

Evaluating Models

Model specification and model fit

Sources of Error in models

I. Model misspecification

A. Failure to identify/include proper variables

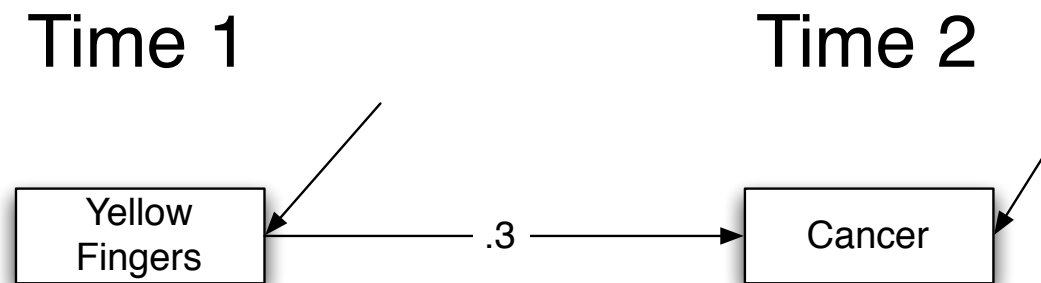
B. Failure to to model relationships

II. Error in Assumptions

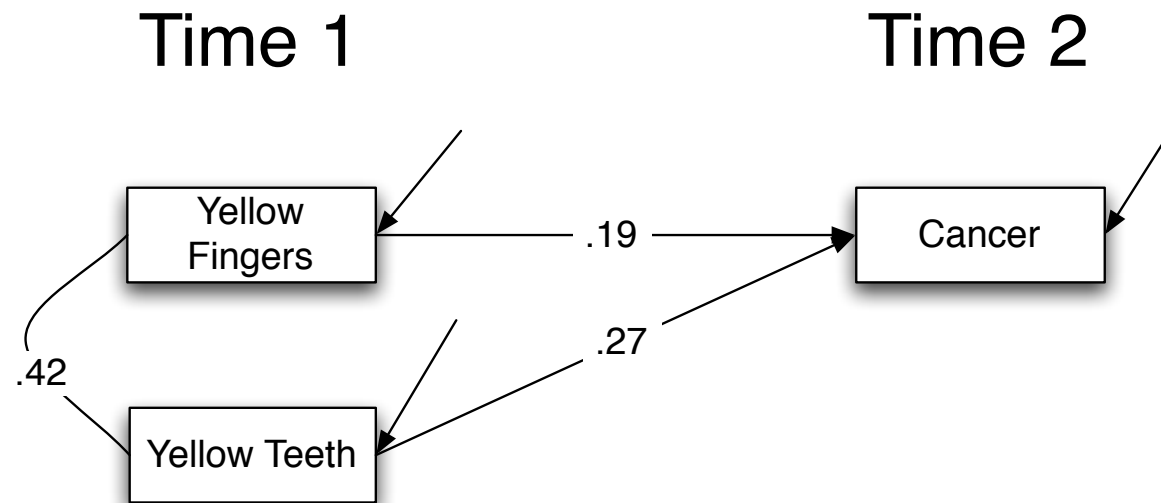
A. Normality

B. Continuous distributions

Effect of yellow fingers on cancer

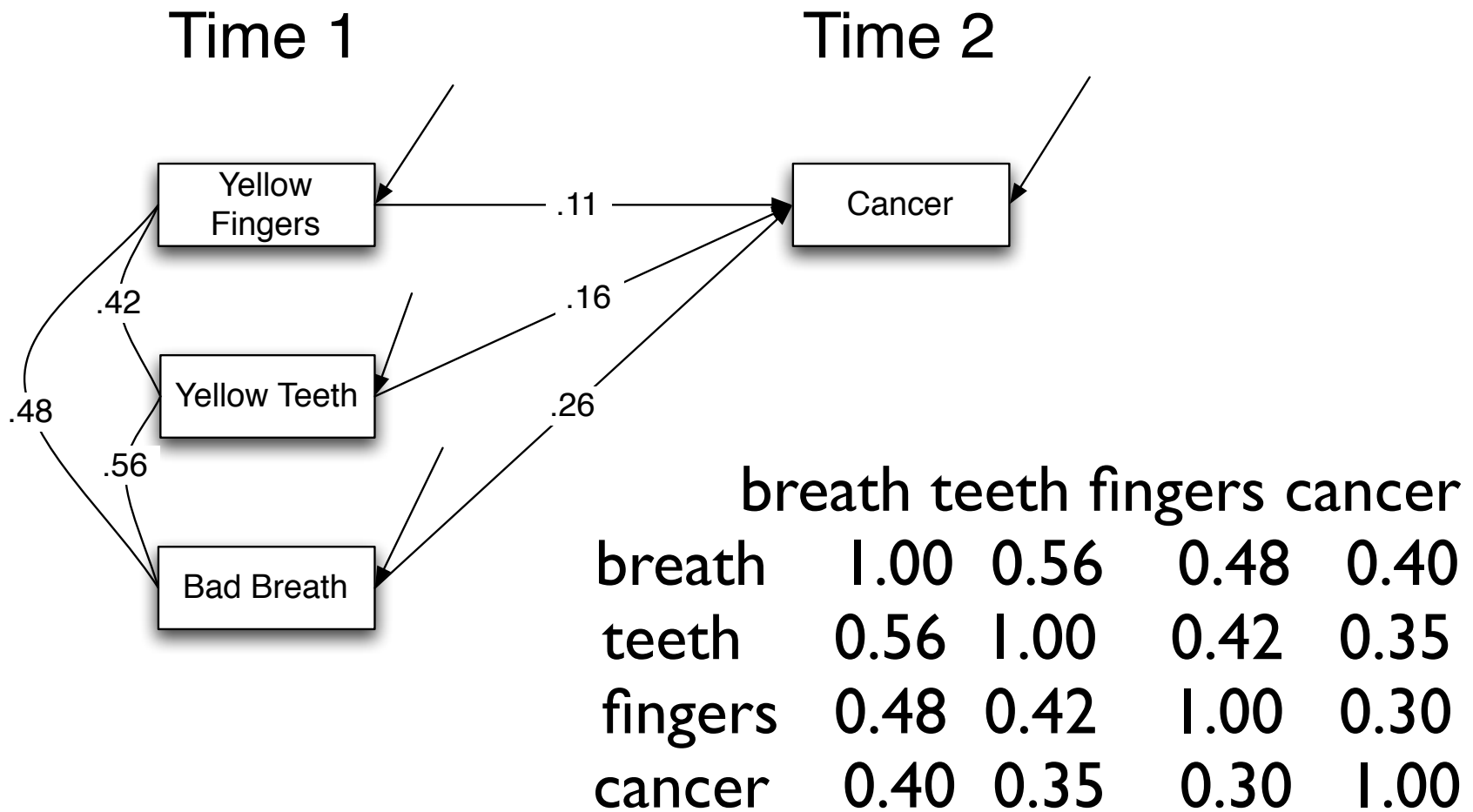


Yellow causes cancer



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

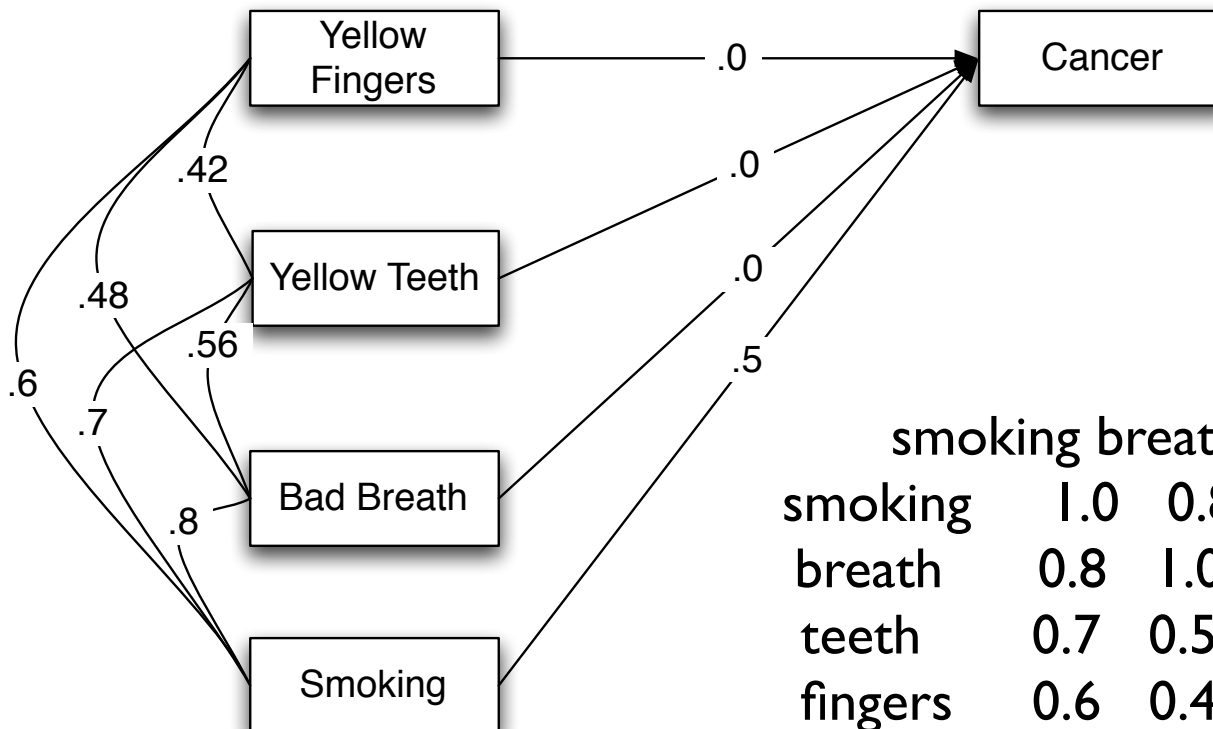
Brush your teeth!



