Confirmatory Factor Analysis with R

James H. Steiger

Traditional *Exploratory factor analysis* (EFA) is often not purely exploratory in nature. The data analyst brings to the enterprise a substantial amount of intellectual baggage that affects the selection of variables, choice of a number of factors, the naming of factors, and in some cases the way factors are rotated to simple structure. So to some extent, EFA is actually confirmatory in nature.

Confirmatory factor analysis (CFA) provides a more explicit framework for confirming prior notions about the structure of a domain of content. CFA adds the ability to test constraints on the parameters of the factor model to the methodology of EFA.

In practice, people frequently combine EFA and CFA, to the extent that the appropriate statistical model is not actually determinable. However, we'll begin with an example of purely confirmatory factor analysis.

1 . "Pure" Confirmatory Factor Analysis

Consider the Athletics Data example we examined in conjunction with EFA. Suppose that, prior to analyzing the data, we hypothesized that there were 3 uncorrelated factors called Endurance, Strength, and Hand-Eye Coordination, and that each factor has non-zero loadings on only 3 variables. Such a hypothesis is, of course, extremely unlikely to be true, a point we will return to later. Taken literally, with a suitable ordering of the 9 observed variables, this hypothesis implies that the common factor pattern is of the form

$$\mathbf{F} = \begin{bmatrix} \theta_1 & 0 & 0 \\ \theta_2 & 0 & 0 \\ \theta_3 & 0 & 0 \\ 0 & \theta_4 & 0 \\ 0 & \theta_5 & 0 \\ 0 & \theta_6 & 0 \\ 0 & 0 & \theta_7 \\ 0 & 0 & \theta_8 \\ 0 & 0 & \theta_9 \end{bmatrix}$$

There are a number of equivalent ways of writing this CFA model. One states that

$$\mathbf{y} = \mathbf{F}\mathbf{x} + \mathbf{e}$$

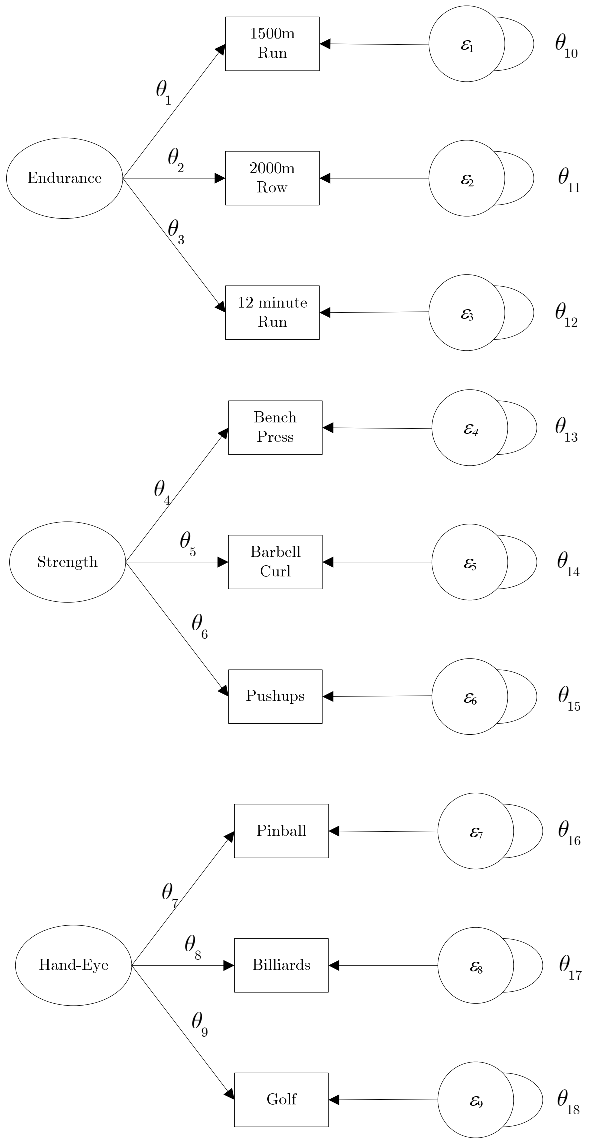
where $\mathbf{F}$ has the form shown above, and $\mathbf{x}$ and $\mathbf{e}$ are vectors of random variables such that $E(\mathbf{x}\mathbf{e}') = \mathbf{0}$, $E(\mathbf{e}\mathbf{e}') = \mathbf{U}^2$, and $E(\mathbf{x}\mathbf{x}') = \mathbf{I}$. $\mathbf{U}^2$ is a diagonal matrix of positive values, and hence may be written in the form (zero entries not shown):

$$\mathbf{U}^2 = \begin{bmatrix} \theta_{10} &&&&&&&& \\ & \theta_{11} &&&&&&& \\ && \theta_{12} &&&&&& \\ &&& \theta_{13} &&&&& \\ &&&& \theta_{14} &&&& \\ &&&&& \theta_{15} &&& \\ &&&&&& \theta_{16} && \\ &&&&&&& \theta_{17} & \\ &&&&&&&& \theta_{18} \end{bmatrix}$$

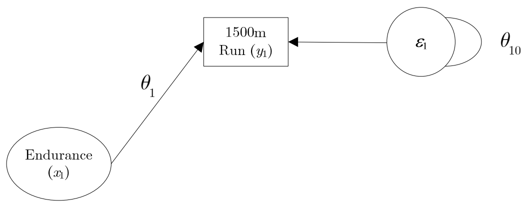
1.1 Diagramming a Confirmatory Factor Model

This model may be written as a path diagram, as shown on the next page. Note that the variances of the common factors are not shown explicitly in the diagram. According to our conventions, they are therefore assumed to have a variance of 1.

Note also that the coefficient from a residual to an observed variable is not labeled in the diagram, while the coefficient from a common factor to an observed variable is labeled. For example, the coefficient from x_1 ("Endurance") to y_1 ("1500 Meter Run") is θ_1. This means that this coefficient is a free parameter that is estimated by the CFA software. On the other hand, the coefficient from ε_1 to y_1 ("1500 Meter Run") is not labeled, and is therefore assumed to be a *fixed value* of 1.



So the top part of the diagram, shown below, stands for the equation $y_1 = \theta_1 x_1 + \varepsilon_1$, where x_1 has a variance of 1 and ε_1 has a variance of θ_{10}.



Recall that, in any path diagram, variables are either manifest or latent, and either exogenous or endogenous. Here are some questions for you. See if you can answer them, then check your answers in the footnote[1] below. What kind of variable is "Endurance" in the preceding diagram? What kind of variable is "1500 Meter Run"? What kind of variable is "ε_1"?

A number of programs are available to fit confirmatory factor analysis models to data. Some of these programs are free. One such program is available as the R package **`sem`**. Another is the program Mx.

Our diagramming system transparently connects with the standard linear equations coding of a structural equation model. Each and every linear equation has a corresponding element in the diagram. Moreover, each path in the diagram can be coded unambiguously in an ASCII computer language called PATH1 (Steiger, 1988).

