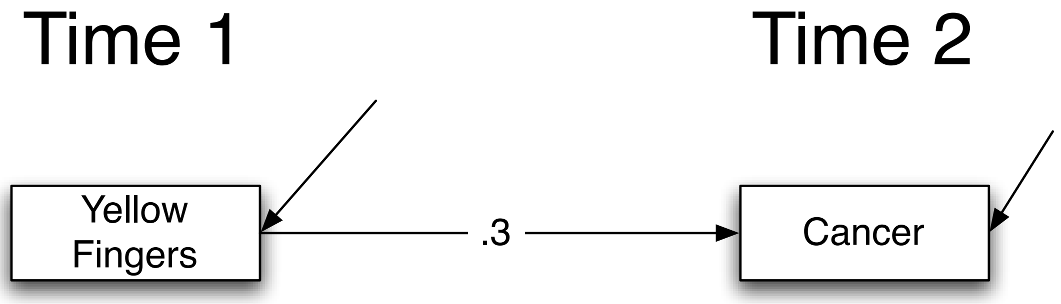
Evaluating Models

Model specification and model fit

Sources of Error in models

- I. Model misspecification
  - A. Failure to identify/include proper variables
  - B. Failure to to model relationships
- II. Error in Assumptions
  - A. Normality
  - B. Continuous distributions

Effect of yellow fingers on cancer



Time 1

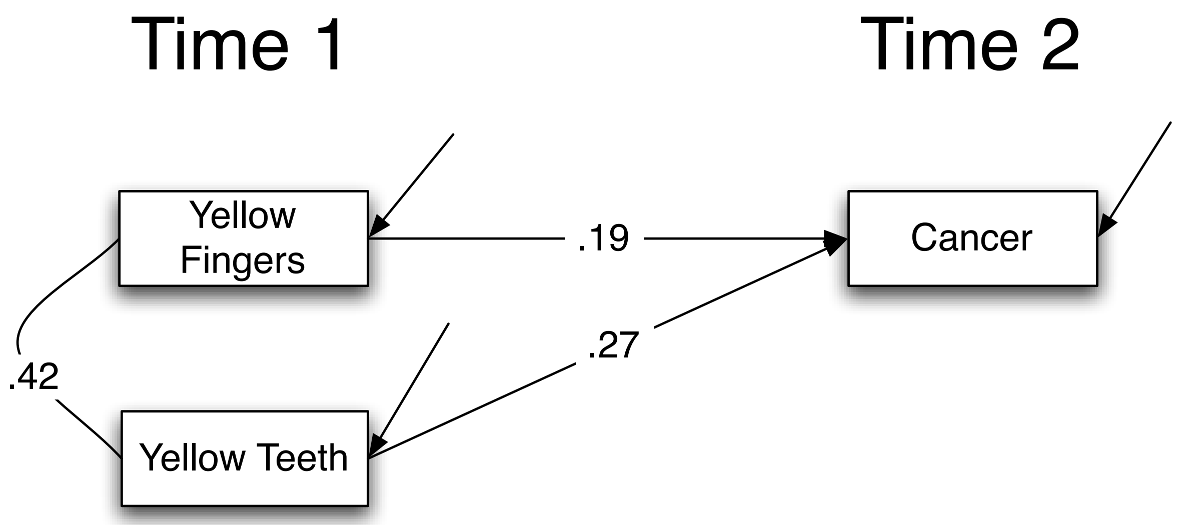
Time 2

Yellow Fingers

.3

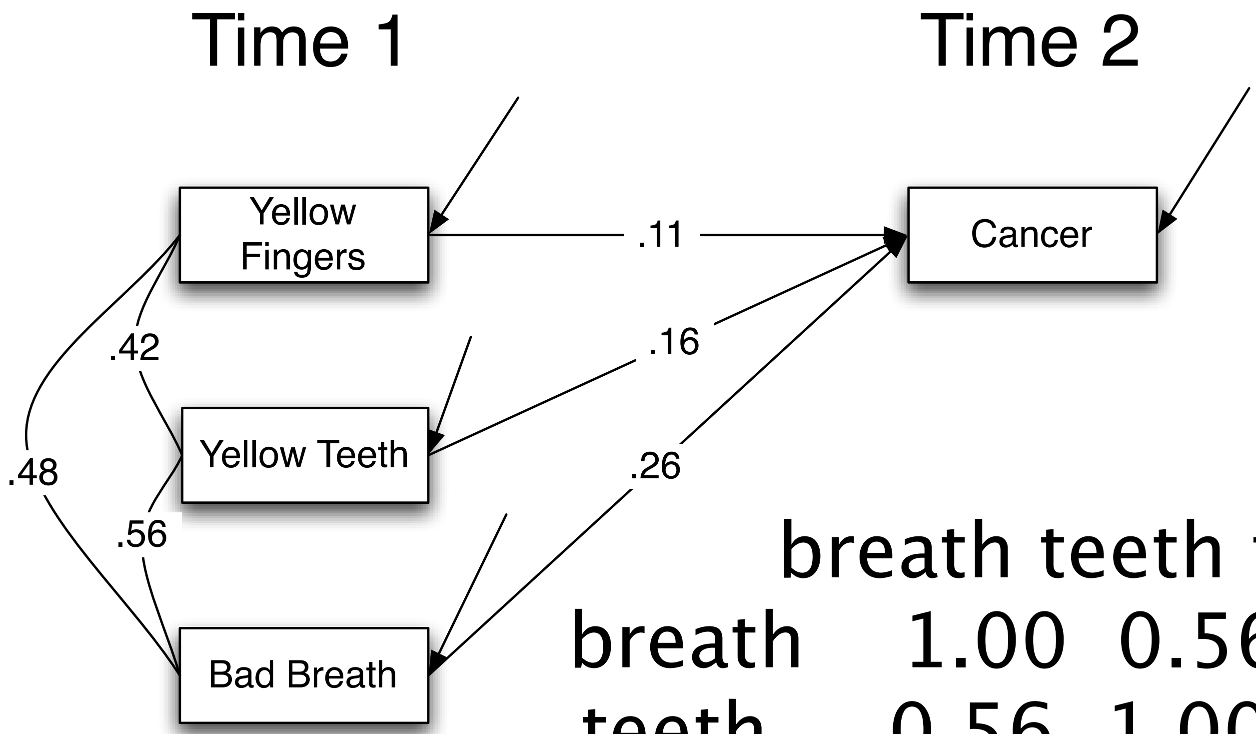
Cancer

Yellow causes cancer



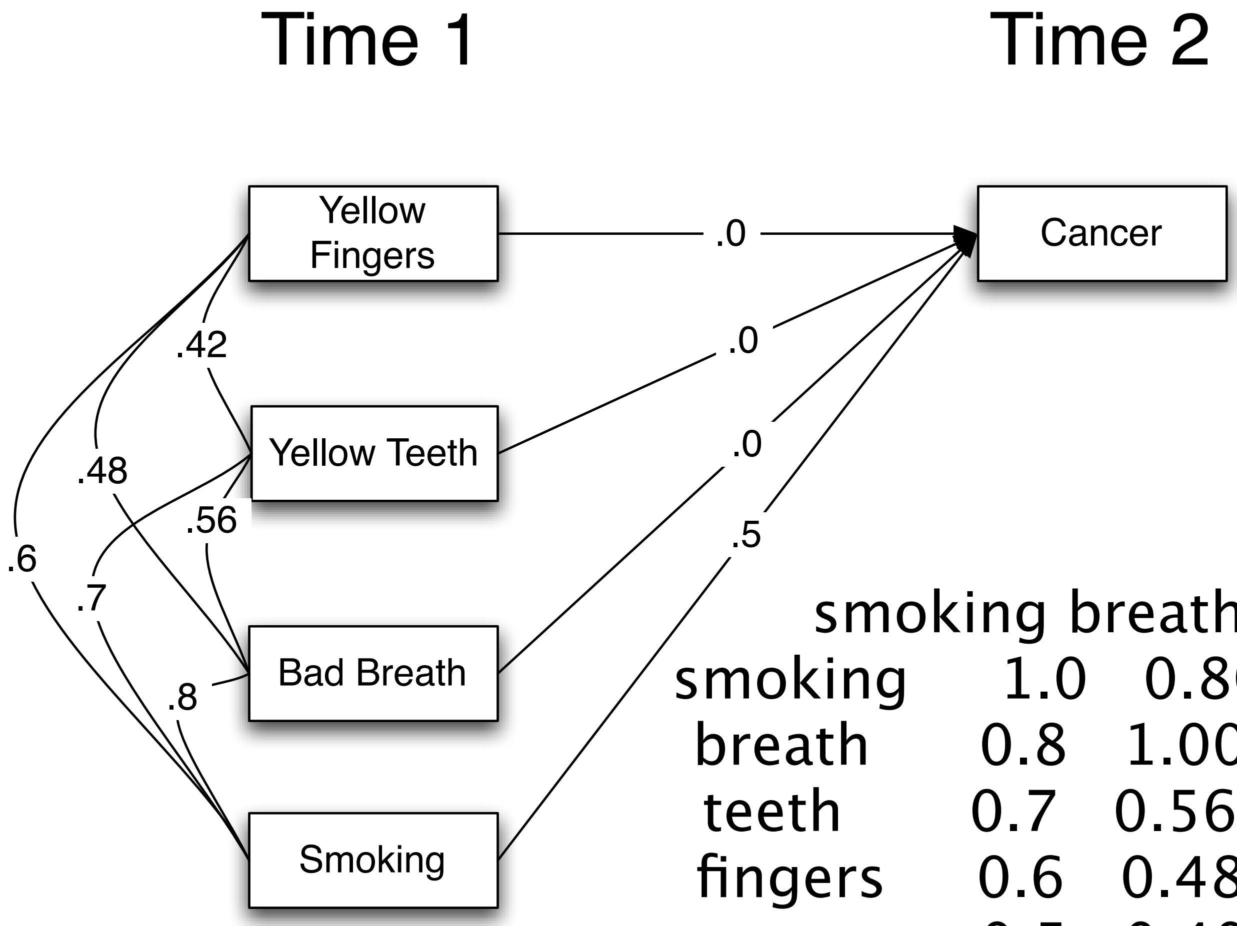
	teeth	fingers	cancer
teeth	1.00	0.42	0.35
fingers	0.42	1.00	0.30
cancer	0.35	0.30	1.00

Brush your teeth!



	breath	teeth	fingers	cancer
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