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

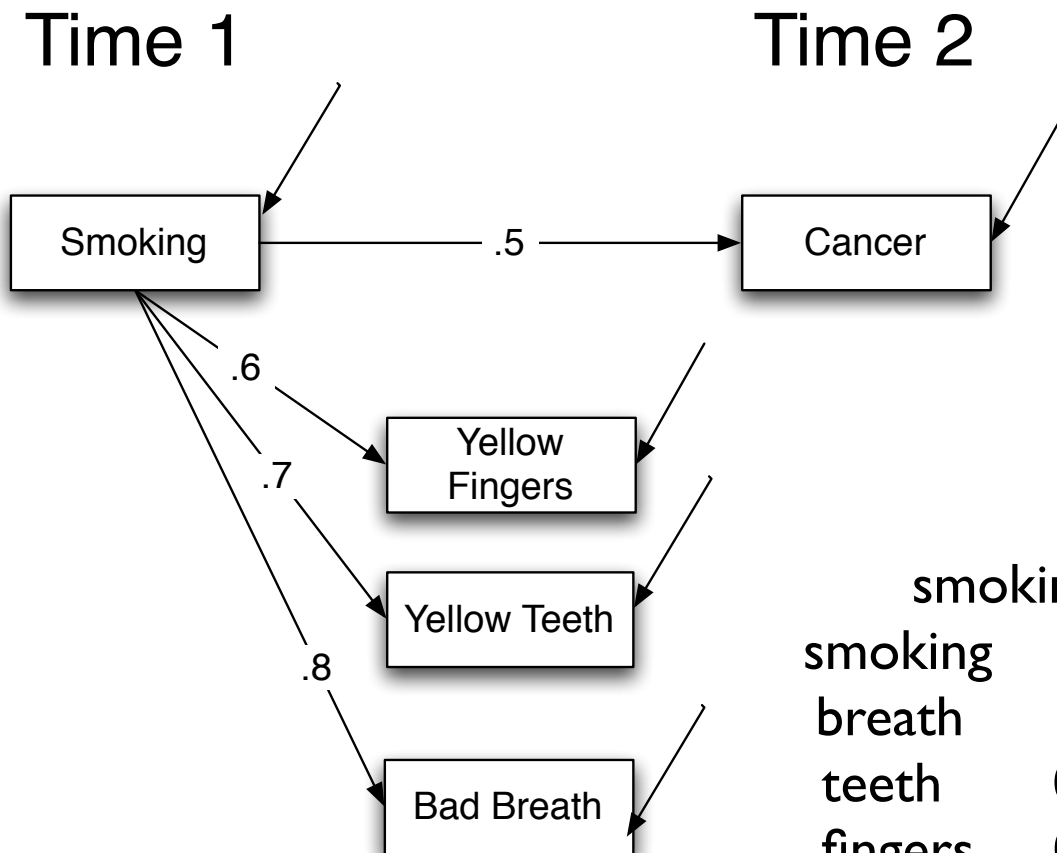
Beta weights

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

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

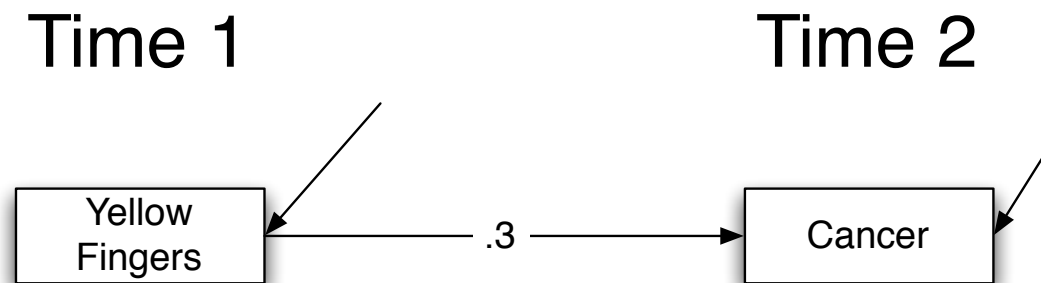
$$R^{-1} = \begin{pmatrix} \frac{r_{22}}{r_{11}r_{22} - r_{12}^2} & -\frac{r_{12}}{r_{11}r_{22} - r_{12}^2} \\ -\frac{r_{12}}{r_{11}r_{22} - r_{12}^2} & \frac{r_{11}}{r_{11}r_{22} - r_{12}^2} \end{pmatrix}$$

Causality?



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

Effect of yellow fingers on cancer



Using SEM for regression

Model Chisquare = $-9.6e-15$ Df = 0 Pr(>Chisq) = NA

Chisquare (null model) = 9.3 Df = 1

Goodness-of-fit index = 1

BIC = $-9.6e-15$

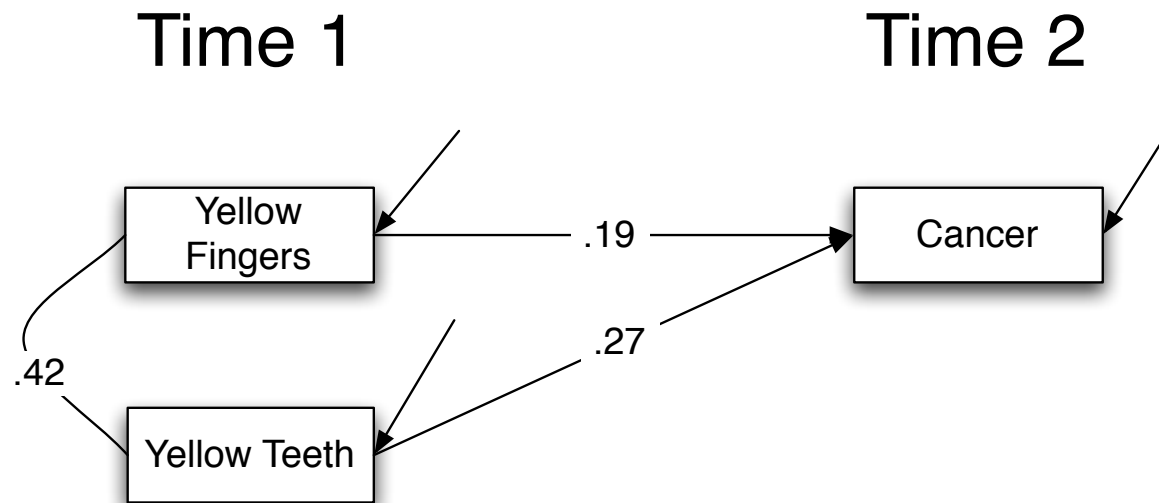
Normalized Residuals

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

Parameter Estimates

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

Yellow causes cancer



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

SEM and multiple R

Parameter Estimates

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

Goodness of fits

Model Chisquare = 19 Df = 1 Pr(>Chisq) = 1.2e-05

Chisquare (null model) = 35 Df = 3

Goodness-of-fit index = 0.9

Adjusted goodness-of-fit index = 0.37

RMSEA index = 0.43 90% CI: (0.28, 0.6)

Bentler-Bonnett NFI = 0.46

Tucker-Lewis NNFI = -0.69

Bentler CFI = 0.44

BIC = 15

Normalized Residuals

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

Residuals

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

SEM multiple R: correlated predictors

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

But model is “saturated”

Model Chisquare = 5.5e-15 Df = 0 Pr(>Chisq) = NA

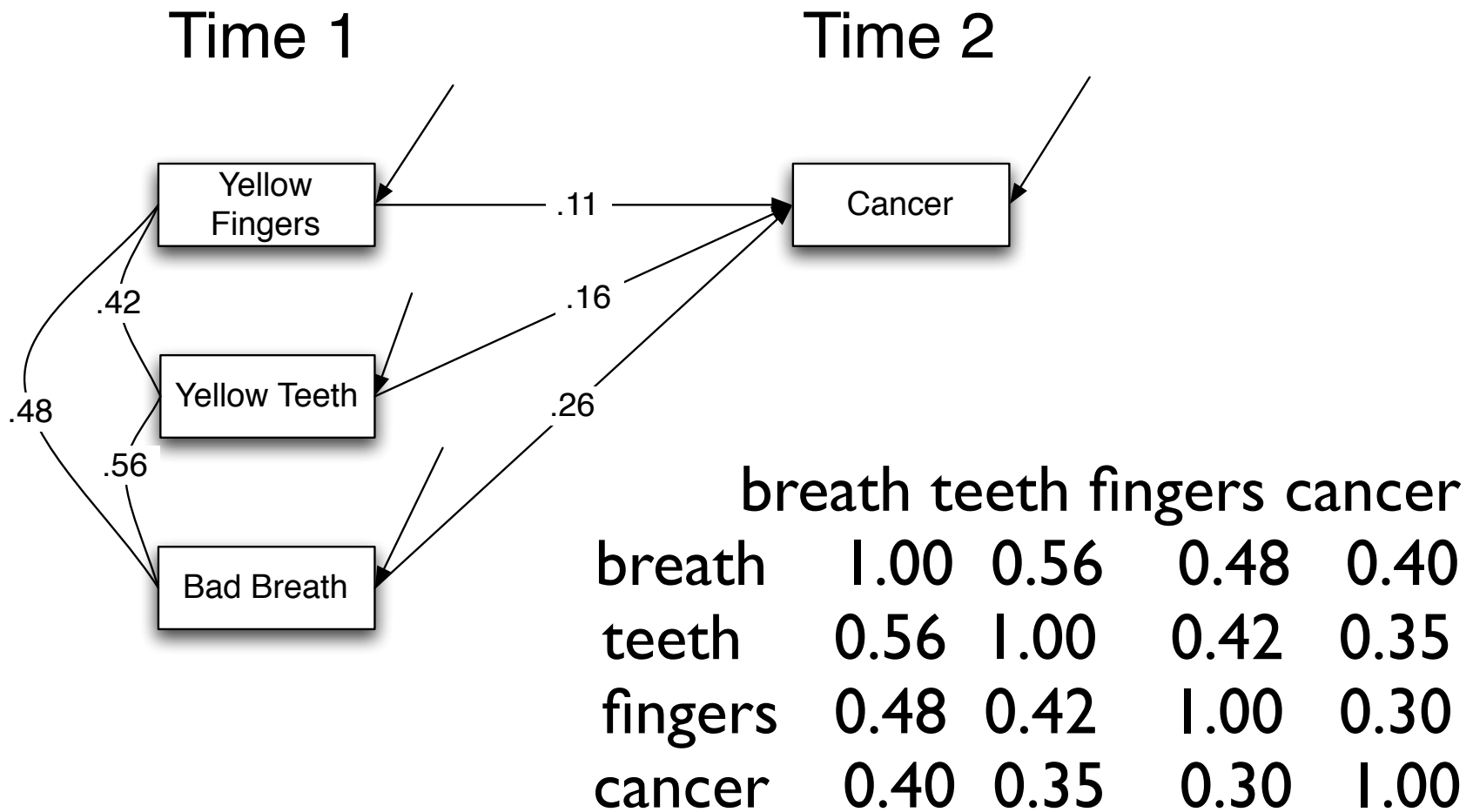
Chisquare (null model) = 35 Df = 3

Goodness-of-fit index = 1

BIC = 5.5e-15

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

Three predictors



3 predictors: uncorrelated

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

Poor measurement/fit

Model Chisquare = 68 Df = 3 Pr(>Chisq) = 1.4e-14

Chisquare (null model) = 89 Df = 6

Goodness-of-fit index = 0.74

Adjusted goodness-of-fit index = 0.12

RMSEA index = 0.47 90% CI: (0.37, 0.57)