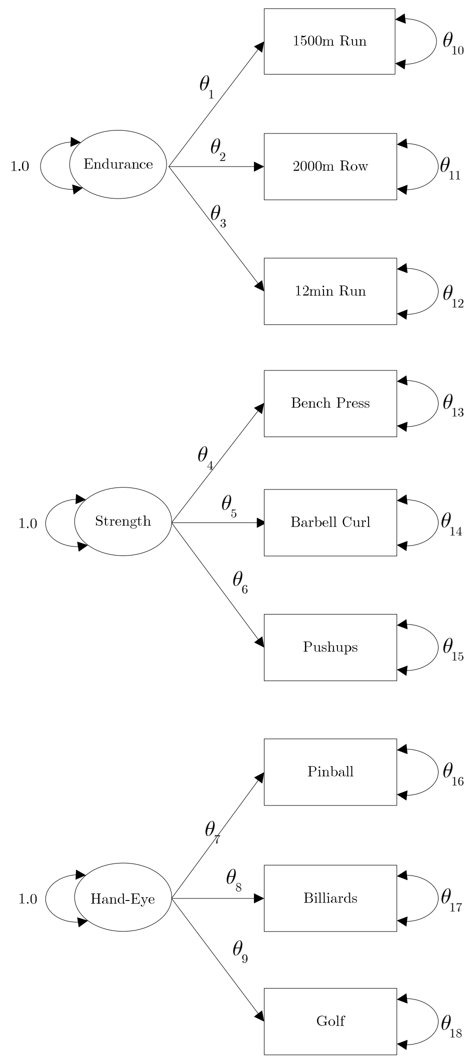
1.2 The `sem` program and the RAM Diagramming System

The **`sem`** package has the capability of decoding a language and diagramming system that follows our general rules for path diagrams (except that it requires latent variable variances of 1 to be represented explicitly). However, it is better designed computationally to handle a slightly abbreviated diagramming system that makes a couple of exceptions to these rules. This latter diagramming system, which I will call RAM, does not maintain a direct visual correspondence with the underlying linear equation system. When we discuss the major algebraic approaches to path models (the LISREL, RAM1, RAM2, Bentler-Weeks, and EzPath models), we will discuss the

[1] "Endurance" is latent-exogenous, "1500 Meter Run" is manifest-endogenous, and "ε_1" is latent-exogenous.

distinction between the original (RAM1) specification of J. J. McArdle, and the improved RAM2 model specification that **sem** is designed around.

The RAM diagramming system is similar to the system we have described above, with one major exception — *residual latent variables* are not represented explicitly. A residual latent variable is an exogenous latent variable that has a single directed path (single headed arrow) to a target endogenous variable. For example, ε_1 is a residual latent variable. In the RAM diagramming system, residual latent variables have their variances and covariances represented as variances and covariances attached to their targets. Below we show the previous path diagram in the RAM system (with unit variances for the factors shown explicitly.



The two-headed arrows, or “slings,” mean something different on the left side of the diagram than they do on the right side of the diagram. On the left side, they stand for the variances of the latent variables, while on right side, they are the variances of the (hidden) residual variables. This system is visually more compact in its use of space than the system described earlier, because some objects are not represented explicitly. On the other hand, this system requires more effort to decode, because (a) there are more arrowheads, and (b) the meaning of a two-headed arrow varies, depending on the status of the target variable it is attached to, which in turn has to be determined by examining whether the target variable is endogenous or exogenous. This double usage of the two-headed arrow also rules out other possible usages in a more complex system. For example, some systems allow unit variance constraints to be placed on the variances of endogenous latent variables, and these constraints are indicated in the path diagram with a two-headed arrow attached to the endogenous latent variable. (The residual variance is indicated with an explicit residual variable.) This system cannot be employed in conjunction with the RAM system.

The **sem** package can decode a model represented in the RAM path diagramming system rather easily. For each sling or arrow, the user includes a line in a rather natural ASCII language. Each line is of the form

```
<Relation>, <Parameter Symbol>, <Parameter Value>
```

`<Relation>` indicates the arrow or sling. Arrows are represented in the form

```
name1 -> name2
```

Slings (two-headed arrows) are represented as

```
name1 <-> name2
```

The **`<Parameter Symbol>`** is a label used to uniquely identify a free parameter. If the parameter symbol is **`NA`**, the path has a fixed value. If two paths have the same free parameter label, the numerical value for that parameter is constrained to be the same for both paths.

The **`<Parameter Value>`** is the starting value for iteration if the parameter is free (a value of **`NA`** will cause the program to use an automatic starting value), the fixed numerical value if the parameter symbol is **`NA`** and the value is fixed.

To see how this system works, compare the code on the following page with the path diagram. Note that you must use the variable names in the data file. I've included some comment lines to set off key areas of the code.

```
## Factor 1 -- Endurance
Endurance -> X.1500M,  theta01, NA
Endurance -> X.2KROW,  theta02, NA
Endurance -> X.12MINTR,theta03, NA
## Factor 2 -- Strength
Strength  -> BENCH,    theta04, NA
Strength  -> CURL,     theta05, NA
Strength  -> MAXPUSHU, theta06, NA
## Factor 3 -- Hand-Eye Coordination
Hand-Eye  -> PINBALL,  theta07, NA
Hand-Eye  -> BILLIARD, theta08, NA
Hand-Eye  -> GOLF,     theta09, NA
## Unique Variances
X.1500M   <->  X.1500M,  theta10, NA
X.2KROW   <->  X.2KROW,  theta11, NA
X.12MINTR <->  X.12MINTR, theta12, NA
BENCH     <->  BENCH, theta13, NA
CURL      <->  CURL, theta14, NA
MAXPUSHU  <->  MAXPUSHU, theta15, NA
PINBALL   <->  PINBALL, theta16, NA
BILLIARD  <->  BILLIARD, theta17, NA
GOLF      <->  GOLF, theta18, NA
## Factor Variances fixed at 1
Endurance <->  Endurance, NA, 1
Strength  <->  Strength,  NA, 1
Hand-Eye  <->  Hand-Eye,  NA, 1
```

Suppose we save the above code into an ASCII file called *CFA1.txt* (say, with NotePad). After loading the Hmisc library, loading the AthleticsData file and attaching it with the following 3 lines, we are ready to go.

```
> library(Hmisc)
> AthleticsData <- spss.get("AthleticsData.sav")
> attach(AthleticsData)
```

We begin by computing a correlation matrix for analysis.

```
> AthleticsData.R <- cor(AthleticsData)
```

After loading the sem package, we then translate the confirmatory factor model

```
> library(sem)
> cfa1.model <- specify.model("CFA1.txt")
```

We are now ready to fit the model and save our results to a model fit object. A single command does the trick.

```
> cfa1.fit <- sem(cfa1.model, AthleticsData.R, 1000)
```

Requesting a summary of the fit produces the following:

```
> summary(cfa1.fit)
Model Chisquare =  526.26   Df =  27 Pr(>Chisq) = 0
Chisquare (null model) =  2330.1   Df =  36
Goodness-of-fit index =  0.90479
Adjusted goodness-of-fit index =  0.84131
RMSEA index =  0.13605   90% CI: (0.12603, 0.14632)
Bentler-Bonnett NFI =  0.77415
Tucker-Lewis NNFI =  0.70983
Bentler CFI =  0.78237
SRMR =  0.12188
BIC =  339.75

Normalized Residuals
    Min.   1st Qu.    Median      Mean   3rd Qu.      Max.
-7.530000 -0.000042  0.823000  1.710000  2.880000 14.000000

Parameter Estimates
        Estimate Std Error z value Pr(>|z|)
theta01 0.71071  0.037397  19.0046 0.0000e+00 X.1500M <--- Endurance
theta02 0.53435  0.035011  15.2623 0.0000e+00 X.2KROW <--- Endurance
theta03 0.75095  0.038010  19.7568 0.0000e+00 X.12MINTR <--- Endurance
theta04 0.78082  0.039534  19.7508 0.0000e+00 BENCH <--- Strength
theta05 0.72157  0.038483  18.7502 0.0000e+00 CURL <--- Strength
theta06 0.48429  0.034890  13.8805 0.0000e+00 MAXPUSHU <--- Strength
theta07 0.59504  0.033551  17.7353 0.0000e+00 PINBALL <--- HandEye
theta08 0.75930  0.034697  21.8836 0.0000e+00 BILLIARD <--- HandEye
theta09 0.74385  0.034580  21.5114 0.0000e+00 GOLF <--- HandEye
theta10 0.49489  0.042484  11.6491 0.0000e+00 X.1500M <--> X.1500M
theta11 0.71447  0.037980  18.8119 0.0000e+00 X.2KROW <--> X.2KROW
theta12 0.43608  0.044934   9.7048 0.0000e+00 X.12MINTR <--> X.12MINTR
theta13 0.39032  0.049199   7.9335 2.2204e-15 BENCH <--> BENCH
theta14 0.47934  0.044755  10.7103 0.0000e+00 CURL <--> CURL
theta15 0.76546  0.038557  19.8527 0.0000e+00 MAXPUSHU <--> MAXPUSHU
theta16 0.64593  0.035543  18.1734 0.0000e+00 PINBALL <--> PINBALL
theta17 0.42346  0.038638  10.9599 0.0000e+00 BILLIARD <--> BILLIARD
theta18 0.44668  0.037998  11.7554 0.0000e+00 GOLF <--> GOLF

Iterations =  19
```

