-style-type: none"> • Articulate research questions (RQs) • Identify items for the measurement model • Identify auxiliary variables to use • Investigate sample size parameter ratio considerations • Decide how variables are going to be coded and modeled (i.e., continuous, dichotomous, multi-categorical). • Visualize model with a path diagram for conceptual understanding 	<p>Introduction:</p> <ul style="list-style-type: none"> • In the framing and potentially at the end of the Introduction, mention and justify the use of latent class analysis and how it addresses RQs (Sinha et al., 2020) • Briefly integrate a rationale for looking at auxiliary variables (both covariates and distal outcome; McCutcheon, 2002) <p>Method:</p> <ul style="list-style-type: none"> • Include justification for selection of items (Nylund-Gibson & Choi, 2018) • Describes auxiliary variables (i.e., covariates and distal outcomes) and rationale for including them • Optionally include a path diagram of final model in methods section or supplementary materials (Online resource (Draw.io)) <p>Limitations:</p> <ul style="list-style-type: none"> • Discussion of tradeoffs around item selection, model complexity, and sample size (Wurpts & Geiser, 2014) • Acknowledge limitation of using sum-scores or any coarse recoding that was done to simplify complexity of model. (Snijders & Bosker 2011 (Ch. 3))
1: Pre-processing & exploration of data	<ul style="list-style-type: none"> • Clean data using best practices for reproducibility (Zurr et al., 2010; Tabachnick & Fidell, 2001) • Explore missing data patterns • Look at descriptive information of variables (i.e., distributions, frequency counts) • Re-code variables (if needed) • Explore response patterns (utility varies by research context; See Response Pattern Tutorial) 	<p>Method:</p> <ul style="list-style-type: none"> • Describe software used, any data recoding/cleaning done, describing prevalence of missing data and how it was handled. • Include a data analysis plan, including how you will evaluate model fit • If including auxiliary variables include rationale for choice of method for integration. (Asparouhov & Muthen, 2014) <p>Results:</p> <ul style="list-style-type: none"> • Create table of descriptive statistics to describe the variables. <p>Limitations:</p> <ul style="list-style-type: none"> • Acknowledge missing data and/or measurement challenges. Also, whether modeling assumptions are realistic or reasonable. (Enders, 2010)
2: Un-conditional model specification	<ul style="list-style-type: none"> • Estimate models with varying number of classes (See Appendix 1.1) • Study information criteria plot to compare model fit (See Appendix 1.3) • Tabulate fit information • Compare conditional item probability plots for contender models (See Appendix 1.4) 	<p>Method:</p> <ul style="list-style-type: none"> • Describe the analytic plan including software and analysis strategy details (Nylund et al., 2007) • Generate Table 2 of model fit indices (See Appendix 1.2) • Describe the pattern of model fit endorsement based on the model fit indices and other considerations

3: Enumeration decision	<ul style="list-style-type: none"> • Study pattern of fit indices model endorsements. Compare conditional item probability plots for each K-class model. • Consult substantive theory in light of emergent classes. • Study classification precision (AvgPP, Entropy, etc.) • Select a subset of candidate models • Re-consult theory • Select final model • Create the conditional item probability plot for final model. 	<p>Results:</p> <ul style="list-style-type: none"> • Figure 1. Conditional item probability plot of the final model (See Appendix 1.5) • In text, describe each emergent class, to clearly translate response pattern shape. • Create a latent class name to label each class. Include relative and absolute class size (e.g., class 1 is 10%; $N=22$). (Masyn, 2013) • Report Entropy and other classification information for selected model (e.g., AvePP, etc.; optionally include in the Appendix; Masyn, 2019) <p>Discussion:</p> <ul style="list-style-type: none"> • Summary of the emergent classes and their labels <p>Limitations:</p> <ul style="list-style-type: none"> • Specific considerations made when deciding on classes (e.g., no clear model, really small class, etc.) (Oberski, 2015) • Mention limitation of solution as needing validation. Not the only model, but the model selected in this context.
4a: Include auxiliary variables	<ul style="list-style-type: none"> • Decide auxiliary variable integration method McLarnon & O'Neill, 2018; Nylund-Gibson et al., 2014 • Follow integration method specification steps based on appropriate method See Appendix 1.6 (ML 3-step) • Specify the moderation model See Appendix 1.7 • Generate figures to communicate results clearly See Appendix 1.8 – 1.9 • When relevant, explore covariate-indicator DIFF Masyn, 2017 	<p>Method:</p> <ul style="list-style-type: none"> • Justify auxiliary variable integration method chosen. <p>Results:</p> <ul style="list-style-type: none"> • Describe covariate/moderation results (e.g., present in a table or figure; Nylund-Gibson et al., 2019) • Create distal outcome comparisons plot. <i>Figure 3</i> in manuscript • Scaffold the results section to talk about covariate relations with the latent class variables. Then distal outcome relations. If relevant, distal and covariate direct relations. <p>Discussion:</p> <ul style="list-style-type: none"> • Summarize patterns of results relating to covariates and distal outcomes.
4b: Moderation	<ul style="list-style-type: none"> • Specify regressions with latent class variable as moderator Muthen et al., 2017; McLarnon & O'Neill, 2018 	<p>Method:</p> <ul style="list-style-type: none"> • In the measures section, hypothesize which variable is given the status of moderator within the interaction term based on theory <p>Results:</p> <ul style="list-style-type: none"> • Include write up of moderation findings in manner accessible to readers with varying familiarity with LCA. (Cooper & Lanza, 2014) • Present moderation results (Table 5 & Figure 5): Create simple slopes plot to ease interpretation. (O'Neill et al., 2016; See Appendix 1.8)