Bentler-Bonnett NFI = 0.24

Tucker-Lewis NNFI = -0.56

Bentler CFI = 0.22

BIC = 54

Residuals

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

Fix variances

	Estimate	Std Error	z value	Pr(> z)	
1	0.11	0.11	1.0	3.0e-01	cancer <--- fingers
2	0.16	0.11	1.4	1.5e-01	cancer <--- teeth
3	0.26	0.12	2.2	2.5e-02	cancer <--- breath
8	0.81	0.11	7.0	2.0e-12	cancer <--> cancer

Better fit statistics (although chi square is same)

Model Chisquare = 68 Df = 6 Pr(>Chisq) = 1.3e-12

Chisquare (null model) = 89 Df = 6

Goodness-of-fit index = 0.74

Adjusted goodness-of-fit index = 0.56

RMSEA index = 0.32 90% CI: (0.26, 0.39)

Bentler-Bonnett NFI = 0.24

Tucker-Lewis NNFI = 0.26

Bentler CFI = 0.26

BIC = 40

Identical residuals

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

Latent Yellow

model.5

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

Latent Yellow misfits

Model Chisquare = 48 Df = 2 Pr(>Chisq) = 3.2e-11

Chisquare (null model) = 89 Df = 6

Goodness-of-fit index = 0.84

Adjusted goodness-of-fit index = 0.19

RMSEA index = 0.48 90% CI: (0.37, 0.61)

Bentler-Bonnett NFI = 0.45

Tucker-Lewis NNFI = -0.68

Bentler CFI = 0.44

BIC = 39

But paths are ok

Parameter Estimates

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

Latent Yellow residuals

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

Latent mouth and yellow

model.6

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

Latent mouth and yellow

Model Chisquare = 26 Df = 1 Pr(>Chisq) = 3.5e-07

Chisquare (null model) = 89 Df = 6

Goodness-of-fit index = 0.9

Adjusted goodness-of-fit index = -0.033

RMSEA index = 0.5 90% CI: (0.35, 0.68)

Bentler-Bonnett NFI = 0.71

Tucker-Lewis NNFI = -0.81

Bentler CFI = 0.7

BIC = 21

two latents - residuals

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

3 correlated predictors

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

Fully saturated

Model Chisquare = 2.2e-14 Df = 0 Pr(>Chisq) = NA

Chisquare (null model) = 89 Df = 6

Goodness-of-fit index = 1

BIC = 2.2e-14

Normalized Residuals

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
0.0e+00	0.0e+00	0.0e+00	1.3e-16	1.3e-16	5.3e-16

But, we can fix variances to 1

Model Chisquare = 2.2e-14 Df = 3 Pr(>Chisq) = 1

Chisquare (null model) = 89 Df = 6

Goodness-of-fit index = 1

Adjusted goodness-of-fit index = 1

RMSEA index = 0 90% CI: (NA, NA)

Bentler-Bonnett NFI = 1

Tucker-Lewis NNFI = 1.1

Bentler CFI = 1

BIC = -14

Fewer paths to estimate

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

Model residuals

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

Or, model one latent

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

A great model

Model Chisquare = 1.9e-10 Df = 2 Pr(>Chisq) = 1

Chisquare (null model) = 89 Df = 6

Goodness-of-fit index = 1

Adjusted goodness-of-fit index = 1

RMSEA index = 0 90% CI: (NA, NA)

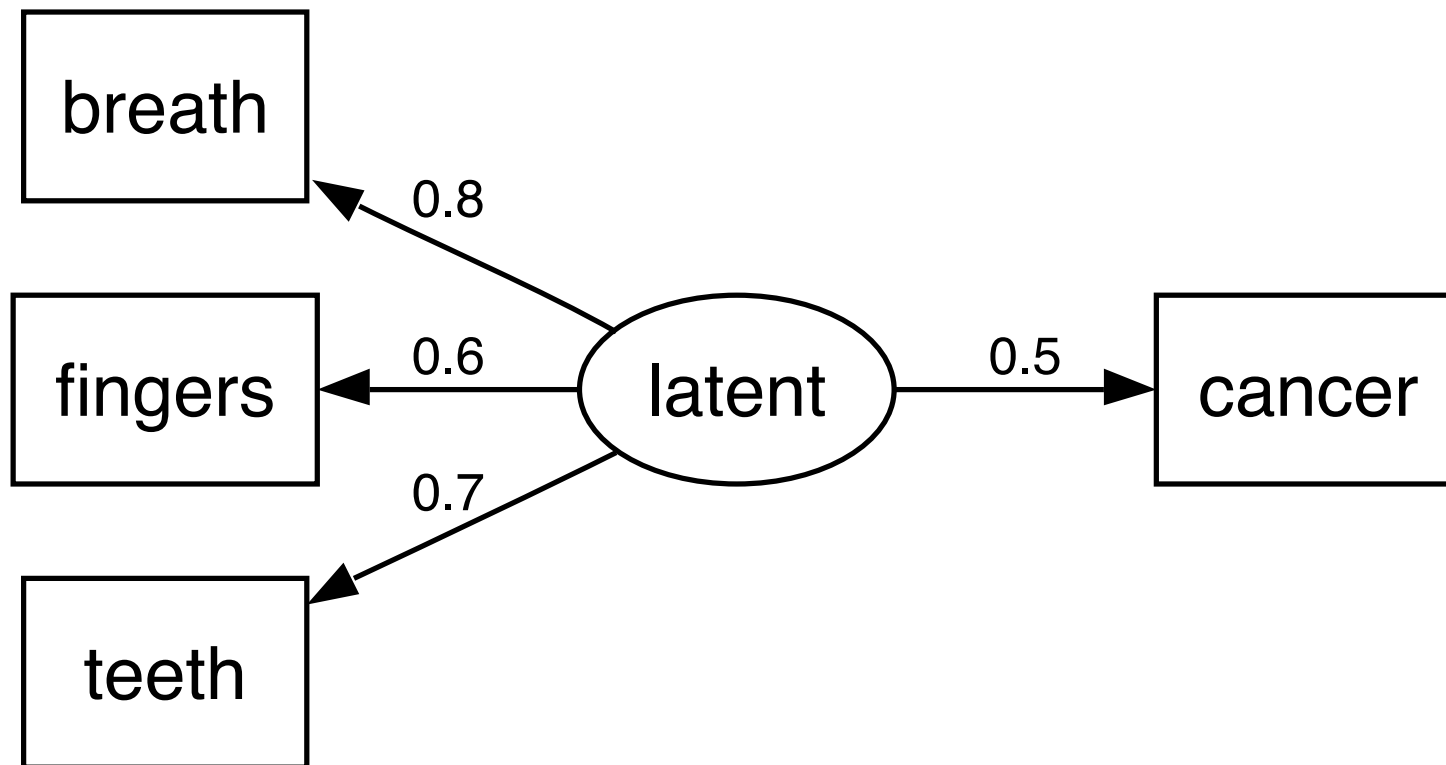
Bentler-Bonnett NFI = 1

Tucker-Lewis NNFI = 1.1

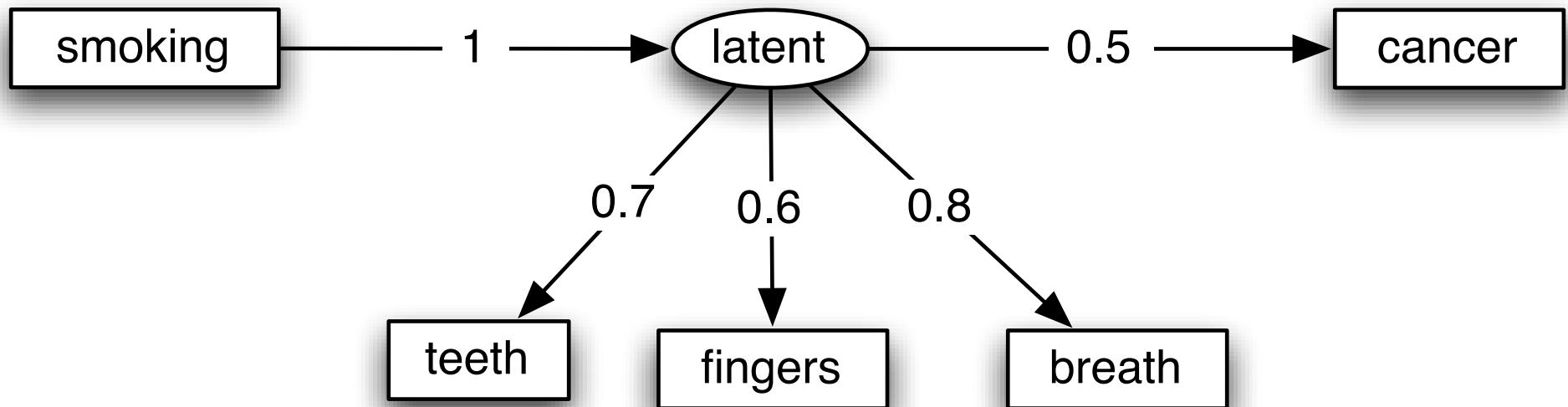
Bentler CFI = 1

BIC = -9.2

SEM alternative: but what is the latent?



