Introduction to Structural Equation Modeling

R Demonstration Notes

Daniel J. Bauer & Patrick J. Curran

May 10-12, 2021

∫CenterStat

CenterStat.org

Table of Contents

Preface: Instructions for Downloading R, RStudio, and R Packages

Downloading R

One of the nice things about R is that it is free to download and use. Just go to

```
https://www.r-project.org/
```

and click the "download R" link. Then run the installer.

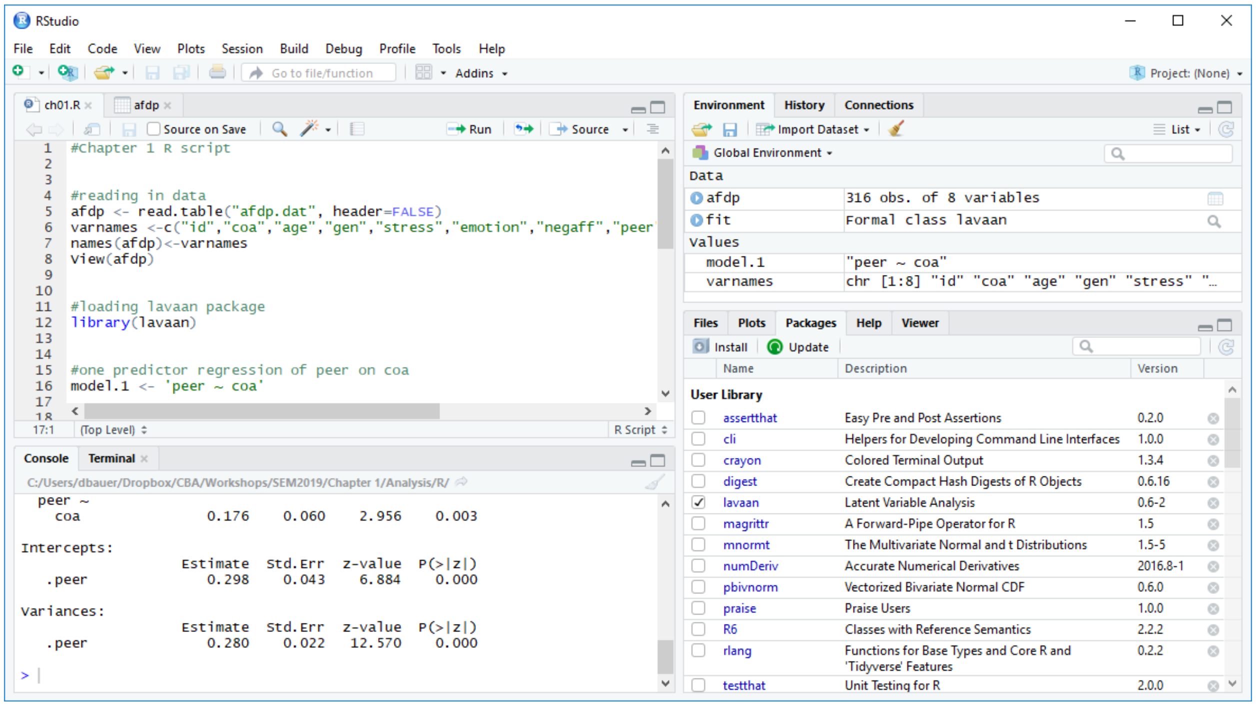
Downloading and Using the RStudio Interface

Another free program, RStudio, provides a convenient interface for using R. The installer for RStudio can be found at

```
https://www.rstudio.com/products/rstudio/download/
```

Select the RStudio Desktop / Open Source License for download and then run the installer.

The default layout for RStudio is shown below



```
#Chapter 1 R script


#reading in data
afdp <- read.table("afdp.dat", header=FALSE)
varnames <-c("id","coa","age","gen","stress","emotion","negaff","peer
names(afdp)<-varnames
View(afdp)


#loading lavaan package
library(lavaan)


#one predictor regression of peer on coa
model.1 <- 'peer ~ coa'
```

```
C:/Users/dbauer/Dropbox/CBA/Workshops/SEM2019/Chapter 1/Analysis/R/
  peer ~
    coa               0.176    0.060    2.956    0.003

Intercepts:
                   Estimate  Std.Err  z-value  P(>|z|)
   .peer              0.298    0.043    6.884    0.000

Variances:
                   Estimate  Std.Err  z-value  P(>|z|)
   .peer              0.280    0.022   12.570    0.000

> |
```

```
Data
afdp        316 obs. of 8 variables
fit         Formal class lavaan
Values
  model.1   "peer ~ coa"
  varnames  chr [1:8] "id" "coa" "age" "gen" "stress" "…
```

	Name	Description	Version
	User Library		
☐	assertthat	Easy Pre and Post Assertions	0.2.0
☐	cli	Helpers for Developing Command Line Interfaces	1.0.0
☐	crayon	Colored Terminal Output	1.3.4
☐	digest	Create Compact Hash Digests of R Objects	0.6.16
✓	lavaan	Latent Variable Analysis	0.6-2
☐	magrittr	A Forward-Pipe Operator for R	1.5
☐	mnormt	The Multivariate Normal and t Distributions	1.5-5
☐	numDeriv	Accurate Numerical Derivatives	2016.8-1
☐	pbivnorm	Vectorized Bivariate Normal CDF	0.6.0
☐	praise	Praise Users	1.0.0
☐	R6	Classes with Reference Semantics	2.2.2
☐	rlang	Functions for Base Types and Core R and 'Tidyverse' Features	0.2.2
☐	testthat	Unit Testing for R	2.0.0

The top left window shows an R script file. Saving R script in a file enables you to share code and re-run analyses quickly. You can highlight individual lines or blocks of lines and click "Run" to submit them to R and obtain the results.

The bottom left window shows the output and also displays a command prompt (the >). When you want to execute a function quickly and don't care to save it to an R script, you can simply type it at the command prompt.

The top right window shows the objects currently in working memory. Here we have two data objects, **afdp** (the data file) and **fit** (containing model results). We also have a model syntax object called **model.1** and a vector of variable labels called **varnames**.

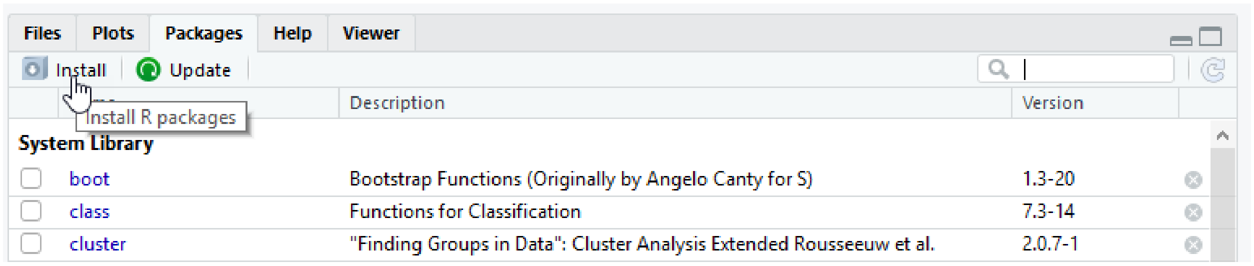
Finally, the bottom right window is useful for a variety of purposes, including viewing and installing packages, displaying plots, etc.

You can rearrange or resize these windows however you like.

Installing and Using Lavaan and other R Packages

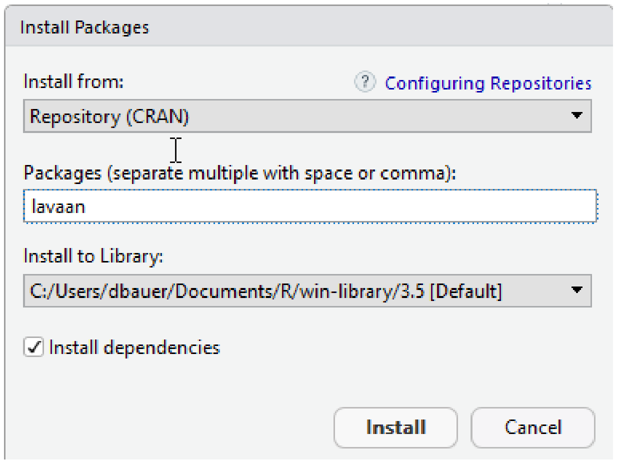
Although R comes with some built in functionality, much of what you can do with R comes through packages contributed by the scientific community. For this workshop, we will be primarily using the **lavaan** (**LA**tent **VA**riable **AN**alaysis) package developed by Yves Rosseel from Ghent University. Although **lavaan** is still considered to be in beta-testing (i.e., experimental, meaning there is no guarantee everything will work as it should), it is widely used and considered to generate accurate results.

There are a couple ways you can download this and other packages in R. Using RStudio, the easiest way to install a package is to click the **packages** tab (in the lower right window under the default configuration) and then click the **install** button, as shown



	Description	Version
System Library		
boot	Bootstrap Functions (Originally by Angelo Canty for S)	1.3-20
class	Functions for Classification	7.3-14
cluster	"Finding Groups in Data": Cluster Analysis Extended Rousseeuw et al.	2.0.7-1

This will bring up the Install Packages dialogue box shown below. Just type "lavaan" on the Packages line, as shown, then click "Install".



Install from: Repository (CRAN)

Packages (separate multiple with space or comma): lavaan

Install to Library: C:/Users/dbauer/Documents/R/win-library/3.5 [Default]

✓ Install dependencies

Alternatively, you can type the following at the command prompt:

```
> install.packages("lavaan", dependencies = TRUE)
```

Regardless of how you install **lavaan**, to actually use the package, you will need to also run the line

```
> library(lavaan)
```

The same steps are used for installing any other package in R (with the exception that some R packages are not provided through the CRAN repository accessed with these commands, in which case they must be downloaded directly from the developer).

Additional packages used in various demonstrations presented in these notes include **plyr**, **semTools**, and **psych**.

If you have questions about **lavaan**, you may wish to consult the discussion group. Go to **`https://groups.google.com/d/forum/lavaan/`** and join the group. Then you can email questions to **`lavaan@googlegroups.com`**.

Chapter 1 Introduction, Background, and Multiple Regression

Multiple Regression Analysis of Deviant Peer Affiliations

The data for this demonstration were provided by Dr. Chassin from the Adolescent and Family Development Project, housed at Arizona State University. ***Note that these data were generously provided for strictly pedagogical purposes and should not be used for any other purposes beyond this workshop.*** The sample includes 316 adolescents, between 10-16 years of age. The study was designed to assess the association between parental alcoholism and adolescent substance use and psychopathology. The data are in the text file **`afdp.dat`** and the accompanying R script is in the **`ch01.R`** file. The variables in the data set that we will use are

`peer`	adolescent report on peer substance use and peer tolerance of use
`coa`	parent report of alcoholism diagnosis where 0=non-alcoholic and 1=alcoholic
`gen`	gender where 0=girl and 1=boy
`age`	age measured in years at assessment
`stress`	self report measure of uncontrollable negative life stressful events
`emotion`	self report measure of temperamental emotional expressiveness
`negaff`	self report measure of depression and anxiety

Reading in the Data

To run our analyses in R, we must first load the data. The first five rows of the **`afdp.dat`** data file (for the first five participants), look like this:

```
1 1 14 0 2.35 1.37 4.4 0.49
2 1 12 0 0.55 1.46 2.34 0
3 1 14 1 2.37 2.12 2.11 1.73
4 1 15 1 1.14 2.83 2.6 1.86
5 1 12 1 1.37 2.11 2.04 0.36
```

The data is in free text format, meaning there are not set column positions for each variable. Instead, variable values are separated only by a space. With this kind of data format, we can use the **`read.table`** function to bring the data into R:

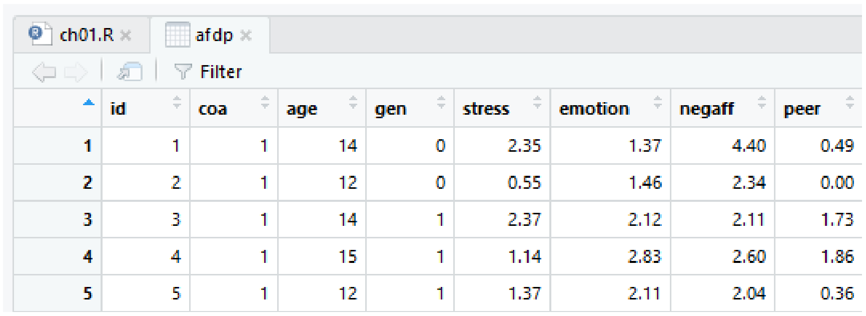
```
afdp <- read.table("afdp.dat", header=FALSE)
varnames <-c("id","coa","age","gen","stress","emotion","negaff","peer")
names(afdp)<-varnames
View(afdp)
```

Note that because we have not specified a full file path (e.g., "C:\Users\dbauer\CBA\SEM\R\afdp.dat"), R will look for **`afdp.dat`** in the current working directory. You can see which directory this is by typing **`getwd()`** at the prompt. You can also reset the working directory by running **`setwd("<new path>")`** or, within RStudio, by clicking **`Session -> Set Working Directory`**. We usually choose to set the working directory to the source file location, meaning the folder within which we have saved our R script file.

The **header** argument of the **read.table** function is set to **FALSE** here to indicate that there are no variable names at the top of the data file. If the first row of the data file included variable names then we would instead set this to **header=TRUE**. Because there are no names for the variables, they will initially have the default names **V1**, **V2**, **V3**, etc.

The next two lines of the script assign labels that are more informative to our variables. First, we define a vector, **varnames**, to hold the variable labels. Here we use the **c** function (for "combine") to put all the labels into one vector. Then we use the **names** function to replace the default variable labels with these new, more useful labels.

Finally, the line **View(afdp)** requests that the data be presented for viewing in spreadsheet form, as shown below.

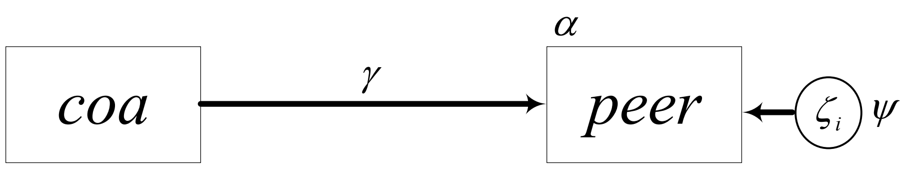


	id	coa	age	gen	stress	emotion	negaff	peer
1	1	1	14	0	2.35	1.37	4.40	0.49
2	2	1	12	0	0.55	1.46	2.34	0.00
3	3	1	14	1	2.37	2.12	2.11	1.73
4	4	1	15	1	1.14	2.83	2.60	1.86
5	5	1	12	1	1.37	2.11	2.04	0.36

We are now ready to run our analyses.

Single Predictor Regression[1]

The single-predictor regression model of COA status predicting deviant peer affiliations is shown in the diagram below:



The model is of the form $peer_i = \alpha + \gamma coa_i + \zeta_i$ where $peer_i$ is an individual's report of their level of association with deviant peers, coa_i is an adolescent's parent report of parent alcoholism status, α represents mean association with deviant peers for children of non-alcoholics (i.e., where $coa_i = 0$), and γ is the expected increase in deviant peer associations for children of alcoholics (i.e. a one unit increase in coa_i). We assume that both **coa** and **peer** contain no measurement error, that $\zeta_i \sim N(0,\psi)$ for all individuals i, and that ζ_i and coa_i are uncorrelated.

[1] The initial model building procedure presented in Chapter 1 of the lecture notes used OLS estimation in traditional regression whereas here we use ML as a way of introducing the SEM procedure in R. The results are virtually identical.

We will fit this regression model using the lavaan package, which we load with the library function as shown:

```
library(lavaan)
```

Under other circumstances, we would use a dedicated regression package to fit such a model, but our intent here is to gain familiarity with how to specify structural equation models within lavaan, starting with the very simple single-predictor regression model.

First, we need to create what's called a model syntax object. The syntax for specifying models in lavaan is quite straightforward and we will show many of the options as we proceed through the demonstrations in this book. For this simple model, we only require a single line:

```
model.1 <- 'peer ~ coa'
```

Here, we have defined the model syntax object **`model.1`**, in which we have specified that **`peer`** is predicted by **`coa`** using the regression operator **~**. That is, the line **`peer ~ coa`** signifies that **`peer`** is regressed on **`coa`**. In general, whatever variable is to the left of **~** is the dependent variable and whatever variable(s) are to the right of **~** are the predictor(s).

We now fit the model using the **`sem`** function, placing the results into the data object **`fit`**. Note that we include the **`meanstructure`** argument with the **`sem`** function so that we will obtain an estimate of the regression intercept. Last, we use the **`summary`** function here to display the primary output.

```
fit <- sem(model.1, data=afdp, meanstructure=TRUE)
summary(fit)
```

We now consider the output produced by the **`summary`** function. First, we obtain some basic information about the model estimation:

```
lavaan 0.6-2 ended normally after 11 iterations

  Optimization method                           NLMINB
  Number of free parameters                          3

  Number of observations                           316

  Estimator                                         ML
  Model Fit Test Statistic                       0.000
  Degrees of freedom                                 0
  Minimum Function Value               0.0000000000000
```

This shows us that we have 316 cases in our sample data and three parameters that we are estimating. Additionally, we are using **`ML`** (maximum likelihood) estimation with the **`nlminb`** optimizer (this is a built-in optimizer in R for finding the minimum of a function).

It is worth pausing here to note that lavaan counts parameters differently than we described in lecture. For this model, we would normally count five parameters, the mean and variance of **`COA`**, the intercept and slope of the regression of **`Peer`** on **`COA`**, and the residual variance of **`Peer`**. But lavaan does not count the mean or variance of the predictor, **`COA`**, as parameters of the model. Nor does it count covariances among predictors (though there are no such covariances in the current model) as free parameters. Fortunately, lavaan also does not count these parameters when determining the number of observed moments, so the degrees of freedom for the test statistic work out regardless (e.g., here it neither counts the mean and variance of COA as observed moments nor does it count them as estimated moments, leaving a net difference of zero when calculating the degrees of freedom).

This output also provides some information about model fit. Multiple regression models are just identified (i.e., every piece of information provided by the sample is 'used up' to estimate model parameters so that no degrees of freedom remain). Therefore, the model fits the data perfectly and it is not worthwhile to interpret the test statistic (this and other fit indices will be discussed in later sections).

The estimates for the model are shown next:

```
Parameter Estimates:

  Information                                 Expected
  Information saturated (h1) model          Structured
  Standard Errors                             Standard

Regressions:
                   Estimate  Std.Err  z-value  P(>|z|)
  peer ~
    coa               0.176    0.060    2.956    0.003

Intercepts:
                   Estimate  Std.Err  z-value  P(>|z|)
   .peer              0.298    0.043    6.884    0.000

Variances:
                   Estimate  Std.Err  z-value  P(>|z|)
   .peer              0.280    0.022   12.570    0.000
```

Recall that our model is

$$peer_i = \alpha + \gamma coa_i + \zeta_i$$

The output is subdivided into three parts, regressions, intercepts, and variances. In the **`Regressions`** section, the **`peer ~ coa`** coefficient is the slope parameter estimate $\hat{\gamma}$. In the **`Intercepts`** section, the coefficient listed for **`.peer`** is the intercept $\hat{\alpha}$. Finally, in the Variances section, the coefficient listed for .peer is the represents represents $\hat{\psi}$, the estimated variance of ζ_i (i.e., residual variance). The **`Estimate`** column lists is the ML point estimate of each parameter. The **`Std.Err`** column gives the standard error for each estimate (where these are computed using the expected information matrix, as noted above). Next, the **`z-value`** column reports the Wald z-statistic for the null hypothesis test that the parameter is significantly different from zero in the population, and the **`P(>|z|)`** column reports the p-value associated with this z-statistic.

Here, we see that the average non-COA has a score of .298 on **peer** and the average COA has a score that is .176 units higher than non-COAs on **peer** (.298 + .176 = .474). Both the intercept and slope are significantly different from zero. Finally, the variance in deviant peer association that is not explained by COA status is .280. This indicates that, although COA status is a significant predictor of **peer**, COA status does not fully account for affiliation with peers.

Because **peer** is not on an intrinsically meaningful scale, we cannot easily interpret the differences among the regression parameters or residual variances. To better interpret these results, we can request standardized estimates. Within lavaan, several methods of standardization are available within the **summary** function. The first type, obtained by including **standardized=TRUE**, is the typical fully standardized solution. In this case, both the independent and dependent variables are standardized to have a variance of 1 (note that lavaan does not, however, also make the means 0, as one might expect). We can see this by running the following line from the R script:

```
summary(fit, standardized=TRUE)
```

The relevant results are shown here:

```
Regressions:
                   Estimate  Std.Err  z-value  P(>|z|)   Std.lv  Std.all
  peer ~
    coa               0.176    0.060    2.956    0.003    0.176    0.164

Intercepts:
                   Estimate  Std.Err  z-value  P(>|z|)   Std.lv  Std.all
   .peer              0.298    0.043    6.884    0.000    0.298    0.554

Variances:
                   Estimate  Std.Err  z-value  P(>|z|)   Std.lv  Std.all
   .peer              0.280    0.022   12.570    0.000    0.280    0.973
```

The **Std.lv** column refers to a solution in which only the latent variables are standardized and not the observed variables. Since the current model contains no latent variables, this is of little use here. The **Std.all** column contains the fully standardized estimates of interest, in which <u>all</u> variables (observed and latent) are standardized to have a variance of one. Thus, we say that a one standard deviation increase in COA status is associated with a .164 standard deviation increase in deviant peer associations.

It may be more useful to retain the original scaling of **COA** while standardizing **peer**. If we include **std.nox=TRUE** in the **summary** function, as shown below, we will obtain estimates in which the latent variables and endogenous observed variables are standardized but the exogenous observed variables are left in their raw scale. These are commonly known as partially standardized estimates.

```
summary(fit, std.nox=TRUE)
```

The relevant output is shown here:

```
Regressions:
                   Estimate  Std.Err  z-value  P(>|z|)   Std.lv  Std.nox
  peer ~
    coa               0.176    0.060    2.956    0.003    0.176    0.329

Intercepts:
                   Estimate  Std.Err  z-value  P(>|z|)   Std.lv  Std.nox
   .peer              0.298    0.043    6.884    0.000    0.298    0.554

Variances:
                   Estimate  Std.Err  z-value  P(>|z|)   Std.lv  Std.nox
   .peer              0.280    0.022   12.570    0.000    0.280    0.973
```

We can interpret these results by saying that the average COA affiliates with deviant peers about .329 standard deviations more than the average non-COA.

Finally, we can also calculate how much variance is explained in peer by coa by requesting that lavaan output the r-squared statistic:

```
summary(fit, rsquare=TRUE)
```

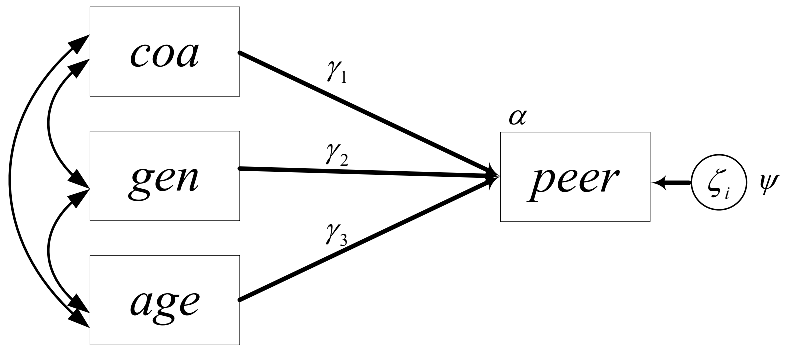
We now obtain a new section of output, shown here:

```
R-Square:
                   Estimate
    peer              0.027
```

`R-Square` is the estimated proportion of variance in **`peer`** that is accounted for by the models (i.e., **`COA`**, the only predictor included in this model). We have explained less than 3% of the total variance in **`peer`** with the **`COA`** predictor. Note, however, that measured variable regression models assume that no measurement error is present. If measurement error is present, the estimated relationship among the variables in the model may be attenuated and the R^2 value will also be underestimated.