Response Patterns

To gain a deeper understanding of LCA, it is meaningful to look at the patterns of responses and their frequency. The top section of Table S3 presents the most frequent observed patterns for the entire sample. The coping pattern that had the highest frequency ($f = 73$), was a pattern where students reported not using any coping strategies (i.e., 0, 0, 0, 0, 0). The next most frequent pattern ($f = 57$) was one where youth used coping strategies 1, 3, and 4 (i.e., pattern of 1, 0, 1, 1, 0). The next three sections of Table S3 allow us to see the most frequent patterns conditioned by class, after an LCA model is estimated. For example, for students whose most likely class membership is the *Externalizing Behavior* class ($k = 2$) the most frequent pattern ($f = 7$) is the response pattern where students reported using coping strategies 2, 3, and 4 (i.e., 0, 1, 1, 1, 0). This table provides a higher resolution of the within class composition than what is depicted in a typical LCA item probability plot.

Table S2.

Response patterns, estimated frequencies ($f > 15$), estimated posterior class probabilities and modal assignments.

	f	Talked to someone	Got Mad	Avoid- ance	Problem Solving	Worried/ Cried	$P_{k=1}$	$P_{k=2}$	$P_{k=3}$	k
<i>Unconditional response patterns ordered by highest frequency, >15</i>										
	73	0	0	0	0	0	.111	.000	.889	3
	57	1	0	1	1	0	.997	.000	.003	1
	39	1	0	0	1	0	.982	.000	.018	1
	38	0	0	1	1	0	.983	.000	.017	1
	33	0	0	1	0	0	.434	.000	.566	3
	32	1	0	0	0	0	.415	.000	.585	3
	25	1	0	1	0	0	.814	.000	.186	1
	22	0	0	0	1	0	.434	.000	.566	3
	22	1	0	1	1	1	.999	.000	.001	1
<i>Conditional response patterns, ordered by modal assignment and pattern frequency</i>										
$k = 1$	57	1	0	1	1	0	.997	.000	.003	1
	39	1	0	0	1	0	.982	.000	.018	1
	38	0	0	1	1	0	.983	.000	.017	1
	22	1	0	1	1	1	.999	.000	.001	1
	7	1	0	0	1	1	.992	.000	.008	1
$k = 2$	7	0	1	1	1	0	.134	.860	.009	2
	7	0	1	1	1	1	.033	.970	.001	2
	5	1	1	1	1	1	.085	.910	.000	2
	2	1	1	0	1	1	.146	.850	.005	2
	1	0	1	0	1	1	.060	.930	.011	2
$k = 3$	73	0	0	0	0	0	.111	.000	.889	3
	7	0	1	1	0	0	.166	.000	.834	3
	5	0	1	0	0	0	.031	.000	.969	3
	2	1	1	0	0	0	.156	.000	.844	3
	1	0	1	0	0	1	.069	.000	.931	3

Note. f = response pattern frequency; P_k = posterior class probabilities.