The above output shows that the solution converged in 19 iterations, yielding a model χ^2 statistic of 526.26 with 27 degrees of freedom. Where did this "degrees of freedom" value come from? In general, it is the number of non-redundant elements of the covariance $p \times p$ matrix minus the number of free parameters. In this case, the covariance matrix is 9×9, so there are $p(p+1)/2 = 9(9+1)/2 = 45$ non-redundant elements. Since there are 18 free parameters (θ_1 through θ_{18}), there are $45 - 18 = 27$ degrees of freedom.

This χ^2 value, of course, has a p-value far below .001, and so the null hypothesis of perfect fit is rejected. The output also includes parameter values, estimates of their standard errors, and asymptotically normal statistics testing the hypothesis that the parameter value is zero in the population. One can also construct an approximate 95% confidence interval by taking the estimate plus or minus two standard errors.

1.3 Evaluating and Improving Model Fit

The fact that the hypothesis of perfect fit is rejected is, in itself, not very informative — the common factor model is highly constrained, and with a sample size of 1000, we have excellent power to detect even minor levels of misfit. The more important statistical questions are, (a) how bad is the misfit, and (b) how precisely have we have we determined the degree of misfit. For a detailed account of several of these indices and their theoretical basis, see the course handout on "Indices of Fit in Structural Equation Modeling."

The fact that the RMSEA confidence interval ranges from .126 to .146 suggests to many people that the model fit, in this case, can definitely be improved. Of course, we know from the earlier exploratory factor analysis of these same data that there are two moderately high "crossover loadings" that are not included in the model we just evaluated, so this model is definitely missing some key elements. However, suppose we did not know that? How would we proceed?

The “pure” confirmatory approach would suggest that we not proceed at all! We had a model, it doesn’t fit, and “well — that’s it.” Of course, in general people do proceed, sometimes at the peril of objective scientific values. Below, we sketch two popular approaches to arriving at a confirmatory factor model through a mixture of exploratory and confirmatory approaches.

2. The “Confirm and Update” Approach

One approach, introduced by Jöreskog, is to start with a confirmatory model based on theory, then update it by adding factor loadings with the aid of “modification indices.” These indices attempt to estimate which missing paths, if added to the current model, would result in the greatest reduction of the χ^2 fit statistic.

Obtaining modification indices from **`sem`** is straightforward.

```
> mod.indices(cfa1.fit)
5 largest modification indices, A matrix:
MAXPUSHU:Endurance   X.2KROW:Strength   MAXPUSHU:X.1500M   MAXPUSHU:X.2KROW
          186.7412           170.2313           147.1726           132.1697
Endurance:MAXPUSHU
          128.8828

  5 largest modification indices, P matrix:
Endurance:MAXPUSHU   Strength:X.2KROW      BENCH:X.1500M   Strength:X.1500M
         186.74117          170.23130           63.26395           59.28328
   Endurance:BENCH
          44.76791
```

Interpreting the above is facilitated by a knowledge of the RAM1 model of McArdle and McDonald. However, essentially it works like this. An entry in the **A** matrix is of the form, **`<endogenous variable>:<exogenous variable>`**. So, the largest modification index, labeled **`MAXPUSHU:Endurance`**, indicates that the model χ^2 fit index would be decreased by roughly 187 if a path from **`Endurance`** to **`MAXPUSHU`** were added to the model. Let’s try it, by simply adding a single line to the previous model. This line is “**`Endurance -> MAXPUSHU, theta19, NA`**”.
We fit the model,

```
> cfa2.model <- specify.model("CFA2.txt")
> cfa2.fit <- sem(cfa2.model, AthleticsData.R, 1000)
```

then examine the results.

```
> summary(cfa2.fit)
 Model Chisquare =  310.32   Df =  26 Pr(>Chisq) = 0
 Chisquare (null model) =  2330.1   Df =  36
 Goodness-of-fit index =  0.93856
 Adjusted goodness-of-fit index =  0.89367
 RMSEA index =  0.10463   90% CI: (0.094363, 0.11522)
 Bentler-Bonnett NFI =  0.86682
 Tucker-Lewis NNFI =  0.8284
 Bentler CFI =  0.87607
 SRMR =  0.093325
 BIC =  130.72

 Normalized Residuals
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
 -7.530  -0.323   0.444   0.910   2.410   7.520

 Parameter Estimates
        Estimate Std Error z value Pr(>|z|)
theta01 0.73778  0.033684  21.9032 0.0000e+00 X.1500M <--- Endurance
theta02 0.56030  0.034651  16.1699 0.0000e+00 X.2KROW <--- Endurance
theta03 0.70195  0.033341  21.0540 0.0000e+00 X.12MINTR <--- Endurance
theta04 0.81307  0.036707  22.1502 0.0000e+00 BENCH <--- Strength
theta05 0.69295  0.035394  19.5781 0.0000e+00 CURL <--- Strength
theta06 0.52020  0.032383  16.0638 0.0000e+00 MAXPUSHU <--- Strength
theta07 0.59503  0.033551  17.7352 0.0000e+00 PINBALL <--- HandEye
theta08 0.75931  0.034697  21.8837 0.0000e+00 BILLIARD <--- HandEye
theta09 0.74385  0.034580  21.5112 0.0000e+00 GOLF <--- HandEye
theta10 0.45568  0.036057  12.6376 0.0000e+00 X.1500M <--> X.1500M
theta11 0.68607  0.037295  18.3959 0.0000e+00 X.2KROW <--> X.2KROW
theta12 0.50726  0.034922  14.5257 0.0000e+00 X.12MINTR <--> X.12MINTR
theta13 0.33892  0.044964   7.5376 4.7962e-14 BENCH <--> BENCH
theta14 0.51982  0.038556  13.4824 0.0000e+00 CURL <--> CURL
theta15 0.53297  0.033166  16.0700 0.0000e+00 MAXPUSHU <--> MAXPUSHU
theta16 0.64594  0.035543  18.1734 0.0000e+00 PINBALL <--> PINBALL
theta17 0.42345  0.038638  10.9594 0.0000e+00 BILLIARD <--> BILLIARD
theta18 0.44669  0.037998  11.7556 0.0000e+00 GOLF <--> GOLF
theta19 0.47879  0.031654  15.1260 0.0000e+00 MAXPUSHU <--- Endurance

 Iterations =  19
```

We see that the new parameter, θ_{19}, has an estimate value of .48, and is highly significant. Moreover, the model χ^2 statistic decreased to 310, a 215 point decrease even greater than the modification index predicted. According to statistical theory in Steiger, Shapiro, and Browne (1984), since the models are nested (The first model is a special case of the second, where one of the parameters is constrained to zero), you can treat the difference in the two χ^2 values as a χ^2 with degrees of freedom equal to the difference in their degrees of freedom (i. e., 1 in this case). The resulting *chi square difference statistic* provides a method for testing whether there is a statistically different improvement in fit. Clearly there is!

