# The P-Technique with lavaan

The purpose of this project is to demonstrate how to fit single-subject structural equation models (SEM) within the p-technique framework. As discussed in the primary manuscript, among the recent introductions to and tutorials on the p-technique family, we believe the method outlined in Little's (2013) text is the most thorough and approachable for non-statistician behavioral researchers. Thus, the approach described herein is based primarily on Little's text.

Here we open our first few packages and load the data

```
library(readxl)
library(tidyverse)
library(lubridate)

d <-
  read_excel("Lindsey.xlsx") %>%
  mutate(Date = ymd(Date))
```

In this document, we'll use functions and syntax from the tidyverse, which you might learn about here or here.

Here we take a glance at the structure of the data.

```
glimpse(d)
```

```
## Observations: 103
## Variables: 9
## $ Date <date> 2016-01-29, 2016-01-30, 2016-01-31, 2016-02-01, 2016-02-02, 2016-02-03, 2016-02-0...
## $ Meds <dbl> 1, NA, NA, NA, 1, 1, 1, NA, NA, 0, 1, 1, 1, 1, NA, 0, 1, 1, 1, 1, 1, 1, NA, 0, 1, ...
## $ A3   <dbl> 3, NA, NA, NA, 4, 3, 5, NA, NA, 4, 3, 3, 3, 4, NA, 4, 3, 4, 3, 2, 3, 2, NA, 4, 4, ...
## $ A8   <dbl> 3, NA, NA, NA, 2, 4, 5, NA, NA, 4, 3, 4, 4, 4, NA, 5, 4, 4, 4, 4, 4, 2, NA, 3, 4, ...
## $ A10  <dbl> 5, NA, NA, NA, 3, 5, 3, NA, NA, 3, 4, 3, 4, 3, NA, 4, 3, 5, 3, 2, 3, 2, NA, 4, 5, ...
## $ A13  <dbl> 4, NA, NA, NA, 5, 4, 4, NA, NA, 2, 4, 4, 3, 3, NA, 1, 4, 5, 5, 2, 3, 2, NA, 2, 5, ...
## $ A14  <dbl> 5, NA, NA, NA, 4, 5, 4, NA, NA, 3, 4, 4, 4, 3, NA, 2, 4, 5, 5, 3, 3, 2, NA, 3, 5, ...
## $ A16  <dbl> 3, NA, NA, NA, 2, 1, 1, NA, NA, 2, 2, 2, 2, 2, NA, 1, 2, 2, 3, 2, 1, 1, NA, 1, 4, ...
## $ A17  <dbl> 3, NA, NA, NA, 1, 2, 3, NA, NA, 1, 3, 3, 4, 3, NA, 4, 3, 4, 3, 2, 3, 2, NA, 3, 5, ...
```

These data are from one participant, who we'll refer to by the pseudonym "Lindsey." The nine columns in the data are composed of three primary types of variables. These are daily-diary data and `Date` contains a sequential list of the dates from the beginning to the end of the study. The next column, `Meds`, is a dummy variable indicating whether Lindsey took her prescribed AHDH medication that day (i.e., coded 0 = "no", 1 = "yes"). The remaining columns `A3` through `A17` are responses to seven of the 18 ASRS items. At the beginning of the study, Lindsey indicated these seven items represented her most salient ADHD symptoms. Because this was a daily-diary study, we reworded the items and their anchors to make sense in a daily context. The five Likert-type anchor were labeled

- 0 (*Not at all*)
- 1 (*A little*)
- 2 (*Moderately*)
- 3 (*Most of the time*)
- 4 (*All day long*)

Her items were worded as follows:

- Was it difficult concentrating on what people said to you, even when they spoke to you directly?
- Were you distracted by activities or noises around you?
- Did you fidget or squirm with your hands or your feet when sitting down?
- Was it difficult unwinding or relaxing when you had time to yourself?

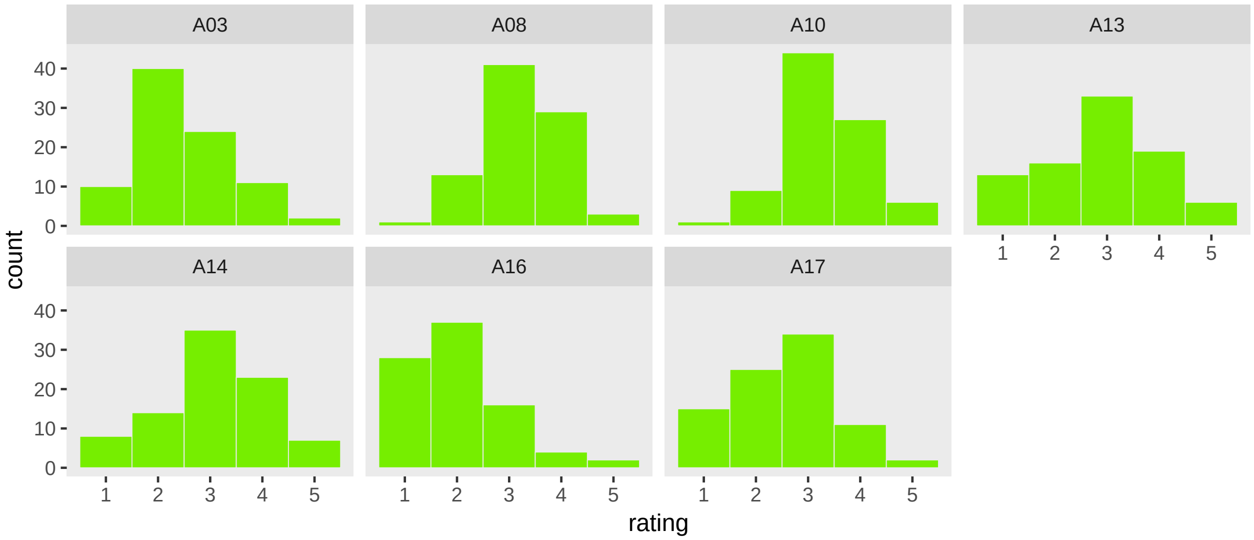
- Did you feel overly active or compelled to do things, like you were driven by a motor?
- Did you finish the sentences of other people before they could finish them themselves?
- Was it difficult waiting your turn in when you were supposed to?

Note how the data are in the long format. That is, although we have one participant, Lindsey, her data are presented in 103 rows, each corresponding to a different calendar day.

## Descriptive statistics

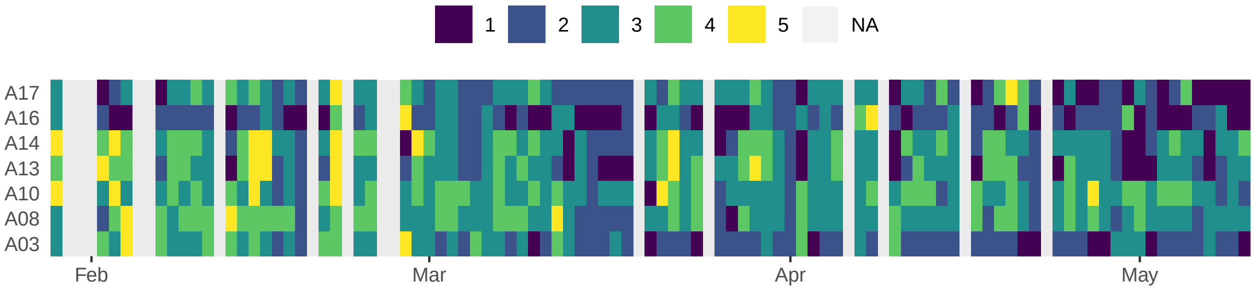
If you wanted to get a sense of the distributions of the ASRS items, histograms might be handy.

```
d %>%
  select(A3:A17) %>%
  rename(A03 = A3,
         A08 = A8) %>%
  gather(item, rating) %>%

  ggplot(aes(x = rating)) +
  geom_histogram(binwidth = 1, fill = "chartreuse2", color = "grey92", size = 1/5) +
  theme(panel.grid = element_blank()) +
  facet_wrap(~item, ncol = 4)
```



Happily, their distributions look reasonable. You can get a sense of their values over time with a sequentially-color-coded tile plot.

```
d %>%
  select(Date, A3:A17) %>%
  rename(A03 = A3,
         A08 = A8) %>%
  gather(item, rating, -Date) %>%
  mutate(rating = factor(rating, levels = c(1:5))) %>%

  ggplot(aes(x = Date, y = item)) +
  geom_tile(aes(fill = rating)) +
  scale_fill_viridis_d(NULL, option = "D",
                     guide = guide_legend(direction = "horizontal",
                                          nrow = 1)) +
  scale_x_date(expand = c(0, 0)) +
  scale_y_discrete(expand = c(0, 0)) +
  labs(x = NULL, y = NULL) +
  theme(panel.grid      = element_blank(),
        axis.ticks.y    = element_blank(),
        axis.text.y     = element_text(hjust = 0),
        legend.position = "top")
```