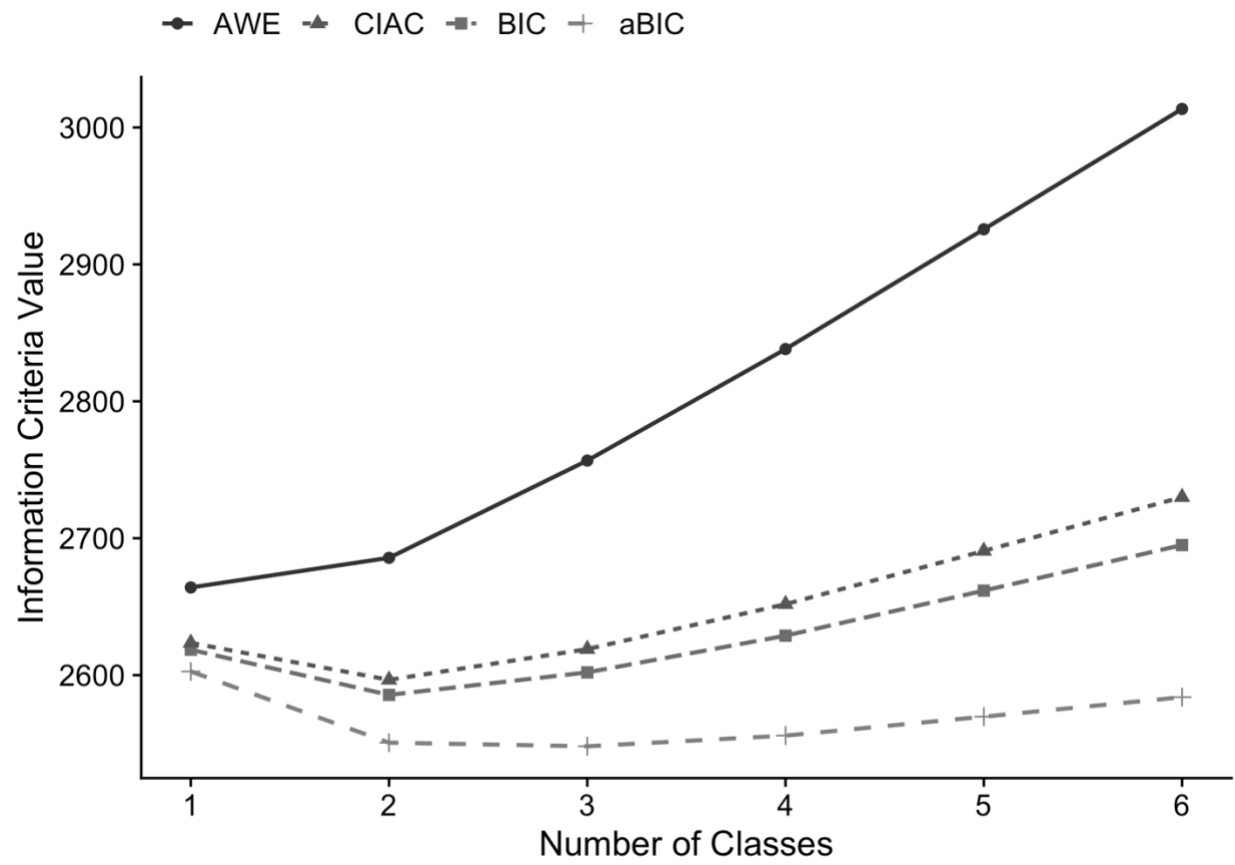


Figure S1. Plot of information criteria values for the unconditional LCA models.

Table S2.

Distal Means and Conditional Means, Moderated by Social Stress.

Outcome Variable	Predictor		
	Mean	Not Social Stress	Social Stress
Positive Mood			
<i>Adaptive Coping</i>	3.16	2.94	3.25
<i>Externalizing Behavior</i>	2.67	2.86	2.60
<i>No Coping</i>	2.72	2.70	2.73
Negative Mood			
<i>Adaptive Coping</i>	1.82	2.12	1.70
<i>Externalizing Behavior</i>	2.31	1.79	2.52
<i>No Coping</i>	1.67	1.84	1.59