Multiple Regression Model with COA Status, Gender, and Age as Predictors

We now expand the model to include gender and age as additional predictors of deviant peer relations as shown in the diagram below. All of the predictors are implicitly allowed to covary with one another.



The model is of the form $peer_i = \alpha + \gamma_1 coa_i + \gamma_2 gen_i + \gamma_3 age_i + \zeta_i$. Each γ is interpreted as the effect of the associated predictor on **peer**, holding the other predictors constant. Unless all predictors are uncorrelated with one another, these estimates will change depending on which other predictors are included in the model. α represents the expected value of **peer** when all predictors are equal to zero.

We assume that none of the variables in our model contain measurement error, that $\zeta_i \sim N(0,\psi)$ for all individuals *i,* that the error variance is constant for all predictors, and that ζ_i is uncorrelated with all of the predictors in the model.

The R script for fitting this model is shown below:

```
model.2 <- 'peer ~ coa + gen + age'

fit <- sem(model.2, data=afdp, meanstructure=TRUE)
summary(fit, std.nox=TRUE, rsquare=TRUE)
```

Here, we have defined a new model syntax object, **model.2**, in which we have specified that **peer** is regression on **coa**, **gen**, and **age**. Note that, again, we use the regression operator **~** to indicate the regression. Now that our model includes multiple predictors, we use the **+** operator in between each predictor.

The results output by the **summary** function (including both partially standardized estimates and r-square) are shown here:

```
lavaan 0.6-2 ended normally after 18 iterations

  Optimization method                           NLMINB
  Number of free parameters                          5

  Number of observations                           316

  Estimator                                         ML
  Model Fit Test Statistic                       0.000
  Degrees of freedom                                 0
  Minimum Function Value               0.0000000000000

Parameter Estimates:

  Information                                 Expected
  Information saturated (h1) model          Structured
  Standard Errors                             Standard

Regressions:
                   Estimate  Std.Err  z-value  P(>|z|)   Std.lv  Std.nox
  peer ~
    coa               0.210    0.054    3.858    0.000    0.210    0.391
    gen              -0.048    0.055   -0.877    0.381   -0.048   -0.089
    age               0.151    0.019    7.993    0.000    0.151    0.281
```

```
Intercepts:
                   Estimate  Std.Err  z-value  P(>|z|)   Std.lv  Std.nox
   .peer             -1.610    0.250   -6.453    0.000   -1.610   -2.999

Variances:
                   Estimate  Std.Err  z-value  P(>|z|)   Std.lv  Std.nox
   .peer              0.232    0.018   12.570    0.000    0.232    0.804

R-Square:
                   Estimate
    peer              0.196
```

We see that **gen** is not a significant predictor of **peer** when **COA** and **age** are also included in the model (*p* = .381). However, **age** is significantly related with **peer** such that older adolescents are more likely to associate with deviant peers. We estimate that a one-year increase in **age** is associated with a .151-increase in deviant peer association ratings. **COA** remains a significant predictor of **peer**, and the regression parameter estimate has not changed much from the single-predictor model to the multiple-predictor model relative to its standard error (i.e., it has increased from .18 to .21). The stability of this coefficient reflects the fact that **COA** is not highly correlated with **gen** or **age**.

The regression coefficients can be interpreted as follows. The slope of **peer** on **COA** is the average effect of being a child of an alcoholic, holding age and gender constant. The slope of **age** is the average effect of **age** on **peer**, holding COA status and gender constant. The intercept is less informative in this model because **age** has not been centered. It now represents the average deviant peer association score for female, non-COAs who are zero years old. This is obviously outside of the range of our data.

To better interpret these results, and to get a sense for the relative contribution of each predictor, we requested the partially standardized solution. We prefer this method of standardization for this example because all three predictors have natural scales. As can be seen in the **Std.nox** column of output, after controlling for **age** and **gender**, COAs affiliate with deviant peers about .391 standard deviation units more than non-COAs. Each additional year of age is associated with a .281 standard deviation increase in self-reported affiliation with deviant peers.

From the R-square output, we can see that the multiple predictor regression model explains more of the variance in peer than the single predictor model. Age and gender account for an additional 17% of the variance in **peer**, over and above COA status. Still, approximately 80% of the variance in **peer** remains unexplained by the variables in our model.

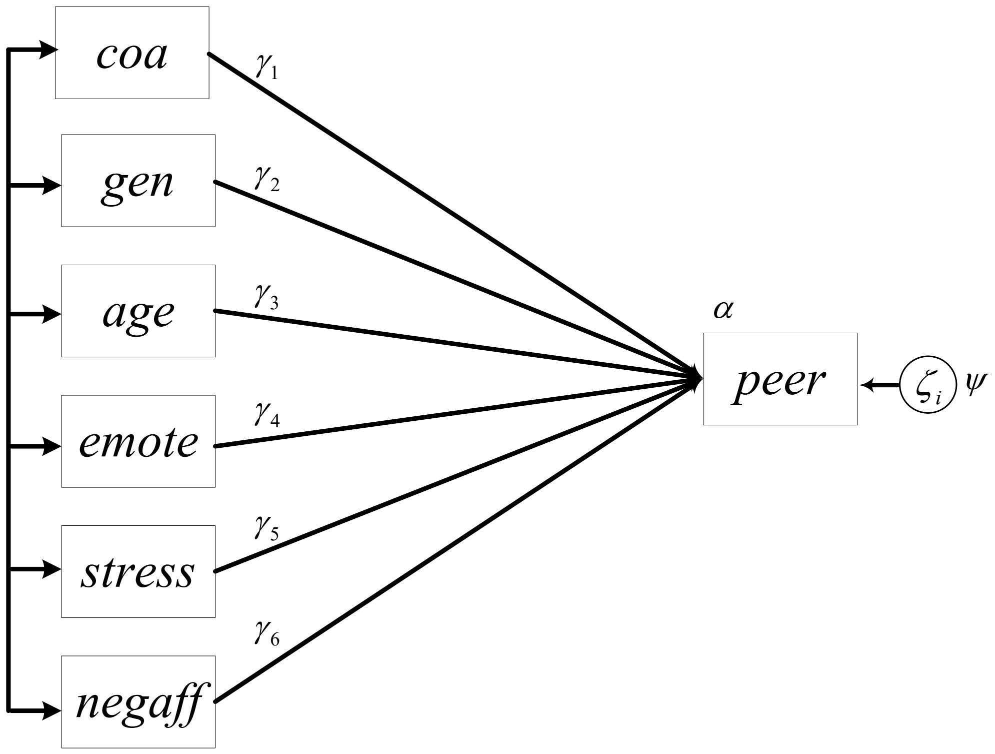
Multiple Regression Model with COA Status, Gender, Age, Stress, Emotion, and Negative Affect as Predictors

To see if we can explain more of the variance in deviant peer associations, we expand the model to include **`stress`**, **`emotion`**, and **`negaff`**, while retaining **`COA`**, **`gen`**, and **`age`**.

The model is now

$$peer_i = \alpha + \gamma_1 coa_i + \gamma_2 gen_i + \gamma_3 age_i + \gamma_4 emote_i + \gamma_5 stress_i + \gamma_6 negaff_i + \zeta_i$$

with the same assumptions as before. Although **`gen`** was not a significant predictor of deviant peer relations in the last model, we do not exclude it from this model because it may covary with the new predictors in such a way that it is important to include it as a control variable in the model. The full model is shown in the diagram.



The R script for fitting this model is shown below:

```
model.3 <- 'peer ~ coa + gen + age + emotion + stress + negaff'

fit <- sem(model.3, data=afdp, meanstructure=TRUE)
summary(fit, standardized=TRUE, rsquare=TRUE)
summary(fit, std.nox=TRUE, rsquare=TRUE)
```

As before, we simply defined a new model syntax object, **`model.3`**, which includes the new predictors of **`peer`**. In this case we requested both the fully standardized and partially standardized solutions in two calls of the **`summary`** function. For **`coa`**, **`gen`**, and **`age`**, the partially standardized coefficients are most interpretable. In contrast, **`emotion`**, **`stress`**, and

negaff do not have intrinsically meaningful scales, so the fully standardized estimates are better. Thus, we consider both. Additionally, by examining the fully standardized estimates across the full set of predictors we can gauge the relative contributions of the predictors, despite the fact that they were originally on quite different scales.

Here, we show the output from the first summary function requesting fully standardized effects:

```
lavaan 0.6-2 ended normally after 22 iterations

  Optimization method                           NLMINB
  Number of free parameters                          8

  Number of observations                           316

  Estimator                                         ML
  Model Fit Test Statistic                       0.000
  Degrees of freedom                                 0

Parameter Estimates:

  Information                                 Expected
  Information saturated (h1) model          Structured
  Standard Errors                             Standard

Regressions:
                   Estimate  Std.Err  z-value  P(>|z|)   Std.lv  Std.all
  peer ~
    coa               0.137    0.055    2.492    0.013    0.137    0.127
    gen              -0.027    0.052   -0.509    0.611   -0.027   -0.025
    age               0.140    0.018    7.660    0.000    0.140    0.378
    emotion           0.030    0.058    0.520    0.603    0.030    0.028
    stress            0.111    0.044    2.546    0.011    0.111    0.140
    negaff            0.109    0.030    3.660    0.000    0.109    0.195

Intercepts:
                   Estimate  Std.Err  z-value  P(>|z|)   Std.lv  Std.all
   .peer             -1.934    0.267   -7.233    0.000   -1.934   -3.602

Variances:
                   Estimate  Std.Err  z-value  P(>|z|)   Std.lv  Std.all
   .peer              0.210    0.017   12.570    0.000    0.210    0.728

R-Square:
                   Estimate
    peer              0.272
```

We see that **gen** is still not a significant predictor of **peer** when other predictors are included in the model (*p* = .611), but that **COA** and **age** remain statistically significant even though the value of their regression coefficients have changed. Importantly, the effect of **COA** on **peer** is not as strong after controlling for **emotion**, **stress**, and **negaff**, indicating that these variables are somewhat related to one another. These new variables could potentially mediate the relationship between **COA** and **peer**; we will later explore this possibility with a path analysis model. Of the new variables, it appears that stressful life events and negative affect are significant predictors of association with deviant peers, but self-reported emotional expressiveness is not significantly related to deviant peer association, after controlling for **age**, **gen**, **stress**, **negaff**, and **COA**.

Examining the standardized estimates in the **Std.all** column, we see that **age** is the strongest relative predictor of **peer**, followed by **negaff**, **stress**, **COA**, **emotion**, and then **gen**. However, determining the "strongest" predictors is always a tricky endeavor, particularly given that **gen** and **COA** are binary predictors for which fully standardized effects are less useful.

We can examine the results from the second **summary** call to see the partially standardized estimates.

```
Regressions:
                   Estimate  Std.Err  z-value  P(>|z|)   Std.lv  Std.nox
  peer ~
    coa               0.137    0.055    2.492    0.013    0.137    0.255
    gen              -0.027    0.052   -0.509    0.611   -0.027   -0.049
    age               0.140    0.018    7.660    0.000    0.140    0.262
    emotion           0.030    0.058    0.520    0.603    0.030    0.056
    stress            0.111    0.044    2.546    0.011    0.111    0.206
    negaff            0.109    0.030    3.660    0.000    0.109    0.204

Intercepts:
                   Estimate  Std.Err  z-value  P(>|z|)   Std.lv  Std.nox
   .peer             -1.934    0.267   -7.233    0.000   -1.934   -3.602

Variances:
                   Estimate  Std.Err  z-value  P(>|z|)   Std.lv  Std.nox
   .peer              0.210    0.017   12.570    0.000    0.210    0.728

R-Square:
                   Estimate
    peer              0.272
```

Finally, examining the R-square output, we see that the final model explains about 27% of the total variance in **peer**.

Chapter 2
Path Analysis: Part I

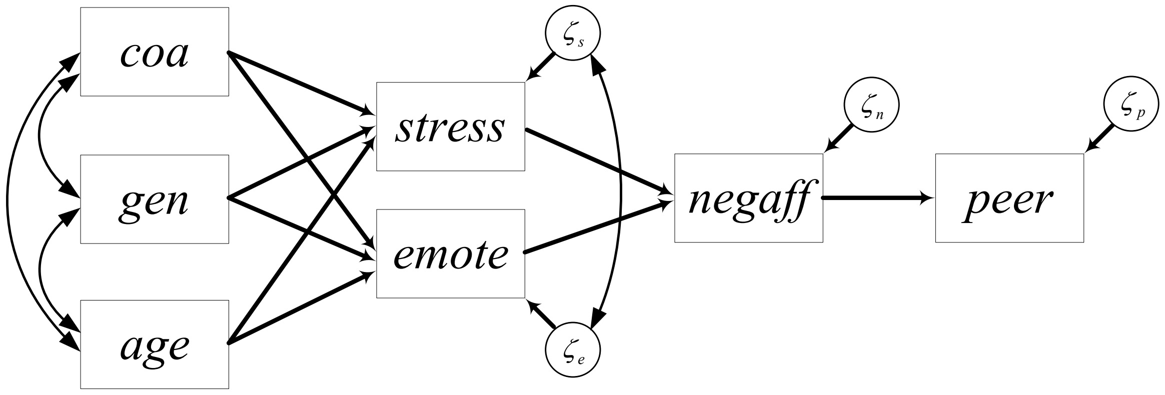
Path Analysis with Deviant Peer Affiliation Data

The data for this demonstration were provided by Dr. Laurie Chassin from the Adolescent and Family Development Project, housed at Arizona State University. ***Note that these data were generously provided for strictly pedagogical purposes and should not be used for any other purposes beyond this workshop.*** The sample includes 316 adolescents, between 10-16 years of age. The study was designed to assess the association between parental alcoholism and adolescent substance use and psychopathology. The data are in the text file **`afdp.dat`** and the accompanying R script is in the **`ch02.R`** file. The variables in the data set that we will use are

`peer`	adolescent report on peer substance use and peer tolerance of use
`coa`	parent report of alcoholism diagnosis where 0=non-alcoholic and 1=alcoholic
`gen`	gender where 0=girl and 1=boy
`age`	age measured in years at assessment
`stress`	self report measure of uncontrollable negative life stressful events
`emotion`	self report measure of temperamental emotional expressiveness
`negaff`	self report measure of depression and anxiety

Path Analysis of Theoretical Peer Affiliation Model

Theory dictates that alcoholic parents increase the number of stressful life events that their children experience, leading to an increase in child negative affect. Further, children of alcoholics are hypothesized to have higher levels of emotionality, leading to more negative affect. Negative affect is thought to be related to higher rates of affiliation with deviant peers. Stressful life events and emotionality should covary, but we hypothesize no directional relation among these variables. We allow **`age`** and **`gen`** to predict **`stress`** and **`emotion`**, and we allow all exogenous characteristics (**`coa`**, **`gen`**, and **`age`**) to covary.



The model is of the form

$$\begin{pmatrix} y_{stress_i} \\ y_{emote_i} \\ y_{negaff_i} \\ y_{peer_i} \end{pmatrix} = \begin{pmatrix} \alpha_{1i} \\ \alpha_{2i} \\ \alpha_{3i} \\ \alpha_{4i} \end{pmatrix} + \begin{pmatrix} \gamma_{11} & \gamma_{12} & \gamma_{13} \\ \gamma_{21} & \gamma_{22} & \gamma_{23} \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix} \begin{pmatrix} coa_i \\ gen_i \\ age_i \end{pmatrix} + \begin{pmatrix} 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ \beta_{31} & \beta_{32} & 0 & 0 \\ 0 & 0 & \beta_{43} & 0 \end{pmatrix} \begin{pmatrix} stress_i \\ emote_i \\ negaff_i \\ peer_i \end{pmatrix} + \begin{pmatrix} \zeta_{1i} \\ \zeta_{2i} \\ \zeta_{3i} \\ \zeta_{4i} \end{pmatrix} \text{where}$$

$$COV(\zeta_i) = \begin{pmatrix} \psi_{11} & & & \\ \psi_{21} & \psi_{22} & & \\ 0 & 0 & \psi_{33} & \\ 0 & 0 & 0 & \psi_{44} \end{pmatrix}$$

The R script that fits this model with the lavaan package is shown below (note that this assumes the data file is in the same directory as the R script file, i.e., the source directory):

```
#reading in data
afdp <- read.table("afdp.dat", header=FALSE)
varnames <-c("id","coa","age","gen","stress","emotion","negaff","peer")
names(afdp)<-varnames

#loading lavaan package
library(lavaan)

#fitting path analysis model
pathmodel.1 <- '
              #regressions
              stress ~ coa + gen + age
              emotion ~ coa + gen + age
              negaff ~ stress + emotion
              peer ~ negaff

              #covariances
              stress ~~ emotion
              '
fit <- sem(pathmodel.1, data=afdp, meanstructure=TRUE)
summary(fit, standardized=TRUE, rsquare=TRUE)
summary(fit, std.nox=TRUE, rsquare=TRUE)

fitted(fit)
resid(fit, type="raw")
resid(fit, type="normalized")
```

We have seen most of this code in Chapter 1, so here we will focus only on what's new in the definition of the model syntax object. Note that some lines in this script, those that are preceded with a **#** character, are comments and are not part of the actual syntax.

In Chapter 1, **`peer`** was the only dependent variable and was regressed on all of the other variables in the model. Here, we have multiple endogenous variables and each has its own regression equation, as specified in the section of the syntax beginning with the **#regressions** comment. Thus, we indicate that there are direct effects of **coa**, **gen**, and **age** on **stress** with the line **stress ~ coa + gen + age**. In each subsequent line, we indicate the direct effects of the predictors for each endogenous variable in the model, ending with **peer** being regressed on **negaff**.

As a default, lavaan allows all exogenous variables to covary but it fixes the residual covariances among endogenous variables to zero. The residual terms of **stress** and **emotion** are freed to covary within the section of the code marked **#covariances**. To designate a covariance (or variance) we use the **~~** operator. Thus, **stress ~~ emotion** tells lavaan to include a residual covariance for **stress** and **emotion**.

In the two **summary** function calls we requested standardized estimates and partially standardized estimates, respectively, to aid interpretation of the results. The final three lines request the model-implied covariance matrix (**fitted(fit)**) and the raw and standardized residual matrices (**resid(fit, type="raw")** and **resid(fit, type="normalized")**, respectively). These residuals represent the differences between the observed covariance matrix and the matrix that is implied by the structure of the model.

Typically, we would evaluate model fit prior to interpreting parameter estimates. For pedagogical purposes, however, we will put aside a discussion of model fit until Chapter 3 and move directly to parameter estimates for our model. Here we see the raw and fully standardized estimates produced by the first **summary** function call:

```
Regressions:
                   Estimate  Std.Err  z-value  P(>|z|)   Std.lv  Std.all
  stress ~
    coa               0.451    0.072    6.223    0.000    0.451    0.331
    gen              -0.016    0.073   -0.215    0.830   -0.016   -0.011
    age               0.002    0.025    0.078    0.938    0.002    0.004
  emotion ~
    coa               0.110    0.056    1.963    0.050    0.110    0.110
    gen              -0.048    0.056   -0.843    0.399   -0.048   -0.047
    age              -0.027    0.019   -1.374    0.170   -0.027   -0.077
  negaff ~
    stress            0.246    0.078    3.134    0.002    0.246    0.175
    emotion           0.553    0.106    5.206    0.000    0.553    0.290
  peer ~
    negaff            0.176    0.030    5.892    0.000    0.176    0.315
Covariances:
                   Estimate  Std.Err  z-value  P(>|z|)   Std.lv  Std.all
 .stress ~~
   .emotion           0.112    0.019    5.896    0.000    0.112    0.352
Intercepts:
                   Estimate  Std.Err  z-value  P(>|z|)   Std.lv  Std.all
   .stress            0.687    0.333    2.066    0.039    0.687    1.010
   .emotion           2.341    0.258    9.088    0.000    2.341    4.663
   .negaff            1.527    0.207    7.373    0.000    1.527    1.594
   .peer             -0.118    0.091   -1.298    0.194   -0.118   -0.220
```

```
Variances:
                   Estimate  Std.Err  z-value  P(>|z|)   Std.lv  Std.all
   .stress            0.412    0.033   12.570    0.000    0.412    0.890
   .emotion           0.247    0.020   12.570    0.000    0.247    0.979
   .negaff            0.778    0.062   12.570    0.000    0.778    0.848
   .peer              0.260    0.021   12.570    0.000    0.260    0.901

R-Square:
                   Estimate
    stress            0.110
    emotion           0.021
    negaff            0.152
    peer              0.099
```

The second summary function call reproduces these same raw parameter estimates but now computes the partially standardized estimates:

```
Regressions:
                   Estimate  Std.Err  z-value  P(>|z|)   Std.lv  Std.nox
  stress ~
    coa               0.451    0.072    6.223    0.000    0.451    0.663
    gen              -0.016    0.073   -0.215    0.830   -0.016   -0.023
    age               0.002    0.025    0.078    0.938    0.002    0.003
  emotion ~
    coa               0.110    0.056    1.963    0.050    0.110    0.219
    gen              -0.048    0.056   -0.843    0.399   -0.048   -0.095
    age              -0.027    0.019   -1.374    0.170   -0.027   -0.053
  negaff ~
    stress            0.246    0.078    3.134    0.002    0.246    0.175
    emotion           0.553    0.106    5.206    0.000    0.553    0.290
  peer ~
    negaff            0.176    0.030    5.892    0.000    0.176    0.315

Covariances:
                   Estimate  Std.Err  z-value  P(>|z|)   Std.lv  Std.nox
 .stress ~~
   .emotion           0.112    0.019    5.896    0.000    0.112    0.352

Intercepts:
                   Estimate  Std.Err  z-value  P(>|z|)   Std.lv  Std.nox
   .stress            0.687    0.333    2.066    0.039    0.687    1.010
   .emotion           2.341    0.258    9.088    0.000    2.341    4.663
   .negaff            1.527    0.207    7.373    0.000    1.527    1.594
   .peer             -0.118    0.091   -1.298    0.194   -0.118   -0.220

Variances:
                   Estimate  Std.Err  z-value  P(>|z|)   Std.lv  Std.nox
   .stress            0.412    0.033   12.570    0.000    0.412    0.890
   .emotion           0.247    0.020   12.570    0.000    0.247    0.979
   .negaff            0.778    0.062   12.570    0.000    0.778    0.848
   .peer              0.260    0.021   12.570    0.000    0.260    0.901
```

```
R-Square:
                   Estimate
    stress            0.110
    emotion           0.021
    negaff            0.152
    peer              0.099
```

We see that the hypothesized pathways to deviant peer affiliation do contain statistically significant components. To aid in interpretation, standardized values are included in the model path diagram, shown below. We report fully standardized effects (from `Std.all` column generated by the first `summary` function call) except for **`coa`**, **`gen`**, and **`age`**, for which we report partially standardized effects (from `Std.nox` column generated by the second `summary` function call). Recall that only the outcome variables are standardized in computing the partially standardized effects, which makes them particularly useful for examining the effects of coding variables (e.g., **`coa`** and **`gen`**) or predictors with natural metrics (e.g., **`age`**).

These partially standardized parameter estimates represent the expected change in standard deviation units in y given a one unit increase in x. By comparison, the fully standardized estimates are computed by standardizing both the predictors and the outcome variables so that parameter estimates represent the expected change in standard deviation units in y given a one standard deviation increase in x. These are most useful for interpreting effects when neither predictors nor outcomes have natural scales and when gauging relative effect sizes across predictors on different scales. For covariance parameters, fully standardized estimates can be interpreted as correlations.

From the `R-Square` section of output, we can also see that only a modest amount of the total variance in any of these variables has been explained by the model.

