Evaluating Models

Model specification and model fit
Sources of Error in models

I. Model misspecification
   A. Failure to identify/include proper variables
   B. Failure to model relationships

II. Error in Assumptions
   A. Normality
   B. Continuous distributions
Effect of yellow fingers on cancer
Yellow causes cancer

Time 1

Yellow Fingers

Yellow Teeth

Time 2

Cancer

<table>
<thead>
<tr>
<th></th>
<th>teeth</th>
<th>fingers</th>
<th>cancer</th>
</tr>
</thead>
<tbody>
<tr>
<td>teeth</td>
<td>1.00</td>
<td>0.42</td>
<td>0.35</td>
</tr>
<tr>
<td>fingers</td>
<td>0.42</td>
<td>1.00</td>
<td>0.30</td>
</tr>
<tr>
<td>cancer</td>
<td>0.35</td>
<td>0.30</td>
<td>1.00</td>
</tr>
</tbody>
</table>
Brush your teeth!

breath     1.00  0.56  0.48  0.40
teeth      0.56  1.00  0.42  0.35
fingers    0.48  0.42  1.00  0.30
cancer     0.40  0.35  0.30  1.00
Properly specified

Time 1

- Yellow Fingers
- Yellow Teeth
- Bad Breath
- Smoking

Time 2

- Cancer

smoking breath teeth fingers cancer

smoking  1.0  0.80  0.70  0.60  0.50
breath   0.8  1.00  0.56  0.48  0.40
teeth    0.7  0.56  1.00  0.42  0.35
fingers  0.6  0.48  0.42  1.00  0.30
cancer   0.5  0.40  0.35  0.30  1.00
Beta weights

\[
\begin{align*}
\beta_1 &= \frac{r_{xy}r_{xx2} - r_{x1x2}r_{x2y}}{r_{x1x1}r_{x2x2} - r_{x1x2}^2} \\
\beta_2 &= \frac{r_{x2y}r_{x1x1} - r_{x1x2}r_{x1y}}{r_{x1x1}r_{x2x2} - r_{x1x2}^2}
\end{align*}
\]

\[
\beta = \beta RR^{-1} = r_{xy}R^{-1}
\]

\[
R^{-1} = \begin{pmatrix}
\frac{r_{12}}{r_{11}r_{22} - r_{12}^2} & -\frac{r_{12}}{r_{11}r_{22} - r_{12}^2} \\
-\frac{r_{12}}{r_{11}r_{22} - r_{12}^2} & \frac{r_{22}}{r_{11}r_{22} - r_{12}^2}
\end{pmatrix}
\]
Causality?

Time 1

Smoking

Yellow Fingers

Yellow Teeth

Bad Breath

Time 2

Cancer

smoking  | 1.0  | 0.80 | 0.70 | 0.60 | 0.50
breath  | 0.8  | 1.00 | 0.56 | 0.48 | 0.40
teeth   | 0.7  | 0.56 | 1.00 | 0.42 | 0.35
fingers | 0.6  | 0.48 | 0.42 | 1.00 | 0.30
cancer  | 0.5  | 0.40 | 0.35 | 0.30 | 1.00
Effect of yellow fingers on cancer

Time 1
Yellow Fingers

Time 2
Cancer

0.3
Using SEM for regression

Model Chisquare = -9.6e-15  Df = 0  Pr(>Chisq) = NA
Chisquare (null model) =  9.3  Df = 1
Goodness-of-fit index = 1
BIC =  -9.6e-15

Normalized Residuals

Min. 1st Qu. Median    Mean 3rd Qu.    Max.
0       0       0       0       0       0

Parameter Estimates

| Estimate | Std Error | z value | Pr(>|z|)          |
|----------|-----------|---------|------------------|
| 1 0.30   | 0.096     | 3.1     | 1.8e-03 cancer <--- fingers |
| 5 1.00   | 0.142     | 7.0     | 2.0e-12 fingers <---> fingers |
| 8 0.91   | 0.129     | 7.0     | 2.0e-12 cancer <---> cancer |
Yellow causes cancer

time 1
Yellow Fingers
Yellow Teeth

time 2
Cancer

teeth fingers cancer

time 1

teeth 1.00 0.42 0.35
fingers 0.42 1.00 0.30
cancer 0.35 0.30 1.00
## SEM and multiple R

| Parameter Estimates | Estimate | Std Error | z value | Pr(>|z|) | Cancer Association |
|---------------------|----------|-----------|---------|----------|-------------------|
| 1                   | 0.19     | 0.10      | 1.8     | 6.9e-02  | cancer <--- fingers |
| 2                   | 0.27     | 0.10      | 2.7     | 7.7e-03  | cancer <--- teeth  |
| 5                   | 1.00     | 0.14      | 7.0     | 2.0e-12  | fingers <--> fingers |
| 6                   | 1.00     | 0.14      | 7.0     | 2.0e-12  | teeth <--> teeth   |
| 8                   | 0.85     | 0.12      | 7.0     | 2.0e-12  | cancer <--> cancer |
Goodness of fits

Model Chisquare = 19   Df = 1  Pr(>Chisq) = 1.2e-05
Chisquare (null model) = 35   Df = 3
Goodness-of-fit index = 0.9
Adjusted goodness-of-fit index = 0.37
RMSEA index = 0.43  90% CI: (0.28, 0.6)
Bentler-Bonnett NFI = 0.46
Tucker-Lewis NNFI = -0.69
Bentler CFI = 0.44
BIC = 15

Normalized Residuals
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
  0.00    0.31    0.76    1.39    1.14    4.18
## Residuals