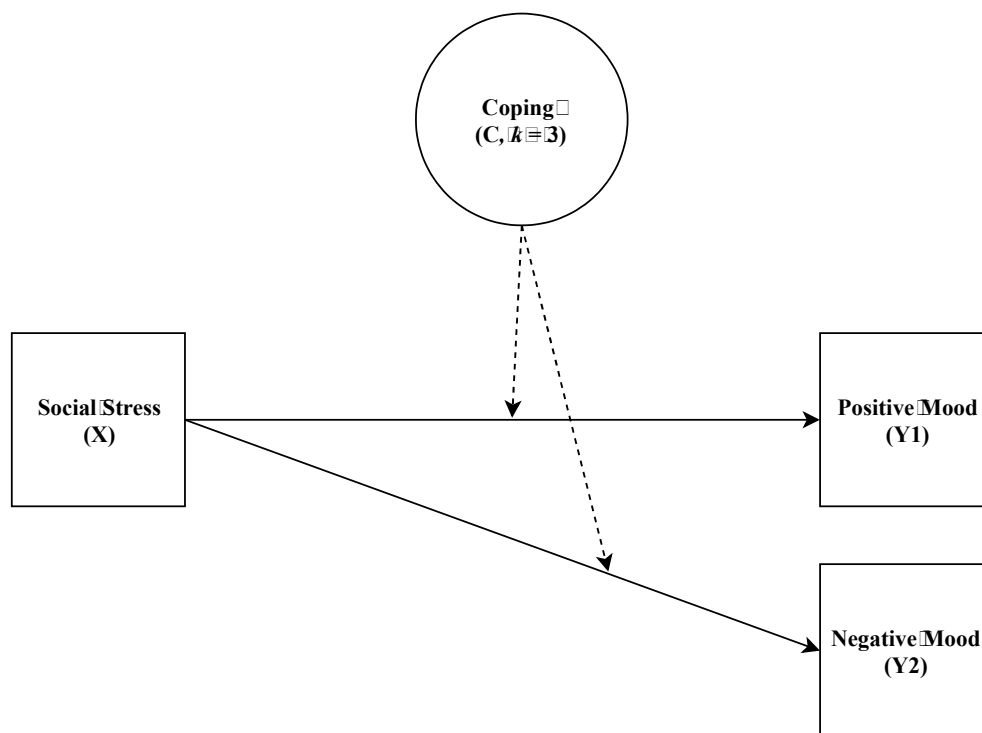


Figure S3. Path Diagram of SEMM Model: The relationship between Social Stress and the outcomes Negative Mood and Positive Mood are moderated by the latent class coping variable.

Coping Behavior Example - Accompanying R Code

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.

Preparation

Download the R-Project

Link to Github repository here: [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.

Note: If preferred users may follow analyses using the Rmarkdown script (.Rmd).

Project folder organization

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

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}

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

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

Load packages

```
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

```
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.


```

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

```
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)

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)))
```

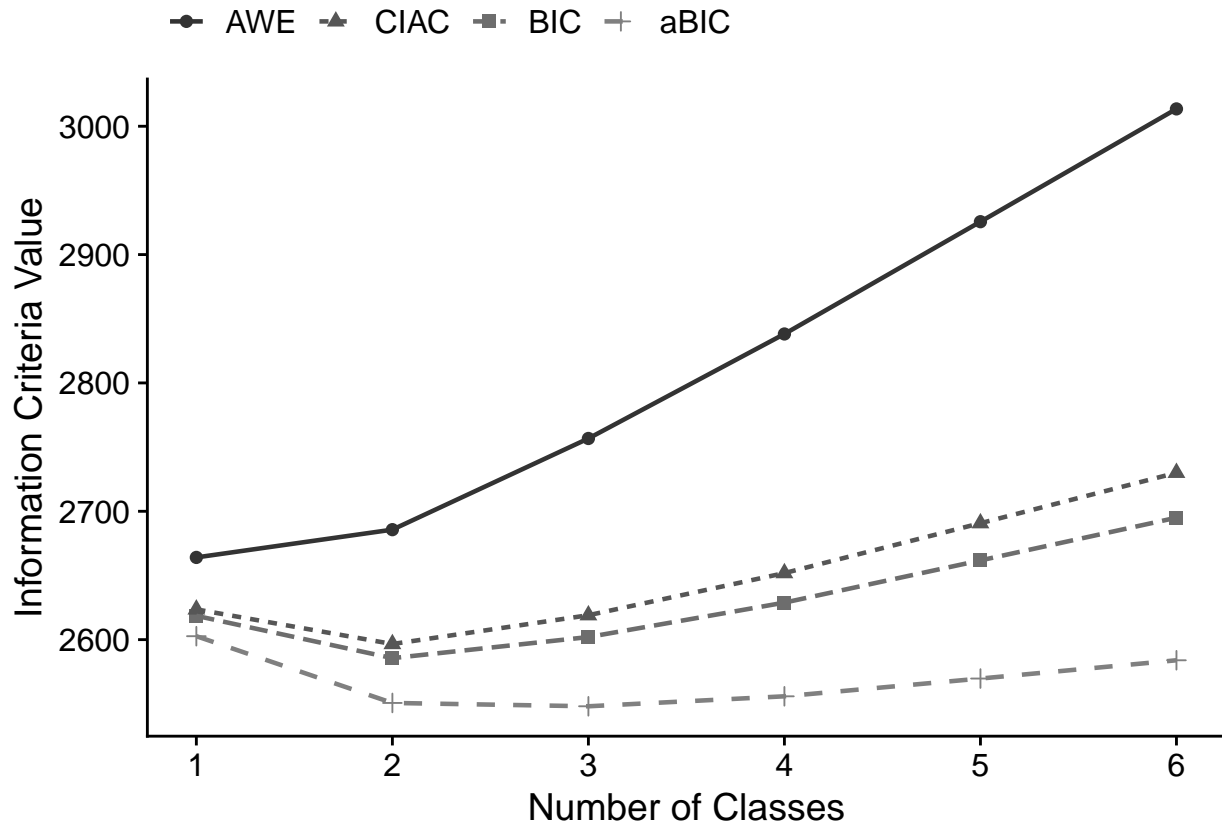
Model Fit Summary Table¹

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

¹Note. 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

