

# 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

## III. Random error from sampling

- A. sampling of people

- B. sampling of items

# Structural $\neq$ Causal

- I. Structural equations are just models of relationships
- II. Causality is sometimes implied by direction of errors, but solving equations does not solve causality problem

# Problem of the missing variable

I. Well known that correlation  $\neq$  causality

A. Large feet and verbal ability

B. Highly paid Methodist ministers and  
Puerto Rican prices

C. Superior learning at superior colleges

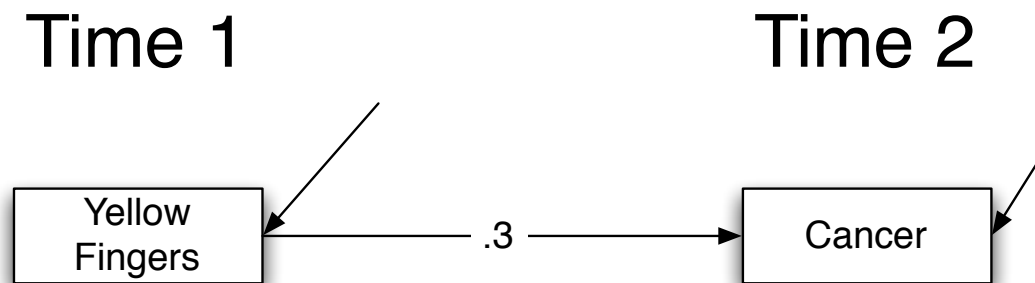
# Temporal ordering as solution?

- I. Basic claim that causality requires temporal ordering
- II. But, temporal ordering  $\neq$  causality
  - A. cocks crow before dawn does not cause sun to come up

# Regression approach

- I. Regression models consider direct and indirect effects
- II. Zero order correlations are decomposed
  - A. direct effects (controlling for other variables)
  - B. indirect effects (due to correlation with other variables)

# Effect of yellow fingers on cancer



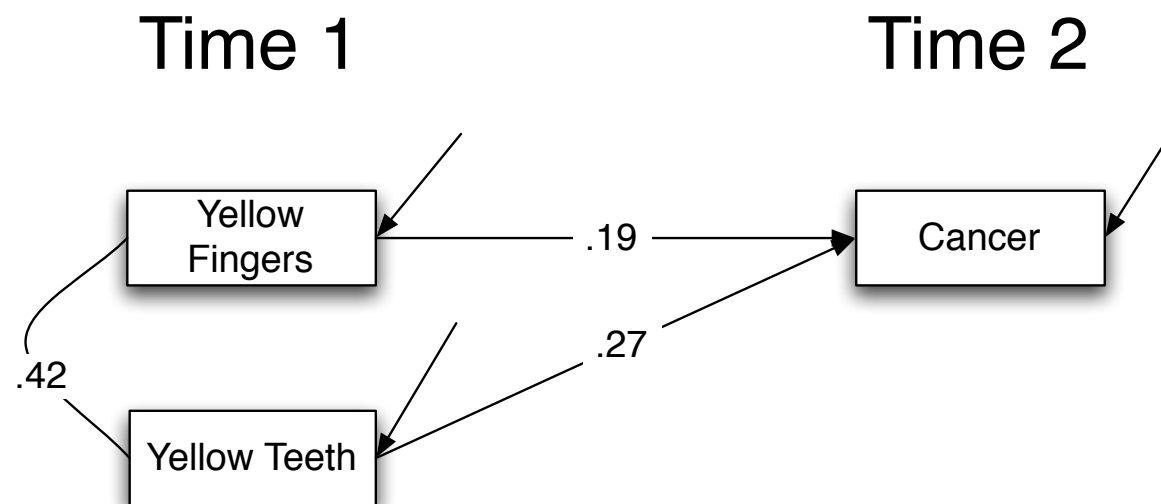
# Beta weights

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

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

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

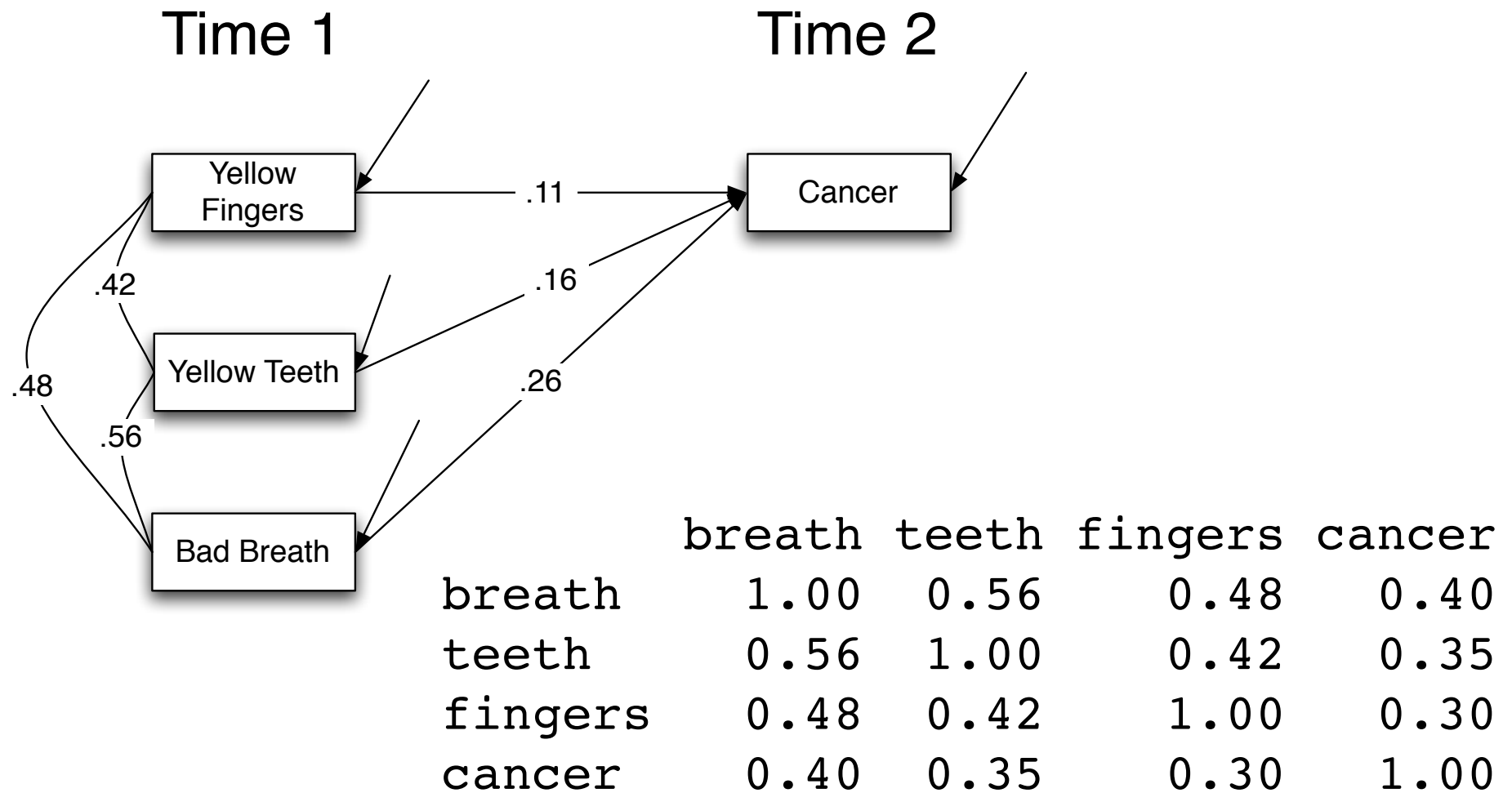
# Yellow causes cancer



|         | teeth | fingers | cancer |
|---------|-------|---------|--------|
| teeth   | 1.00  | 0.42    | 0.35   |
| fingers | 0.42  | 1.00    | 0.30   |
| cancer  | 0.35  | 0.30    | 1.00   |

Yellow fingers have an effect even when controlling for yellow teeth

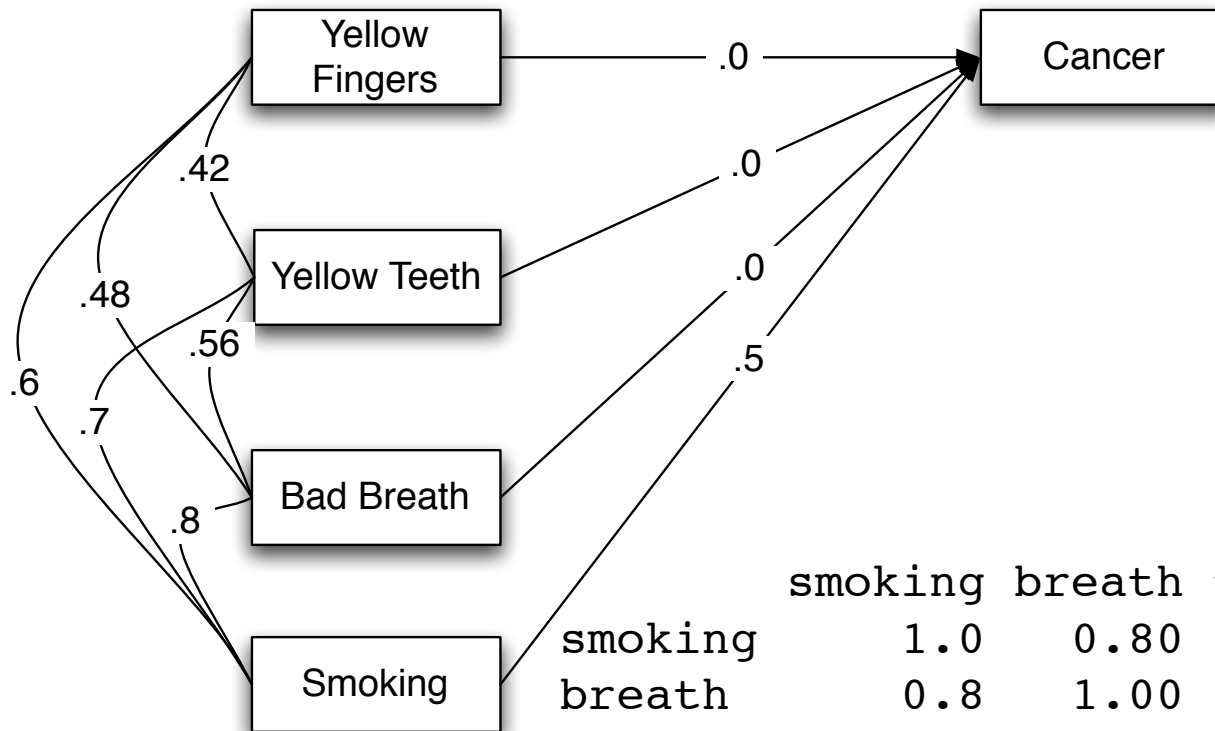
# Brush your teeth!



