12/5/16

Outline

1. Assessing model fit: the $\chi^2$
   - Related indices
2. Evaluating Residuals for Normality
3. Adjusting for non-normality
4. Model comparison
5. Testing mediation

Evaluating Fit of Modeled Covariances Matrix

The log likelihood ratio, $F_{ML}$ follows $\chi^2$ distribution such that

$$\chi^2 = (n-1)F_{ML}$$

- Note scaling by sample size
- Large $\chi^2$ implies LACK of fit
The Classic Test using P Values

\[ \chi^2 = 1.78 \text{ with 50 samples} \]
\[ p = 0.182 \]

\[ \chi^2 = 3.60 \text{ with 100 samples} \]
\[ p = 0.058 \]

\[ \chi^2 = 7.24 \text{ with 200 samples} \]
\[ p = 0.007 \]

Kline (2012) recommends 4 measures of model fit:

1. Model Chi-Square with its df and p-value.
   - prefer p-value greater than 0.05

2. Root Mean Square Error of Approximation (RMSEA).
   - prefer lower 90%CI to be < 0.05

3. Comparative Fit Index (CFI).
   - prefer value greater than 0.90

4. Standardized Root Mean Square Residual (SRMR).
   - prefer value less than 0.10

---

RMSEA for Our Example

<table>
<thead>
<tr>
<th>Samples</th>
<th>RMSEA</th>
<th>LO90</th>
<th>HI90</th>
<th>PCLOSE</th>
</tr>
</thead>
<tbody>
<tr>
<td>50</td>
<td>.126</td>
<td>.000</td>
<td>.426</td>
<td>.208</td>
</tr>
<tr>
<td>100</td>
<td>.162</td>
<td>.000</td>
<td>.356</td>
<td>.089</td>
</tr>
<tr>
<td>200</td>
<td>.177</td>
<td>.074</td>
<td>.307</td>
<td>.024</td>
</tr>
</tbody>
</table>

We are still affected by sample size / power.
(which is reasonable)

As our sample size increases, we can expect our data to support more and more complex models.

Measures of Goodness of Fit that don’t involve p-values

CFI: uses Centrality of model \( \chi^2 \)

50 samples = 0.96
100 samples = 0.94
200 samples = 0.94
Evaluating Fit of A Model

issue: should there be a path from x to y2?

\[ r_{xy2} \text{ expected to be } 0.2 = (0.40 \times 0.50) \]

\[
\begin{array}{ccc}
  & y1 & y2 \\
  x & 0.40 & 0.50 \\
  y1 & & 1.0 \\
  y2 & & 0.40 \\
  x & 0.35 & 0.5 \\
  y2 & & 1.0 \\
  x & 0.40 & 0.35 \\
\end{array}
\]

\[
\text{std. covariance matrix}
\]

standardized residual = 0.35 – 0.2 = 0.15

Diagnosing Causes of Lack of Fit with Residuals (misspecification)

\[
\text{But how much will including a path increase model fit?}
\]

Modification Indices

- **Lagrange Multipliers**: The amount that \( \chi^2 \) would decrease due to including a path.

- **Wald W statistic**: How much \( \chi^2 \) would increase if a path is trimmed.
  - Dropping a path can increase parameter variability

- Be very careful here for data dredging.

Fully Mediated Fire

```
fullMedModel<-' firesev ~ age
cover ~ firesev'
```

```
fullMedSEM<-sem(fullMedModel, data=keeley)
```
### Fit of the Fully Mediated Model

| age | cover | firesev |

> summary(fullMedSEM)
lavaan (0.5-17) converged normally after 19 iterations

<table>
<thead>
<tr>
<th>Number of observations</th>
<th>90</th>
</tr>
</thead>
<tbody>
<tr>
<td>Estimator</td>
<td>ML</td>
</tr>
<tr>
<td>Minimum Function Chi-square</td>
<td>3.297</td>
</tr>
<tr>
<td>Degrees of freedom</td>
<td>1</td>
</tr>
<tr>
<td>P-value</td>
<td>0.069</td>
</tr>
</tbody>
</table>

