

Chapter 6: Evaluating models

William Revelle

Northwestern University

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Abstract

Evaluating model fit in SEM may be done by examining the various indices of fit and misfit supplied by the programs used. The R `sem` package provides 8 indices which we will discuss in this chapter. LISREL, EQS, and Mplus provide even more.

However, the goodness of fit statistics do not address fundamental errors in model specification. The first part of the chapter address errors in model specification. The latter part of the chapter addresses measures of fit.

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Evaluating model fit in SEM may be done by examining the various indices of fit and misfit supplied by the programs used. The R `sem` package provides 8 indices which we will discuss in this chapter. LISREL, EQS, and Mplus provide even more.

However, before considering the various indices of fit, it is important to consider the reasons that models do not fit.

1. Errors in theory
 - (a) Failure to include the appropriate variables
 - (b) Failure to model the appropriate relationships
2. Errors in assumptions
 - (a) Problems in distributions
 - (b) Methods or correlated error factors

6.1 Model misspecification: failure to include variables

A classic problem in statements of causal structure is the failure to include appropriate variables. Such model misspecification is the bane of using correlations to infer anything about causality, for there is always the lurking third variable that could explain the relationship.

In an attempt to demonstrate this effect, consider the correlation between three variables at time 1 as predictors of an important outcome at time 2. The measured variables at time 1 are Yellow Fingers, Yellow Teeth and Bad Breath. The outcome variable is probability of Lung Cancer (rescored with a logistic transformation to be a continuous variable ranging from -3 to 3.)¹

For the purposes of this demonstration, we create an artificial correlation matrix of these four variables by defining a latent variable, θ , with factor loadings θ . The product of $\theta\theta^T$ is the observed correlation matrix:

```
> theta <- matrix(c(0.8, 0.7, 0.6, 0.5), nrow = 4)
> observed <- theta %*% t(theta)
> diag(observed) <- 1
> rownames(observed) <- colnames(observed) <- c("breath", "teeth",
+       "fingers", "cancer")
> observed
```

	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

6.1.1 Misspecified Linear Regression

Using classical linear regression, we can predict cancer risk given 1, 2, or 3 predictors. To do this from the observed correlation matrix, we can use the `solve` function in base R, or alternatively the `mat.regress` function in the `psych` package. This latter function will take a correlation matrix and then find the beta weights for a set of X predictors of Y variables. We do this multiple times, first to regress smoking on yellow fingers, then upon yellow teeth and yellow fingers, and then finally, on breath, yellow teeth and yellow fingers. Finally, compare the `mat.regress` output with using the `solve` function.

Remember to load the `psych` package before running this analysis.

¹As I hope is obvious, this is an artificial example. It was inspired, in part, by the webpage on causal and statistical reasoning at Carnegie Mellon University (www.cmu.edu/CSR/index.html)

```

> library(psych)
> mat.regress(observed, 3, 4)
$beta
fingers
  0.3

$R2
cancer
  0.09
> mat.regress(observed, c(2, 3), 4)
$beta
  teeth fingers
  0.27   0.19

$R2
cancer
  0.15
> mat.regress(observed, c(1:3), 4)
$beta
  breath  teeth fingers
  0.26   0.16   0.11

$R2
cancer
  0.19
> beta <- solve(observed[1:3, 1:3], observed[4, 1:3])
> round(beta, 2)
  breath  teeth fingers
  0.26   0.16   0.11

```

Note how the beta weight for yellow fingers decreases as we add more variables into the model. The final model with all three predictors may be summarized as in Figure 6.1.

6.1.2 Regression with the correct variables included

We can restate the θ term in the generating model (6.1) as “smoking” and generate the correlation matrix again, as well as the regressions. This time we add the “smoking” variable with a loading of 1.0 on the latent variable.

```

> theta <- matrix(c(1, 0.8, 0.7, 0.6, 0.5), nrow = 5)
> observed <- theta %*% t(theta)
> diag(observed) <- 1
> rownames(observed) <- colnames(observed) <- c("smoking", "breath",
+       "teeth", "fingers", "cancer")
> observed
      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
> mat.regress(observed, 4, 5)
$beta
fingers
  0.3

```

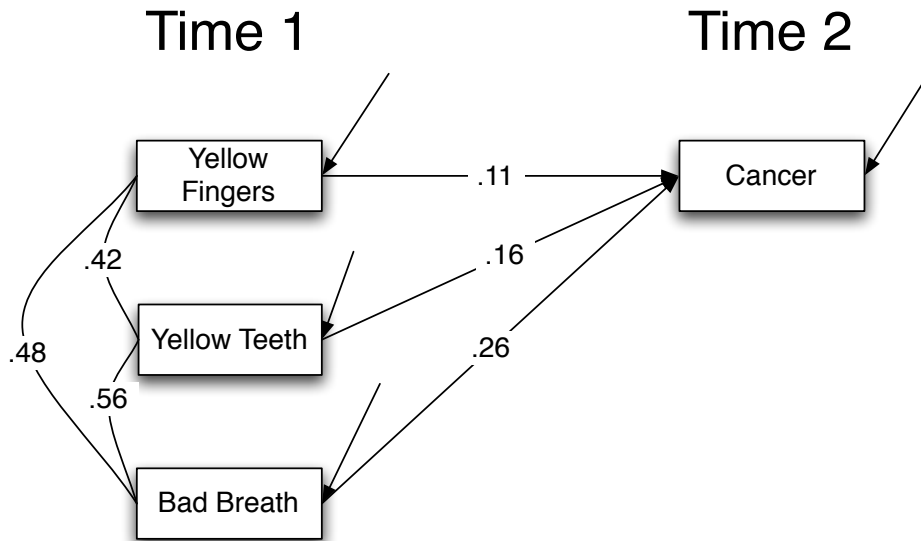


Figure 6.1: The direct and indirect effect of three predictors upon a criterion variable. The “real”, causal variable is missing from the model.

```

$R2
cancer
  0.09
> mat.regress(observed, c(3, 4), 5)
$beta
  teeth fingers
  0.27    0.19
  
```

```

$R2
cancer
  0.15
> mat.regress(observed, c(2:4), 5)
$beta
  breath  teeth fingers
  0.26    0.16    0.11
  
```

```

$R2
cancer
  0.19
> mat.regress(observed, c(1:4), 5)
$beta
smoking  breath  teeth fingers
  0.5     0.0    0.0    0.0
  
```

```

$R2
cancer
  0.25
  
```

Notice how if the model is correctly specified (i.e., the causal variable, smoking, is introduced), the beta weights for the non-causal variables go to zero. This is understandable