# Properly specified

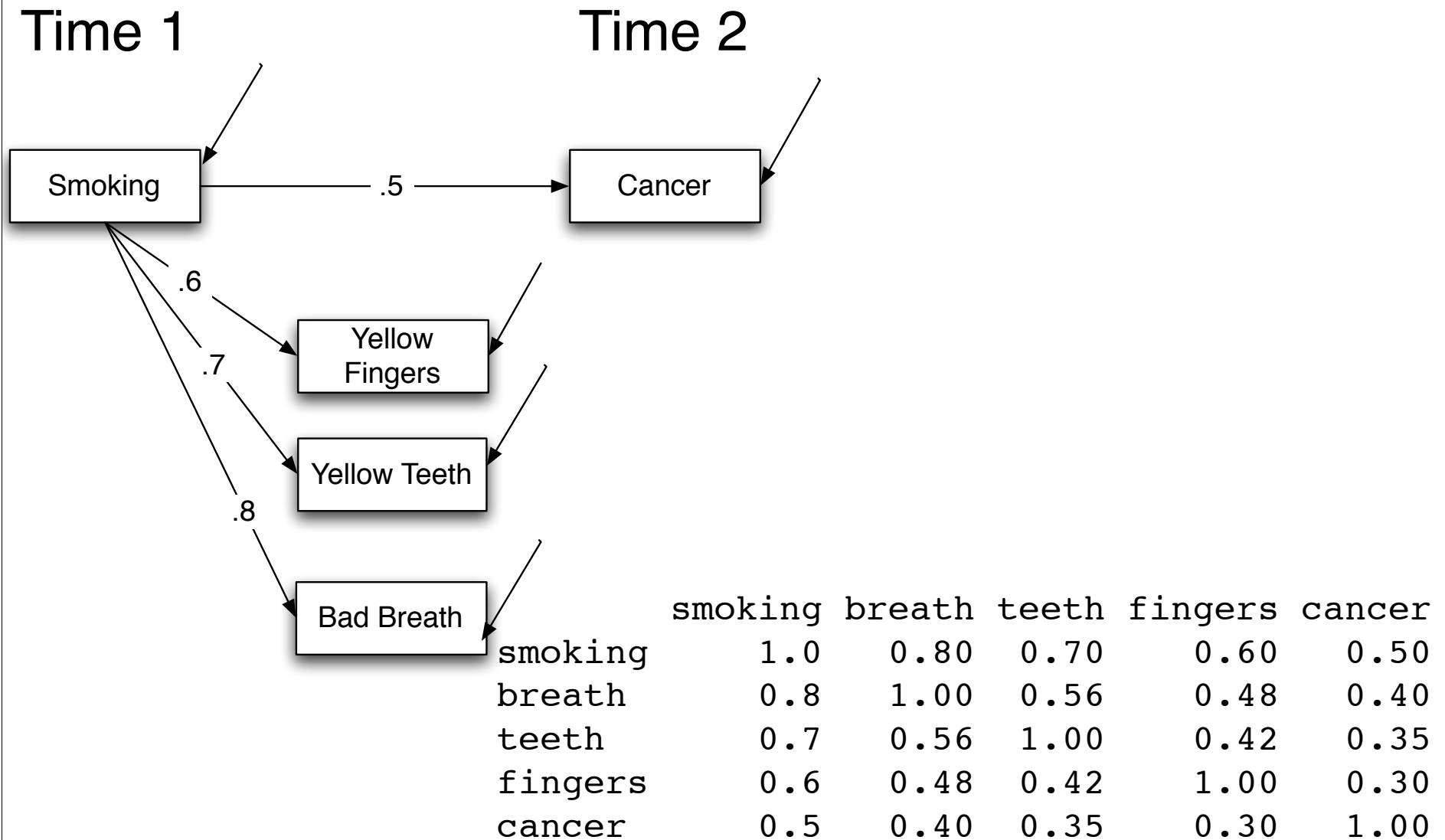
Time 1

Time 2

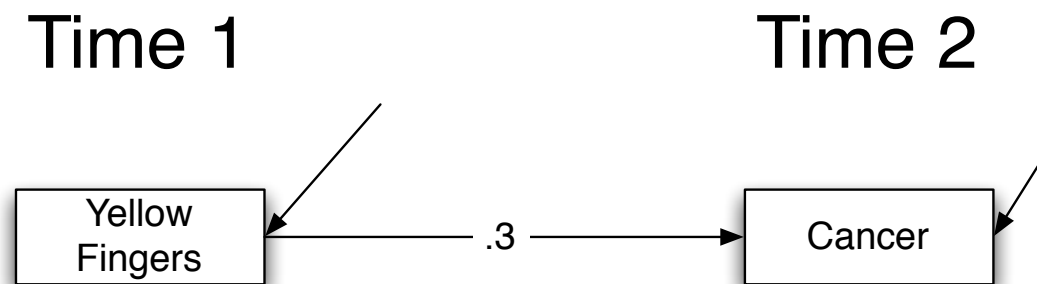


|         | smoking | breath | teeth | fingers | cancer |
|---------|---------|--------|-------|---------|--------|
| smoking | 1.0     | 0.80   | 0.70  | 0.60    | 0.50   |
| breath  | 0.8     | 1.00   | 0.56  | 0.48    | 0.40   |
| teeth   | 0.7     | 0.56   | 1.00  | 0.42    | 0.35   |
| fingers |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

# Causality?



# Effect of yellow fingers on cancer



# Can use sem as a regression program

- I. By using the fixed.x option, sem allows the x predictors to be correlated.
- II. Without using this option, the model misses the correlations between the predictors but still estimates the regression paths
- III. Can decompose the regression problem to identify critical paths

# The model

```
model <- matrix(c(
  "breath -> cancer", "a1", "NA",
  "teeth -> cancer", "a2", "NA",
  "fingers -> cancer", "a3", "NA",
  "cancer <->
cancer", "e1", "NA"), ncol=3, byrow=TRUE)
> class(model) <- "mod"
> model
```

|   | Path              | Parameter |
|---|-------------------|-----------|
| 1 | breath -> cancer  | a1        |
| 2 | teeth -> cancer   | a2        |
| 3 | fingers -> cancer | a3        |
| 4 | cancer <-> cancer | e1        |

# sem regression

```
sem.can <- sem(model,cancer,400,fixed.x  
=c("breath","teeth","fingers"))
```

```
> summary(sem.can,digits=2)
```

```
Model Chisquare = 4.4e-14    Df = 0 Pr(>Chisq) = NA
```

```
Chisquare (null model) = 357    Df = 6
```

```
Goodness-of-fit index = 1
```

```
BIC = 4.4e-14
```

```
Normalized Residuals
```

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. |
|------|---------|--------|------|---------|------|
|------|---------|--------|------|---------|------|

|         |         |         |         |         |         |
|---------|---------|---------|---------|---------|---------|
| 0.0e+00 | 0.0e+00 | 0.0e+00 | 3.9e-16 | 2.7e-16 | 2.1e-15 |
|---------|---------|---------|---------|---------|---------|

```
Parameter Estimates
```

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

|    |      |       |      |         |                     |
|----|------|-------|------|---------|---------------------|
| a1 | 0.26 | 0.057 | 4.5  | 6.9e-06 | cancer <--- breath  |
| a2 | 0.16 | 0.056 | 2.9  | 4.1e-03 | cancer <--- teeth   |
| a3 | 0.11 | 0.052 | 2.1  | 3.8e-02 | cancer <--- fingers |
| e1 | 0.81 | 0.057 | 14.1 | 0.0e+00 | cancer <--> cancer  |

# sem regression with uncorrelated predictors (wrong model)

```
model.1 <- matrix(c(
  "breath -> cancer", "a1", "NA",
  "teeth -> cancer", "a2", "NA",
  "fingers -> cancer", "a3", "NA",
  "cancer <-> cancer", "e1", "NA",
  "breath <-> breath", "NA", "1",
  "teeth <-> teeth", "NA", "1",
  "fingers <-> fingers", "NA",
  "1"), ncol=3, byrow=TRUE)

> sem.can1 <- sem(model.1, cancer, 400)
```

# Poor measurement/fit

Model Chisquare = 272      Df = 5      Pr(>Chisq) = 0  
Chisquare (null model) = 357      Df = 6  
Goodness-of-fit index = 0.74  
Adjusted goodness-of-fit index = 0.47  
RMSEA index = 0.37      90% CI: (0.33, 0.4)  
Bentler-Bonnett NFI = 0.24  
Tucker-Lewis NNFI = 0.087  
Bentler CFI = 0.24  
SRMR = 0.29  
BIC = 242

# Regression betas are right

## Normalized Residuals

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. |
|------|---------|--------|------|---------|------|
| 0.0  | 2.5     | 4.0    | 5.1  | 8.7     | 11.2 |

## Parameter Estimates

|    | Estimate | Std Error | z value | Pr(> z ) |                     |
|----|----------|-----------|---------|----------|---------------------|
| a1 | 0.26     | 0.057     | 4.5     | 6.9e-06  | cancer <--- breath  |
| a2 | 0.16     | 0.056     | 2.9     | 4.1e-03  | cancer <--- teeth   |
| a3 | 0.11     | 0.052     | 2.1     | 3.8e-02  | cancer <--- fingers |
| e1 | 0.81     | 0.057     | 14.1    | 0.0e+00  | cancer <--> cancer  |
| NA | 1.00     | 0.041     | 24.5    | 0.0e+00  | breath <--> breath  |

Iterations = 0

# 3 predictors: uncorrelated (prior version of sem)

|   | 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   |

# 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   |

# Adjusting the model

- I. Prior model had three uncorrelated latent variables
- II. Add in the correlations between the latents  
(as would be done in a regression model)
- III. Can examine the correlations between the latent predictors

# Constructing the model

```
model.3 <- matrix(c(
  "breath -> cancer", "a1", "NA",
  "teeth -> cancer", "a2", "NA",
  "fingers -> cancer", "a3", "NA",
  "cancer <-> cancer", "e4", "NA",
  "breath <-> breath", "e1", "NA",
  "teeth <-> teeth", "e2", "NA",
  "fingers <-> fingers", "e3", "NA",
  "teeth <-> fingers", "r12", "NA",
  "teeth <-> breath", "r13", "NA",
  "fingers <-> breath",
  "r23", "NA"), ncol=3, byrow=TRUE)

sem.can3 <- sem(model.3, cancer, 400)
```

# The model

```
> model.3
```

|       | [,1]                  | [,2]  | [,3] |
|-------|-----------------------|-------|------|
| [1,]  | "breath -> cancer"    | "a1"  | "NA" |
| [2,]  | "teeth -> cancer"     | "a2"  | "NA" |
| [3,]  | "fingers -> cancer"   | "a3"  | "NA" |
| [4,]  | "cancer <-> cancer"   | "e4"  | "NA" |
| [5,]  | "breath <-> breath"   | "e1"  | "NA" |
| [6,]  | "teeth <-> teeth"     | "e2"  | "NA" |
| [7,]  | "fingers <-> fingers" | "e3"  | "NA" |
| [8,]  | "teeth <-> fingers"   | "r12" | "NA" |
| [9,]  | "teeth <-> breath"    | "r13" | "NA" |
| [10,] | "fingers <-> breath"  | "r23" | "NA" |

# Model is “saturated”

```
> summary(sem.can3)
```

```
Model Chisquare = 4.4298e-14    Df = 0
Pr(>Chisq) = NA
Chisquare (null model) = 357.29    Df = 6
Goodness-of-fit index = 124

BIC = 4.4298e-14

Normalized Residuals
      Min.   1st Qu.   Median       Mean   3rd Qu.
Max.
0.00e+00 0.00e+00 0.00e+00 3.90e-16 2.66e-16
2.06e-15
```

# Paths are correct

## Parameter Estimates

|     | Estimate | Std Error | z value | Pr(> z ) |                      |
|-----|----------|-----------|---------|----------|----------------------|
| a1  | 0.26     | 0.057     | 4.5     | 6.9e-06  | cancer <--- breath   |
| a2  | 0.16     | 0.056     | 2.9     | 4.1e-03  | cancer <--- teeth    |
| a3  | 0.11     | 0.052     | 2.1     | 3.8e-02  | cancer <--- fingers  |
| e4  | 0.81     | 0.057     | 14.1    | 0.0e+00  | cancer <--> cancer   |
| e1  | 1.00     | 0.071     | 14.1    | 0.0e+00  | breath <--> breath   |
| e2  | 1.00     | 0.071     | 14.1    | 0.0e+00  | teeth <--> teeth     |
| e3  | 1.00     | 0.071     | 14.1    | 0.0e+00  | fingers <--> fingers |
| r12 | 0.42     | 0.054     | 7.7     | 1.0e-14  | fingers <--> teeth   |
| r13 | 0.56     | 0.057     | 9.8     | 0.0e+00  | breath <--> teeth    |
| r23 | 0.48     | 0.056     | 8.6     | 0.0e+00  | breath <--> fingers  |

Iterations = 0

# Residuals are zero

```
> round(residuals(sem.can3,4))
```

|         | breath | teeth | fingers | cancer |
|---------|--------|-------|---------|--------|
| breath  | 0      | 0     | 0       | 0      |
| teeth   | 0      | 0     | 0       | 0      |
| fingers | 0      | 0     | 0       | 0      |
| cancer  | 0      | 0     | 0       | 0      |