```
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)
}

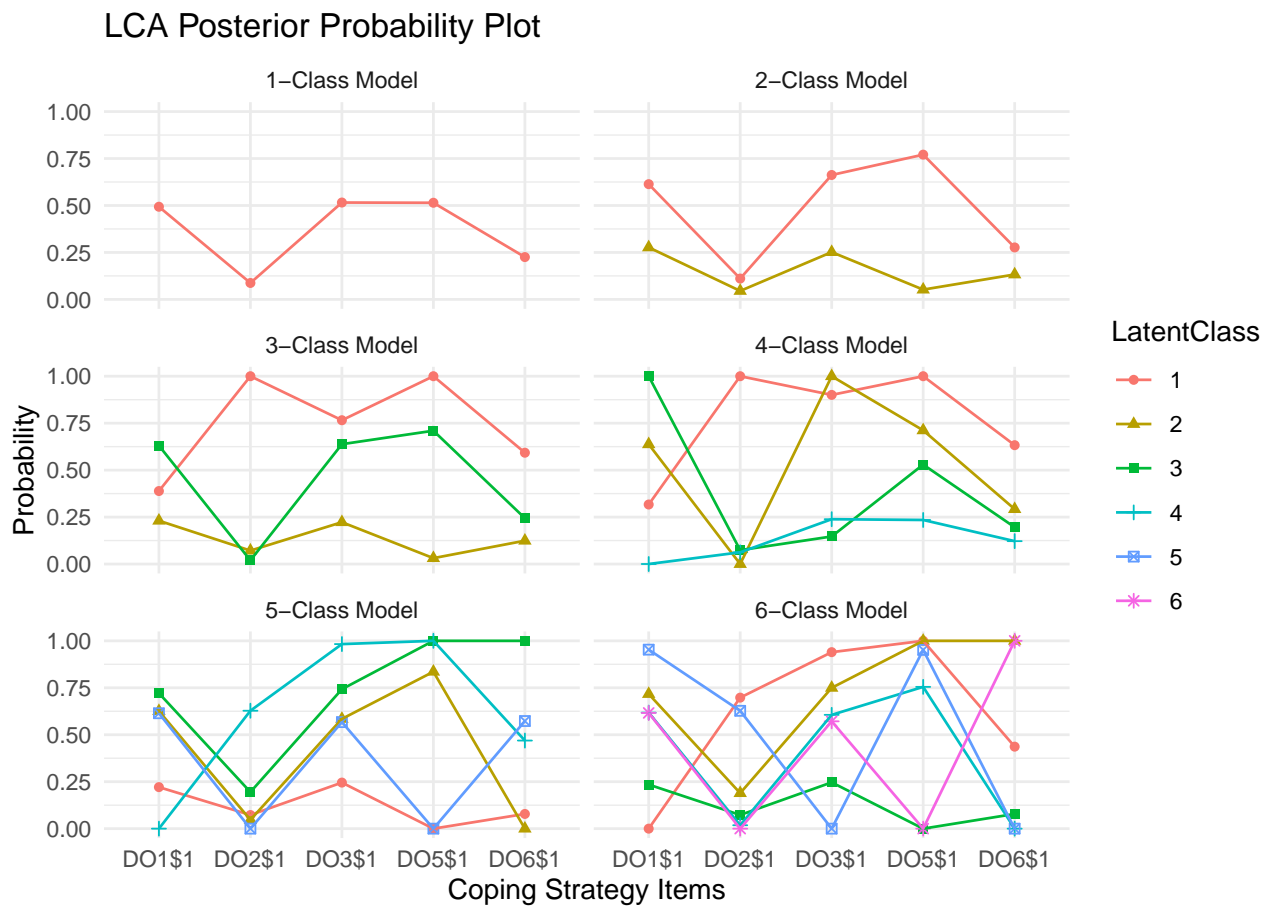
model_results <- model_results %>%
```

```

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`

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

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")