	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

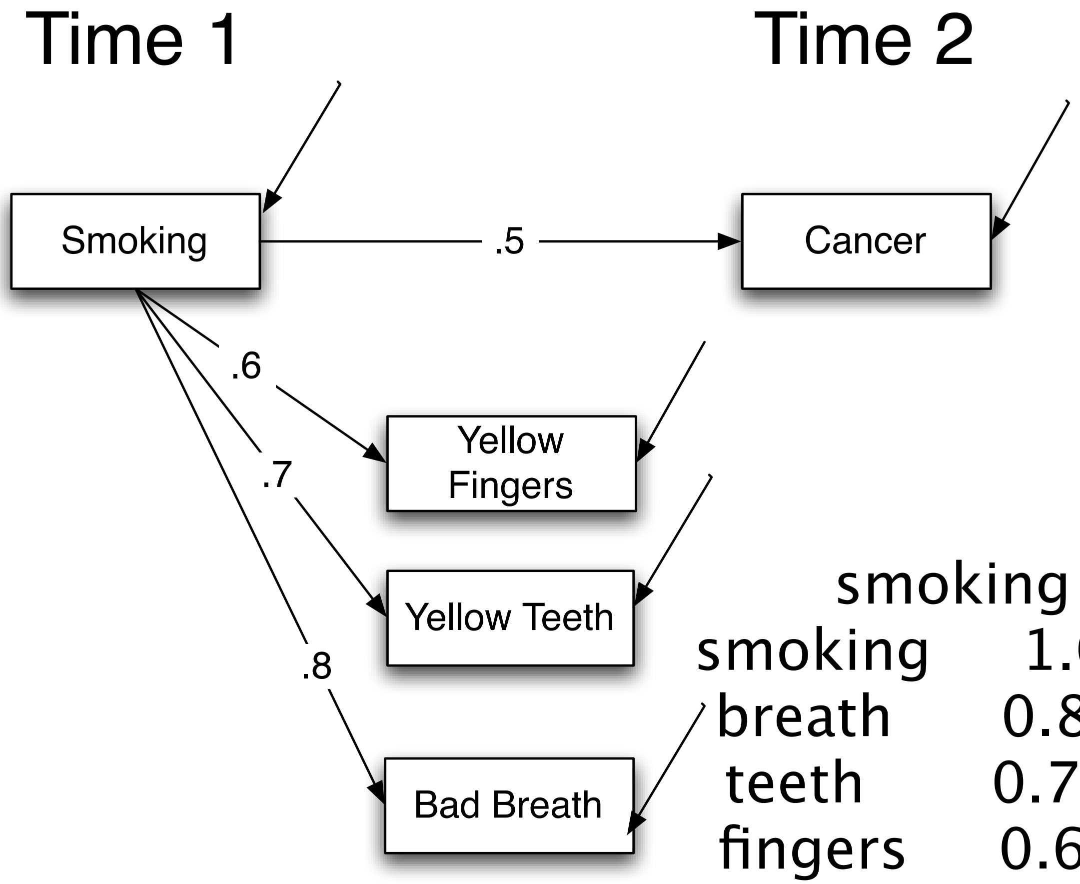
Beta weights

$$\left\{ \begin{array}{l} \beta_1 = (r_{x1y} r_{x2x2} - r_{x1x2} r_{x2y}) / (r_{x1x1} r_{x2x2} - r_{x1x2}^2) \\ \beta_2 = (r_{x2y} r_{x1x1} - r_{x1x2} r_{x1y}) / (r_{x1x1} r_{x2x2} - r_{x1x2}^2) \end{array} \right\}$$

$$\beta = \beta R R^{-1} = r_{xy} R^{-1}$$

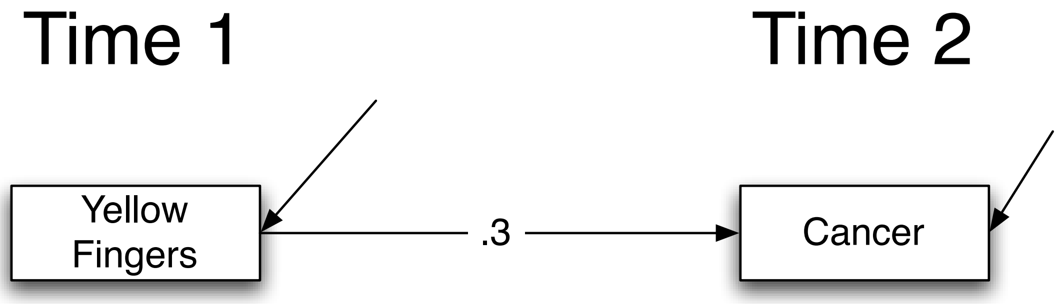
$$R^{-1} = \begin{pmatrix} \frac{r_{22}}{r_{11} r_{22} - r_{12}^2} & -\frac{r_{12}}{r_{11} r_{22} - r_{12}^2} \\ -\frac{r_{12}}{r_{11} r_{22} - r_{12}^2} & \frac{r_{11}}{r_{11} r_{22} - r_{12}^2} \end{pmatrix}$$

Causality?



	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

Effect of yellow fingers on cancer



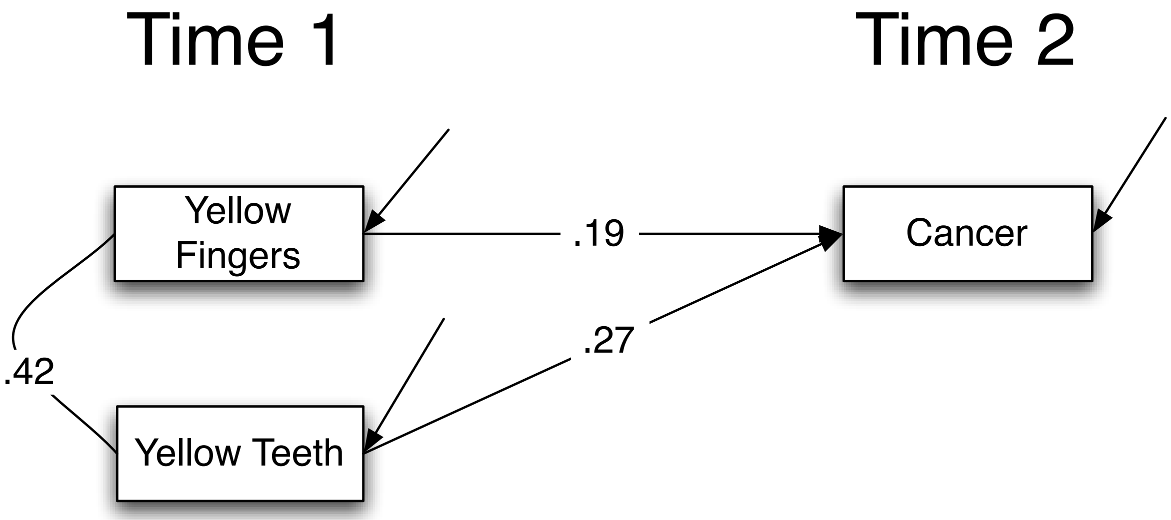
Using SEM for regression

```
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



	teeth	fingers	cancer
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|)
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

	teeth	fingers	cancer
teeth	0.000	0.42	0.078
fingers	0.420	0.00	0.114
cancer	0.078	0.11	0.042

SEM multiple R: correlated predictors

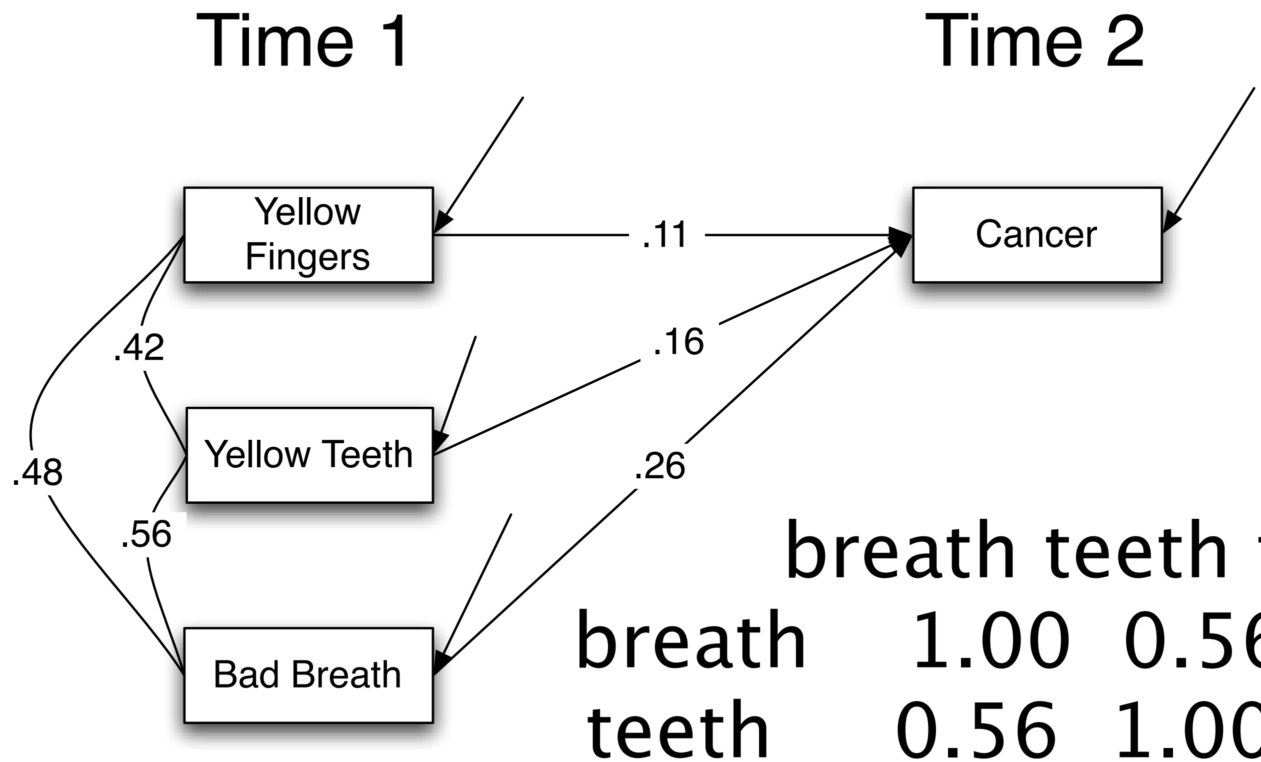
```
  Estimate Std Error z value Pr(>|z|)
1 0.19     0.10      1.8     6.9e-02  cancer <--- fingers
2 0.27     0.10      2.7     7.7e-03  cancer <--- teeth
5 1.00     0.14      7.0     2.0e-12  fingers <--> fingers
6 1.00     0.14      7.0     2.0e-12  teeth <--> teeth
7 0.42     0.11      3.9     1.2e-04  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


          teeth fingers cancer
    teeth       0       0      0
   fingers     0       0      0
   cancer      0       0      0
```

Three predictors



	breath	teeth	fingers	cancer
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

3 predictors:uncorrelated

```
 Estimate Std Error z value Pr(>|z|)
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

	breath	teeth	fingers	cancer
breath	0.00	0.56	0.48	0.142
teeth	0.56	0.00	0.42	0.190
fingers	0.48	0.42	0.00	0.191
cancer	0.14	0.19	0.19	0.088

Fix variances

```
  Estimate Std Error z value Pr(>|z|)
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

	breath	teeth	fingers	cancer
breath	0.00	0.56	0.48	0.142
teeth	0.56	0.00	0.42	0.190
fingers	0.48	0.42	0.00	0.191
cancer	0.14	0.19	0.19	0.088

Latent Yellow