However, the RMSEA statistic for the improved model is still larger (.10) than the recommended value. We recompute the modification indices:

```
> mod.indices(cfa2.fit)

 5 largest modification indices, A matrix:
X.2KROW:Strength    X.2KROW:BENCH     X.2KROW:CURL    X.1500M:BENCH
       164.62477        137.49080        103.45883         89.50040
X.1500M:Strength
        84.81637
```

The largest modification index is for a path from **`Strength`** to **`X.2KROW`**. Adding this path to the model with the line "**`Strength -> X.2KROW, theta20, NA`**" we refit the model again,

```
> cfa3.model <- specify.model("CFA3.txt")
> cfa3.fit <- sem(cfa3.model, AthleticsData.R, 1000)
> summary(cfa3.fit)
Model Chisquare =  125.32   Df =  25 Pr(>Chisq) = 2.5535e-15
 Chisquare (null model) =  2330.1   Df =  36
 Goodness-of-fit index =  0.97393
 Adjusted goodness-of-fit index =  0.95307
 RMSEA index =  0.06338   90% CI: (0.052591, 0.074631)
 Bentler-Bonnett NFI =  0.94622
 Tucker-Lewis NNFI =  0.93703
 Bentler CFI =  0.95627
 SRMR =  0.080264
 BIC =  -47.369

 Normalized Residuals
     Min.   1st Qu.    Median      Mean   3rd Qu.      Max.
-7.530000 -1.520000  0.000013  0.108000  1.350000  5.890000

 Parameter Estimates
        Estimate Std Error z value Pr(>|z|)
theta01 0.77177  0.033156  23.2768 0        X.1500M <--- Endurance
theta02 0.60940  0.032238  18.9033 0        X.2KROW <--- Endurance
theta03 0.69222  0.032997  20.9786 0        X.12MINTR <--- Endurance
theta04 0.81218  0.033343  24.3581 0        BENCH <--- Strength
theta05 0.69416  0.033125  20.9555 0        CURL <--- Strength
theta06 0.56438  0.032014  17.6293 0        MAXPUSHU <--- Strength
theta07 0.59503  0.033551  17.7352 0        PINBALL <--- HandEye
theta08 0.75930  0.034697  21.8836 0        BILLIARD <--- HandEye
theta09 0.74385  0.034580  21.5113 0        GOLF <--- HandEye
theta10 0.40437  0.035668  11.3370 0        X.1500M <--> X.1500M
theta11 0.52207  0.031609  16.5165 0        X.2KROW <--> X.2KROW
theta12 0.52083  0.034224  15.2180 0        X.12MINTR <--> X.12MINTR
theta13 0.34037  0.037359   9.1107 0        BENCH <--> BENCH
theta14 0.51815  0.034470  15.0318 0        CURL <--> CURL
theta15 0.54321  0.031522  17.2329 0        MAXPUSHU <--> MAXPUSHU
theta16 0.64593  0.035543  18.1734 0        PINBALL <--> PINBALL
theta17 0.42346  0.038638  10.9597 0        BILLIARD <--> BILLIARD
theta18 0.44668  0.037998  11.7554 0        GOLF <--> GOLF
theta19 0.45936  0.031381  14.6382 0        MAXPUSHU <--- Endurance
theta20 0.42293  0.030938  13.6703 0        X.2KROW <--- Strength

 Iterations =  16
```

The new parameter, θ_{20}, has an impressive value of .42, and is highly significant. The model χ^2 dropped to 125 (the chi square difference test is overwhelmingly significant)+, and the RMSEA, at .063, is now definitely in the range considered acceptable by many experts.

Of course, we can continue to examine modification indices, but we may be reaching a point of diminishing returns where we are capitalizing on chance.

```
mod.indices(cfa3.fit)

 5 largest modification indices, A matrix:
Strength:X.1500M  Endurance:BENCH    X.1500M:BENCH X.1500M:Strength
        47.51062         40.07892         39.82350         34.17247
   BENCH:X.1500M
        33.91703

  5 largest modification indices, P matrix:
  Strength:X.1500M Strength:Endurance   HandEye:Strength    Endurance:BENCH
          34.17247           32.66084           26.38424           24.81201
     BENCH:X.1500M
          22.04953
```

Notice how all the modification indices are rather close, and are now much smaller than before. Remember that the first variable in the **A** matrix is the variable the arrow goes to, so we are looking only at paths from a latent variable to a manifest variable. Let's add a path from `Strength` to `X.1500M` and see what happens.

```
> cfa4.model <- specify.model("CFA4.txt")
> cfa4.fit <- sem(cfa4.model, AthleticsData.R, 1000)
> summary(cfa4.fit)

Model Chisquare =  81.641   Df =  24 Pr(>Chisq) = 3.3251e-08
 Chisquare (null model) =  2330.1   Df =  36
 Goodness-of-fit index =  0.983
 Adjusted goodness-of-fit index =  0.96812
 RMSEA index =  0.049032   90% CI: (0.037601, 0.060921)
 Bentler-Bonnett NFI =  0.96496
 Tucker-Lewis NNFI =  0.96231
 Bentler CFI =  0.97487
 SRMR =  0.061516
 BIC =  -84.145

 Normalized Residuals
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
-3.3500 -0.3240  0.0666  0.6760  1.3800  5.8900

 Parameter Estimates
        Estimate Std Error z value Pr(>|z|)
theta01  0.76727 0.032380  23.6957 0.0000e+00 X.1500M <--- Endurance
theta02  0.61213 0.031840  19.2251 0.0000e+00 X.2KROW <--- Endurance
theta03  0.67383 0.032764  20.5664 0.0000e+00 X.12MINTR <--- Endurance
theta04  0.82465 0.032818  25.1282 0.0000e+00 BENCH <--- Strength
theta05  0.68468 0.032785  20.8841 0.0000e+00 CURL <--- Strength
```

```
theta06  0.50656 0.032462  15.6048 0.0000e+00 MAXPUSHU <--- Strength
theta07  0.59503 0.033551  17.7352 0.0000e+00 PINBALL <--- HandEye
theta08  0.75930 0.034697  21.8836 0.0000e+00 BILLIARD <--- HandEye
theta09  0.74385 0.034580  21.5113 0.0000e+00 GOLF <--- HandEye
theta10  0.35235 0.035665   9.8796 0.0000e+00 X.1500M <--> X.1500M
theta11  0.52539 0.031764  16.5406 0.0000e+00 X.2KROW <--> X.2KROW
theta12  0.54595 0.033784  16.1600 0.0000e+00 X.12MINTR <--> X.12MINTR
theta13  0.31995 0.036578   8.7470 0.0000e+00 BENCH <--> BENCH
theta14  0.53121 0.033818  15.7081 0.0000e+00 CURL <--> CURL
theta15  0.54467 0.031649  17.2100 0.0000e+00 MAXPUSHU <--> MAXPUSHU
theta16  0.64593 0.035543  18.1734 0.0000e+00 PINBALL <--> PINBALL
theta17  0.42346 0.038638  10.9596 0.0000e+00 BILLIARD <--> BILLIARD
theta18  0.44669 0.037998  11.7555 0.0000e+00 GOLF <--> GOLF
theta19  0.47520 0.030764  15.4466 0.0000e+00 MAXPUSHU <--- Endurance
theta20  0.35239 0.032025  11.0035 0.0000e+00 X.2KROW <--- Strength
theta21 -0.20340 0.030502  -6.6685 2.5845e-11 X.1500M <--- Strength

 Iterations =  18
```

We can see that the added parameter has a value of $-.20$, and the RMSEA has decreased appreciably to .049, a value generally considered to represent excellent fit. This latest coefficient seems to imply that increased strength actually hurts performance in the 1500 meter run!

In practical circumstances, there is no way of determining which model is “correct.” Indeed, one might argue that it is extremely unlikely that factor loadings (other than a certain small number of loadings that can always be forced to zero by rotation, as we will discuss later) are truly zero. On the other hand, “minor loadings” contribute little to the ability of the factor model to fit data, and, because of sampling error, including them in the model may be contributing nearly as much signal as noise.