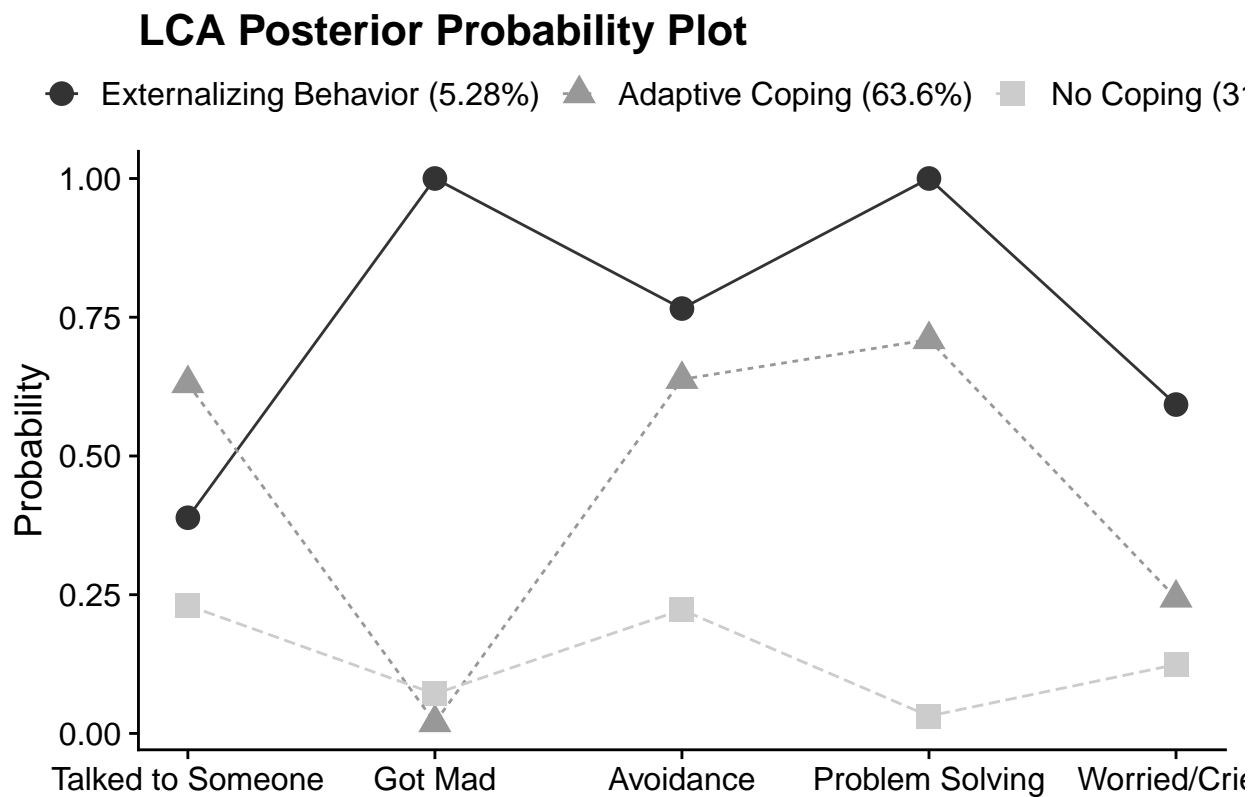
  # This syntax uses the data-frame created above to produce the plot with `ggplot()`

  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*)

```
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"  
)
```



```
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;
NEGMOOD1 on SOC_STRS (s01);    !!! estimate conditional intercept !!!
                                !!! 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)

```

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)