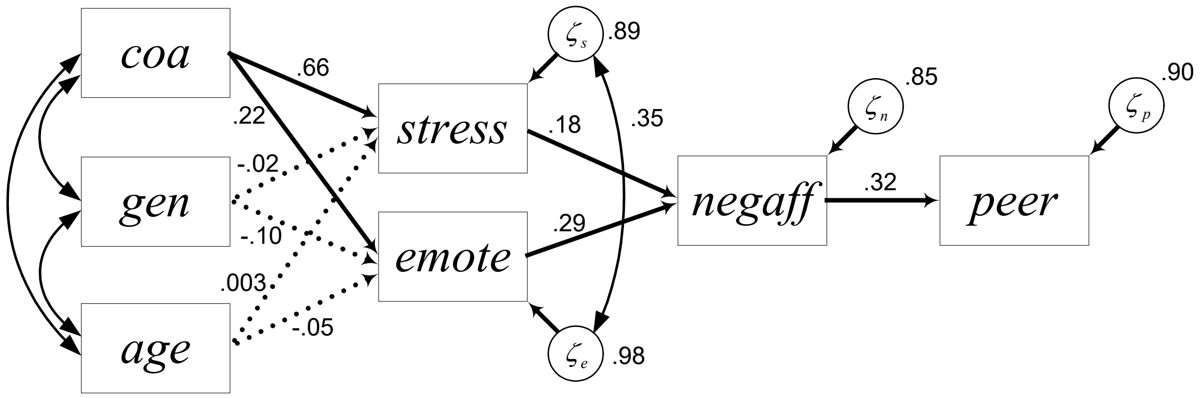
Finally, the model-implied covariance matrix and the raw and standardized residuals between the observed and model-implied covariance matrices are:

```
> fitted(fit)
$`cov`
        stress emotin negaff peer   coa    gen    age   
stress   0.463                                          
emotion  0.125  0.252                                   
negaff   0.183  0.170  0.917                            
peer     0.032  0.030  0.162  0.288                     
coa      0.112  0.029  0.044  0.008  0.249              
gen     -0.003 -0.010 -0.006 -0.001  0.002  0.249       
age     -0.019 -0.059 -0.037 -0.007 -0.055 -0.070  2.095

$mean
 stress emotion  negaff    peer     coa     gen     age 
  0.941   2.034   2.883   0.390   0.525   0.538  12.718 
```

```
> resid(fit, type="raw")
$`type`
[1] "raw"

$cov
        stress emotin negaff peer   coa    gen    age
stress   0.000
emotion  0.000  0.000
negaff   0.000  0.000  0.000
peer     0.055  0.006  0.000  0.000
coa      0.000  0.000 -0.004  0.036  0.000
gen      0.000  0.000 -0.042 -0.021  0.000  0.000
age      0.000  0.000  0.247  0.314  0.000  0.000  0.000

$mean
 stress emotion  negaff    peer     coa     gen     age
      0       0       0       0       0       0       0

> resid(fit, type="normalized")
$`type`
[1] "normalized"

$cov
        stress emotin negaff peer   coa    gen    age
stress   0.000
emotion  0.000  0.000
negaff   0.000  0.000  0.000
peer     2.657  0.395  0.000  0.000
coa      0.000  0.000 -0.163  2.685  0.000
gen      0.000  0.000 -1.580 -1.548  0.000  0.000
age      0.000  0.000  3.229  8.015  0.000  0.000  0.000

$mean
 stress emotion  negaff    peer     coa     gen     age
      0       0       0       0       0       0       0
```

The normalized residuals are rescaled to follow a standard normal distribution and values exceeding plus or minus two are often taken as potentially meaningful in magnitude. The normalized residuals for this model suggest that the hypothesized structure is doing a poor job in reproducing the observed covariances between several variables, most notably between *age* and *peer*, between *age* and *negaff*, and between *stress* and *peer*. We will explore methods for more formally assessing overall model fit in the next chapter.

Finally, below is a path diagram denoting all estimated parameters. Significant effects are denoted with solid lines (*p*<.05) and non-significant with dashed lines. Partially standardized effects are presented for COA, gender, and age and fully standardized are presented for all other predictors.



Chapter 3
Path Analysis: Part II

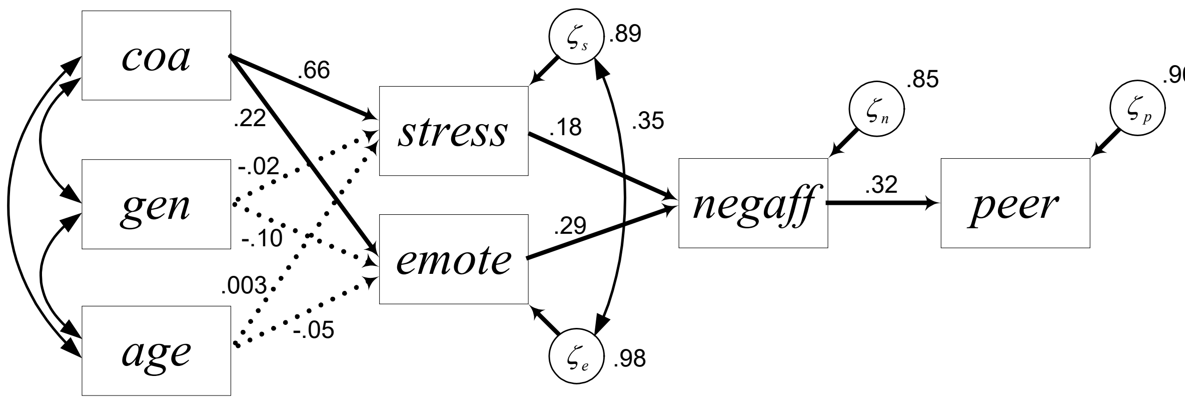
Path Analysis with Deviant Peer Affiliation Data

The data for this demonstration were provided by Dr. Laurie Chassin from the Adolescent and Family Development Project, housed at Arizona State University. ***Note that these data were generously provided for strictly pedagogical purposes and should not be used for any other purposes beyond this workshop.*** The sample includes 316 adolescents, between 10-16 years of age. The study was designed to assess the association between parental alcoholism and adolescent substance use and psychopathology. The data are in the text file **`afdp.dat`** and the accompanying R script is in the **`ch03.R`** file. The variables in the data set that we will use are

`peer`	adolescent report on peer substance use and peer tolerance of use
`coa`	parent report of alcoholism diagnosis where 0=non-alcoholic and 1=alcoholic
`gen`	gender where 0=girl and 1=boy
`age`	age measured in years at assessment
`stress`	self report measure of uncontrollable negative life stressful events
`emotion`	self report measure of temperamental emotional expressiveness
`negaff`	self report measure of depression and anxiety

Theoretical Model

We tested our hypothesized theoretical model of pathways to deviant peer affiliation for COAs and non-COAs. The original model is illustrated below with standardized parameter estimates overlaid on the path diagram (regression paths from **`coa`**, **`gen`**, **`age`** are partially standardized; all other estimates are fully standardized):



The R script for fitting this model was shown in Chapter 2 and is included here again for reference.

```
pathmodel.1 <-'
              #regressions
              stress ~ coa + gen + age
              emotion ~ coa + gen + age
              negaff ~ stress + emotion
              peer ~ negaff

              #covariances
              stress ~~ emotion
              '
fit.1 <- sem(pathmodel.1, data=afdp, meanstructure=TRUE)
```

The only modification to the script is that the object previously named **`fit`** has been renamed **`fit.1`**, as we will be comparing fit across multiple models in this chapter.

We obtain measures of fit, appropriately enough, by including **`fit.measures=TRUE`** as an argument to the summary function, as shown here:

```
summary(fit.1, fit.measures=TRUE)
```

Although the output includes the parameter estimates, we will focus here only on output related to model fit. Some of this information is already included in the default output header:

```
lavaan 0.6-2 ended normally after 43 iterations

  Optimization method                           NLMINB
  Number of free parameters                         18

  Number of observations                           316

  Estimator                                         ML
  Model Fit Test Statistic                      81.173
  Degrees of freedom                                 8
  P-value (Chi-square)                           0.000
```

Lavaan lists the number of free parameters as 18, but recall that it does not count the means, variances, or covariances of the exogenous predictors (**`coa`**, **`gen`**, and **`age`**) as estimated parameters. The number of free parameters reported by lavaan for this model thus does not equal what we computed by the *t*-rule (27 free parameters, including 3 means, 3 variances, and 3 covariances for **`coa`**, **`gen`**, and **`age`**; 16 + 9 = 27). The *t*-rule still works out to 8 degrees of freedom for the chi-square, however, because the observed means, variances, and covariances of the covariates are also not counted in the number of sample means and variances *k*.

As we can see, the chi square-distributed likelihood ratio test of model fit rejects the null hypothesis that the model fits the data. However, to get a full understanding of model fit we must also consider other fit indices.

The additional output generated by **`fit.measures=TRUE`** is shown below

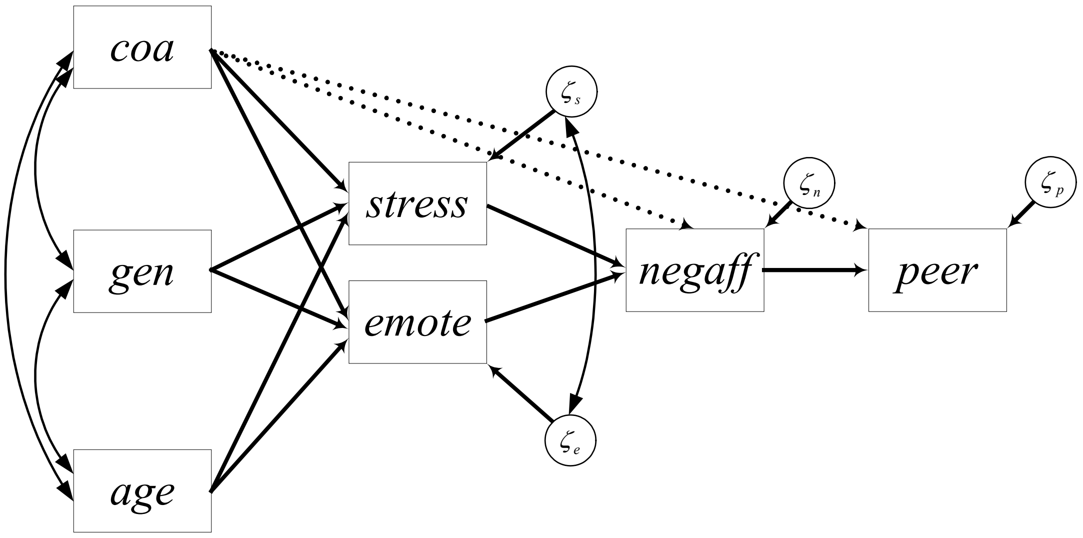
```
Model test baseline model:

  Minimum Function Test Statistic              251.027
  Degrees of freedom                                18
  P-value                                        0.000

User model versus baseline model:

  Comparative Fit Index (CFI)                    0.686
  Tucker-Lewis Index (TLI)                       0.293

Loglikelihood and Information Criteria:

  Loglikelihood user model (H0)              -1158.938
  Loglikelihood unrestricted model (H1)      -1118.351

  Number of free parameters                         18
  Akaike (AIC)                                2353.875
  Bayesian (BIC)                              2421.479
  Sample-size adjusted Bayesian (BIC)         2364.387

Root Mean Square Error of Approximation:

  RMSEA                                          0.170
  90 Percent Confidence Interval          0.138  0.205
  P-value RMSEA <= 0.05                          0.000

Standardized Root Mean Square Residual:

  SRMR                                           0.085
```

In addition to poor model chi-square, the CFI and the TLI are far lower than .9, the standard lower bound for a good-fitting model. Finally, the 90% confidence interval for the RMSEA does not even include .10 at the lower bound, indicating terrible fit. As such, we cannot interpret the obtained parameter estimates with any confidence given the severe misfit of the model.

Modification to Peer Affiliation Model: Likelihood Ratio Test

Since the theoretical model of deviant peer affiliation that was presented in Chapter 2 did not fit the data well, we will consider model modifications to improve our representation of the data. First, theory might suggest that it is an excessively severe restriction to require that the influence of parental alcoholism be conveyed entirely by the mediators. Thus we can allow **`coa`** to directly predict **`negaff`** and **`peer`**, over and above its indirect relationship with these variables via **`stress`** and **`emotion`**.

The new paths are illustrated with dotted lines in the path diagram below.



The model is now of the form:

$$\begin{pmatrix} y_{stress_i} \\ y_{emote_i} \\ y_{negaff_i} \\ y_{peer_i} \end{pmatrix} = \begin{pmatrix} \alpha_{1i} \\ \alpha_{2i} \\ \alpha_{3i} \\ \alpha_{4i} \end{pmatrix} + \begin{pmatrix} \gamma_{11} & \gamma_{12} & \gamma_{13} \\ \gamma_{21} & \gamma_{22} & \gamma_{23} \\ \gamma_{31} & 0 & 0 \\ \gamma_{41} & 0 & 0 \end{pmatrix} \begin{pmatrix} coa_i \\ gen_i \\ age_i \end{pmatrix} + \begin{pmatrix} 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ \beta_{31} & \beta_{32} & 0 & 0 \\ 0 & 0 & \beta_{43} & 0 \end{pmatrix} \begin{pmatrix} stress_i \\ emote_i \\ negaff_i \\ peer_i \end{pmatrix} + \begin{pmatrix} \zeta_{1i} \\ \zeta_{2i} \\ \zeta_{3i} \\ \zeta_{4i} \end{pmatrix}$$

where

$$COV(\zeta_i) = \begin{pmatrix} \psi_{11} & & & \\ \psi_{21} & \psi_{22} & & \\ 0 & 0 & \psi_{33} & \\ 0 & 0 & 0 & \psi_{44} \end{pmatrix}$$

The R script for this model is shown below:

```
pathmodel.2 <- '
               #regressions
               stress ~ coa + gen + age
               emotion ~ coa + gen + age
               negaff ~ stress + emotion + coa
               peer ~ negaff + coa

               #covariances
               stress ~~ emotion
               '
fit.2 <- sem(pathmodel.2, data=afdp, meanstructure=TRUE)
summary(fit.2, fit.measures=TRUE)
```

The only difference from the **pathmodel.1** model syntax object is that **coa** is included as a predictor in the lines for **peer** and **negaff**.

Let us now turn to the model fit to determine whether freeing these two regression parameters has led to a significant improvement in model fit.

```
lavaan 0.6-2 ended normally after 47 iterations

  Optimization method                           NLMINB
  Number of free parameters                         20

  Number of observations                           316

  Estimator                                         ML
  Model Fit Test Statistic                      74.321
  Degrees of freedom                                 6
  P-value (Chi-square)                           0.000

Model test baseline model:

  Minimum Function Test Statistic              251.027
  Degrees of freedom                                18
  P-value                                        0.000

User model versus baseline model:

  Comparative Fit Index (CFI)                    0.707
  Tucker-Lewis Index (TLI)                       0.120

Loglikelihood and Information Criteria:

  Loglikelihood user model (H0)              -1155.511
  Loglikelihood unrestricted model (H1)      -1118.351

  Number of free parameters                         20
  Akaike (AIC)                                2351.023
  Bayesian (BIC)                              2426.138
  Sample-size adjusted Bayesian (BIC)         2362.703

Root Mean Square Error of Approximation:

  RMSEA                                          0.190
  90 Percent Confidence Interval          0.153  0.230
  P-value RMSEA <= 0.05                          0.000

Standardized Root Mean Square Residual:

  SRMR                                           0.081
```

The likelihood for the original model (Model A) was $T_A = 81.17$ on 8 degrees of freedom. We have used two addition model parameters for the modified model (Model B), and the likelihood test statistic for this model is 74.32. These models are nested, so we can conduct a Likelihood Ratio Test (LRT) to determine whether Model B fits significantly better than Model A. Lavaan nicely provides a function for conducting the LRT, **`lavTestLRT`**, in which you simply provide the fit objects from Models B and A (in that order, where A is more restricted than B), as shown here for the present example:

```
lavTestLRT(fit.2, fit.1)
```

This generates the output

```
Chi Square Difference Test

      Df    AIC    BIC  Chisq Chisq diff Df diff Pr(>Chisq)
fit.2  6 2351.0 2426.1 74.321
fit.1  8 2353.9 2421.5 81.173     6.8522       2    0.03251 *
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

Thus we have

$$T_\Delta = T_A - T_B = 81.17 - 74.32 = 6.85$$
$$df_\Delta = df_A - df_B = 8 - 6 = 2$$
$$T_\Delta \sim \chi^2(df_\Delta) \rightarrow p = .033$$

Given that $p < .05$, we can reject the null hypothesis that there is no difference in model fit between Model A and Model B. There is thus support for including the two additional paths. However, given that the sample size is rather large and the effect size (gain in model improvement) is rather small, the LRT suggests only a trivial gain in model fit associated with this modification.

Examining relative tests of model fit for this new model, however, we see that the fit is still terrible. Our attempt to modify the model based upon a priori hypotheses has failed to produce an acceptable model.

Modification to Peer Affiliation Model: Modification Indices

Returning to the original hypothesized model, we will take a different approach to model modification. We can request that lavaan suggest changes to our model based on the expected change in model chi-square if a fixed parameter were freed; these are the modification indices (MIs). We can obtain MIs with the **`modindices`** function, as shown here:

```
modindices(fit.1, sort.=TRUE, minimum.value=10)
```

The first argument is the fit/results object generated by lavaan for the model of interest, here **`fit.1`**. The **`sort.`** argument is set to **`TRUE`** so that lavaan will present the largest MIs first. Additionally, the **`minimum.value`** argument is set to suppress printing of any MIs less than 10.

The **minimum.value** argument can be changed to a smaller or larger number, as desired, or omitted entirely to look at all possible MIs.

Model modification indices are shown below:

```
      lhs op    rhs     mi   epc sepc.lv sepc.all sepc.nox
63    age  ~   peer 53.942 1.114   1.114    0.413    0.413
47   peer  ~    age 42.540 0.129   0.129    0.348    0.241
42 negaff  ~    age 11.889 0.119   0.119    0.179    0.124
62    age  ~ negaff 10.877 0.303   0.303    0.201    0.201
```

Here, **lhs** stands for "on the left-hand side of the operator" and **rhs** stands for "on the right-hand side of the operator." The operator, denoted **op**, for these parameters is **~**, indicating these are regression slopes. **mi** denotes the expected improvement in the model chi square test statistic if the modification is accepted. **epc** denotes "expected parameter change (EPC)" and gives the expected parameter value if the modification is implemented (since it is changing from zero). **sepc.lv** re-scales the EPC by standardizing any latent variables in the model, **sepc.all** re-scales the EPC by standardizing all variables (observed and latent), and **sepc.nox** re-scales the EPC by standardizing all variables except exogenous predictors. Here, **sepc.lv** is equivalent to the EPC because there are no latent variables in the model. It can be helpful to rely on standardized EPC values in order to get a sense of the relative magnitude of each potential modification.

Note the overlap in suggested modification indices. This tells us that our original model does not allow for a significant relation between **age** and **negaff** or between **age** and **peer**. These suggestions are not independent from one another; allowing **negaff** to relate directly with **age** would imply an increased correlation between **negaff** and **peer**.

It is more theoretically justifiable to regress **peer** on **age** than to regress **negaff** on **age**; thus, we will proceed with this model modification, as shown in the code below.

```
pathmodel.3 <-'
              #regressions
              stress ~ coa + gen + age
              emotion ~ coa + gen + age
              negaff ~ stress + emotion
              peer ~ negaff + age

              #covariances
              stress ~~ emotion
              '
fit.3 <- sem(pathmodel.3, data=afdp, meanstructure=TRUE)
summary(fit.3, fit.measures=TRUE)
```

Relative to the model syntax object for our first model, all we have done is add **age** as a predictor to the right of the **~** statement for **peer**.

We obtain the following model fit:

```
lavaan 0.6-2 ended normally after 49 iterations

  Optimization method                           NLMINB
  Number of free parameters                         19

  Number of observations                           316

  Estimator                                         ML
  Model Fit Test Statistic                      34.368
  Degrees of freedom                                 7
  P-value (Chi-square)                           0.000

Model test baseline model:

  Minimum Function Test Statistic              251.027
  Degrees of freedom                                18
  P-value                                        0.000

User model versus baseline model:

  Comparative Fit Index (CFI)                    0.883
  Tucker-Lewis Index (TLI)                       0.698

Loglikelihood and Information Criteria:

  Loglikelihood user model (H0)              -1135.535
  Loglikelihood unrestricted model (H1)      -1118.351

  Number of free parameters                         19
  Akaike (AIC)                                2309.070
  Bayesian (BIC)                              2380.429
  Sample-size adjusted Bayesian (BIC)         2320.166

Root Mean Square Error of Approximation:

  RMSEA                                          0.111
  90 Percent Confidence Interval          0.076  0.150
  P-value RMSEA <= 0.05                          0.003

Standardized Root Mean Square Residual:

  SRMR                                           0.057
```

We can statistically compare the fit of this model with that of the original model using a LRT:

```
lavTestLRT(fit.3, fit.1)
```

```
Chi Square Difference Test

      Df    AIC    BIC  Chisq Chisq diff Df diff Pr(>Chisq)
fit.3  7 2309.1 2380.4 34.368
fit.1  8 2353.9 2421.5 81.173     46.805       1  7.841e-12 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

In other words, we have

$$T_{\Delta} = T_A - T_B = 81.17 - 34.37 = 46.80$$
$$df_{\Delta} = df_A - df_B = 8 - 7 = 1$$
$$T_{\Delta} \sim \chi^2(df_{\Delta}) \rightarrow p < .001$$

Thus, including age as a predictor of deviant peer affiliation has significantly improved the fit of the model. However, the relative model fit is still poor. We can again examine the modification indices to determine whether a justifiable model modification would lead to further improvements in model fit.

```
modindices(fit.3, sort.=TRUE, minimum.value=10)
```

```
      lhs op    rhs     mi   epc sepc.lv sepc.all sepc.nox
44   peer  ~ stress 13.381 0.149   0.149    0.192    0.192
63    age  ~   peer 12.858 1.977   1.977    0.721    0.721
43 negaff  ~    age 11.889 0.119   0.119    0.179    0.124
46   peer  ~    coa 11.853 0.185   0.185    0.175    0.350
62    age  ~ negaff 10.859 0.303   0.303    0.200    0.200
```

The MIs continue to suggest that **negaff** be directly regressed on **age**, even after we have regressed **peer** on **age**. However, the MIs also suggest regressing **peer** on **coa**, a modification that we consider to be the most theoretically defensible of the suggested modifications.

