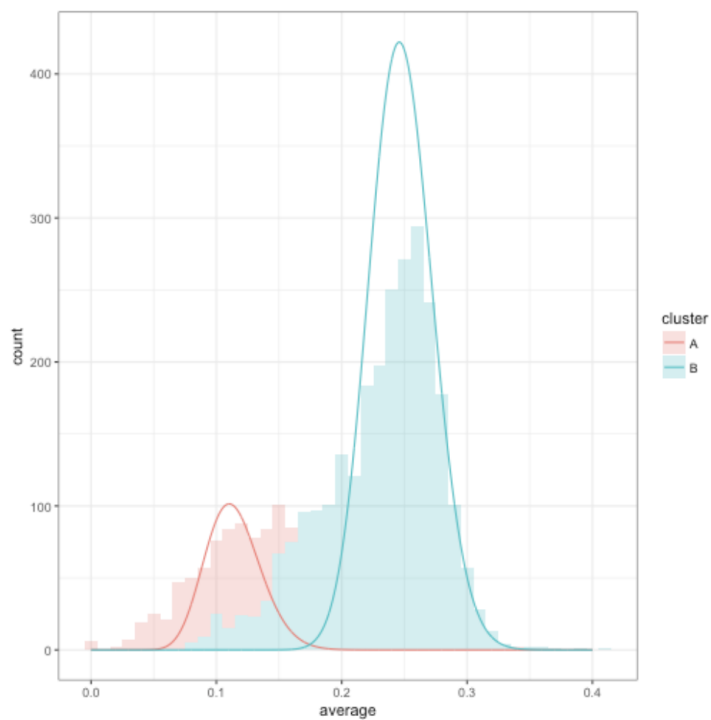


# Introduction to Latent Profile Analysis

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*Figure.* Gaussian mixture models. Data simulated from a 2-class model.

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## Lab preparation

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### Data source:

1. The first example closely follows the vignette used to demonstrate the `tidyLPA` package (Rosenberg, 2019): [See detailed documentation of this model here](#)

This model utilizes the PISA data collected in the U.S. in 2015. To learn more about this data [see here](#).

To access the 2015 US PISA data in R use the following code: `devtools::install_github("jrosen48/pisaUSA15")`  
`library(pisaUSA15)` `open_codebook()`

2. The second examples utilizes 4 test score measures from the public-use dataset, *The Longitudinal Survey of American Youth* (**LSAY**): [See documentation here](#)

---

Load packages

```
library(naniar)
library(tidyverse)
library(haven)
library(glue)
library(MplusAutomation)
library(here)
library(janitor)
library(gt)
library(tidyLPA)
```

Load data

```
pisa <- pisaUSA15
```

---

## Latent Profile Analysis

---

$$\begin{bmatrix} \sigma_1^2 & \sigma_{21} & \sigma_{31} & \sigma_{41} \\ \sigma_{12} & \sigma_2^2 & \sigma_{23} & \sigma_{24} \\ \sigma_{13} & \sigma_{12} & \sigma_3^2 & \sigma_{33} \\ \sigma_{14} & \sigma_{12} & \sigma_{12} & \sigma_4^2 \end{bmatrix}$$

*Figure.* Picture adapted from tutorial (Rosenberg, 2019).

- **model 1** Class-invariant / Diagonal: Equal variances, and covariances fixed to 0
- **model 2** Class-varying / Diagonal: Free variances and covariances fixed to 0

- `model 3` Class-invariant / Non-Diagonal: Equal variances and equal covariances
- `model 4` Free variances, and equal covariances
- `model 5` Equal variances, and free covariances
- `model 6` Class Varying / Non-Diagonal: Free variances and free covariances

---

Example 1: PISA dataset from the `tidyLPA` package

---

Enumerate using `estimate_profiles()`:

- Estimate models with classes  $K = 1 : 3$
- Model has 4 continuous indicators
- Default variance-covariance specifications (model 1)
- Add line `scale() %>%` to center indicator means

```
lpa_models <- pisa[1:500,] %>%
  select(broad_interest, enjoyment, instrumental_mot, self_efficacy) %>%
  estimate_profiles(1:3,
    package = "MplusAutomation",
    ANALYSIS = "starts = 100, 20;",
    variances = c("equal", "varying"),
    covariances = c("zero", "varying"))

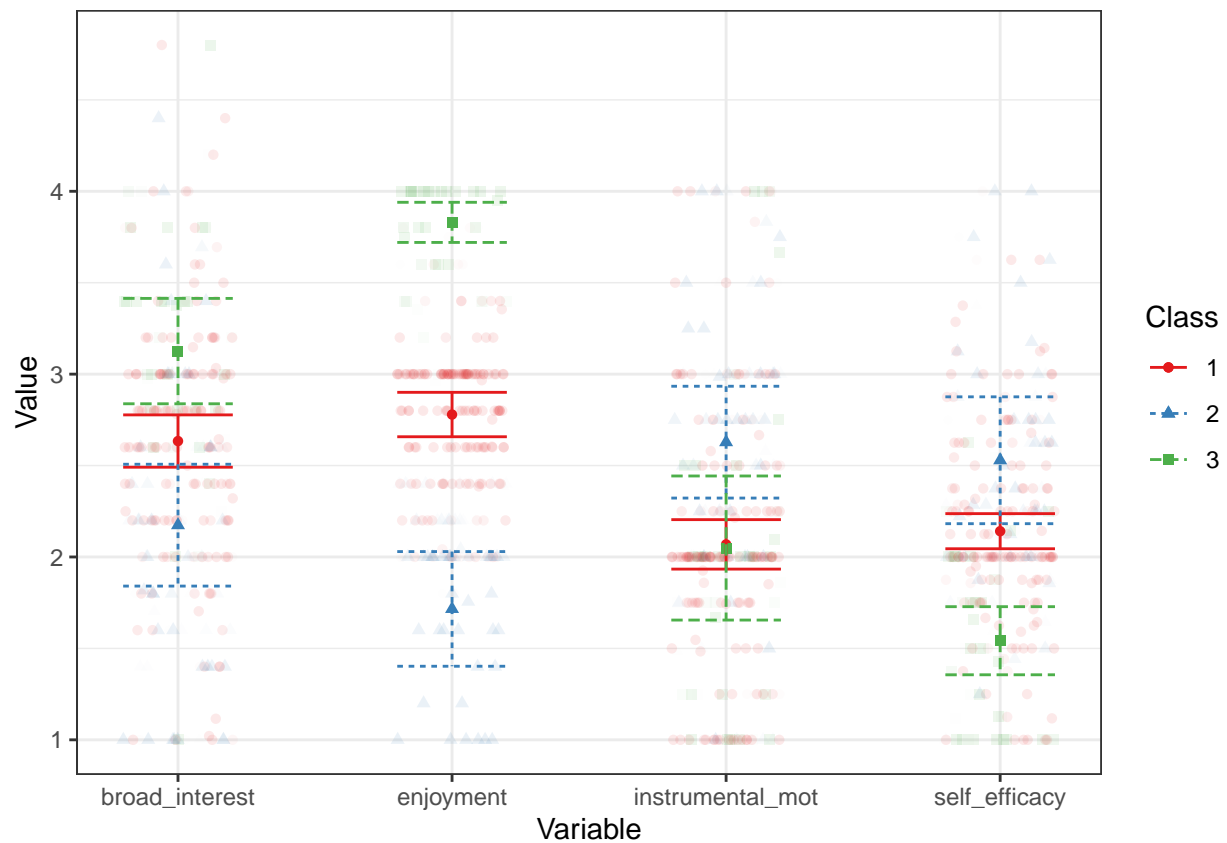
get_fit(lpa_models)
```