And with the psych package, we can use the `describe()` function to get the typical descriptive statistics.

```
library(psych)

d %>%
  select(A3:A17) %>%
  describe()
```

```
##     vars  n mean   sd median trimmed  mad min max range  skew kurtosis   se
## A3     1 87 2.48 0.94      2    2.45 1.48   1   5     4  0.51    -0.17 0.10
## A8     2 87 3.23 0.79      3    3.25 1.48   1   5     4 -0.14    -0.19 0.08
## A10    3 87 3.32 0.80      3    3.32 0.00   1   5     4  0.05     0.10 0.09
## A13    4 87 2.87 1.13      3    2.87 1.48   1   5     4 -0.09    -0.72 0.12
## A14    5 87 3.08 1.06      3    3.11 1.48   1   5     4 -0.22    -0.44 0.11
## A16    6 87 2.02 0.95      2    1.92 1.48   1   5     4  0.91     0.69 0.10
## A17    7 87 2.54 1.00      3    2.52 1.48   1   5     4  0.10    -0.55 0.11
```

If you look at the tile plot, above, you'll note the several light-gray stripes. Those are occasions for missing values. Here's the breakdown of missing values on the ASRS items by count and percent.

```
d %>%
  mutate(missing = is.na(A10)) %>%
  group_by(missing) %>%
  count() %>%
  ungroup() %>%
  mutate(percent = 100 * n / sum(n)) %>%
  mutate_if(is.double, round, digits = 1)
```

```
## # A tibble: 2 x 3
##   missing     n percent
##   <lgl>   <int>   <dbl>
## 1 FALSE      87    84.5
## 2 TRUE       16    15.5
```

Recall that the items in the ASRS correspond to the 18 criterion A symptoms, with the first nine classified as Inattentive and the last nine as hyperactive/impulsive. For the sake of this example, we'll focus on Lindsey's hyperactive/impulsive symptoms, ASRS items 10, 13, 14, 16, and 17. The following code drops the other two, items 3 and 8.

```
d <-
  d %>%
  select(everything(), -A3, -A8)
```

## P-technique CFA

Here we open our primary statistical package, lavaan, which you might learn more about here or here.

```
library(lavaan)
```

### *0-lag.*

The simplest starting place is a p-technique factor analysis. Using this approach, the model syntax looks much like that of a typical group-level CFA. First, we specify the model, which we call `CFA_0_lag`. We define our sole factor `H` by the five items. By default, lavaan fixes the first loading of each factor to 1 in order to set the latent scale. With the `NA*A10` syntax, we relax that constraint, allowing lavaan to freely estimate all loadings. Correspondingly, we used the `H ~~ 1*H` syntax to set the latent variance to 1, which then set the scale of the latent by putting it in a standardized metric.

The way one scales a factor is largely a matter of taste. Interested readers might learn more about the three most common methods in Little, Slegers and Card's (2006) article on the topic. We use the fixed factor method, here, to aid the interpretation of the effects in subsequent models.

```
CFA_0_lag <- '
H =~ NA*A10 + A13 + A14 + A16 + A17

# Standardize the variance
H ~~ 1*H
'
```

Now we've defined the model, here we estimate the parameters. Note we've selected a robust estimator with the `estimator = "MLR"` syntax. The lavaan package offers a variety of estimators, in addition to conventional maximum likelihood. With the `missing = "ML"` syntax, you'll note we're also handling the missing data with full information maximum likelihood (FIML) under the typical MAR assumption. As our p-technique models are just special cases of SEM, all of the modern missing data techniques (e.g., auxiliary variables with the saturated-correlates approach, multiple imputation) are available. For an approachable introduction contemporary missing data methods, see Enders' (2010) text, *Applied missing data analysis*. As our primary focus in this project is practicing with the p-technique models, we'll keep things simple and just use FIML.

```
fit.CFA_0_lag <-
  cfa(CFA_0_lag,
      data = d,
      estimator = "MLR",
      missing = "ML")
```

Now we use the `summary()` function to return the results, including the typical fit indices and 95% CIs for good measure.

```
summary(fit.CFA_0_lag,
        fit.measures = T,
        standardized = T,
        ci = T)
```

```
## lavaan 0.6-3 ended normally after 16 iterations
##
```

```
##   Optimization method                           NLMINB
##   Number of free parameters                         15
##
##                                                   Used       Total
##   Number of observations                            87         103
##   Number of missing patterns                         1
##
##   Estimator                                         ML      Robust
##   Model Fit Test Statistic                       7.452       6.768
##   Degrees of freedom                                 5           5
##   P-value (Chi-square)                           0.189       0.238
##   Scaling correction factor                                  1.101
##     for the Yuan-Bentler correction (Mplus variant)
##
## Model test baseline model:
##
##   Minimum Function Test Statistic              123.262     105.281
##   Degrees of freedom                                10          10
##   P-value                                        0.000       0.000
##
## User model versus baseline model:
##
##   Comparative Fit Index (CFI)                    0.978       0.981
##   Tucker-Lewis Index (TLI)                       0.957       0.963
##
##   Robust Comparative Fit Index (CFI)                         0.983
##   Robust Tucker-Lewis Index (TLI)                            0.965
##
## Loglikelihood and Information Criteria:
##
##   Loglikelihood user model (H0)               -548.428    -548.428
##   Scaling correction factor                                  1.061
##     for the MLR correction
##   Loglikelihood unrestricted model (H1)       -544.702    -544.702
##   Scaling correction factor                                  1.071
##     for the MLR correction
##
##   Number of free parameters                         15          15
##   Akaike (AIC)                                1126.856    1126.856
##   Bayesian (BIC)                              1163.845    1163.845
##   Sample-size adjusted Bayesian (BIC)         1116.515    1116.515
##
## Root Mean Square Error of Approximation:
##
##   RMSEA                                          0.075       0.064
##   90 Percent Confidence Interval          0.000  0.179       0.000  0.167
##   P-value RMSEA <= 0.05                          0.295       0.354
##
##   Robust RMSEA                                               0.067
##   90 Percent Confidence Interval                             0.000  0.180
##
## Standardized Root Mean Square Residual:
##
##   SRMR                                           0.049       0.049
```

```
##
## Parameter Estimates:
##
##   Information                                 Observed
##   Observed information based on                Hessian
##   Standard Errors                    Robust.huber.white
##
## Latent Variables:
##                    Estimate  Std.Err  z-value  P(>|z|) ci.lower ci.upper   Std.lv  Std.all
##   H =~
##     A10               0.222    0.099    2.237    0.025    0.027    0.417    0.222    0.279
##     A13               1.063    0.104   10.252    0.000    0.860    1.266    1.063    0.947
##     A14               0.885    0.102    8.659    0.000    0.684    1.085    0.885    0.840
##     A16               0.056    0.107    0.523    0.601   -0.153    0.265    0.056    0.059
##     A17               0.488    0.107    4.574    0.000    0.279    0.697    0.488    0.492
##
## Intercepts:
##                    Estimate  Std.Err  z-value  P(>|z|) ci.lower ci.upper   Std.lv  Std.all
##    .A10               3.322    0.085   38.973    0.000    3.155    3.489    3.322    4.178
##    .A13               2.874    0.120   23.879    0.000    2.638    3.109    2.874    2.560
##    .A14               3.080    0.113   27.291    0.000    2.859    3.302    3.080    2.926
##    .A16               2.023    0.101   19.934    0.000    1.824    2.222    2.023    2.137
##    .A17               2.540    0.106   23.885    0.000    2.332    2.749    2.540    2.561
##     H                 0.000                               0.000    0.000    0.000    0.000
##
## Variances:
##                    Estimate  Std.Err  z-value  P(>|z|) ci.lower ci.upper   Std.lv  Std.all
##     H                 1.000                               1.000    1.000    1.000    1.000
##    .A10               0.583    0.088    6.591    0.000    0.409    0.756    0.583    0.922
##    .A13               0.130    0.163    0.799    0.424   -0.189    0.449    0.130    0.103
##    .A14               0.326    0.126    2.577    0.010    0.078    0.574    0.326    0.294
##    .A16               0.893    0.162    5.498    0.000    0.575    1.211    0.893    0.997
##    .A17               0.746    0.126    5.929    0.000    0.500    0.993    0.746    0.758
```

The measures of model fit generally look good. We might note, however, that since this model has a small number of degrees of freedom (i.e., $df = 10$), the RMSEA is of limited utility, here. For more on the topic, see Kenney, Kaniskan and McCoach (2015). But RMSEA aside, the model $\chi^2$ and the CFI both look great.

If you inspect the `Std.all` column, you'll see that for Lindsey, items 10 and 16 have very low standardized loadings. Results like this are where p-technique methods shine. Even though both items have high loadings in group-level factor analyses, those results do not necessarily hold for individuals. Even though Lindsey selected both items as among her primary ADHD concerns, they provide little information to her hyperactive factor.