<table>
<thead>
<tr>
<th></th>
<th>teeth</th>
<th>fingers</th>
<th>cancer</th>
</tr>
</thead>
<tbody>
<tr>
<td>teeth</td>
<td>0.000</td>
<td>0.420</td>
<td>0.078</td>
</tr>
<tr>
<td>fingers</td>
<td>0.420</td>
<td>0.000</td>
<td>0.114</td>
</tr>
<tr>
<td>cancer</td>
<td>0.078</td>
<td>0.111</td>
<td>0.042</td>
</tr>
</tbody>
</table>
### SEM multiple R: correlated predictors

|   | Estimate | Std Error | z value | Pr(>|z|) | Relationship          |
|---|----------|-----------|---------|---------|-----------------------|
| 1 | 0.19     | 0.10      | 1.8     | 6.9e-02 | cancer <--- fingers   |
| 2 | 0.27     | 0.10      | 2.7     | 7.7e-03 | cancer <--- teeth     |
| 5 | 1.00     | 0.14      | 7.0     | 2.0e-12 | fingers <--> fingers  |
| 6 | 1.00     | 0.14      | 7.0     | 2.0e-12 | teeth <--> teeth      |
| 7 | 0.42     | 0.11      | 3.9     | 1.2e-04 | teeth <--> fingers    |
| 8 | 0.85     | 0.12      | 7.0     | 2.0e-12 | cancer <--> cancer    |
But model is “saturated”

Model Chisquare = 5.5e-15  Df = 0  Pr(>Chisq) = NA
Chisquare (null model) = 35  Df = 3
Goodness-of-fit index = 1
BIC = 5.5e-15

<table>
<thead>
<tr>
<th></th>
<th>teeth</th>
<th>fingers</th>
<th>cancer</th>
</tr>
</thead>
<tbody>
<tr>
<td>teeth</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>fingers</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>cancer</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
</tbody>
</table>
Three predictors

<table>
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<tr>
<th></th>
<th>breath</th>
<th>teeth</th>
<th>fingers</th>
<th>cancer</th>
</tr>
</thead>
<tbody>
<tr>
<td>breath</td>
<td>1.00</td>
<td>0.56</td>
<td>0.48</td>
<td>0.40</td>
</tr>
<tr>
<td>teeth</td>
<td>0.56</td>
<td>1.00</td>
<td>0.42</td>
<td>0.35</td>
</tr>
<tr>
<td>fingers</td>
<td>0.48</td>
<td>0.42</td>
<td>1.00</td>
<td>0.30</td>
</tr>
<tr>
<td>cancer</td>
<td>0.40</td>
<td>0.35</td>
<td>0.30</td>
<td>1.00</td>
</tr>
</tbody>
</table>
3 predictors: uncorrelated

|   | Estimate | Std Error | z value | Pr(>|z|)   | Association                |
|---|----------|-----------|---------|-----------|-----------------------------|
| 1 | 0.11     | 0.11      | 1.0     | 3.0e-01   | cancer <----> fingers       |
| 2 | 0.16     | 0.11      | 1.4     | 1.5e-01   | cancer <----> teeth         |
| 3 | 0.26     | 0.12      | 2.2     | 2.5e-02   | cancer <----> breath        |
| 5 | 1.00     | 0.14      | 7.0     | 2.0e-12   | fingers <----> fingers      |
| 6 | 1.00     | 0.14      | 7.0     | 2.0e-12   | teeth <----> teeth          |
| 7 | 1.00     | 0.14      | 7.0     | 2.0e-12   | breath <----> breath        |
| 8 | 0.81     | 0.11      | 7.0     | 2.0e-12   | cancer <----> cancer        |
Poor measurement/fit

Model Chisquare = 68  Df = 3  Pr(>Chisq) = 1.4e-14
Chisquare (null model) = 89  Df = 6
Goodness-of-fit index = 0.74
Adjusted goodness-of-fit index = 0.12
RMSEA index = 0.47  90% CI: (0.37, 0.57)
Bentler-Bonnett NFI = 0.24
Tucker-Lewis NNFI = -0.56
Bentler CFI = 0.22
BIC = 54
## Residuals

<table>
<thead>
<tr>
<th></th>
<th>breath</th>
<th>teeth</th>
<th>fingers</th>
<th>cancer</th>
</tr>
</thead>
<tbody>
<tr>
<td>breath</td>
<td>0.00</td>
<td>0.56</td>
<td>0.48</td>
<td>0.142</td>
</tr>
<tr>
<td>teeth</td>
<td>0.56</td>
<td>0.00</td>
<td>0.42</td>
<td>0.190</td>
</tr>
<tr>
<td>fingers</td>
<td>0.48</td>
<td>0.42</td>
<td>0.00</td>
<td>0.191</td>
</tr>
<tr>
<td>cancer</td>
<td>0.14</td>
<td>0.19</td>
<td>0.19</td>
<td>0.088</td>
</tr>
</tbody>
</table>
## Fix variances

|   | Estimate | Std Error | z value | Pr(>|z|) | Cancer Location       |
|---|----------|-----------|---------|---------|-----------------------|
| 1 | 0.11     | 0.11      | 1.0     | 3.0e-01 | cancer <---- fingers  |
| 2 | 0.16     | 0.11      | 1.4     | 1.5e-01 | cancer <---- teeth    |
| 3 | 0.26     | 0.12      | 2.2     | 2.5e-02 | cancer <---- breath   |
| 8 | 0.81     | 0.11      | 7.0     | 2.0e-12 | cancer <--> cancer    |
Better fit statistics
(although chi square is same)