```
 model.5
      [,1]                    [,2] [,3]
 [1,] "fingers -> cancer"   "1"  NA
 [2,] "teeth -> cancer"     "2"  NA
 [3,] "breath -> cancer"    "3"  NA
 [4,] "fingers <-> fingers" "5"  NA
 [5,] "teeth <-> teeth"     "6"  NA
 [6,] "breath <-> breath"   "7"  NA
 [7,] "cancer <-> cancer"   "8"  NA
 [8,] "yellow <-> yellow"   NA   "1"
 [9,] "yellow -> fingers"   "10" NA
[10,] "yellow -> teeth"     NA   "1"
```

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

```
 Parameter Estimates
   Estimate Std Error z value  Pr(>|z|)
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

```
        breath   teeth fingers cancer
breath    0.00 5.6e-01 4.8e-01  0.142
teeth     0.56 6.5e-07 7.8e-07  0.145
fingers   0.48 7.8e-07 4.0e-07  0.124
cancer    0.14 1.4e-01 1.2e-01  0.073
```

Latent mouth and yellow

```
model.6
     [,1]                      [,2] [,3]
 [1,] "fingers -> cancer"   "1"  NA
 [2,] "teeth -> cancer"     "2"  NA
 [3,] "breath -> cancer"    "3"  NA
 [4,] "fingers <-> fingers" "5"  NA
 [5,] "teeth <-> teeth"     "6"  NA
 [6,] "breath <-> breath"   "7"  NA
 [7,] "cancer <-> cancer"   "8"  NA
 [8,] "yellow <-> yellow"   NA   "1"
 [9,] "yellow -> fingers"   "10" NA
[10,] "yellow -> teeth"     NA   "1"
[11,] "mouth -> teeth"      NA   "1"
[12,] "mouth -> breath"     "11" NA
[13,] "mouth <-> mouth"     NA   "1"
```

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

```
         breath teeth  fingers cancer
breath  1.3e-07 0.094  4.8e-01  0.067
teeth   9.4e-02 0.088  2.2e-01  0.063
fingers 4.8e-01 0.224 -1.3e-07  0.160
cancer  6.7e-02 0.063  1.6e-01  0.045
```

3 correlated predictors

```
 Estimate Std Error z value Pr(>|z|)
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|)
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

```
        breath teeth fingers  cancer
breath  0.0e+00     0 0.0e+00 5.6e-17
teeth   0.0e+00     0 0.0e+00 0.0e+00
fingers 0.0e+00     0 0.0e+00 5.6e-17
cancer  5.6e-17     0 5.6e-17 0.0e+00
```

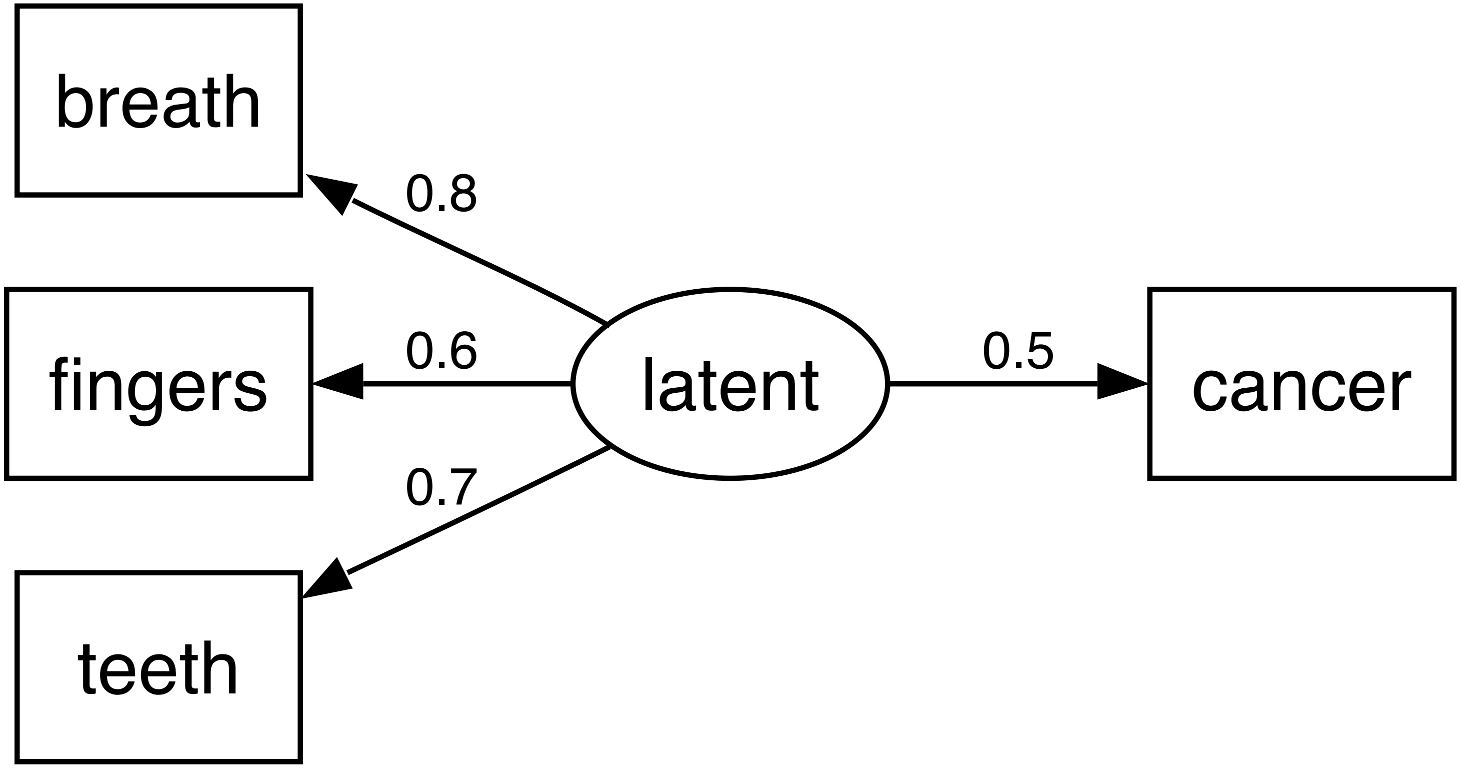
Or, model one latent

```
  Estimate Std Error z value Pr(>|z|)
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
```

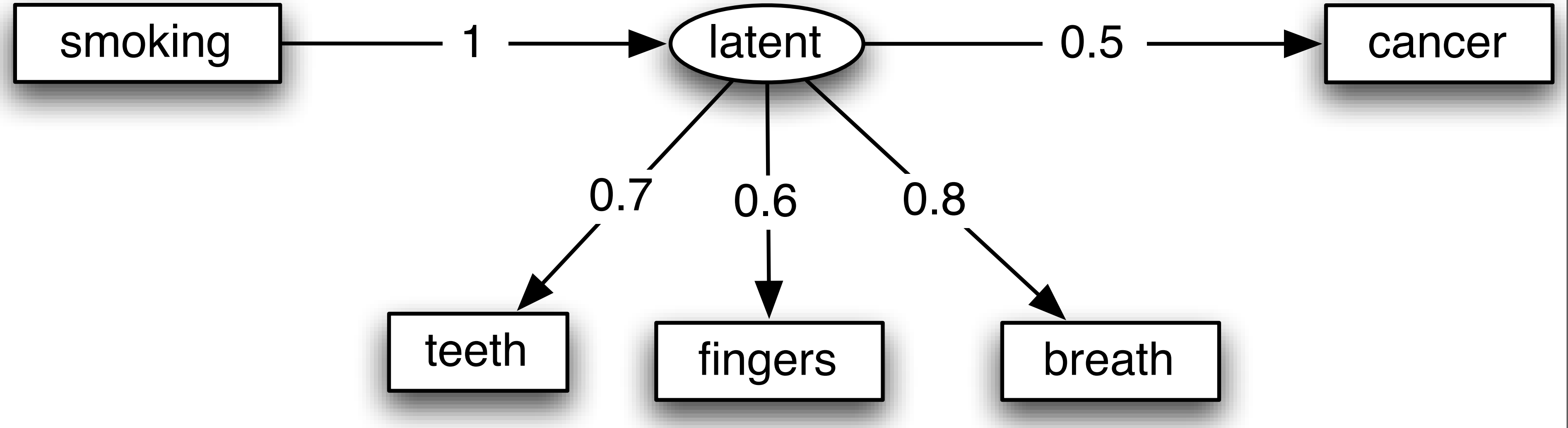
A great model