To make this modification, we run the following script:

```
pathmodel.4 <-'
              #regressions
              stress ~ coa + gen + age
              emotion ~ coa + gen + age
              negaff ~ stress + emotion
              peer ~ negaff + age + coa

              #covariances
              stress ~~ emotion
              '
fit.4 <- sem(pathmodel.4, data=afdp, meanstructure=TRUE)
summary(fit.4, fit.measures=TRUE)
```

We obtain the following model fit:

```
lavaan 0.6-2 ended normally after 50 iterations

  Optimization method                           NLMINB
  Number of free parameters                         20

  Number of observations                           316

  Estimator                                         ML
  Model Fit Test Statistic                      22.274
  Degrees of freedom                                 6
  P-value (Chi-square)                           0.001

Model test baseline model:

  Minimum Function Test Statistic              251.027
  Degrees of freedom                                18
  P-value                                        0.000

User model versus baseline model:

  Comparative Fit Index (CFI)                    0.930
  Tucker-Lewis Index (TLI)                       0.790

Loglikelihood and Information Criteria:

  Loglikelihood user model (H0)              -1129.488
  Loglikelihood unrestricted model (H1)      -1118.351

  Number of free parameters                         20
  Akaike (AIC)                                2298.977
  Bayesian (BIC)                              2374.092
  Sample-size adjusted Bayesian (BIC)         2310.657

Root Mean Square Error of Approximation:

  RMSEA                                          0.093
  90 Percent Confidence Interval          0.054  0.135
  P-value RMSEA <= 0.05                          0.038

Standardized Root Mean Square Residual:

  SRMR                                           0.044
```

A LRT would show that the inclusion of a direct path from **coa** to **peer** results in a significant improvement to the model fit; however, we are still not satisfied with the relative model fit. Once again, we turn to the modification indices.

```
modindices(fit.4, sort.=TRUE, minimum.value=10)
```

```
      lhs op    rhs     mi   epc sepc.lv sepc.all sepc.nox
44 negaff  ~    age 11.889 0.119   0.119    0.179    0.124
62    age  ~ negaff 10.875 0.303   0.303    0.201    0.201
```

Modification indices persist in suggesting that **age** is directly related with **negaff**. This is the only remaining modification that has an expected change in model fit that is greater than 10. Because this is not an unreasonable modification, we will make this change as well:

```
pathmodel.5 <-'
              #regressions
              stress ~ coa + gen + age
              emotion ~ coa + gen + age
              negaff ~ stress + emotion + age
              peer ~ negaff + age + coa

              #covariances
              stress ~~ emotion
              '
fit.5 <- sem(pathmodel.5, data=afdp, meanstructure=TRUE)
summary(fit.5, fit.measures=TRUE)
```

And we obtain the following fit to the data:

```
lavaan 0.6-2 ended normally after 55 iterations

  Optimization method                           NLMINB
  Number of free parameters                         21

  Number of observations                           316

  Estimator                                         ML
  Model Fit Test Statistic                      10.156
  Degrees of freedom                                 5
  P-value (Chi-square)                           0.071

Model test baseline model:

  Minimum Function Test Statistic              251.027
  Degrees of freedom                                18
  P-value                                        0.000

User model versus baseline model:

  Comparative Fit Index (CFI)                    0.978
  Tucker-Lewis Index (TLI)                       0.920

Loglikelihood and Information Criteria:

  Loglikelihood user model (H0)              -1123.429
  Loglikelihood unrestricted model (H1)      -1118.351

  Number of free parameters                         21
  Akaike (AIC)                                  2288.858
  Bayesian (BIC)                                2367.728
  Sample-size adjusted Bayesian (BIC)           2301.122

Root Mean Square Error of Approximation:

  RMSEA                                            0.057
  90 Percent Confidence Interval          0.000  0.108
  P-value RMSEA <= 0.05                            0.345

Standardized Root Mean Square Residual:

  SRMR                                             0.027
```

By including three data-driven but theoretically acceptable modifications to our original model, we have obtained good model fit. The CFI and the TLI are both above .9 and the 90% confidence interval for the RMSEA includes 0. Note, however, that the confidence interval also includes values greater than .10, so the model fit is not outstanding.

We turn now to the raw and standardized parameter estimates associated with our final model, again computing both fully and partially standardized estimates.

```
summary(fit.5, standardized=TRUE, rsquare=TRUE)
summary(fit.5, std.nox=TRUE, rsquare=TRUE)
```

Here we see the raw and fully standardized estimates:

```
Regressions:
                   Estimate  Std.Err  z-value  P(>|z|)   Std.lv  Std.all
  stress ~
    coa               0.451    0.072    6.223    0.000    0.451    0.331
    gen              -0.016    0.073   -0.215    0.830   -0.016   -0.011
    age               0.002    0.025    0.078    0.938    0.002    0.004
  emotion ~
    coa               0.110    0.056    1.963    0.050    0.110    0.110
    gen              -0.048    0.056   -0.843    0.399   -0.048   -0.047
    age              -0.027    0.019   -1.374    0.170   -0.027   -0.077
  negaff ~
    stress            0.243    0.077    3.157    0.002    0.243    0.173
    emotion           0.582    0.105    5.568    0.000    0.582    0.305
    age               0.119    0.034    3.515    0.000    0.119    0.179
  peer ~
    negaff            0.137    0.028    4.942    0.000    0.137    0.244
    age               0.138    0.018    7.525    0.000    0.138    0.372
    coa               0.185    0.053    3.512    0.000    0.185    0.172

Covariances:
                   Estimate  Std.Err  z-value  P(>|z|)   Std.lv  Std.all
 .stress ~~
   .emotion           0.112    0.019    5.896    0.000    0.112    0.352

```

```
Intercepts:
                   Estimate  Std.Err  z-value  P(>|z|)   Std.lv  Std.all
   .stress            0.687    0.333    2.066    0.039    0.687    1.010
   .emotion           2.341    0.258    9.088    0.000    2.341    4.663
   .negaff           -0.038    0.489   -0.078    0.938   -0.038   -0.040
   .peer             -1.856    0.239   -7.771    0.000   -1.856   -3.457

Variances:
                   Estimate  Std.Err  z-value  P(>|z|)   Std.lv  Std.all
   .stress            0.412    0.033   12.570    0.000    0.412    0.890
   .emotion           0.247    0.020   12.570    0.000    0.247    0.979
   .negaff            0.749    0.060   12.570    0.000    0.749    0.816
   .peer              0.216    0.017   12.570    0.000    0.216    0.748
```

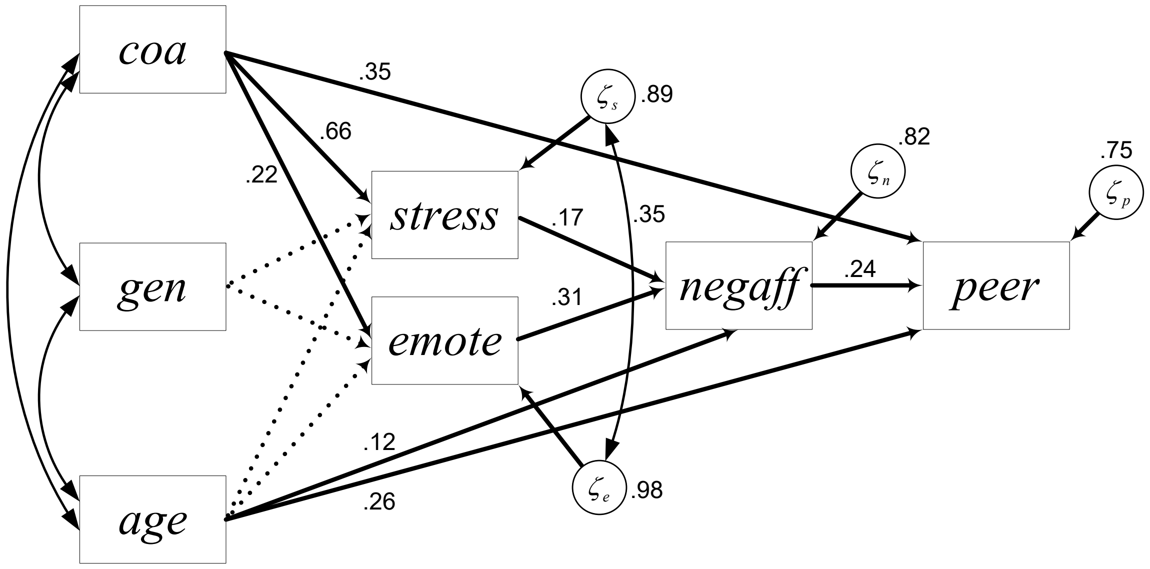
And here we see the raw and partially standardized estimates (just shown for the regression slopes):

```
Regressions:
                   Estimate  Std.Err  z-value  P(>|z|)   Std.lv  Std.nox
  stress ~
    coa               0.451    0.072    6.223    0.000    0.451    0.663
    gen              -0.016    0.073   -0.215    0.830   -0.016   -0.023
    age               0.002    0.025    0.078    0.938    0.002    0.003
  emotion ~
    coa               0.110    0.056    1.963    0.050    0.110    0.219
    gen              -0.048    0.056   -0.843    0.399   -0.048   -0.095
    age              -0.027    0.019   -1.374    0.170   -0.027   -0.053
  negaff ~
    stress            0.243    0.077    3.157    0.002    0.243    0.173
    emotion           0.582    0.105    5.568    0.000    0.582    0.305
    age               0.119    0.034    3.515    0.000    0.119    0.124
  peer ~
    negaff            0.137    0.028    4.942    0.000    0.137    0.244
    age               0.138    0.018    7.525    0.000    0.138    0.257
    coa               0.185    0.053    3.512    0.000    0.185    0.345
```

Finally, the r-square values for the model are given here:
`R-Square:`

```
                   Estimate
    stress            0.110
    emotion           0.021
    negaff            0.184
    peer              0.252
```

The final path diagram with standardized estimates overlaid is shown below. Note that, as before, partially standardized estimates (from the **std.nox** output) are reported for regression paths emanating from the exogenous variables, **COA**, **gen**, and **age**, as all of these predictors have meaningful metrics. All other values are fully standardized.



We originally hypothesized that **coa** would lead to an increase in uncontrolled stressful life events, and this was supported by the model. COA status leads to a moderately high increase in **stress**. We hypothesized that being a COA would lead to an increase in emotionality, and this was supported: **coa** leads to a small-to-moderate increase in **emotion**. We hypothesized that stress and **emotion** would increase **negaff**, and model results suggest a small, positive effect of **stress** on **negaff** and a moderate effect of **emotion** on **negaff**. Finally, we hypothesized that negative affect would increase affiliation with deviant peers, and we estimated a moderately positive direct relation between **negaff** and **peer**.

Additionally, we found support for a direct effect of **coa** on **peer**, suggesting that **stress**, **emotion**, and **negaff** do not fully account for the total relation between COA status and affiliation with deviant peers. Furthermore, age appears to account for a significant amount of the variation in negative affect and affiliation with deviant peers, but age does not appear to be related to uncontrolled stressful life events or emotionality.

Tests of Direct, Indirect, and Specific Effects

Significant links in a mediational pathway are not sufficient to infer mediation. In order to formally test the full mediation effect, we need an inferential test of the entire specific indirect effect in question. Here, we want to know whether the specific mediational pathway of COA status on deviant peer affiliation via stressful events and negative affect is statistically significant, whether the specific mediational effect of **coa** on **peer** via emotionality and negative affect is significant, and whether the overall indirect effect of **coa** on **peer** is significant. Finally, we would like to have an estimate of the total effect of **coa** on **peer** considering both direct and indirect pathways.

The first thing we need to do is define the effects of interest in a new model syntax object, as shown below:

```
effects.5 <-'
            #regressions
            stress ~ c_s*coa + gen + age
            emotion ~ c_e*coa + gen + age
            negaff ~ s_n*stress + e_n*emotion + age
            peer ~ n_p*negaff + age + c_p*coa

            #covariances
            stress ~~ emotion

            #direct effect
            dir := c_p

            #specific indirect effects
            ind_s := c_s*s_n*n_p
            ind_e := c_e*e_n*n_p

            #total indirect effect
            tot_ind := c_s*s_n*n_p + c_e*e_n*n_p

            #total effect
            tot := c_s*s_n*n_p + c_e*e_n*n_p + c_p
```

This is precisely the same model as was defined in the **pathmodel.5** syntax object. What's new here is that we've added parameter labels for the paths involved in the direct and indirect effects of **coa** on **peer**. For instance, in the line **stress ~ c_s*coa + gen + age**, we have supplied the label **c_s** for the effect of **coa** on **stress**. Likewise, the other paths involved in computing the effects of interest have also been labeled. To help keep track of things, our labels consist of the first letter of the predictor, an underscore, and first letter of outcome, but any labels are fine. We can now refer to these labels when defining direct, indirect, and total effects.

Following the core model specification, we have new lines to define the direct, specific indirect, total indirect, and total effects. This is done using the "define" operator **:=**. For instance, **ind_s := c_s*s_n*n_p** requests that lavvan compute the quantity **ind_s** as the product of the three paths previously labeled **c_s**, **s_n**, and **n_p**.

If we were to fit this model using the default options, lavaan would generate point estimates for all of the newly defined effects as well as delta-method standard errors. As we noted in lecture, however, the current best practices is to conduct inferential tests of indirect effects using bootstrapped confidence intervals. Fortunately, it is straightforward to compute these using lavaan.

The script for computing bootrapped confidence intervals is shown below:

```
set.seed(62973)
fit.5b <- sem(effects.5, data=afdp, meanstructure=TRUE, se="bootstrap",
bootstrap=1000)
parameterEstimates(fit.5b, boot.ci.type = "perc")
parameterEstimates(fit.5b, boot.ci.type = "bca.simple")
```

Note that we have used the **set.seed** function to set the random number seed for selecting the bootstrapped samples so that we can reproduce exactly these same results each time we run the script.

Then, in the **sem** function, we specified **se="bootstrap", bootstrap=1000** to request that lavaan compute bootstrapped standard errors with 1000 bootstrapped samples. We actually don't care much about the standard errors. What we really want are bootstrapped confidence intervals, which are generated in the **parameterEstimates** function with the **boot.ci.type** argument. The **parameterEstimates** function produces a simple list of the parameter estimates from the model. By including the **boot.ci.type** argument, we request that this output include 95% boostrapped confidence intervals.

Note that there exist multiple methods for calculating bootrapped CIs. The percentile method is probably easiest to understand – the 1000 boostrapped estimates are ordered by magnitude and the 25th estimate (2.5th percentile) and 975th estimate (97.5th percentile) are taken as the confidence limits, yielding a 95% confidence interval. This method, which is widely available in many software programs, is obtained via **boot.ci.type = "perc"**. That is the method we used in the lecture notes. A slightly preferable approach, however, is to use bias-corrected bootstrapped confidence intervals, and these are readily available in lavaan. To obtain the bias-corrected confidence intervals, we simply use **boot.ci.type = "bca.simple"**. The bias-corrected intervals are shown in the output below. In terms of null hypothesis testing, the same conclusions are generated with the bias-corrected CIs as with the percentile CIs presented in lecture, but there are some slight differences in the specific values of the confidence limits.

```
       lhs op                        rhs   label    est    se      z pvalue ci.lower ci.upper
1   stress  ~                        coa     c_s  0.451 0.071  6.385  0.000    0.319    0.597
2   stress  ~                        gen         -0.016 0.075 -0.209  0.835   -0.163    0.126
3   stress  ~                        age          0.002 0.026  0.075  0.940   -0.050    0.055
4  emotion  ~                        coa     c_e  0.110 0.058  1.908  0.056   -0.004    0.226
5  emotion  ~                        gen         -0.048 0.056 -0.843  0.399   -0.167    0.062
6  emotion  ~                        age         -0.027 0.022 -1.215  0.225   -0.072    0.018
7   negaff  ~                     stress     s_n  0.243 0.091  2.674  0.007    0.080    0.430
8   negaff  ~                    emotion     e_n  0.582 0.109  5.324  0.000    0.354    0.787
9   negaff  ~                        age          0.119 0.030  3.891  0.000    0.062    0.180
10    peer  ~                     negaff     n_p  0.137 0.030  4.526  0.000    0.077    0.196
11    peer  ~                        age          0.138 0.016  8.636  0.000    0.108    0.169
12    peer  ~                        coa     c_p  0.185 0.052  3.529  0.000    0.069    0.280
13  stress ~~                    emotion          0.112 0.019  6.006  0.000    0.076    0.150
14  stress ~~                     stress          0.412 0.041 10.132  0.000    0.343    0.507
15 emotion ~~                    emotion          0.247 0.017 14.356  0.000    0.217    0.286
16  negaff ~~                     negaff          0.749 0.066 11.352  0.000    0.637    0.896
17    peer ~~                       peer          0.216 0.029  7.426  0.000    0.162    0.277
18     coa ~~                        coa          0.249 0.000     NA     NA    0.249    0.249
19     coa ~~                        gen          0.002 0.000     NA     NA    0.002    0.002
20     coa ~~                        age         -0.055 0.000     NA     NA   -0.055   -0.055
21     gen ~~                        gen          0.249 0.000     NA     NA    0.249    0.249
```

```
22     gen ~~                        age        -0.070 0.000     NA     NA   -0.070   -0.070
23     age ~~                        age         2.095 0.000     NA     NA    2.095    2.095
24  stress ~1                                    0.687 0.339  2.028  0.043    0.016    1.346
25 emotion ~1                                    2.341 0.291  8.033  0.000    1.777    2.939
26  negaff ~1                                   -0.038 0.449 -0.085  0.932   -0.950    0.880
27    peer ~1                                   -1.856 0.195 -9.514  0.000   -2.236   -1.474
28     coa ~1                                    0.525 0.000     NA     NA    0.525    0.525
29     gen ~1                                    0.538 0.000     NA     NA    0.538    0.538
30     age ~1                                   12.718 0.000     NA     NA   12.718   12.718
31     dir :=                        c_p     dir  0.185 0.052  3.527  0.000    0.069    0.280
32   ind_s :=                c_s*s_n*n_p   ind_s  0.015 0.007  2.024  0.043    0.005    0.036
33   ind_e :=                c_e*e_n*n_p   ind_e  0.009 0.005  1.647  0.100    0.000    0.022
34 tot_ind :=     c_s*s_n*n_p+c_e*e_n*n_p tot_ind  0.024 0.010  2.477  0.013    0.009    0.047
35     tot := c_s*s_n*n_p+c_e*e_n*n_p+c_p     tot  0.209 0.054  3.900  0.000    0.094    0.306
```

Here, we are principally concerned with the estimates and bias-adjusted bootstrapped confidence intervals given in lines 31-35.

The total effect of **`coa`** on **`peer`** is equal to .209 and represents a combination of the direct effect (.185) and the total indirect effect (.024). The 95% CI is equal to .094 and .306; because this does not contain zero, the total effect is deemed to be significant.

Examining the mediational pathways, we see that the specific indirect effect **`coa`→`stress`→`negaff`→`peer`**, labeled **`ind_s`** to indicate it is the indirect effect through **`stress`**, is equal to .015 (95% CI=.005, .036) and is significant (does not include zero). The biological pathway from **`coa`→`emotion`→`negaff`→`peer`**, labeled **`ind_e`** to indicate it is the indirect effect through **`emotion`**, is equal to .009 (95% CI=0, .022) and thus does not reach statistical significance (because the lower CI is equal to zero).

In sum, examining the specific indirect mediational pathways has provided a more nuanced understanding of how parental alcoholism is related to children's affiliation with deviant peers.

Chapter 4
Confirmatory Factor Analysis

Confirmatory Factor analysis of Holzinger-Swineford Data

The data for this demonstration were provided by Holzinger & Swineford in their 1939 monograph *A Study in Factor Analysis: The Stability of a Bi-Factor Solution*. The sample includes 301 7th and 8th grade students, between 11-16 years of age, drawn from two schools. The data is in the text file **`hs.dat`** and the accompanying R-script file is **`ch04.R`**. The variables in the data set that we will use are

`visperc`	visual perception test in which participants select the next image in a series
`cubes`	visual perception test in which participants must mentally rotate a cube
`lozenges`	visual perception test involving mental "flipping" of a parallelogram ("lozenge")
`parcomp`	paragraph comprehension test
`sencomp`	sentence completion task in which participants select most appropriate word to put at the end of a sentence
`wordmean`	verbal ability test in which participants must select a word most similar in meaning to a word used in a sentence.
`addition`	participants have 2 minutes to complete as many 2-number addition problems as they can
`countdot`	participants have 4 minutes to count the number of dots in each of a series of dot pictures
`sccaps`	participants have 3 minutes to indicate whether capital letters are composed entirely of straight lines or include curved lines.

Other variables in the data not included in the models fit here are **`school`**, **`female`**, **`age`**, and **`month`**.

Preliminary Steps

We begin by reading in the data and assigning variable names, as follows (where the working directory has been set to the source file directory as described in Chapter 1):

```
hs <- read.table("hs.dat", header=FALSE)
names(hs) <- c("school", "female", "age", "month",
               "visperc", "cubes", "lozenges",
               "parcomp", "sencomp", "wordmean",
               "addition", "countdot", "sccaps")
```

Next, we rescaled the variables **`addition`**, **`countdot`**, and **`sccaps`** by dividing by four:

```
hs$addition <- hs$addition/4
hs$countdot <- hs$countdot/4
hs$sccaps <- hs$sccaps/4
```

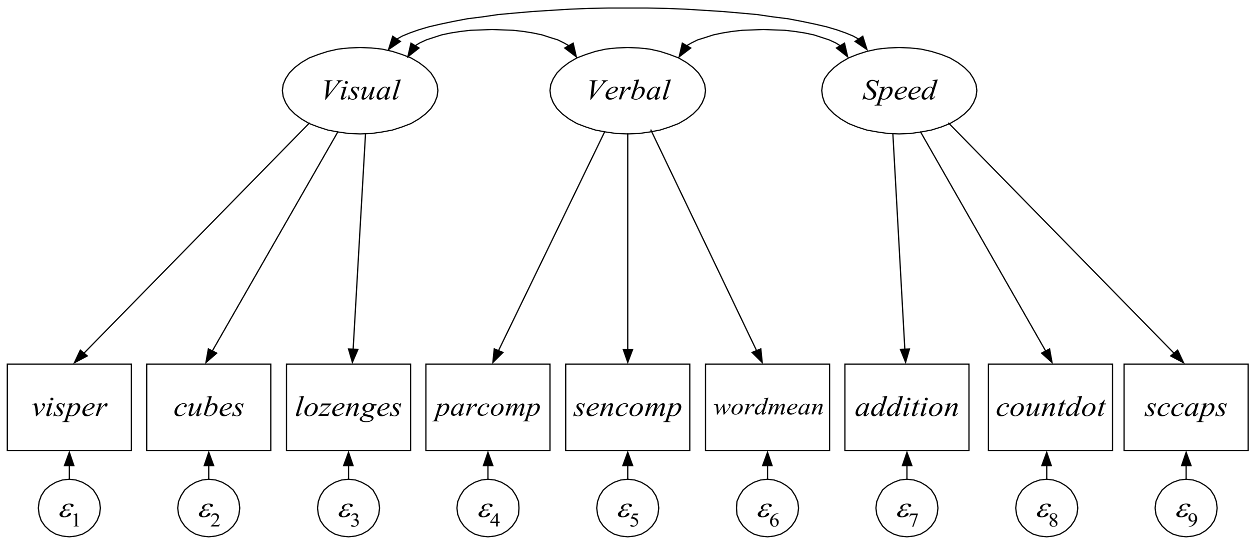
This was done to facilitate model estimation, as numerical instability problems can arise when using variables on widely differing scales. Dividing these variables by four brings their standard deviations closer to the standard deviations of the other observed variables.