Model Chisquare = 68  Df = 6  Pr(>Chisq) = 1.3e-12
Chisquare (null model) = 89  Df = 6
Goodness-of-fit index = 0.74
Adjusted goodness-of-fit index = 0.56
RMSEA index = 0.32  90% CI: (0.26, 0.39)
Bentler-Bonnett NFI = 0.24
Tucker-Lewis NNFI = 0.26
Bentler CFI = 0.26
BIC = 40
Identical residuals

<table>
<thead>
<tr>
<th></th>
<th>breath</th>
<th>teeth</th>
<th>fingers</th>
<th>cancer</th>
</tr>
</thead>
<tbody>
<tr>
<td>breath</td>
<td>0.00</td>
<td>0.56</td>
<td>0.48</td>
<td>0.142</td>
</tr>
<tr>
<td>teeth</td>
<td>0.56</td>
<td>0.00</td>
<td>0.42</td>
<td>0.190</td>
</tr>
<tr>
<td>fingers</td>
<td>0.48</td>
<td>0.42</td>
<td>0.00</td>
<td>0.191</td>
</tr>
<tr>
<td>cancer</td>
<td>0.14</td>
<td>0.19</td>
<td>0.19</td>
<td>0.088</td>
</tr>
</tbody>
</table>
Latent Yellow

<p>| | | |</p>
<table>
<thead>
<tr>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>fingers -&gt; cancer</td>
<td>1</td>
</tr>
<tr>
<td>2</td>
<td>teeth -&gt; cancer</td>
<td>2</td>
</tr>
<tr>
<td>3</td>
<td>breath -&gt; cancer</td>
<td>3</td>
</tr>
<tr>
<td>4</td>
<td>fingers &lt;-&gt; fingers</td>
<td>5</td>
</tr>
<tr>
<td>5</td>
<td>teeth &lt;-&gt; teeth</td>
<td>6</td>
</tr>
<tr>
<td>6</td>
<td>breath &lt;-&gt; breath</td>
<td>7</td>
</tr>
<tr>
<td>7</td>
<td>cancer &lt;-&gt; cancer</td>
<td>8</td>
</tr>
<tr>
<td>8</td>
<td>yellow &lt;-&gt; yellow</td>
<td>NA</td>
</tr>
<tr>
<td>9</td>
<td>yellow -&gt; fingers</td>
<td>10</td>
</tr>
<tr>
<td>10</td>
<td>yellow -&gt; teeth</td>
<td>NA</td>
</tr>
</tbody>
</table>
Latent Yellow misfits

Model Chisquare = 48   Df = 2   Pr(>Chisq) = 3.2e-11
Chisquare (null model) = 89   Df = 6
Goodness-of-fit index = 0.84
Adjusted goodness-of-fit index = 0.19
RMSEA index = 0.48   90% CI: (0.37, 0.61)
Bentler-Bonnett NFI = 0.45
Tucker-Lewis NNFI = -0.68
Bentler CFI = 0.44
BIC = 39
But paths are ok

|   | Estimate  | Std Error | z value | Pr(>|z|)        | Value          |
|---|-----------|-----------|---------|----------------|----------------|
| 1 | 1.1e-01   | 0.11      | 1.0e+00 | 3.0e-01        | cancer <--- fingers |
| 2 | 1.6e-01   | 0.11      | 1.4e+00 | 1.5e-01        | cancer <--- teeth |
| 3 | 2.6e-01   | 0.12      | 2.2e+00 | 2.5e-02        | cancer <--- breath |
| 5 | 8.2e-01   | 0.12      | 6.9e+00 | 6.1e-12        | fingers <--> fingers |
| 6 | -6.5e-07  | 0.14      | -4.6e-06| 1.0e+00        | teeth <--> teeth |
| 7 | 1.0e+00   | 0.14      | 7.0e+00 | 2.0e-12        | breath <--> breath |
| 8 | 8.1e-01   | 0.11      | 7.0e+00 | 2.0e-12        | cancer <--> cancer |
| 10| 4.2e-01   | 0.11      | 3.9e+00 | 1.2e-04        | fingers <--- yellow |
## Latent Yellow residuals

<table>
<thead>
<tr>
<th></th>
<th>breath</th>
<th>teeth</th>
<th>fingers</th>
<th>cancer</th>
</tr>
</thead>
<tbody>
<tr>
<td>breath</td>
<td>0.00</td>
<td>5.6e-01</td>
<td>4.8e-01</td>
<td>0.142</td>
</tr>
<tr>
<td>teeth</td>
<td>0.56</td>
<td>6.5e-07</td>
<td>7.8e-07</td>
<td>0.145</td>
</tr>
<tr>
<td>fingers</td>
<td>0.48</td>
<td>7.8e-07</td>
<td>4.0e-07</td>
<td>0.124</td>
</tr>
<tr>
<td>cancer</td>
<td>0.14</td>
<td>1.4e-01</td>
<td>1.2e-01</td>
<td>0.073</td>
</tr>
</tbody>
</table>
Latent mouth
and yellow