In the above example, we started with a strong “confirmatory” position, based on a prior understanding about the state of the world, i.e., there are 3 factors, and each factor has 3 indicator variables. We used modification indices to “upgrade” the model, and quickly ended up with a model that is parsimonious, seems to “make sense,” and fits well.

Note that we can continue this process, by recomputing modification indices and upgrading the model still further. Ultimately however, we have to worry seriously about the extent to which we are capitalizing on chance.

3. The "Exploratory-Confirmatory" Approach

An alternative approach, which *begins* with a purely exploratory factor analysis, was described by Karl Jöreskog in his 1978 Presidential Address to the Psychometric Society.

Jöreskog's approach is as follows:

- Perform an exploratory factor analysis, and decide on the number of factors, m. In many textbook examples, the decision is relatively clear cut. Be forewarned — in practice the decision may be quite difficult.
- Fit an m-factor model, and rotate to simple structure using varimax or promax. (In the original article, Jöreskog said to use promax, but used varimax in his numerical example. We'll use varimax.)
- For each column of the factor pattern, find the largest loading, then constrain *all the other loadings in that row to be zero*, and fit the resulting model as a confirmatory factor model. This confirmatory model will have exactly the same discrepancy function and χ^2 value as the exploratory factor analysis that preceded it.
- Examine the factor pattern, and test all factor loadings. Delete "non-significant" loadings from the model. After checking the fit, the user can decide whether to terminate the process, or look for more loadings to delete.

A detailed commentary on the final steps may prove helpful. Due to the well-known fact of rotational indeterminacy, the parameters in the exploratory factor model (where every factor loading is free to vary) are not uniquely determined. In the broader language of structural equation modeling, we say that the parameters are not "identified."

A parameter is a fixed numerical value. To estimate a "parameter," it obviously follows that the parameter has to be identified! So in general, a model must be identified in some way before iteration to a best-fitting solution can be attempted. Therefore, a model with parameters that are not identified can propose a severe problem for general structural equation modeling programs like **sem**.

Exploratory factor analysis programs achieve identification automatically during iteration by a variety of means, so while doing exploratory factor analysis *with a program designed to do exploratory factor analysis,* you don't need to worry about it. However, when doing a "completely unrestricted" confirmatory factor analysis with 2 or more factors, you cannot simply start by letting all the possible $p \times m$ factor loadings be free parameters. You'd discover that the solution is not identified. Depending on the sophistication of your program, you'd either converge to a solution and get an error indicator, or you'd fail to converge with a cryptic error message. **sem**, unfortunately, falls into the latter category. Try fitting the following unrestricted 3 factor model in **sem**.

```
## Factor 1 -- Endurance
Endurance -> X.1500M,  theta01, NA
Endurance -> X.2KROW,  theta02, NA
Endurance -> X.12MINTR,theta03, NA
Endurance  -> BENCH,    theta04, NA
Endurance  -> CURL,     theta05, NA
Endurance  -> MAXPUSHU, theta06, NA
Endurance  -> PINBALL,  theta07, NA
Endurance  -> BILLIARD, theta08, NA
Endurance  -> GOLF,     theta09, NA
## Factor 2 -- Strength
Strength -> X.1500M,  theta10, NA
Strength -> X.2KROW,  theta11, NA
Strength -> X.12MINTR,theta12, NA
Strength  -> BENCH,    theta13, NA
Strength  -> CURL,     theta14, NA
Strength  -> MAXPUSHU, theta15, NA
Strength  -> PINBALL,  theta16, NA
Strength  -> BILLIARD, theta17, NA
Strength  -> GOLF,     theta18, NA
## Factor 3 -- Hand-Eye Coordination
Hand-Eye -> X.1500M,  theta19, NA
Hand-Eye -> X.2KROW,  theta20, NA
Hand-Eye -> X.12MINTR,theta21, NA
Hand-Eye  -> BENCH,    theta22, NA
Hand-Eye  -> CURL,     theta23, NA
Hand-Eye  -> MAXPUSHU, theta24, NA
Hand-Eye  -> PINBALL,  theta25, NA
Hand-Eye  -> BILLIARD, theta26, NA
```

```
Hand-Eye  -> GOLF,     theta27, NA
## Unique Variances
X.1500M   <->  X.1500M,  theta28, NA
X.2KROW   <->  X.2KROW,  theta29, NA
X.12MINTR <->  X.12MINTR, theta30, NA
BENCH     <->  BENCH, theta31, NA
CURL      <->  CURL, theta32, NA
MAXPUSHU  <->  MAXPUSHU, theta33, NA
PINBALL   <->  PINBALL, theta34, NA
BILLIARD  <->  BILLIARD, theta35, NA
GOLF      <->  GOLF, theta36, NA
## Factor Variances
Endurance <->  Endurance, NA, 1
Strength  <->  Strength,  NA, 1
Hand-Eye  <->  Hand-Eye,  NA, 1
## Factor Correlations
Endurance <->  Strength, theta37, NA
Endurance <->  Hand-Eye, theta38, NA
Strength  <->  Hand-Eye, theta39, NA
```

You'll see the following error message:

```
Error in solve.default(C[ind, ind]) :
  Lapack routine dgesv: system is exactly singular
```

With the advantage of a substantial amount of experience, you might be able to interpret this message as follows:

- During iteration, the program tries to invert a matrix that is a scalar multiple of an estimated variance-covariance matrix of the parameter estimates.
- If some parameters are functionally related to others, this estimated asymptotic covariance matrix will be singular
- The system is not "identified," because some parameters are not needed — they are determinate functions of other parameters

According to Jöreskog (1978), you can identify a common factor model by setting at least $k-1$ loadings in each column of the factor pattern to zero. He provides a scheme for doing this automatically, based on examination of the pattern after rotating to simple structure. Jöreskog's explanation of this step was somewhat terse, and he does not describe in detail why the system works. In looking carefully at the algebra, we'll discover that some of the "free parameters" in a common factor pattern are not "really free" as you might expect. In other words, if you set up a confirmatory factor model with all p variables loading on all m factors, and all m factors allowed to correlate with each other, you will have pm factor loadings and p unique variances, plus $m(m-1)/2$ nonredundant factor intercorrelations, yet the "true number of free parameters" is not really $pm + p + m(m-1)/2$. Why not?

The answer stems from the following facts. First, suppose the orthogonal factor model fits, and

$$\mathbf{y} = \mathbf{F}\mathbf{x} + \mathbf{e}$$

with $\mathbf{F}$ a $p \times m$ factor pattern of full column rank, with the standard restrictions in place. First of all, recall the fact of rotational indeterminacy, and assume the factors are allowed to be correlated after rotation by a matrix **T**. Then if $\mathbf{y} = \mathbf{F}\mathbf{x} + \mathbf{e}$, it must also be true that $\mathbf{y} = \mathbf{F}\mathbf{T}\mathbf{T}^{-1}\mathbf{x} + \mathbf{e}$ for any nonsingular matrix **T**, so the common factor model must still fit with new pattern $\mathbf{F}^* = \mathbf{F}\mathbf{T}$ and new factors $\mathbf{x}^* = \mathbf{T}^{-1}\mathbf{x}$ with covariance matrix $\mathbf{T}^{-1}\mathbf{T}^{-1\prime}$. In general, we wish to retain the restriction that the common factors have unit variance after rotation by $\mathbf{T}^{-1}$. So we impose the restriction on $\mathbf{T}^{-1}$ that $\operatorname{diag}(\mathbf{T}^{-1}\mathbf{T}^{-1\prime}) = \operatorname{diag}(\mathbf{I})$.