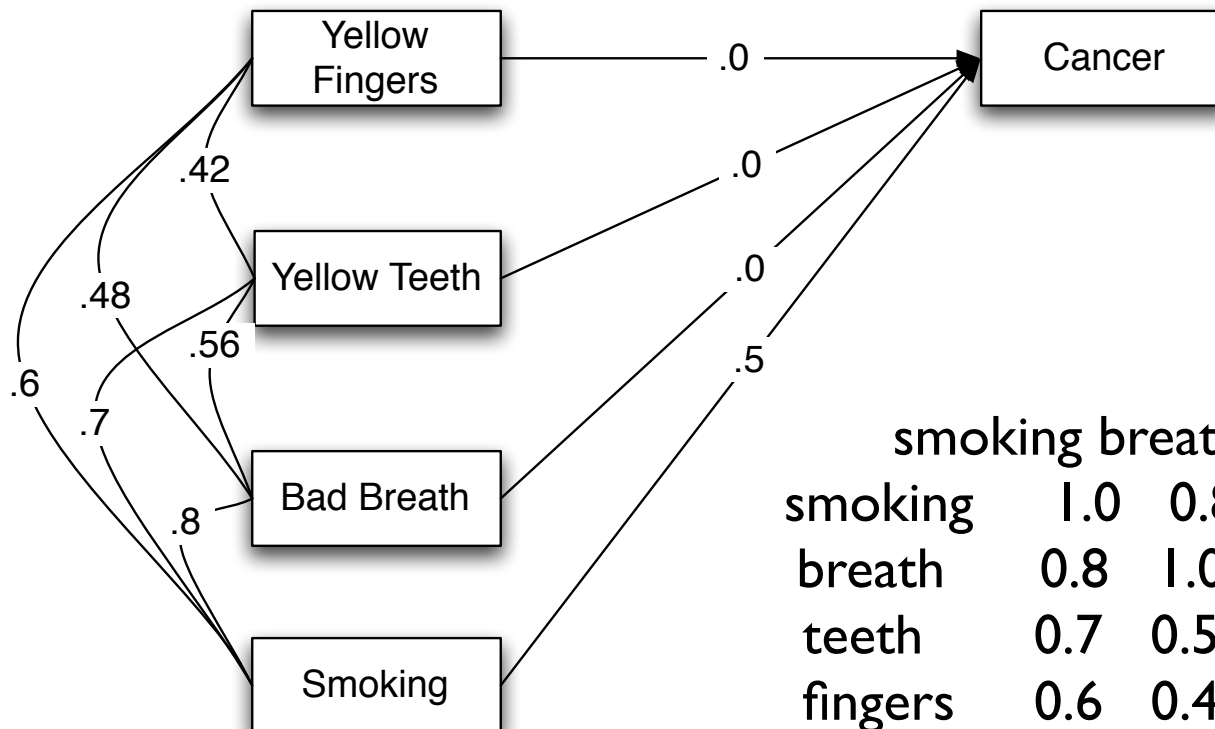
Smoking is measured perfectly



Properly specified

Time 1

Time 2

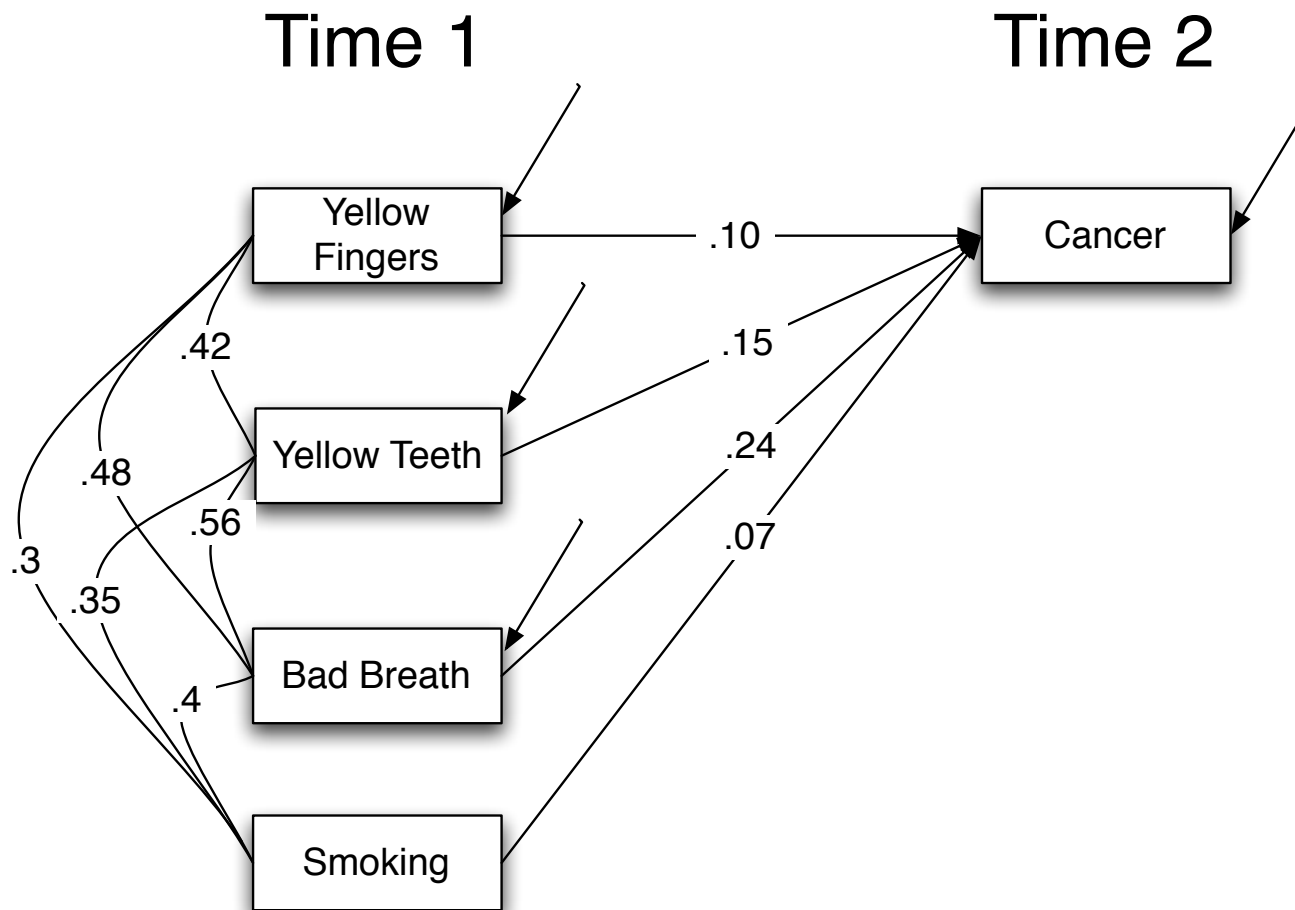


	smoking	breath	teeth	fingers	cancer
smoking	1.0	0.80	0.70	0.60	0.50
breath	0.8	1.00	0.56	0.48	0.40
teeth	0.7	0.56	1.00	0.42	0.35
fingers	0.6	0.48	0.42	1.00	0.30
cancer	0.5	0.40	0.35	0.30	1.00

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)