```
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
```

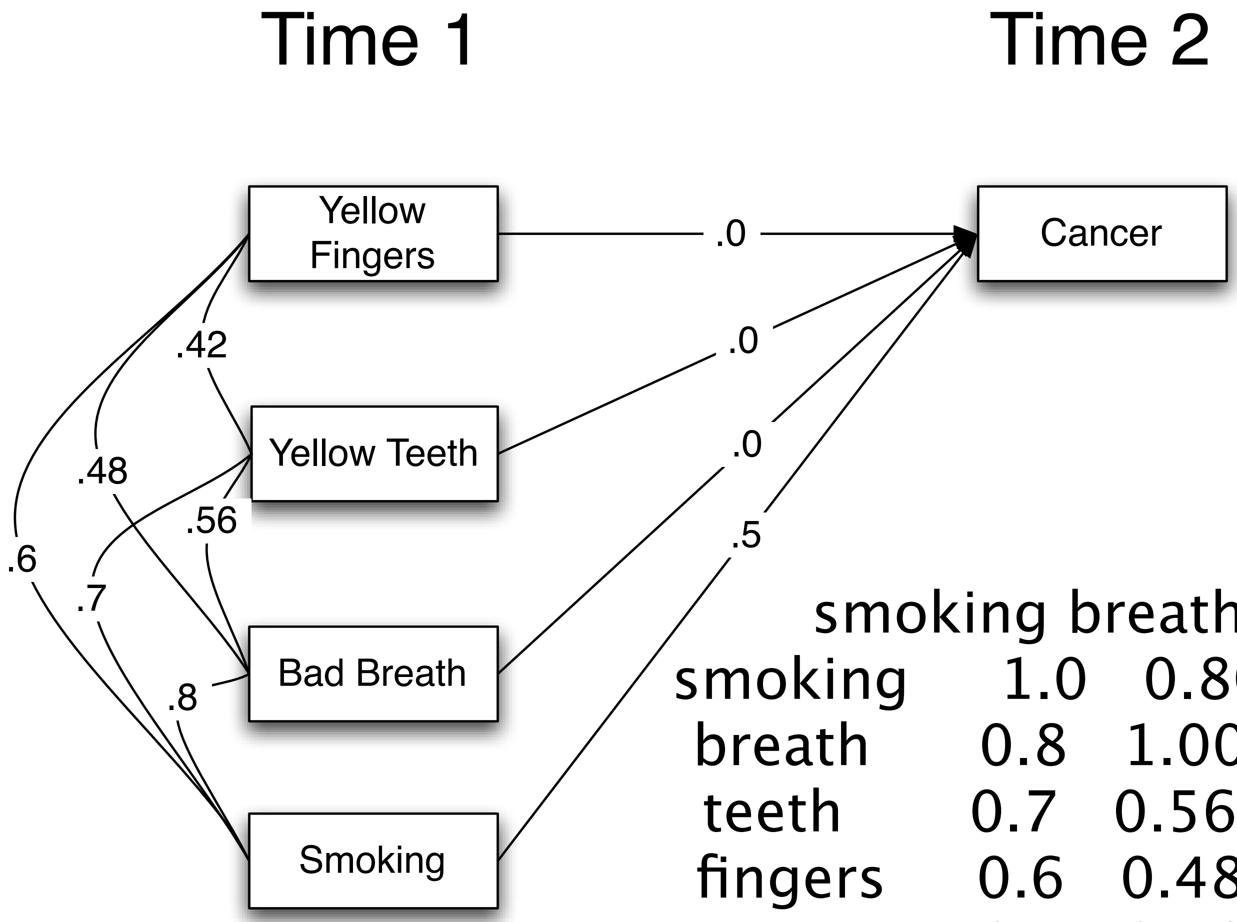
SEM alternative: but what is the latent?



Smoking is measured perfectly



Properly specified

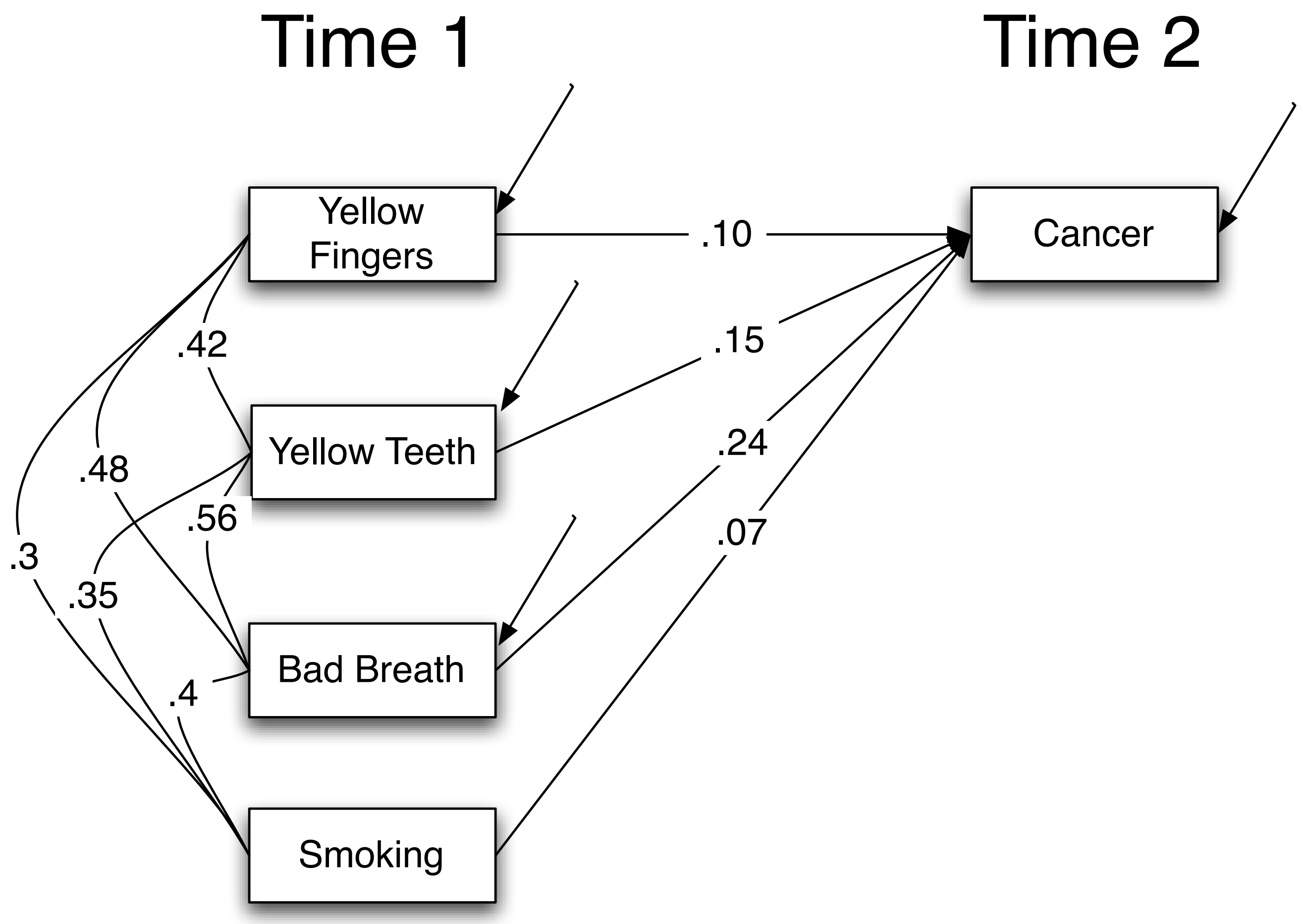


	smoking	breath	teeth	fingers	cancer
smoking	1.0	0.80	0.70	0.60	0.50
breath	0.8	1.00	0.56	0.48	0.40
teeth	0.7	0.56	1.00	0.42	0.35
fingers	0.6	0.48	0.42	1.00	0.30
cancer	0.5	0.40	0.35	0.30	1.00

Regression if measurement error

	smoking	breath	teeth	fingers	cancer
smoking	1.00	0.40	0.35	0.30	0.25
breath	0.40	1.00	0.56	0.48	0.40
teeth	0.35	0.56	1.00	0.42	0.35
fingers	0.30	0.48	0.42	1.00	0.30
cancer	0.25	0.40	0.35	0.30	1.00

Failure of regression



Try SEM

```
      [,1]                      [,2] [,3]
 [1,] "latent -> cancer"    "1"  NA
 [2,] "latent -> breath"    "2"  NA
 [3,] "latent -> fingers"   "3"  NA
 [4,] "latent -> teeth"     "4"  NA
 [5,] "latent -> smoking"   "9"  NA
 [6,] "fingers <-> fingers" "5"  NA
 [7,] "teeth <-> teeth"     "6"  NA
 [8,] "breath <-> breath"   "7"  NA
 [9,] "cancer <-> cancer"   "8"  NA
[10,] "smoking <-> smoking" "10" NA
[11,] "latent <-> latent"   NA   "1"
```

Good data

```
1   5.0e-01 0.095      5.3e+00 1.3e-07  cancer <--- latent
2   8.0e-01 0.085      9.4e+00 0.0e+00  breath <--- latent
3   6.0e-01 0.092      6.5e+00 7.5e-11  fingers <--- latent
4   7.0e-01 0.089      7.9e+00 3.6e-15  teeth <--- latent
9   1.0e+00 0.075       1.3e+01 0.0e+00  smoking <--- 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
10 -7.1e-08 0.048     -1.5e-06 1.0e+00  smoking <--> smoking
```

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
```

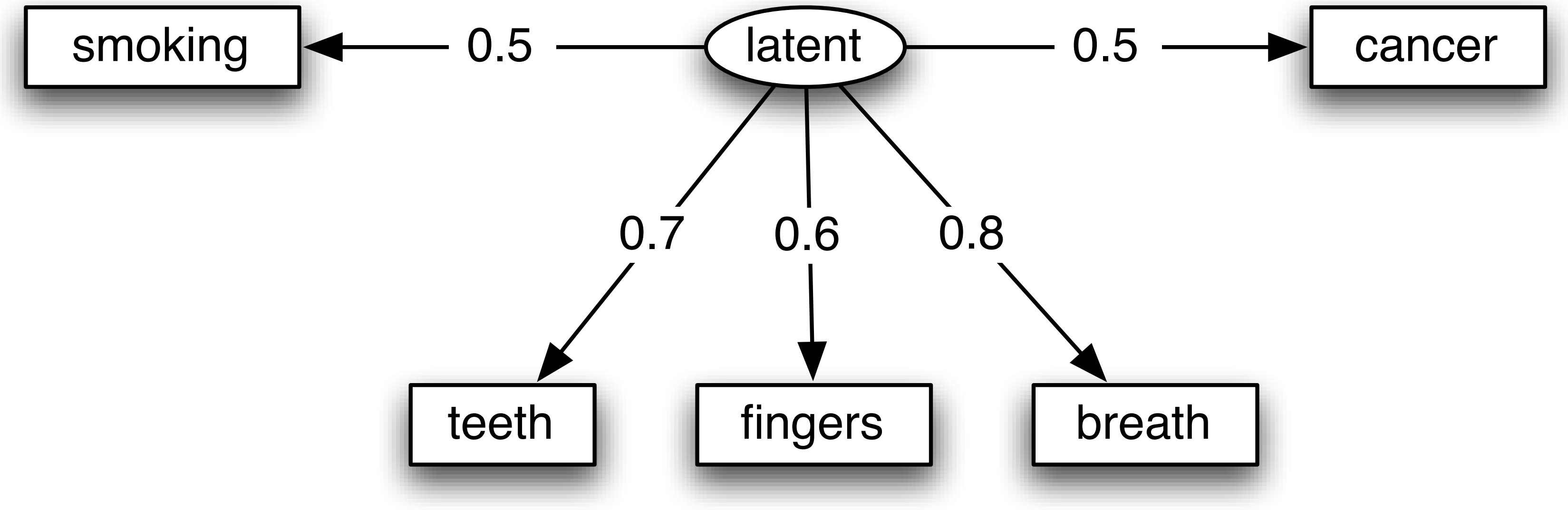
Bad data, correct model

```
  Estimate Std Error z value Pr(>|z|)
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



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
```

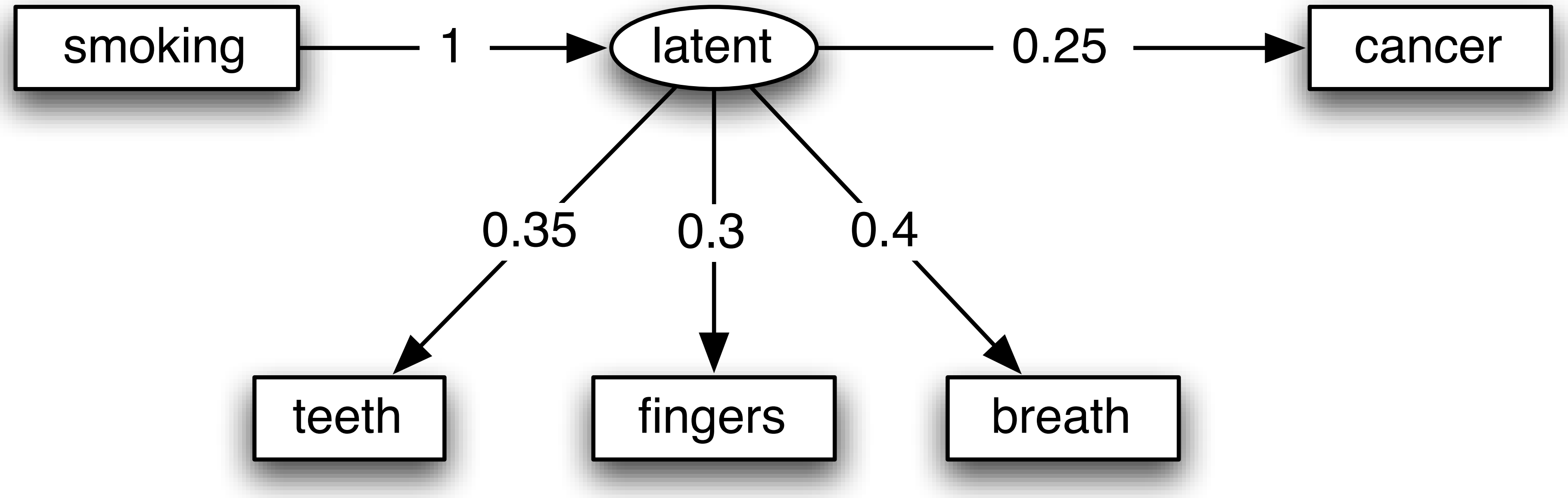
Perfect smoking

```
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
```