Finally, we load the lavaan package that we will use to fit the CFA models:

```
library(lavaan)
```

Initial Model with Standardized Factors

The hypothesized model for the data includes three factors and is shown in the diagram below:



The model is of the form

$$\begin{pmatrix} visper_i \\ cubes_i \\ lozenges_i \\ parcomp_i \\ sencomp_i \\ wordmean_i \\ addition_i \\ countdot_i \\ sccaps_i \end{pmatrix} = \begin{pmatrix} \nu_1 \\ \nu_2 \\ \nu_3 \\ \nu_4 \\ \nu_5 \\ \nu_6 \\ \nu_7 \\ \nu_8 \\ \nu_9 \end{pmatrix} + \begin{pmatrix} \lambda_{11} & 0 & 0 \\ \lambda_{21} & 0 & 0 \\ \lambda_{31} & 0 & 0 \\ 0 & \lambda_{42} & 0 \\ 0 & \lambda_{52} & 0 \\ 0 & \lambda_{62} & 0 \\ 0 & 0 & \lambda_{73} \\ 0 & 0 & \lambda_{83} \\ 0 & 0 & \lambda_{93} \end{pmatrix} \begin{pmatrix} visual_i \\ verbal_i \\ speed_i \end{pmatrix} + \begin{pmatrix} \varepsilon_{1i} \\ \varepsilon_{2i} \\ \varepsilon_{3i} \\ \varepsilon_{4i} \\ \varepsilon_{5i} \\ \varepsilon_{6i} \\ \varepsilon_{7i} \\ \varepsilon_{8i} \\ \varepsilon_{9i} \end{pmatrix}$$

where

$$COV(\boldsymbol{\varepsilon}_i) = \boldsymbol{\Theta} = DIAG(\theta_{11}, \theta_{22}, \theta_{33}, \theta_{44}, \theta_{55}, \theta_{66}, \theta_{77}, \theta_{88}, \theta_{99})$$

$$E(\boldsymbol{\eta}_i) = \boldsymbol{\alpha} = \begin{pmatrix} \alpha_1 \\ \alpha_2 \\ \alpha_3 \end{pmatrix}; \quad COV(\boldsymbol{\eta}_i) = \boldsymbol{\Psi} = \begin{pmatrix} \psi_{11} & & \\ \psi_{21} & \psi_{22} & \\ \psi_{31} & \psi_{32} & \psi_{33} \end{pmatrix}$$

Recall that to identify the model we must set the scale of the latent variables. Two options for doing so are to (1) standardize the latent variables or (2) set the intercept and factor loading of one item per factor to zero and one, respectively. We shall begin with the standardized scaling by setting these parameters as fixed:

$$E(\boldsymbol{\eta}_i) = \boldsymbol{\alpha} = \begin{pmatrix} 0 \\ 0 \\ 0 \end{pmatrix}; \quad COV(\boldsymbol{\eta}_i) = \boldsymbol{\Psi} = \begin{pmatrix} 1 & & \\ \psi_{21} & 1 & \\ \psi_{31} & \psi_{32} & 1 \end{pmatrix}$$

The R script to specify and fit this model is shown below:

```
cfa.1a <-'#factor loadings
          visual =~ visperc + cubes + lozenges
          verbal =~ parcomp + sencomp + wordmean
          speed =~ addition + countdot + sccaps
         '

fit.1a <- cfa(cfa.1a, data=hs, meanstructure=TRUE, std.lv=TRUE)
summary(fit.1a, fit.measures=TRUE, standardized=TRUE, rsquare=TRUE)
```

We have seen most of this syntax before, so here we will highlight only portions of the syntax, especially new syntax that involves the use of latent variables.

First, we will use the **cfa** function in lavaan to fit the model. This function imposes a number of defaults consistent with how CFA models are typically specified and enables us to specify models with compact model syntax objects. The default scaling for the latent variables is a hybrid of the approaches we described in lecture. By default, the latent variables will have means set to zero but freely estimated variance. Additionally, the factor loading of the first indicator for each latent variable will be set to one but the intercept for this indicator will be freely estimated. We will override these defaults to implement the scaling options described in lecture.

Second, in defining the model syntax object, we implement the **=~** operator, which is used to define latent variables (left hand side) and to specify the variables that load on them (right hand side). Thus, **visual =~ visperc + cubes + lozenges** defines a new latent variable, **visual**, and indicates that **visperc**, **cubes**, and **lozenges** are indicator variables.

Third, in fitting the model, we specify **std.lv=TRUE** within the **cfa** function call. This overrides the default hybrid scaling and instead asks lavaan to (1) standardize the factors and (2) freely estimate all loadings.

Let us now turn to the output, considering first the fit indices for the model:

```
lavaan 0.6-2 ended normally after 28 iterations

  Optimization method                           NLMINB
  Number of free parameters                         30
  Number of observations                           301
  Estimator                                         ML
  Model Fit Test Statistic                      85.306
  Degrees of freedom                                24
  P-value (Chi-square)                           0.000

Model test baseline model:

  Minimum Function Test Statistic              918.852
  Degrees of freedom                                36
  P-value                                        0.000

User model versus baseline model:

  Comparative Fit Index (CFI)                    0.931
  Tucker-Lewis Index (TLI)                       0.896

Loglikelihood and Information Criteria:

  Loglikelihood user model (H0)              -8326.241
  Loglikelihood unrestricted model (H1)      -8283.589

  Number of free parameters                         30
  Akaike (AIC)                               16712.483
  Bayesian (BIC)                             16823.696
  Sample-size adjusted Bayesian (BIC)        16728.553

Root Mean Square Error of Approximation:

  RMSEA                                          0.092
  90 Percent Confidence Interval          0.071  0.114
  P-value RMSEA <= 0.05                          0.001

Standardized Root Mean Square Residual:

  SRMR                                           0.060
```

We see here that the fit indices indicate that the model does not fit the data particularly well.

The estimates (both raw and fully standardized) for the model are shown next. These values must be interpreted cautiously, given the lack of fit of the model.

```
Latent Variables:
                   Estimate  Std.Err  z-value  P(>|z|)   Std.lv  Std.all
  visual =~
    visperc           5.398    0.485   11.128    0.000    5.398    0.772
    cubes             1.992    0.310    6.429    0.000    1.992    0.424
    lozenges          5.249    0.595    8.817    0.000    5.249    0.581
  verbal =~
    parcomp           2.969    0.170   17.474    0.000    2.969    0.852
    sencomp           4.406    0.251   17.576    0.000    4.406    0.855
    wordmean          6.416    0.376   17.082    0.000    6.416    0.838
  speed =~
    addition          3.562    0.400    8.903    0.000    3.562    0.570
    countdot          3.655    0.330   11.090    0.000    3.655    0.723
    sccaps            6.030    0.585   10.305    0.000    6.030    0.665

Covariances:
                   Estimate  Std.Err  z-value  P(>|z|)   Std.lv  Std.all
  visual ~~
    verbal            0.459    0.064    7.189    0.000    0.459    0.459
    speed             0.471    0.073    6.461    0.000    0.471    0.471
  verbal ~~
    speed             0.283    0.069    4.117    0.000    0.283    0.283

Intercepts:
                   Estimate  Std.Err  z-value  P(>|z|)   Std.lv  Std.all
   .visperc          29.615    0.403   73.473    0.000   29.615    4.235
   .cubes            24.352    0.271   89.855    0.000   24.352    5.179
   .lozenges         18.003    0.521   34.579    0.000   18.003    1.993
   .parcomp           9.183    0.201   45.694    0.000    9.183    2.634
   .sencomp          17.362    0.297   58.452    0.000   17.362    3.369
   .wordmean         15.299    0.441   34.667    0.000   15.299    1.998
   .addition         24.069    0.360   66.766    0.000   24.069    3.848
   .countdot         27.635    0.291   94.854    0.000   27.635    5.467
   .sccaps           48.367    0.523   92.546    0.000   48.367    5.334
    visual            0.000                               0.000    0.000
    verbal            0.000                               0.000    0.000
    speed             0.000                               0.000    0.000

Variances:
                   Estimate  Std.Err  z-value  P(>|z|)   Std.lv  Std.all
   .visperc          19.766    4.090    4.833    0.000   19.766    0.404
   .cubes            18.141    1.628   11.146    0.000   18.141    0.821
   .lozenges         54.037    5.800    9.317    0.000   54.037    0.662
   .parcomp           3.341    0.429    7.779    0.000    3.341    0.275
   .sencomp           7.140    0.934    7.642    0.000    7.140    0.269
   .wordmean         17.454    2.109    8.277    0.000   17.454    0.298
   .addition         26.430    2.691    9.823    0.000   26.430    0.676
   .countdot         12.192    1.855    6.573    0.000   12.192    0.477
   .sccaps           45.857    5.730    8.003    0.000   45.857    0.558
```

```
    visual            1.000                                    1.000    1.000
    verbal            1.000                                    1.000    1.000
    speed             1.000                                    1.000    1.000
```

Note that the standard error, z-statistic, and p-value for the factor means and variances are all missing. This simply indicates that these parameters were not estimated, and hence no inferential tests were conducted on their values.

Because the items are on different scales, we cannot easily interpret the differences among the raw estimates for the factor loadings or residual variances. To better interpret these results, we requested the standardized solution. Note that because we have already standardized the latent variables, the column labeled `Std.lv` is redundant with the raw estimates. We are more interested in the fully-standardized `Std.all` values. The fully-standardized factor loadings can be compared directly (e.g., **`visperc`** is a better indicator than **`cubes`** for the **`visual`** factor).

One odd thing to note is that the indicator intercepts are not zero in the standardized output, as you would expect if the observed variables had been standardized in the usual way of deviating the mean and dividing by the standard deviation. In lavaan, the standardized solution merely rescales the observed variables to have standard deviations of one, and does not center the variables to have means of zero. This is of no consequence here, as the mean structure is saturated and of little interest.

Last, the standardized residual variances of the indicators are interpretable as the proportion of variance unexplained by the latent factors (or 1 – communality). The communalities themselves were obtained by setting the **`rsquare`** argument of the **`summary`** function to **`TRUE`**:

```
R-Square:
                   Estimate
    visperc           0.596
    cubes             0.179
    lozenges          0.338
    parcomp           0.725
    sencomp           0.731
    wordmean          0.702
    addition          0.324
    countdot          0.523
    sccaps            0.442
```

Items with high communality are generally regarded as better items. Given the poor model fit, we may wish to examine modification indices to get an idea of where the model may be misspecified.

The modification indices for the model are obtained from the **`modindices`** function as follows:

```
modindices(fit.1a, sort.=TRUE, minimum.value=10)
```

```
        lhs op      rhs     mi     epc sepc.lv sepc.all sepc.nox
42   visual =~   sccaps 36.411   4.672   4.672    0.515    0.515
88 addition ~~ countdot 34.145  15.423  15.423    0.859    0.859
40   visual =~ addition 18.631  -2.182  -2.182   -0.349   -0.349
90 countdot ~~   sccaps 14.946 -19.039 -19.039   -0.805   -0.805
```

Here we see the largest modification indices are associated with a cross-loading for **`sccaps`** on **`visual`**, and a correlated uniqueness for **`countdot`** with **`addition`**. It is important to keep in mind that both modification indices may be related to the same misspecification.

Before proceeding to respecify the model, let us also consider how the model would be input into lavaan if we chose to scale the latent variables using scaling items rather than standardizing.

Initial Model with Scaling Items

We shall choose the first indicator for each factor to be the scaling item. The intercept and factor loading for each scaling item is set to zero and one, respectively. This scaling option permits the means and variances of the latent factors to be estimated. The model is thus now specified as

$$\begin{pmatrix} visper_i \\ cubes_i \\ lozenges_i \\ parcomp_i \\ sencomp_i \\ wordmean_i \\ addition_i \\ countdot_i \\ sccaps_i \end{pmatrix} = \begin{pmatrix} 0 \\ \nu_2 \\ \nu_3 \\ 0 \\ \nu_5 \\ \nu_6 \\ 0 \\ \nu_8 \\ \nu_9 \end{pmatrix} + \begin{pmatrix} 1 & 0 & 0 \\ \lambda_{21} & 0 & 0 \\ \lambda_{31} & 0 & 0 \\ 0 & 1 & 0 \\ 0 & \lambda_{52} & 0 \\ 0 & \lambda_{62} & 0 \\ 0 & 0 & 1 \\ 0 & 0 & \lambda_{83} \\ 0 & 0 & \lambda_{93} \end{pmatrix} \begin{pmatrix} visual_i \\ verbal_i \\ speed_i \end{pmatrix} + \begin{pmatrix} \varepsilon_{1i} \\ \varepsilon_{2i} \\ \varepsilon_{3i} \\ \varepsilon_{4i} \\ \varepsilon_{5i} \\ \varepsilon_{6i} \\ \varepsilon_{7i} \\ \varepsilon_{8i} \\ \varepsilon_{9i} \end{pmatrix}$$

where

$$COV(\boldsymbol{\varepsilon}_i) = \boldsymbol{\Theta} = DIAG(\theta_{11}, \theta_{22}, \theta_{33}, \theta_{44}, \theta_{55}, \theta_{66}, \theta_{77}, \theta_{88}, \theta_{99})$$

$$E(\boldsymbol{\eta}_i) = \boldsymbol{\alpha} = \begin{pmatrix} \alpha_1 \\ \alpha_2 \\ \alpha_3 \end{pmatrix}; \quad COV(\boldsymbol{\eta}_i) = \boldsymbol{\Psi} = \begin{pmatrix} \psi_{11} & & \\ \psi_{21} & \psi_{22} & \\ \psi_{31} & \psi_{32} & \psi_{33} \end{pmatrix}$$

and all elements in $\boldsymbol{\alpha}$ and $\boldsymbol{\Psi}$ are now estimated.

The corresponding R script for fitting the model and displaying the results is given here:

```
cfa.1b <-'#factor loadings
          visual =~ visperc + cubes + lozenges
          verbal =~ parcomp + sencomp + wordmean
          speed =~ addition + countdot + sccaps

          #means/intercepts
          visual ~ 1
          verbal ~ 1
          speed ~ 1
          visperc ~ 0*1
          parcomp ~ 0*1
          addition ~ 0*1
         '

fit.1b <- cfa(cfa.1b, data=hs, meanstructure=TRUE)
summary(fit.1b, fit.measures=TRUE, standardized=TRUE, rsquare=TRUE)
```

In this case, we will not invoke the **`std.lv`** option when fitting the model as we do not wish to standardize the factors. Here, we wish to use a scaling indicator instead. We can rely on the default that the factor loading for the first indicator per factor will be fixed to one (this need not be specified explicitly). We must, however, assign a numeric value of zero to the intercept for each of the anchor items, e.g., via **`visperc ~ 0*1`**, to override the default of freely estimating intercepts for all observed variables.

Similarly, we can rely on the default that the factor variances will be freely estimated but we need to indicate that lavvan should estimate the factor means, e.g., via **`visual ~ 1`**. (Since there are no predictors of the factors, their intercepts are interpretable as means).

The model fit output is shown here:

```
lavaan 0.6-2 ended normally after 180 iterations

  Optimization method                           NLMINB
  Number of free parameters                         30

  Number of observations                           301

  Estimator                                         ML
  Model Fit Test Statistic                      85.306
  Degrees of freedom                                24
  P-value (Chi-square)                           0.000

Model test baseline model:

  Minimum Function Test Statistic              918.852
  Degrees of freedom                                36
  P-value                                        0.000
```

```
User model versus baseline model:

  Comparative Fit Index (CFI)                    0.931
  Tucker-Lewis Index (TLI)                       0.896

Loglikelihood and Information Criteria:

  Loglikelihood user model (H0)              -8326.241
  Loglikelihood unrestricted model (H1)      -8283.589

  Number of free parameters                         30
  Akaike (AIC)                               16712.483
  Bayesian (BIC)                             16823.696
  Sample-size adjusted Bayesian (BIC)        16728.553

Root Mean Square Error of Approximation:

  RMSEA                                          0.092
  90 Percent Confidence Interval          0.071  0.114
  P-value RMSEA <= 0.05                          0.001

Standardized Root Mean Square Residual:

  SRMR                                           0.060
```

Note that the tests of model fit are identical to the standardized factor model presented previously. The two models are equivalent, and merely scaled differently.

The difference in scales is apparent when considering the model estimates:

```
Parameter Estimates:

  Information                                 Expected
  Information saturated (h1) model          Structured
  Standard Errors                             Standard

Latent Variables:
                   Estimate  Std.Err  z-value  P(>|z|)   Std.lv  Std.all
  visual =~
    visperc           1.000                               5.398    0.772
    cubes             0.369    0.066    5.554    0.000    1.992    0.424
    lozenges          0.972    0.145    6.685    0.000    5.249    0.581
  verbal =~
    parcomp           1.000                               2.969    0.852
    sencomp           1.484    0.087   17.014    0.000    4.406    0.855
    wordmean          2.161    0.129   16.703    0.000    6.416    0.838
  speed =~
    addition          1.000                               3.562    0.570
    countdot          1.026    0.143    7.152    0.000    3.655    0.723
    sccaps            1.693    0.237    7.155    0.000    6.030    0.665
```

```
Covariances:
                   Estimate  Std.Err  z-value  P(>|z|)   Std.lv  Std.all
  visual ~~
    verbal            7.348    1.323    5.552    0.000    0.459    0.459
    speed             9.047    1.942    4.660    0.000    0.471    0.471
  verbal ~~
    speed             2.993    0.851    3.518    0.000    0.283    0.283

Intercepts:
                   Estimate  Std.Err  z-value  P(>|z|)   Std.lv  Std.all
    visual           29.615    0.403   73.473    0.000    5.487    5.487
    verbal            9.183    0.201   45.694    0.000    3.093    3.093
    speed            24.069    0.360   66.766    0.000    6.757    6.757
   .visperc           0.000                               0.000    0.000
   .parcomp           0.000                               0.000    0.000
   .addition          0.000                               0.000    0.000
   .cubes            13.424    1.985    6.762    0.000   13.424    2.855
   .lozenges        -10.797    4.336   -2.490    0.013  -10.797   -1.195
   .sencomp           3.734    0.831    4.496    0.000    3.734    0.725
   .wordmean         -4.545    1.233   -3.685    0.000   -4.545   -0.594
   .countdot          2.940    3.472    0.847    0.397    2.940    0.582
   .sccaps            7.622    5.730    1.330    0.183    7.622    0.841

Variances:
                   Estimate  Std.Err  z-value  P(>|z|)   Std.lv  Std.all
   .visperc          19.766    4.090    4.833    0.000   19.766    0.404
   .cubes            18.141    1.628   11.146    0.000   18.141    0.821
   .lozenges         54.037    5.800    9.317    0.000   54.037    0.662
   .parcomp           3.341    0.429    7.779    0.000    3.341    0.275
   .sencomp           7.140    0.934    7.642    0.000    7.140    0.269
   .wordmean         17.454    2.109    8.277    0.000   17.454    0.298
   .addition         26.430    2.691    9.823    0.000   26.430    0.676
   .countdot         12.192    1.855    6.573    0.000   12.192    0.477
   .sccaps           45.857    5.730    8.003    0.000   45.857    0.558
    visual           29.135    5.237    5.564    0.000    1.000    1.000
    verbal            8.815    1.009    8.737    0.000    1.000    1.000
    speed            12.688    2.850    4.451    0.000    1.000    1.000

R-Square:
                   Estimate
    visperc           0.596
    cubes             0.179
    lozenges          0.338
    parcomp           0.725
    sencomp           0.731
    wordmean          0.702
    addition          0.324
    countdot          0.523
    sccaps            0.442
```

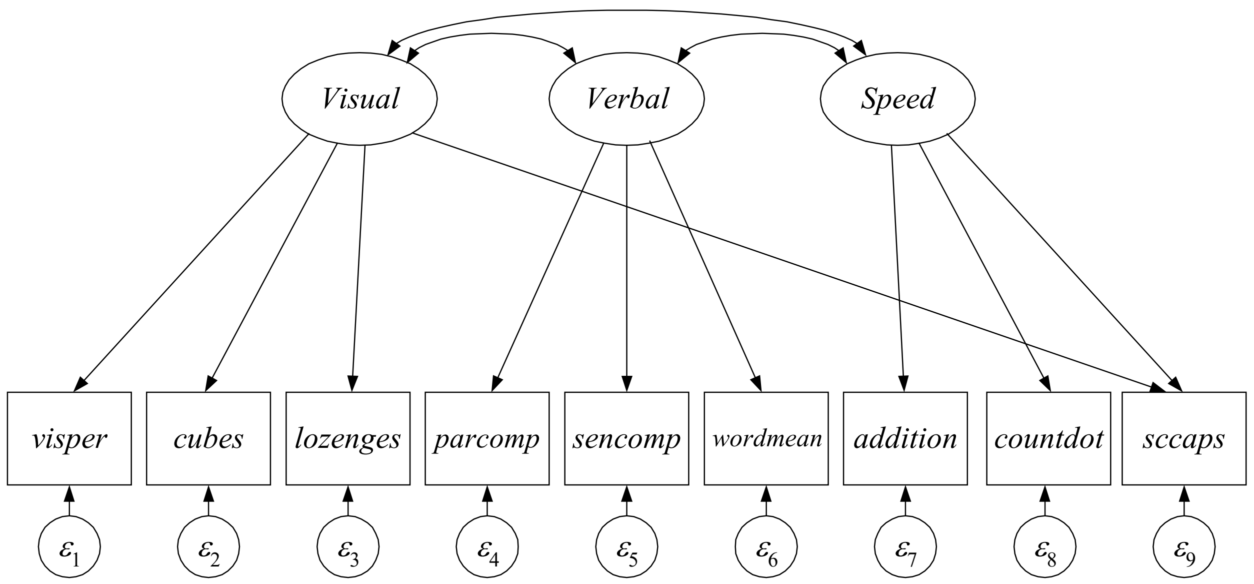
The raw estimates for the factor loadings and intercepts are now interpreted in a relative scale, with reference to the scaling item. Further, because the factor variances are no longer set to one, the covariances among the factors can no longer be interpreted as correlations.

Again, the difference in metric across the tests makes interpretation of differences in intercepts and loadings somewhat difficult. The standardized solution can again be considered to aid in interpretation. Note that it is identical to the standardized solution shown previously. Similarly, modification indices are no different with this scaling option and are not repeated here.

We now consider respecification of the model, returning to the standardized scaling option to set the metric of the latent variables.

Model Modification

We first introduce a cross loading of **`sccaps`** on **`visual`**, as shown in the diagram below:



The model is now of the form

$$\begin{pmatrix} visper_i \\ cubes_i \\ lozenges_i \\ parcomp_i \\ sencomp_i \\ wordmean_i \\ addition_i \\ countdot_i \\ sccaps_i \end{pmatrix} = \begin{pmatrix} \nu_1 \\ \nu_2 \\ \nu_3 \\ \nu_4 \\ \nu_5 \\ \nu_6 \\ \nu_7 \\ \nu_8 \\ \nu_9 \end{pmatrix} + \begin{pmatrix} \lambda_{11} & 0 & 0 \\ \lambda_{21} & 0 & 0 \\ \lambda_{31} & 0 & 0 \\ 0 & \lambda_{42} & 0 \\ 0 & \lambda_{52} & 0 \\ 0 & \lambda_{62} & 0 \\ 0 & 0 & \lambda_{73} \\ 0 & 0 & \lambda_{83} \\ \lambda_{91} & 0 & \lambda_{93} \end{pmatrix} \begin{pmatrix} visual_i \\ verbal_i \\ speed_i \end{pmatrix} + \begin{pmatrix} \varepsilon_{1i} \\ \varepsilon_{2i} \\ \varepsilon_{3i} \\ \varepsilon_{4i} \\ \varepsilon_{5i} \\ \varepsilon_{6i} \\ \varepsilon_{7i} \\ \varepsilon_{8i} \\ \varepsilon_{9i} \end{pmatrix}$$

where

$$COV(\boldsymbol{\varepsilon}_i) = \boldsymbol{\Theta} = DIAG(\theta_{11}, \theta_{22}, \theta_{33}, \theta_{44}, \theta_{55}, \theta_{66}, \theta_{77}, \theta_{88}, \theta_{99})$$

$$E(\boldsymbol{\eta}_i) = \boldsymbol{\alpha} = \begin{pmatrix} 0 \\ 0 \\ 0 \end{pmatrix}; \quad COV(\boldsymbol{\eta}_i) = \boldsymbol{\Psi} = \begin{pmatrix} 1 & & \\ \psi_{21} & 1 & \\ \psi_{31} & \psi_{32} & 1 \end{pmatrix}$$

The difference between the modified model and the original CFA is that the element in 9th row (corresponding to **sccaps**) and 1st column (corresponding to **visual**) of the factor loading matrix has been freed from zero to λ_{91}.

The new cross-loading can be estimated by defining and fitting a slightly modified model syntax object, **cfa.2**, as follows:

```
cfa.2 <- '#factor loadings
          visual =~ visperc + cubes + lozenges + sccaps
          verbal =~ parcomp + sencomp + wordmean
          speed =~ addition + countdot + sccaps
         '
fit.2 <- cfa(cfa.2, data=hs, meanstructure=TRUE, std.lv=TRUE)
summary(fit.2, fit.measures=TRUE, standardized=TRUE, rsquare=TRUE)
```

Notice that **sccaps** now appears twice: once on **speed** and once on **visual**. Factor loadings for **sccaps** are freely estimated for both factors.