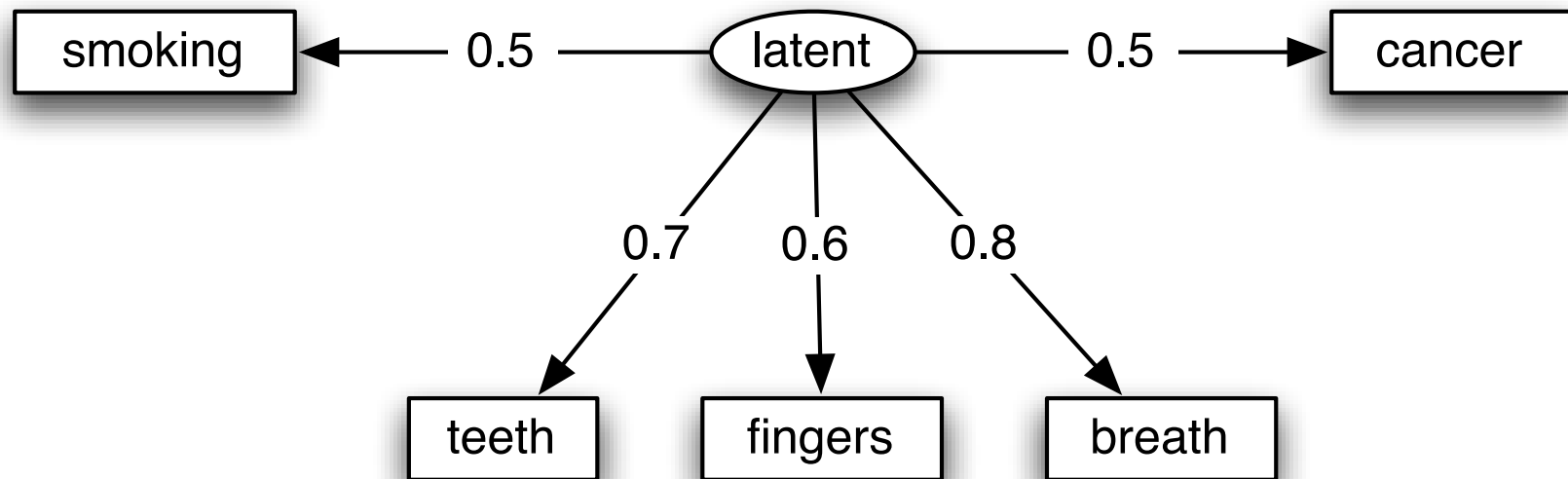
Bentler-Bonnett NFI = 1

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

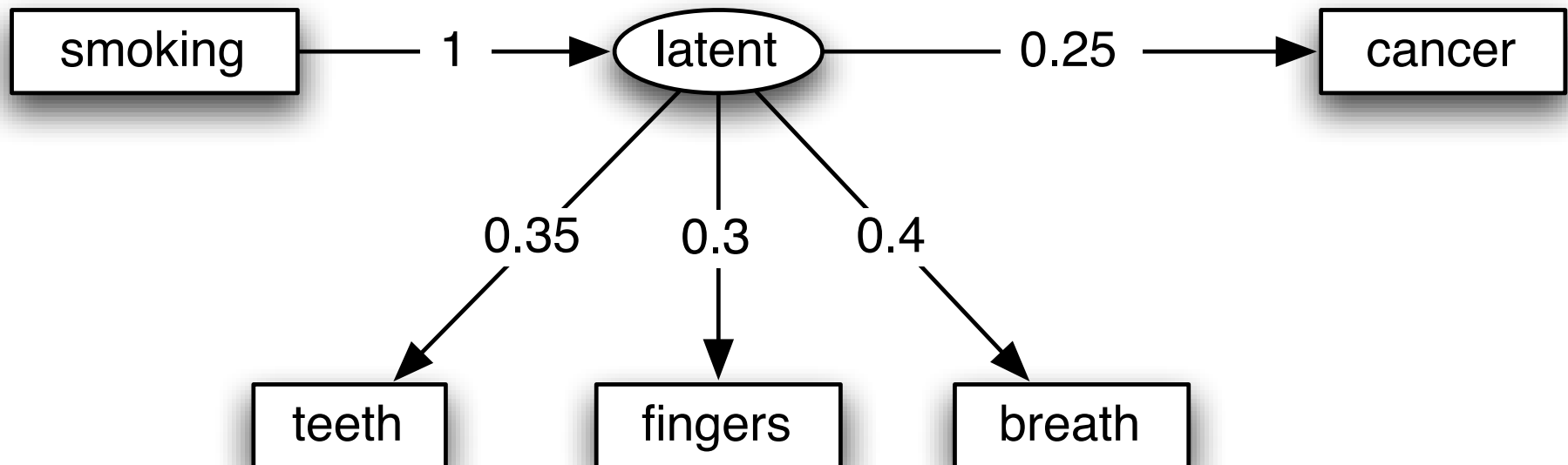
Bentler CFI = 1

BIC = -28

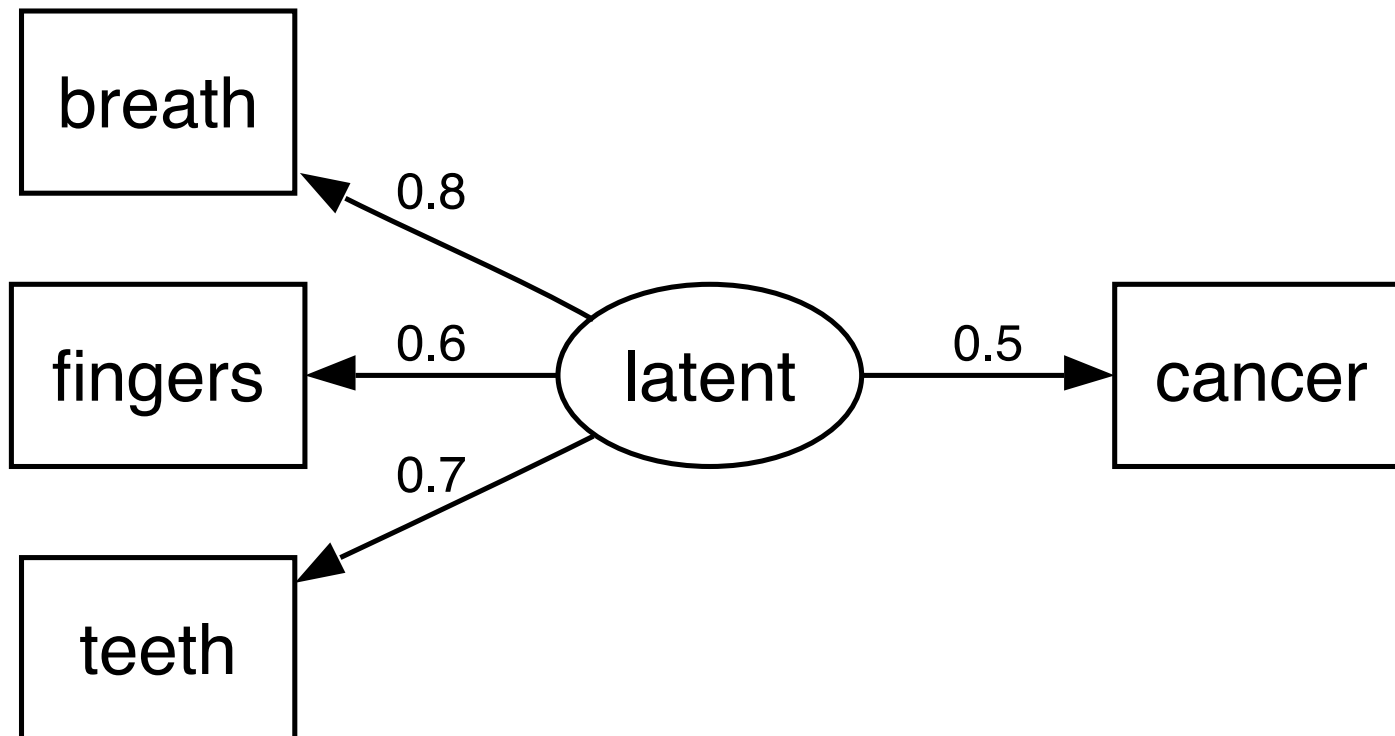
“Imperfect” smoking, modeled with no error