Now, suppose that we isolate an $m \times m$ submatrix of **F**. Note that by suitable permutation of the (arbitrary) ordering of the variables in **y**, we can always manipulate this submatrix into the upper m rows of **F**. So we can write **F** in partitioned form as

$$\mathbf{F} = \begin{bmatrix} \mathbf{F}_1 \\ \mathbf{F}_2 \end{bmatrix}$$

Suppose that $\mathbf{F}_1$ is nonsingular, and let $\mathbf{T} = \mathbf{F}_1^{-1}\mathbf{D}^{-1}$, where **D** is a positive definite diagonal scaling matrix. Then

$$\mathbf{F}^* = \mathbf{F}\mathbf{T} = \begin{bmatrix} \mathbf{F}_1 \\ \mathbf{F}_2 \end{bmatrix} \mathbf{T} = \begin{bmatrix} \mathbf{F}_1\mathbf{T} \\ \mathbf{F}_2\mathbf{T} \end{bmatrix} = \begin{bmatrix} \mathbf{D}^{-1} \\ \mathbf{F}_2\mathbf{F}_1^{-1}\mathbf{D}^{-1} \end{bmatrix}$$

Note that the upper $m \times m$ submatrix of $\mathbf{F}^*$ is diagonal, and contains $m^2 - m = m(m-1)$ zeroes. In other words, it is inevitable that any factor pattern can be rotated obliquely to include that many zeroes. Notice that rotation to this position has absolutely no effect on how well the model fits. So instead of "really" having pm free factor loadings, we have $pm - m(m-1)$ loadings that are actually free to be nonzero.

In the previous formula, we did not specify how to calculate the scaling matrix **D**. However, it is determined by the restriction that the rotated factors still have unit variance. This requirement means that $\text{diag}(\mathbf{T}^{-1}\mathbf{T}^{-1\prime}) = \text{diag}(\mathbf{I})$. Since $\text{diag}(\mathbf{T}^{-1}\mathbf{T}^{-1\prime}) = \text{diag}(\mathbf{D}\mathbf{F}_1\mathbf{F}_1'\mathbf{D})$, it is clear that we can force the latter matrix to have ones on its diagonal by simply setting $\mathbf{D} = \text{diag}^{-1/2}(\mathbf{F}_1\mathbf{F}_1')$, or, equivalently

$$\mathbf{T} = \mathbf{F}_1^{-1}\mathbf{D}^{-1} = \mathbf{F}_1^{-1}\,\text{diag}^{1/2}(\mathbf{F}_1\mathbf{F}_1') \tag{1}$$

Since **T** operates on the rows of **F** independently, we *do not need to rearrange* the rows of **F** to manipulate desired rows into the upper $m \times m$ submatrix. Rather, we simply construct $\mathbf{F}_1$ from the desired rows and apply Equation 1.

A purely hypothetical example constructed using R should help make the above ideas clear. Suppose we have a factor analysis based on 6 variables and two factors. We observe the following factor pattern:

```
> F <- matrix(c(.6,.5,.58,.2,.1,.05,.09,.11,.07,.71,.62,.66),6,2)
> F
     [,1] [,2]
[1,] 0.60 0.09
[2,] 0.50 0.11
[3,] 0.58 0.07
[4,] 0.20 0.71
[5,] 0.10 0.62
[6,] 0.05 0.66
```

Notice that row 1 has the highest loading for factor 1, and row 4 has the highest loading for factor 2. The preceding algebra says that we can actually rotate these two "marker" rows (and the rest of **F**) so that the other two values in the "marker" rows are zero.

Pull out rows 1 and 4, and call them $\mathbf{F}_1$.

```
> F1 <- rbind(F[1,], F[4,])
> F1
     [,1] [,2]
[1,]  0.6 0.09
[2,]  0.2 0.71
```

Then construct $\mathbf{T}$ via Equation 1 as

```
> T <- solve(F1) %*% diag ( sqrt( diag(F1 %*% t(F1) ) ) )
```

We can readily verify that the resulting $\mathbf{T}$ rotates $\mathbf{F}$ into the desired configuration, and that $\mathrm{diag}(\mathbf{T}^{-1}\mathbf{T}^{-1\prime}) = \mathrm{diag}(\mathbf{I})$:

```
> zapsmall(F %*% T) ## use zapsmall to eliminate scientific notation
           [,1]       [,2]
[1,]  0.6067125  0.0000000
[2,]  0.4951844  0.0379663
[3,]  0.5915446 -0.0184408
[4,]  0.0000000  0.7376313
[5,] -0.0788131  0.6562749
[6,] -0.1434994  0.7078007

> solve(T) %*% t (solve(T))
          [,1]      [,2]
[1,] 1.0000000 0.4109221
[2,] 0.4109221 1.0000000
```

This rotated version of the original F will exactly match the F we get if we fit a confirmatory factor model with correlated factors and fixed zeroes in the appropriate positions. Let's try this with the AthleticsData example. We pull the factor loadings out of the results, place them in a matrix, and add the variable names to help us keep track

```
> exploratory <- factanal(AthleticsData, factors = 3)
> F <- matrix(exploratory$loadings[1:27],9,3)
> rownames(F) <- colnames(AthleticsData)
> F
                 [,1]        [,2]       [,3]
PINBALL   -0.005893274  0.13056931 0.58976923
BILLIARD   0.023633952  0.03187533 0.76469736
GOLF       0.048166786  0.05164699 0.73454363
X.1500M    0.778911631 -0.17862424 0.01582561
X.2KROW    0.584828226  0.37187300 0.01224432
X.12MINTR  0.677605546 -0.03963524 0.03780637
BENCH     -0.118897796  0.81551057 0.13732357
CURL      -0.022681822  0.67410438 0.09591605
MAXPUSHU   0.432998769  0.52198807 0.02011158
```

The highest loading in the first column is in row 4, the highest loading in the second column is in row 7, and the highest loading in the third column is in row 2. We extract these three rows, bind them into the matrix $\mathbf{F}_1$, and then construct $\mathbf{T}$ as before.

```
> F1 <- rbind(F[4,], F[7,],F[2,])
> F1
            [,1]        [,2]       [,3]
[1,]  0.77891163 -0.17862424 0.01582561
[2,] -0.11889780  0.81551057 0.13732357
[3,]  0.02363395  0.03187533 0.76469736
> T <- solve(F1) %*% diag ( sqrt(diag(F1 %*% t(F1))))
> rotated.F <- zapsmall (F %*% T)
> rotated.F
                [,1]      [,2]       [,3]
PINBALL   -0.0085167 0.1073794  0.5730588
BILLIARD   0.0000000 0.0000000  0.7657262
GOLF       0.0304990 0.0287544  0.7301948
X.1500M    0.7992874 0.0000000  0.0000000
X.2KROW    0.6819869 0.5409817 -0.0902969
X.12MINTR  0.7131092 0.1225123  0.0035555
BENCH      0.0000000 0.8354950  0.0000000
CURL       0.0811407 0.7101584 -0.0224437
MAXPUSHU   0.5444078 0.6636849 -0.0998862
```

The rotation worked, and the new rotated factors have the following correlation matrix:

```
> solve(T) %*% t( solve(T) )
            [,1]       [,2]       [,3]
[1,]  1.00000000 -0.3535600 0.04054807
[2,] -0.35355999  1.0000000 0.20038064
[3,]  0.04054807  0.2003806 1.00000000
```

Let's verify that we get exactly the same solution if we set up a confirmatory factor model with all loadings free except for the zeroes we rotated into position in rows 2,4 and 7. It'll help if we add column names to the factor pattern:

```
> colnames(rotated.F) <- c("Endurance","Strength","Hand-Eye")
> rotated.F
           Endurance  Strength   Hand-Eye
PINBALL   -0.0085167 0.1073794  0.5730588
BILLIARD   0.0000000 0.0000000  0.7657262
GOLF       0.0304990 0.0287544  0.7301948
X.1500M    0.7992874 0.0000000  0.0000000
X.2KROW    0.6819869 0.5409817 -0.0902969
X.12MINTR  0.7131092 0.1225123  0.0035555
BENCH      0.0000000 0.8354950  0.0000000
CURL       0.0811407 0.7101584 -0.0224437
MAXPUSHU   0.5444078 0.6636849 -0.0998862
```