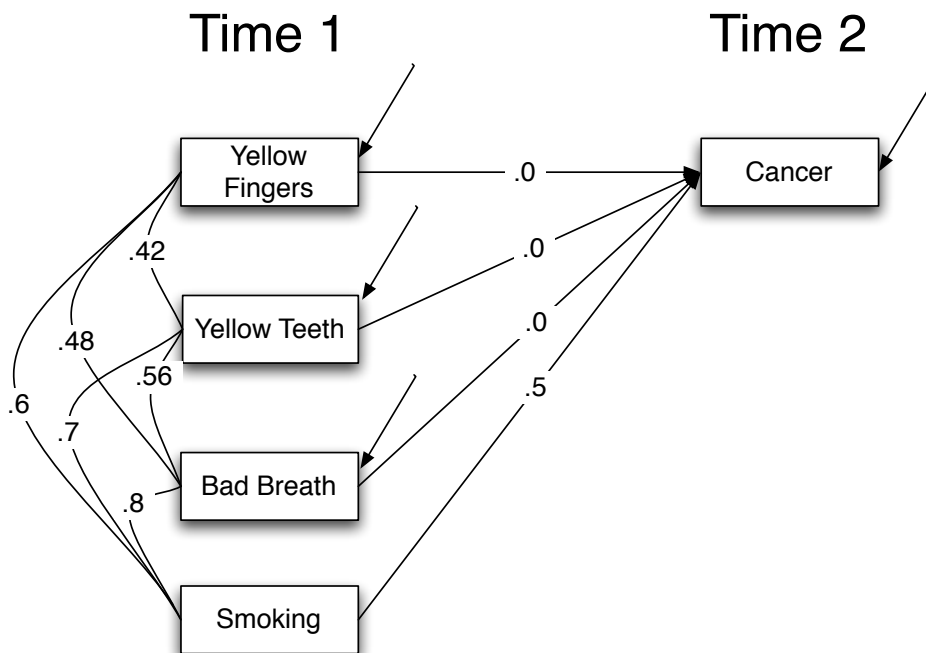


Figure 6.2: .

The direct and indirect effect of four predictors upon a criterion variable. If the “correct” causal variable is specified, the β weights of the remaining variables are reduced to zero. Compare the β weights with those in Figure 6.1

if we consider the beta weights in the two predictor case:

$$\left\{ \begin{array}{l} \beta_1 = (r_{x_1y}r_{x_2x_2} - r_{x_1x_2}r_{x_2y}) / (r_{x_1x_1}r_{x_2x_2} - r_{x_1x_2}^2) \\ \beta_2 = (r_{x_2y}r_{x_1x_1} - r_{x_1x_2}r_{x_1y}) / (r_{x_1x_1}r_{x_2x_2} - r_{x_1x_2}^2) \end{array} \right\} \quad (6.1)$$

In the more general case,

$$\beta R = r_{xy} \quad (6.2)$$

and we can solve 6.2 for β by multiplying both sides by the inverse of R.

$$\beta = \beta R R^{-1} = r_{xy} R^{-1} \quad (6.3)$$

In the two variable case (see Appendix 2), finding the inverse of a two by two matrix is discussed and is shown to be

$$R^{-1} = \begin{pmatrix} \frac{r_{22}}{r_{11}r_{22} - r_{12}^2} & -\frac{r_{12}}{r_{11}r_{22} - r_{12}^2} \\ -\frac{r_{12}}{r_{11}r_{22} - r_{12}^2} & \frac{r_{11}}{r_{11}r_{22} - r_{12}^2} \end{pmatrix} \quad (6.4)$$

6.1.3 Misspecified Structural Equation Models

The regression models in 6.1 are misspecified in that the “real” causal variable is not included in the model. This same problem can arise in structural equations. That is, we can fit the data very well with a model which is, in fact, incorrect. In parallel with the misspecification of the linear regression, compare a series of structural equation models. The first one is fully saturated (has no degrees of freedom), and models the effect of yellow fingers as leading to cancer. Note how we are using a subset of the correlation matrix. Remember to load the **sem** package before running this analysis.

one predictor

```

      path                parameter initial value
[1,] "fingers -> cancer"    "1"          NA
[2,] "fingers <-> fingers"  "5"          NA
[3,] "cancer <-> cancer"    "8"          NA
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

```

Iterations = 0

Note how the path coefficient for fingers -> cancer is identical to the beta weight found in the regression model for one predictor variable (and is, in the one predictor case equal, of course, to the zero order correlation). Also note that the unexplained variance of cancer is equal to $1 - r^2$.

Compare this result to the model that just models the correlation between yellow fingers and cancer:

```

      path                parameter initial value
[1,] "fingers <-> cancer"  "1"          NA
[2,] "fingers <-> fingers" "5"          NA
[3,] "cancer <-> cancer"   "8"          NA
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 0.3      0.10      2.9    4.2e-03 cancer <--> fingers
5 1.0      0.14      7.0    2.0e-12 fingers <--> fingers
8 1.0      0.14      7.0    2.0e-12 cancer <--> cancer

```

Iterations = 0

Two predictors, don't model the correlation

A slightly more complicated model adds the effects of having yellow teeth.

```

      path                parameter initial value
[1,] "fingers -> cancer"  "1"          NA
[2,] "teeth -> cancer"    "2"          NA
[3,] "fingers <-> fingers" "5"          NA
[4,] "teeth <-> teeth"    "6"          NA
[5,] "cancer <-> cancer"  "8"          NA
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

```

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

```

Iterations = 0

```

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

```

Even with 100 subjects, the model does not fit in terms of χ^2 or any of the conventional fit statistics. Although the path coefficients predicting cancer exactly match the regression betas, the failure to fit is due to the failure to model the correlations between the predictor variables. That is, our measurement model is faulty (because we are not actually trying to measure it.)

Two predictors, model the correlation

```

      path                parameter initial value
[1,] "fingers -> cancer"   "1"          NA
[2,] "teeth -> cancer"     "2"          NA
[3,] "fingers <-> fingers" "5"          NA
[4,] "teeth <-> teeth"     "6"          NA
[5,] "fingers <-> teeth"   "7"          NA
[6,] "cancer <-> cancer"   "8"          NA
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

```

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 0.19      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

```

Iterations = 0

```

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

```

Fitting the correlation between fingers and teeth produces a fully saturated model (with no degrees of freedom). The paths are the correct beta weights.

6.1.4 Three predictors - alternative models

There are a variety of ways to model the effect of three predictors on the outcome variable. The model that is logically the equivalent of the regression model is to consider the three predictors as independent. Alternatives to this consider various ways in which the predictors could be related.

Three predictors, don't model the correlations

```

      path                parameter initial value
[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
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

```

Normalized Residuals

```

      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
      0.0    1.2    2.0    2.5    4.3    5.6

```

Parameter Estimates

```

      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

```

Iterations = 0

```

      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

```

As we saw before, although the prediction paths from the predictors to the criterion match the beta weights, the model does not fit, because this model fails to model the correlation between the predictors. Once again, our failure to have a measurement model is at fault.

We can fix the variance of the predictors to increase the degrees of freedom, but we are still not modeling the covariances.

```

      path                parameter initial value
[1,] "fingers -> cancer"    "1"          NA
[2,] "teeth -> cancer"      "2"          NA
[3,] "breath -> cancer"     "3"          NA
[4,] "fingers <-> fingers"  NA           "1"
[5,] "teeth <-> teeth"      NA           "1"
[6,] "breath <-> breath"    NA           "1"
[7,] "cancer <-> cancer"    "8"          NA

```

```

> summary(sem.4a, digits = 2)
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

Normalized Residuals
  Min. 1st Qu. Median Mean 3rd Qu. Max.
  0.0  1.2  2.0  2.5  4.3  5.6

Parameter Estimates
  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

Iterations = 0
> print(standardized.residuals(sem.4a), digits = 2)
      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

```

Three predictors, model the correlations, case 1

Revise the previous model to include a “yellow” latent variable. That is, we notice from the residuals that yellow teeth and fingers seem to go together. Perhaps, with a bit of creativity, we can explain this as due to the influence of yellowing agents which need to be controlled.

```

      path                parameter initial value
[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"
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