	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

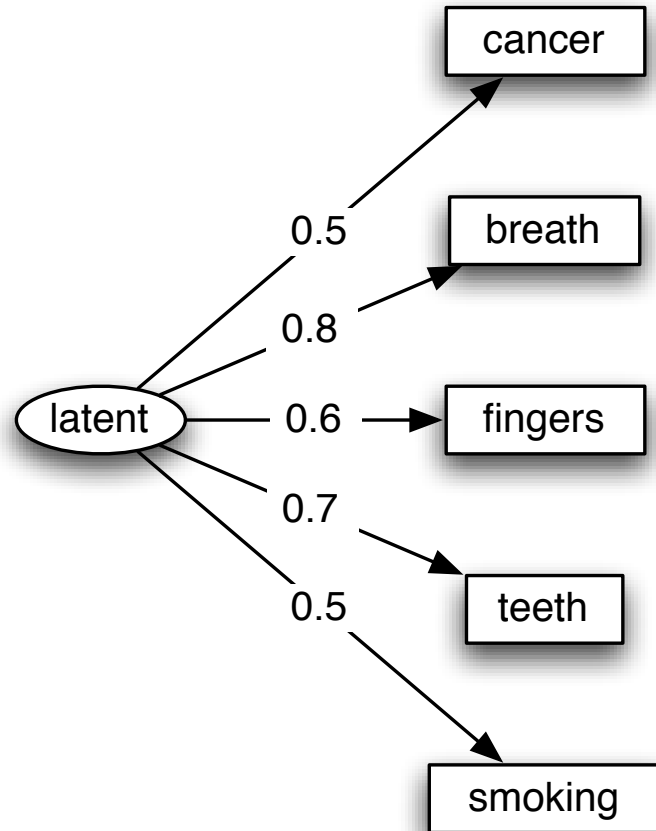
Smoking is not measured perfectly



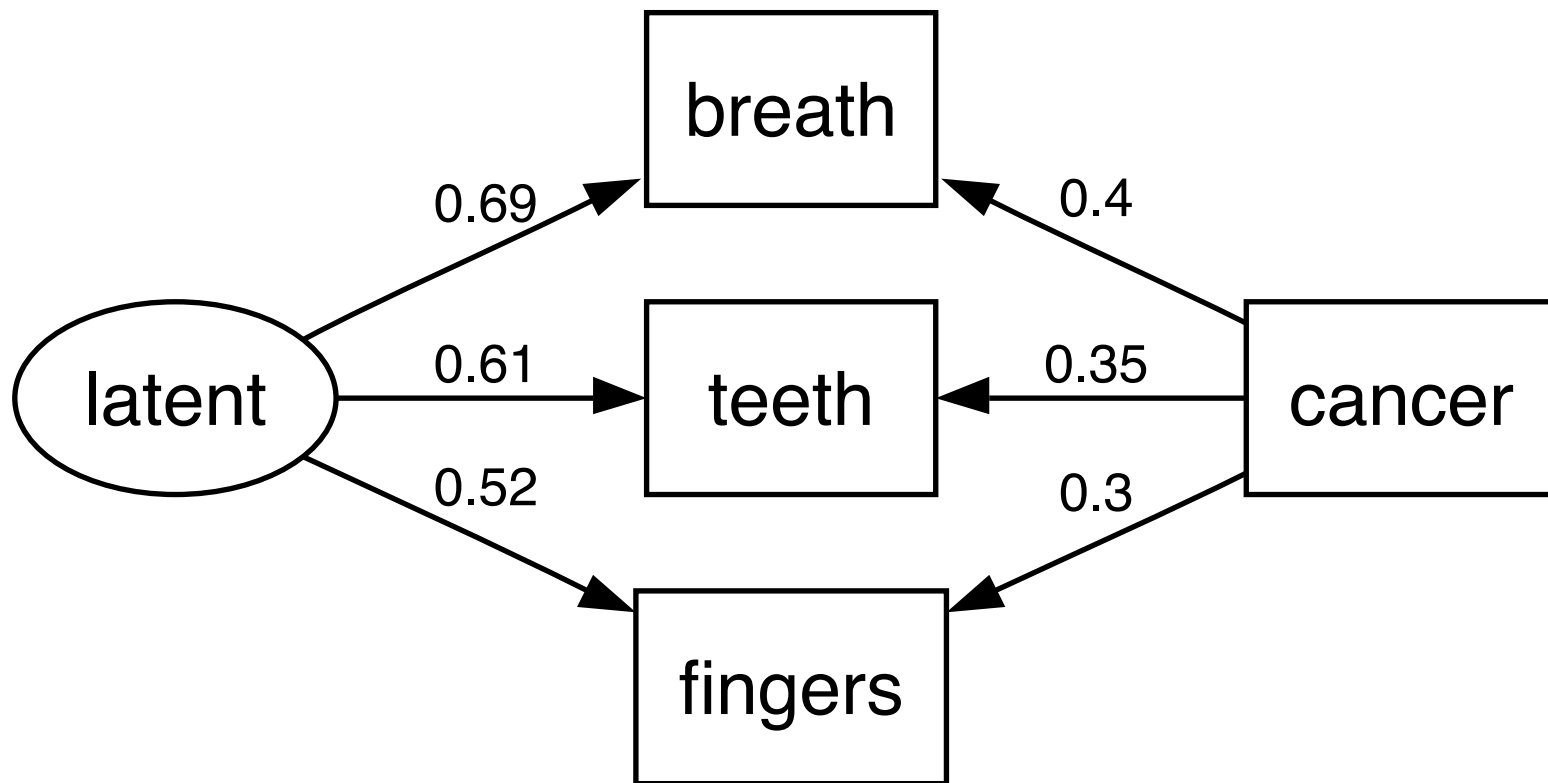
What is the causal variable



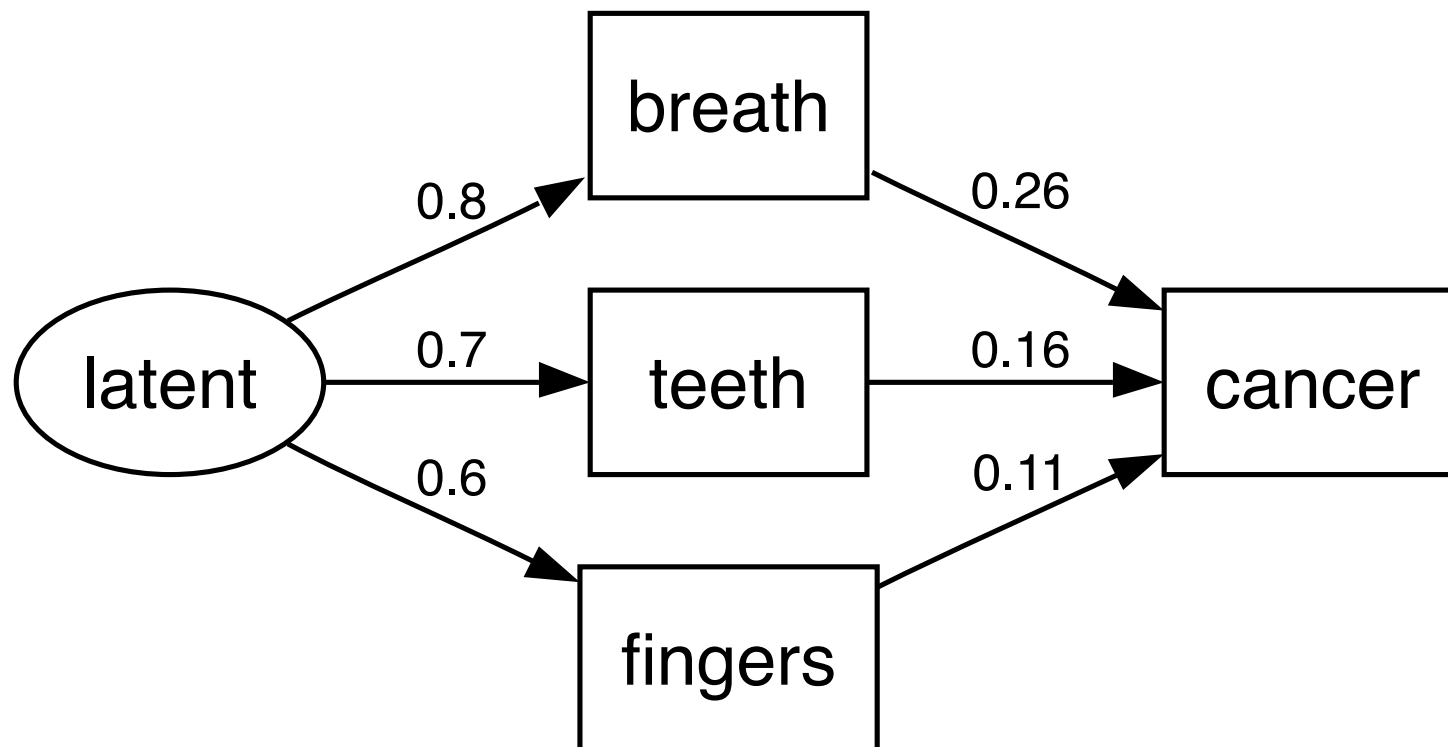
Something causes one to smoke and get cancer: is it E?



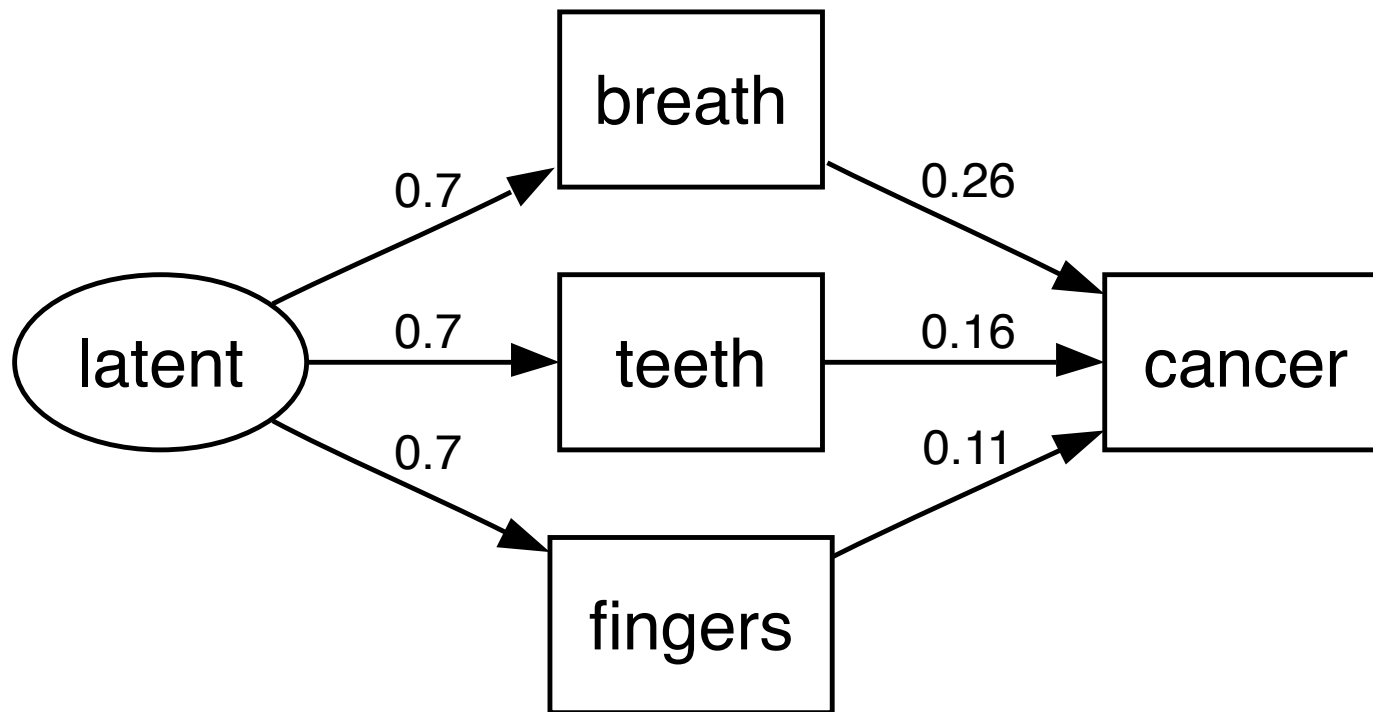
Cancer as cause

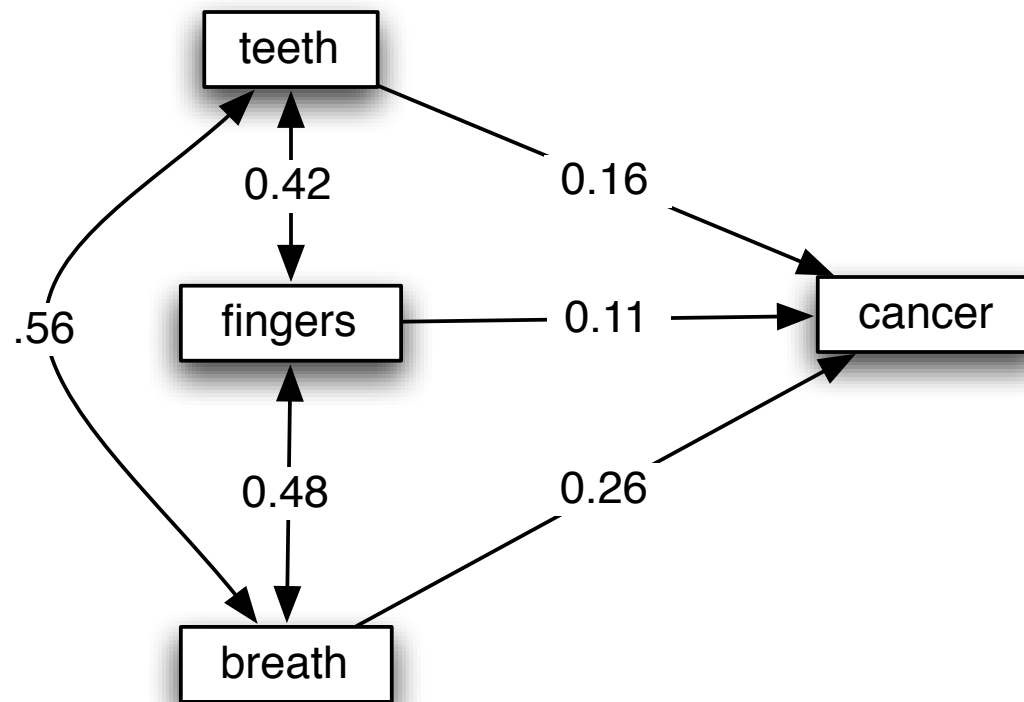


Cancer as caused



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)