The easiest way to construct the initial confirmatory factor model is to take a complete model with all loadings, then simply eliminate the zero loadings by erasing their lines from the model file, or by commenting them out with **##** as shown below. There is no need to “renumber” the names given to the parameter numbers.

```
## Factor 1 -- Endurance
Endurance -> X.1500M,  theta01, NA
Endurance -> X.2KROW,  theta02, NA
Endurance -> X.12MINTR,theta03, NA
## Endurance  -> BENCH,theta04, NA
Endurance  -> CURL,     theta05, NA
Endurance  -> MAXPUSHU, theta06, NA
Endurance  -> PINBALL,  theta07, NA
## Endurance  -> BILLIARD, theta08, NA
Endurance  -> GOLF,     theta09, NA
## Factor 2 -- Strength
## Strength -> X.1500M,  theta10, NA
Strength -> X.2KROW,  theta11, NA
Strength -> X.12MINTR,theta12, NA
Strength  -> BENCH,    theta13, NA
Strength  -> CURL,     theta14, NA
Strength  -> MAXPUSHU, theta15, NA
Strength  -> PINBALL,  theta16, NA
## Strength  -> BILLIARD, theta17, NA
Strength  -> GOLF,     theta18, NA
## Factor 3 -- Hand-Eye Coordination
## Hand-Eye -> X.1500M,  theta19, NA
Hand-Eye -> X.2KROW,  theta20, NA
Hand-Eye -> X.12MINTR,theta21, NA
##  Hand-Eye  -> BENCH,    theta22, NA
Hand-Eye  -> CURL,     theta23, NA
Hand-Eye  -> MAXPUSHU, theta24, NA
Hand-Eye  -> PINBALL,  theta25, NA
Hand-Eye  -> BILLIARD, theta26, NA
Hand-Eye  -> GOLF,     theta27, NA
## Unique Variances
X.1500M   <->  X.1500M,  theta28, NA
X.2KROW   <->  X.2KROW,  theta29, NA
X.12MINTR <->  X.12MINTR, theta30, NA
BENCH     <->  BENCH, theta31, NA
CURL      <->  CURL, theta32, NA
MAXPUSHU  <->  MAXPUSHU, theta33, NA
PINBALL   <->  PINBALL, theta34, NA
BILLIARD  <->  BILLIARD, theta35, NA
GOLF      <->  GOLF, theta36, NA
## Factor Variances
Endurance <->  Endurance, NA, 1
Strength  <->  Strength,  NA, 1
Hand-Eye  <->  Hand-Eye,  NA, 1
## Factor Correlations
Endurance <->  Strength, theta37, NA
Endurance <->  Hand-Eye, theta38, NA
Strength  <->  Hand-Eye, theta39, NA
```

We save this model definition to a file called “Full AthleticsData Model.txt” and fit it with the following commands:

```
> base.model <-  specify.model("Full AthleticsData Model.txt")
Read 36 records
> base.model.fit <- sem(base.model, AthleticsData.R, 1000)
> summary(base.model.fit)

 Model Chisquare =  13.016   Df =  12 Pr(>Chisq) = 0.36787
 Chisquare (null model) =  2330.1   Df =  36
 Goodness-of-fit index =  0.99718
 Adjusted goodness-of-fit index =  0.98943
 RMSEA index =  0.0092067   90% CI: (NA, 0.034233)
 Bentler-Bonnett NFI =  0.99441
 Tucker-Lewis NNFI =  0.99867
 Bentler CFI =  0.99956
 SRMR =  0.0083836
 BIC =  -69.877

 Normalized Residuals
     Min.   1st Qu.    Median      Mean   3rd Qu.      Max.
-7.28e-01 -6.03e-02  3.58e-06  2.03e-03  5.30e-02  6.75e-01

 Parameter Estimates
        Estimate   Std Error z value  Pr(>|z|)
theta01  0.7992863 0.032454  24.62791 0.0000e+00 X.1500M <--- Endurance
theta02  0.6819851 0.037465  18.20328 0.0000e+00 X.2KROW <--- Endurance
theta03  0.7131082 0.035756  19.94376 0.0000e+00 X.12MINTR <--- Endurance
theta05  0.0811397 0.033591   2.41551 1.5713e-02 CURL <--- Endurance
theta06  0.5444060 0.036702  14.83334 0.0000e+00 MAXPUSHU <--- Endurance
theta07 -0.0085169 0.036086  -0.23601 8.1342e-01 PINBALL <--- Endurance
theta09  0.0304986 0.035300   0.86399 3.8759e-01 GOLF <--- Endurance
theta11  0.5409809 0.038606  14.01292 0.0000e+00 X.2KROW <--- Strength
theta12  0.1225113 0.035842   3.41809 6.3062e-04 X.12MINTR <--- Strength
theta13  0.8354945 0.032119  26.01248 0.0000e+00 BENCH <--- Strength
theta14  0.7101566 0.036427  19.49523 0.0000e+00 CURL <--- Strength
theta15  0.6636826 0.038615  17.18738 0.0000e+00 MAXPUSHU <--- Strength
theta16  0.1073757 0.036889   2.91075 3.6057e-03 PINBALL <--- Strength
theta18  0.0287492 0.036641   0.78461 4.3268e-01 GOLF <--- Strength
theta20 -0.0902962 0.036492  -2.47439 1.3346e-02 X.2KROW <--- HandEye
theta21  0.0035565 0.034536   0.10298 9.1798e-01 X.12MINTR <--- HandEye
theta23 -0.0224436 0.033400  -0.67197 5.0160e-01 CURL <--- HandEye
theta24 -0.0998858 0.036133  -2.76440 5.7027e-03 MAXPUSHU <--- HandEye
theta25  0.5730593 0.034658  16.53460 0.0000e+00 PINBALL <--- HandEye
theta26  0.7657239 0.034999  21.87871 0.0000e+00 BILLIARD <--- HandEye
theta27  0.7301998 0.036511  19.99932 0.0000e+00 GOLF <--- HandEye
theta28  0.3611397 0.034815  10.37297 0.0000e+00 X.1500M <--> X.1500M
theta29  0.5195373 0.031951  16.26021 0.0000e+00 X.2KROW <--> X.2KROW
theta30  0.5378512 0.033371  16.11730 0.0000e+00 X.12MINTR <--> X.12MINTR
theta31  0.3019493 0.035269   8.56143 0.0000e+00 BENCH <--> BENCH
theta32  0.5358710 0.033143  16.16860 0.0000e+00 CURL <--> CURL
theta33  0.5396369 0.031860  16.93766 0.0000e+00 MAXPUSHU <--> MAXPUSHU
theta34  0.6350901 0.034811  18.24382 0.0000e+00 PINBALL <--> PINBALL
theta35  0.4136680 0.039453  10.48518 0.0000e+00 BILLIARD <--> BILLIARD
theta36  0.4554507 0.037795  12.05056 0.0000e+00 GOLF <--> GOLF
theta37 -0.3535592 0.042714  -8.27737 2.2204e-16 Strength <--> Endurance
theta38  0.0405418 0.050557   0.80190 4.2261e-01 HandEye <--> Endurance
theta39  0.2003873 0.047973   4.17704 2.9532e-05 HandEye <--> Strength

 Iterations =  88
```

As you can see, the above output precisely matches our rotated simple structure solution, except now we have standard error estimates and test statistics associated with all the parameters. The hypothesis of perfect fit is no longer even rejected ($p = .37$), and the fit indices are better than one usually sees in practice.

One aspect of the above output might confuse the novice, so let me digress for a moment. I stated that this “identified” unrestricted model has exactly the same fit as an unrestricted model fit by a “dedicated” factor analysis program such as **`factanal`**.

However, in this case, we see a chi square statistic of 13.016, while in our previous investigation using factanal gave a chi square of 12.94. Why the discrepancy?

