PSY792F SEM

Week 6 – Latent Variable Modeling

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Overview of today's lecture

- Today will be a lot of lecture
- Rather than give all the background then the code I will sprinkle in the code throughout
- As with regression where you don't write up the results of your assumption testing *(unless something is violated)*, a lot of the preliminary work with SEM doesn't make it into the write up, unless there are issues where you have to deviate from what is expected.

Testing theory – all models are wrong

- Using the scientific method we develop a theory, design a study to test that theory, collect data, and then run analyses….

…. "the best one can hope for is to identify a parsimonious, substantively meaningful model that fits the observed data adequately well…."

- MacCallum and Austin, 2000

Latent Variable Structural Equation Modeling

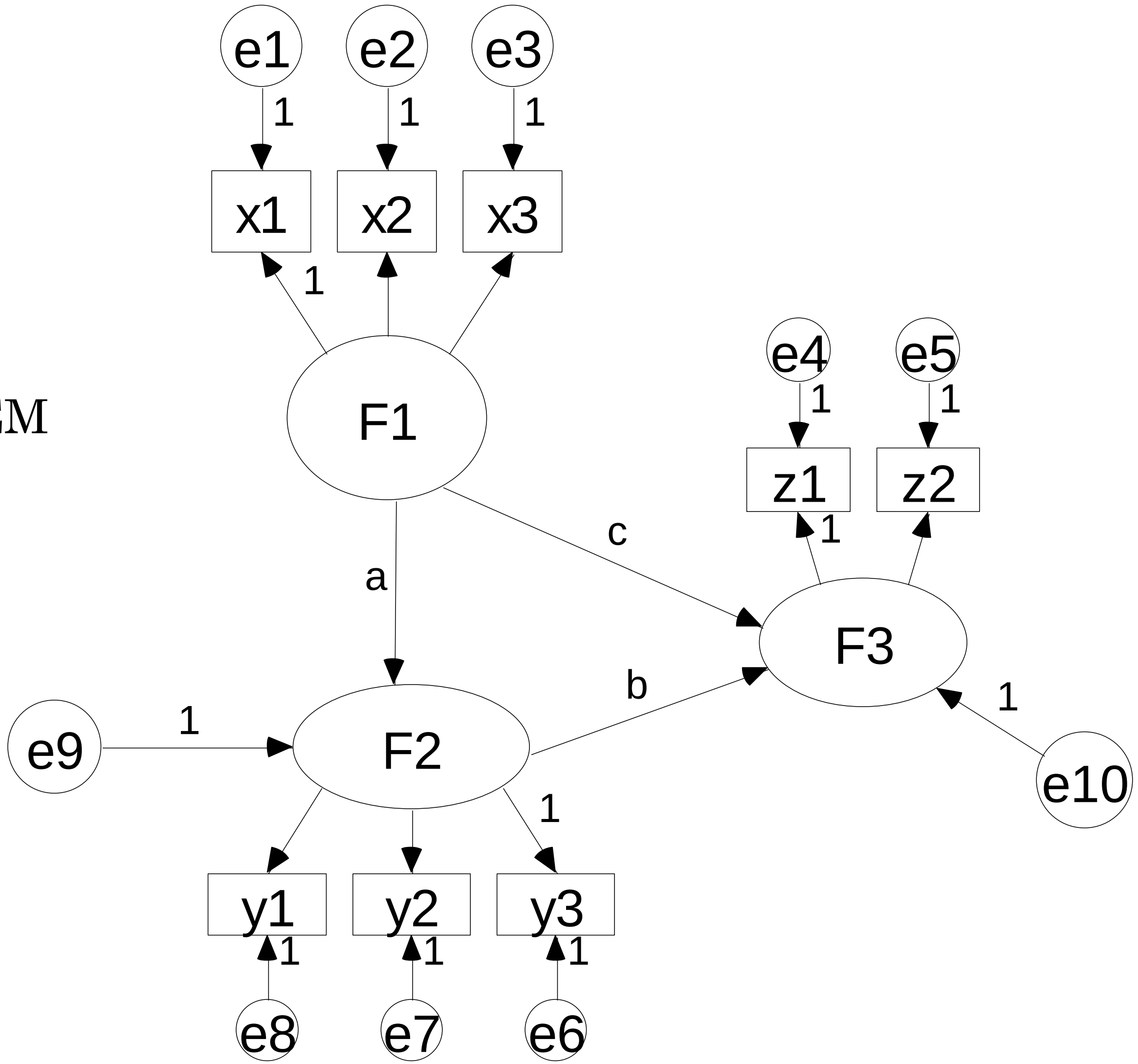
- Used to study relationships among multiple outcomes involving latent variables.
- Estimate and test direct and indirect effects in a system of regression equations for observed and latent variables.
- Model identification, estimation, testing, and modification are the same as for CFA.