### Fit-A-Palooza

**summary(fullMedSEM, fit.measures=T)**

> summary(fullMedSEM, fit.measures=T)
lavaan (0.4-12) converged normally after 21 iterations

<table>
<thead>
<tr>
<th>Number of observations</th>
<th>90</th>
</tr>
</thead>
<tbody>
<tr>
<td>Estimator</td>
<td>ML</td>
</tr>
<tr>
<td>Minimum Function Chi-square</td>
<td>43.143</td>
</tr>
<tr>
<td>Degrees of freedom</td>
<td>3</td>
</tr>
<tr>
<td>P-value</td>
<td>0.000</td>
</tr>
</tbody>
</table>

Chi-square test baseline model:

<table>
<thead>
<tr>
<th>Comparative Fit Index (CFI)</th>
<th>0.943</th>
</tr>
</thead>
<tbody>
<tr>
<td>Tucker-Lewis Index (TLI)</td>
<td>0.828</td>
</tr>
</tbody>
</table>

Loglikelihood and Information Criteria:

<table>
<thead>
<tr>
<th>Loglikelihood</th>
<th>user model (H0)</th>
<th>-531.341</th>
</tr>
</thead>
<tbody>
<tr>
<td>Loglikelihood</td>
<td>unrestricted model (H1)</td>
<td>-529.693</td>
</tr>
<tr>
<td>Number of free parameters</td>
<td>4</td>
<td></td>
</tr>
<tr>
<td>Akaike (AIC)</td>
<td>1070.683</td>
<td></td>
</tr>
<tr>
<td>Bayesian (BIC)</td>
<td>1080.682</td>
<td></td>
</tr>
<tr>
<td>Sample-size adjusted Bayesian (BIC)</td>
<td>1068.057</td>
<td></td>
</tr>
<tr>
<td>Root Mean Square Error of Approximation:</td>
<td></td>
<td></td>
</tr>
<tr>
<td>RMSEA</td>
<td>0.160</td>
<td></td>
</tr>
<tr>
<td>90 Percent Confidence Interval</td>
<td>0.000 0.365</td>
<td></td>
</tr>
<tr>
<td>P-value RMSEA &lt;= 0.05</td>
<td>0.101</td>
<td></td>
</tr>
</tbody>
</table>

### Fit-A-Palooza2

**fitMeasures(fullMedSEM)**

> fitMeasures(fullMedSEM)

<table>
<thead>
<tr>
<th>Parameter</th>
<th>RMSEA</th>
<th>90 Percent Confidence Interval</th>
<th>P-value RMSEA &lt;= 0.05</th>
</tr>
</thead>
<tbody>
<tr>
<td>-531.460</td>
<td>0.160</td>
<td>0.000 0.365</td>
<td>0.101</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Unstandardized</th>
<th>Standardized</th>
</tr>
</thead>
<tbody>
<tr>
<td>c</td>
<td>4.000</td>
<td>0.018</td>
</tr>
<tr>
<td>tli</td>
<td>3.297</td>
<td>0.160</td>
</tr>
<tr>
<td>pvalue</td>
<td>0.069</td>
<td>1.000</td>
</tr>
</tbody>
</table>

### Fit-A-Palooza3

**summary(fullMedSEM, fit.measures=T)**

> summary(fullMedSEM, fit.measures=T)
lavaan (0.5-17) converged normally after 19 iterations

<table>
<thead>
<tr>
<th>Number of observations</th>
<th>90</th>
</tr>
</thead>
<tbody>
<tr>
<td>Estimator</td>
<td>ML</td>
</tr>
<tr>
<td>Minimum Function Chi-square</td>
<td>3.297</td>
</tr>
<tr>
<td>Degrees of freedom</td>
<td>1</td>
</tr>
<tr>
<td>P-value</td>
<td>0.069</td>
</tr>
</tbody>
</table>

Chi-square test baseline model:

<table>
<thead>
<tr>
<th>Comparative Fit Index (CFI)</th>
<th>0.943</th>
</tr>
</thead>
<tbody>
<tr>
<td>Tucker-Lewis Index (TLI)</td>
<td>0.828</td>
</tr>
</tbody>
</table>

Loglikelihood and Information Criteria:

<table>
<thead>
<tr>
<th>Loglikelihood</th>
<th>user model (H0)</th>
<th>-531.341</th>
</tr>
</thead>
<tbody>
<tr>
<td>Loglikelihood</td>
<td>unrestricted model (H1)</td>
<td>-529.693</td>
</tr>
<tr>
<td>Number of free parameters</td>
<td>4</td>
<td></td>
</tr>
<tr>
<td>Akaike (AIC)</td>
<td>1070.683</td>
<td></td>
</tr>
<tr>
<td>Bayesian (BIC)</td>
<td>1080.682</td>
<td></td>
</tr>
<tr>
<td>Sample-size adjusted Bayesian (BIC)</td>
<td>1068.057</td>
<td></td>
</tr>
<tr>
<td>Root Mean Square Error of Approximation:</td>
<td></td>
<td></td>
</tr>
<tr>
<td>RMSEA</td>
<td>0.160</td>
<td></td>
</tr>
<tr>
<td>90 Percent Confidence Interval</td>
<td>0.000 0.365</td>
<td></td>
</tr>
<tr>
<td>P-value RMSEA &lt;= 0.05</td>
<td>0.101</td>
<td></td>
</tr>
</tbody>
</table>
Observed v. Fitted

```
observed <- inspect(fullMedSEM, "sample")
fitted <- fitted(fullMedSEM)
```

<table>
<thead>
<tr>
<th></th>
<th>firesev</th>
<th>cover</th>
<th>age</th>
</tr>
</thead>
<tbody>
<tr>
<td>firesev</td>
<td>2.700</td>
<td>0.100</td>
<td>1.381</td>
</tr>
<tr>
<td>cover</td>
<td>-0.227</td>
<td>0.100</td>
<td>-0.782</td>
</tr>
<tr>
<td>age</td>
<td>9.319</td>
<td>-1.156</td>
<td>156.157</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th></th>
<th>firesev</th>
<th>cover</th>
<th>age</th>
</tr>
</thead>
<tbody>
<tr>
<td>mean</td>
<td>4.565</td>
<td>0.691</td>
<td>25.567</td>
</tr>
</tbody>
</table>

Residual Covariance

```
residuals <- residuals(fullMedSEM)
```

<table>
<thead>
<tr>
<th></th>
<th>firesev</th>
<th>cover</th>
<th>age</th>
</tr>
</thead>
<tbody>
<tr>
<td>firesev</td>
<td>0.000</td>
<td>0.000</td>
<td>0.000</td>
</tr>
<tr>
<td>cover</td>
<td>0.000</td>
<td>0.000</td>
<td>0.000</td>
</tr>
<tr>
<td>age</td>
<td>0.000</td>
<td>-0.599</td>
<td>0.000</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th></th>
<th>firesev</th>
<th>cover</th>
<th>age</th>
</tr>
</thead>
<tbody>
<tr>
<td>mean</td>
<td>0.000</td>
<td>0.000</td>
<td>0.000</td>
</tr>
</tbody>
</table>

Residual Correlation

```
residuals <- residuals(fullMedSEM)
```

<table>
<thead>
<tr>
<th></th>
<th>firesev</th>
<th>cover</th>
<th>age</th>
</tr>
</thead>
<tbody>
<tr>
<td>firesev</td>
<td>0.000</td>
<td>0.000</td>
<td>0.000</td>
</tr>
<tr>
<td>cover</td>
<td>0.000</td>
<td>0.000</td>
<td>0.000</td>
</tr>
<tr>
<td>age</td>
<td>0.000</td>
<td>-0.152</td>
<td>0.000</td>
</tr>
</tbody>
</table>

Modification Indices

```
modificationIndices <- modificationIndices(fullMedSEM, standardized=F)
```