The p-technique literature is surfeit with analyses showing the mismatch between group-based factor structures and those of single-case data. For introductions to the topic, consider Fisher, Medaglia, and Jeronimus (2018) or Molenaar and Campbell (2009).

#### *1-lag.*

#### *First, we need to process the data a bit.*

Before we proceed to fit a dynamic-p CFA, we'll need to lag our data file. In short, a lag is the difference from one measurement occasion to another. The duration of a lag will depend on study design. From the clinical process literature, for example, lags have ranged from utterance to utterance to the span between therapy sessions (Russell, Jones, & Miller, 2007). Since Lindsey's data are from a daily-diary study, each lag is a day in separation.

Before we lag the data file, we'll add a row to the end of the data. Because this row corresponds to `Date = "2016-05-11"`, a day for which we don't have any information other than it was a Wednesday, we'll insert NAs into most of the columns.

```r
d_lagged <-
  tibble(Date = ymd("2016-01-18"),
         Meds = NA,
         A10 = NA, A13 = NA, A14 = NA, A16 = NA, A17 = NA) %>%
  bind_rows(d)
```

With the `lead()` function, we'll add lagged values for our `Meds` dummy and our ASRS items. For each of the lagged columns, we'll add the suffix `_1` to help differentiate them from the original columns.

```r
d_lagged <-
  d_lagged %>%
  mutate(Meds_1 = lead(Meds),
         A10_1  = lead(A10),
         A13_1  = lead(A13),
         A14_1  = lead(A14),
         A16_1  = lead(A16),
         A17_1  = lead(A17))

glimpse(d_lagged)
```

```
## Observations: 104
## Variables: 13
## $ Date   <date> 2016-01-18, 2016-01-29, 2016-01-30, 2016-01-31, 2016-02-01, 2016-02-02, 2016-02...
## $ Meds   <dbl> NA, 1, NA, NA, NA, 1, 1, 1, NA, NA, 0, 1, 1, 1, 1, NA, 0, 1, 1, 1, 1, 1, 1, NA, ...
## $ A10    <dbl> NA, 5, NA, NA, NA, 3, 5, 3, NA, NA, 3, 4, 3, 4, 3, NA, 4, 3, 5, 3, 2, 3, 2, NA, ...
## $ A13    <dbl> NA, 4, NA, NA, NA, 5, 4, 4, NA, NA, 2, 4, 4, 3, 3, NA, 1, 4, 5, 5, 2, 3, 2, NA, ...
## $ A14    <dbl> NA, 5, NA, NA, NA, 4, 5, 4, NA, NA, 3, 4, 4, 4, 3, NA, 2, 4, 5, 5, 3, 3, 2, NA, ...
## $ A16    <dbl> NA, 3, NA, NA, NA, 2, 1, 1, NA, NA, 2, 2, 2, 2, 2, NA, 1, 2, 2, 3, 2, 1, 1, NA, ...
## $ A17    <dbl> NA, 3, NA, NA, NA, 1, 2, 3, NA, NA, 1, 3, 3, 4, 3, NA, 4, 3, 4, 3, 2, 3, 2, NA, ...
## $ Meds_1 <dbl> 1, NA, NA, NA, 1, 1, 1, NA, NA, 0, 1, 1, 1, 1, NA, 0, 1, 1, 1, 1, 1, 1, NA, 0, 1...
## $ A10_1  <dbl> 5, NA, NA, NA, 3, 5, 3, NA, NA, 3, 4, 3, 4, 3, NA, 4, 3, 5, 3, 2, 3, 2, NA, 4, 5...
## $ A13_1  <dbl> 4, NA, NA, NA, 5, 4, 4, NA, NA, 2, 4, 4, 3, 3, NA, 1, 4, 5, 5, 2, 3, 2, NA, 2, 5...
## $ A14_1  <dbl> 5, NA, NA, NA, 4, 5, 4, NA, NA, 3, 4, 4, 4, 3, NA, 2, 4, 5, 5, 3, 3, 2, NA, 3, 5...
## $ A16_1  <dbl> 3, NA, NA, NA, 2, 1, 1, NA, NA, 2, 2, 2, 2, 2, NA, 1, 2, 2, 3, 2, 1, 1, NA, 1, 4...
## $ A17_1  <dbl> 3, NA, NA, NA, 1, 2, 3, NA, NA, 1, 3, 3, 4, 3, NA, 4, 3, 4, 3, 2, 3, 2, NA, 3, 5...
```

Let's focus on the last four rows to take a closer look at what we've done. Here we'll just consider the `Date` and the original and lagged versions of items 10 and 13.

```r
d_lagged %>%
  select(Date, A10:A13, A10_1:A13_1) %>%
  slice(c(101:104)) %>%
  knitr::kable()
```

| Date | A10 | A13 | A10_1 | A13_1 |
|---|---|---|---|---|
| 2016-05-07 | 3 | 1 | 2 | 2 |
| 2016-05-08 | 2 | 2 | 3 | 3 |
| 2016-05-09 | 3 | 3 | 2 | 3 |
| 2016-05-10 | 2 | 3 | NA | NA |

Notice how the values of `A10` and `A13` in one row are always the same as `A10_1` and `A13_1` in the row above them. That's because when we created the lagged variables, those with the `_1` suffixes, we took the values from the original columns and shifted them up one. As such, the new lagged columns always have missing values in their last row. Because we did not collect data from Lindsey on May 11, we have no values to on her ASRS items to shift up one and insert into the lagged columns for May 10.

In principle, we could add more lags. Kim, Nesselroade, and McCullough (2009), for example, used a 2-lag structure in their study on worldview, self-concept, and physical health in older individuals. For our present analysis, you might consider the original columns as depicting the data at *lag 0* and the new lagged columns as depicting the data at *lag 1*. Conceptually, lag 0 corresponds to "today" and lag 1 to "tomorrow." That is, the 1-lag data structure for daily-diary data allows to ask questions about how today will predict or influence tomorrow. If this is still confusing, see Little's (2013) text, particularly his Figure 7.7 and the prose surrounding it. This should also become more clear with a little practice.

### ***We digress into measurement theory.***

Now we have our lagged data, `d_lagged`, we are almost ready to specify and fit the 1-lag CFA model.

Because of the way the data are copied to create a lagged dataset, model estimation involving multiple lags entails a number of specific constraints because the information across the lags is essentially equivalent (Little, 2013). These constraints are all connected to the issue of measurement invariance. Typical group-level longitudinal CFAs require that analysts assess the extent to which the factors are invariant across time (for detailed discussions, see Brown, 2015; Little, 2013; Newsom, 2015; Widaman, Ferrer, & Conger, 2010). Factorial invariance across time suggests the variables of interest were reliably measured across time and that the constructs themselves were stable. For dynamic p-technique models, we expect "strict factorial invariance" (Little, 2013), which entails that the item loadings, item intercepts, and residual variances are equivalent across lags.

We will specify those constraints using parameter labels in the code that follows. If you are completely new to measurement invariance within the SEM context, we provide a brief walk-through at the end of this project. But for a more thorough introduction, do spend some time with one or a few of the references, above.

### ***Finally, we're ready to specify and estimate the model.***

Within lavaan, assigning two or more parameters the same label will constrain them to equality. For example, consider the loading code, below. We define the lag-0 factor with the following: `H0 =~ l1*A10 + l2*A13 + l3*A14 + l4*A16 + l5*A17`. With the `l[i]*` prefixes, we labeled the loading of ASRS item 10 as `l1`, the loading for item 13 as `l2`, and so on. If you look at the second line, you'll see we used the same parameter labels for the lag-1 items. In this way, we constrain the loadings of the same items to equality across lags. We followed the same approach for the item intercepts and residual variances.