```

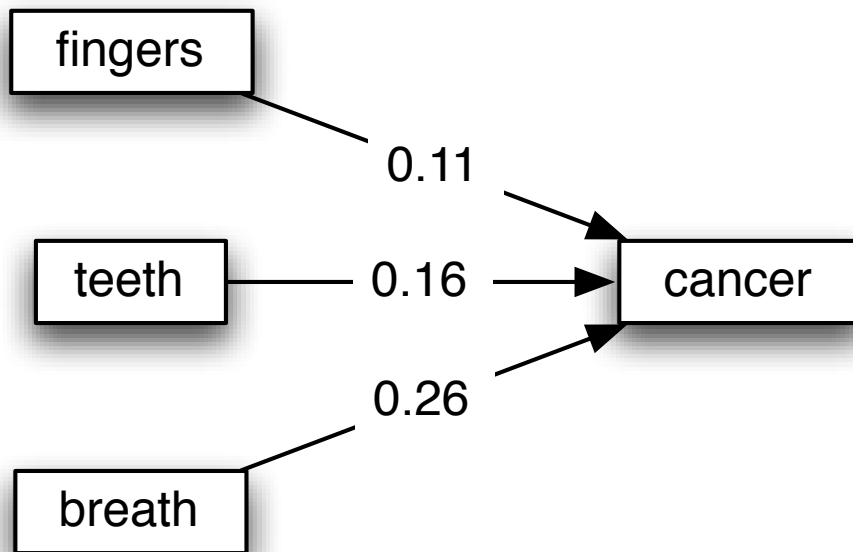


Figure 6.3: The direct effect of three predictors upon a criterion variable. The “real”, causal variable is missing from the model. Although the direct paths are correct (match the beta weights), the model has a poor fit because the predictors are modeled as uncorrelated. That is, it is not possible to see the indirect effects from this model.

```

Tucker-Lewis NNFI = -0.68
Bentler CFI = 0.44
BIC = 39
  
```

```

Normalized Residuals
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
0.0e+00 7.1e-06 1.3e+00 1.9e+00 2.3e+00 5.6e+00
  
```

```

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
  
```

```

Iterations = 14
      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
  
```

This model is significant improvement over the previous model, (examine the change in χ^2 for the one degree of freedom used), but still does not fit very well.

Three predictors, model the correlations, case 2

Looking at the residuals suggests perhaps we should model a latent mouth variable as well. Perhaps the yellowing of the teeth have an additional component related to being in the mouth.

```

      path                parameter initial value
[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"
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

```

```

Normalized Residuals
      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
-8.9e-07 6.4e-01 7.8e-01 1.4e+00 1.8e+00 4.8e+00

```

```

Parameter Estimates
      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
5  0.96  0.136    7.1  1.7e-12 fingers <--> fingers
6 -1.09  0.124   -8.7  0.0e+00 teeth <--> teeth
7  0.78  0.118    6.6  3.4e-11 breath <--> breath
8  0.81  0.115    7.0  2.0e-12 cancer <--> cancer
10 0.20  0.097    2.0  4.3e-02 fingers <--- yellow
11 0.47  0.114    4.1  4.4e-05 breath <--- mouth

```

```

Iterations = 21
      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

This is a great improvement (once again, look at the change in χ^2 for the 1 degree of freedom more complex model), but the model still does not fit at all well.

Three predictors, model the correlations, case 3

Alternatively, we could just allow all the predictors to correlate:

```
path                parameter initial value
[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,] "teeth <-> breath"   "9"      NA
[9,] "teeth <-> fingers"  "10"     NA
[10,] "fingers <-> breath" "11"     NA
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
```

```
Parameter Estimates
  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
```

```
Iterations = 0
      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
```

This model is fully saturated, and thus the χ^2 statistic is meaningless. The β weights match the regression model, and the modeled correlations match the data.

However, if we fix the variances of the three predictors to be 1, then we have gained 3 degrees of freedom and now the model looks great!

```
path                parameter initial value
[1,] "fingers -> cancer"  "1"      NA
[2,] "teeth -> cancer"    "2"      NA
```

```

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

```

```

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

```

```

Parameter Estimates
  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

```

```

Iterations = 0
      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

```

6.1.5 Three predictors, model the correlations with one latent variable

An alternative model to that in Figure 6.4 is to note that the three predictors correlate and to consider that perhaps they reflect an unknown, latent variable. Perhaps it is this latent variable which leads to cancer.

```

path          parameter initial value
[1,] "latent -> cancer"    "1"      NA
[2,] "latent -> breath"    "2"      NA
[3,] "latent -> fingers"   "3"      NA
[4,] "latent -> teeth"     "4"      NA
[5,] "fingers <-> fingers" "5"      NA
[6,] "teeth <-> teeth"     "6"      NA
[7,] "breath <-> breath"   "7"      NA

```

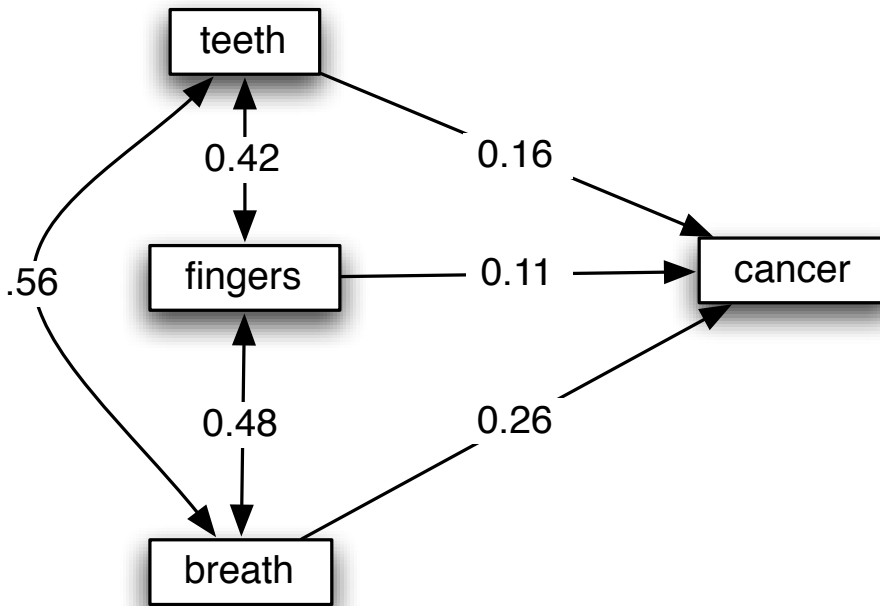


Figure 6.4: The direct and indirect effect of three predictors upon a criterion variable using sem. The “real”, causal variable is missing from the model. The direct paths are correct (match the beta weights), and the model has an excellent fit because the correlations between the predictors are modeled.