SEM in Model Form

Note: no error on F1
Because it is purely
Exogenous

This is a mediation SEM

F1 – F2 – F3



# of indicators:
"Two might be fine,
three is better,
four is best,
and anything more
is gravy" (Kenny,1979)

Matrix Notation

- SEM made up of 8 different matrices (Β, Γ, Λy, Λx, ϕ, ψ, Θε, Θδ)
- Measurement models *(for the CFAs)*: $Y = \Lambda_y \eta + \varepsilon$ and $X = \Lambda_x \xi + \delta$

  Λ_y and Λ_x (p x m) matrices of loadings

  ε (p x 1) vector of measurement errors for y dependent vars, with covariance matrix Θε

  δ (q x 1) vector of measurement errors for x independent vars, with covariance matrix Θδ

- Structural model: $\eta = B\eta + \Gamma\xi + \zeta$

  η (m x 1) vector of endogenous latent variables

  Β (m x m) matrix of structural coefficients relate latent dependent variables to one another (with elements β)

  Γ (m x n) matrix of structural coefficients relate latent independent to latent dependent variables (with elements γ)

  ξ (n x 1) vector of exogenous latent variables, with (n x n) matrix of covariances among exogenous variables, Φ

  ζ (m x 1) vector of errors in the conceptual model, with (m x m) matrix of covariances among errors, ψ

Advantages over Path Analysis:

- Can explicitly incorporate/account for measurement error in the model
  - Measurement error in independent variables → Attenuation in regression slopes
  - Measurement error in dependent variables → Increased standard errors
  - *Path analysis assumes variables are measured without error.*

  - Single indicator: with known amount of measurement error
  - Multiple indicators: CFA

Considerations in SEM

- Model specification (a priori, confirmatory)
  - Misspecification in measurement model
  - Misspecification in structural model
- Identifiability
  - Identifiable measurement model
  - Identifiable structural model
- Believability (plausibility); theoretically justifiable
- Quality (fit, estimates, power)

How to approach SEM?

- There are a variety of strategies.

SEM 5 Step approach

1. Establish a CFA model (when latent variables are involved)
2. Establish a model of the relationships among the observed and/or latent variables
3. Estimate the model
4. Modify the model
5. Interpret the model

Two-step modeling

1. Develop measurement model (CFA) relating observed variables to latent variables. Examine goodness of fit of this model on its own. Examine correlations between all variables (usually latent variables) of interest by looking at correlations between factors from CFA.

2. Develop full structural equation model. That is, change the "spuriously correlated" relationships in the CFA to impose theoretical causal direct effects between variables and drop relationships not assumed by theory. Examine goodness of fit of this model as a whole.

Anderson, J.C. and Gerbing, D.W. (1988) Psychological Bulletin

Four-step modeling

- Each factor must have at least 4 indicators

Steps:

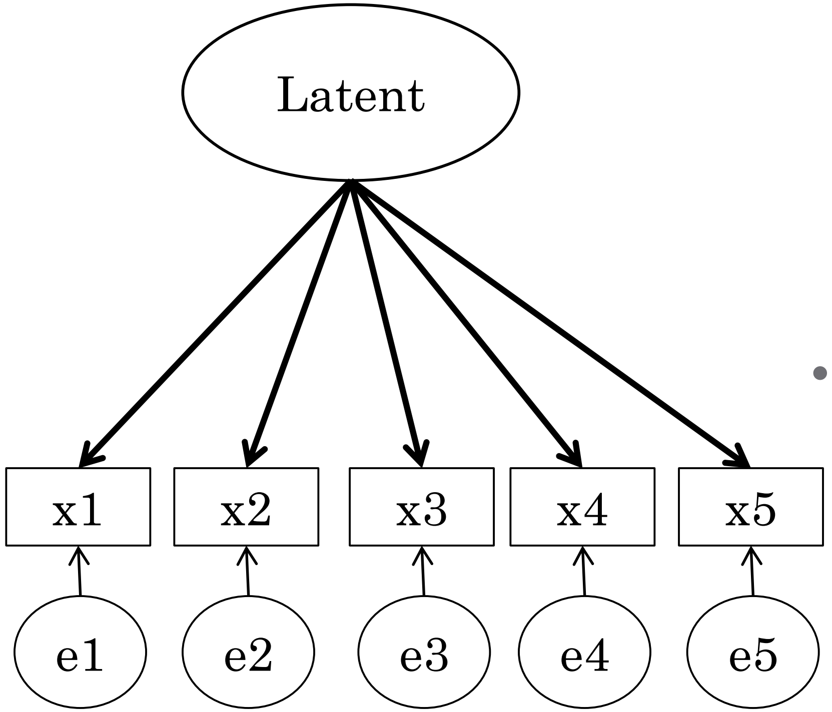
1. Exploratory common factor model
2. CFA with some coefficients fixed to 0
3. Structural model where at least one unanalyzed association is re-specified as direct effect
4. Test a priori hypotheses about parameters, e.g., add equality constraints

- If the fit of a model with fewer constraints (EFA) fits poor then models with more constraints will fit worse

Which approach to use?

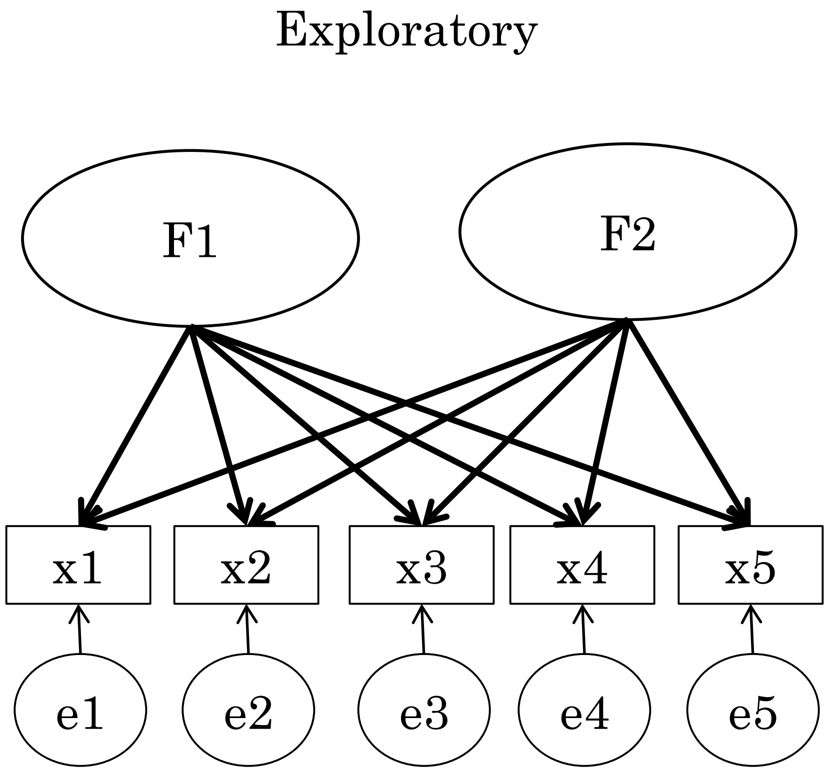
- All are acceptable.
- Essentially, you need to feel confident with:
  - Your measurement model
    - Number of factors (latent variables)
    - Factor loadings
    - Model fit
    - Invariance (if applicable)
  - Your structural model
    - The model makes sense according to theory
    - The model tests what you want it to test
    - Model fit
    - A more parsimonious model won’t get the job done