The particular names you use for your labels are, of course, arbitrary. We could have named our first loading `dog` if we wanted to. Buy my stance is it makes sense to serially name parameters in the order they come in (e.g., `l1`, `l2`, . . . ) and to give groups of parameters the same prefix (e.g., `l` for loadings, `i` for intercepts).

```
CFA_1_lag <- '
# loadings
H0 =~ l1*A10   + l2*A13   + l3*A14   + l4*A16   + l5*A17
H1 =~ l1*A10_1 + l2*A13_1 + l3*A14_1 + l4*A16_1 + l5*A17_1

# item intercepts
A10 ~ i1*1
A13 ~ i2*1
A14 ~ i3*1
A16 ~ i4*1
A17 ~ i5*1
```

```
A10_1 ~ i1*1
A13_1 ~ i2*1
A14_1 ~ i3*1
A16_1 ~ i4*1
A17_1 ~ i5*1

# residual variances
A10 ~~ rv1*A10
A13 ~~ rv2*A13
A14 ~~ rv3*A14
A16 ~~ rv4*A16
A17 ~~ rv5*A17

A10_1 ~~ rv1*A10_1
A13_1 ~~ rv2*A13_1
A14_1 ~~ rv3*A14_1
A16_1 ~~ rv4*A16_1
A17_1 ~~ rv5*A17_1

# cross-lag residual covariances
A10 ~~ A10_1
A13 ~~ A13_1
A14 ~~ A14_1
A16 ~~ A16_1
A17 ~~ A17_1

# Structural model
H1 ~ H0

# latent variances
H0 ~~ 1*H0
H1 ~~ NA*H1 # Because of the structural model, the residual variance for H1 is freely estimated

# latent means/intercepts
H0 ~ 0
H1 ~ 1 # Because of the structural model, the latent intercept for H1 is freely estimated
'
```

We fit the model, here.

```
fit.CFA_1_lag <-
  cfa(CFA_1_lag,
      data = d_lagged,
      estimator = "MLR",
      missing = "ML",
      std.lv = T)
```

The summary:

```
summary(fit.CFA_1_lag,
        fit.measures = T,
        standardized = T,
        ci = T)
```

```
## lavaan 0.6-3 ended normally after 37 iterations
```

```
##
##   Optimization method                           NLMINB
##   Number of free parameters                         38
##   Number of equality constraints                    15
##
##                                                   Used       Total
##   Number of observations                           100         104
##   Number of missing patterns                         3
##
##   Estimator                                         ML      Robust
##   Model Fit Test Statistic                      31.919      31.394
##   Degrees of freedom                                42          42
##   P-value (Chi-square)                           0.870       0.884
##   Scaling correction factor                                  1.017
##     for the Yuan-Bentler correction (Mplus variant)
##
## Model test baseline model:
##
##   Minimum Function Test Statistic              290.043     266.514
##   Degrees of freedom                                45          45
##   P-value                                        0.000       0.000
##
## User model versus baseline model:
##
##   Comparative Fit Index (CFI)                    1.000       1.000
##   Tucker-Lewis Index (TLI)                       1.044       1.051
##
##   Robust Comparative Fit Index (CFI)                         1.000
##   Robust Tucker-Lewis Index (TLI)                            1.048
##
## Loglikelihood and Information Criteria:
##
##   Loglikelihood user model (H0)              -1083.604   -1083.604
##   Scaling correction factor                                  0.676
##     for the MLR correction
##   Loglikelihood unrestricted model (H1)      -1067.644   -1067.644
##   Scaling correction factor                                  1.052
##     for the MLR correction
##
##   Number of free parameters                         23          23
##   Akaike (AIC)                                2213.208    2213.208
##   Bayesian (BIC)                              2273.127    2273.127
##   Sample-size adjusted Bayesian (BIC)         2200.487    2200.487
##
## Root Mean Square Error of Approximation:
##
##   RMSEA                                          0.000       0.000
##   90 Percent Confidence Interval          0.000  0.036       0.000  0.033
##   P-value RMSEA <= 0.05                          0.981       0.984
##
##   Robust RMSEA                                               0.000
##   90 Percent Confidence Interval                             0.000  0.034
##
## Standardized Root Mean Square Residual:
```

```
##
##   SRMR                                           0.076       0.076
##
## Parameter Estimates:
##
##   Information                                 Observed
##   Observed information based on                Hessian
##   Standard Errors                   Robust.huber.white
##
## Latent Variables:
##                    Estimate  Std.Err  z-value  P(>|z|) ci.lower ci.upper   Std.lv  Std.all
##   H0 =~
##     A10       (l1)    0.219    0.068    3.200    0.001    0.085    0.352    0.219    0.275
##     A13       (l2)    1.056    0.091   11.558    0.000    0.877    1.235    1.056    0.940
##     A14       (l3)    0.895    0.076   11.849    0.000    0.747    1.043    0.895    0.848
##     A16       (l4)    0.050    0.080    0.621    0.535   -0.107    0.207    0.050    0.052
##     A17       (l5)    0.488    0.080    6.129    0.000    0.332    0.644    0.488    0.491
##   H1 =~
##     A10_1     (l1)    0.219    0.068    3.200    0.001    0.085    0.352    0.218    0.275
##     A13_1     (l2)    1.056    0.091   11.558    0.000    0.877    1.235    1.056    0.940
##     A14_1     (l3)    0.895    0.076   11.849    0.000    0.747    1.043    0.895    0.848
##     A16_1     (l4)    0.050    0.080    0.621    0.535   -0.107    0.207    0.050    0.052
##     A17_1     (l5)    0.488    0.080    6.129    0.000    0.332    0.644    0.488    0.491
##
## Regressions:
##                    Estimate  Std.Err  z-value  P(>|z|) ci.lower ci.upper   Std.lv  Std.all
##   H1 ~
##     H0                0.511    0.117    4.378    0.000    0.282    0.740    0.511    0.511
##
## Covariances:
##                    Estimate  Std.Err  z-value  P(>|z|) ci.lower ci.upper   Std.lv  Std.all
##  .A10 ~~
##    .A10_1            -0.065    0.080   -0.818    0.413   -0.221    0.091   -0.065   -0.112
##  .A13 ~~
##    .A13_1            -0.068    0.071   -0.962    0.336   -0.207    0.071   -0.068   -0.460
##  .A14 ~~
##    .A14_1            -0.039    0.074   -0.527    0.598   -0.184    0.106   -0.039   -0.124
##  .A16 ~~
##    .A16_1             0.170    0.140    1.217    0.224   -0.104    0.445    0.170    0.190
##  .A17 ~~
##    .A17_1             0.220    0.106    2.080    0.038    0.013    0.427    0.220    0.294
##
## Intercepts:
##                    Estimate  Std.Err  z-value  P(>|z|) ci.lower ci.upper   Std.lv  Std.all
##    .A10       (i1)    3.316    0.058   57.605    0.000    3.203    3.429    3.316    4.174
##    .A13       (i2)    2.842    0.117   24.266    0.000    2.612    3.071    2.842    2.528
##    .A14       (i3)    3.052    0.105   29.125    0.000    2.846    3.257    3.052    2.891
##    .A16       (i4)    2.026    0.078   25.882    0.000    1.873    2.180    2.026    2.138
##    .A17       (i5)    2.526    0.091   27.672    0.000    2.348    2.705    2.526    2.545
##    .A10_1     (i1)    3.316    0.058   57.605    0.000    3.203    3.429    3.316    4.174
##    .A13_1     (i2)    2.842    0.117   24.266    0.000    2.612    3.071    2.842    2.528
##    .A14_1     (i3)    3.052    0.105   29.125    0.000    2.846    3.257    3.052    2.891
##    .A16_1     (i4)    2.026    0.078   25.882    0.000    1.873    2.180    2.026    2.138
##    .A17_1     (i5)    2.526    0.091   27.672    0.000    2.348    2.705    2.526    2.545
##     H0                 0.000                               0.000    0.000    0.000    0.000
##    .H1                 0.052    0.121    0.427    0.669   -0.185    0.289    0.052    0.052
##
## Variances:
##                     Estimate  Std.Err  z-value  P(>|z|) ci.lower ci.upper   Std.lv  Std.all
##    .A10       (rv1)    0.584    0.065    9.000    0.000    0.456    0.711    0.584    0.924
##    .A13       (rv2)    0.148    0.098    1.515    0.130   -0.044    0.339    0.148    0.117
##    .A14       (rv3)    0.314    0.080    3.912    0.000    0.157    0.471    0.314    0.282
##    .A16       (rv4)    0.896    0.122    7.317    0.000    0.656    1.136    0.896    0.997
##    .A17       (rv5)    0.748    0.097    7.745    0.000    0.559    0.937    0.748    0.758
##    .A10_1     (rv1)    0.584    0.065    9.000    0.000    0.456    0.711    0.584    0.924
##    .A13_1     (rv2)    0.148    0.098    1.515    0.130   -0.044    0.339    0.148    0.117
##    .A14_1     (rv3)    0.314    0.080    3.912    0.000    0.157    0.471    0.314    0.282
##    .A16_1     (rv4)    0.896    0.122    7.317    0.000    0.656    1.136    0.896    0.997
##    .A17_1     (rv5)    0.748    0.097    7.745    0.000    0.559    0.937    0.748    0.759
##     H0                 1.000                               1.000    1.000    1.000    1.000
##    .H1                 0.738    0.156    4.734    0.000    0.433    1.044    0.739    0.739
```

The model fits the data great. You'll note that the autoregressive parameter, `H1 ~ H0`, is about .5. The metric is standardized and suggests that a one-unit increase in Lindsey's ASRS ratings, today, would predict about a half unit increase, tomorrow. You might interpret this as a carryover effect, or a kind of behavioral inertia. For more on the inertia interpretation, see Hamaker, Asparouhov, Brose, Schmiedek, and Muthén (2018).