The model fit information is shown here:

```
lavaan 0.6-2 ended normally after 29 iterations

  Optimization method                           NLMINB
  Number of free parameters                         31

  Number of observations                           301

  Estimator                                         ML
  Model Fit Test Statistic                      52.382
  Degrees of freedom                                23
  P-value (Chi-square)                           0.000

Model test baseline model:

  Minimum Function Test Statistic              918.852
  Degrees of freedom                                36
  P-value                                        0.000

User model versus baseline model:

  Comparative Fit Index (CFI)                    0.967
  Tucker-Lewis Index (TLI)                       0.948
```

```
Loglikelihood and Information Criteria:

  Loglikelihood user model (H0)             -8309.780
  Loglikelihood unrestricted model (H1)     -8283.589

  Number of free parameters                        31
  Akaike (AIC)                              16681.560
  Bayesian (BIC)                            16796.480
  Sample-size adjusted Bayesian (BIC)       16698.166

Root Mean Square Error of Approximation:

  RMSEA                                         0.065
  90 Percent Confidence Interval         0.042  0.089
  P-value RMSEA <= 0.05                         0.133

Standardized Root Mean Square Residual:

  SRMR                                          0.041
```

Freeing the cross-loading significantly improved the model fit according to a likelihood ratio test of the original CFA and the model estimated above:

```
lavTestLRT(fit.2, fit.1a)
```

```
Chi Square Difference Test

       Df   AIC   BIC  Chisq Chisq diff Df diff Pr(>Chisq)
fit.2  23 16682 16797 52.382
fit.1a 24 16713 16824 85.305     32.923       1  9.586e-09 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

Thus we have:

$$\chi^2\left(df_{Original} - df_{CrossLoad}\right) = \chi^2{}_{Original} - \chi^2{}_{CrossLoad}$$
$$\chi^2\left(24-23\right) = 85.305 - 52.382$$
$$\chi^2\left(1\right) = 32.923, p < .001$$

Other fit indices suggest that the modified model may have satisfactory fit to the data.

The estimates for the model are shown next. To the extent that we are justified in including the new cross loading, we can have more faith in these estimates due to improved model fit.

```
Latent Variables:
                   Estimate  Std.Err  z-value  P(>|z|)   Std.lv  Std.all
  visual =~
    visperc           5.308    0.454   11.685    0.000    5.308    0.759
    cubes             2.046    0.305    6.698    0.000    2.046    0.435
    lozenges          5.333    0.577    9.241    0.000    5.333    0.590
    sccaps            3.480    0.577    6.034    0.000    3.480    0.384
  verbal =~
    parcomp           2.967    0.170   17.455    0.000    2.967    0.851
    sencomp           4.411    0.251   17.602    0.000    4.411    0.856
    wordmean          6.414    0.376   17.073    0.000    6.414    0.838
  speed =~
    addition          3.830    0.419    9.134    0.000    3.830    0.612
    countdot          4.021    0.368   10.934    0.000    4.021    0.795
    sccaps            4.049    0.593    6.824    0.000    4.049    0.447

Covariances:
                   Estimate  Std.Err  z-value  P(>|z|)   Std.lv  Std.all
  visual ~~
    verbal            0.453    0.062    7.242    0.000    0.453    0.453
    speed             0.301    0.080    3.763    0.000    0.301    0.301
  verbal ~~
    speed             0.206    0.070    2.937    0.003    0.206    0.206

Intercepts:
                   Estimate  Std.Err  z-value  P(>|z|)   Std.lv  Std.all
   .visperc          29.615    0.403   73.473    0.000   29.615    4.235
   .cubes            24.352    0.271   89.855    0.000   24.352    5.179
   .lozenges         18.003    0.521   34.579    0.000   18.003    1.993
   .sccaps           48.367    0.523   92.546    0.000   48.367    5.334
   .parcomp           9.183    0.201   45.694    0.000    9.183    2.634
   .sencomp          17.362    0.297   58.452    0.000   17.362    3.369
   .wordmean         15.299    0.441   34.667    0.000   15.299    1.998
   .addition         24.069    0.360   66.766    0.000   24.069    3.848
   .countdot         27.635    0.291   94.854    0.000   27.635    5.467
    visual            0.000                               0.000    0.000
    verbal            0.000                               0.000    0.000
    speed             0.000                               0.000    0.000

Variances:
                   Estimate  Std.Err  z-value  P(>|z|)   Std.lv  Std.all
   .visperc          20.726    3.616    5.731    0.000   20.726    0.424
   .cubes            17.924    1.607   11.153    0.000   17.924    0.811
   .lozenges         53.148    5.586    9.515    0.000   53.148    0.651
   .sccaps           45.234    4.845    9.336    0.000   45.234    0.550
   .parcomp           3.353    0.430    7.800    0.000    3.353    0.276
   .sencomp           7.098    0.934    7.602    0.000    7.098    0.267
   .wordmean         17.483    2.110    8.285    0.000   17.483    0.298
   .addition         24.450    2.845    8.595    0.000   24.450    0.625
   .countdot          9.383    2.362    3.973    0.000    9.383    0.367
    visual            1.000                               1.000    1.000
    verbal            1.000                               1.000    1.000
    speed             1.000                               1.000    1.000
```

```
R-Square:
                   Estimate
    visperc           0.576
    cubes             0.189
    lozenges          0.349
    sccaps            0.450
    parcomp           0.724
    sencomp           0.733
    wordmean          0.702
    addition          0.375
    countdot          0.633
```

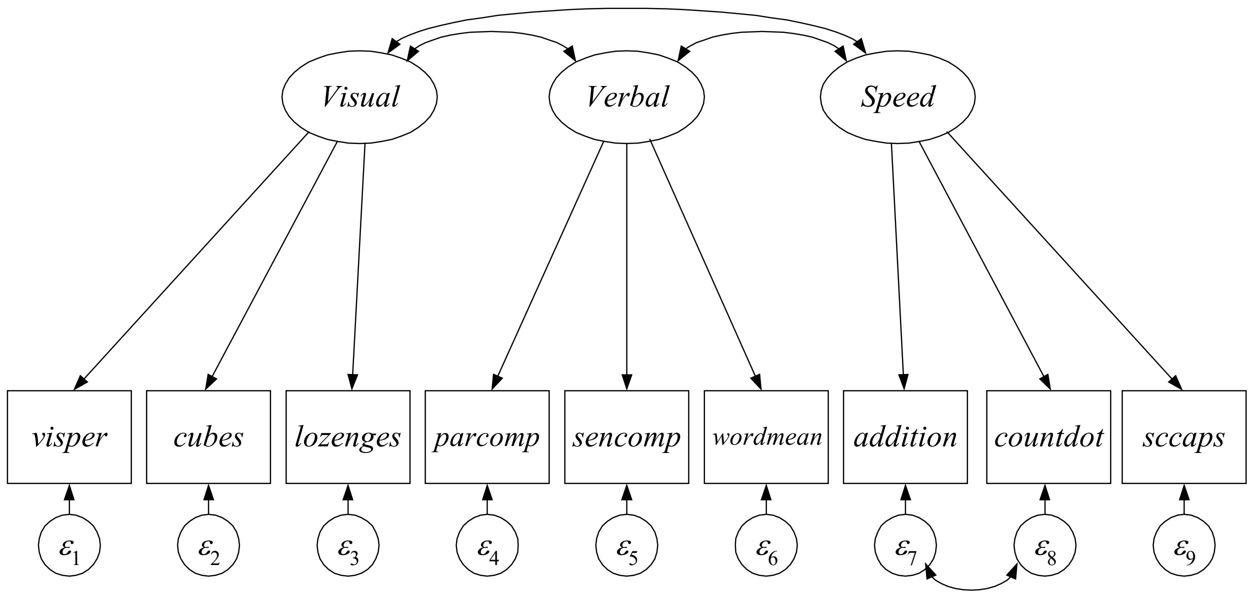
In the results, note that **`sccaps`** loads significantly on **`visual`**. The residual variance of **`sccaps`** remains fairly high and the correlation between **`visual`** and **`speed`** is still statistically significant. The new modification indices exceeding 10 are reported below:

```
modindices(fit.2, sort.=TRUE, minimum.value=10)
```

```
[1] lhs      op       rhs      mi       epc      sepc.lv  sepc.all sepc.nox
<0 rows> (or 0-length row.names)
```

Note that no further changes are suggested for the model.

Next, we illustrate how implementing a different model modification might affect conclusions drawn from the model. We allow the residual errors for **`addition`** and **`countdot`** to correlate, as shown in the diagram below:



The model is now of the form

$$\begin{pmatrix} visper_i \\ cubes_i \\ lozenges_i \\ parcomp_i \\ sencomp_i \\ wordmean_i \\ addition_i \\ countdot_i \\ sccaps_i \end{pmatrix} = \begin{pmatrix} \nu_1 \\ \nu_2 \\ \nu_3 \\ \nu_4 \\ \nu_5 \\ \nu_6 \\ \nu_7 \\ \nu_8 \\ \nu_9 \end{pmatrix} + \begin{pmatrix} \lambda_{11} & 0 & 0 \\ \lambda_{21} & 0 & 0 \\ \lambda_{31} & 0 & 0 \\ 0 & \lambda_{42} & 0 \\ 0 & \lambda_{52} & 0 \\ 0 & \lambda_{62} & 0 \\ 0 & 0 & \lambda_{73} \\ 0 & 0 & \lambda_{83} \\ 0 & 0 & \lambda_{93} \end{pmatrix} \begin{pmatrix} visual_i \\ verbal_i \\ speed_i \end{pmatrix} + \begin{pmatrix} \varepsilon_{1i} \\ \varepsilon_{2i} \\ \varepsilon_{3i} \\ \varepsilon_{4i} \\ \varepsilon_{5i} \\ \varepsilon_{6i} \\ \varepsilon_{7i} \\ \varepsilon_{8i} \\ \varepsilon_{9i} \end{pmatrix}$$

where

$$COV(\boldsymbol{\varepsilon}_i) = \boldsymbol{\Theta} = \begin{pmatrix} \theta_{11} &&&&&&&& \\ 0 & \theta_{22} &&&&&&& \\ 0 & 0 & \theta_{33} &&&&&& \\ 0 & 0 & 0 & \theta_{44} &&&&& \\ 0 & 0 & 0 & 0 & \theta_{55} &&&& \\ 0 & 0 & 0 & 0 & 0 & \theta_{66} &&& \\ 0 & 0 & 0 & 0 & 0 & 0 & \theta_{77} && \\ 0 & 0 & 0 & 0 & 0 & 0 & \theta_{87} & \theta_{88} & \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & \theta_{99} \end{pmatrix}$$

$$E(\boldsymbol{\eta}_i) = \boldsymbol{\alpha} = \begin{pmatrix} 0 \\ 0 \\ 0 \end{pmatrix}; \quad COV(\boldsymbol{\eta}_i) = \boldsymbol{\Psi} = \begin{pmatrix} 1 && \\ \psi_{21} & 1 & \\ \psi_{31} & \psi_{32} & 1 \end{pmatrix}$$

The difference between the modified model and the original CFA is that $\boldsymbol{\Theta}$ is no longer diagonal; it contains a covariance between the residual terms for **`addition`** and **`countdot`**. This change can be included in the model by defining and fitting a new model syntax object, **`cfa.3`**, as follows:

```
cfa.3 <- '#factor loadings
          visual =~ visperc + cubes + lozenges
          verbal =~ parcomp + sencomp + wordmean
          speed =~ addition + countdot + sccaps

          #covariances
          addition ~~ countdot
         '
fit.3 <- cfa(cfa.3, data=hs, meanstructure=TRUE, std.lv=TRUE)
summary(fit.3, fit.measures=TRUE, standardized=TRUE, rsquare=TRUE)
```

The difference between this input and the original input is the final statement: **`addition ~~ countdot`**. In lavaan, when observed variable names are joined by the ~~ operator, it indicates that the residuals associated with those variables should covary (i.e., be correlated).

We first consider the model fit:

```
lavaan 0.6-2 ended normally after 51 iterations

  Optimization method                           NLMINB
  Number of free parameters                         31

  Number of observations                           301

  Estimator                                         ML
  Model Fit Test Statistic                      53.272
  Degrees of freedom                                23
  P-value (Chi-square)                           0.000

Model test baseline model:

  Minimum Function Test Statistic              918.852
  Degrees of freedom                                36
  P-value                                        0.000

User model versus baseline model:

  Comparative Fit Index (CFI)                    0.966
  Tucker-Lewis Index (TLI)                       0.946

Loglikelihood and Information Criteria:

  Loglikelihood user model (H0)              -8310.225
  Loglikelihood unrestricted model (H1)      -8283.589

  Number of free parameters                         31
  Akaike (AIC)                               16682.450
  Bayesian (BIC)                             16797.370
  Sample-size adjusted Bayesian (BIC)        16699.056

Root Mean Square Error of Approximation:

  RMSEA                                          0.066
  90 Percent Confidence Interval          0.043  0.090
  P-value RMSEA <= 0.05                          0.118

Standardized Root Mean Square Residual:

  SRMR                                           0.043
```

Allowing a single residual correlation among these items resulted in a large improvement in model fit, which we can evaluate via a likelihood ratio test (i.e., chi-square difference test):

```
lavTestLRT(fit.3, fit.1a)
```

```
Chi Square Difference Test

       Df   AIC   BIC  Chisq Chisq diff Df diff Pr(>Chisq)
fit.3  23 16682 16797 53.272
fit.1a 24 16713 16824 85.305     32.033       1  1.516e-08 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

The improvement in model fit is highly significant:

$$\chi^2\left(df_{Original} - df_{ResCorr}\right) = \chi^2{}_{Original} - \chi^2{}_{ResCorr}$$
$$\chi^2\left(24-23\right) = 85.305 - 53.272$$
$$\chi^2\left(1\right) = 32.033, p < .001$$

Other fit indices suggest that the modified model may also have satisfactory overall fit to the data.

The estimates for the model are shown next. To the extent that we are justified in including the unhypothesized cross loading, we can have more faith in these estimates due to improved model fit.

```
Latent Variables:
                   Estimate  Std.Err  z-value  P(>|z|)   Std.lv  Std.all
  visual =~
    visperc           5.308    0.457   11.620    0.000    5.308    0.759
    cubes             2.037    0.305    6.673    0.000    2.037    0.433
    lozenges          5.323    0.576    9.238    0.000    5.323    0.589
  verbal =~
    parcomp           2.967    0.170   17.458    0.000    2.967    0.851
    sencomp           4.411    0.251   17.601    0.000    4.411    0.856
    wordmean          6.413    0.376   17.068    0.000    6.413    0.838
  speed =~
    addition          2.202    0.421    5.229    0.000    2.202    0.352
    countdot          2.383    0.366    6.505    0.000    2.383    0.471
    sccaps            8.667    0.958    9.051    0.000    8.667    0.956

Covariances:
                   Estimate  Std.Err  z-value  P(>|z|)   Std.lv  Std.all
 .addition ~~
   .countdot         10.140    1.936    5.239    0.000   10.140    0.389
  visual ~~
    verbal            0.457    0.064    7.142    0.000    0.457    0.457
    speed             0.544    0.078    6.965    0.000    0.544    0.544
  verbal ~~
    speed             0.270    0.065    4.141    0.000    0.270    0.270
```

```
Intercepts:
                   Estimate  Std.Err  z-value  P(>|z|)   Std.lv  Std.all
   .visperc          29.615    0.403   73.473    0.000   29.615    4.235
   .cubes            24.352    0.271   89.855    0.000   24.352    5.179
   .lozenges         18.003    0.521   34.579    0.000   18.003    1.993
   .parcomp           9.183    0.201   45.694    0.000    9.183    2.634
   .sencomp          17.362    0.297   58.452    0.000   17.362    3.369
   .wordmean         15.299    0.441   34.667    0.000   15.299    1.998
   .addition         24.069    0.360   66.766    0.000   24.069    3.848
   .countdot         27.635    0.291   94.854    0.000   27.635    5.467
   .sccaps           48.367    0.523   92.546    0.000   48.367    5.334
    visual            0.000                               0.000    0.000
    verbal            0.000                               0.000    0.000
    speed             0.000                               0.000    0.000

Variances:
                   Estimate  Std.Err  z-value  P(>|z|)   Std.lv  Std.all
   .visperc          20.730    3.651    5.678    0.000   20.730    0.424
   .cubes            17.960    1.608   11.171    0.000   17.960    0.812
   .lozenges         53.255    5.576    9.552    0.000   53.255    0.653
   .parcomp           3.350    0.430    7.791    0.000    3.350    0.276
   .sencomp           7.099    0.934    7.600    0.000    7.099    0.267
   .wordmean         17.496    2.111    8.287    0.000   17.496    0.298
   .addition         34.268    2.980   11.501    0.000   34.268    0.876
   .countdot         19.870    1.989    9.988    0.000   19.870    0.778
   .sccaps            7.090   15.210    0.466    0.641    7.090    0.086
    visual            1.000                               1.000    1.000
    verbal            1.000                               1.000    1.000
    speed             1.000                               1.000    1.000

R-Square:
                   Estimate
    visperc           0.576
    cubes             0.188
    lozenges          0.347
    parcomp           0.724
    sencomp           0.733
    wordmean          0.702
    addition          0.124
    countdot          0.222
    sccaps            0.914
```

Note that the newly freed parameter, **`addition ~~ countdot`** is statistically significantly different from zero. The standardized estimate indicates that **`addition`** and **`countdots`** are moderately correlated above and beyond the correlation implied by the common **`speed`** factor (r = .389). Note further the substantial reduction in residual variance estimates for items loading on **`speed`**. Specifically, even though **`sccaps`** is not directly involved in the residual correlation between **`addition`** and **`countdot`**, its residual variance was substantially reduced. By accounting for the local dependence between **`addition`** and **`countdot`** with the residual covariance, **`speed`** was able to account for more of the variance in **`sccaps`**. This is further evidenced by the fact that **sccaps** is now the highest loading item on the factor. It now appears that **sccaps** is almost definitional of the **speed** factor, with a communality of .914, whereas the communalities of **countdots** and **addition** are much lower.

As with the previous example, introducing this single new parameter resulted in no further sizeable modification indices.

```
modindices(fit.3, sort.=TRUE, minimum.value=10)
```

```
[1] lhs      op       rhs      mi       epc      sepc.lv  sepc.all sepc.nox
<0 rows> (or 0-length row.names)
```

This model is not nested with the alternative modified model; however, the two models provide nearly equivalent fit (RMSEA=.065 versus .066, TLI=.948 versus .946, etc.). Thus, model selection should be based on which modification is most plausible, and upon the interpretability of parameter estimates.

Chapter 5
Structural Equation Models with Latent Variables

Structural Equation Modeling of Şenol-Durak and Ayvaşik's Posttraumatic Growth Data

The data for this demonstration were provided by Şenol-Durak & Ayvaşik in their 2010 *Journal of Health Psychology* manuscript, "Factors associated with posttraumatic growth among the spouses of myocardial infraction patients." The sample includes 132 spouses of myocardial infarction patients. The correlation matrix is in the text file `mip.dat`. We will enter the means and standard deviations into R directly. The R script for this chapter is contained in the file `ch05.R`.

The variables in the data set that we will use are

`fa`	social support from family	
`fr`	social support from friends	*Environmental Resources*
`si`	social support from significant others	
`lo`	Locus of Control Scale score	
`comt`	Commitment score	
`con`	Control score	*Individual Resources*
`cha`	Challenge score	
`es`	Rosenberg Self Esteem Scale score	
`pro`	subjective evaluation of prognosis	
`th`	threat to future health	*Event Related Factors*
`time`	time since diagnosis	
`em`	emotion focused coping	
`ind`	indirect coping (labeled `in` in diagrams)	
`ru`	rumination	*Cognitive Process Coping*
`av`	avoidance	
`hy`	hypervigilance	
`rb`	religious beliefs	
`ptgi1`	improved relationships	
`ptgi2`	new possibilities for one's life	
`ptgi3`	greater appreciation of life	*Posttraumatic Growth*
`ptgi4`	greater sense of personal strength	
`ptgi5`	spiritual development	

Refer to the article for definitions of variables not included in the model.

Preliminary Steps

This example illustrates how summary statistics can be used to fit structural equation models in lavaan. To do so, we require the covariance matrix of the observed variables. For generality, we will also bring in the mean vector, although it plays no part in the fit of this particular model (because the model is saturated in the means). In this case, we have the correlation matrix and thus must construct the covariance matrix from the correlations and standard deviations.

To begin, we load the lavaan package

```
library(lavaan)
```

We then define the variable names (this includes variables not used in the models fit here):

```
names <- c("ptgi","ptgi1", "ptgi2", "ptgi3", "ptgi4", "ptgi5",
           "marital", "fa", "fr", "si", "child", "child18",
           "age", "gender", "depres", "comt", "con", "cha",
           "es", "lo", "pro", "th", "diord", "time", "problem",
           "em", "ind", "ru", "av", "hy", "relipart", "rb")
```

As a side note, here we used the name **ind** for indirect coping rather than **in** because the latter has a special meaning and thus cannot be used as a variable name.

Next, we enter the means and standard deviations reported in the manuscript (in the same order as the variable names):

```
mip.mns <- c(59.18, 19.84, 10.53, 12.65, 9.80, 6.35,
             9.53, 24.96, 19.89, 18.24, 2.68, .45,
             52.04, .11, 9.37, 10.36, 10.35, 9.93,
             30.33, 80.47, 2.67, 1.78, .47, 3.91, 70.58,
             38.87, 24.34, 12.26, 11.80, 9.17, .81, 2.74)

mip.sds <- c(24.24, 9.00, 6.89, 5.22, 3.73, 3.05,
             2.59, 3.87, 6.07, 7.48, 1.07, .81,
            11.04, .318, 6.57, 2.65, 3.27, 2.45,
            5.92, 18.12, .74, 1.14, .50, 8.05, 11.94,
            11.41, 6.83, 7.51, 5.51, 5.94, 1.24, .92)
```

Finally, we read in the correlations from the file **mip.dat** using the **read.table** function and convert the correlation matrix to a covariance matrix with the following commands:

```
mip.cor <- read.table("mip.dat", header=FALSE, row.names=names, col.names=names)
mip.cor <- data.matrix(mip.cor)
mip.cov <- cor2cov(mip.cor,sds=mip.sds)
```

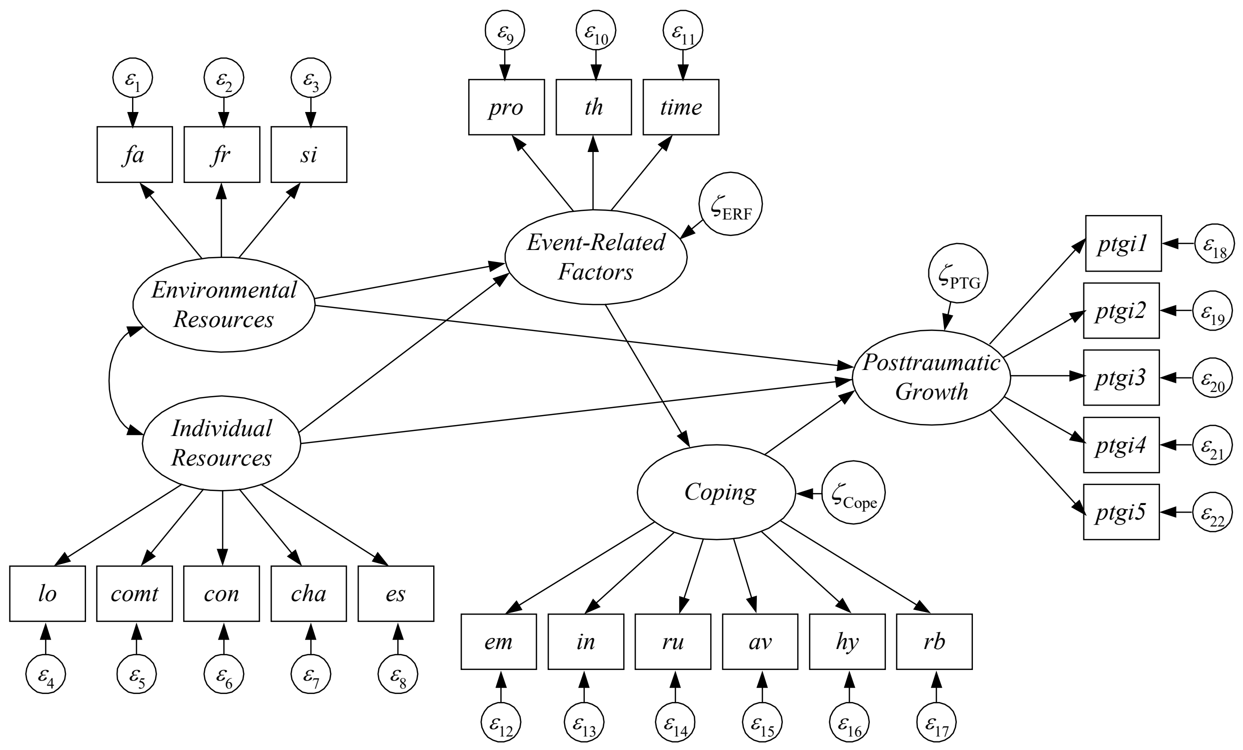
The **mip.dat** file is a space-delimited text file that contains a full correlation matrix (diagonal of 1's as well as all elements above and below the diagonal). The **read.table** function creates a data frame from this file called **mip.cor** with rows and columns labeled by the variable names we input previously. We then convert **mip.cor** to a numeric matrix using the **data.matrix** function. Finally, we use the **cor2cov** function of lavaan to convert the correlation matrix into a covariance matrix, utilizing the information we provided on the standard deviations in the vector **mip.sds**.