<p>| | | |</p>
<table>
<thead>
<tr>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>fingers -&gt; cancer</td>
<td>1</td>
</tr>
<tr>
<td>2</td>
<td>teeth -&gt; cancer</td>
<td>2</td>
</tr>
<tr>
<td>3</td>
<td>breath -&gt; cancer</td>
<td>3</td>
</tr>
<tr>
<td>4</td>
<td>fingers &lt;-&gt; fingers</td>
<td>5</td>
</tr>
<tr>
<td>5</td>
<td>teeth &lt;-&gt; teeth</td>
<td>6</td>
</tr>
<tr>
<td>6</td>
<td>breath &lt;-&gt; breath</td>
<td>7</td>
</tr>
<tr>
<td>7</td>
<td>cancer &lt;-&gt; cancer</td>
<td>8</td>
</tr>
<tr>
<td>8</td>
<td>yellow &lt;-&gt; yellow</td>
<td>NA</td>
</tr>
<tr>
<td>9</td>
<td>yellow -&gt; fingers</td>
<td>10</td>
</tr>
<tr>
<td>10</td>
<td>yellow -&gt; teeth</td>
<td>NA</td>
</tr>
<tr>
<td>11</td>
<td>mouth -&gt; teeth</td>
<td>NA</td>
</tr>
<tr>
<td>12</td>
<td>mouth -&gt; breath</td>
<td>11</td>
</tr>
<tr>
<td>13</td>
<td>mouth &lt;-&gt; mouth</td>
<td>NA</td>
</tr>
</tbody>
</table>
Latent mouth and yellow

Model Chisquare = 26  Df = 1  Pr(>Chisq) = 3.5e-07
Chisquare (null model) = 89  Df = 6
Goodness-of-fit index = 0.9
Adjusted goodness-of-fit index = -0.033
RMSEA index = 0.5  90% CI: (0.35, 0.68)
Bentler-Bonnett NFI = 0.71
Tucker-Lewis NNFI = -0.81
Bentler CFI = 0.7
BIC = 21
two latents - residuals

<table>
<thead>
<tr>
<th></th>
<th>breath</th>
<th>teeth</th>
<th>fingers</th>
<th>cancer</th>
</tr>
</thead>
<tbody>
<tr>
<td>breath</td>
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<td>0.094</td>
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<td>0.067</td>
</tr>
<tr>
<td>teeth</td>
<td>9.4e-02</td>
<td>0.088</td>
<td>2.2e-01</td>
<td>0.063</td>
</tr>
<tr>
<td>fingers</td>
<td>4.8e-01</td>
<td>0.224</td>
<td>-1.3e-07</td>
<td>0.160</td>
</tr>
<tr>
<td>cancer</td>
<td>6.7e-02</td>
<td>0.063</td>
<td>1.6e-01</td>
<td>0.045</td>
</tr>
</tbody>
</table>
3 correlated predictors

|   | Estimate | Std Error | z value | Pr(>|z|)    | Relationship          |
|---|----------|-----------|---------|-------------|-----------------------|
| 1 | 0.11     | 0.11      | 1.0     | 3.0e-01     | cancer <---- fingers   |
| 2 | 0.16     | 0.11      | 1.4     | 1.5e-01     | cancer <---- teeth     |
| 3 | 0.26     | 0.12      | 2.2     | 2.5e-02     | cancer <---- breath    |
| 5 | 1.00     | 0.14      | 7.0     | 2.0e-12     | fingers <--> fingers   |
| 6 | 1.00     | 0.14      | 7.0     | 2.0e-12     | teeth <--> teeth       |
| 7 | 1.00     | 0.14      | 7.0     | 2.0e-12     | breath <--> breath     |
| 8 | 0.81     | 0.11      | 7.0     | 2.0e-12     | cancer <--> cancer     |
| 9 | 0.56     | 0.12      | 4.9     | 1.2e-06     | breath <--> teeth      |
|10 | 0.42     | 0.11      | 3.9     | 1.2e-04     | fingers <--> teeth     |
|11 | 0.48     | 0.11      | 4.3     | 1.7e-05     | breath <--> fingers    |
Fully saturated

Model Chisquare = 2.2e-14  Df = 0  Pr(>Chisq) = NA
Chisquare (null model) = 89  Df = 6
Goodness-of-fit index = 1
BIC = 2.2e-14

Normalized Residuals
  Min. 1st Qu. Median  Mean 3rd Qu.  Max.
  0.0e+00  0.0e+00  0.0e+00  1.3e-16  1.3e-16  5.3e-16
But, we can fix variances to 1

Model Chisquare = 2.2e-14  Df = 3  Pr(>Chisq) = 1
Chisquare (null model) = 89  Df = 6
Goodness-of-fit index = 1
Adjusted goodness-of-fit index = 1
RMSEA index = 0  90% CI: (NA, NA)
Bentler-Bonnett NFI = 1
Tucker-Lewis NNFI = 1.1
Bentler CFI = 1
BIC = -14
Fewer paths to estimate

|   | Estimate | Std Error | z value | Pr(>|z|) | Relation |
|---|----------|-----------|---------|----------|----------|
| 1 | 0.11     | 0.105     | 1.0     | 3.0e-01  | cancer <-- fingers |
| 2 | 0.16     | 0.111     | 1.4     | 1.5e-01  | cancer <-- teeth   |
| 3 | 0.26     | 0.115     | 2.2     | 2.5e-02  | cancer <-- breath  |
| 8 | 0.81     | 0.115     | 7.0     | 2.0e-12  | cancer --> cancer  |
| 9 | 0.56     | 0.060     | 9.3     | 0.0e+00  | breath --> teeth   |
|10 | 0.42     | 0.075     | 5.6     | 2.6e-08  | fingers --> teeth  |
|11 | 0.48     | 0.069     | 6.9     | 4.6e-12  | breath --> fingers |
# Model residuals