As an aside, you might also note that now our degrees of freedom are large enough (i.e., $df = 42$) that the RMSEA should be more informative. For example, the width of its upper 90% CI is much more narrow than it was in the first model. Happily, the RMSEA coheres with the other fit statistics, which all suggest the model fits the data well.

## Dynamic-p SEM part 1: Adding a covariate

Here we move from measurement model concerns to include a covariate. With the data in hand, we can use `Meds_1` to predict lag-1 ADHD values, `H1`, while still controlling for the previous day's ADHD values (i.e., `H1 ~ H0`). The same measurement invariance constraints remain imposed.

```
SEM_1_lag <- '
# loadings
H0 =~ l1*A10   + l2*A13   + l3*A14   + l4*A16   + l5*A17
H1 =~ l1*A10_1 + l2*A13_1 + l3*A14_1 + l4*A16_1 + l5*A17_1

# item intercepts
A10 ~ i1*1
A13 ~ i2*1
A14 ~ i3*1
A16 ~ i4*1
A17 ~ i5*1

A10_1 ~ i1*1
A13_1 ~ i2*1
A14_1 ~ i3*1
A16_1 ~ i4*1
A17_1 ~ i5*1

# residual variances
A10 ~~ rv1*A10
```

```
A13 ~~ rv2*A13
A14 ~~ rv3*A14
A16 ~~ rv4*A16
A17 ~~ rv5*A17

A10_1 ~~ rv1*A10_1
A13_1 ~~ rv2*A13_1
A14_1 ~~ rv3*A14_1
A16_1 ~~ rv4*A16_1
A17_1 ~~ rv5*A17_1

# cross-lag residual covariances
A10 ~~ A10_1
A13 ~~ A13_1
A14 ~~ A14_1
A16 ~~ A16_1
A17 ~~ A17_1

# Structural model
H1 ~ H0 + Meds_1

# LV variances
H0 ~~ 1*H0
H1 ~~ NA*H1 # Because of the structural model, the resitual variance for H1 is freely estimated

# latent means/intercepts
H0 ~ 0
H1 ~ 1 # Because of the structural model, the latent intercept for H1 is freely estimated
'
```

Fit the model.

```
fit.SEM_1_lag <-
  cfa(SEM_1_lag,
      data = d_lagged,
      estimator = "MLR",
      missing = "ML",
      std.lv = T)
```

Now we summarize.

```
summary(fit.SEM_1_lag,
        fit.measures = T,
        standardized = T,
        ci = T)
```

```
## lavaan 0.6-3 ended normally after 39 iterations
##
##   Optimization method                           NLMINB
##   Number of free parameters                         39
##   Number of equality constraints                    15
##
##                                                   Used       Total
##   Number of observations                            87         104
##   Number of missing patterns                         2
##
```

```
##   Estimator                                         ML      Robust
##   Model Fit Test Statistic                      52.201      51.923
##   Degrees of freedom                                51          51
##   P-value (Chi-square)                           0.427       0.438
##   Scaling correction factor                                  1.005
##     for the Yuan-Bentler correction (Mplus variant)
##
## Model test baseline model:
##
##   Minimum Function Test Statistic              328.939     308.051
##   Degrees of freedom                                55          55
##   P-value                                        0.000       0.000
##
## User model versus baseline model:
##
##   Comparative Fit Index (CFI)                    0.996       0.996
##   Tucker-Lewis Index (TLI)                       0.995       0.996
##
##   Robust Comparative Fit Index (CFI)                         0.997
##   Robust Tucker-Lewis Index (TLI)                            0.996
##
## Loglikelihood and Information Criteria:
##
##   Loglikelihood user model (H0)               -975.687    -975.687
##   Scaling correction factor                                  0.690
##     for the MLR correction
##   Loglikelihood unrestricted model (H1)       -949.587    -949.587
##   Scaling correction factor                                  1.043
##     for the MLR correction
##
##   Number of free parameters                         24          24
##   Akaike (AIC)                                1999.374    1999.374
##   Bayesian (BIC)                              2058.556    2058.556
##   Sample-size adjusted Bayesian (BIC)         1982.828    1982.828
##
## Root Mean Square Error of Approximation:
##
##   RMSEA                                          0.016       0.014
##   90 Percent Confidence Interval          0.000  0.071       0.000  0.071
##   P-value RMSEA <= 0.05                          0.788       0.796
##
##   Robust RMSEA                                               0.014
##   90 Percent Confidence Interval                             0.000  0.071
##
## Standardized Root Mean Square Residual:
##
##   SRMR                                           0.117       0.117
##
## Parameter Estimates:
##
##   Information                                 Observed
##   Observed information based on                Hessian
##   Standard Errors                   Robust.huber.white
##
```

```
## Latent Variables:
##                    Estimate  Std.Err  z-value  P(>|z|) ci.lower ci.upper   Std.lv  Std.all
##   H0 =~
##     A10       (l1)    0.183    0.060    3.062    0.002    0.066    0.300    0.183    0.235
##     A13       (l2)    1.038    0.095   10.872    0.000    0.851    1.225    1.038    0.926
##     A14       (l3)    0.904    0.087   10.402    0.000    0.734    1.074    0.904    0.858
##     A16       (l4)    0.008    0.081    0.103    0.918   -0.150    0.167    0.008    0.009
##     A17       (l5)    0.454    0.083    5.473    0.000    0.291    0.617    0.454    0.457
##   H1 =~
##     A10_1     (l1)    0.183    0.060    3.062    0.002    0.066    0.300    0.177    0.228
##     A13_1     (l2)    1.038    0.095   10.872    0.000    0.851    1.225    1.002    0.921
##     A14_1     (l3)    0.904    0.087   10.402    0.000    0.734    1.074    0.872    0.849
##     A16_1     (l4)    0.008    0.081    0.103    0.918   -0.150    0.167    0.008    0.009
##     A17_1     (l5)    0.454    0.083    5.473    0.000    0.291    0.617    0.438    0.444
##
## Regressions:
##                    Estimate  Std.Err  z-value  P(>|z|) ci.lower ci.upper   Std.lv  Std.all
##   H1 ~
##     H0                  0.264    0.102    2.599    0.009    0.065    0.463    0.274    0.274
##     Meds_1              1.577    0.200    7.894    0.000    1.185    1.969    1.634    0.688
##
## Covariances:
##                    Estimate  Std.Err  z-value  P(>|z|) ci.lower ci.upper   Std.lv  Std.all
##  .A10 ~~
##    .A10_1             -0.068    0.076   -0.892    0.372   -0.217    0.081   -0.068   -0.119
##  .A13 ~~
##    .A13_1             -0.025    0.071   -0.354    0.723   -0.165    0.115   -0.025   -0.142
##  .A14 ~~
##    .A14_1             -0.068    0.067   -1.012    0.312   -0.200    0.064   -0.068   -0.231
##  .A16 ~~
##    .A16_1              0.152    0.125    1.212    0.226   -0.094    0.397    0.152    0.180
##  .A17 ~~
##    .A17_1              0.227    0.113    1.999    0.046    0.004    0.449    0.227    0.290
##
## Intercepts:
##                    Estimate  Std.Err  z-value  P(>|z|) ci.lower ci.upper   Std.lv  Std.all
##    .A10       (i1)    3.319    0.058   57.060    0.000    3.205    3.433    3.319    4.272
##    .A13       (i2)    2.825    0.127   22.224    0.000    2.576    3.074    2.825    2.520
##    .A14       (i3)    3.032    0.115   26.410    0.000    2.807    3.258    3.032    2.878
##    .A16       (i4)    2.008    0.078   25.670    0.000    1.855    2.162    2.008    2.191
##    .A17       (i5)    2.518    0.096   26.110    0.000    2.329    2.707    2.518    2.533
##    .A10_1     (i1)    3.319    0.058   57.060    0.000    3.205    3.433    3.319    4.280
##    .A13_1     (i2)    2.825    0.127   22.224    0.000    2.576    3.074    2.825    2.598
##    .A14_1     (i3)    3.032    0.115   26.410    0.000    2.807    3.258    3.032    2.953
##    .A16_1     (i4)    2.008    0.078   25.670    0.000    1.855    2.162    2.008    2.191
##    .A17_1     (i5)    2.518    0.096   26.110    0.000    2.329    2.707    2.518    2.551
##     H0                  0.000                               0.000    0.000    0.000    0.000
##    .H1                 -1.166    0.176   -6.632    0.000   -1.511   -0.821   -1.208   -1.208
##
## Variances:
##                    Estimate  Std.Err  z-value  P(>|z|) ci.lower ci.upper   Std.lv  Std.all
##    .A10      (rv1)    0.570    0.068    8.392    0.000    0.437    0.703    0.570    0.945
##    .A13      (rv2)    0.178    0.097    1.843    0.065   -0.011    0.368    0.178    0.142
##    .A14      (rv3)    0.294    0.067    4.368    0.000    0.162    0.426    0.294    0.264
##    .A16      (rv4)    0.840    0.120    7.007    0.000    0.605    1.075    0.840    1.000
##    .A17      (rv5)    0.782    0.103    7.587    0.000    0.580    0.984    0.782    0.791
##    .A10_1    (rv1)    0.570    0.068    8.392    0.000    0.437    0.703    0.570    0.948
##    .A13_1    (rv2)    0.178    0.097    1.843    0.065   -0.011    0.368    0.178    0.151
##    .A14_1    (rv3)    0.294    0.067    4.368    0.000    0.162    0.426    0.294    0.279
##    .A16_1    (rv4)    0.840    0.120    7.007    0.000    0.605    1.075    0.840    1.000
##    .A17_1    (rv5)    0.782    0.103    7.587    0.000    0.580    0.984    0.782    0.803
##     H0                 1.000                               1.000    1.000    1.000    1.000
##    .H1                 0.421    0.106    3.958    0.000    0.213    0.630    0.452    0.452
```

The model fit the data well. Recall that the latent variables are in a standardized metric. Because `Meds_1` is a dummy variable, this puts its coefficient in a Cohen's *d* like metric.