Note that it is also possible to read in a lower triangular correlation matrix and convert it to a full covariance matrix using the **getCov** function in lavaan. Here, however, the data was originally entered as a full correlation matrix.

We now have the sufficient statistics, the covariance matrix **mip.cov** and the mean vector **mip.mns**, ready for use with lavaan. We can thus proceed to specify and fit the hypothesized structural equation model.

Initial Hypothesized Model

The hypothesized model for the data predicts that both individual and environmental resources directly lead to increased posttraumatic growth, but also indirectly lead to somewhat decreased posttraumatic growth by reducing event-related hardship, thus decreasing the need for coping and reducing opportunities for posttraumatic growth. The hypothesized model also predicts that neither environmental nor individual resources have a direct impact on cognitive coping. Further, the effect of event-related factors on posttraumatic growth is hypothesized to be purely mediated by coping.



We can also express the model using matrix algebra, as shown on the next page.

The measurement model is:

$$\begin{bmatrix} fa_i \\ fr_i \\ si_i \\ lo_i \\ comt_i \\ con_i \\ cha_i \\ es_i \\ pro_i \\ th_i \\ time_i \\ em_i \\ in_i \\ ru_i \\ av_i \\ hy_i \\ rb_i \\ ptgi_{1i} \\ ptgi_{2i} \\ ptgi_{3i} \\ ptgi_{4i} \\ ptgi_{5i} \end{bmatrix} = \begin{bmatrix} \nu_{1i} \\ \nu_{2i} \\ \nu_{3i} \\ \nu_{4i} \\ \nu_{5i} \\ \nu_{6i} \\ \nu_{7i} \\ \nu_{8i} \\ \nu_{9i} \\ \nu_{10i} \\ \nu_{11i} \\ \nu_{12i} \\ \nu_{13i} \\ \nu_{14i} \\ \nu_{15i} \\ \nu_{16i} \\ \nu_{17i} \\ \nu_{18i} \\ \nu_{19i} \\ \nu_{20i} \\ \nu_{21i} \\ \nu_{22i} \end{bmatrix} + \begin{bmatrix} \lambda_{11} & 0 & 0 & 0 & 0 \\ \lambda_{21} & 0 & 0 & 0 & 0 \\ \lambda_{31} & 0 & 0 & 0 & 0 \\ 0 & \lambda_{42} & 0 & 0 & 0 \\ 0 & \lambda_{52} & 0 & 0 & 0 \\ 0 & \lambda_{62} & 0 & 0 & 0 \\ 0 & \lambda_{72} & 0 & 0 & 0 \\ 0 & \lambda_{82} & 0 & 0 & 0 \\ 0 & 0 & \lambda_{93} & 0 & 0 \\ 0 & 0 & \lambda_{10,3} & 0 & 0 \\ 0 & 0 & \lambda_{11,3} & 0 & 0 \\ 0 & 0 & 0 & \lambda_{12,4} & 0 \\ 0 & 0 & 0 & \lambda_{13,4} & 0 \\ 0 & 0 & 0 & \lambda_{14,4} & 0 \\ 0 & 0 & 0 & \lambda_{15,4} & 0 \\ 0 & 0 & 0 & \lambda_{16,4} & 0 \\ 0 & 0 & 0 & \lambda_{17,4} & 0 \\ 0 & 0 & 0 & 0 & \lambda_{18,5} \\ 0 & 0 & 0 & 0 & \lambda_{19,5} \\ 0 & 0 & 0 & 0 & \lambda_{20,5} \\ 0 & 0 & 0 & 0 & \lambda_{21,5} \\ 0 & 0 & 0 & 0 & \lambda_{22,5} \end{bmatrix} \begin{bmatrix} \eta_{ERi} \\ \eta_{IRi} \\ \eta_{ERFi} \\ \eta_{COPE_i} \\ \eta_{PTGi} \end{bmatrix} + \begin{bmatrix} \varepsilon_{1i} \\ \varepsilon_{2i} \\ \varepsilon_{3i} \\ \varepsilon_{4i} \\ \varepsilon_{5i} \\ \varepsilon_{6i} \\ \varepsilon_{7i} \\ \varepsilon_{8i} \\ \varepsilon_{9i} \\ \varepsilon_{10i} \\ \varepsilon_{11i} \\ \varepsilon_{12i} \\ \varepsilon_{13i} \\ \varepsilon_{14i} \\ \varepsilon_{15i} \\ \varepsilon_{16i} \\ \varepsilon_{17i} \\ \varepsilon_{18i} \\ \varepsilon_{19i} \\ \varepsilon_{20i} \\ \varepsilon_{21i} \\ \varepsilon_{22i} \end{bmatrix}$$

where $\mathbf{\Theta} = DIAG\left(\theta_{11}, \theta_{22}, \ldots, \theta_{22,22}\right)$

The latent variable model is:

$$\begin{bmatrix} \eta_{ERi} \\ \eta_{IRi} \\ \eta_{ERFi} \\ \eta_{COPE_i} \\ \eta_{PTGi} \end{bmatrix} = \begin{bmatrix} 0 \\ 0 \\ 0 \\ 0 \\ 0 \end{bmatrix} + \begin{bmatrix} 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ \beta_{31} & \beta_{32} & 0 & 0 & 0 \\ 0 & 0 & \beta_{43} & 0 & 0 \\ \beta_{51} & \beta_{52} & 0 & \beta_{54} & 0 \end{bmatrix} \begin{bmatrix} \eta_{ERi} \\ \eta_{IRi} \\ \eta_{ERFi} \\ \eta_{COPE_i} \\ \eta_{PTGi} \end{bmatrix} + \begin{bmatrix} \zeta_{ERi} \\ \zeta_{IRi} \\ \zeta_{ERFi} \\ \zeta_{COPE_i} \\ \zeta_{PTGi} \end{bmatrix}$$

where $\mathbf{\Psi} = \begin{bmatrix} 1 & & & & \\ \psi_{21} & 1 & & & \\ 0 & 0 & 1 & & \\ 0 & 0 & 0 & 1 & \\ 0 & 0 & 0 & 0 & 1 \end{bmatrix}$

Note that the means/intercepts and (residual) variances of the factors have been fixed to 0 and 1, respectively to scale the latent variables. In class, we used the *t*-rule and the two-step rule to verify that the model is identified. We can thus go on to specify the model in lavaan.

Here we specify the model syntax object for the hypothesized SEM and fit the model.

```
mod.1 <-'#specifying measurement model portion
         ER =~ fa + fr + si
         IR =~ comt + con + cha + es + lo
         ERF =~ pro + th + time
         CPP =~ em + ind + ru + av + hy + rb
         PTG =~ ptgi1 + ptgi2 + ptgi3 + ptgi4 + ptgi5

         #specifying structural model portion
         ERF ~ ER + IR
         CPP ~ ERF
         PTG ~ ER + IR + CPP
        '

fit.1 <- sem(mod.1, sample.cov=mip.cov, sample.mean=mip.mns, sample.nobs=132,
             meanstructure=TRUE, std.lv=TRUE)
summary(fit.1, fit.measures=TRUE, estimates=FALSE)
```

We have seen most of these commands before, so here we will highlight only portions of the code.

Lavaan accepts either raw data or summary data (i.e., means, standard deviations, and correlations among variables). As a default, lavaan assumes that data are in raw format. Since the data from this example are in summary form, we used the **`sample.cov`**, **`sample.mean`**, and **`sample.nobs`** arguments of the **`sem`** function, indicating the covariance matrix, mean vector, and number of observations in the data, respectively.

As in Chapter 4, the measurement model for the latent variables is specified using the **=~** operator. As in Chapters 1-3, regression equations are specified via the **~** operator, the only difference here being that we are referencing the latent variables.

To set the scale of the latent factors, we have standardized the factor (residual) variances by using **`std.lv=TRUE`** in the **`sem`** function call.

Within the **`summary`** function, we requested only the fit measures. We will examine the model estimates only after obtaining a model that we deem to fit the data reasonably well.

Let us now turn to the fit indices for the model:

```
lavaan 0.6-2 ended normally after 53 iterations

  Optimization method                           NLMINB
  Number of free parameters                         73

  Number of observations                           132

  Estimator                                         ML
  Model Fit Test Statistic                     350.000
  Degrees of freedom                               202
  P-value (Chi-square)                           0.000

Model test baseline model:

  Minimum Function Test Statistic             1205.231
  Degrees of freedom                               231
  P-value                                        0.000

User model versus baseline model:

  Comparative Fit Index (CFI)                    0.848
  Tucker-Lewis Index (TLI)                       0.826

Loglikelihood and Information Criteria:

  Loglikelihood user model (H0)              -8012.004
  Loglikelihood unrestricted model (H1)      -7837.004

  Number of free parameters                         73
  Akaike (AIC)                               16170.009
  Bayesian (BIC)                             16380.453
  Sample-size adjusted Bayesian (BIC)        16149.553

Root Mean Square Error of Approximation:

  RMSEA                                          0.075
  90 Percent Confidence Interval          0.061  0.087
  P-value RMSEA <= 0.05                          0.002

Standardized Root Mean Square Residual:

  SRMR                                           0.101
```

The fit indices indicate that the model does not fit the data well. Rather than examining the parameter estimates, we will next look at the modification indices to get a sense for what might be causing the model to fit poorly, keeping in mind that any model modification must be theoretically justifiable.

```
modindices(fit.1, sort.=TRUE, minimum.value=10)
```

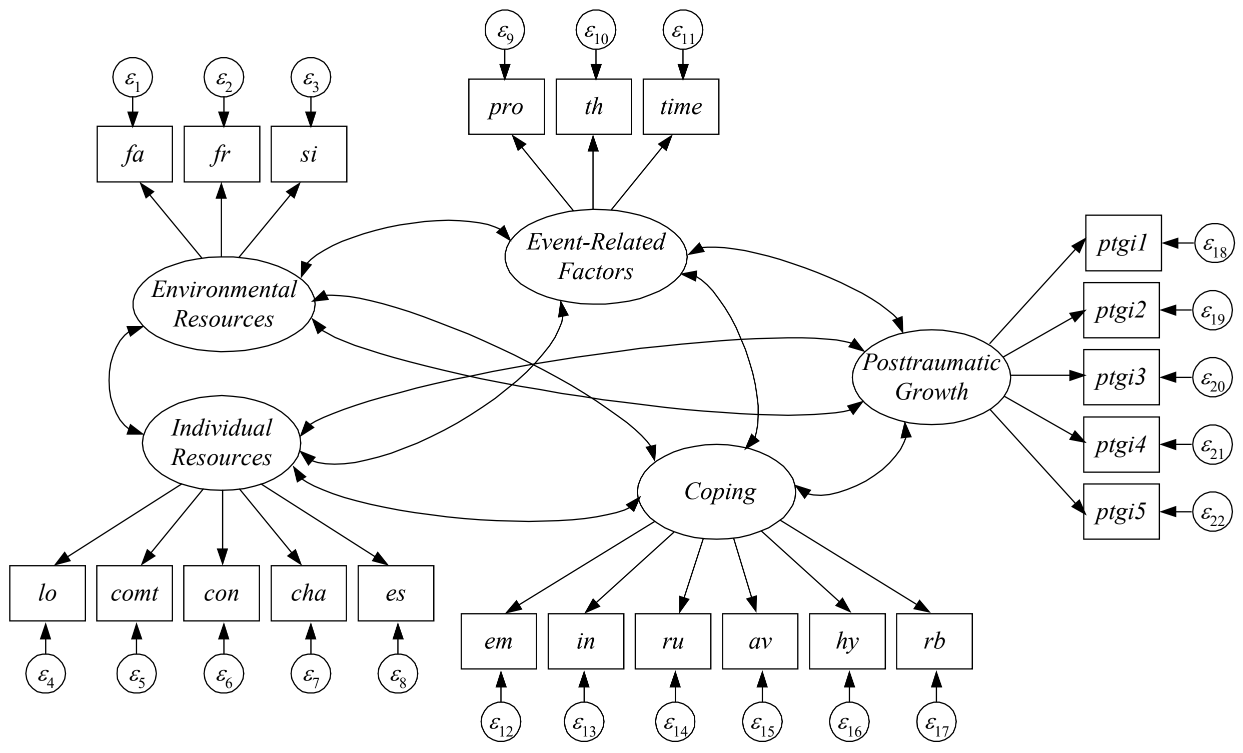
```
     lhs op   rhs     mi     epc sepc.lv sepc.all sepc.nox
368   ru ~~    hy 32.238  34.381  34.381    4.461    4.461
233 comt ~~   cha 27.844   2.684   2.684    0.546    0.546
348   em ~~   ind 21.340 -26.655 -26.655   -0.410   -0.410
183   fa ~~   ind 14.250  -7.574  -7.574   -0.333   -0.333
250  con ~~   cha 12.343  -2.215  -2.215   -0.381   -0.381
119   IR =~ ptgi5 11.877  -0.730  -0.730   -0.241   -0.241
256  con ~~    em 10.695  -8.717  -8.717   -0.304   -0.304
160  PTG =~   cha 10.321   0.590   0.688    0.282    0.282
```

Modification indices suggest that the largest improvement to the model chi-square could be achieved by allowing hypervigilance to correlate with rumination, over and above the correlation implied by the coping factor, allowing challenge to correlate with commitment over and above the individual resources factor, and allowing indirect and emotional coping to correlate above and beyond the correlation implied by the coping factor. These modifications reflect misspecification in the measurement model.

Confirmatory Factor Analysis

When building a structural equation model, a useful strategy to isolate misspecification is to begin by ensuring that the foundation of the overall model, the measurement model, is correctly specified. Once the measurement model has been properly specified, one can consider misfit introduced by the structural model. Thus, we turn next to a CFA with saturated covariances among factors. This strategy will allow us to get measurement right so that measurement misspecification is not confounded with structural misfit.

The CFA model is shown below.



The corresponding script to specify and fit this model is

```
mod.2 <-'#specifying measurement model
         ER =~ fa + fr + si
         IR =~ comt + con + cha + es + lo
         ERF =~ pro + th + time
         CPP =~ em + ind + ru + av + hy + rb
         PTG =~ ptgi1 + ptgi2 + ptgi3 + ptgi4 + ptgi5
        '

fit.2 <- sem(mod.2, sample.cov=mip.cov, sample.mean=mip.mns, sample.nobs=132,
             meanstructure=TRUE, std.lv=TRUE)
summary(fit.2, fit.measures=TRUE, estimates=FALSE)
```

The model fit information is shown below:

```
lavaan 0.6-2 ended normally after 53 iterations

  Optimization method                           NLMINB
  Number of free parameters                         76

  Number of observations                           132

  Estimator                                         ML
  Model Fit Test Statistic                     348.636
  Degrees of freedom                               199
  P-value (Chi-square)                           0.000

Model test baseline model:

  Minimum Function Test Statistic             1205.231
  Degrees of freedom                               231
  P-value                                        0.000

User model versus baseline model:

  Comparative Fit Index (CFI)                    0.846
  Tucker-Lewis Index (TLI)                       0.822

Loglikelihood and Information Criteria:

  Loglikelihood user model (H0)              -8011.322
  Loglikelihood unrestricted model (H1)      -7837.004

  Number of free parameters                         76
  Akaike (AIC)                               16174.645
  Bayesian (BIC)                             16393.738
  Sample-size adjusted Bayesian (BIC)        16153.348
```

```
Root Mean Square Error of Approximation:

  RMSEA                                         0.075
  90 Percent Confidence Interval         0.062  0.088
  P-value RMSEA <= 0.05                         0.001

Standardized Root Mean Square Residual:

  SRMR                                          0.099
```

The model still does not fit the data well, confirming our hypothesis that the measurement model, and not the structural model, is misspecified. Indeed, we can conduct a likelihood ratio test comparing the CFA model with the originally hypothesized SEM because the hypothesized model is a constrained version of the CFA with three structural parameters fixed to zero.

```
lavTestLRT(fit.2, fit.1)
```

```
Chi Square Difference Test

       Df   AIC   BIC  Chisq Chisq diff Df diff Pr(>Chisq)
fit.2 199 16175 16394 348.64
fit.1 202 16170 16380 350.00     1.3639       3      0.714
```

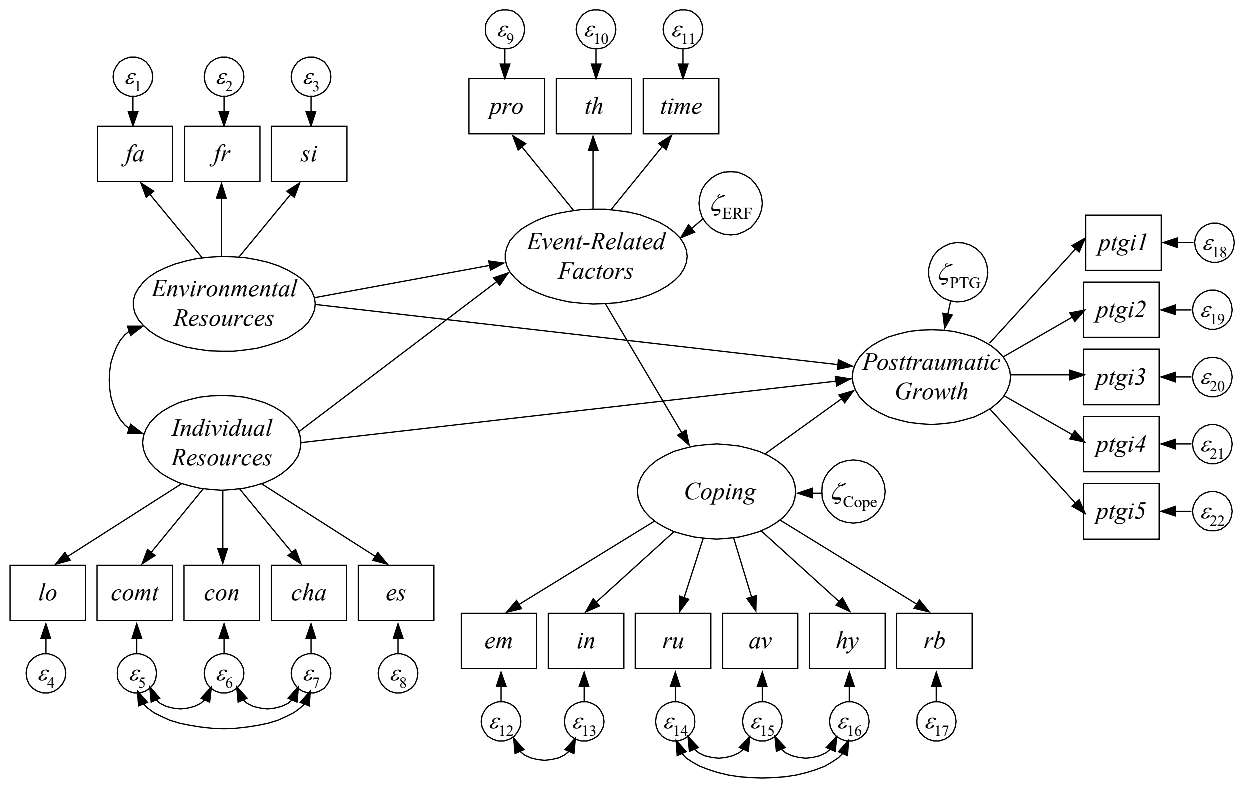
Thus, there is no significant decrement in fit associated with restricting the relationships among the latent variables:

$$\Delta\chi^2(3) = 350.00 - 348.64 = 1.36, p = .71$$

Combining this information with the information provided earlier from the modification indices, we can conclude that the measurement model is the primary source of misfit and requires respecification. Theoretically, allowing some residuals to correlate (as suggested by the MIs) makes sense because some factors include multiple subscale scores as indicators. When combined with other items from different scales, we would expect some degree of local dependence for subscales from a common measure. Specifically, the **IR** factor includes three Psychological Hardiness subscale scores as indicators (**comt**, **con**, and **cha**), but also two indicators from independent scales (**lo** and **es**). The coping factor includes two indicators from the Ways of Coping Inventory (**em** and **ind**), three indicators from the Impact of Event Scale (**ru**, **av**, and **hy**), and a religious beliefs score from another scale (**rb**).

Revised Model

We now introduce correlated uniquenesses for **comt**, **con**, and **cha** on the individual resources factor, between **em** and **ind** on the coping factor, and among **ru**, **av**, and **hy** on the coping factor.



These correlated uniquenesses are included in a new model syntax object:

```
mod.3 <-'#specifying measurement model portion
         ER =~ fa + fr + si
         IR =~ comt + con + cha + es + lo
         ERF =~ pro + th + time
         CPP =~ em + ind + ru + av + hy + rb
         PTG =~ ptgi1 + ptgi2 + ptgi3 + ptgi4 + ptgi5

         #specifying structural model portion
         ERF ~ ER + IR
         CPP ~ ERF
         PTG ~ ER + IR + CPP

         #correlating uniquenesses of same-scale items
         comt ~~ con + cha
         con ~~ cha
         em ~~ ind
         ru ~~ av + hy
         av ~~ hy
        '
```

```
fit.3 <- sem(mod.3, sample.cov=mip.cov, sample.mean=mip.mns, sample.nobs=132,
             meanstructure=TRUE, std.lv=TRUE)
summary(fit.3, fit.measures=TRUE, standardized=TRUE, rsquare=TRUE)
```

Lavaan does not use separate names for uniquenesses/residuals/disturbances. Instead, uniquenesses or disturbances are referred to by the referent variable. Thus, the line **`comt ~~ con + cha`** thus includes a covariance between the uniquenesses of **`comt`** and **`con`** and between **`comt`** and **`cha`**.