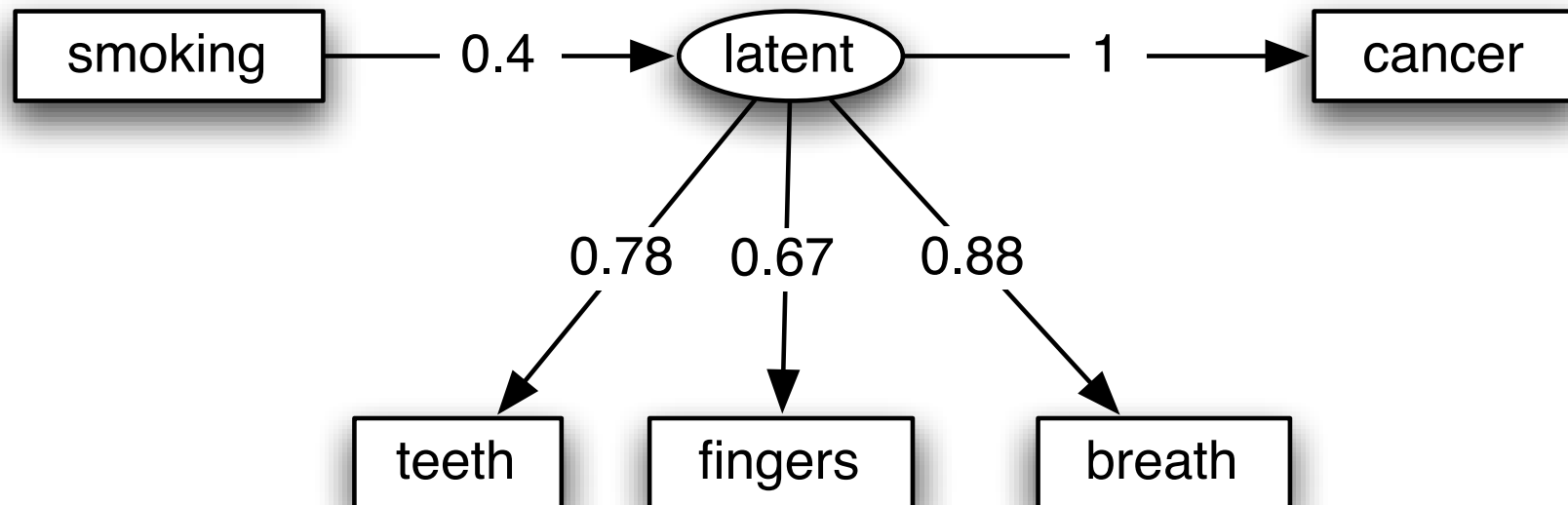
Bentler-Bonnett NFI = 0.76

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. Σ is the modeled covariance matrix

D. if model is correct, F is asymptotically chi square

Distribution free Fit functions (after Browne)

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

II. Let Σ 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. $RMSEA = \sqrt{\frac{\text{Chi}^2/df - 1}{N - 1}}$

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

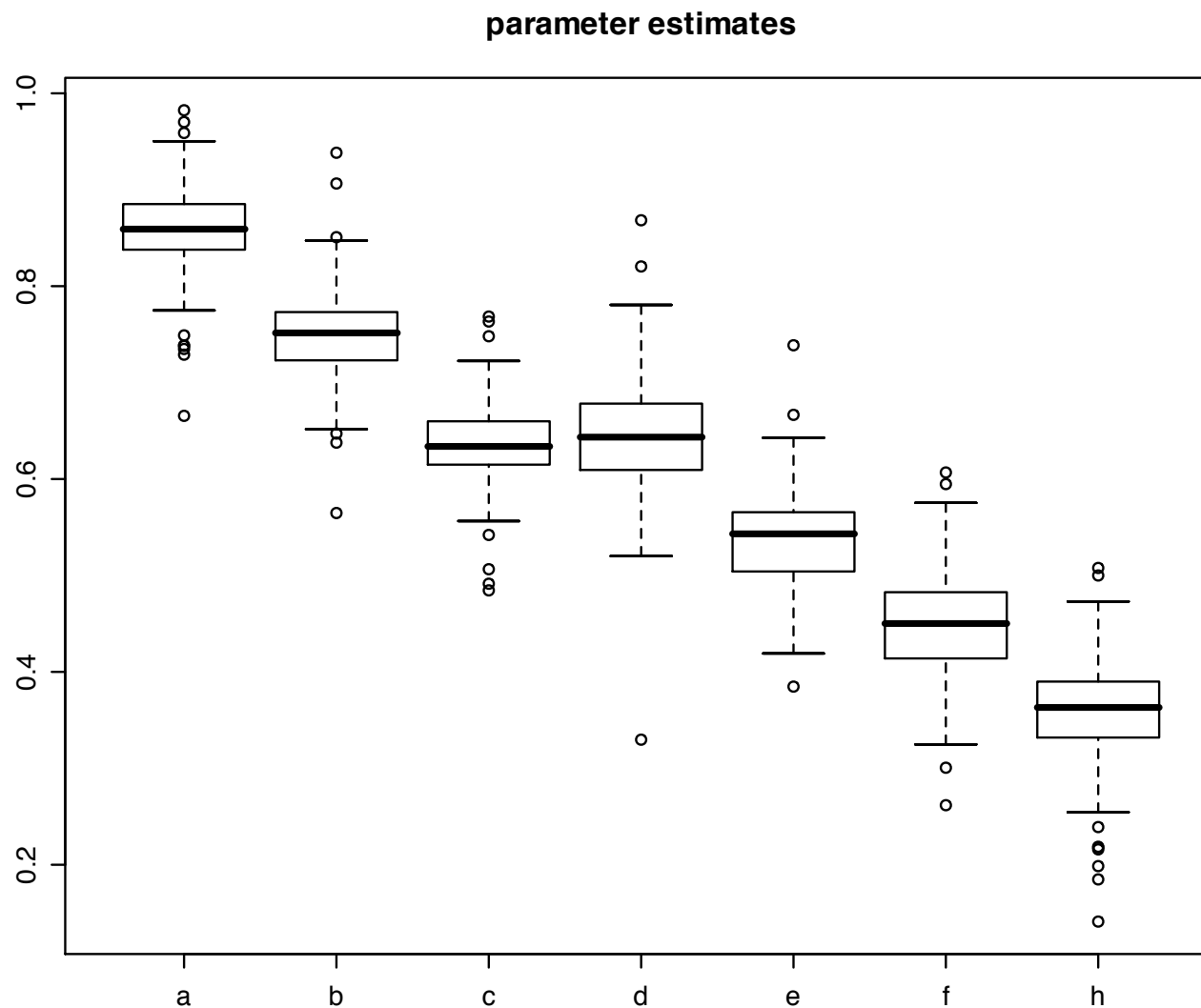
Examples of fit (2 factors - 6 variables)