## Dynamic-p SEM part 2: Longitudinal mediation

To demonstrate the flexibility of the dynamic p-technique SEM framework, we might reparameterize the structural model to make a longitudinal mediation model. We will continue to regress `H1` on both `H0` and `Meds_1`. Now we also regress `Meds_1` on `H0`. Within that context, the consider the typical mediation path diagram.

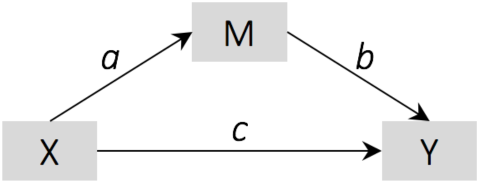


Figure 1: Behold the simple mediation model.

If we are interested in quantifying the strength of the indirect effect of X on Y through M, we multiply the *a* and *b* pathways. Because the sampling distribution of the *ab* coefficient is not necessarily Gaussian, contemporary methodologists typically recommend using the bootstrap to compute the 95% confidence intervals rather than rely on analytic standard errors (e.g., Hayes & Rockwood, 2017). All of this is available with lavaan.

Now consider our new structural model.

```
'
H1     ~ H0 + Meds_1
Meds_1 ~ H0
'
```

In this model, we might consider `H1` as the $Y$ variable, `H0` as the $X$, and `Meds_1` as the mediator $M$. As such, we can label the parameters like so.

```
'
H1     ~ c*H0 + b*Meds_1
Meds_1 ~ a*H0
'
```

Now all we need to do is use the `:=` operator to define the `ab` parameter and fit the model.

```
MED_1_lag <- '
# loadings
H0 =~ l1*A10   + l2*A13   + l3*A14   + l4*A16   + l5*A17
H1 =~ l1*A10_1 + l2*A13_1 + l3*A14_1 + l4*A16_1 + l5*A17_1

```

```
# item intercepts
A10 ~ i1*1
A13 ~ i2*1
A14 ~ i3*1
A16 ~ i4*1
A17 ~ i5*1

A10_1 ~ i1*1
A13_1 ~ i2*1
A14_1 ~ i3*1
A16_1 ~ i4*1
A17_1 ~ i5*1

# residual variances
A10 ~~ rv1*A10
A13 ~~ rv2*A13
A14 ~~ rv3*A14
A16 ~~ rv4*A16
A17 ~~ rv5*A17

A10_1 ~~ rv1*A10_1
A13_1 ~~ rv2*A13_1
A14_1 ~~ rv3*A14_1
A16_1 ~~ rv4*A16_1
A17_1 ~~ rv5*A17_1

# cross-lag residual covariances
A10 ~~ A10_1
A13 ~~ A13_1
A14 ~~ A14_1
A16 ~~ A16_1
A17 ~~ A17_1

# Structural model
H1     ~ c*H0 + b*Meds_1
Meds_1 ~ a*H0

# LV variances
H0 ~~ 1*H0
H1 ~~ NA*H1 # Because of the structural model, the resitual variance for H1 is freely estimated

# latent means/intercepts
H0 ~ 0
H1 ~ 1 # Because of the structural model, the latent intercept for H1 is freely estimated

# model constraint
ab := a * b
'
```

lavaan offers at least two ways to bootstrap. Perhaps the simplest is to include `se = "bootstrap"` within the `cfa()` or `sem()` functions. By default, it returns results from 1000 iterations. Note, however, that this requires we set `estimator = "ML"`.

```
fit.MED_1_lag <-
  cfa(MED_1_lag,
      data = d_lagged,
      estimator = "ML",
      missing = "ML",
      std.lv = T,
      se = "bootstrap")
```

Behold the summary.

```
summary(fit.MED_1_lag,
        fit.measures = T,
        ci = T)
```

```
## lavaan 0.6-3 ended normally after 42 iterations
##
##   Optimization method                           NLMINB
##   Number of free parameters                         42
##   Number of equality constraints                    15
##
##                                                   Used       Total
##   Number of observations                           100         104
##   Number of missing patterns                         3
##
##   Estimator                                         ML
##   Model Fit Test Statistic                      46.774
##   Degrees of freedom                                50
##   P-value (Chi-square)                           0.604
##
## Model test baseline model:
##
##   Minimum Function Test Statistic              360.130
##   Degrees of freedom                                55
##   P-value                                        0.000
##
## User model versus baseline model:
##
##   Comparative Fit Index (CFI)                    1.000
##   Tucker-Lewis Index (TLI)                       1.012
##
## Loglikelihood and Information Criteria:
##
##   Loglikelihood user model (H0)              -1104.120
##   Loglikelihood unrestricted model (H1)      -1080.733
##
##   Number of free parameters                         27
##   Akaike (AIC)                                2262.240
##   Bayesian (BIC)                              2332.580
##   Sample-size adjusted Bayesian (BIC)         2247.307
##
## Root Mean Square Error of Approximation:
##
##   RMSEA                                          0.000
##   90 Percent Confidence Interval          0.000  0.057
##   P-value RMSEA <= 0.05                          0.910
```

```
##
## Standardized Root Mean Square Residual:
##
##   SRMR                                           0.088
##
## Parameter Estimates:
##
##   Standard Errors                            Bootstrap
##   Number of requested bootstrap draws             1000
##   Number of successful bootstrap draws            1000
##
## Latent Variables:
##                    Estimate  Std.Err  z-value  P(>|z|) ci.lower ci.upper
##   H0 =~
##     A10       (l1)    0.224    0.063    3.533    0.000    0.101    0.351
##     A13       (l2)    1.039    0.093   11.198    0.000    0.838    1.196
##     A14       (l3)    0.922    0.082   11.266    0.000    0.765    1.086
##     A16       (l4)    0.051    0.086    0.588    0.557   -0.103    0.243
##     A17       (l5)    0.480    0.082    5.864    0.000    0.299    0.630
##   H1 =~
##     A10_1     (l1)    0.224    0.063    3.533    0.000    0.101    0.351
##     A13_1     (l2)    1.039    0.093   11.198    0.000    0.838    1.196
##     A14_1     (l3)    0.922    0.082   11.266    0.000    0.765    1.086
##     A16_1     (l4)    0.051    0.086    0.588    0.557   -0.103    0.243
##     A17_1     (l5)    0.480    0.082    5.864    0.000    0.299    0.630
##
## Regressions:
##                    Estimate  Std.Err  z-value  P(>|z|) ci.lower ci.upper
##   H1 ~
##     H0         (c)    0.266    0.121    2.210    0.027    0.002    0.484
##     Meds_1     (b)    1.466    0.223    6.563    0.000    1.093    1.960
##   Meds_1 ~
##     H0         (a)    0.164    0.047    3.464    0.001    0.097    0.289
##
## Covariances:
##                    Estimate  Std.Err  z-value  P(>|z|) ci.lower ci.upper
##  .A10 ~~
##    .A10_1            -0.070    0.082   -0.853    0.394   -0.271    0.058
##  .A13 ~~
##    .A13_1            -0.014    0.066   -0.205    0.838   -0.138    0.119
##  .A14 ~~
##    .A14_1            -0.076    0.065   -1.171    0.242   -0.211    0.049
##  .A16 ~~
##    .A16_1             0.169    0.148    1.149    0.251   -0.093    0.489
##  .A17 ~~
##    .A17_1             0.215    0.108    1.996    0.046   -0.078    0.352
##
## Intercepts:
##                    Estimate  Std.Err  z-value  P(>|z|) ci.lower ci.upper
##    .A10       (i1)    3.314    0.057   58.451    0.000    3.236    3.467
##    .A13       (i2)    2.832    0.115   24.695    0.000    2.641    3.079
##    .A14       (i3)    3.042    0.106   28.584    0.000    2.846    3.259
##    .A16       (i4)    2.026    0.079   25.527    0.000    1.888    2.196
##    .A17       (i5)    2.523    0.086   29.500    0.000    2.417    2.754
##    .A10_1     (i1)    3.314    0.057   58.451    0.000    3.236    3.467
##    .A13_1     (i2)    2.832    0.115   24.695    0.000    2.641    3.079
##    .A14_1     (i3)    3.042    0.106   28.584    0.000    2.846    3.259
##    .A16_1     (i4)    2.026    0.079   25.527    0.000    1.888    2.196
##    .A17_1     (i5)    2.523    0.086   29.500    0.000    2.417    2.754
##     H0                0.000                               0.000    0.000
##    .H1               -1.078    0.184   -5.867    0.000   -1.542   -0.785
##    .Meds_1            0.777    0.045   17.399    0.000    0.675    0.852
##
## Variances:
##                    Estimate  Std.Err  z-value  P(>|z|) ci.lower ci.upper
##    .A10      (rv1)    0.582    0.067    8.628    0.000    0.432    0.706
##    .A13      (rv2)    0.190    0.091    2.091    0.036    0.044    0.402
##    .A14      (rv3)    0.278    0.066    4.197    0.000    0.117    0.379
##    .A16      (rv4)    0.896    0.127    7.082    0.000    0.644    1.143
##    .A17      (rv5)    0.754    0.096    7.879    0.000    0.511    0.893
##    .A10_1    (rv1)    0.582    0.067    8.628    0.000    0.432    0.706
##    .A13_1    (rv2)    0.190    0.091    2.091    0.036    0.044    0.402
##    .A14_1    (rv3)    0.278    0.066    4.197    0.000    0.117    0.379
##    .A16_1    (rv4)    0.896    0.127    7.082    0.000    0.644    1.143
##    .A17_1    (rv5)    0.754    0.096    7.879    0.000    0.511    0.893
##     H0                1.000                               1.000    1.000
##    .H1                0.416    0.113    3.688    0.000    0.236    0.654
##    .Meds_1            0.150    0.021    7.285    0.000    0.101    0.185
##
## Defined Parameters:
##                    Estimate  Std.Err  z-value  P(>|z|) ci.lower ci.upper
##     ab                0.241    0.086    2.811    0.005    0.138    0.478
```