# Constrain the model

```
> model.4
```

|       | [,1]                  | [,2]  | [,3] |
|-------|-----------------------|-------|------|
| [1,]  | "breath -> cancer"    | "a1"  | "NA" |
| [2,]  | "teeth -> cancer"     | "a2"  | "NA" |
| [3,]  | "fingers -> cancer"   | "a3"  | "NA" |
| [4,]  | "cancer <-> cancer"   | "e4"  | "NA" |
| [5,]  | "breath <-> breath"   | "e1"  | "NA" |
| [6,]  | "teeth <-> teeth"     | "e2"  | "NA" |
| [7,]  | "fingers <-> fingers" | "e3"  | "NA" |
| [8,]  | "teeth <-> fingers"   | "r12" | "NA" |
| [9,]  | "teeth <-> breath"    | "r12" | "NA" |
| [10,] | "fingers <-> breath"  | "r12" | "NA" |

# Not very good

```
> summary(sem.can4,digits=2)
```

```
Model Chisquare = 7.6    Df = 2 Pr(>Chisq) =  
0.022
```

```
Chisquare (null model) = 357    Df = 6
```

```
Goodness-of-fit index = 1
```

```
Adjusted goodness-of-fit index = 0.95
```

```
RMSEA index = 0.084    90% CI: (0.027, 0.15)
```

```
Bentler-Bonnett NFI = 0.98
```

```
Tucker-Lewis NNFI = 0.95
```

```
Bentler CFI = 0.98
```

```
SRMR = 0.047
```

```
BIC = -4.3
```

# Regression paths are correct

## Parameter Estimates

|         | Estimate | Std Error | z value | Pr(> z ) |                     |
|---------|----------|-----------|---------|----------|---------------------|
| a1      | 0.26     | 0.057     | 4.5     | 6.9e-06  | cancer <--- breath  |
| a2      | 0.16     | 0.056     | 2.9     | 4.1e-03  | cancer <--- teeth   |
| a3      | 0.11     | 0.052     | 2.1     | 3.8e-02  | cancer <--- fingers |
| e4      | 0.81     | 0.057     | 14.1    | 0.0e+00  | cancer <--> cancer  |
| e1      | 0.94     | 0.060     | 15.8    | 0.0e+00  | breath <--> breath  |
| e2      | 0.99     | 0.064     | 15.5    | 0.0e+00  | teeth <--> teeth    |
| e3      | 1.08     | 0.072     | 15.0    | 0.0e+00  | fingers <-->        |
| fingers |          |           |         |          |                     |
| r12     | 0.50     | 0.048     | 10.3    | 0.0e+00  | fingers <--> teeth  |

# Residuals are not bad

```
> round(residuals(sem.can4), 2)
```

|         | breath | teeth | fingers | cancer |
|---------|--------|-------|---------|--------|
| breath  | 0.06   | 0.06  | -0.02   | 0.02   |
| teeth   | 0.06   | 0.01  | -0.08   | 0.01   |
| fingers | -0.02  | -0.08 | -0.08   | -0.03  |
| cancer  | 0.02   | 0.01  | -0.03   | 0.00   |

# Constrain betas to be identical

```
model.5 <- matrix(c(
  "breath -> cancer", "a1", "NA",
  "teeth -> cancer", "a1", "NA",
  "fingers -> cancer", "a1", "NA",
  "cancer <-> cancer", "e4", "NA",
  "breath <-> breath", "e1", "NA",
  "teeth <-> teeth", "e2", "NA",
  "fingers <-> fingers", "e3", "NA",
  "teeth <-> fingers", "r12", "NA",
  "teeth <-> breath", "r13", "NA",
  "fingers <-> breath",
  "r23", "NA"), ncol=3, byrow=TRUE)

sem.can5 <- sem(model.5, cancer, 400)
```

# Fit is fine

```
> summary(sem.can5,digits=2)
```

```
Model Chisquare = 2.8    Df = 2 Pr(>Chisq) = 0.25  
Chisquare (null model) = 357    Df = 6  
Goodness-of-fit index = 1  
Adjusted goodness-of-fit index = 0.98  
RMSEA index = 0.031    90% CI: (NA, 0.11)  
Bentler-Bonnett NFI = 1  
Tucker-Lewis NNFI = 1  
Bentler CFI = 1  
SRMR = 0.017  
BIC = -9.2
```

# Regression betas are wrong

## Parameter Estimates

|         | Estimate | Std Error | z value | Pr(> z ) |                     |
|---------|----------|-----------|---------|----------|---------------------|
| a1      | 0.18     | 0.019     | 9.6     | 0.0e+00  | cancer <--- breath  |
| e4      | 0.81     | 0.058     | 14.1    | 0.0e+00  | cancer <--> cancer  |
| e1      | 1.00     | 0.071     | 14.1    | 0.0e+00  | breath <--> breath  |
| e2      | 1.00     | 0.071     | 14.1    | 0.0e+00  | teeth <--> teeth    |
| e3      | 1.00     | 0.071     | 14.1    | 0.0e+00  | fingers <-->        |
| fingers |          |           |         |          |                     |
| r12     | 0.42     | 0.054     | 7.7     | 1.0e-14  | fingers <--> teeth  |
| r13     | 0.56     | 0.057     | 9.8     | 0.0e+00  | breath <--> teeth   |
| r23     | 0.48     | 0.056     | 8.6     | 0.0e+00  | breath <--> fingers |

# But residuals are small

```
> round(residuals(sem.can5), 2)
```

|         | breath | teeth | fingers | cancer |
|---------|--------|-------|---------|--------|
| breath  | 0.00   | 0     | 0.00    | 0.04   |
| teeth   | 0.00   | 0     | 0.00    | 0.00   |
| fingers | 0.00   | 0     | 0.00    | -0.04  |
| cancer  | 0.04   | 0     | -0.04   | 0.00   |

# Base model and simplified model do not differ

```
> anova(sem.can, sem.can5)
```

LR Test for Difference Between Models

|         | Model | Df | Model | Chisq    | Df | LR     | Chisq | Pr(>Chisq) |
|---------|-------|----|-------|----------|----|--------|-------|------------|
| Model 1 |       | 0  |       | 4.43e-14 |    |        |       |            |
| Model 2 |       | 2  |       | 2.7758   | 2  | 2.7758 |       | 0.2496     |

# 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

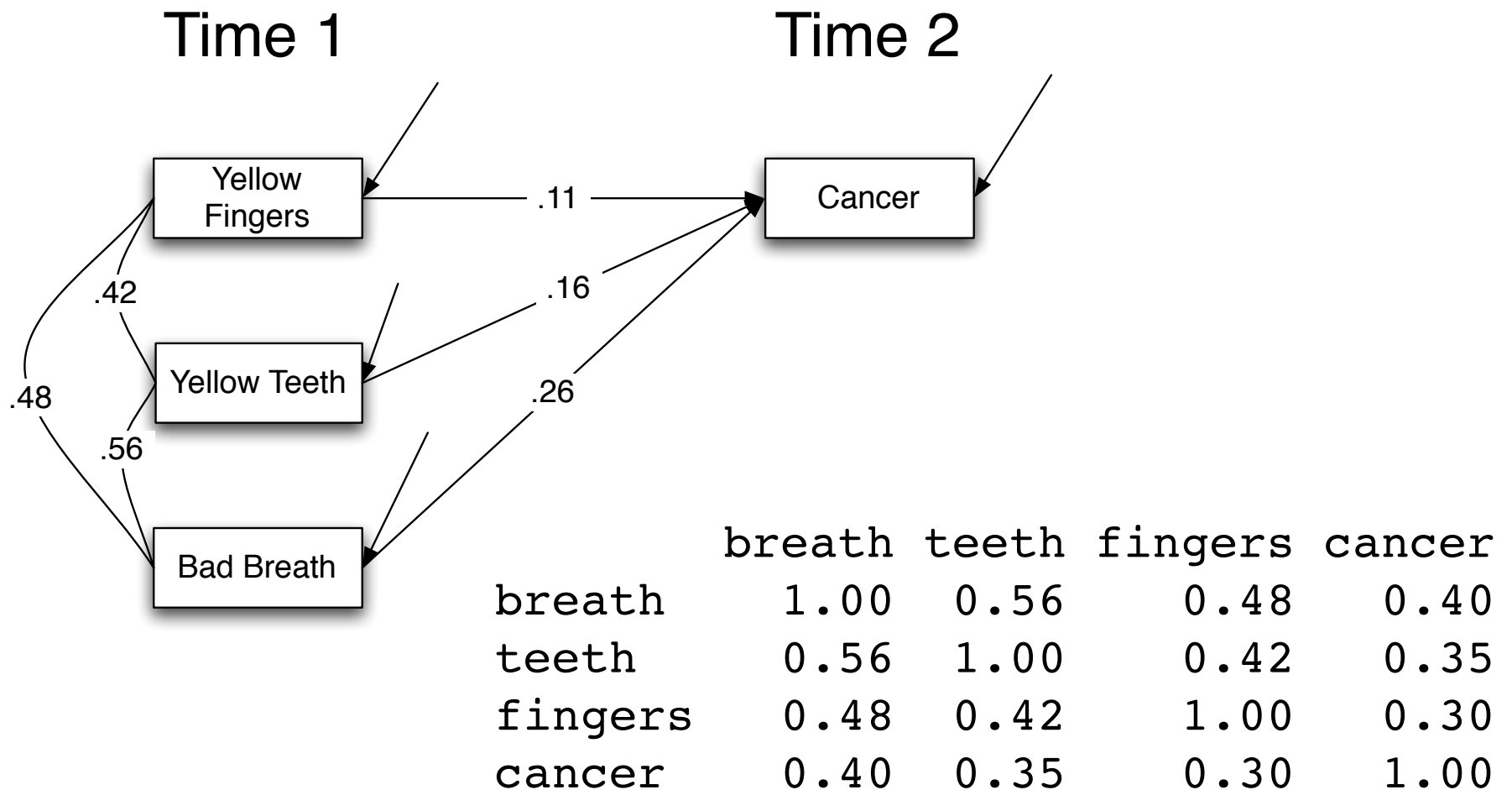
## Normalized Residuals

| 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  |

# Three predictors



# Residuals show the problem

```
> round(residuals(sem.can1), 2)
```

|         | breath | teeth | fingers | cancer |
|---------|--------|-------|---------|--------|
| breath  | 0.00   | 0.56  | 0.48    | 0.14   |
| teeth   | 0.56   | 0.00  | 0.42    | 0.19   |
| fingers | 0.48   | 0.42  | 0.00    | 0.19   |
| cancer  | 0.14   | 0.19  | 0.19    | 0.09   |

# 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.y <- matrix(c(
  "breath -> cancer", "a1", "NA",
  "teeth -> cancer", "a2", "NA",
  "fingers -> cancer", "a3", "NA",
  "yellow -> breath", "y1", "NA",
  "yellow -> teeth", "y2", "NA",
  "yellow -> fingers", "y3", "NA",
  "yellow <-> yellow", "NA", "1",
  "cancer <-> cancer", "e1", "NA",
  "breath <-> breath", "e2", "NA",
  "teeth <-> teeth", "e3", "NA",
  "fingers <-> fingers", "NA", "1"), ncol=3, byrow=TRUE)

sem.yellow <- sem(model.y, cancer, 400)
```

# But this is just the regression

Model Chisquare = 4e-10 Df = 0 Pr(>Chisq) = NA

Chisquare (null model) = 357 Df = 6

Goodness-of-fit index = 1

BIC = 4e-10

## Parameter Estimates

|    | Estimate | Std Error | z value | Pr(> z ) |                     |
|----|----------|-----------|---------|----------|---------------------|
| a1 | 0.26     | 0.057     | 4.5     | 6.9e-06  | cancer <--- breath  |
| a2 | 0.16     | 0.056     | 2.9     | 4.1e-03  | cancer <--- teeth   |
| a3 | 0.11     | 0.052     | 2.1     | 3.8e-02  | cancer <--- fingers |
| y1 | 1.00     | 0.076     | 13.2    | 0.0e+00  | breath <--- yellow  |
| y2 | 0.88     | 0.079     | 11.1    | 0.0e+00  | teeth <--- yellow   |
| y3 | 0.75     | 0.083     | 9.0     | 0.0e+00  | fingers <--- yellow |
| NA | 0.64     | 0.056     | 11.4    | 0.0e+00  | yellow <--> yellow  |

# Yellow as mediator