<table>
<thead>
<tr>
<th></th>
<th>breath</th>
<th>teeth</th>
<th>fingers</th>
<th>cancer</th>
</tr>
</thead>
<tbody>
<tr>
<td>breath</td>
<td>0.0e+00</td>
<td>0</td>
<td>0.0e+00</td>
<td>5.6e-17</td>
</tr>
<tr>
<td>teeth</td>
<td>0.0e+00</td>
<td>0</td>
<td>0.0e+00</td>
<td>0.0e+00</td>
</tr>
<tr>
<td>fingers</td>
<td>0.0e+00</td>
<td>0</td>
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Or, model one latent

|   | Estimate | Std Error | z value | Pr(>|z|) | association       |
|---|----------|-----------|---------|----------|-------------------|
| 1 | 0.50     | 0.11      | 4.7     | 2.8e-06  | cancer <---- latent |
| 2 | 0.80     | 0.10      | 7.8     | 5.1e-15  | breath <---- latent |
| 3 | 0.60     | 0.10      | 5.8     | 8.2e-09  | fingers <---- latent |
| 4 | 0.70     | 0.10      | 6.8     | 9.8e-12  | teeth <---- latent |
| 5 | 0.64     | 0.11      | 5.9     | 4.8e-09  | fingers ---> fingers |
| 6 | 0.51     | 0.10      | 4.9     | 1.2e-06  | teeth ---> teeth |
| 7 | 0.36     | 0.11      | 3.3     | 9.1e-04  | breath ---> breath |
| 8 | 0.75     | 0.12      | 6.4     | 2.0e-10  | cancer ---> cancer |
A great model

Model Chisquare = 1.9e-10  Df = 2  Pr(>Chisq) = 1
Chisquare (null model) = 89  Df = 6
Goodness-of-fit index = 1
Adjusted goodness-of-fit index = 1
RMSEA index = 0  90% CI: (NA, NA)
Bentler-Bonnett NFI = 1
Tucker-Lewis NNFI = 1.1
Bentler CFI = 1
BIC = -9.2
SEM alternative: but what is the latent?

breath

fingers

teeth

latent

cancer

0.8

0.6

0.7

0.5
Smoking is measured perfectly

- Smoking
- Latent cancer (0.5)
  - Teeth (0.7)
  - Fingers (0.6)
  - Breath (0.8)
- Cancer
Properly specified

Time 1

- Yellow Fingers
- Yellow Teeth
- Bad Breath
- Smoking

Time 2

- Cancer

Smoking breath teeth fingers cancer

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<thead>
<tr>
<th></th>
<th>smoking</th>
<th>breath</th>
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<th>fingers</th>
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Regression if measurement error

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<td>0.56</td>
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<td>0.40</td>
<td>0.35</td>
<td>0.30</td>
<td>1.00</td>
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</table>
Failure of regression

Time 1

- Yellow Fingers
- Yellow Teeth
- Bad Breath
- Smoking

Time 2

Cancer

Correlations:

- Yellow Fingers → Cancer: 0.10
- Yellow Teeth → Cancer: 0.15
- Bad Breath → Cancer: 0.24
- Smoking → Cancer: 0.07
- Other correlations (0.3, 0.35, 0.4, 0.48, 0.56)
Try SEM

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<tr>
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Good fits

Model Chisquare = 1.8e-11  Df = 5  Pr(>Chisq) = 1
Chisquare (null model) = 240  Df = 10
Goodness-of-fit index = 1
Adjusted goodness-of-fit index = 1
RMSEA index = 0  90% CI: (NA, NA)
Bentler-Bonnett NFI = 1
Tucker-Lewis NNFI = 1.0
Bentler CFI = 1
BIC = -23
Not perfect data

|   | Estimate | Std Error | z value | Pr(>|z|)   |     |
|---|----------|-----------|---------|------------|-----|
| 1 | 0.50     | 0.099     | 5.0     | 5.0e-07    | cancer <--- latent |
| 2 | 0.80     | 0.088     | 9.1     | 0.0e+00    | breath <--- latent |
| 3 | 0.60     | 0.096     | 6.2     | 4.5e-10    | fingers <--- latent |
| 4 | 0.70     | 0.092     | 7.6     | 3.3e-14    | teeth <--- latent |
| 9 | 0.90     | 0.084     | 10.7    | 0.0e+00    | smoking <--- latent |
| 5 | 0.64     | 0.098     | 6.5     | 7.7e-11    | fingers --> fingers |
| 6 | 0.51     | 0.084     | 6.1     | 1.1e-09    | teeth --> teeth    |
| 7 | 0.36     | 0.070     | 5.1     | 3.0e-07    | breath --> breath  |
| 8 | 0.75     | 0.111     | 6.7     | 1.7e-11    | cancer --> cancer  |
| 10| 0.19     | 0.064     | 3.0     | 2.8e-03    | smoking --> smoking |
Good fit

Model Chisquare = 1.1e-10  Df = 5  Pr(>Chisq) = 1
Chisquare (null model) = 188  Df = 10
Goodness-of-fit index = 1
Adjusted goodness-of-fit index = 1
RMSEA index = 0  90% CI: (NA, NA)
Bentler-Bonnett NFI = 1
Tucker-Lewis NNFI = 1.1
Bentler CFI = 1
BIC = -23
Bad data, correct model

|   | Estimate | Std. Error | z value | Pr(>|z|)       | Relation                      |
|---|----------|------------|---------|---------------|-------------------------------|
| 1 | 0.50     | 0.105      | 4.7     | 2.1e-06       | cancer <-- latent             |
| 2 | 0.80     | 0.098      | 8.2     | 2.2e-16       | breath <-- latent             |
| 3 | 0.60     | 0.102      | 5.9     | 4.6e-09       | fingers <-- latent            |
| 4 | 0.70     | 0.100      | 7.0     | 2.3e-12       | teeth <-- latent              |
| 9 | 0.50     | 0.105      | 4.7     | 2.1e-06       | smoking <-- latent            |
| 5 | 0.64     | 0.107      | 6.0     | 2.2e-09       | fingers --> fingers           |
| 6 | 0.51     | 0.099      | 5.1     | 2.7e-07       | teeth --> teeth               |
| 7 | 0.36     | 0.097      | 3.7     | 2.1e-04       | breath --> breath             |
| 8 | 0.75     | 0.117      | 6.4     | 1.3e-10       | cancer --> cancer             |
| 10| 0.75     | 0.117      | 6.4     | 1.3e-10       | smoking --> smoking           |
Good fit