- 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

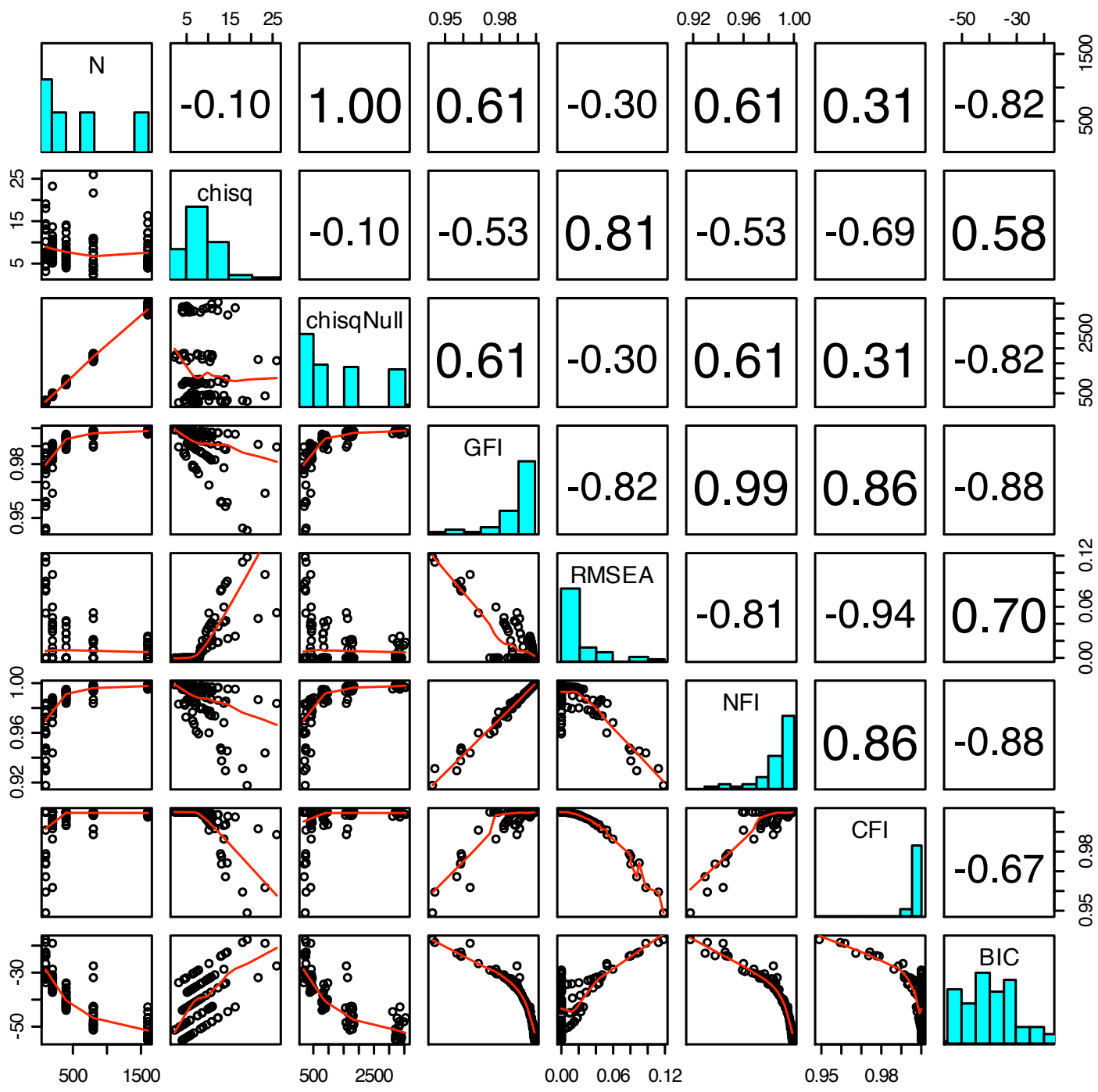
Estimation

	[,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

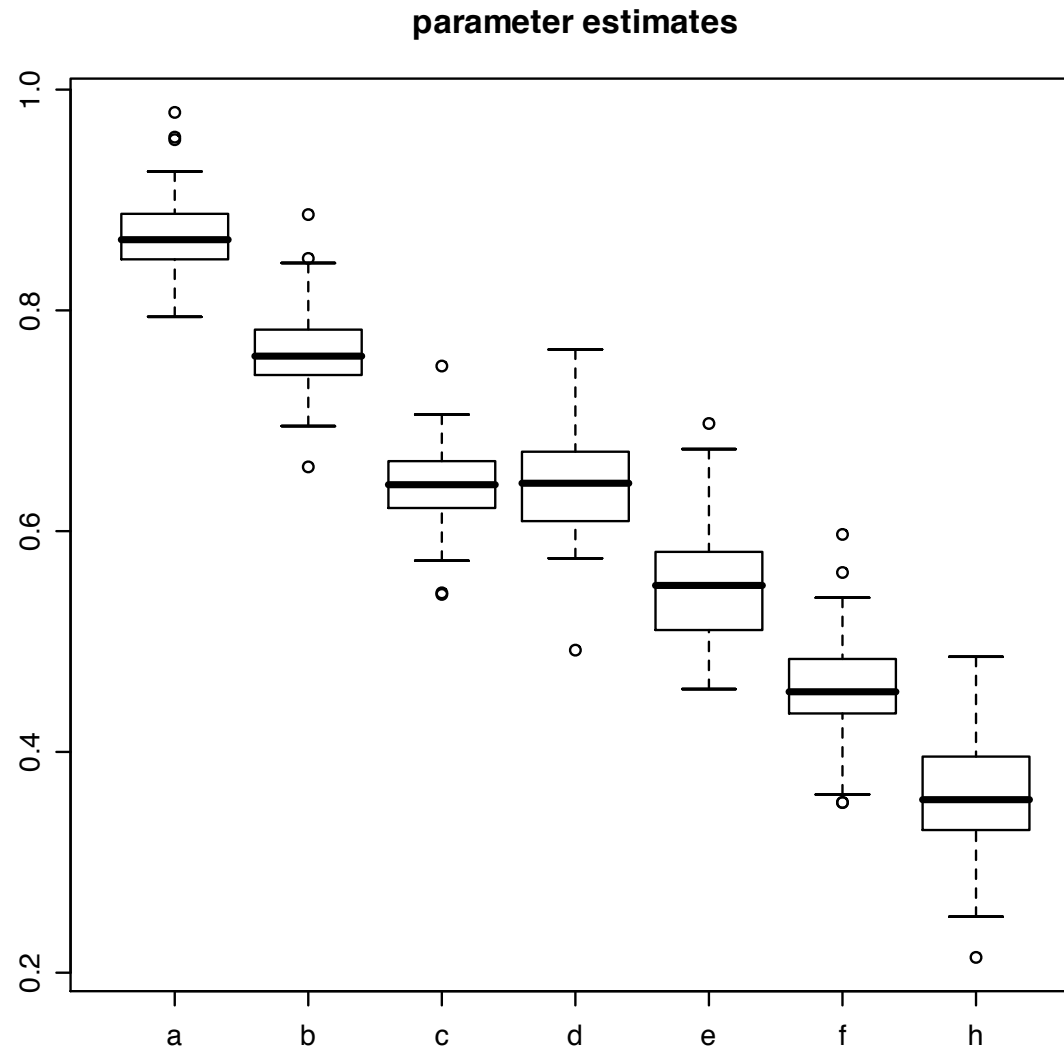
$\phi = .4$

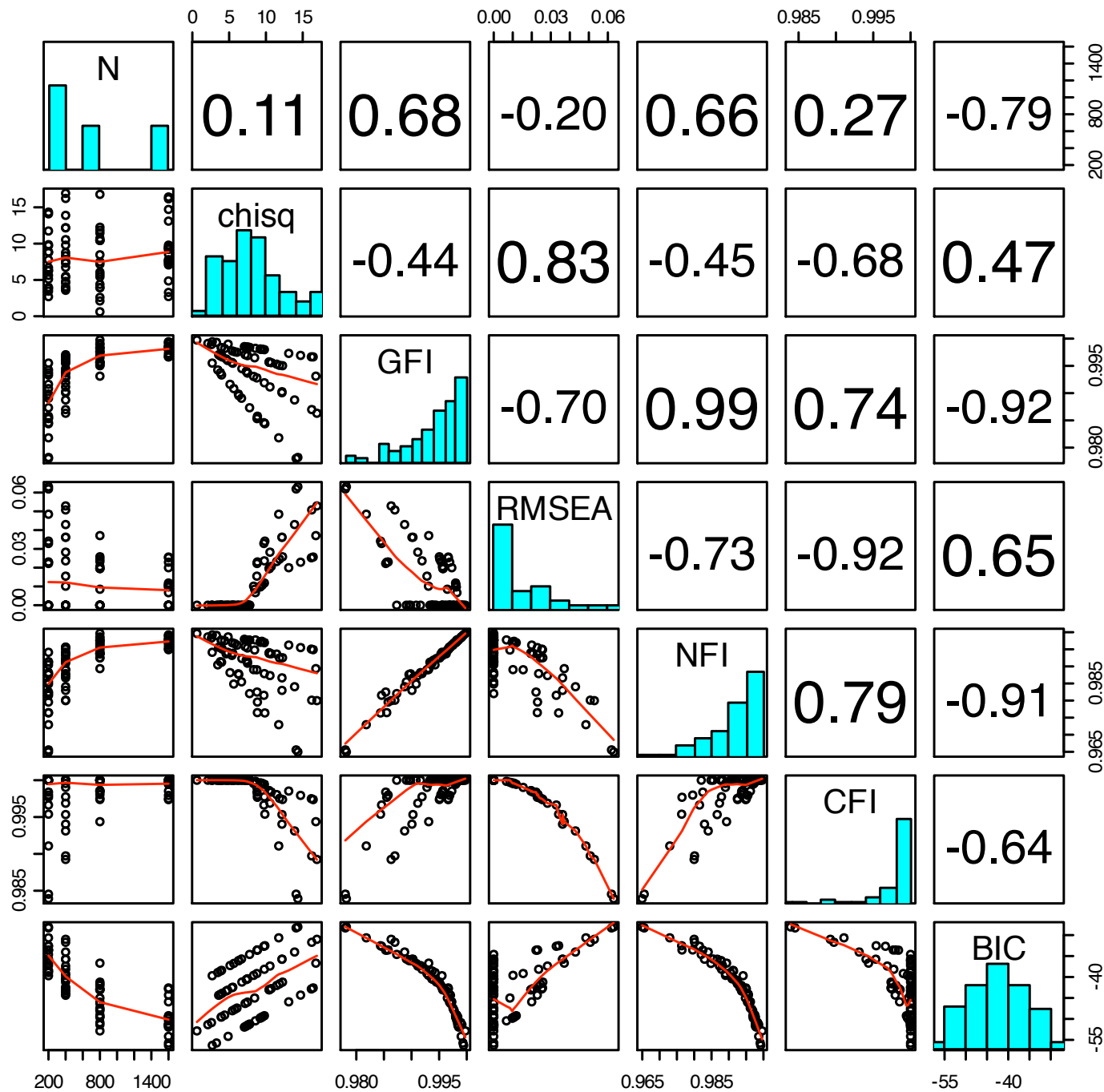


n=
100,
200,
400,
800,
1600



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

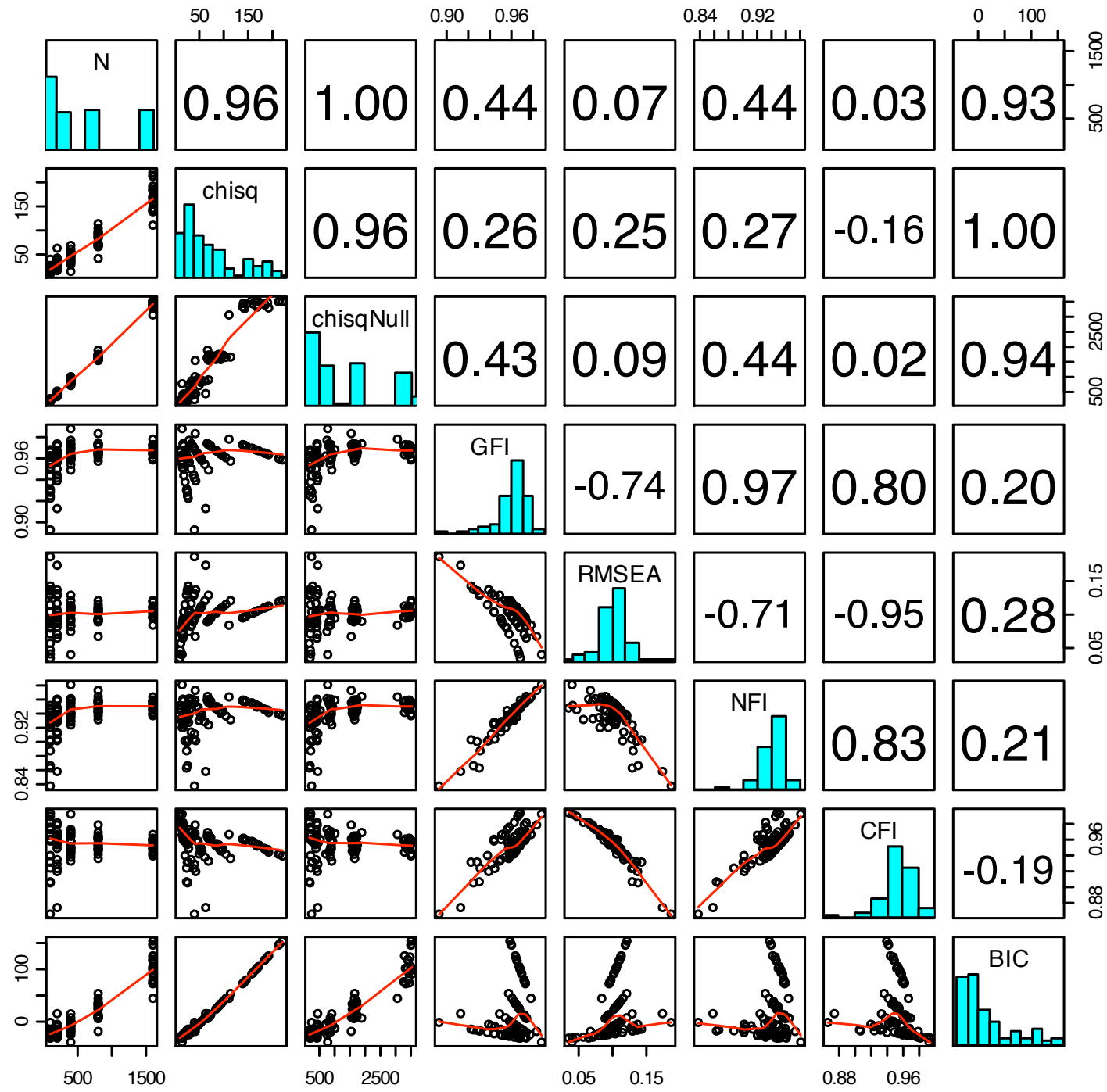




n=
200,
400,
800,
1600

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