<table>
<thead>
<tr>
<th></th>
<th>firesev</th>
<th>cover</th>
<th>age</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>firesev</td>
<td>firesev</td>
<td>3.238</td>
</tr>
<tr>
<td>2</td>
<td>firesev</td>
<td>cover</td>
<td>3.238</td>
</tr>
<tr>
<td>3</td>
<td>firesev</td>
<td>age</td>
<td>NA</td>
</tr>
<tr>
<td>4</td>
<td>cover</td>
<td>cover</td>
<td>0.000</td>
</tr>
<tr>
<td>5</td>
<td>cover</td>
<td>age</td>
<td>-0.755</td>
</tr>
<tr>
<td>6</td>
<td>age</td>
<td>age</td>
<td>0.000</td>
</tr>
<tr>
<td>7</td>
<td>firesev</td>
<td>cover</td>
<td>3.238</td>
</tr>
<tr>
<td>8</td>
<td>firesev</td>
<td>age</td>
<td>0.000</td>
</tr>
<tr>
<td>9</td>
<td>cover</td>
<td>firesev</td>
<td>0.000</td>
</tr>
<tr>
<td>10</td>
<td>cover</td>
<td>age</td>
<td>1.238</td>
</tr>
<tr>
<td>11</td>
<td>age</td>
<td>firesev</td>
<td>0.000</td>
</tr>
<tr>
<td>12</td>
<td>age</td>
<td>cover</td>
<td>2.884</td>
</tr>
</tbody>
</table>

12/5/16
Exercise: Diagnosing Misspecification

- Fit and assess model
- Look at measures of misspecification

Solution: Diagnosing Misspecification

# Full Mediation
```
distModel2 <- 'rich ~ abiotic + hetero
    hetero ~ distance
    abiotic ~ distance'

distFit2 <- sem(distModel2, data=keeley)
```

Solution: Model Doesn't Fit Data

```
> summary(distFit2)
lavaan (0.5-17) converged normally after 36 iterations
   Number of observations                           90
   Estimator                                         ML
   Minimum Function Test Statistic                 17.831
   Degrees of freedom                                 2
   P-value (Chi-square)                           0.000
```

Solution: Large Residual rich->distance correlation

```
> residuals(distFit2, type="cor")
$r

<table>
<thead>
<tr>
<th></th>
<th>rich</th>
<th>hetero</th>
<th>abiotic</th>
<th>distance</th>
</tr>
</thead>
<tbody>
<tr>
<td>rich</td>
<td>0.000</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>hetero</td>
<td>0.042</td>
<td>0.000</td>
<td></td>
<td></td>
</tr>
<tr>
<td>abiotic</td>
<td>0.032</td>
<td>0.118</td>
<td>0.000</td>
<td></td>
</tr>
<tr>
<td>distance</td>
<td>0.271</td>
<td>0.000</td>
<td>0.000</td>
<td>0.000</td>
</tr>
</tbody>
</table>
```
Solution: Large Residual rich->distance correlation

```r
# modification indices, with a trick to only see big ones
> modI <- modificationIndices(distFit2, standardized=F)
> modI[which(modI$mi > 3),]

   lhs  op rhs  mi  epc
1  rich --  hetero 15.181 -1.690
2  rich --  abiotic 15.181 -76.202
3  rich --  distance 15.181  0.662
4   abiotic --  rich  3.811  0.196
5  distance --  rich  10.672  0.251
```

Additional Points about Overall Model Fit

1. SEM focuses on assessing overall model fit
   • Is your model adequate?
   • Are you missing any paths?

2. When you are missing important paths your parameter estimates may be incorrect
   • your model is *misspecified*

Outline

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Partial Mediation Model

```r
partialMedModel<-'firesev ~ age
cover ~ firesev + age'

partialMedSEM<-$\text{sem}(\text{partialMedModel, data=keeley, meanstructure=TRUE})$
```
What is the distribution of our residuals?

```r
> source("./fitted_lavaan.R")
> partialResid <- residuals_lavaan(partialMedSEM)

> head(partialResid)
firesev  cover
1 -1.9263673  0.4752431
2 -0.4811819 -0.2186521
3 -1.3343917  0.1642312
4 -1.0343917  0.4101956
5 -0.1118239  0.5842525
6 -0.4715029  0.4683961
```