Model Chisquare = 4.2e-10  Df = 5  Pr(>Chisq) = 1
Chisquare (null model) = 110  Df = 10
Goodness-of-fit index = 1
Adjusted goodness-of-fit index = 1
RMSEA index = 0  90% CI: (NA, NA)
Bentler-Bonnett NFI = 1
Tucker-Lewis NNFI = 1.1
Bentler CFI = 1
BIC = -23
Measurement is considered latent cancer

smoking

0.5

latent

0.5

cancer

0.7

0.6

0.8

teeth

fingers

breath

0.5

0.5

0.5
Change causality-
perfect smoking

|   | Estimate | Std Error | z value | Pr(>|z|)    |     |
|---|----------|-----------|---------|------------|-----|
| 1 | 5.0e-01  | 0.087     | 5.7e+00 | 9.2e-09    | cancer <--- latent |
| 2 | 8.0e-01  | 0.060     | 1.3e+01 | 0.0e+00    | breath <--- latent |
| 3 | 6.0e-01  | 0.080     | 7.5e+00 | 8.5e-14    | fingers <--- latent |
| 4 | 7.0e-01  | 0.072     | 9.8e+00 | 0.0e+00    | teeth <--- latent  |
| 5 | 6.4e-01  | 0.093     | 6.9e+00 | 4.9e-12    | fingers -->-- fingers |
| 6 | 5.1e-01  | 0.076     | 6.7e+00 | 2.3e-11    | teeth -->-- teeth  |
| 7 | 3.6e-01  | 0.060     | 6.0e+00 | 1.7e-09    | breath -->-- breath |
| 8 | 7.5e-01  | 0.107     | 7.0e+00 | 2.8e-12    | cancer -->-- cancer |
| 12| 9.7e-09  | 0.048     | 2.0e-07 | 1.0e+00    | latent -->-- latent |
Perfect smoking

Model Chisquare = 4.9e-12  Df = 6  Pr(>Chisq) = 1
Chisquare (null model) = 240  Df = 10
Goodness-of-fit index = 1
Adjusted goodness-of-fit index = 1
RMSEA index = 0  90% CI: (NA, NA)
Bentler-Bonnett NFI = 1
Tucker-Lewis NNFI = 1.0
Bentler CFI = 1
BIC = -28
“Imperfect” smoking, modeled with no error

|     | Estimate | Std Error | z value | Pr(>|z|)         | Relationship          |
|-----|----------|-----------|---------|------------------|-----------------------|
| 1   | 0.25     | 0.070     | 3.6     | 3.6e-04          | cancer <--- latent    |
| 2   | 0.40     | 0.087     | 4.6     | 4.0e-06          | breath <--- latent    |
| 3   | 0.30     | 0.075     | 4.0     | 7.1e-05          | fingers <--- latent   |
| 4   | 0.35     | 0.082     | 4.3     | 1.8e-05          | teeth <--- latent     |
| 5   | 0.64     | 0.107     | 6.0     | 2.2e-09          | fingers ---> fingers   |
| 6   | 0.51     | 0.099     | 5.1     | 2.7e-07          | teeth ---> teeth       |
| 7   | 0.36     | 0.097     | 3.7     | 2.1e-04          | breath ---> breath     |
| 8   | 0.75     | 0.117     | 6.4     | 1.3e-10          | cancer ---> cancer     |
| 12  | 3.00     | 1.364     | 2.2     | 2.8e-02          | latent ---> latent     |
Smoking is not measured perfectly.

The diagram shows:
- Smoking (1) influences latent cancer (0.25).
- Latent cancer influences:
  - Teeth (0.35)
  - Fingers (0.3)
  - Breath (0.4)
- Teeth, fingers, and breath influence cancer.
What is the causal variable

breath

fingers

teeth

latent

0.8
0.6
0.7

0.5

cancer
Something causes one to smoke and get cancer: is it E?
Cancer as cause

- latent
- breath (0.69)
- teeth (0.61)
- fingers (0.52)
- cancer (0.4, 0.35)
- cancer (0.3)
Cancer as caused

- Latent
- Breath: 0.8
- Teeth: 0.7
- Fingers: 0.6
- Cancer: 0.26, 0.16, 0.1, 1
Cancer as caused: equal error
Consider error in smoking