---

Plot 3-class model

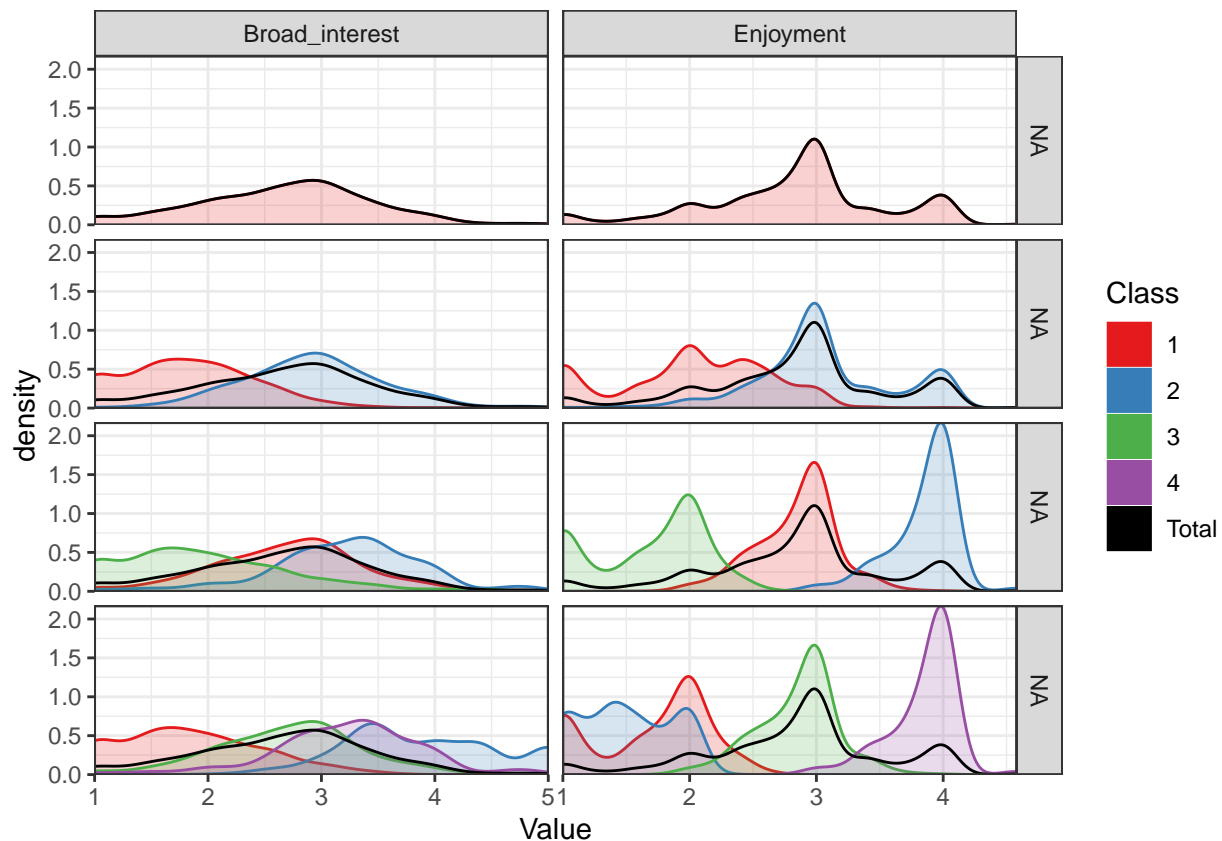
**Note:** single imputation is used in this example as `plot_profiles()` requires complete cases

```
pisa[1:200,] %>%
  select(broad_interest, enjoyment, instrumental_mot, self_efficacy) %>%
  single_imputation() %>%
  estimate_profiles(3, package = "MplusAutomation") %>%
  plot_profiles(sd=FALSE)
```



Plot densities for classes `k = 1:4`

```
pisa[1:500, c("broad_interest", "enjoyment")] %>%
  single_imputation() %>%
  estimate_profiles(1:4, package = "MplusAutomation") %>%
  plot_density()
```




---

**Example 2: Math, Science, Physics, and Biology measures (LSAY).**

---

Read in data

```
lsay_data <- read_csv("https://garberadamc.github.io/project-site/data/lsay_lab10.2_lpa.csv")
```

---

Run a quick enumeration

```
lpa_k14 <- lapply(1:4, function(k) {
  lpa_enum <- mplusObject(
    TITLE = glue("Class {k}"),
    VARIABLE = glue(
      "usevar = mth_scor-bio_scor;
      classes = c({k}); "),
    ANALYSIS =
```

```

    "estimator = mlr;
    type = mixture;
    starts = 200 50;
    processors = 10;";

OUTPUT = "sampstat residual tech11 tech14;";

PLOT =
    "type = plot3;
    series = mth_scor-bio_scor(*)";

usevariables = colnames(lsay_data),
rdata = lsay_data)

lpa_enum_fit <- mplusModeler(lpa_enum,
    dataout=glue(here("22-LPA", "enum_lpa", "lpa_lsay.dat")),
    modelout=glue(here("22-LPA", "enum_lpa", "c{k}_lpa_lsay.inp")) ,
    check=TRUE, run = TRUE, hashfilename = FALSE)
})

```

---

Plot 3-class profile

```

lsay_data[1:500,5:8] %>%
  single_imputation() %>%
  estimate_profiles(1:4, package = "MplusAutomation") %>%
  plot_profiles(sd=FALSE)