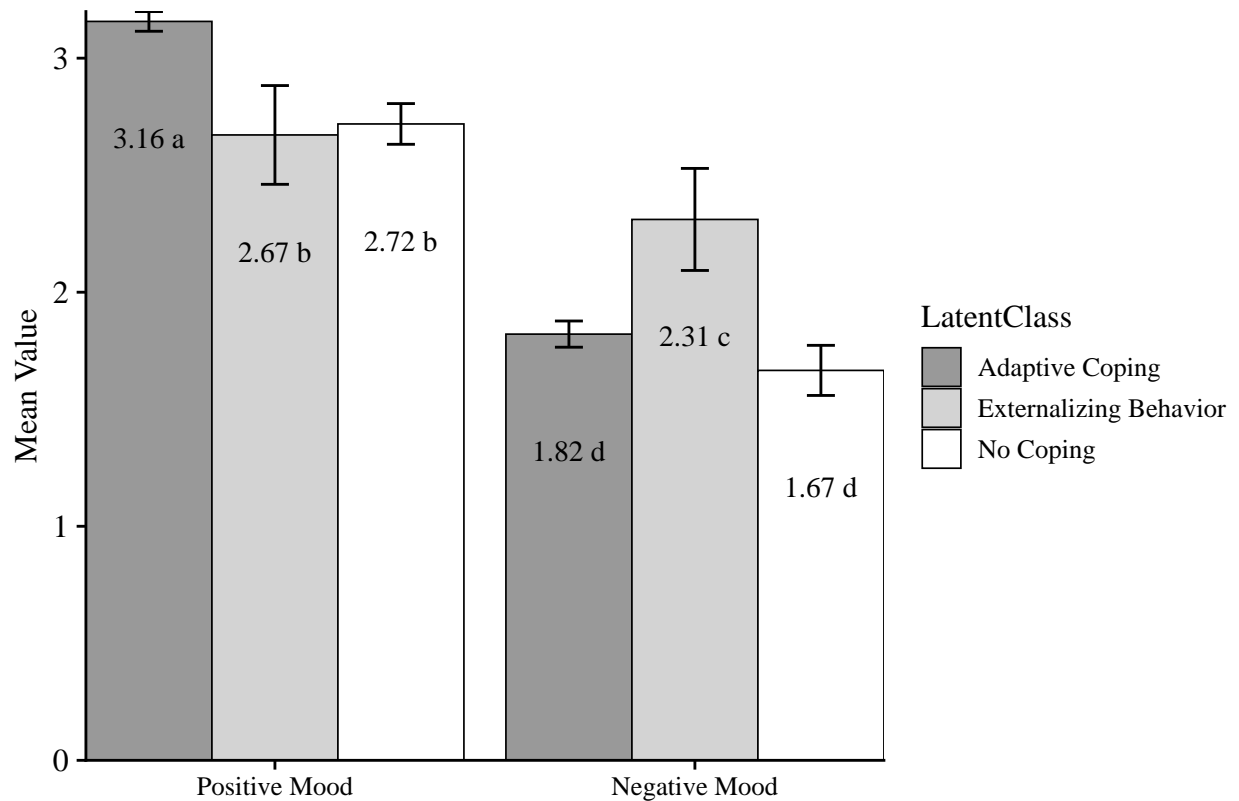
model_step3 <- data.frame(model_step3$parameters$unstandardized)
```

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

```
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

```
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