```

[8,] "cancer <-> cancer"  "8"      NA
[9,] "latent <-> latent"  NA      "1"
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
  
```

```

Normalized Residuals
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
9.4e-07 1.7e-06 3.0e-06 3.5e-06 4.7e-06 1.2e-05
  
```

```

Parameter Estimates
  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
  
```

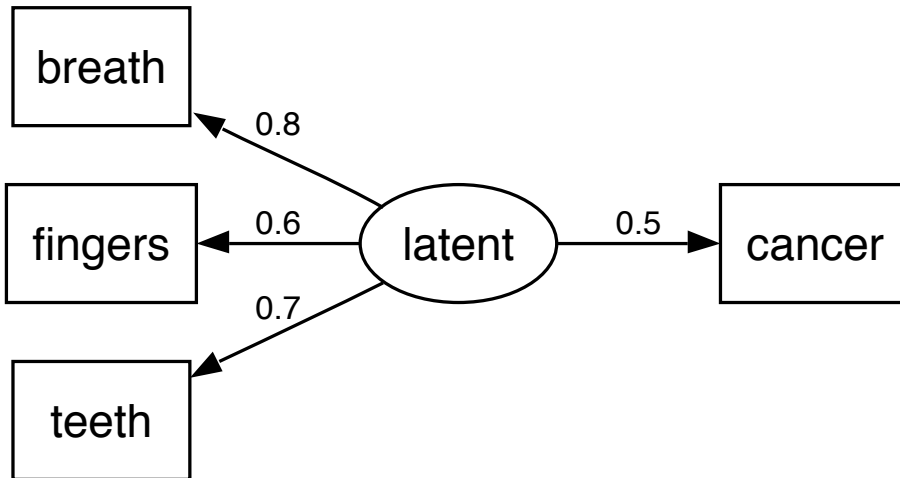


Figure 6.5: Faulty inference can be the result of a misspecified model. Whatever is common to bad breadth, yellow teeth, and yellow hands seems to lead to lung cancer. Thus, one should use mouth freshners, visit your dentist, and wear latex gloves.

```
8 0.75      0.12      6.4      2.0e-10  cancer <--> cancer
```

```
Iterations = 13
      breath  teeth fingers  cancer
breath 6.1e-07 5.4e-07 3.5e-07 5.2e-07
teeth  5.4e-07 2.8e-07 1.1e-07 2.9e-07
fingers 3.5e-07 1.1e-07 1.3e-07 1.8e-07
cancer 5.2e-07 2.9e-07 1.8e-07 1.7e-06
```

Ah, that did it. We now understand the “causal” structure (although our inference about what is common between bad breath, yellow teeth and yellow fingers will probably ignore the real cause). The secret to solving lung cancer is to use mouth freshners, visit your dentist, and wear latex gloves! (See Figure 6.5)

6.1.6 Three predictors with shared “error”

An alternative model is to consider the latent variable as accounting for the correlations between the three observed variables, and then to have direct paths from yellow teeth, yellow fingers, and bad breath to cancer. (This is functionally equivalent to the regression model.) Note how this model is conceptually very different from the previous one in which the latent variable was seen as common to all four variables.

	path	parameter	initial value
[1,]	"breath -> cancer"	"A"	NA
[2,]	"teeth -> cancer"	"B"	NA
[3,]	"fingers -> cancer"	"C"	NA
[4,]	"latent -> breath"	"2"	NA
[5,]	"latent -> fingers"	"3"	NA
[6,]	"latent -> teeth"	"4"	NA
[7,]	"fingers <-> fingers"	"5"	NA
[8,]	"teeth <-> teeth"	"6"	NA
[9,]	"breath <-> breath"	"7"	NA
[10,]	"cancer <-> cancer"	"8"	NA

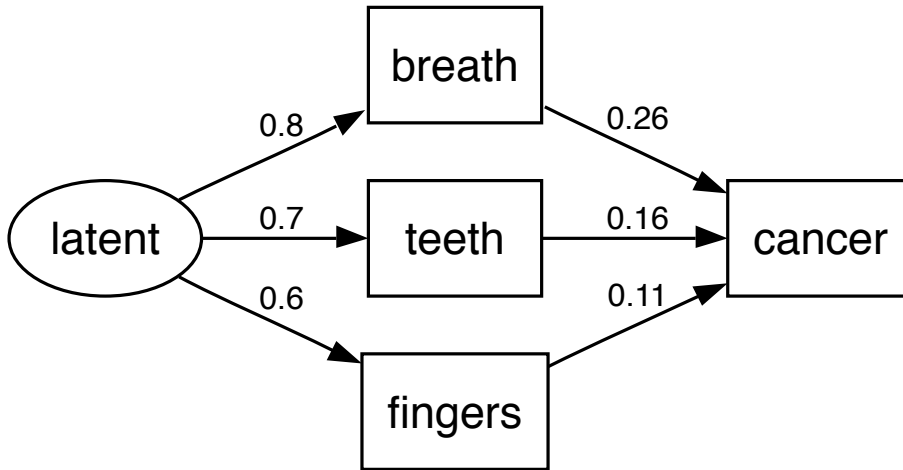


Figure 6.6: Correlated errors not associated with the criterion. Alternatively, there is something in common to yellow teeth, yellow fingers, and bad breath, but whatever it is that they do not share leads to cancer.

```

[11,] "latent <-> latent"  NA      "1"
Model Chi-square = 1.5e-10  Df = 0  Pr(>ChiSq) = NA
Chi-square (null model) = 89  Df = 6
Goodness-of-fit index = 1
BIC = 1.5e-10

Normalized Residuals
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
-4.8e-06 -1.4e-06 -7.0e-07 -1.0e-06 -1.6e-07  1.5e-06

Parameter Estimates
  Estimate Std Error z value Pr(>|z|)
A 0.26     0.12     2.2    2.5e-02 cancer <--- breath
B 0.16     0.11     1.4    1.5e-01 cancer <--- teeth
C 0.11     0.11     1.0    3.0e-01 cancer <--- fingers
2 0.80     0.11     7.2    7.1e-13 breath <--- latent
3 0.60     0.11     5.6    1.9e-08 fingers <--- latent
4 0.70     0.11     6.4    1.3e-10 teeth <--- latent
5 0.64     0.11     5.7    1.5e-08 fingers <--> fingers
6 0.51     0.12     4.4    1.2e-05 teeth <--> teeth
7 0.36     0.13     2.8    5.5e-03 breath <--> breath
8 0.81     0.11     7.0    2.0e-12 cancer <--> cancer

Iterations = 15
      breath  teeth  fingers  cancer
breath  1.1e-07 -5.5e-07 -2.6e-07 -8.8e-08
teeth  -5.5e-07  2.1e-07 -1.7e-08 -1.1e-07
fingers -2.6e-07 -1.7e-08  8.5e-08 -6.1e-08
cancer  -8.8e-08 -1.1e-07 -6.1e-08 -4.7e-08
  
```

But the previous model is fully saturated. We can revise the model somewhat by forcing all three paths with the latent variable to be equal. This frees up two degrees of freedom

and results in a very good fit.