The answer is that the chi square statistic is, in general, computed by multiplying the maximum likelihood discrepancy function by a "multiplier." Most general purpose structural equation modeling programs use a multiplier of $N-1$, while many dedicated factor analysis programs use the "Bartlett multiplier"

$$N-1-\frac{p}{3}-\frac{4m+5}{6}$$

If you examine the factanal output with the command

```
> exploratory$criteria
      objective counts.function counts.gradient
     0.01302917     11.00000000     11.00000000
```

you discover that the discrepancy function is .01302917. The Bartlett multiplier is 992.1667, which when multipled by the discrepancy function gives the stated chi square value of 12.94. If we multiply the discrepancy by $N-1$, we obtain 13.016, the value given by **sem**. We can also examine the discrepancy function directly, with the command

```
> base.model.fit$criterion
[1] 0.01302917
```

The next step, according to Jöreskog (1978), is to pare down the model by eliminating factor loadings that are not significant, and then re-estimating the model. If we eliminate all paths that are not significant with $p < .05$, two-tailed, this amounts to eliminating all paths with z-statistics less than 1.96 in absolute value. I highlighted all the loading (directed) paths in the output above. Effectively eliminating them by placing **##** in front of them, and fitting the revised model, we get

```
 Model Chisquare =  14.824   Df =  17 Pr(>Chisq) = 0.60814
 Chisquare (null model) =  2330.1   Df =  36
 Goodness-of-fit index =  0.99678
 Adjusted goodness-of-fit index =  0.99147
 RMSEA index =  0   90% CI: (NA, 0.024988)
 Bentler-Bonnett NFI =  0.99364
 Tucker-Lewis NNFI =  1.002
 Bentler CFI =  1
 SRMR =  0.010374
 BIC =  -102.61

 Normalized Residuals
     Min.   1st Qu.    Median      Mean   3rd Qu.      Max.
-7.48e-01 -1.48e-01 -9.49e-06 -1.56e-02  6.34e-02  1.12e+00

 Parameter Estimates
        Estimate  Std Error z value Pr(>|z|)
theta01  0.798679 0.032453  24.6106 0.0000e+00 X.1500M <--- Endurance
theta02  0.682514 0.037419  18.2398 0.0000e+00 X.2KROW <--- Endurance
theta03  0.714667 0.035439  20.1663 0.0000e+00 X.12MINTR <--- Endurance
theta05  0.079109 0.033130   2.3878 1.6949e-02 CURL <--- Endurance
theta06  0.545619 0.036620  14.8994 0.0000e+00 MAXPUSHU <--- Endurance
theta11  0.540617 0.038419  14.0717 0.0000e+00 X.2KROW <--- Strength
theta12  0.123926 0.034505   3.5915 3.2875e-04 X.12MINTR <--- Strength
theta13  0.837604 0.032037  26.1446 0.0000e+00 BENCH <--- Strength
theta14  0.703326 0.034641  20.3035 0.0000e+00 CURL <--- Strength
theta15  0.663589 0.038425  17.2695 0.0000e+00 MAXPUSHU <--- Strength
theta16  0.103959 0.031970   3.2517 1.1471e-03 PINBALL <--- Strength
theta20 -0.085985 0.033327  -2.5801 9.8785e-03 X.2KROW <--- HandEye
theta24 -0.094708 0.033368  -2.8382 4.5363e-03 MAXPUSHU <--- HandEye
theta25  0.574036 0.034090  16.8387 0.0000e+00 PINBALL <--- HandEye
theta26  0.762281 0.034516  22.0849 0.0000e+00 BILLIARD <--- HandEye
theta27  0.740866 0.034353  21.5664 0.0000e+00 GOLF <--- HandEye
theta28  0.362112 0.034793  10.4077 0.0000e+00 X.1500M <--> X.1500M
theta29  0.520594 0.031931  16.3039 0.0000e+00 X.2KROW <--> X.2KROW
theta30  0.536656 0.033361  16.0861 0.0000e+00 X.12MINTR <--> X.12MINTR
theta31  0.298420 0.035146   8.4910 0.0000e+00 BENCH <--> BENCH
theta32  0.538503 0.032873  16.3815 0.0000e+00 CURL <--> CURL
theta33  0.540087 0.031881  16.9410 0.0000e+00 MAXPUSHU <--> MAXPUSHU
theta34  0.635539 0.034737  18.2958 0.0000e+00 PINBALL <--> PINBALL
theta35  0.418927 0.038344  10.9256 0.0000e+00 BILLIARD <--> BILLIARD
theta36  0.451118 0.037473  12.0386 0.0000e+00 GOLF <--> GOLF
theta37 -0.354331 0.042603  -8.3170 0.0000e+00 Strength <--> Endurance
theta38  0.049396 0.042759   1.1552 2.4800e-01 HandEye <--> Endurance
theta39  0.202231 0.041354   4.8902 1.0071e-06 HandEye <--> Strength

 Iterations =  23
```

A final step, according to Jöreskog, is to check modification indices to see if any zero loadings might be relaxed.

```
> mod.indices(pared.model.fit)
```

The results show that no potential loading from a factor to an observed variable makes the list of highest modification indices in the **A** matrix, and only one of them suggests a significant improvement in the chi square statistic, because the significance value for a χ^2 with one degree of freedom is 3.84.

```
 5 largest modification indices, A matrix:
   GOLF:X.2KROW BILLIARD:X.2KROW     X.2KROW:GOLF        CURL:GOLF X.1500M:MAXPUSHU
       3.933301         2.005178         1.417790         1.128748         0.968813

  5 largest modification indices, P matrix:
     X.2KROW:GOLF     X.12MINTR:GOLF   X.2KROW:BILLIARD   MAXPUSHU:X.1500M MAXPUSHU:X.12MINTR
         4.427690           2.845399           2.576033           2.101112           2.016665
```

This final model has fit statistics that are incredibly good. The point estimate for the RMSEA is zero, and the p-value for the test of perfect fit is .61. The hypothesis of perfect fit cannot be rejected.

Before ending this discussion, I'd like to sound some cautionary notes, and add some food for thought. First and foremost, the statistics generated by sem and several other programs like it assume that (a) a sample covariance matrix with (b) a Wishart distribution is being analyzed. The distribution theory, overall test of fit, and standard error estimates are all based on that assumption. Assumption (a) is clearly violated in this situation, as, true to tradition, we actually analyzed the correlation matrix. Now, in a sense, a correlation matrix *is* a covariance matrix, but the sample correlation matrix does not have the same distribution as the sample covariance matrix from which it is calculated. To see why, simply look at each element of the correlation matrix. The diagonal entries do not vary randomly — they are always 1 — while the elements on the diagonal of a sample covariance matrix are, of course, free to vary. Lawley and Maxwell (1970) pointed this out in their book on factor analysis, and showed the extent of the error in the standard error estimates that could result from analyzing the sample correlation matrix as though it were a correlation matrix. The earliest commercial software program, LISREL, was based on a computational engine that assumed a covariance matrix was being analyzed. For years, LISREL produced incorrect standard error estimates from a sample correlation matrix, and, in fact, featured examples of the same in its manual. The chi square statistic and parameter estimates are not affected by this error when a factor model is estimated, but the standard errors can be substantially in error.

In practice, assumption (b), which amounts in practice to an assumption of multivariate normality, is also violated frequently. Although "asymptotically distribution free" (ADF) methods are available to compensate for this, they don't work very well unless sample sizes are quite large.

If you think carefully about what we did in our two approaches to confirmatory factor analysis, you will realize that a number of aspects were questionable, because the procedures violated some long established principles of statistical analysis. In addition to some truly questionable aspects of the procedures, other things we did were somewhat arbitrary. For example, we decided to stop freeing up factor loadings in our first approach, when the modification indices showed we could continue to produce significant improvements in the overall fit statistic. In the second procedure, we used the .05 significance level to establish our cutoff for deciding if a loading is "insignificant." What would have happened if we'd considered familywise error rate? These are issues we will discuss in class.