```

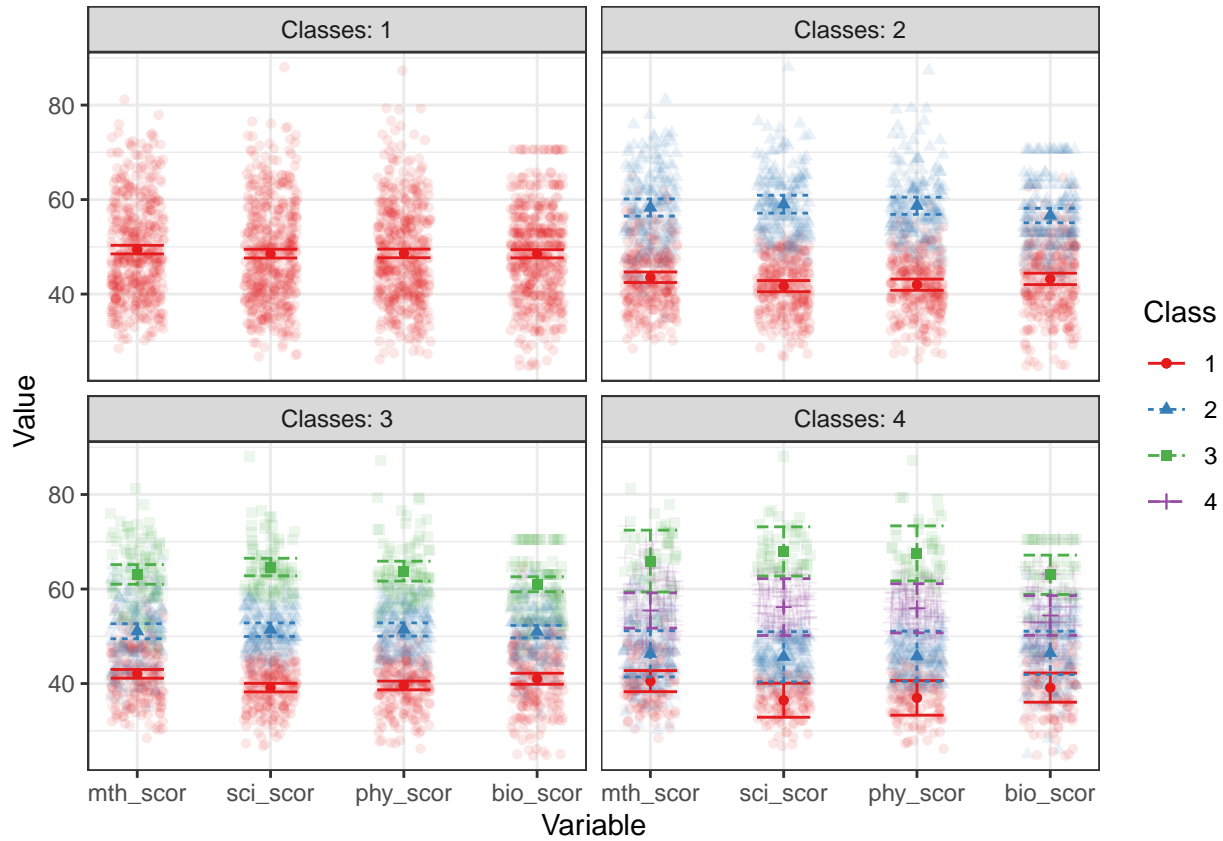


Figure. Here we see ordered solutions.

Compare model fit.

```
all_output <- readModels(here("22-LPA", "enum_lpa"), quiet = TRUE)

enum_extract <- LatexSummaryTable(all_output,
  keepCols=c("Title", "Parameters", "LL", "BIC",
    "aBIC", "BLRT_PValue", "T11_VLMR_PValue"),
  sortBy = "Title")

enum_extract %>% gt()
```

| Title   | Parameters | LL        | BIC      | aBIC     | BLRT_PValue | T11_VLMR_PValue |
|---------|------------|-----------|----------|----------|-------------|-----------------|
| Class 1 | 8          | -46288.29 | 92640.89 | 92615.47 | NA          | NA              |
| Class 2 | 13         | -43352.36 | 86809.23 | 86767.93 | 0           | 0               |
| Class 3 | 18         | -42126.11 | 84396.93 | 84339.74 | 0           | 0               |
| Class 4 | 23         | -41433.72 | 83052.37 | 82979.29 | 0           | 0               |

## References

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- 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/>
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