```
> model.8b <- matrix(c("breath -> cancer", "A", NA, "teeth -> cancer",  
+ "B", NA, "fingers -> cancer", "C", NA, "latent -> breath",  
+ 2, NA, "latent -> fingers", 2, NA, "latent -> teeth", 2,  
+ NA, "fingers <-> fingers", 5, NA, "teeth <-> teeth", 6, NA,  
+ "breath <-> breath", 7, NA, "cancer <-> cancer", 8, NA, "latent <-> latent",  
+ NA, 1), byrow = TRUE, ncol = 3)
```

```
> model.8b  
      [,1]      [,2] [,3]  
[1,] "breath -> cancer" "A" NA  
[2,] "teeth -> cancer" "B" NA  
[3,] "fingers -> cancer" "C" NA  
[4,] "latent -> breath" "2" NA  
[5,] "latent -> fingers" "2" NA  
[6,] "latent -> teeth" "2" NA  
[7,] "fingers <-> fingers" "5" NA  
[8,] "teeth <-> teeth" "6" NA  
[9,] "breath <-> breath" "7" NA  
[10,] "cancer <-> cancer" "8" NA  
[11,] "latent <-> latent" NA "1"
```

```
> sem.8b <- sem(model.8b, observed[2:5, 2:5], 100)
```

```
> summary(sem.8b, digits = 2)
```

```
Model Chisquare = 1.9 Df = 2 Pr(>Chisq) = 0.39  
Chisquare (null model) = 89 Df = 6  
Goodness-of-fit index = 1  
Adjusted goodness-of-fit index = 0.95  
RMSEA index = 0 90% CI: (NA, 0.20)  
Bentler-Bonnett NFI = 0.98  
Tucker-Lewis NNFI = 1  
Bentler CFI = 1  
BIC = -7.3
```

Normalized Residuals

	Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
	-0.660	-0.233	0.039	-0.020	0.223	0.583

Parameter Estimates

	Estimate	Std Error	z value	Pr(> z)	
A	0.26	0.115	2.2	2.5e-02	cancer <--- breath
B	0.16	0.111	1.4	1.5e-01	cancer <--- teeth
C	0.11	0.105	1.0	3.0e-01	cancer <--- fingers
2	0.70	0.069	10.3	0.0e+00	breath <--- latent
5	0.59	0.108	5.4	5.3e-08	fingers <--> fingers
6	0.50	0.096	5.2	2.4e-07	teeth <--> teeth
7	0.45	0.091	4.9	8.2e-07	breath <--> breath
8	0.81	0.115	7.0	2.0e-12	cancer <--> cancer

Iterations = 10

```
> print(standardized.residuals(sem.8b), digits = 2)
```

	breath	teeth	fingers	cancer
breath	0.058	0.0637	-0.016	0.0232
teeth	0.064	0.0065	-0.076	0.0092
fingers	-0.016	-0.0763	-0.083	-0.0255

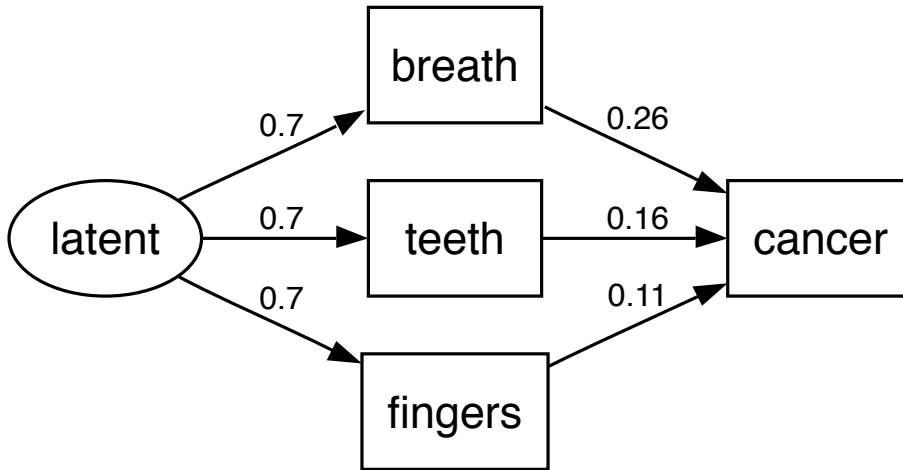


Figure 6.7: Fixing the correlated errors paths. There is something in common to yellow teeth, yellow fingers, and bad breath, but whatever it is that they do not share leads to cancer. By fixing the paths to the latent variable to be the same the model has gained two degrees of freedom. The fit is very good.

```
cancer 0.023 0.0092 -0.025 0.0047
```

6.1.7 Reverse the causal paths

Yet another alternative model is to think of cancer as the cause of bad breath, yellow teeth and yellow fingers. (That is to say, to reverse the causal arrows from the previous model.) The paths from cancer to the former “predictors” are now longer β weights, but have become the zero order correlation coefficients.

```

> model.8c <- matrix(c("breath <- cancer", "A", NA, "teeth <- cancer",
+   "B", NA, "fingers <- cancer", "C", NA, "latent -> breath",
+   1, NA, "latent -> fingers", 2, NA, "latent -> teeth", 3,
+   NA, "fingers <-> fingers", 5, NA, "teeth <-> teeth", 6, NA,
+   "breath <-> breath", 7, NA, "cancer <-> cancer", NA, 1, "latent <-> latent",
+   NA, 1), byrow = TRUE, ncol = 3)
> model.8c
      [,1]           [,2] [,3]
[1,] "breath <- cancer"  "A"  NA
[2,] "teeth <- cancer"   "B"  NA
[3,] "fingers <- cancer" "C"  NA
[4,] "latent -> breath"  "1"  NA
[5,] "latent -> fingers" "2"  NA
[6,] "latent -> teeth"  "3"  NA
[7,] "fingers <-> fingers" "5"  NA
[8,] "teeth <-> teeth"   "6"  NA
[9,] "breath <-> breath" "7"  NA
[10,] "cancer <-> cancer" NA  "1"
[11,] "latent <-> latent" NA  "1"
> sem.8c <- sem(model.8c, observed[2:5, 2:5], 100)
> summary(sem.8c, digits = 2)

```

```

Model Chisquare = 1.0e-10  Df = 1  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 = -4.6

```

```

Normalized Residuals
  Min.  1st Qu.  Median    Mean  3rd Qu.    Max.
-6.5e-06 -4.7e-06 -4.0e-06 -3.2e-06 -1.5e-06  4.8e-08

```

```

Parameter Estimates
  Estimate Std Error z value Pr(>|z|)
A 0.40      0.092    4.3    1.4e-05  breath <--- cancer
B 0.35      0.094    3.7    2.0e-04  teeth <--- cancer
C 0.30      0.096    3.1    1.8e-03  fingers <--- cancer
1 0.69      0.116    6.0    2.4e-09  breath <--- latent
2 0.52      0.110    4.7    2.1e-06  fingers <--- latent
3 0.61      0.113    5.4    7.3e-08  teeth <--- latent
5 0.64      0.113    5.7    1.5e-08  fingers <--> fingers
6 0.51      0.117    4.4    1.2e-05  teeth <--> teeth
7 0.36      0.130    2.8    5.5e-03  breath <--> breath

```

```

Iterations = 16
> print(standardized.residuals(sem.8c), digits = 2)
      breath  teeth  fingers  cancer
breath -6.1e-08 -5.5e-07 -2.1e-07  5.2e-09
teeth  -5.5e-07 -6.6e-07 -4.4e-07 -6.9e-07
fingers -2.1e-07 -4.4e-07 -5.7e-07 -4.5e-07
cancer  5.2e-09 -6.9e-07 -4.5e-07  0.0e+00

```

6.2 Including the correct variables, but misspecifying the models

Based upon the previous model fitting in section 6.1 we have concluded that there is some latent variable that ties our four variables together. We now examine what happens when we add yet another variable to the mix.

We use the correlation matrix from section 6.1. Note that the correlation matrix is identical for the previous four variables, and that the smoking variable is equivalent to the latent factor that generated the data.

6.2.1 Including the correct variables in linear regression

Remember that if we include smoking into the linear regression, the effect of the other variables vanishes (Figure 6.2