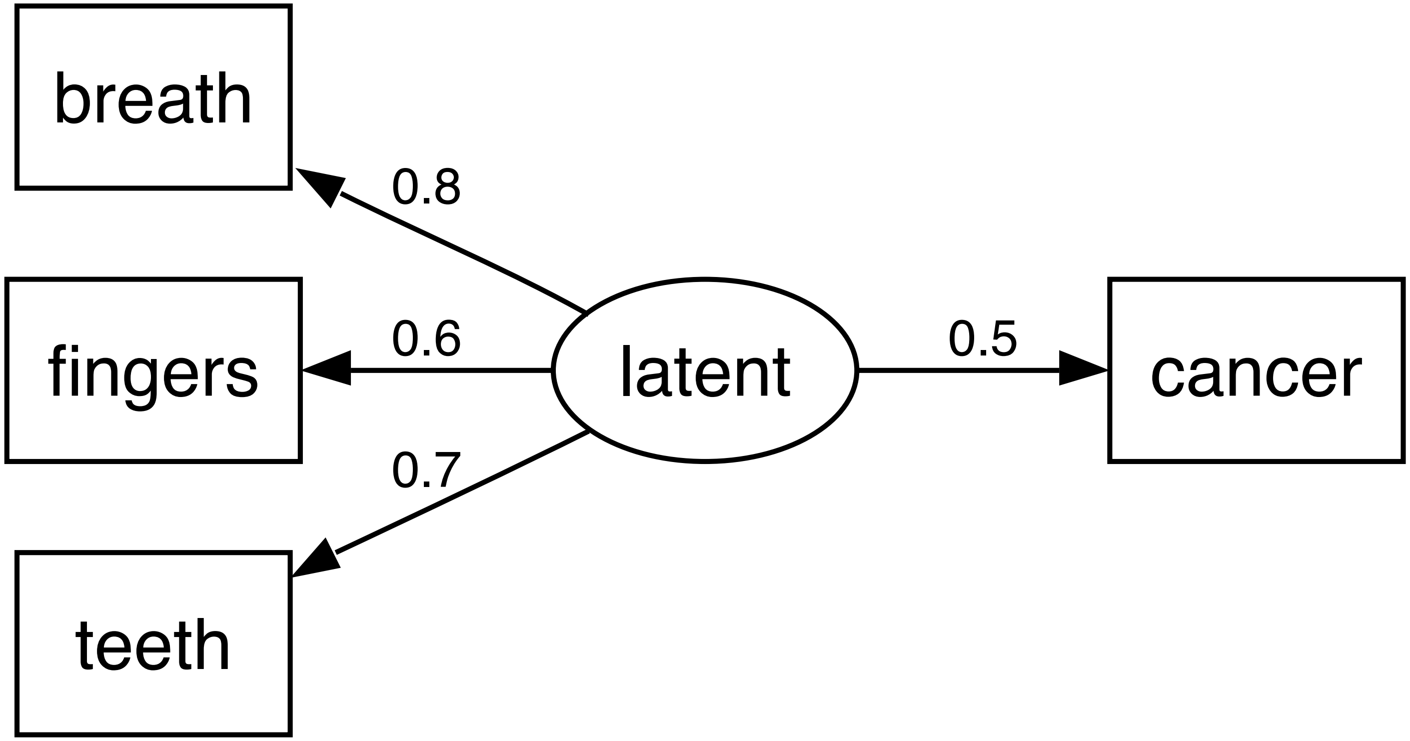
“Imperfect” smoking, modeled with no error

```
  Estimate Std Error z value Pr(>|z|)
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
```