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<td>&quot;latent &lt;-&gt; latent&quot;</td>
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<td>&quot;1&quot;</td>
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</table>
Error in smoking

|   | Estimate | Std Error | z value | Pr(>|z|)         | Relationship  |
|---|----------|-----------|---------|------------------|---------------|
| 2 | 0.88     | 0.108     | 8.1     | 6.7e-16          | breath <--- latent |
| 3 | 0.67     | 0.114     | 5.9     | 4.4e-09          | fingers <--- latent |
| 4 | 0.78     | 0.110     | 7.1     | 1.6e-12          | teeth <--- latent  |
| 11| 0.40     | 0.113     | 3.6     | 3.7e-04          | latent <--- smoking |
| 5 | 0.64     | 0.107     | 6.0     | 1.9e-09          | fingers ---> fingers |
| 6 | 0.52     | 0.098     | 5.3     | 1.4e-07          | teeth ---> teeth   |
| 7 | 0.39     | 0.096     | 4.1     | 4.5e-05          | breath ---> breath |
| 8 | 0.77     | 0.144     | 5.4     | 8.3e-08          | cancer ---> cancer |
| 10| 1.00     | 0.142     | 7.0     | 2.0e-12          | smoking ---> smoking |
Model Chisquare = 26  Df = 6 Pr(>Chisq) = 0.00021
Chisquare (null model) = 110  Df = 10
Goodness-of-fit index = 0.92
Adjusted goodness-of-fit index = 0.8
RMSEA index = 0.18  90% CI: (0.12, 0.26)
Bentler-Bonnett NFI = 0.76
Tucker-Lewis NNFI = 0.67
Bentler CFI = 0.8
BIC = -1.5
Measurement is considered

- Smoking (0.4) → Latent Cancer
- Teeth (0.78) → Latent Cancer
- Fingers (0.67) → Latent Cancer
- Breath (0.88) → Latent Cancer
- Latent Cancer (1) → Cancer
Conclusion

I. Model specification is vital to model testing
II. Good fit does not imply correct model
III. Poor fit does not imply all of model is incorrect
   A. consider what parts have failed and why
   B. Specification
   C. Quality of measurement?
What do the fit tests measure?

I. Chi Square
II. Chi Square / df (expected value is 1)
III. GFI/NFI/AGFI
IV. BIC
V. RMSEA
Fit function (F) Joreskog

I. Ordinary least squares: \( F = \frac{1}{2}\text{tr}[(S-\Sigma)^2] \)

II. Generalized least squares \( F = \frac{1}{2}\text{tr}[(I-S^{-1}\Sigma)^2] \)

III. Maximum likelihood: \( F = \log|\Sigma| + \text{tr}(S\Sigma^{-1}) - \log|S| - p \)

A. \( p \) is total number of variables

B. \( S \) is the observed covariance matrix

C. \( \Sigma \) is the modeled covariance matrix

D. if model is correct, \( F \) is asymptotically chi square
Distribution free Fit functions (after Browne)

I. Let $S$ be the “strung out” data matrix

II. Let $\Sigma$ be the “strung out” model matrix

III. $\text{Fit} = (S - \Sigma)^T W^{-1} (S - \Sigma)$

IV. where $W =$

   A. Ordinary Least Squares  ($W = I$)

   B. Generalized least squares: $W = (SS')$

   C. Maximum likelihood:  $W = (\Sigma \Sigma')$
Measures of fit

I. Taken from David Kenny
   A. http://davidakenny.net/cm/fit.htm

II. and
Bentler-Bonnet Normed Fit Index

I. (Chi square null - Chi square model) square null

II. between .90 and .95 is “acceptable”

III. > .95 is “good”
Tucker Lewis Normed fit

I. \( \frac{\text{Chi2(Null)}}{\text{df(null)}} - \frac{\text{Chi2 (model)}}{\text{df(model)}} \)
\( \frac{\text{Chi2(Null)}}{\text{df(null)}} - 1 \)

II. Penalizes models for estimating more parameters

III.a “parsimony” correction
Comparative Fit Index

I. let \( d = \text{Chi square} - \text{df} \)

II. \( CFI = \frac{d(\text{Null}) - d(\text{model})}{d(\text{model})} \)
Root Mean Square Error of Approximation (RMSEA)

I. let d = Chi square - df

II. RMSEA = sqrt{(Chi^2/df-1)/(N-1)]

III. if Chi square < df then RMSEA = 0

IV. “good” models have RMSEA < .05

V. “poor” models have RMSEA > .10
p of close fit

I. Null hypothesis is that RMSEA is .05
II. test if RMSEA is > .05
III. Claim good fit if p(RMSEA > .05) > .05
Standardized Root Mean Square Residual

I. What is the square root of the average squared residual?

II. Kenny: “< .08 is good”
Akaike Information Criterion (AIC)

I. Chi Square + k(k-1) - 2df where k is the number of variables in the model and df is the degrees of freedom

II. useful for comparing models

III. Note the penalty is 2 for every parameter estimated
GFI and AGFI

I. GFI and AGFI are LISREL estimates

II. Kenny: “consensus is not to use them” for they are affected by sample size and can be large even for bad models
Examples of fit
(2 factors - 6 variables)

I. Monte Carlo simulation of 100, 200, 400, 800, 1600 subjects
II. 2 factors with 6 variables (see chapter 2)
III. Plot parameter estimates
IV. Plot correlations of size of estimates
Estimation