```

> mat.regress(observed, c(2:4), 5)
$beta
  breath  teeth  fingers
    0.26   0.16   0.11

```

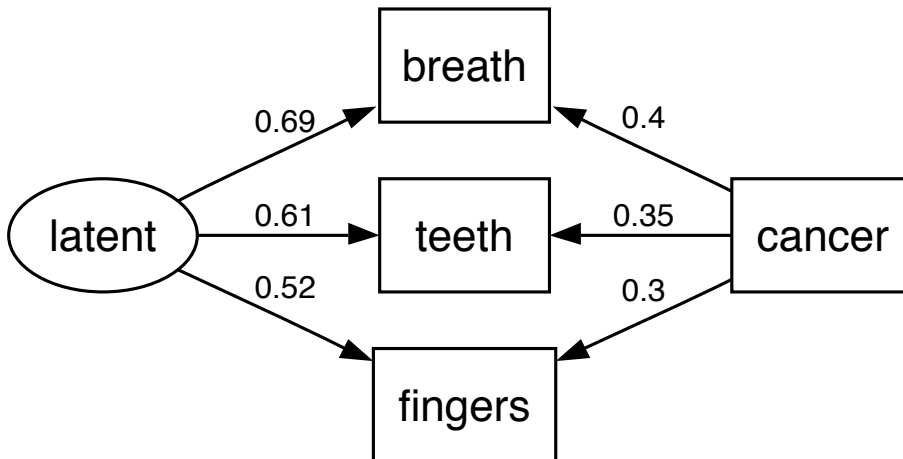


Figure 6.8: Changing the direction of causation. Perhaps cancer is the causal agent and breath, teeth, and fingers are merely signs of the underlying disease. In addition, perhaps they have some shared error.

```

$R2
cancer
  0.19
> mat.regress(observed, c(1:4), 5)
$beta
smoking  breath  teeth fingers
      0.5    0.0    0.0    0.0

```

```

$R2
cancer
  0.25

```

If, however, we were to make smoking an unreliable measure and thus not perfectly correlated with the latent factor, the other variables still seem to have an effect. We show this by making the latent path from θ to smoking less than one. In the first case, we make the path .9. This is the same as making the reliability of smoking .81. Call this new correlation matrix `observed1`.

```

> theta <- matrix(c(0.9, 0.8, 0.7, 0.6, 0.5), nrow = 5)
> observed1 <- theta %% t(theta)
> diag(observed1) <- 1
> rownames(observed1) <- colnames(observed1) <- c("smoking", "breath",
+ "teeth", "fingers", "cancer")
> observed1
      smoking  breath  teeth  fingers  cancer
smoking  1.00   0.72  0.63   0.54   0.45
breath   0.72   1.00  0.56   0.48   0.40
teeth    0.63   0.56  1.00   0.42   0.35
fingers  0.54   0.48  0.42   1.00   0.30
cancer   0.45   0.40  0.35   0.30   1.00
> mat.regress(observed1, c(2:4), 5)

```

```

$beta
  breath  teeth fingers
    0.26   0.16   0.11

$R2
cancer
  0.19
> mat.regress(observed1, c(1:4), 5)
$beta
smoking  breath  teeth fingers
    0.28   0.13   0.08   0.05

```

```

$R2
cancer
  0.22

```

Compare the regression weights for the two data sets (observed and observed1). Note how the other variables still contribute to the regression unless smoking is measured perfectly reliably.

To show it even more clearly, make the θ to smoking path = .5 (This is the equivalent of having a reliability of smoking of .25)

```

> theta <- matrix(c(0.5, 0.8, 0.7, 0.6, 0.5), nrow = 5)
> observed2 <- theta %*% t(theta)
> diag(observed2) <- 1
> rownames(observed2) <- colnames(observed2) <- c("smoking", "breath",
+         "teeth", "fingers", "cancer")
> observed2
      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
> mat.regress(observed2, c(2:4), 5)
$beta
  breath  teeth fingers
    0.26   0.16   0.11

```

```

$R2
cancer
  0.19
> mat.regress(observed2, c(1:4), 5)
$beta
smoking  breath  teeth fingers
    0.07   0.24   0.15   0.10

```

```

$R2
cancer
  0.2

```

Note that in this case, we completely over estimate the contribution of the other variables and underestimate the contribution of smoking. In regression, there is no way to correct for this, but structural equation modeling does allow for various ways of correcting this problem.

6.2.2 Including the correct variables in the Structural Equation

Here we apply the identical model to our three different correlation matrices.

```
> model.9 <- matrix(c("latent -> cancer", 1, NA, "latent -> breath",
+ 2, NA, "latent -> fingers", 3, NA, "latent -> teeth", 4,
+ NA, "latent -> smoking", 9, NA, "fingers <-> fingers", 5,
+ NA, "teeth <-> teeth", 6, NA, "breath <-> breath", 7, NA,
+ "cancer <-> cancer", 8, NA, "smoking <-> smoking", 10, NA,
+ "latent <-> latent", NA, 1), byrow = TRUE, ncol = 3)
> model.9
```

```
      [,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"
```

```
> sem.9 <- sem(model.9, observed, 100)
```

```
> summary(sem.9, digits = 2)
```

```
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
```

Normalized Residuals

	Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
	-8.2e-07	-3.6e-07	5.1e-08	2.3e-07	8.5e-07	1.2e-06

Parameter Estimates

	Estimate	Std Error	z value	Pr(> z)	
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

Iterations = 15

```
> print(standardized.residuals(sem.9), digits = 2)
```

```

      smoking  breath  teeth  fingers  cancer
smoking -1.9e-08 -3.1e-08 -1.0e-07 -2.4e-08 1.2e-07
breath  -3.1e-08  9.0e-08 -5.1e-08  5.7e-09 1.2e-07
teeth   -1.0e-07 -5.1e-08 -6.0e-08 -3.9e-08 6.7e-08
fingers -2.4e-08  5.7e-09 -3.9e-08  1.7e-07 8.9e-08
cancer  1.2e-07  1.2e-07  6.7e-08  8.9e-08 1.6e-07

```

Note that with the perfect data set, the estimate for the error variance of smoking is appropriately very small.

Repeat this analysis with the less than perfect reliability of smoking of the observed1 data set:

```

> sem.10 <- sem(model.9, observed1, 100)
> summary(sem.10, digits = 2)
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

```

```

Normalized Residuals
      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
-3.8e-06 -2.5e-06  3.1e-07  2.7e-07  2.7e-06  5.7e-06

```

```

Parameter Estimates
      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

```

```

Iterations = 12
> print(standardized.residuals(sem.10), digits = 2)
      smoking  breath  teeth  fingers  cancer
smoking 1.5e-07  8.2e-08 -1.8e-07  6.5e-07 -2.7e-07
breath  8.2e-08  4.4e-08 -2.2e-07  5.3e-07 -2.8e-07
teeth  -1.8e-07 -2.2e-07  2.9e-09  3.0e-07 -3.9e-07
fingers 6.5e-07  5.3e-07  3.0e-07  5.1e-07  1.2e-07
cancer -2.7e-07 -2.8e-07 -3.9e-07  1.2e-07 -5.4e-07

```

Repeat this analysis with the even less reliability of smoking of the observed2 data set:

```

> sem.11 <- sem(model.9, observed2, 100)
> summary(sem.11, digits = 2)
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

```

Normalized Residuals

	Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
	-1.0e-05	-2.4e-06	-1.1e-06	-5.4e-07	2.2e-06	5.5e-06

Parameter Estimates

	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

```
Iterations = 11
```

```

> print(standardized.residuals(sem.11), digits = 2)
      smoking  breath  teeth  fingers  cancer
smoking  7.7e-07 -2.4e-07  5.2e-07 -2.6e-07  2.3e-07
breath   -2.4e-07 -6.2e-07 -1.4e-08 -1.1e-06 -2.4e-07
teeth    5.2e-07 -1.4e-08 -2.7e-07 -1.2e-07  5.2e-07
fingers  -2.6e-07 -1.1e-06 -1.2e-07 -1.1e-07 -2.6e-07
cancer   2.3e-07 -2.4e-07  5.2e-07 -2.6e-07  7.7e-07

```

We now see the real power of the SEM approach. For by modeling the correlations between the X predictor set, we are able to estimate how unreliable each variable is (the path from a variable to itself reflects the unreliability) and see the structure of the data. But, the conclusion is still wrong, because now we are forced to interpret that whatever it is that is common to smoking, bad breath, yellow fingers and yellow teeth lead to cancer. Although our latent modeling approach has helped and is able to reproduce the data perfectly, it has not led to the correct conclusion as to causality. (See Figure ??).

6.2.3 Direct the causal path

What happens if we make smoking a causal variable that leads to the latent variable?