Based on the $\chi^2$ and so forth, the model continues to fit the data just fine. The `ab` parameter is small but with modestly narrow intervals not overlapping zero. Here we have statistical evidence of a single-subject mediational process.

To be clear, this is not a theory-based model and we would not encourage our readers to over interpret these results. But we do hope applied researchers might find the example provocative. By combining sound theory, carefully-collected single-case data, and the dynamic p-technique framework, researchers can fit single-case mediation models and more.

## Happy modeling

Consider again the challenge made by Hayes and colleagues:

> Individual human lives are contextual and longitudinal, as are the change processes that alter these life trajectories. From a process-based point of view, practitioners need coherent and broadly applicable models of change processes that are relevant for the individual in context, that provide increased treatment utility and intervention guidance, and that simplify human complexity. The most popular methodological and analytic tools in use in intervention science are not fully adequate to that task, even when they are turned in the direction of change processes. (p. 3)

We believe the p-technique framework may be up to the task.

Happy modeling.

## What's the deal with measurement invariance?

If you haven't waded into the measurement invariance literature before, their waters can seem deep and cold at first touch. But don't recoil yet. The basic ideas are simple enough. In brief, we want to make sure our tools (i.e., our self-report questionnaires) work the same across contexts. If they do, we say we have measurement invariance, which we generally like. If our tools work differently across contexts, we say we have some degree of measurement variance.

With group-level data, we typically assess measurement invariance in two contexts. First, when the data are cross-sectional, the we often ask whether a measure is invariant across two or more groups. These are often demographic groups, such as subgroupings of sex or ethnicity (e.g., Melka, Lancaster, Bryant, & Rodriguez, 2011). Within the clinical literature, they are also often between clinical and non-clinical samples (e.g., Meganck, Vanheule, & Desmet, 2008). In the second context, measurement invariance may be assessed over multiple assessment points in a longitudinal study (e.g., Fried et al., 2016). In this way, the question is to what extent the tool worked the same over time.

In line with contemporary psychometrics, we usually assess measurement invariance within the context of the latent variable framework. As such, it's often operationalized by the term *factorial invariance*. Let's say we have a given questionnaire, like the ASRS. The latent variable model proposes we can describe the 18 ASRS items with a smaller number of latent variables. In so doing, the model entails the items have loadings (i.e., $\lambda$s), intercepts (i.e., $\tau$s), residual variances (i.e., $\theta$s), and possibly residual covariances (i.e., $\theta_{ij}$s). It's beyond the scope of this tutorial to expound on these terms in depth. For that, the interested reader should consult an introductory SEM textbook, such as those by Brown (2015) or Kline (2016). But the point, here, is that if we wanted to assess whether the ASRS was factorially invariant across two groups (e.g., boys and girls), we'd assess whether those $\lambda$s, $\tau$s, and $\theta$s were the same across the two groups.

There are other kinds of factorial invariance, too, such as invariance of latent means, variances, and covariances. In principle, those can apply to our p-technique framework. However, they are not applicable to the models in this tutorial and in order to keep some semblance of focus, we will not consider them further.

Factorial invariance can be thought of as on a continuum or gradation. In practice, we typically assess factorial invariance by imposing a sequence of increasingly strict equality constraints. The levels in this sequence go by several names and there is some dispute among psychometricians on how to order them. Here we present an approach consistent with Little (2013) and Newsom (2015). The levels of factorial invariance we will consider are:

1. Configural invariance
2. Weak invariance
3. Strong invariance
4. Strict invariance

### *Configural invariance (i.e., invariance of gross structure).*

To use a simple example, let's say we have a 3-item questionnaire. We'll call those items $y_1$, $y_2$, and $y_3$. Their content might be for depression, ADHD, or whatever you like. Now say we've given our brief questionnaire to the same group of people at two time points. Our theory proposes we can measure those three items as defining a single latent variable. Following common SEM notation, we'll call that latent variable $\eta$. Let's call those two time points were $t = 1$ and $t = 2$. We can then differentiate our latent variable on those two time points as $\eta_1$ and $\eta_2$. Accordingly, we can depict our longitudinal SEM in the path diagrams in Figure 2.

In the applied literature, SEM path diagrams aren't usually this detailed. To keep things simple, researchers often leave out the mean structure—which we've depicted by the triangles and the associated arrows showing the $\tau$ parameters and the $\alpha$ parameters. Those are the item intercepts and latent means, respectively.

For the sake of our factorial invariance discussion, the main thing to notice is that both $\eta_1$ and $\eta_2$ are defined by the same items, $y_1$ through $y_3$, but just at different time points. Thus, $y_{11}$ is the first item measured at $t = 1$ and $y_{12}$ is that same item measured at $t = 2$. That is, both latent variables have the same general

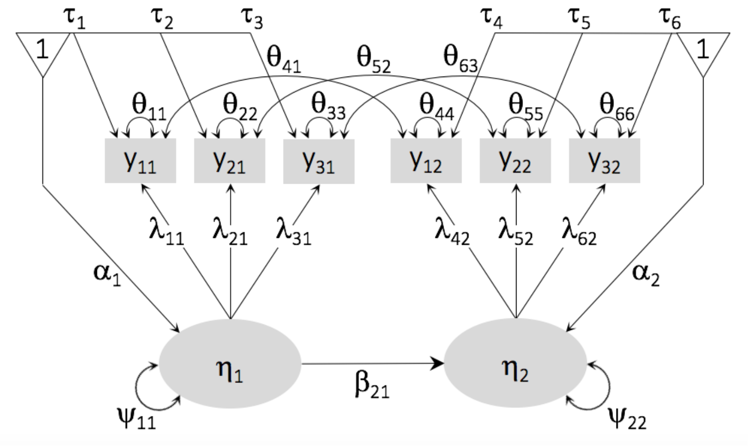


Figure 2: The configural model.

factor structure; they have the same number of item loadings, which are connected to the same items. This is *configural invariance*. You might think of this as the foundation of all other levels of factorial invariance. If this assumption isn't tenable, well, you'll have a lot to write about in your discussion section.

We typically determine configural invariance is tenable if the overall fit statistics (e.g., the model $\chi^2$, the CFI) are within reasonable ranges.