```
> model.yell <- matrix(c(
+   "yellow -> cancer", "Y", "NA",
+   "yellow -> breath", "y1", "NA",
+   "yellow -> teeth", "y2", "NA",
+   "yellow -> fingers", "y3", "NA",
+   "yellow <-> yellow", "NA", "1",
+   "cancer <-> cancer", "e1", "NA",
+   "breath <-> breath", "e2", "NA",
+   "teeth <-> teeth", "e3", "NA",
+   "fingers <-> fingers", "NA",
+   "1"), ncol=3, byrow=TRUE)
>
> sem.yellow <- sem(model.yell, cancer, 400)
```

# Fit is very good

```
> summary(sem.yellow,digits=2)
```

```
Model Chisquare = 8.4e-10    Df = 2 Pr(>Chisq) = 1  
Chisquare (null model) = 357    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 = 1.0  
Bentler CFI = 1  
SRMR = 6.9e-07  
BIC = -12
```

# Parameters are hard to interpret

## Parameter Estimates

|        | Estimate | Std Error | z value | Pr(> z ) |                    |
|--------|----------|-----------|---------|----------|--------------------|
| Y      | 0.63     | 0.072     | 8.7     | 0.0e+00  | cancer <--- yellow |
| y1     | 1.00     | 0.073     | 13.8    | 0.0e+00  | breath <--- yellow |
| y2     | 0.87     | 0.074     | 11.8    | 0.0e+00  | teeth <--- yellow  |
| y3     | 0.75     | 0.080     | 9.4     | 0.0e+00  | fingers <---       |
| yellow |          |           |         |          |                    |
| NA     | 0.64     | 0.054     | 11.7    | 0.0e+00  | yellow <--> yellow |
| e1     | 0.75     | 0.059     | 12.8    | 0.0e+00  | cancer <--> cancer |
| e2     | 0.36     | 0.054     | 6.7     | 2.8e-11  | breath <--> breath |
| e3     | 0.51     | 0.052     | 9.8     | 0.0e+00  | teeth <--> teeth   |

# But standardized paths are easy to understand