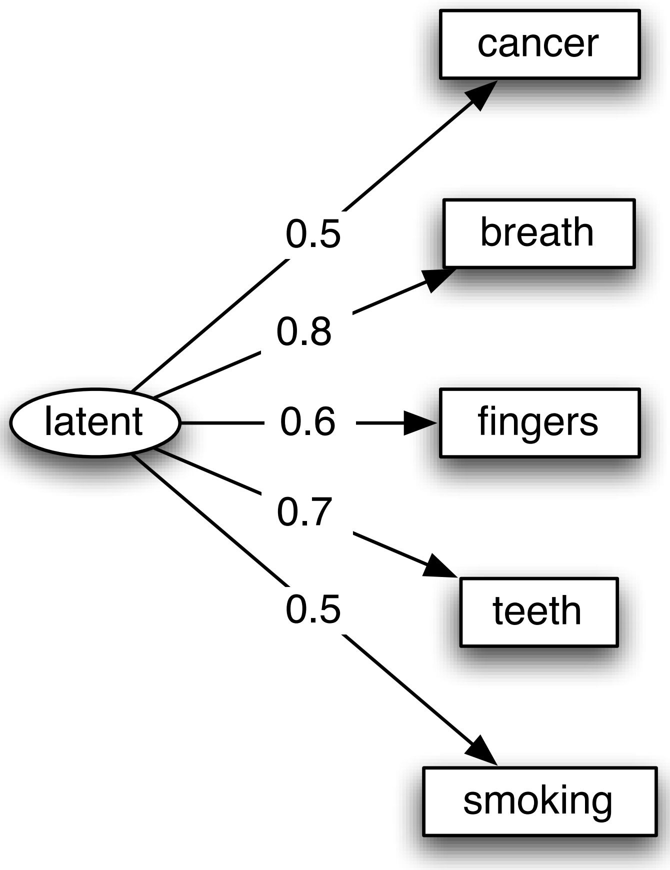
Smoking is not measured perfectly



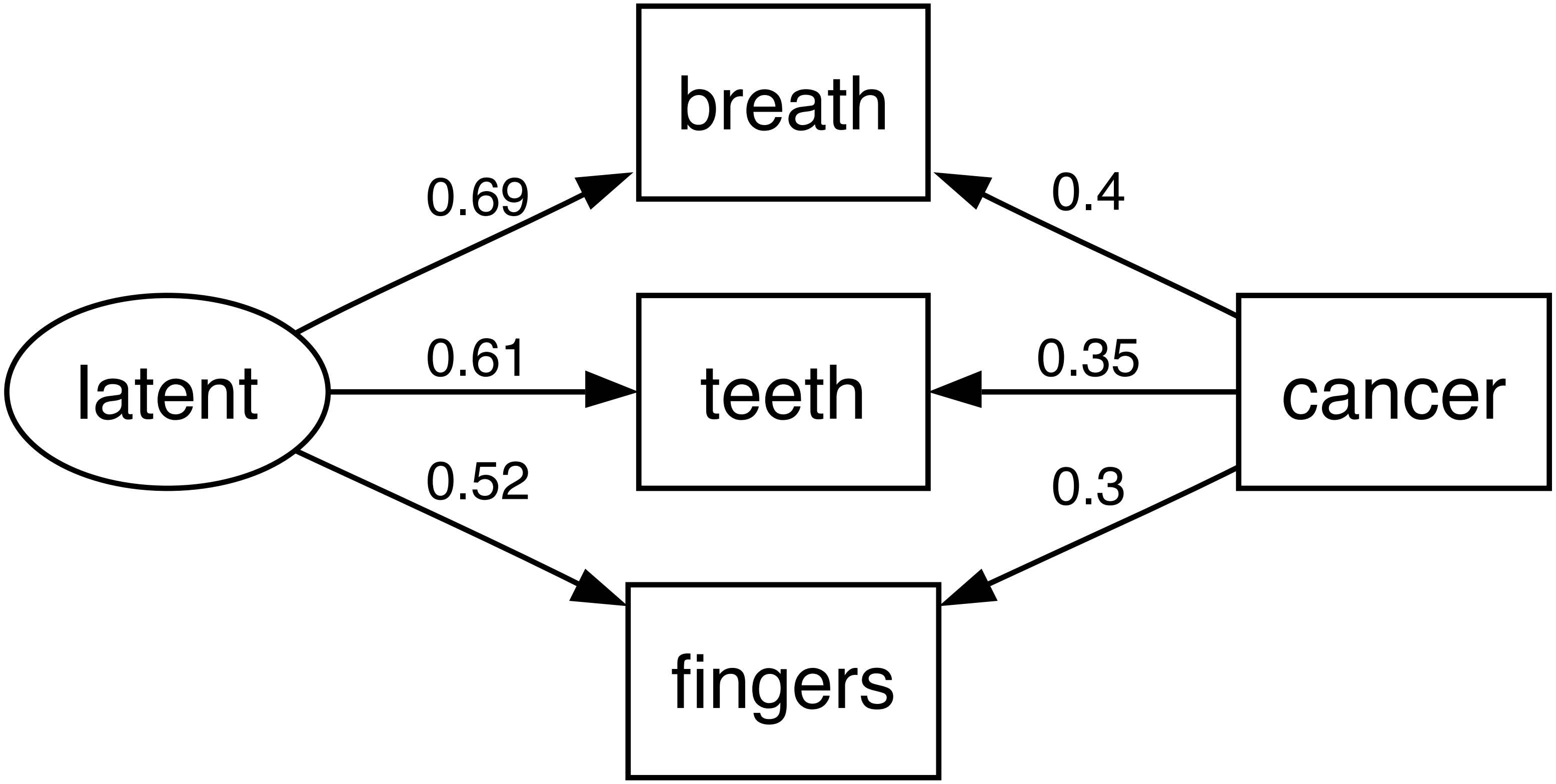
What is the causal variable



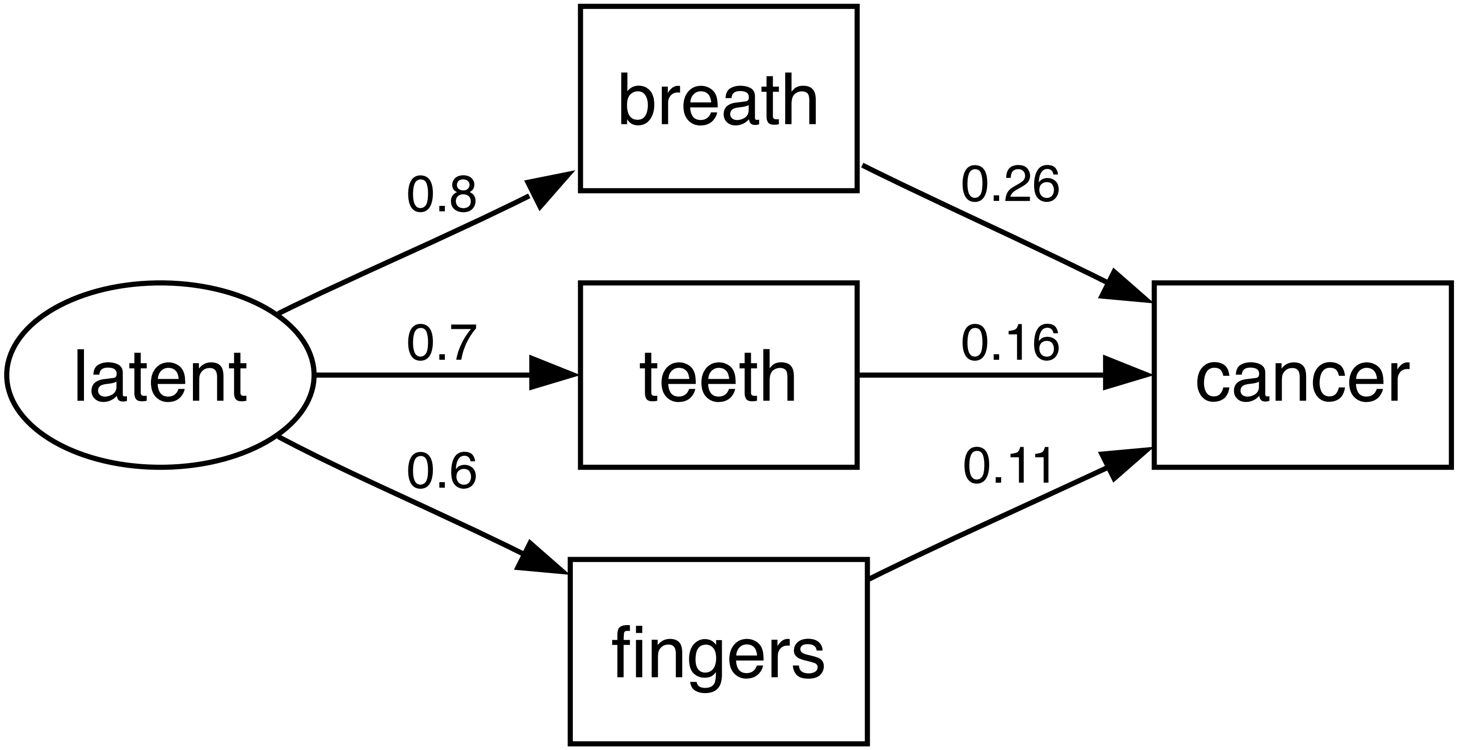
Something causes one to smoke and get cancer: is it E?



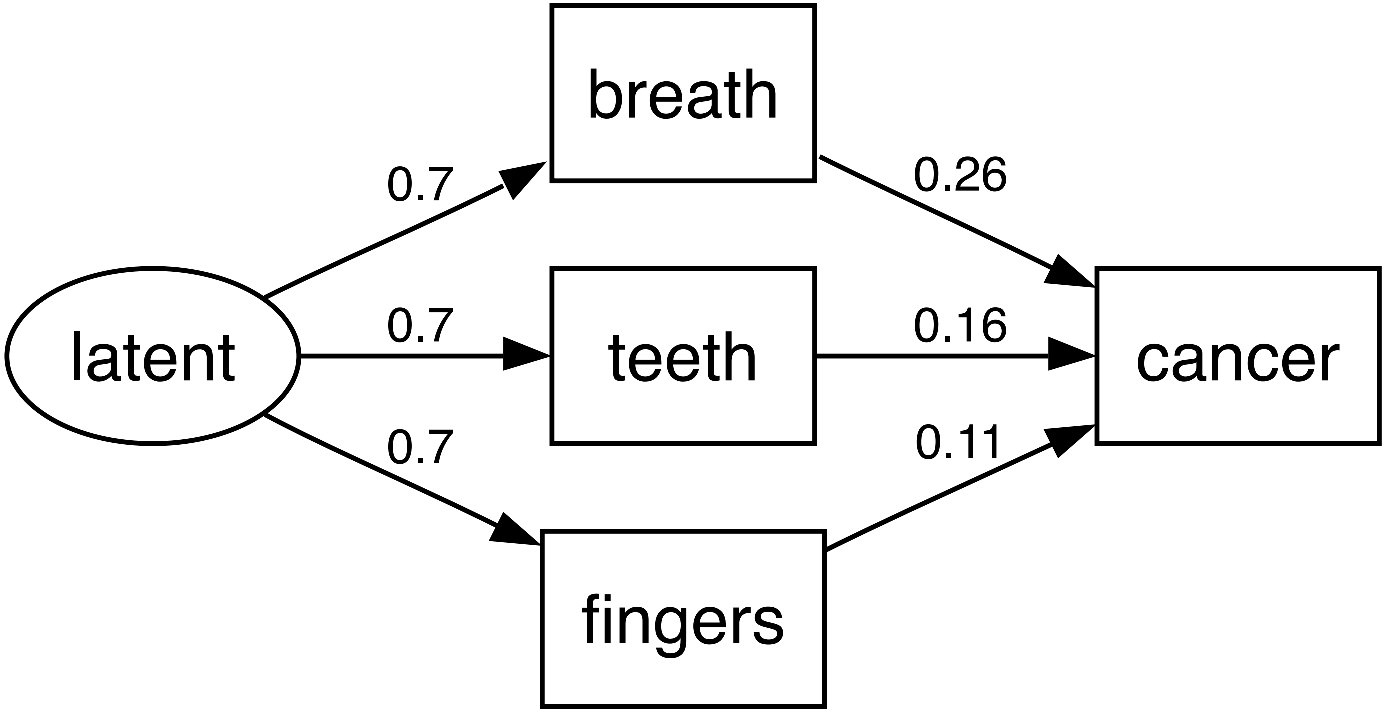
Cancer as cause

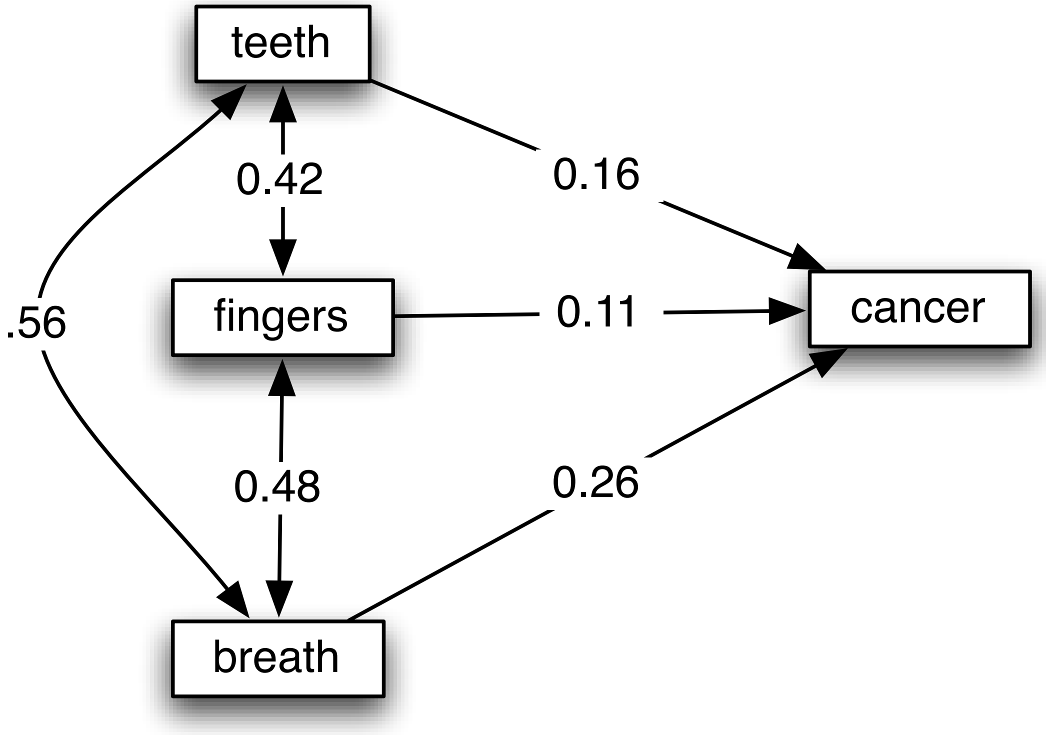


Cancer as caused



Cancer as caused:equal error




teeth
0.42
0.16
.56
fingers
0.11
cancer
0.48
0.26
breath

Consider error in smoking

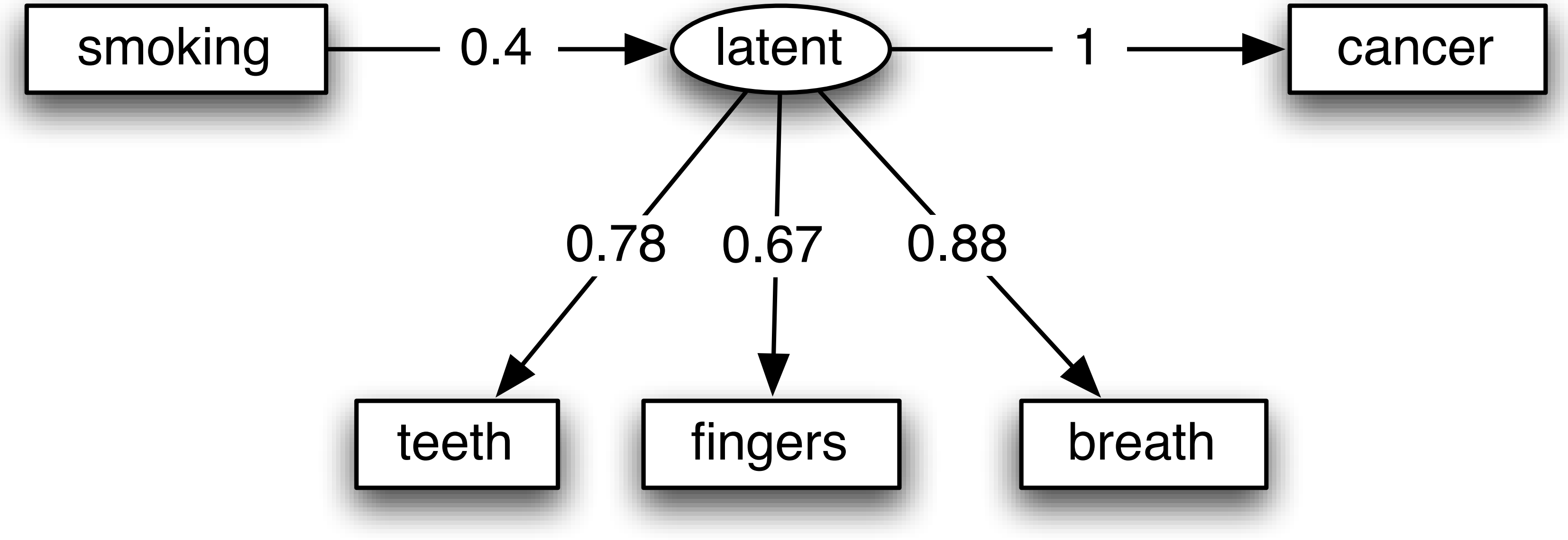
```
      [,1]                      [,2] [,3]
 [1,] "latent -> cancer"        NA   "1"
 [2,] "latent -> breath"        "2"  NA
 [3,] "latent -> fingers"       "3"  NA
 [4,] "latent -> teeth"         "4"  NA
 [5,] "smoking -> latent"       "11" NA
 [6,] "fingers <-> fingers"     "5"  NA
 [7,] "teeth <-> teeth"         "6"  NA
 [8,] "breath <-> breath"       "7"  NA
 [9,] "cancer <-> cancer"       "8"  NA
[10,] "smoking <-> smoking"     "10" NA
[11,] "latent <-> latent"       NA   "1"
```