### *Weak invariance (i.e., invariance of the loadings).*

Assuming configural invariance holds, which is typical but not a guarantee (see Fried et al., 2016), the next step is to test for *weak factorial invariance*–invariance across intercepts. Continuing on with our 3-item example, in this step we would specify the following constraints: $\lambda_{11} = \lambda_{12}$, $\lambda_{21} = \lambda_{22}$, and $\lambda_{31} = \lambda_{32}$. We have depicted those constraints in Figure 3. Note how the $\lambda$s are all colored red. This is just to bring them to attention. More importantly, notice how both $\lambda_{11}$ and $\lambda_{12}$ have the $a$ superscript. This is just to indicate that their values are constrained to equality. The same relationship is also true for the other two items across time.

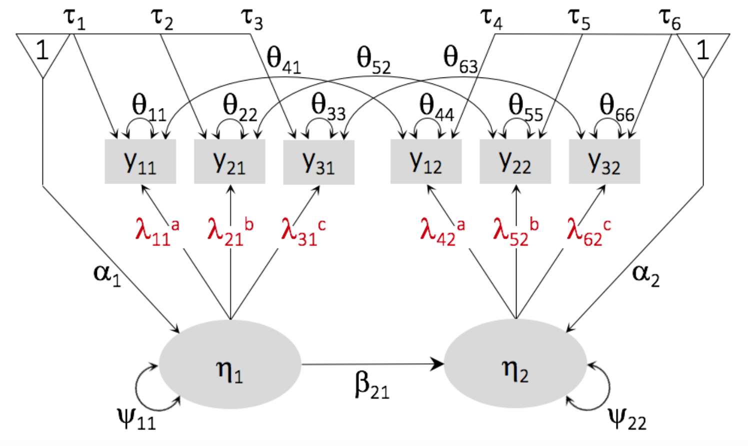


Figure 3: The weak invariance model.

If the model fit statistics do not degrade substantially after including these constraints, we generally determine weak measurement invariance holds. There is continuing debate in the psychometric literature on how stringent analysts should be when assessing model fit degradation, as well as which fit statistics are the best ones to consult. But those discussions are beyond the scope of this tutorial. Any of the text books (e.g., Newsom, 2015) or methodological papers (e.g., Widaman et al., 2010) we have already mentioned are fine starting points for those topics.

***Strong invariance (i.e., invariance of item intercepts).***

Generally speaking, though not necessarily (see Newsom, 2015), analysts next proceed to assess whether the item intercepts are invariant. Invariance across item intercepts is often termed *strong factorial invariance*. This is less often examined in the applied literature, though see Neumann, van Lier, Gratz, and Koot (2010) for an example. We depict these constraints in Figure 4.

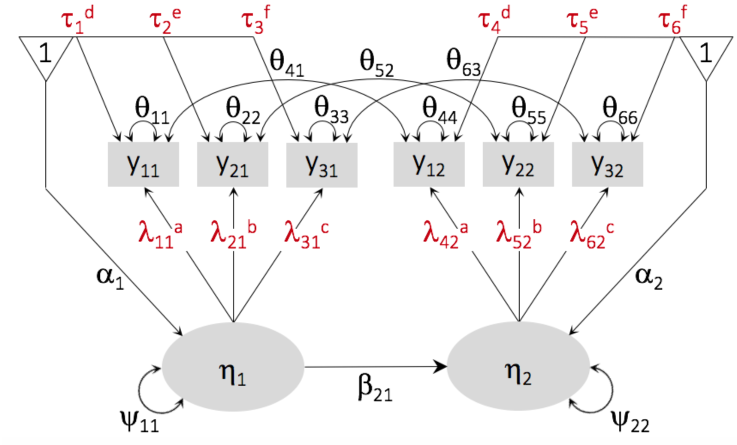


Figure 4: The strong invariance model.

In addition to the $\lambda$ constraints carried over from the weak invariance model, out strong invariance model added the constraints that: $\tau_1 = \tau_4$, $\tau_2 = \tau_5$, and $\tau_3 = \tau_6$. That is, now our first item, $y_1$, has the same intercept at both $t = 1$ and $t = 2$. The same holds for $y_2$ and $y_3$. If the model fit does not degrade past our chosen threshold, we declare strong factorial invariance.

In many applications, this is the desired level of factorial invariance to declare the items measure the same constructs across the groups and/or time points under consideration. However, we can take one more step.

***Strict invariance (i.e., invariance of residual variances).***

Residual variances are the parts of the item variances that are not explained by the latent variable, $\eta$. In classical test theory, these are considered pure measurement error (Lord & Novick, 1968). In contemporary latent variable theory, they are seen as containing both random error and possibly systemic variation associated with constructs other than the focal latent variable. These can be any number of things, ranging from other substantive variables to method effects. But at any rate, *strict factorial invariance* entails imposing equality constraints on residual variances.

For typical contexts, psychometricians often recommend against testing imposing strict invariance. Little (2013):

> Why do I have a problem with enforcing strict invariance? The reason is that the variances of the indicator residuals contain both the indicator-specific information and the random unreliability of measurement. Strict factorial invariance is a test that the sum of these two sources of variance (indicator specific and random error) is *exactly* the same across time (or groups). Although it might be reasonable to assume that the indicator-specific information would be invariant across

> time (or groups), I don't think it is reasonable to assume that the amount of random error present in each indicator at each time point (or across groups) would be the same. (p. 143, *emphasis* in the original)

We depict the constraints entailed in strict factorial invariance in Figure 5.

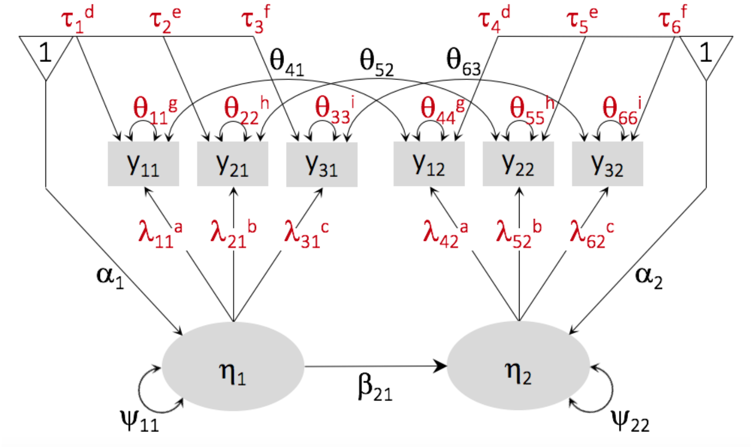


Figure 5: The strict invariance model.

Though Little's warning is well-headed in most contexts, it is poorly applied with dynamic p-technique analyses. Why? Recall how we lagged our data, above. We copy/pasted the information from lag 0 to make lag 1. All we did was shift the rows up 1. So, as Little explained in his section on dynamic SEM, "because the within-lag information is essentially equivalent, all parameters associated with a given construct would be invariant in the CFA build up to the structural model" (p. 236). This includes the residual variances. This is the key to understanding the invariance constraints we imposed on all our dynamic p-technique models. Because we used a 1-lag data structure, our $\lambda$s, $\tau$s, and $\theta$s were a priori invariant across lags. We didn't even need to follow the typical nested model comparisons with the $\chi^2$, CFI, or other fit indices. We knew they would be invariant from the outset.

***There are other possibilities.***

Due to the nature of the simple 1-lag dynamic models we fit in this tutorial, those are the only kinds of measurement invariance we'll explore in detail. But we'd be remiss not to mention other possibilities. In models with 2+ lags, there may be additional invariance constraints, such as cross-lag residual covariances or structural parameters, such as the autoregressive parameters. In p-technique analyses with data from multiple participants, analysts can use multigroup CFA procedures to text factorial invariance across participants. And some recent works have proposed models with time/varying parameters, opening up the possibility of temporal measurement invariance. For more on these possibilities, consult Little's (2013) text and also the paper by Adolf, Schuurman, Borkenau, Borsboom, and Dolan (2014).

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## Session Info

To help make this work more reproducible, here's the session information.

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sessionInfo()
```

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## Running under: macOS High Sierra 10.13.6
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## Matrix products: default
## BLAS: /Library/Frameworks/R.framework/Versions/3.5/Resources/lib/libRblas.0.dylib
## LAPACK: /Library/Frameworks/R.framework/Versions/3.5/Resources/lib/libRlapack.dylib
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## [1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8
##
## attached base packages:
## [1] stats     graphics  grDevices utils     datasets  methods   base
##
## other attached packages:
##  [1] lavaan_0.6-3    psych_1.8.4     bindrcpp_0.2.2  lubridate_1.7.4 forcats_0.3.0   stringr_1.3.1
##  [7] dplyr_0.7.6     purrr_0.2.5     readr_1.1.1     tidyr_0.8.1     tibble_1.4.2    ggplot2_3.1.0
## [13] tidyverse_1.2.1 readxl_1.1.0
##
## loaded via a namespace (and not attached):
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##  [6] stats4_3.5.1      viridisLite_0.3.0 htmltools_0.3.6   yaml_2.1.19       utf8_1.1.4
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