```
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")))
```

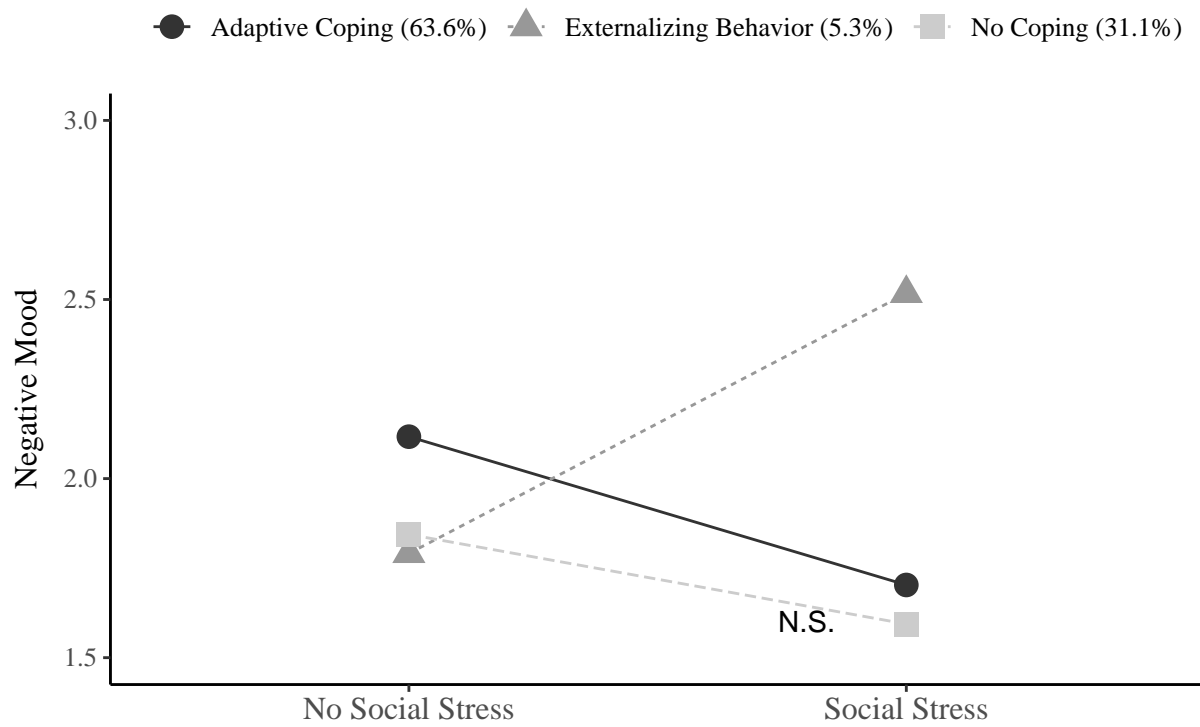
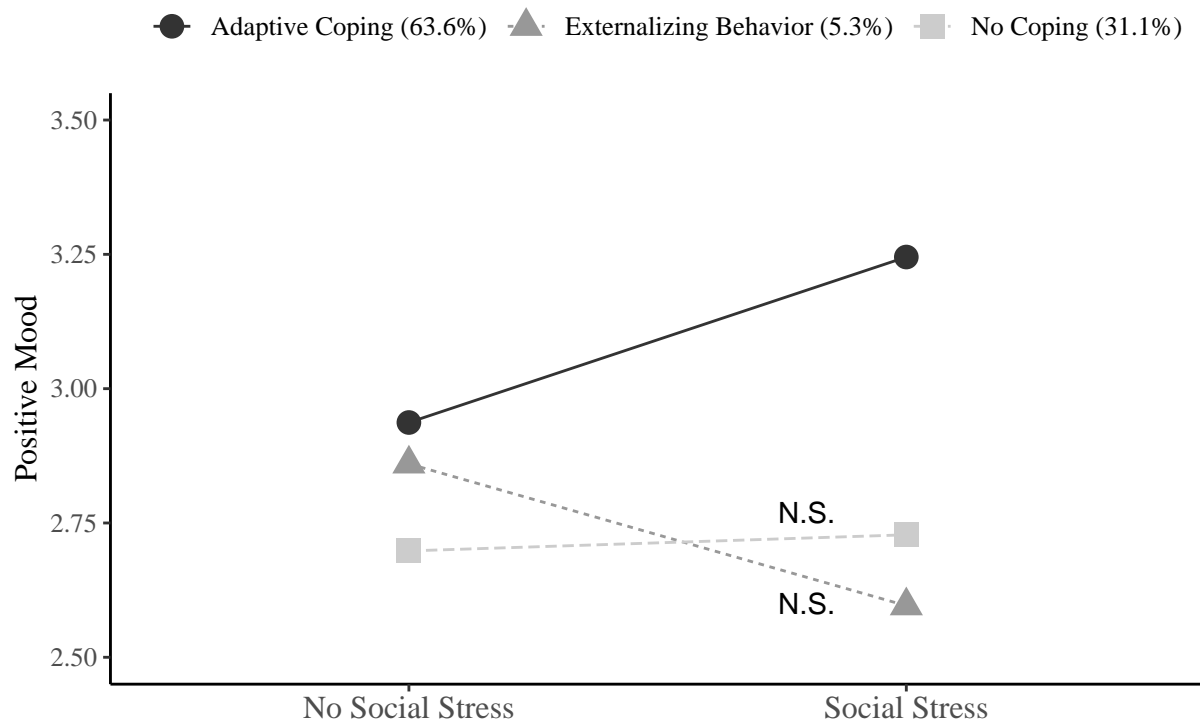
Plot negative mood simple slope graph

```
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.

p_plot / n_plot



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

2.0 Repsonse Pattern Table

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

Lab10.1-Response-Patterns

Additional `R/MplusAutomation` Examples

Tidy-Workflow-with-MplusAutomation

References:

- 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>.
- 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>.
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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.