```

> model.12 <- matrix(c("latent -> cancer", 1, NA, "latent -> breath",
+   2, NA, "latent -> fingers", 3, NA, "latent -> teeth", 4,
+   NA, "smoking -> latent", NA, 1, "fingers <-> fingers", 5,
+   NA, "teeth <-> teeth", 6, NA, "breath <-> breath", 7, NA,
+   "cancer <-> cancer", 8, NA, "smoking <-> smoking", NA, 1,
+   "latent <-> latent", 12, NA), byrow = TRUE, ncol = 3)
> sem.12 <- sem(model.12, observed, 100)
> summary(sem.12, digits = 2)
Model Chisquare = 4.9e-12  Df = 6  Pr(>Chisq) = 1
Chisquare (null model) = 240  Df = 10

```

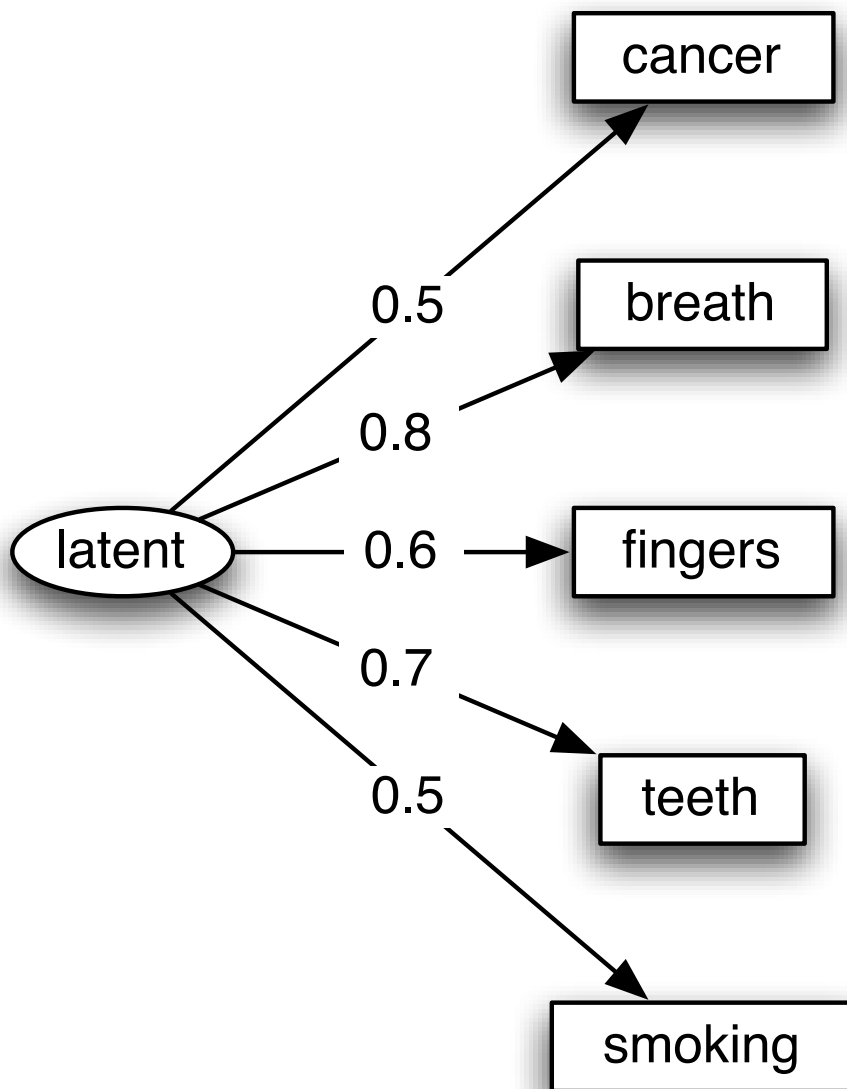


Figure 6.9: Good fit does not imply “causality”—the problem of incorrect inference. Whatever is common to smoking, bad breath, yellow teeth, and yellow hands also seems to lead to lung cancer. Thus, one should use mouth fresheners, visit your dentist, and wear latex gloves. It is unclear why the latent variable leads to smoking.

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

Normalized Residuals

	Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
	-5.8e-07	-1.0e-07	1.7e-07	3.1e-07	4.4e-07	1.2e-06

Parameter Estimates

	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

Iterations = 15

```

> print(standardized.residuals(sem.12), digits = 2)
      smoking  breath  teeth  fingers  cancer
smoking  0.0e+00  5.5e-08  1.0e-07 -1.4e-08 -1.2e-08
breath   5.5e-08  1.4e-07  1.2e-07  1.7e-08  1.5e-08
teeth    1.0e-07  1.2e-07  1.7e-07  4.8e-08  4.0e-08
fingers -1.4e-08  1.7e-08  4.8e-08  2.5e-08 -1.7e-08
cancer  -1.2e-08  1.5e-08  4.0e-08 -1.7e-08 -8.2e-08
  
```

Repeat this analysis with noisy data from observed2. (Remember that in this case, smoking is not measured reliably).

```

> sem.13 <- sem(model.12, observed2, 100)
> summary(sem.13, digits = 2)
Model Chisquare = 7.4e-11 Df = 6 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 = -28
  
```

Normalized Residuals

	Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
	-5.1e-06	-2.7e-06	-2.4e-06	-2.3e-06	-1.1e-06	6.4e-07

Parameter Estimates

	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

Iterations = 18

```
> print(standardized.residuals(sem.13), digits = 2)
      smoking  breath  teeth  fingers  cancer
smoking  0.0e+00 -3.0e-07 -1.2e-07 -1.2e-07 -2.4e-07
breath   -3.0e-07 -7.3e-07 -3.1e-07 -2.9e-07 -4.8e-07
teeth    -1.2e-07 -3.1e-07  9.1e-08 -8.8e-08 -2.8e-07
fingers  -1.2e-07 -2.9e-07 -8.8e-08 -7.1e-07 -2.5e-07
cancer   -2.4e-07 -4.8e-07 -2.8e-07 -2.5e-07 -2.8e-07
```

We can also model smoking as a noisy variable, and then fix one path (in this case, the latent to cancer) to estimate the model for pure, moderate, and very noisy smoking.