```
> std.coef(sem.yellow)
```

|    |    | Std. Estimate |                     |
|----|----|---------------|---------------------|
| Y  | Y  | 0.5           | cancer <--- yellow  |
| y1 | y1 | 0.8           | breath <--- yellow  |
| y2 | y2 | 0.7           | teeth <--- yellow   |
| y3 | y3 | 0.6           | fingers <--- yellow |

# But paths are ok

## Parameter Estimates

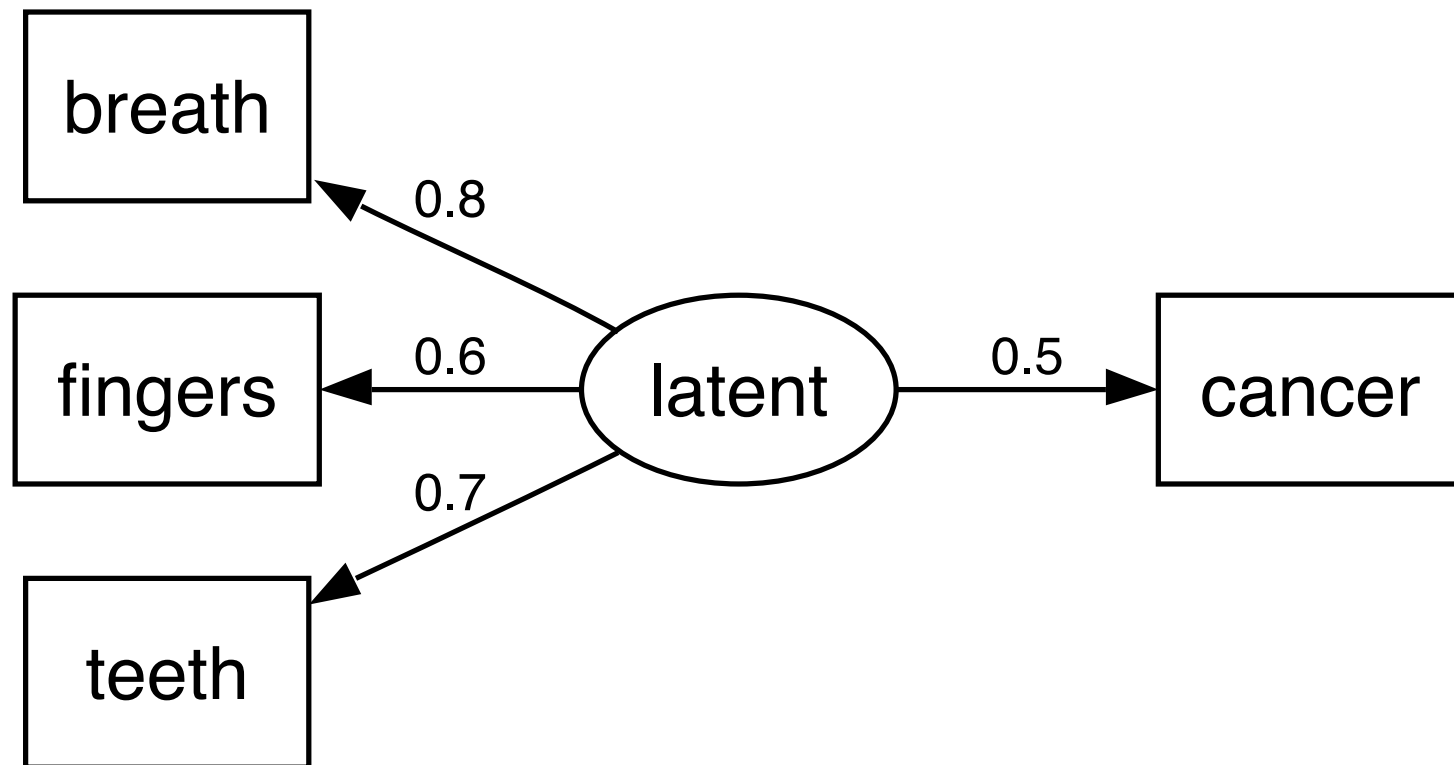
|    | Estimate | Std Error | z value  | Pr(> z ) |                      |
|----|----------|-----------|----------|----------|----------------------|
| 1  | 1.1e-01  | 0.11      | 1.0e+00  | 3.0e-01  | cancer <--- fingers  |
| 2  | 1.6e-01  | 0.11      | 1.4e+00  | 1.5e-01  | cancer <--- teeth    |
| 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 mouth and yellow

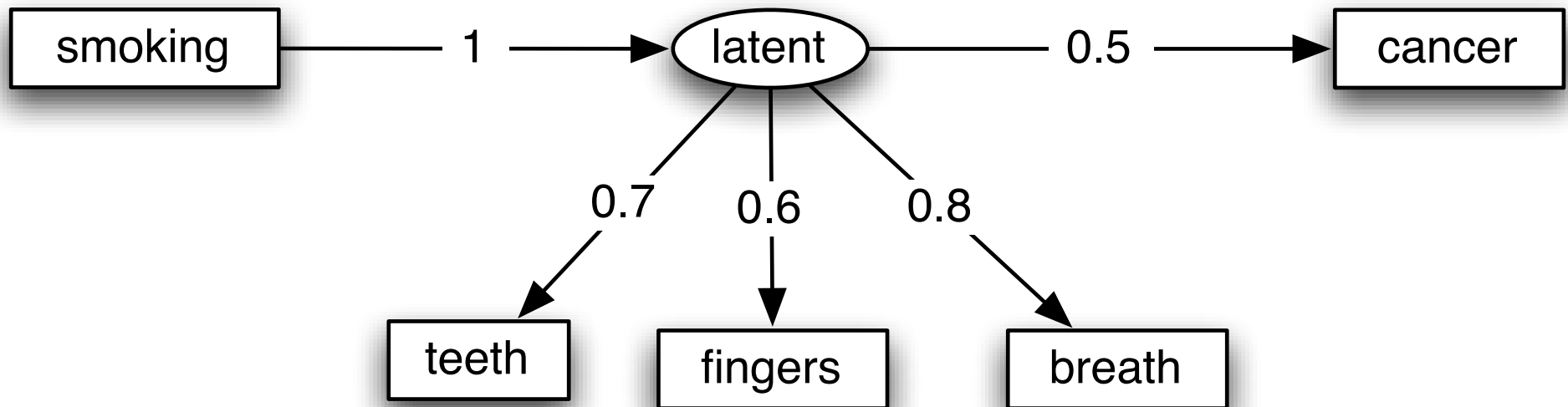
model.6

|       | [,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"  |

# SEM alternative: but what is the latent?



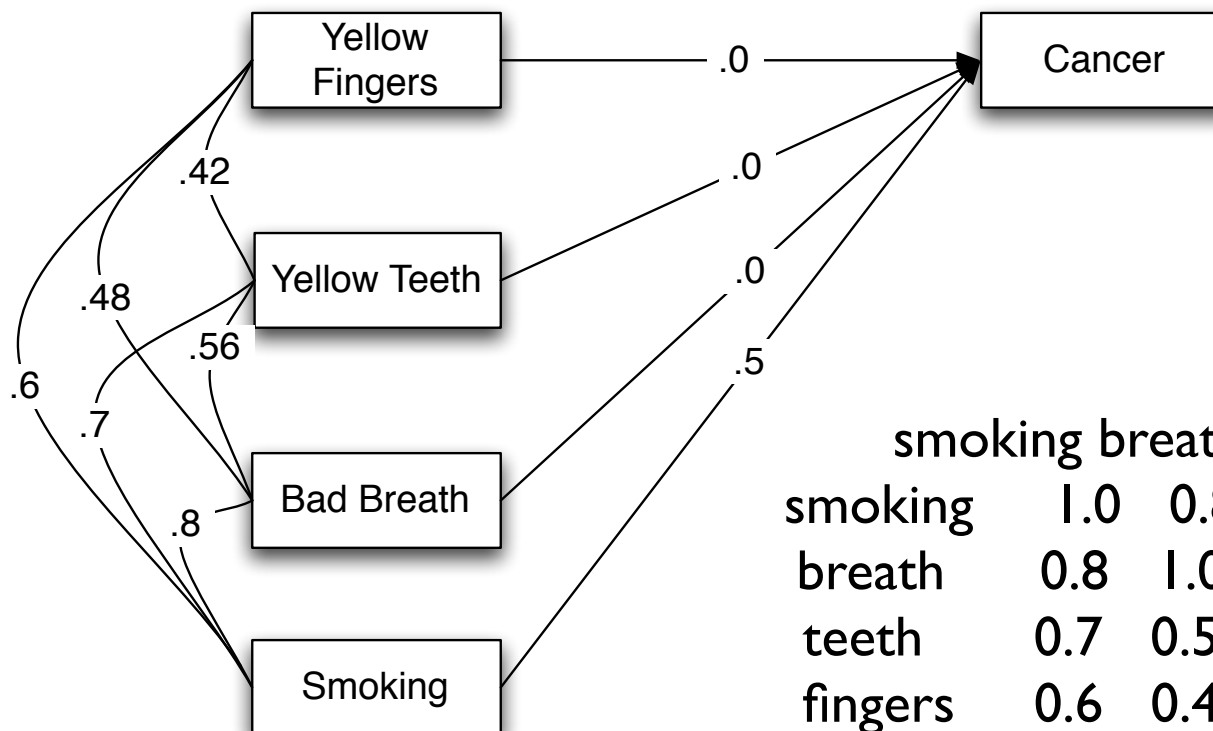