Error in smoking

```
 Parameter Estimates
   Estimate Std Error z value Pr(>|z|)
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



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: $F = 1/2\mathrm{tr}[(S-\Sigma)^{2}]$

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

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

   A. p is total number of variables

   B. S is the observed covariance matrix

   C. Σ 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 $\sum$ be the “strung out” model matrix

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

IV. where W =

   A. Ordinary Least Squares (W = I)

   B. Generalized least squares: W = (SS’)

   C. Maximum likelihood: W = ($\sum\sum$’)

Measures of fit

1. Taken from David Kenny
    - A. http://davidakenny.net/cm/fit.htm
2. 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. $$\frac{\text{Chi2(Null)/df(null) - Chi2 (model)/df(model)}}{\text{Chi2(Null)/df(null) - 1}}$$

II. Penalizes models for estimating more parameters

III. a “parsimony” correction

Comparative Fit Index

I. let d = Chi square -df

II. CFI = $\dfrac{d(\mathrm{Null}) - d(\mathrm{model})}{d(\mathrm{model})}$

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)

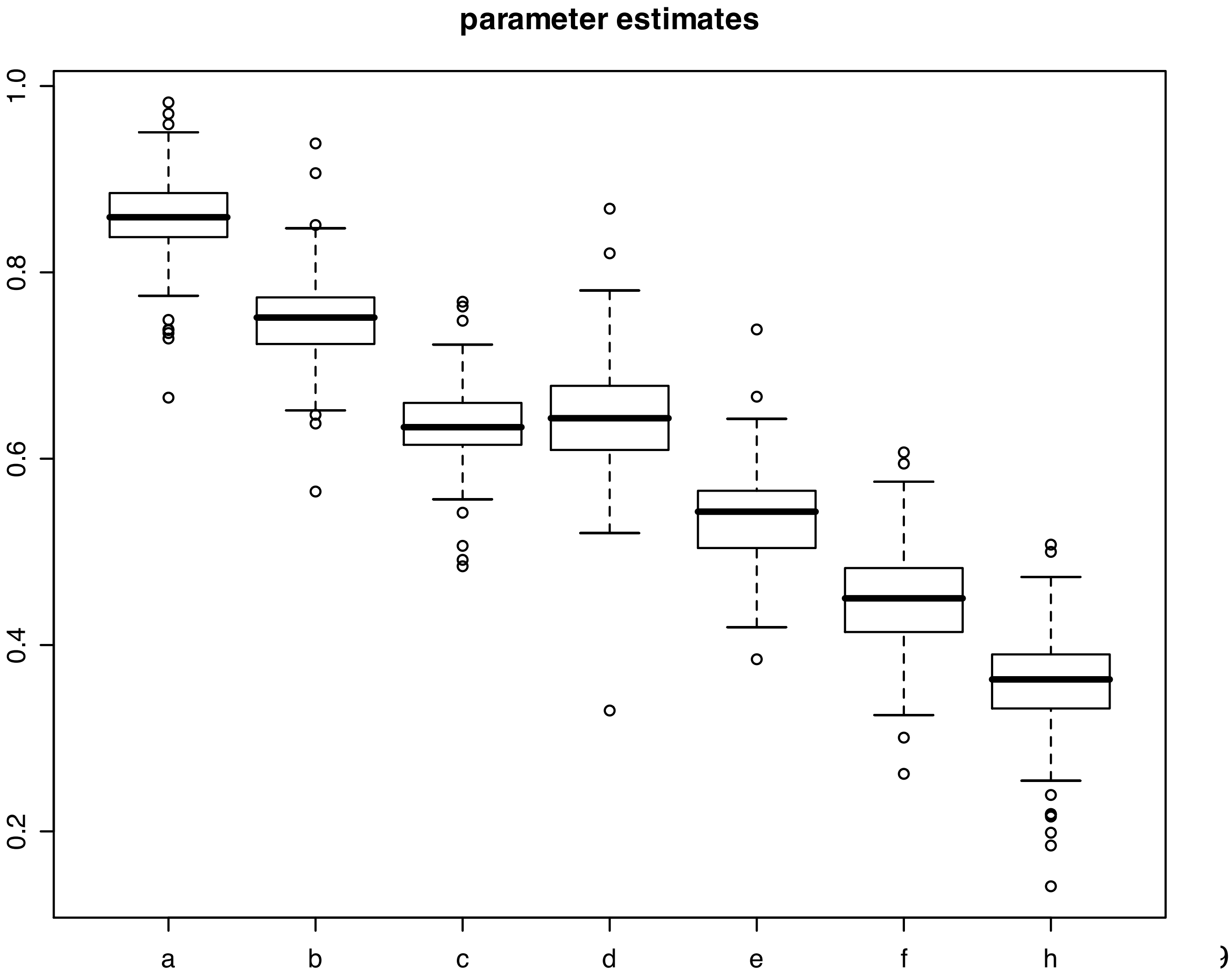
III. Plot parameter estimates

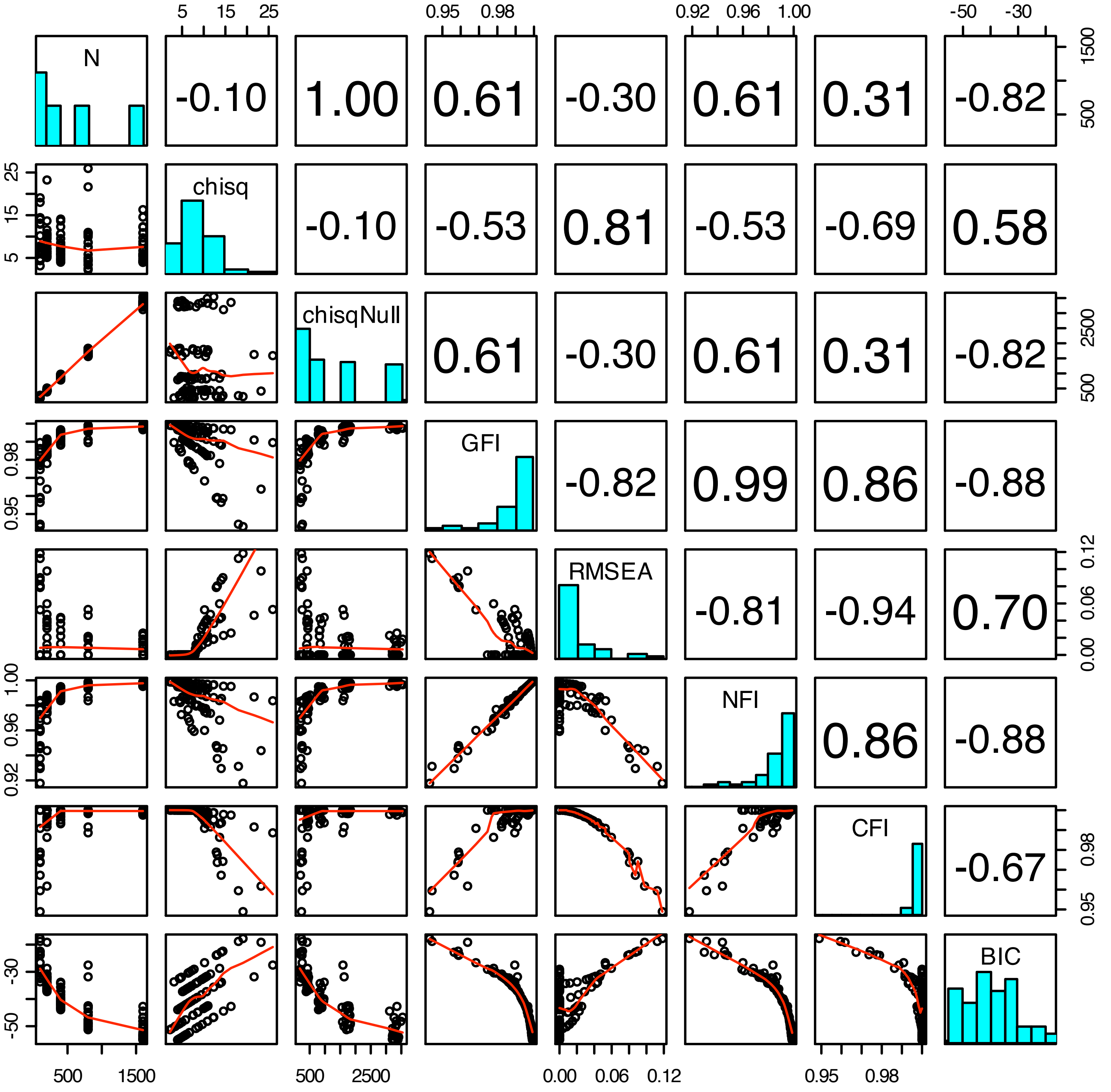
IV. Plot correlations of size of estimates

Estimation