QQ Plots Help

```r
par(mfrow=c(1,2))
apply(partialResid, 2, function(x){
  qqnorm(x)
  qqline(x))
par(mfrow=c(1,1))
```

Multivariate Shapiro-Wilks Test

```r
library(mvnormtest)
> mshapiro.test(t(partialResid))

  Shapiro-Wilk normality test

  data: Z
  W = 0.96889, p-value = 0.02954
```

Often too sensitive of a test

Formal Tests from MVN

```r
library(MVN)
mt <- mardiaTest(partialResid, qqplot=F)
Mardia’s Multivariate Normality Test
```

```r
data : partialResid

  q1p : 0.6205411
c1.skew : 9.3088116
  p.value.skew : 0.05384291
  
g2p : 7.249683
  z.kurtosis : -0.8897668
  p.value.kurt : 0.3735911
  
  chi.small.skew : 9.83453
  p.value.small : 0.04330918

Result : Data are multivariate normal.
```
Outline

1. Assessing model fit: the $\chi^2$
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Our Model for Correction

```
# Full Mediation
distModel2 <- 'rich ~ abiotic + hetero
              hetero ~ distance
              abiotic ~ distance'
```

```
distFit2 <- sem(distModel2, data=keeley, meanstructure=TRUE)
```

Are these Residuals Multivariate Normal?
Multivariate Shapiro-Wilks Test

> library(mvnormtest)
> mshapiro.test(t(res))

Shapiro-Wilk normality test

data:  Z
W = 0.98579, p-value = 0.4367

These residuals are fine

- Can be overly sensitive
- Skew most important

Correcting for Violation of Normality: The Satorra-Bentler Chi Square

Sensitivity to Parameter Change
Weights derived From Cov Matrix

Correlation coefficient for $\chi^2$ and Standard Errors

distFitSB <- sem(distModel2, data = keeley, estimator = "mlm")

Mardia’s Multivariate Skew

> library(semTools)
> mardiaSkew(res)

b1d        chi         df          p
0.5693772  8.5406580 10.0000000  0.5761788

This is fine

Satorra-Bentler Output

> summary(distFit2SB)
lavaan (0.5-17) converged normally after 44 iterations

Number of observations                             90
Estimator                                         ML      Robust
Minimum Function Test Statistic               17.831      17.854
Degrees of freedom                                 2           2
P-value (Chi-square)                           0.000       0.000
Scaling correction factor                                  0.999
Violation of Multivariate Normality: The Bollen-Stine Bootstrap

To get accurate bootstrap, you can calculate a bootstrapped \( \chi^2 \) on transformed data

Bollen-Stine Bootstrap Output

```r
> distFitBoot <- sem(distModel, data=keeley, test="bollen.stine", se="boot", bootstrap=100)
```

Typically want ~ 1000 bootstrap replicates

Bollen-Stine Bootstrap Output

```r
> summary(distFitBoot)
lavaan (0.5-17) converged normally after 37 iterations

Number of observations                    90
Estimator                                ML
Minimum Function Test Statistic          1.810
Degrees of freedom                      1
P-value (Chi-square)                    0.178
P-value (Bollen-Stine Bootstrap)        0.140
```

Questions?
Outline

1. Assessing model fit: the $\chi^2$
   - Related indices
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The Likelihood Ratio Test Revisited for Mediation

<table>
<thead>
<tr>
<th>Model</th>
<th>$\chi^2$</th>
<th>DF</th>
<th>p</th>
</tr>
</thead>
<tbody>
<tr>
<td>Model 1</td>
<td>1.78</td>
<td>1</td>
<td>0.18</td>
</tr>
<tr>
<td>Model 2</td>
<td>0.00</td>
<td>0</td>
<td></td>
</tr>
</tbody>
</table>

\[ \text{Suggests Model 1 fits as well as model 2 with fewer paths – parsimony wins!} \]