# Smoking is measured perfectly



# Properly specified

Time 1

Time 2

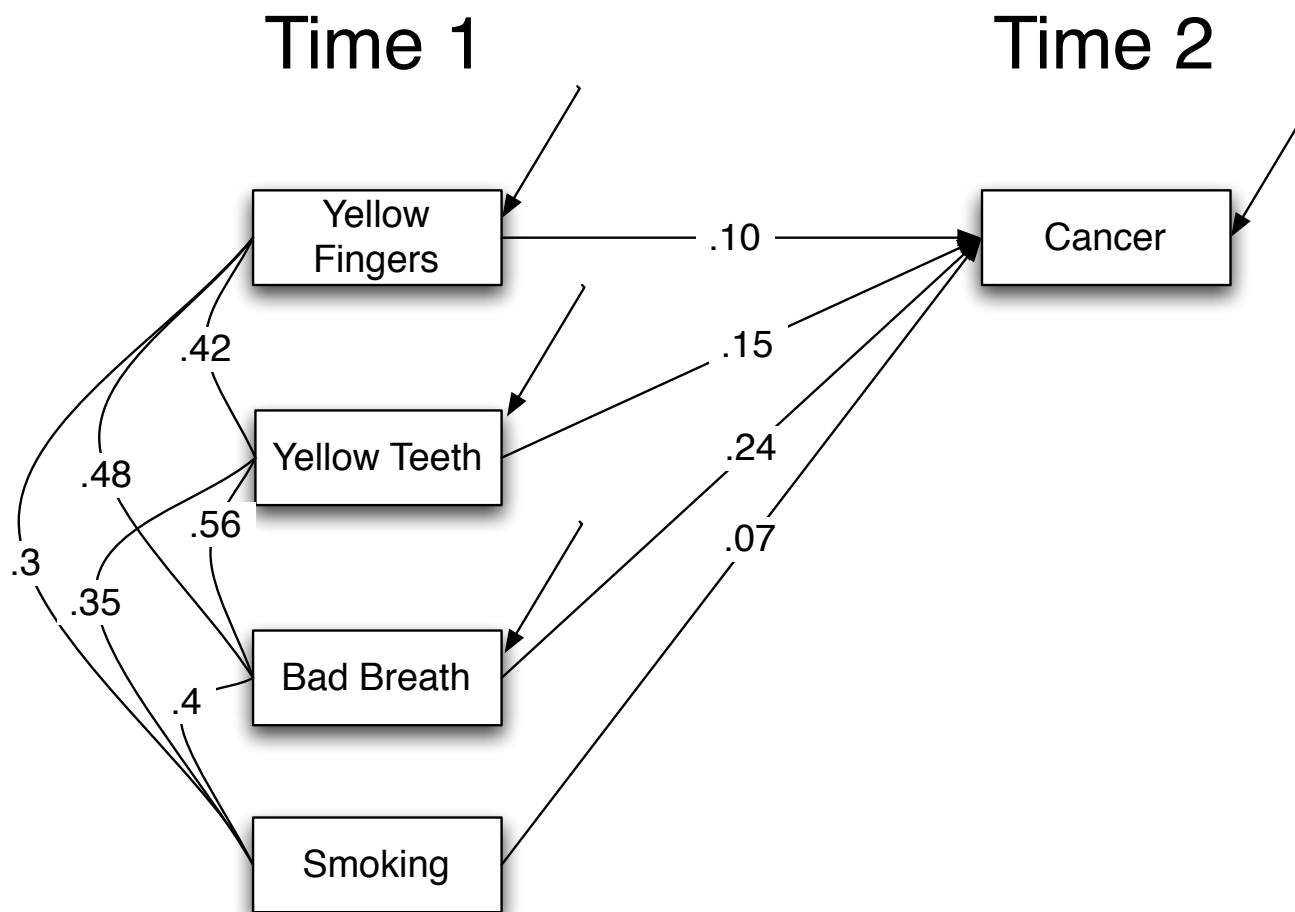


|         | smoking | breath | teeth | fingers | cancer |
|---------|---------|--------|-------|---------|--------|
| smoking | 1.0     | 0.80   | 0.70  | 0.60    | 0.50   |
| breath  | 0.8     | 1.00   | 0.56  | 0.48    | 0.40   |
| teeth   | 0.7     | 0.56   | 1.00  | 0.42    | 0.35   |
| fingers | 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)

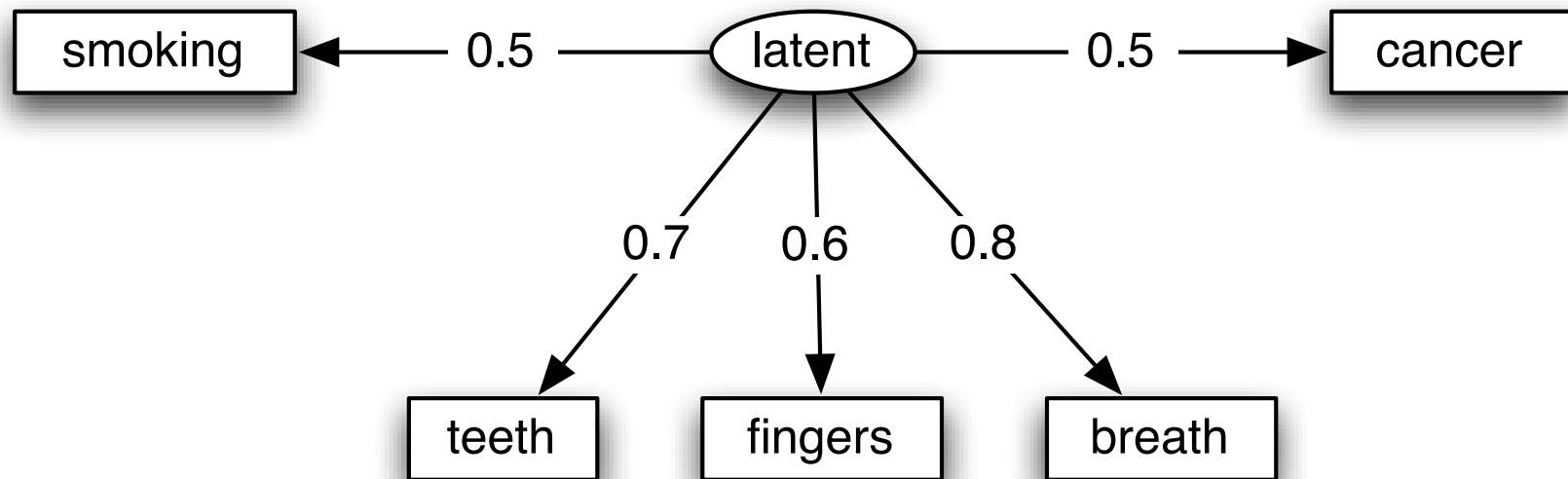
Bentler-Bonnett NFI = 1

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

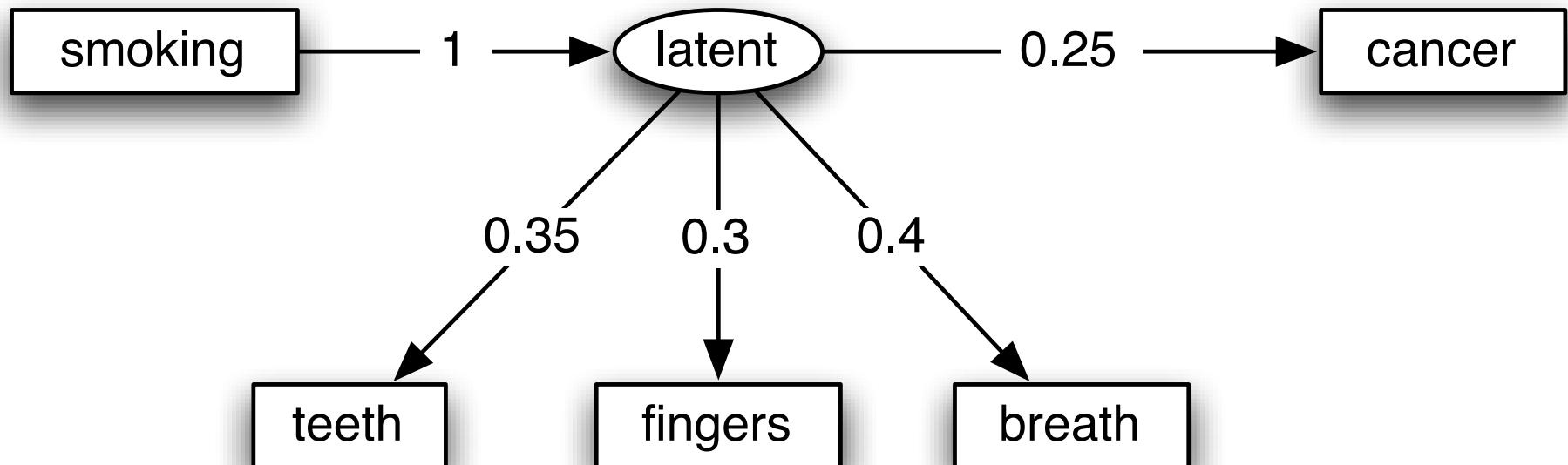
Bentler CFI = 1

BIC = -28

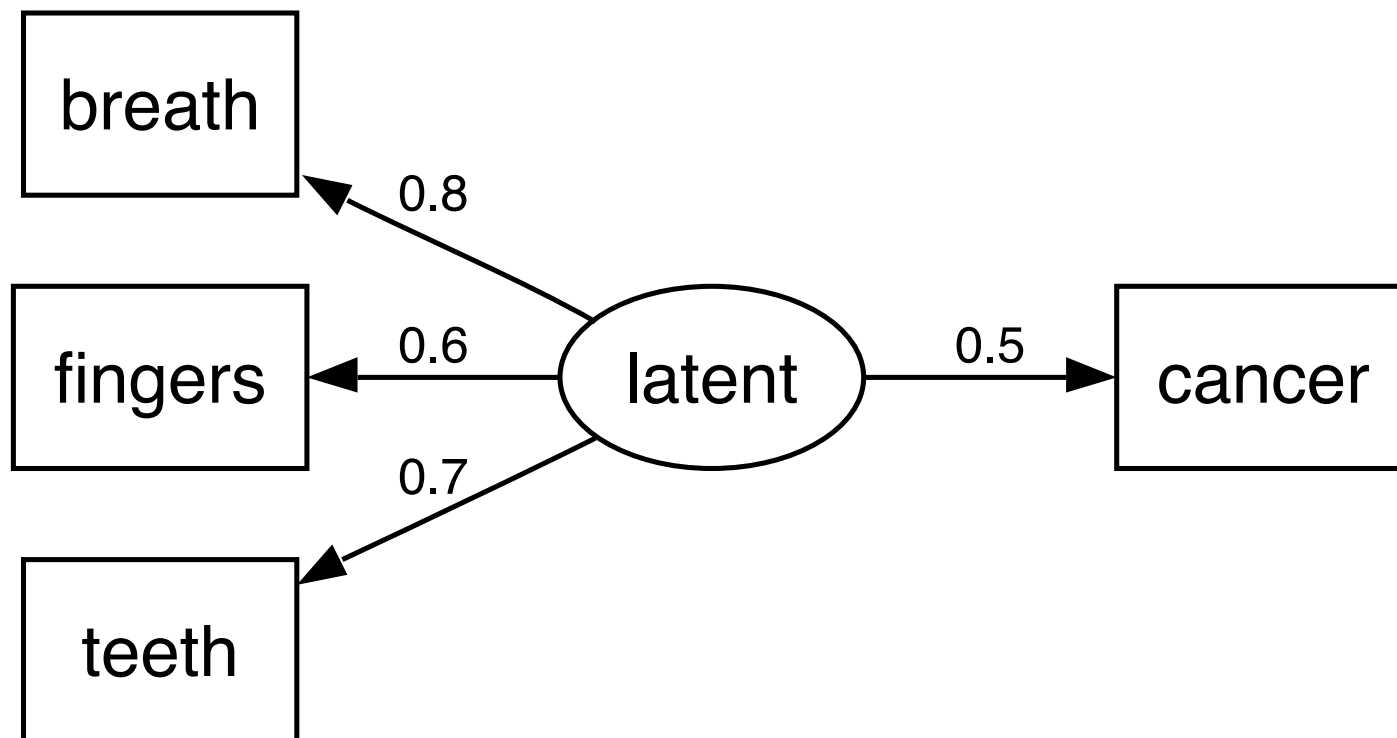
# “Imperfect” smoking, modeled with no error

|    | 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   |

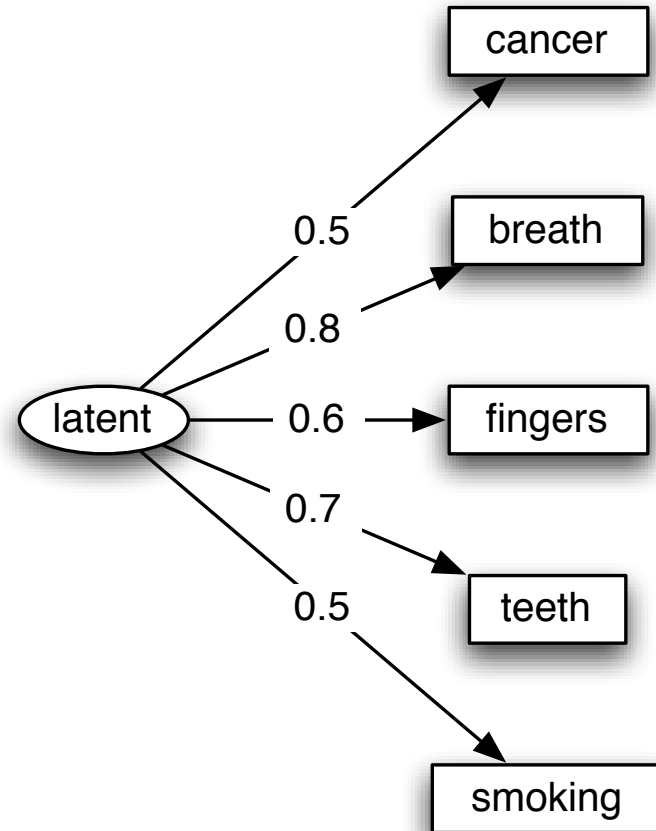
# Smoking is not measured perfectly



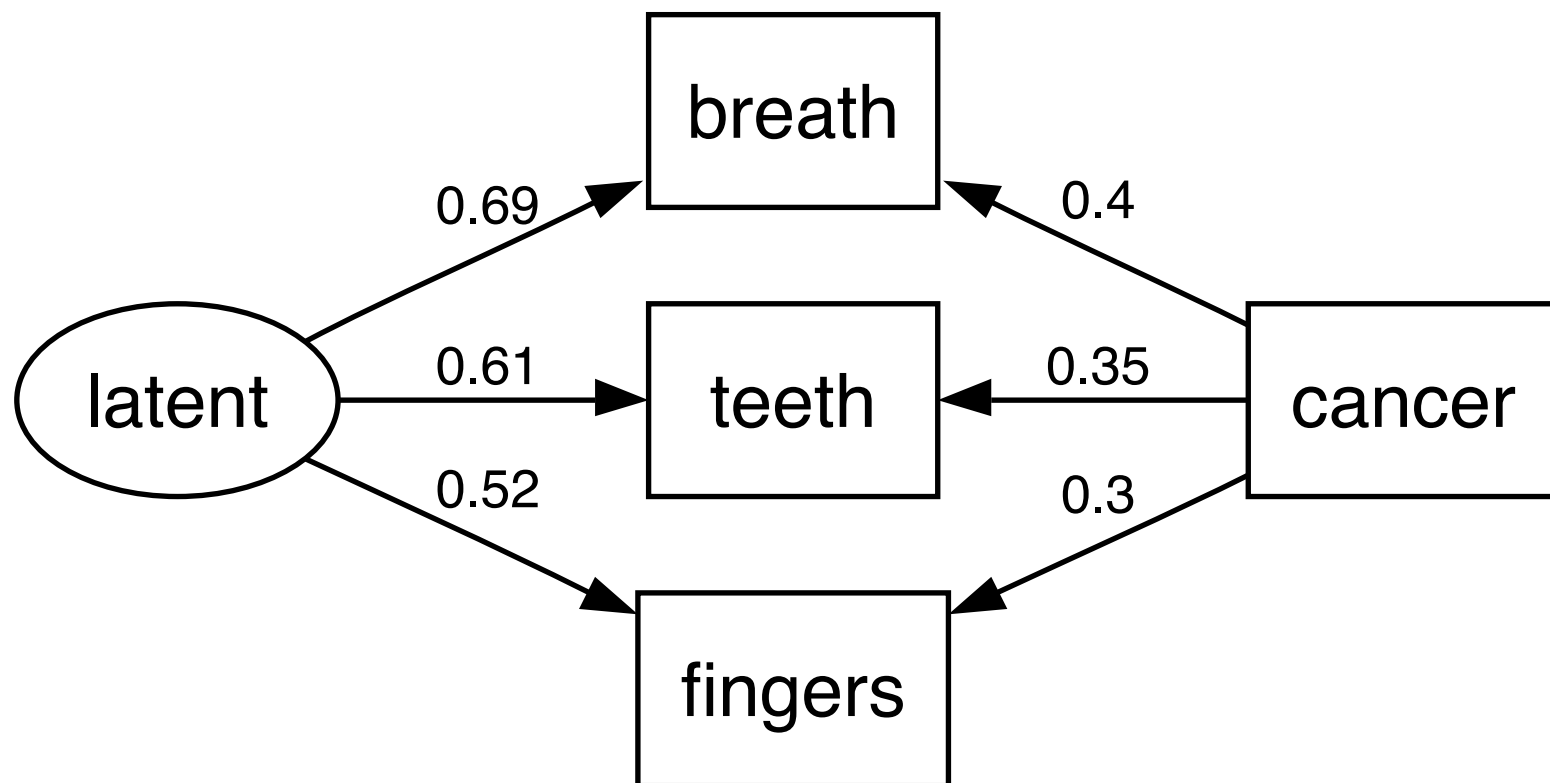