The model fit is shown here:

```
lavaan 0.6-2 ended normally after 138 iterations

  Optimization method                           NLMINB
  Number of free parameters                         80

  Number of observations                           132

  Estimator                                         ML
  Model Fit Test Statistic                     270.278
  Degrees of freedom                               195
  P-value (Chi-square)                           0.000

Model test baseline model:

  Minimum Function Test Statistic             1205.231
  Degrees of freedom                               231
  P-value                                        0.000

User model versus baseline model:

  Comparative Fit Index (CFI)                    0.923
  Tucker-Lewis Index (TLI)                       0.908

Loglikelihood and Information Criteria:

  Loglikelihood user model (H0)              -7972.143
  Loglikelihood unrestricted model (H1)      -7837.004

  Number of free parameters                         80
  Akaike (AIC)                               16104.287
  Bayesian (BIC)                             16334.911
  Sample-size adjusted Bayesian (BIC)        16081.869

Root Mean Square Error of Approximation:

  RMSEA                                          0.054
  90 Percent Confidence Interval          0.037  0.069
  P-value RMSEA <= 0.05                          0.325
```

```
Standardized Root Mean Square Residual:

  SRMR                                           0.090
```

We can evaluate the improvement in fit associated with adding these 7 new free parameters to the hypothesized model via the chi-square difference (likelihood ratio) test:

```
lavTestLRT(fit.3, fit.1)
```

```
Chi Square Difference Test

       Df   AIC   BIC  Chisq Chisq diff Df diff Pr(>Chisq)
fit.3 195 16104 16335 270.28
fit.1 202 16170 16380 350.00     79.722       7  1.569e-14 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

These results show that the correlated uniquenesses significantly improved the fit of the model:

$$\Delta\chi^2(7) = 350.00 - 270.28 = 79.72, p < .001 .$$

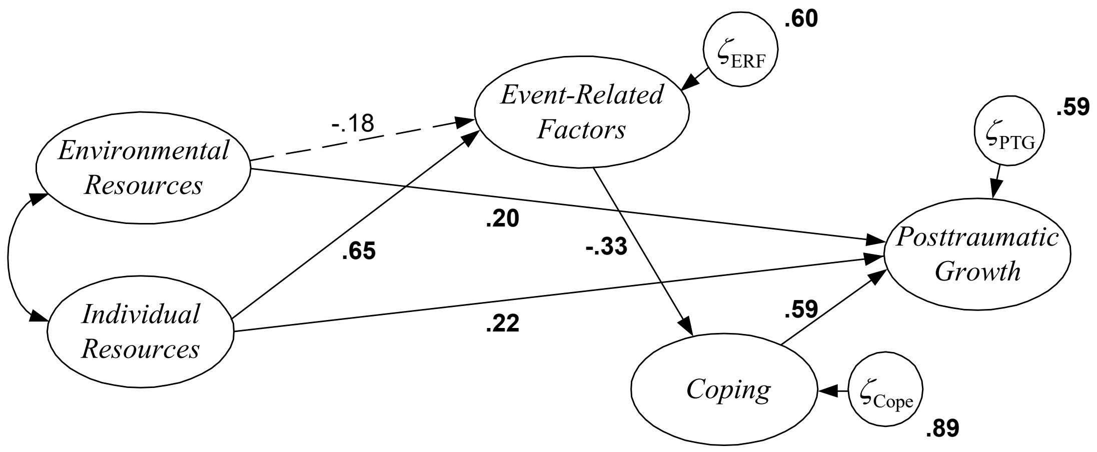
Other fit indices suggest that the modified model fits the data reasonably well (though not wonderfully).

Raw and fully standardized parameter estimates are presented below.

```
Latent Variables:
                   Estimate  Std.Err  z-value  P(>|z|)   Std.lv  Std.all
  ER =~
    fa                1.317    0.362    3.637    0.000    1.317    0.342
    fr                5.855    0.767    7.634    0.000    5.855    0.968
    si                4.457    0.776    5.740    0.000    4.457    0.598
  IR =~
    comt              1.028    0.290    3.538    0.000    1.028    0.389
    con               2.312    0.325    7.105    0.000    2.312    0.710
    cha               1.141    0.264    4.323    0.000    1.141    0.468
    es                3.007    0.551    5.453    0.000    3.007    0.510
    lo              -11.555    1.675   -6.897    0.000  -11.555   -0.640
  ERF =~
    pro               0.347    0.103    3.365    0.001    0.446    0.606
    th               -0.342    0.114   -3.012    0.003   -0.440   -0.387
    time              1.316    0.743    1.772    0.076    1.693    0.211
  CPP =~
    em                6.060    1.103    5.495    0.000    6.429    0.566
    ind              -3.100    0.668   -4.645    0.000   -3.289   -0.483
    ru                4.173    0.798    5.229    0.000    4.427    0.592
    av                2.958    0.587    5.039    0.000    3.138    0.572
    hy                3.725    0.625    5.962    0.000    3.952    0.668
    rb                0.221    0.088    2.515    0.012    0.235    0.256
  PTG =~
    ptgi1             6.035    0.633    9.538    0.000    7.837    0.874
    ptgi2             4.578    0.484    9.457    0.000    5.945    0.866
    ptgi3             2.974    0.365    8.146    0.000    3.862    0.743
    ptgi4             2.259    0.261    8.649    0.000    2.933    0.790
    ptgi5             1.879    0.214    8.794    0.000    2.440    0.803

Regressions:
                   Estimate  Std.Err  z-value  P(>|z|)   Std.lv  Std.all
  ERF ~
    ER               -0.236    0.181   -1.305    0.192   -0.183   -0.183
    IR                0.834    0.293    2.840    0.005    0.648    0.648
  CPP ~
    ERF              -0.276    0.130   -2.120    0.034   -0.334   -0.334
  PTG ~
    ER                0.259    0.118    2.201    0.028    0.200    0.200
    IR                0.284    0.139    2.039    0.041    0.219    0.219
    CPP               0.722    0.168    4.299    0.000    0.590    0.590

Covariances:
                   Estimate  Std.Err  z-value  P(>|z|)   Std.lv  Std.all
 .comt ~~
   .con              -1.601    0.699   -2.292    0.022   -1.601   -0.287
   .cha               2.242    0.601    3.729    0.000    2.242    0.427
 .con ~~
   .cha              -1.923    0.648   -2.967    0.003   -1.923   -0.388
 .em ~~
   .ind             -16.748    6.617   -2.531    0.011  -16.748   -0.300
 .ru ~~
   .av                2.123    3.766    0.564    0.573    2.123    0.078
   .hy               19.248    4.875    3.948    0.000   19.248    0.725
 .av ~~
   .hy               -0.383    2.978   -0.129    0.898   -0.383   -0.019
  ER ~~
    IR                0.244    0.101    2.407    0.016    0.244    0.244

Intercepts:
                   Estimate  Std.Err  z-value  P(>|z|)   Std.lv  Std.all
   .fa               24.960    0.336   74.382    0.000   24.960    6.474
   .fr               19.890    0.526   37.791    0.000   19.890    3.289
   .si               18.240    0.649   28.123    0.000   18.240    2.448
   .comt             10.360    0.230   45.087    0.000   10.360    3.924
   .con              10.350    0.284   36.503    0.000   10.350    3.177
   .cha               9.930    0.212   46.744    0.000    9.930    4.069
   .es               30.330    0.513   59.087    0.000   30.330    5.143
   .lo               80.470    1.571   51.217    0.000   80.470    4.458
   .pro               2.670    0.064   41.612    0.000    2.670    3.622
   .th                1.780    0.099   18.008    0.000    1.780    1.567
   .time              3.910    0.698    5.602    0.000    3.910    0.488
   .em               38.870    0.989   39.289    0.000   38.870    3.420
   .ind              24.340    0.592   41.100    0.000   24.340    3.577
   .ru              12.260    0.651   18.827    0.000   12.260    1.639
   .av              11.800    0.478   24.698    0.000   11.800    2.150
   .hy               9.170    0.515   17.804    0.000    9.170    1.550
   .rb               2.740    0.080   34.348    0.000    2.740    2.990
   .ptgi1           19.840    0.780   25.432    0.000   19.840    2.214
   .ptgi2           10.530    0.597   17.632    0.000   10.530    1.535
   .ptgi3           12.650    0.453   27.956    0.000   12.650    2.433
   .ptgi4            9.800    0.323   30.309    0.000    9.800    2.638
   .ptgi5            6.350    0.264   24.018    0.000    6.350    2.091
    ER               0.000                               0.000    0.000
    IR               0.000                               0.000    0.000
   .ERF              0.000                               0.000    0.000
   .CPP              0.000                               0.000    0.000
   .PTG              0.000                               0.000    0.000

Variances:
                  Estimate  Std.Err  z-value  P(>|z|)   Std.lv  Std.all
   .fa              13.130    1.669    7.867    0.000   13.130    0.883
   .fr               2.287    7.782    0.294    0.769    2.287    0.063
   .si              35.663    6.303    5.658    0.000   35.663    0.642
   .comt             5.913    0.825    7.170    0.000    5.913    0.848
   .con              5.269    1.182    4.457    0.000    5.269    0.496
   .cha              4.654    0.694    6.704    0.000    4.654    0.781
   .es              25.739    3.570    7.209    0.000   25.739    0.740
   .lo             192.339   31.799    6.049    0.000  192.339    0.590
   .pro              0.344    0.083    4.156    0.000    0.344    0.633
   .th               1.096    0.157    6.966    0.000    1.096    0.850
   .time            61.446    7.847    7.830    0.000   61.446    0.955
   .em              87.866   14.001    6.276    0.000   87.866    0.680
   .ind             35.475    5.157    6.879    0.000   35.475    0.766
   .ru              36.371    6.685    5.441    0.000   36.371    0.650
   .av              20.284    3.598    5.638    0.000   20.284    0.673
   .hy              19.397    4.201    4.618    0.000   19.397    0.554
   .rb               0.785    0.099    7.895    0.000    0.785    0.934
   .ptgi1           18.908    3.311    5.711    0.000   18.908    0.235
   .ptgi2           11.741    1.995    5.886    0.000   11.741    0.249
   .ptgi3           12.112    1.676    7.227    0.000   12.112    0.448
   .ptgi4            5.196    0.752    6.911    0.000    5.196    0.377
   .ptgi5            3.275    0.482    6.789    0.000    3.275    0.355
    ER               1.000                               1.000    1.000
    IR               1.000                               1.000    1.000
   .ERF              1.000                               0.604    0.604
   .CPP              1.000                               0.888    0.888
   .PTG              1.000                               0.593    0.593
```

We focus on the structural parameter estimates in this chapter because interpretation of measurement models has been discussed previously. **`IR`** has a significant direct effect on **`ERF`** ($\gamma = .834$; S.E. = .293; *p* = .005) and **`PTG`** ($\gamma = .284$; S.E. = .139; *p* = .041). **`ER`** has a significant direct effect on **`PTG`** ($\gamma = .259$; S.E. = .118; *p* = .28) and **`coping`** ($\gamma = -.276$; S.E. = .130; *p* = .034). **`Coping`** is significantly related to **`PTG`** ($\gamma = .722$; S.E. = .168 *p* < .001).

The standardized structural parameter estimates have been drawn on the path diagram below to enhance interpretation of the model results. The non-significant path from environmental resources to event-related factors is dashed. All other paths are statistically significant and shown with solid lines.



We can also examine the R-square statistics to get a sense of the magnitude of these effects:

```
R-Square:
                  Estimate
    fa               0.117
    fr               0.937
    si               0.358
    comt             0.152
    con              0.504
    cha              0.219
    es               0.260
    lo               0.410
    pro              0.367
    th               0.150
    time             0.045
    em               0.320
    ind              0.234
    ru               0.350
    av               0.327
    hy               0.446
    rb               0.066
    ptgi1            0.765
    ptgi2            0.751
    ptgi3            0.552
    ptgi4            0.623
    ptgi5            0.645
    ERF              0.396
    CPP              0.112
    PTG              0.407
```

Together, these results suggest that environmental and individual resources have a moderate, direct, positive influence on posttraumatic growth, cognitive coping has a strong, direct, positive influence on posttraumatic growth, individual resources strongly predict more event-related factors (shorter time since prognosis, poorer prognosis, and greater threat), and more positive event-related factors predicts moderately less cognitive coping. Individual resources and event related factors have a complex relationship with posttraumatic growth. To better understand these relationships, we must consider direct, indirect, and total effects.

Examining Direct, Indirect and Total Effects

As in Chapter 3, to compute and test indirect and total effects, we need to modify the model syntax object to include parameter labels for the paths involved in the effects so that we can define the effects of interest. Here we will focus on the effects on post-traumatic growth.

```
mod.3b <-'#specifying measurement model portion
          ER =~ fa + fr + si
          IR =~ comt + con + cha + es + lo
          ERF =~ pro + th + time
          CPP =~ em + ind + ru + av + hy + rb
          PTG =~ ptgi1 + ptgi2 + ptgi3 + ptgi4 + ptgi5

          #specifying structural model portion
          ERF ~ a1*ER + a2*IR
          CPP ~ b*ERF
          PTG ~  d1*ER + d2*IR + c*CPP

          #correlating uniquenesses of same-scale items
          comt ~~ con + cha
          con ~~ cha
          em ~~ ind
          ru ~~ av + hy
          av ~~ hy

          #effects of ERF
          dir_ERF := 0
          ind_ERF := b*c
          tot_ERF := 0 + b*c

          #effects of ER
          dir_ER := d1
          ind_ER := a1*b*c
          tot_ER := d1 + a1*b*c

          #effects of IR
          dir_IR := d2
          ind_IR := a2*b*c
          tot_IR := d2 + a2*b*c
         '
fit.3b <- sem(mod.3b, sample.cov=mip.cov, sample.mean=mip.mns,
              sample.nobs=132, meanstructure=TRUE, std.lv=TRUE)
summary(fit.3b, fit.measures=TRUE, standardized=TRUE, rsquare=TRUE)
```

We will thus obtain direct, indirect and total effect estimates of **ERF**, **IR**, and **ER** on **PTG**.

Most of the results obtained by fitting this model are identical to those presented previously, so only the new information associated with the effect decomposition is shown below:

```
Defined Parameters:
                   Estimate  Std.Err  z-value  P(>|z|)   Std.lv  Std.all
    dir_ERF           0.000                                0.000    0.000
    ind_ERF          -0.199    0.100   -1.982    0.047   -0.197   -0.197
    tot_ERF          -0.199    0.100   -1.982    0.047   -0.197   -0.197
    dir_ER            0.259    0.118    2.201    0.028    0.200    0.200
    ind_ER            0.047    0.041    1.152    0.249    0.036    0.036
    tot_ER            0.306    0.123    2.494    0.013    0.236    0.236
    dir_IR            0.284    0.139    2.039    0.041    0.219    0.219
    ind_IR           -0.166    0.091   -1.833    0.067   -0.128   -0.128
    tot_IR            0.118    0.132    0.893    0.372    0.091    0.091
```

For each predictor-to-outcome effect, we have directed lavaan to first compute the direct effect, then the indirect effect, and finally the total effect (along with standard errors and significance tests). Standard errors are computed using the delta method (producing what is known as the Sobel test for the indirect effects). Unlike in Chapter 3, we cannot use non-parametric bootstrapping to obtain more accurate standard errors because we do not have access to the raw data.

We will closely examine the effect of **IR** on **PTG**. We start by noting that the total effect of **IR** on **PTG** is nonsignificant (*p* = .372). Upon closer examination, however, it is apparent that **IR** is related to **PTG** both directly and indirectly. These effects are in opposite directions such that the net, total effect is nearly zero. The direct effect of **IR** on **PTG** is positive and significant (*p* = .041), whereas the indirect effect is negative and marginally significant (*p* = .067).

Appendix A: Generating Path Diagrams in R

This appendix presents a fully worked example drawn from class demonstrating the creation of path diagrams from lavaan fit objects using the **`semPlot`** package developed by Sacha Epskamp. There are likely other packages that could be used for the same purpose.

Some software programs also offer the ability to draw a path diagram and infer the model specification syntax from the diagram. For instance, the free stand-alone program Ωnyx can produce lavaan script based on a user-specified diagram (see http://onyx.brandmaier.de).

Holzinger-Swineford CFA (Chapter 4)

The data for this demonstration were provided by Holzinger & Swineford in their 1939 monograph *A Study in Factor Analysis: The Stability of a Bi-Factor Solution*. The sample includes 301 7th and 8th grade students, between 11-16 years of age, drawn from two schools. The data is in the text file **`hs.dat`** and the script file is **`app_ex1.R`**. The variables in the data set that we will use are

`visperc`	visual perception test in which participants select the next image in a series
`cubes`	visual perception test in which participants must mentally rotate a cube
`lozenges`	visual perception test involving mental "flipping" of a parallelogram ("lozenge")
`parcomp`	paragraph comprehension test
`sencomp`	sentence completion task in which participants select most appropriate word to put at the end of a sentence
`wordmean`	verbal ability test in which participants must select a word most similar in meaning to a word used in a sentence.
`addition`	participants have 2 minutes to complete as many 2-number addition problems as they can
`countdot`	participants have 4 minutes to count the number of dots in each of a series of dot pictures
`sccaps`	participants have 3 minutes to indicate whether capital letters are composed entirely of straight lines or include curved lines.

Other variables in the data not included in the models fit here are **`school`**, **`female`**, **`age`**, and **`month`**. We can read in the data with the following:

```
hs <- read.table("hs.dat", header=FALSE)
names(hs) <- c("school", "female", "age", "month",
               "visperc", "cubes", "lozenges",
               "parcomp", "sencomp", "wordmean",
               "addition", "countdot", "sccaps")
hs$addition <- hs$addition/4
hs$countdot <- hs$countdot/4
hs$sccaps <- hs$sccaps/4
```

As described in Chapter 4, we rescaled the last three variables to give them a similar range to the other indicators.

We will also load the two packages we need (install **`semPlot`** first if you have not already):

```
library(lavaan)
library(semPlot)
```

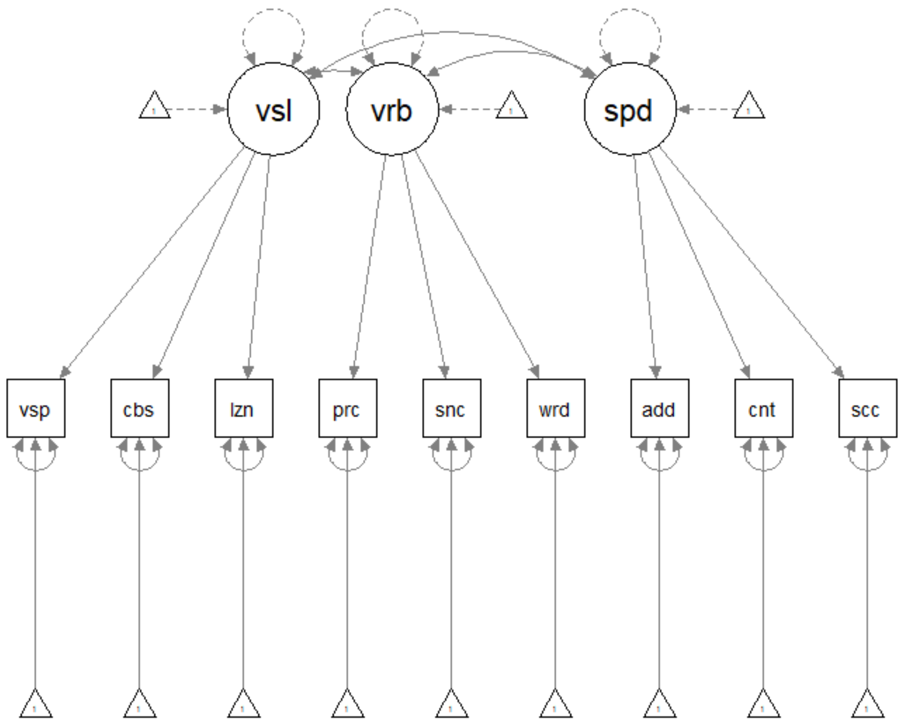
The initial model we fit to this data posited three factors, **`visual`** (with indicators **`visperc`**, **`cubes`** and **`lozenges`**), **`verbal`** (with indicators **`parcomp`**, **`sencomp`**, and **`wordmean`**), and **`speed`** (with indicators **`addition`**, **`countdot`**, and **`sccaps`**). We scaled the latent variables by setting their means to zero and variances to one, permitting all factor loadings and intercepts to be freely estimated. The corresponding script for specifying and fitting this model in lavaan is

```
cfa.1a <-'#factor loadings
          visual =~ visperc + cubes + lozenges
          verbal =~ parcomp + sencomp + wordmean
          speed =~ addition + countdot + sccaps
         '
fit.1a <- cfa(cfa.1a, data=hs, meanstructure=TRUE, std.lv=TRUE)
```

We can now use the fit object **fit.1a** to generate a path diagram.

We first show the default diagram generated by the **semPaths** function:

```
semPaths(fit.1a)
```



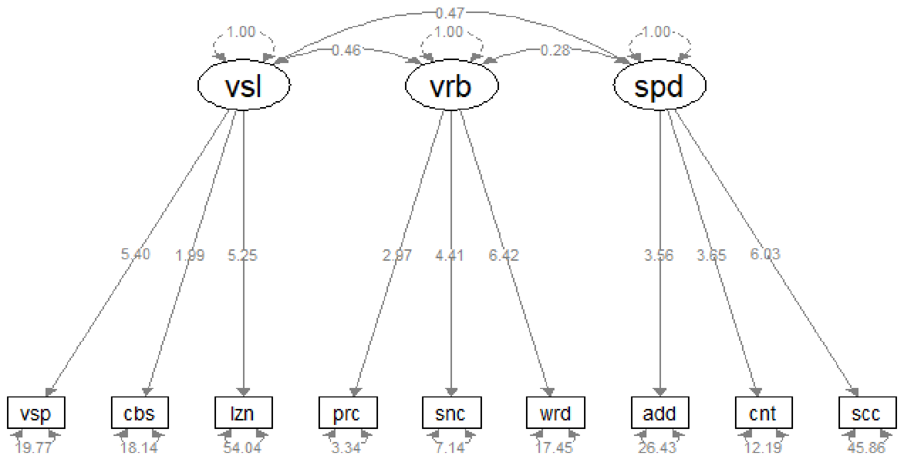
Clearly, some aspects of this plot can be improved upon. The triangles used to convey intercepts create a great deal of clutter and the covariances and variances among the latent variables are overlapping. Further, we might like to display the model estimates on the diagram for ease of interpretation.

Fortunately, there are many options for modifying the layout and information provided in the plot. Fiddling with these a bit, we invoked the following options:

```
semPaths(fit.1a, whatLabels="est", intercepts="FALSE", curve=1.75)
```

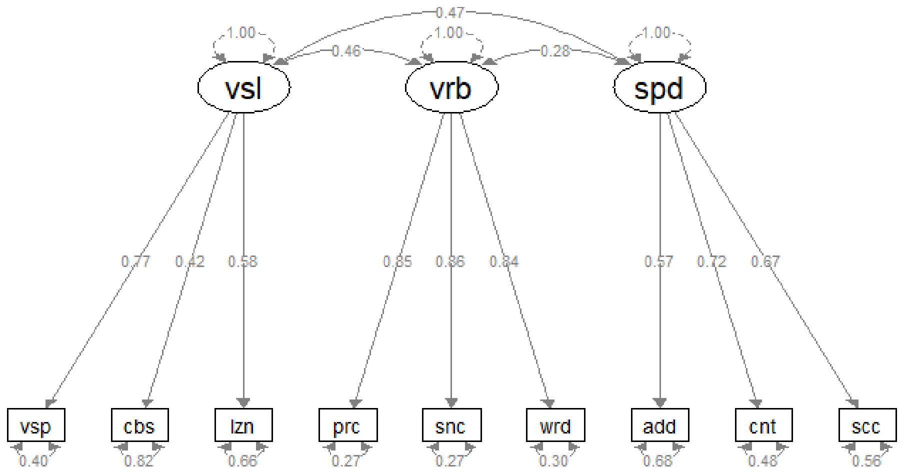
With these commands we will display the estimates (unstandardized) on the paths, remove the triangles for the intercepts, and increase the curvature of the double-headed arrows for the covariances so that they no longer overlap with the variances.

The resulting plot is shown here:



We can also switch the path labels to standardized estimates using the following options:

```
semPaths(fit.1a, whatLabels="std", intercepts="FALSE", curve=1.75)
```



Because the factors were already standardized, the displayed values for the latent variable variances and covariances are unchanged, but we now see standardized factor loadings and residuals (equal to one minus the communality for the indicator).

There are many other ways to modify the plot, as described in the documentation for the package.