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\begin{align*}
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\begin{bmatrix}
1, & 1 \\
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\end{bmatrix}
\end{align*}
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<th>100, 200, 400, 800, 1600</th>
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<td>NFI</td>
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</tr>
<tr>
<td>CFI</td>
<td>-0.67</td>
</tr>
<tr>
<td>BIC</td>
<td>-0.00 0.06 0.12 0.95 0.98</td>
</tr>
</tbody>
</table>
Redo this with $n = 200, 400, 800, 1600$

parameter estimates
<table>
<thead>
<tr>
<th>$\text{n}$</th>
<th>200</th>
<th>400</th>
<th>800</th>
<th>1600</th>
</tr>
</thead>
<tbody>
<tr>
<td>$N$</td>
<td>0.11</td>
<td>0.68</td>
<td>-0.20</td>
<td>0.66</td>
</tr>
<tr>
<td>chi sq</td>
<td>-0.44</td>
<td>0.83</td>
<td>-0.45</td>
<td>-0.68</td>
</tr>
<tr>
<td>GFI</td>
<td>-0.70</td>
<td>0.99</td>
<td>0.74</td>
<td>-0.92</td>
</tr>
<tr>
<td>RMSEA</td>
<td>-0.73</td>
<td>-0.92</td>
<td>0.65</td>
<td></td>
</tr>
<tr>
<td>NFI</td>
<td>0.79</td>
<td>-0.91</td>
<td></td>
<td></td>
</tr>
<tr>
<td>CFI</td>
<td>-0.64</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>BIC</td>
<td></td>
<td></td>
<td></td>
<td>-55</td>
</tr>
</tbody>
</table>

N = 200, 400, 800, 1600
Goodness of fit of bad model

I. Previous slides were the correlations of the goodness of fit for correct model

II. What happens if we examine an incorrect model for various sample sizes?

A. 6 variables, 2 correlated factors
B. model as 6 variables, 2 uncorrelated factors
C. Sample sizes of 100, 200, 400, 800, 1600
Numerical fits to poor model

<table>
<thead>
<tr>
<th>var</th>
<th>n</th>
<th>mean</th>
<th>sd</th>
<th>median</th>
<th>min</th>
<th>max</th>
<th>chisq</th>
<th>chisqNull</th>
<th>GFI</th>
<th>AGFI</th>
<th>RMSEA</th>
<th>NFI</th>
<th>CFI</th>
</tr>
</thead>
<tbody>
<tr>
<td>N</td>
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<td>95</td>
<td>641.05</td>
<td>554.19</td>
<td>400</td>
<td>100</td>
<td>1600</td>
<td>71.14</td>
<td>0.96</td>
<td>0.91</td>
<td>0.1</td>
<td>0.94</td>
<td>0.95</td>
</tr>
<tr>
<td>chisq</td>
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<td>95</td>
<td>71.14</td>
<td>57.97</td>
<td>51.41</td>
<td>10.1</td>
<td>220.46</td>
<td>1354.58</td>
<td>0.01</td>
<td>0.03</td>
<td>0.02</td>
<td>0.02</td>
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</tr>
<tr>
<td>chisqNull</td>
<td>3</td>
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<td>1177.23</td>
<td>874.45</td>
<td>174.06</td>
<td>3538.64</td>
<td>1177.23</td>
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<td>0.92</td>
<td>0.1</td>
<td>0.94</td>
<td>0.96</td>
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<tr>
<td>GFI</td>
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<td>0.01</td>
<td>0.96</td>
<td>0.89</td>
<td>0.99</td>
<td>1.14</td>
<td>0.03</td>
<td>0.02</td>
<td>0.04</td>
<td>0.84</td>
<td>0.87</td>
</tr>
<tr>
<td>AGFI</td>
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<td>0.91</td>
<td>0.03</td>
<td>0.92</td>
<td>0.75</td>
<td>0.97</td>
<td>0.98</td>
<td>0.1</td>
<td>0.1</td>
<td>0.19</td>
<td>0.84</td>
<td>0.98</td>
</tr>
<tr>
<td>RMSEA</td>
<td>6</td>
<td>95</td>
<td>0.1</td>
<td>0.02</td>
<td>0.1</td>
<td>0.04</td>
<td>0.19</td>
<td>0.98</td>
<td>0.84</td>
<td>0.84</td>
<td>0.98</td>
<td>0.87</td>
<td>0.99</td>
</tr>
<tr>
<td>NFI</td>
<td>10</td>
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<td>0.94</td>
<td>0.02</td>
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<td>0.84</td>
<td>0.98</td>
<td>0.98</td>
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<td>0.84</td>
<td>0.98</td>
<td>0.87</td>
<td>0.99</td>
</tr>
<tr>
<td>CFI</td>
<td>11</td>
<td>95</td>
<td>0.95</td>
<td>0.02</td>
<td>0.96</td>
<td>0.87</td>
<td>0.99</td>
<td>0.98</td>
<td>0.87</td>
<td>0.87</td>
<td>0.99</td>
<td>0.87</td>
<td>0.99</td>
</tr>
</tbody>
</table>

Notice that all the “golden rules of thumb” will have type I errors
Considering rules of thumb and fit

I. Fit functions have distributions and thus are susceptible to problems of type I and type II error.

A. Compare the fits for correct model as well as those for a simple incorrect

II. Should we just use chi square and reject models that don’t fit, or should we reason about why they don’t fit
What does it mean if the model does not fit

I. Model is wrong
II. Measurement is wrong
III. Structure is wrong
IV. Assumptions are wrong
V. at least one of above, but which one?
Specification & Respecification

I. Is the measurement model consistent
   
   A. revise it
      
      1. evaluate loadings
      2. evaluate error variances
      3. more or fewer factors
      4. correlated errors?

from Kenny: http://davidakenny.net/cm/respec.htm
Respecification
(continued)

I. Structural model:
   A. adjust paths
   B. drop paths
   C. add paths
Equivalent models

I. What models are equivalent?

II. Do they make equally good sense

Conclusion

I. Latent variable models are a powerful theoretical aid but do not replace theory

II. Nor do latent modeling algorithms replace the need for good scale development

III. Latent variable models are a supplement to the conventional regression models of observed scores.

IV. Other latent models (not considered) include
   A. Item Response Theory
   B. Latent Class Analysis
   C. Latent Growth Curve analysis