# What is the causal variable



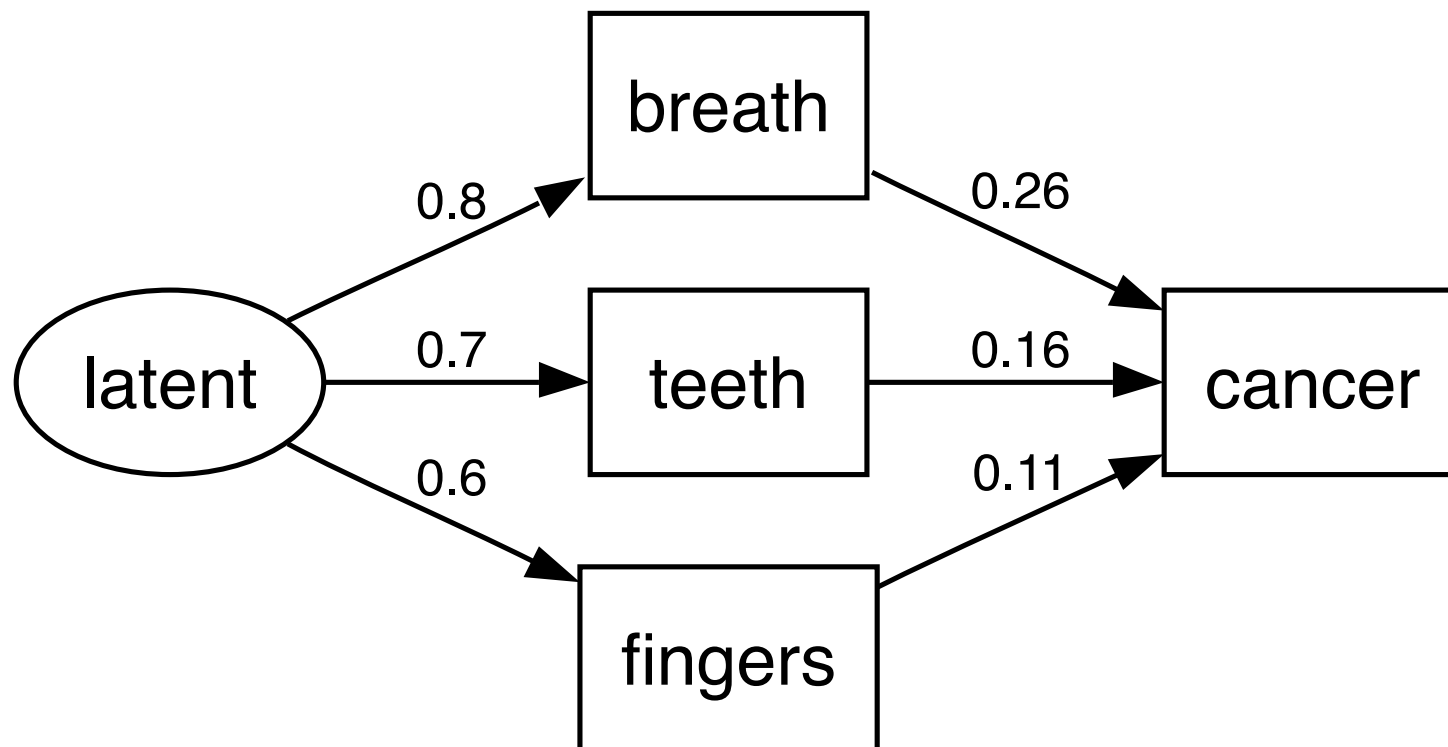
# Something causes one to smoke and get cancer: is it E?



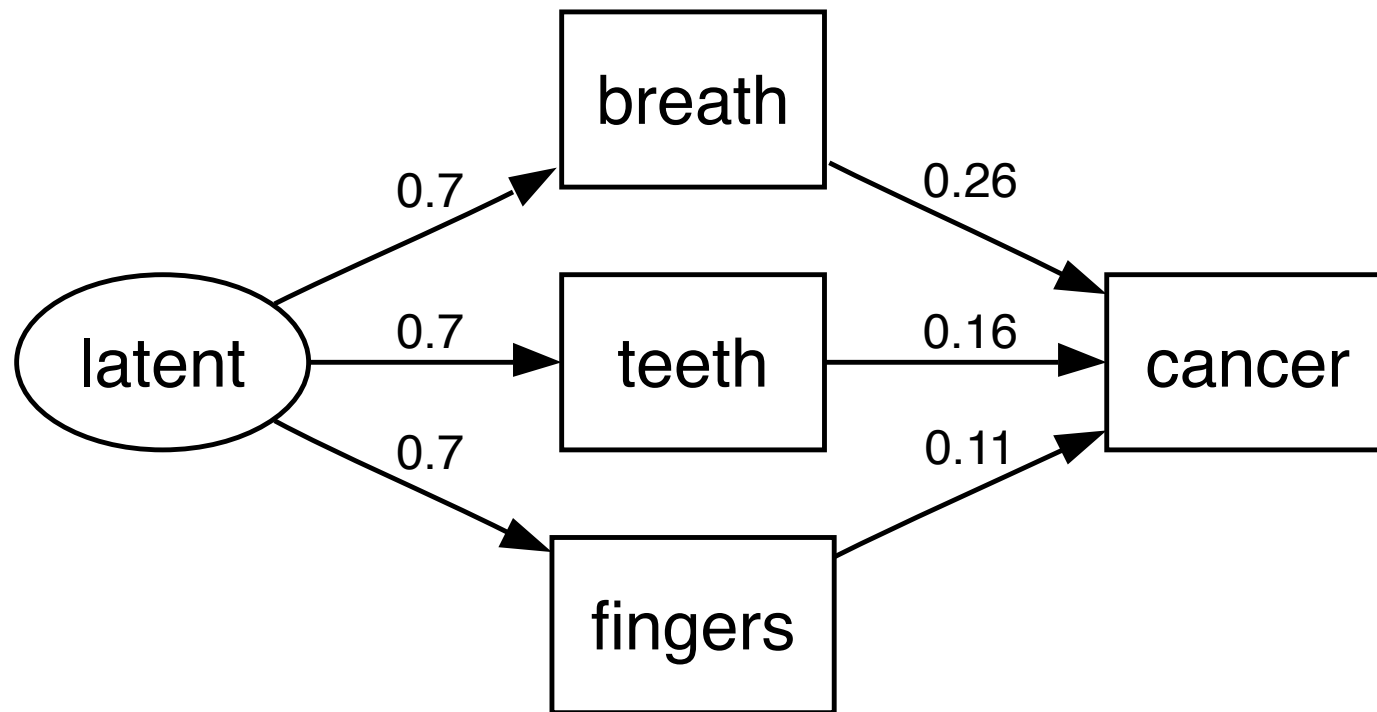
# Cancer as cause

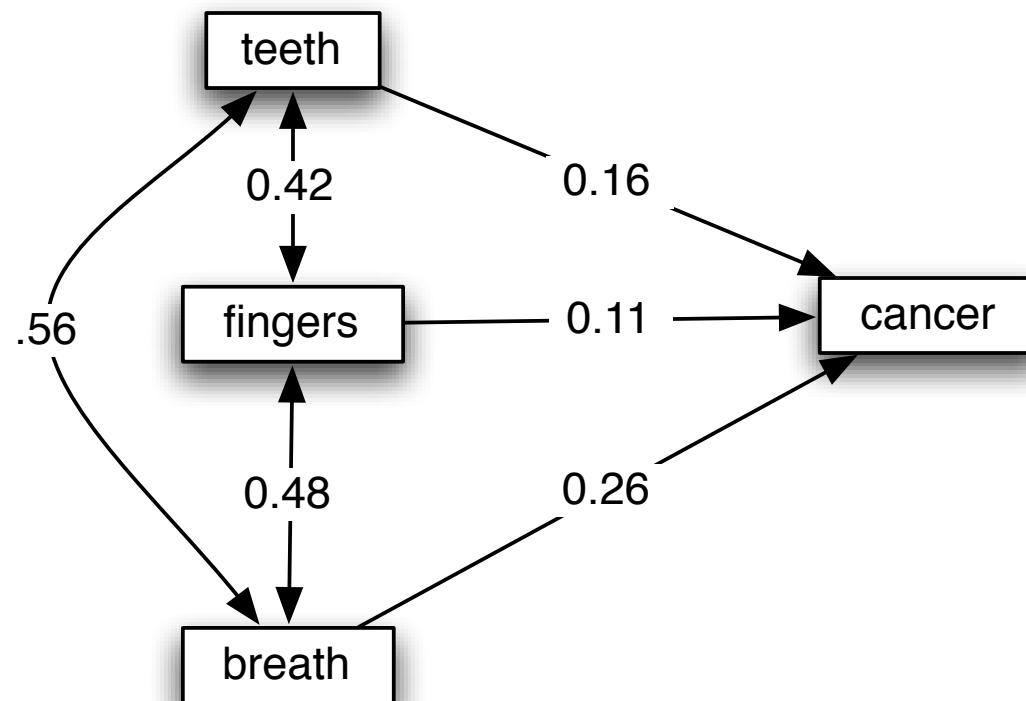


# Cancer as caused



# Cancer as caused:equal error





# 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)

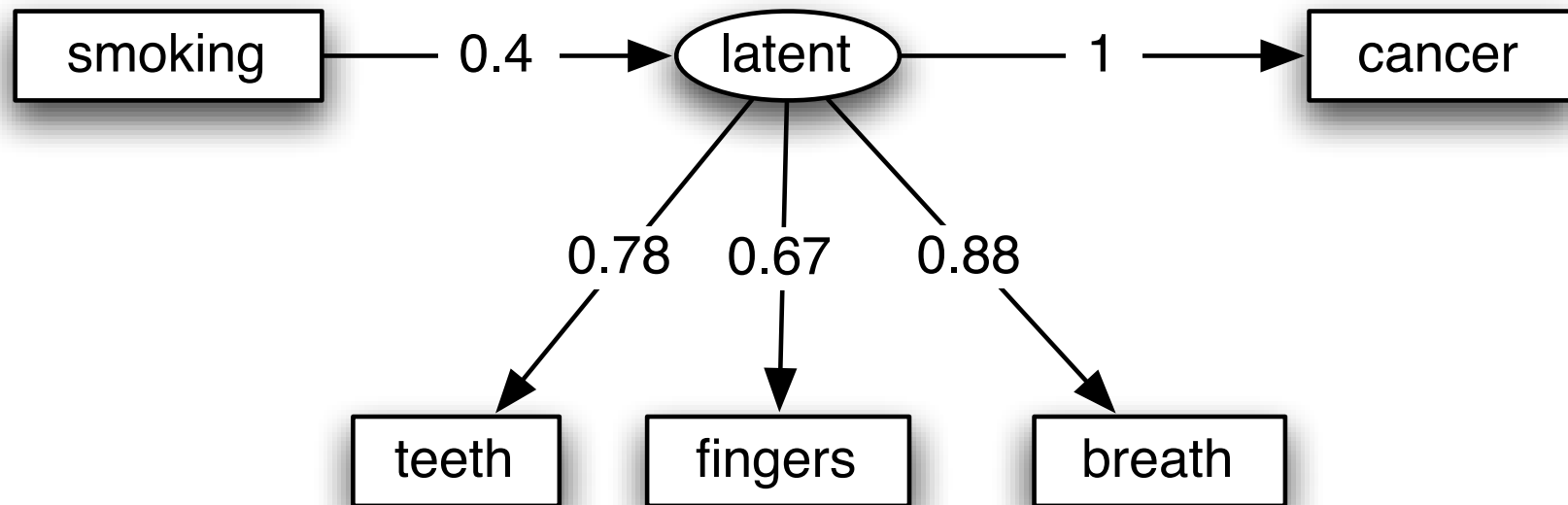
Bentler-Bonnett NFI = 0.76

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

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

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

II. Penalizes models for estimating more parameters

III.a “parsimony” correction

# Comparative Fit Index

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

II. CFI = 
$$\frac{d(\text{Null}) - d(\text{model})}{d(\text{model})}$$

# Root Mean Square Error of Approximation (RMSEA)

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