AIC Comparisons: Because You Will Only Ever Know Your Sampled Population

\[ f(x) = \text{“True” value at point } x \]
\[ \text{Discrepancy between fit model and } f(x) \text{ conveys information loss} \]

Models Provide Varying Degrees of Information about Reality

\[ G_i(x|\theta) = \text{estimate of model } i \text{ at point } x \text{ given parameters } \theta \]
Kulback-Leibler Information

\[ I(f, g) = \int f(x) \log \frac{f(x)}{g(x | \theta)} \, dx \]

\( I(f, g) \) = information loss when \( g \) is used to approximate \( f \) – integrated over all values of \( x \)

Note: \( f(x) \) can be pulled out as a constant when comparing multiple models! No need to know the true value of \( f(x) \)

Likelihood and Information

For likelihood, information loss is conveyed by the following with \( K = \# \) of parameters:

\[ \log(\hat{L}(\hat{\theta} | \text{data})) - K = \text{constant} - I(f, \hat{g}) \]

This gives rise to Akaike’s Information Criterion – lower AIC means less information is lost by a model

\[ \text{AIC} = -2\log(L(\hat{\theta} | \text{data})) + 2K \]

Principal of Parsimony:
How many parameters does it take to fit an elephant?
Correcting for Sample Size: the AICc

\[ AICc = AIC + \frac{2t(t+1)}{n-t-1} \]

where \( t \) = number of estimated parameters in the model and \( n \) = the number of samples

Note, this is not the “consistent AIC” reported as CAIC by many pieces of software

Model Weights to Compare Models

• In a set of models, the difference between model I and the model with the best fit is
  \[ \Delta I = AIC_I - AIC_{\text{min}} \]

• We can then define the relative support for a model as a model weight
  \[ w_i = \frac{\exp\left(-\frac{1}{2}\Delta_i \right)}{\sum_{i=1}^r \exp\left(-\frac{1}{2}\Delta_i \right)} \]

• N.B. model weights summed together = 1

AIC and SEM

• AIC – most predictive model
  \[ AIC = \chi^2 + 2K \]

• Small Sample-Size Adjusted AIC
  \[ AICc = \chi^2 + 2K*(K-1)/(N-K-1) \]

• Bayesian Information Criterion – most ‘correct’ model
  \[ BIC = \chi^2 - DF \times \log(N) \]

AIC difference criteria

<table>
<thead>
<tr>
<th>AIC diff</th>
<th>support for equivalency of models</th>
</tr>
</thead>
<tbody>
<tr>
<td>0-2</td>
<td>substantial</td>
</tr>
<tr>
<td>4-7</td>
<td>weak</td>
</tr>
<tr>
<td>&gt; 10</td>
<td>none</td>
</tr>
</tbody>
</table>

Note: Models are not required to be nested, as in using LRT tests

LR Testing v. AIC

1. SEM provides a framework that aids the application of scientific judgment to selecting an appropriate model of the world.
2. Growing interest in an information-based approach that focuses on model selection and effect sizes.
3. Many viewpoints on utility of Neyman-Pearson hypothesis testing.
4. The two can be used complementarily, however!

Outline

1. Assessing model fit: the $\chi^2$
   - Related indices
2. Evaluating Residuals for Normality
3. Adjusting for non-normality
4. Model comparison
5. Testing mediation

Fully Mediated Model

```
fullMedModel<-' firesev ~ age
cover ~ firesev'

fullMedSEM<-sem(fullMedModel, data=keeley)
```
Partially Mediated Model

```r
partialMedModel <- ' firesev ~ age
cover ~ firesev + age'
partialMedSEM <- sem(partialMedModel, data = keeley)
```