```
> model.14 <- matrix(c("latent -> cancer", NA, 1, "latent -> breath",
+ 2, NA, "latent -> fingers", 3, NA, "latent -> teeth", 4,
+ NA, "smoking -> latent", 11, NA, "fingers <-> fingers", 5,
+ NA, "teeth <-> teeth", 6, NA, "breath <-> breath", 7, NA,
+ "cancer <-> cancer", 8, NA, "smoking <-> smoking", 10, NA,
+ "latent <-> latent", NA, 1), byrow = TRUE, ncol = 3)
> sem.14 <- sem(model.14, observed, 100)
> summary(sem.14, digits = 2)
```

```
Model Chisquare = 111 Df = 6 Pr(>Chisq) = 0
Chisquare (null model) = 240 Df = 10
Goodness-of-fit index = 0.76
Adjusted goodness-of-fit index = 0.39
RMSEA index = 0.42 90% CI: (0.35, 0.49)
Bentler-Bonnett NFI = 0.54
Tucker-Lewis NNFI = 0.24
Bentler CFI = 0.55
BIC = 83
```

Normalized Residuals

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
-4.63	-3.38	-1.81	-1.68	0.00	0.81

Parameter Estimates

	Estimate	Std Error	z value	Pr(> z)	
2	0.73	0.082	8.9	0.0e+00	breath <--- latent
3	0.54	0.090	6.0	2.2e-09	fingers <--- latent
4	0.63	0.087	7.2	6.0e-13	teeth <--- latent
11	0.95	0.133	7.2	8.5e-13	latent <--- smoking
5	0.63	0.102	6.2	5.4e-10	fingers <--> fingers
6	0.50	0.091	5.5	3.5e-08	teeth <--> teeth
7	0.32	0.082	3.9	8.5e-05	breath <--> breath
8	1.02	0.208	4.9	9.7e-07	cancer <--> cancer
10	1.00	0.142	7.0	2.0e-12	smoking <--> smoking

```

Iterations = 13
> print(standardized.residuals(sem.14), digits = 2)
      smoking breath teeth fingers cancer
smoking  0.00  0.10  0.10   0.09 -0.45
breath   0.10 -0.34 -0.31  -0.27 -0.99
teeth    0.10 -0.31 -0.25  -0.22 -0.84
fingers  0.09 -0.27 -0.22  -0.18 -0.72
cancer   -0.45 -0.99 -0.84  -0.72 -1.92
> sem.15 <- sem(model.14, observed1, 100)
> summary(sem.15, digits = 2)
Model Chisquare = 71  Df = 6 Pr(>Chisq) = 2.1e-13
Chisquare (null model) = 188  Df = 10
Goodness-of-fit index = 0.81
Adjusted goodness-of-fit index = 0.53
RMSEA index = 0.33  90% CI: (0.27, 0.4)
Bentler-Bonnett NFI = 0.62
Tucker-Lewis NNFI = 0.39
Bentler CFI = 0.63
BIC = 44

```

Normalized Residuals

	Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
	-4.31	-3.26	-1.73	-1.61	0.00	0.72

Parameter Estimates

	Estimate	Std Error	z value	Pr(> z)	
2	0.77	0.088	8.7	0.0e+00	breath <--- latent
3	0.57	0.096	6.0	2.2e-09	fingers <--- latent
4	0.67	0.093	7.2	5.1e-13	teeth <--- latent
11	0.81	0.125	6.5	9.1e-11	latent <--- smoking
5	0.64	0.104	6.2	7.6e-10	fingers <--> fingers
6	0.51	0.093	5.5	4.6e-08	teeth <--> teeth
7	0.35	0.086	4.0	5.3e-05	breath <--> breath
8	0.92	0.181	5.1	3.6e-07	cancer <--> cancer
10	1.00	0.142	7.0	2.0e-12	smoking <--> smoking

```

Iterations = 13
> print(standardized.residuals(sem.15), digits = 2)
      smoking breath teeth fingers cancer
smoking  0.000  0.095  0.087   0.075 -0.36
breath   0.095 -0.330 -0.295  -0.252 -0.88
teeth    0.087 -0.295 -0.249  -0.216 -0.76
fingers  0.075 -0.252 -0.216  -0.183 -0.65
cancer   -0.362 -0.878 -0.760  -0.651 -1.58
> sem.16 <- sem(model.14, observed2, 100)
> summary(sem.16, digits = 2)
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

```

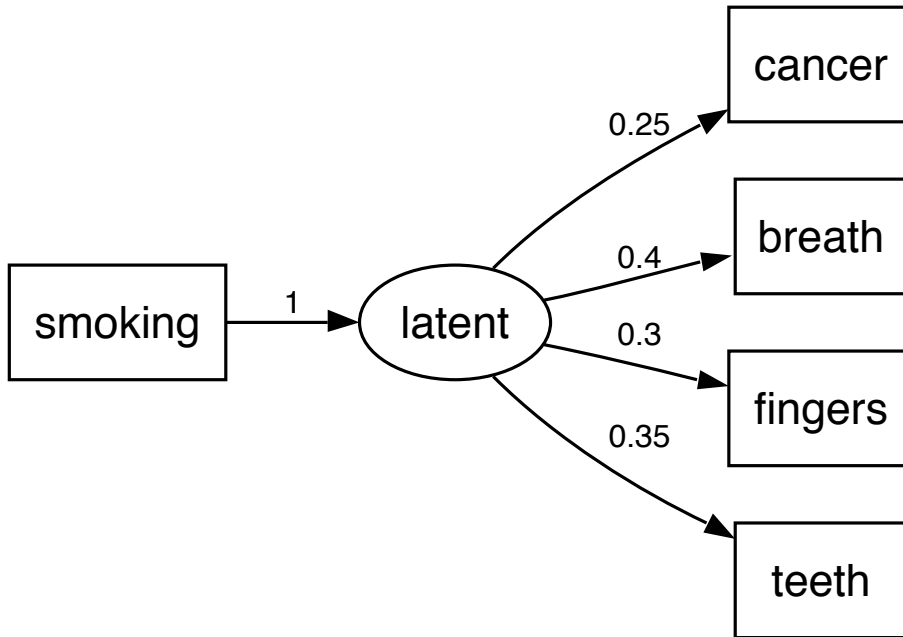


Figure 6.10: The correct model does not necessarily fit better. Smoking seems to affect something that leads to bad breadth, yellow teeth, and yellow hands as well as lung cancer.

Bentler CFI = 0.8
 BIC = -1.5

Normalized Residuals

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
-3.4	-2.8	-1.4	-1.4	0.0	0.4

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

Iterations = 14

6.3 Measures of fit

As has been seen in the previous sections, the use of fit statistics does not guarantee meaningful models. If we do not specify the model correctly, either because we do not include the correct variables or because we fail to use the appropriate measurement model,

we will lead to incorrect conclusions.

Even if we have a very good fit, we are unable to determine causal structure from the model, even if we bother to add time into the model.

6.3.1 χ^2

As we saw in the previous chapter, χ^2 is very sensitive to many sources of error in our model specification. χ^2 is sensitive to failures of our distributional assumptions (continuous, multivariate normal) as well as to our failures to correctly specify the structure.

6.3.2 GFI, NFI, ...

6.3.3 RMSEA

6.4 What does it mean to fit a model

What should we do when the model does not fit? This is a recurring controversy, discussed, for instance in the March, 2007 issue of *Personality and Individual Differences*. It is also a continuing source of debate on the SEM-net list serve. There are those who treat fit statistics (particularly χ^2) as the definitive test and evidence for model adequacy. There are others who do not take such an all or none approach, and are concerned with comparisons of models to alternative models.

6.5 References