II.  $RMSEA = \sqrt{\{(\text{Chi}^2/df - 1)/(N - 1)\}}$

III. if  $\text{Chi square} < df$  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  $p(\text{RMSEA} > .05) > .05$

# 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

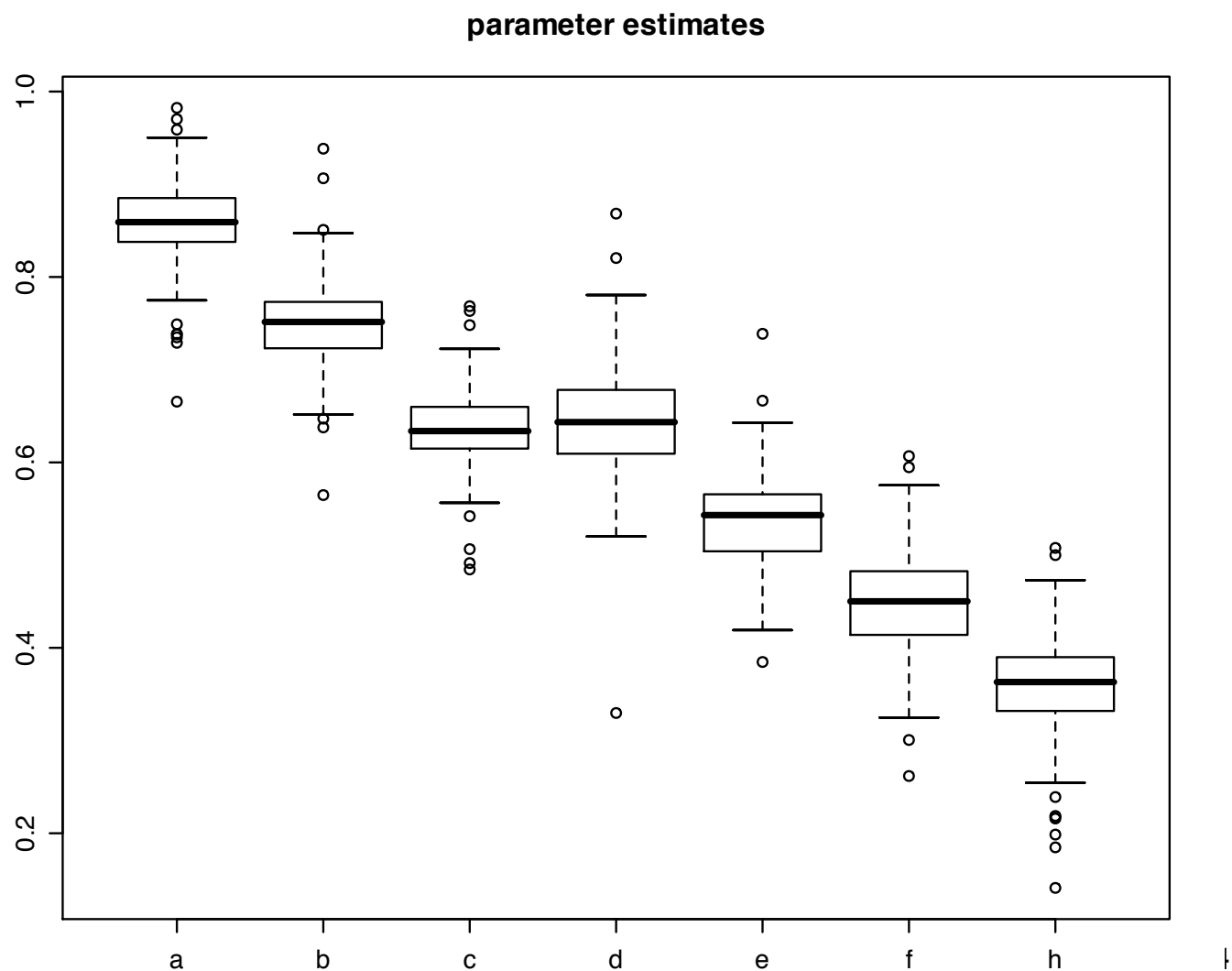
# Examples of fit (2 factors - 6 variables)

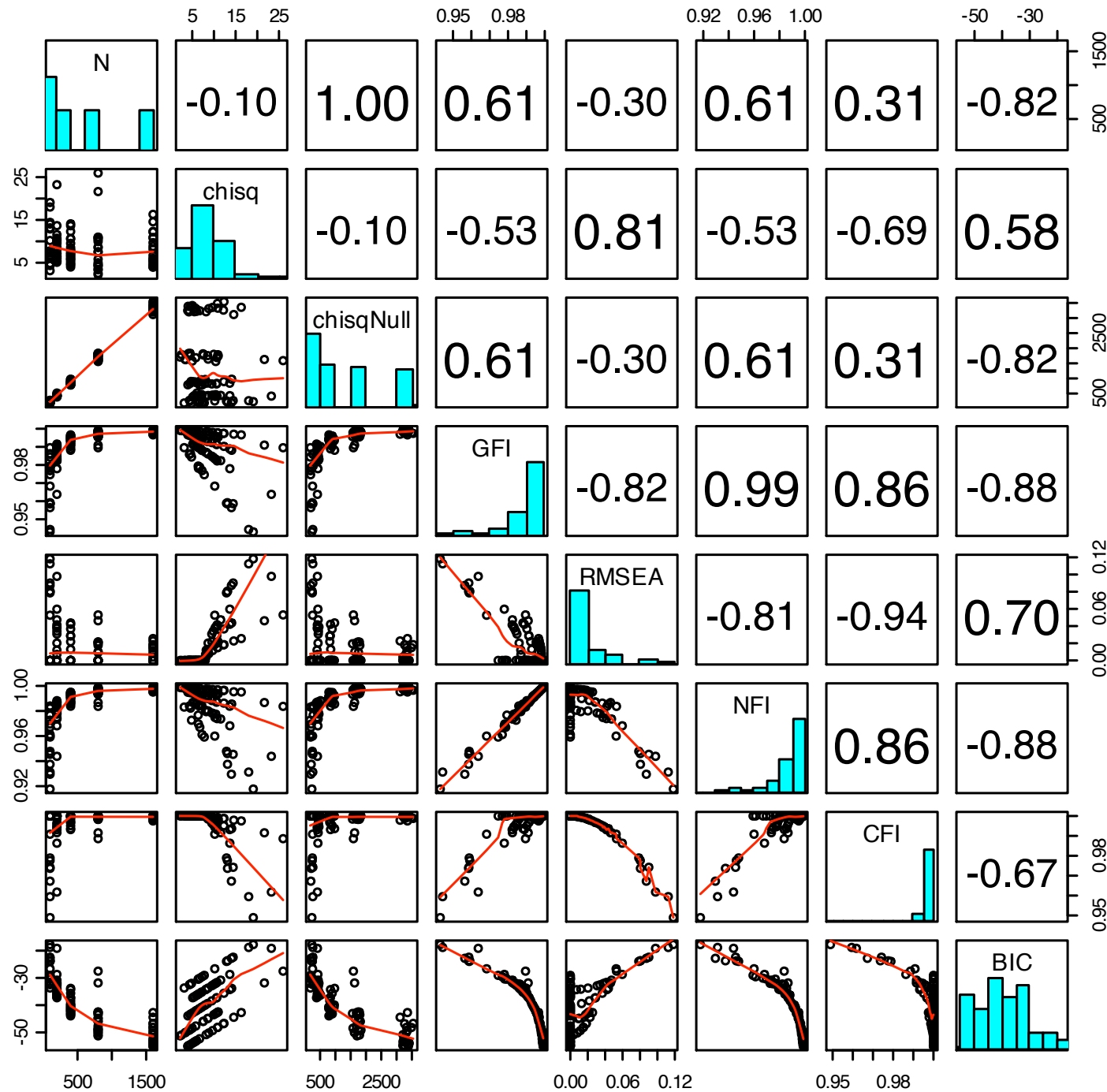
- I. Monte Carlo simulation of 100, 200, 400, 800, 1600 subjects
- II. 2 factors with 6 variables (see chapter 2)
- III. Plot parameter estimates
- IV. Plot correlations of size of estimates

# 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,

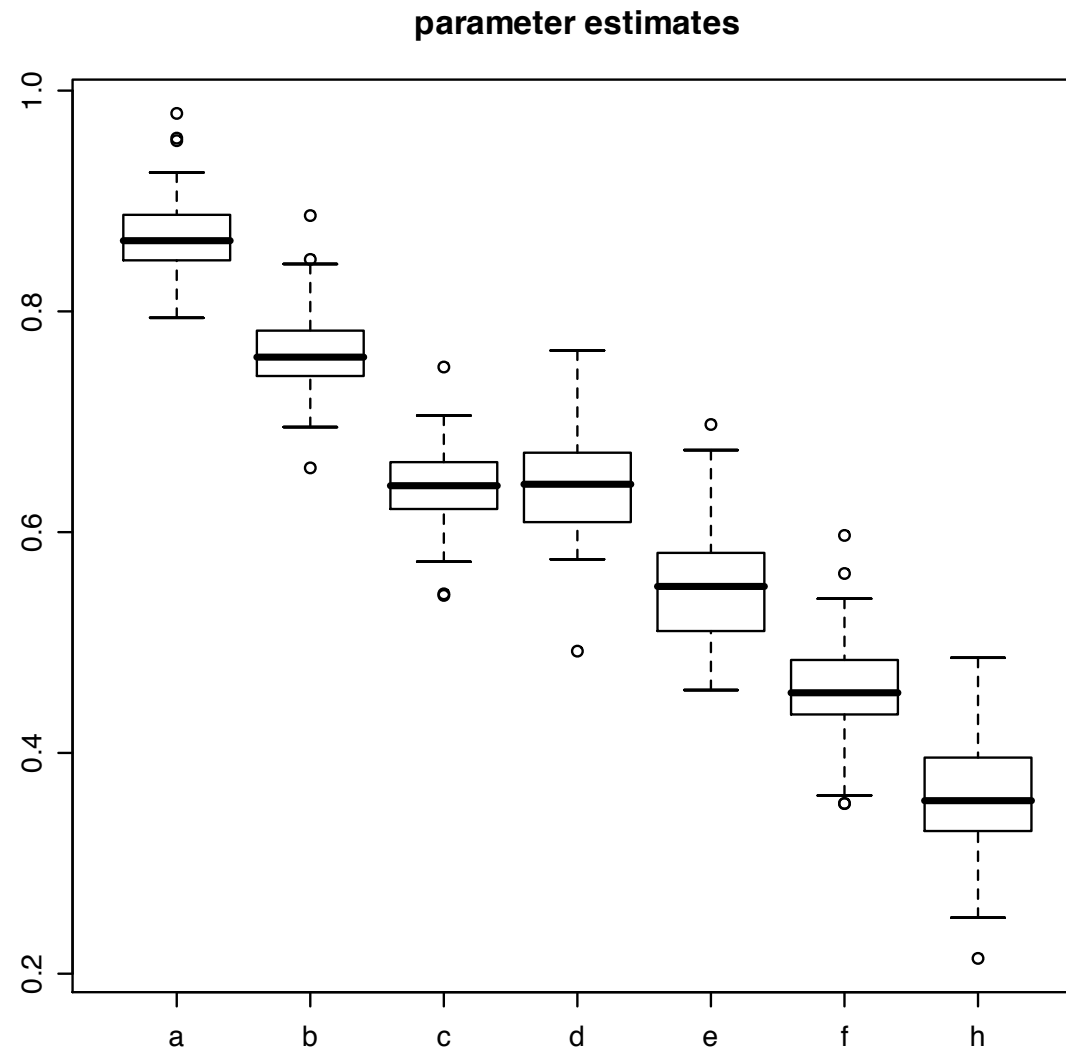
200,

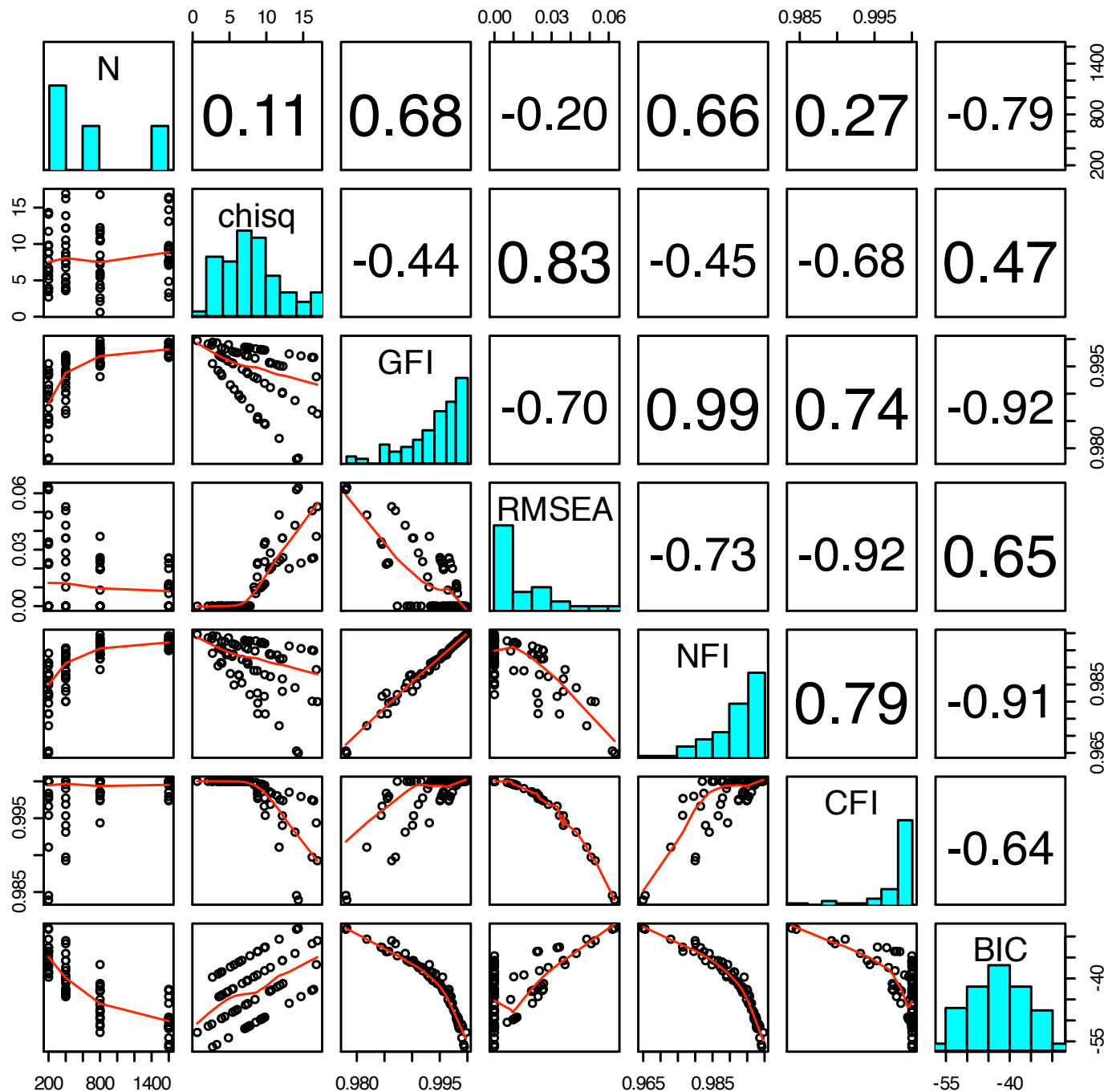
400,

800,

1600

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

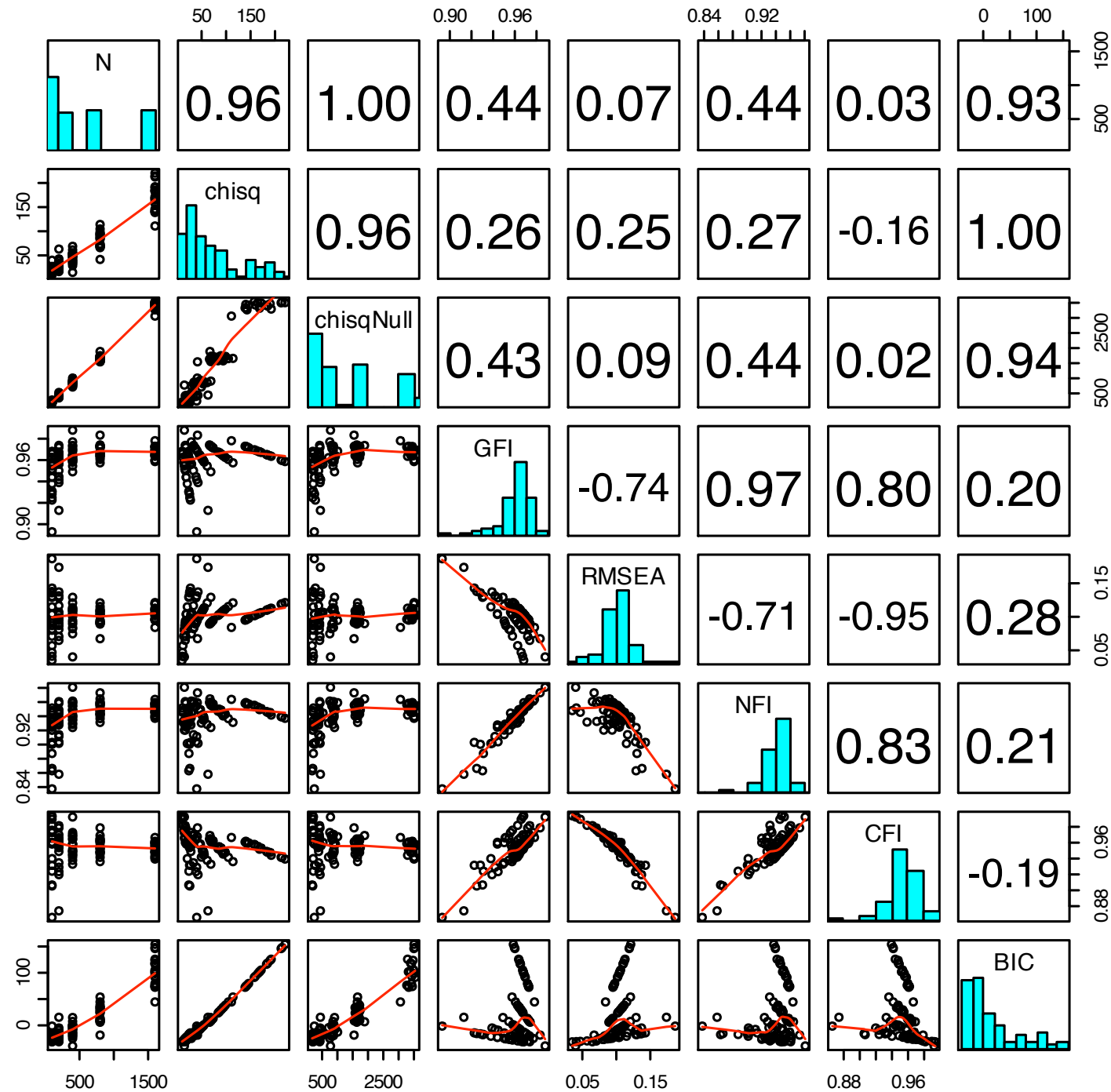




$n=$   
200,  
400,  
800,  
1600

# 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



# 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