Comparing Models with a Likelihood Ratio Test

```r
> anova(partialMedSEM, fullMedSEM)
Chi Square Difference Test

<table>
<thead>
<tr>
<th></th>
<th>Df</th>
<th>AIC</th>
<th>BIC</th>
<th>Chisq</th>
<th>Chisq.dif</th>
<th>Df</th>
<th>Pr(&gt;Chisq)</th>
</tr>
</thead>
<tbody>
<tr>
<td>partialMedSEM</td>
<td>0</td>
<td>1069.4</td>
<td>1081.9</td>
<td>0.000</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>fullMedSEM</td>
<td>1</td>
<td>1070.7</td>
<td>1080.7</td>
<td>3.297</td>
<td>3.297</td>
<td>1</td>
<td>0.06939</td>
</tr>
</tbody>
</table>
```

Comparing Models with AICc

```r
> source('./lavaan.modavg.R')
> aictab.lavaan(list(fullMedSEM, partialMedSEM),
c("Full", "Partial"))
```

<table>
<thead>
<tr>
<th>Model</th>
<th>K</th>
<th>AICc</th>
<th>Delta_AICc</th>
<th>AICcWt</th>
<th>Cum.Wt</th>
<th>LL</th>
</tr>
</thead>
<tbody>
<tr>
<td>Partial</td>
<td>5</td>
<td>1069.66</td>
<td>0.00</td>
<td>0.64</td>
<td>0.64</td>
<td>-529.69</td>
</tr>
<tr>
<td>Full</td>
<td>4</td>
<td>1070.82</td>
<td>1.16</td>
<td>0.36</td>
<td>1.00</td>
<td>-531.34</td>
</tr>
</tbody>
</table>

Exercises

Perform a test of mediation for the following model
Bonus: Calculate summed direct and indirect effects
Solution: The Models

- **Partial Mediation**
  
  ```
  distModel <- 'rich ~ distance + abiotic + hetero
  hetero ~ distance
  abiotic ~ distance'
  ```

- **Full Mediation**
  
  ```
  distModel2 <- 'rich ~ abiotic + hetero
  hetero ~ distance
  abiotic ~ distance'
  ```

Solution 3: Model Comparison with LRT

```
> anova(distFit, distFit2)
Chi Square Difference Test

<table>
<thead>
<tr>
<th></th>
<th>Df</th>
<th>AIC</th>
<th>BIC</th>
<th>Chisq</th>
<th>Chisq diff</th>
<th>Df</th>
<th>diff Pr(&gt;Chisq)</th>
</tr>
</thead>
<tbody>
<tr>
<td>distFit</td>
<td>1</td>
<td>1801.7</td>
<td>1821.7</td>
<td>1.81</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>distFit2</td>
<td>2</td>
<td>1815.8</td>
<td>1833.2</td>
<td>17.83</td>
<td>16.02</td>
<td>16</td>
<td>6.267e-05</td>
</tr>
</tbody>
</table>
```

Signif. codes: 0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Solution 3: Model Comparison with AICc

```
> aictab.lavaan(list(distFit2, distFit), c("Partial", "Full"))
Model selection based on AICc :

<table>
<thead>
<tr>
<th></th>
<th>K</th>
<th>AICc</th>
<th>Delta_AICc</th>
<th>AICcWt</th>
<th>Cum.Wt</th>
<th>LL</th>
</tr>
</thead>
<tbody>
<tr>
<td>Partial</td>
<td>8</td>
<td>1802.44</td>
<td>0.00</td>
<td>1</td>
<td>1</td>
<td>-892.87</td>
</tr>
<tr>
<td>Full</td>
<td>7</td>
<td>1816.22</td>
<td>13.78</td>
<td>0</td>
<td>1</td>
<td>-900.88</td>
</tr>
</tbody>
</table>
```

Mediation & SEM

- A central goal of SEM analyses is the evaluation of mediation.
- We can use complementary sources of information to determine mediation.
- Models that we evaluate for AIC analyses, etc., must fit the data before using in calculating AIC differences, etc.
We Should Not have Used the Fully Mediated Model for AIC Analyses

![diagram]

lavaan (0.5-17) converged normally after 36 iterations

- Number of observations: 90
- Estimator: ML
- Minimum Function Test Statistic: 17.831
- Degrees of freedom: 2
- P-value (Chi-square): 0.000

Questions?