```
     [,1] [,2]
[1,]  0.8  0.0
[2,]  0.7  0.0
[3,]  0.6  0.0
[4,]  0.0  0.7
[5,]  0.0  0.6
[6,]  0.0  0.5
```

phi = .4





n=

100,

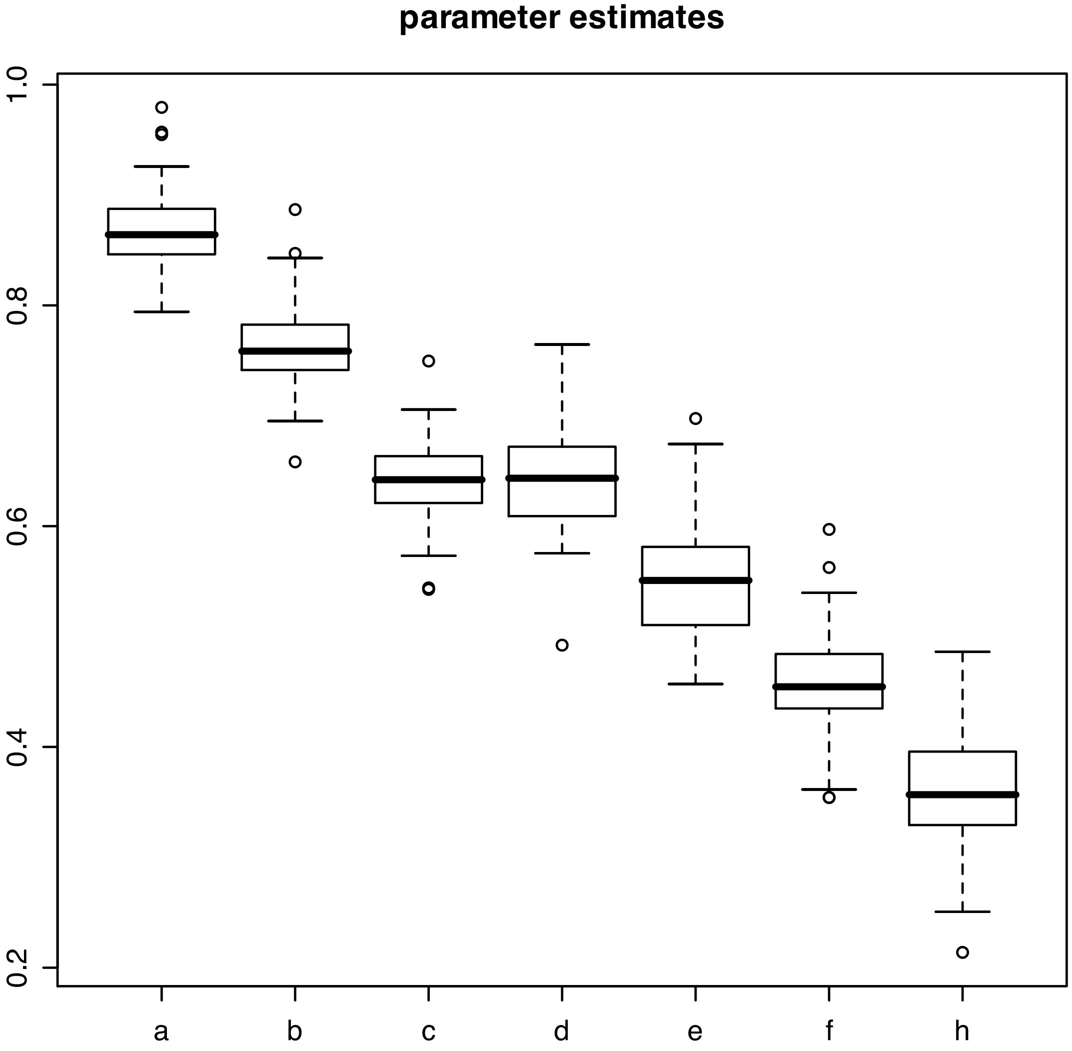
200,

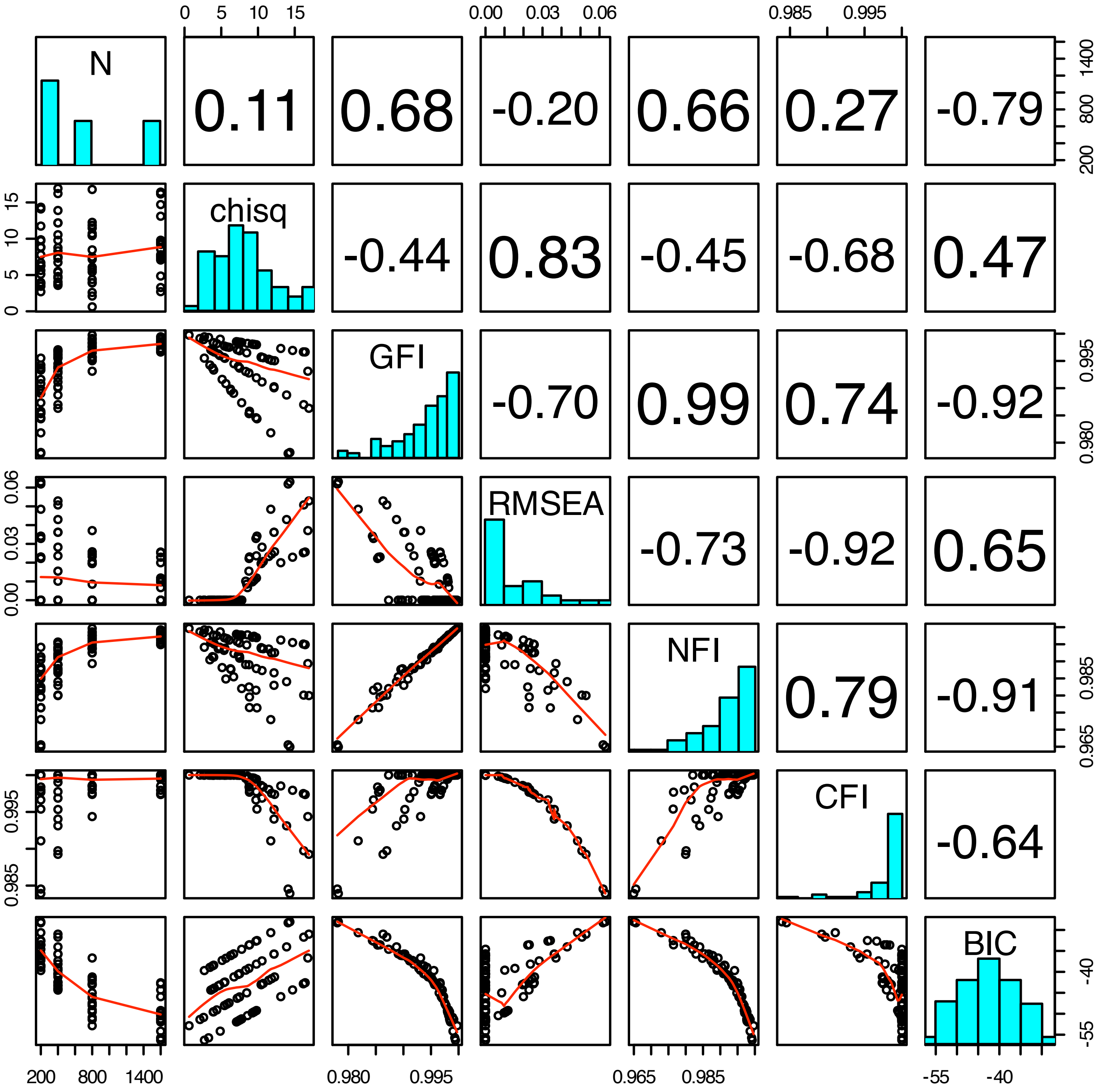
400,

800,

1600

Redo this with n = 200, 400, 800, 1600





n=
200,
400,
800,
1600

Goodness of fit of bad model

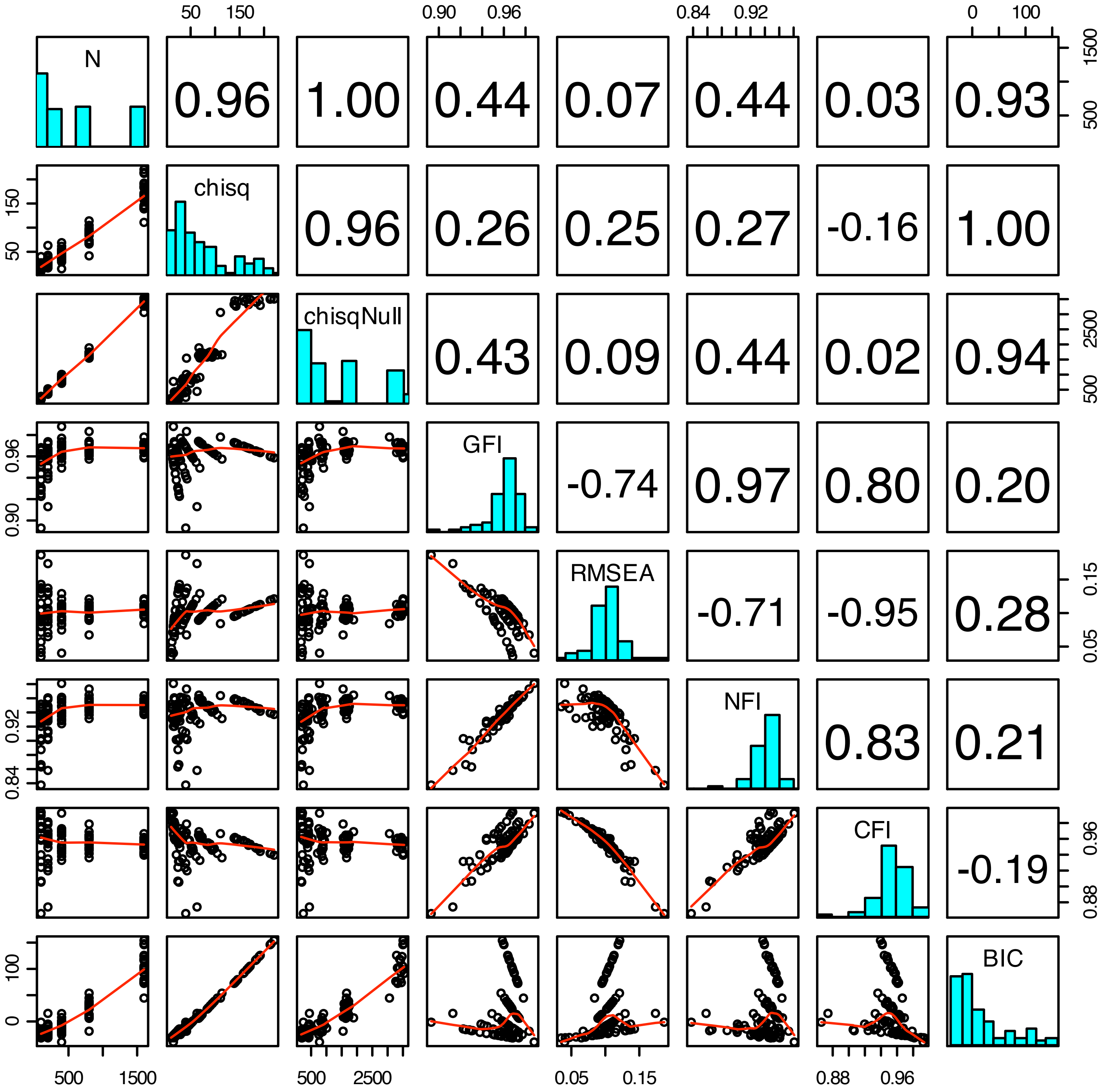
I. Previous slides were the correlations of the goodness of fit for correct model

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


N
chisq
chisqNull
GFI
RMSEA
NFI
CFI
BIC
0.96
1.00
0.44
0.07
0.44
0.03
0.93
0.96
0.26
0.25
0.27
-0.16
1.00
0.43
0.09
0.44
0.02
0.94
-0.74
0.97
0.80
0.20
-0.71
-0.95
0.28
0.83
0.21
-0.19
50
150
0.90
0.96
0.84
0.92
0
100
1500
500
2500
500
0.15
0.05
0.96
0.88
150
50
0.96
0.90
0.92
0.84
100
0
500
1500
500
2500
0.05
0.15
0.88
0.96

Numerical fits to poor model

	var	n	mean	sd	median	min	max
N	1	95	641.05	554.19	400	100	1600
chisq	2	95	71.14	57.97	51.41	10.1	220.46
chisqNull	3	95	1354.58	1177.23	874.45	174.06	3538.64
GFI	4	95	0.96	0.01	0.96	0.89	0.99
AGFI	5	95	0.91	0.03	0.92	0.75	0.97
RMSEA	6	95	0.1	0.02	0.1	0.04	0.19
NFI	10	95	0.94	0.02	0.94	0.84	0.98
CFI	11	95	0.95	0.02	0.96	0.87	0.99

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

III. MacCallum, R. C., Wegener, D. T., Uchino, B. N., & Fabrigar, L. R. (1993). The problem of equivalent models in applications of covariance structure analysis. Psychological Bulletin, 114, 185-199.

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