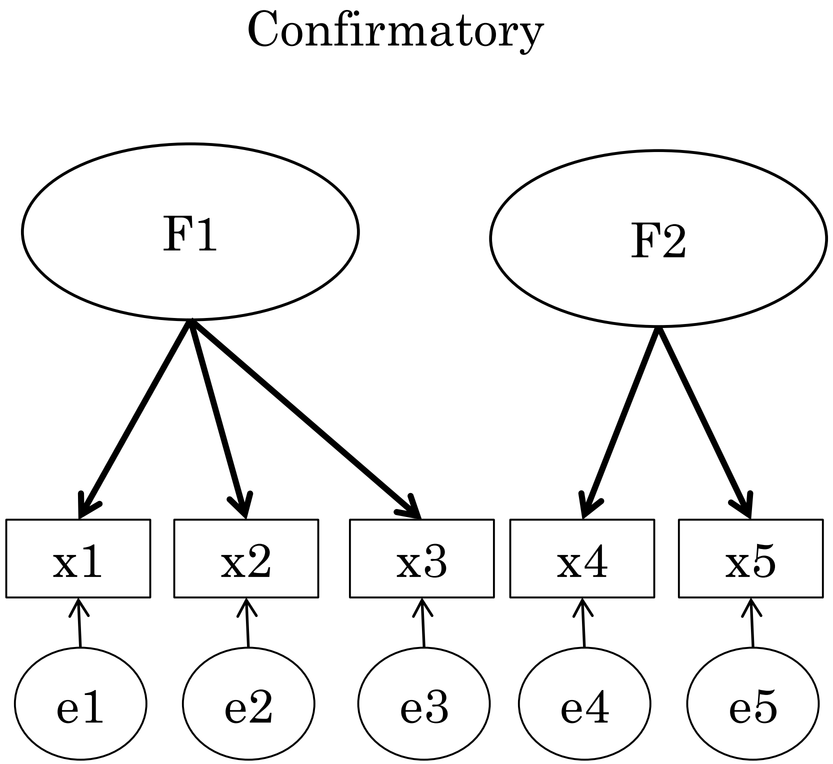
Measurement Models



- Exploratory factor analysis
  - Data driven
  - Obtain “simple structure”
  - Can be done in SPSS
- Confirmatory factor analysis
  - Theory driven
  - Based on model fit
  - Should not be done in SPSS

Measurement Models





Exploratory Factor Analysis

- EFA is generally used to explore the factor structure of a measure and examine its internal reliability and is often recommended when researchers have few hypotheses about the underlying factor structure of their measure (all items load on all factors).
- EFA has three basic decision points:
  - (1) decide the number of factors (or Kaiser-Guttman rule)
  - (2) choose an extraction method
    - e.g., PCA, PFA, ML, ULS, GLS
  - (3) choose a rotation method
    - e.g., orthogonal, oblique

  *The defaults in Mplus are good choices

Eigenvalues

- Variance in all variables which is accounted for by a factor
- *Interpretation:* Eigenvalues measure the amount of variation in the total sample accounted for by each factor
- *Extraction sums of squared loadings:* A factor's eigenvalue may be computed as the sum of its squared factor loadings for all the variables.

Total Variance Explained

Factor	Initial Eigenvalues			Extraction Sums of Squared Loadings			Rotation Sums of Squared Loadings		
	Total	% of Variance	Cumulative %	Total	% of Variance	Cumulative %	Total	% of Variance	Cumulative %
1	4.179	41.793	41.793	3.784	37.843	37.843	2.486	24.865	24.865
2	1.442	14.416	56.209	1.094	10.936	48.779	1.685	16.846	41.711
3	1.205	12.046	68.255	.732	7.318	56.097	1.439	14.385	56.097
4	.757	7.568	75.823						
5	.677	6.773	82.596						
6	.549	5.491	88.088						
7	.424	4.240	92.327						
8	.396	3.959	96.286						
9	.261	2.609	98.895						
10	.110	1.105	100.000						

Extraction Method: Principal Axis Factoring.

Rotation

- Rotation serves to make the output more understandable and is usually necessary to facilitate the interpretation of factors, by maximizing high correlations between factors and variables and minimizing low correlations
  - No rotation
  - Orthogonal - no factor correlation matrix is produced, "varimax"
  - Oblique - allow the factors to be correlated, "promax"
- The sum of eigenvalues is not affected by rotation, but rotation will alter the eigenvalues (and % of variance explained) of particular factors and will change the factor loadings

Factor (Component) Loading Matrices

- Orthogonal rotation – coefficients represent variance in a measured variable explained by a factor for each eigenvalue
- Oblique rotation - structure and pattern matrices
  - *structure matrix* is simply the factor loading matrix as in orthogonal rotation, coefficients represent unique and common variance explained by each factor
  - *pattern matrix*, in contrast, contains coefficients which just represent unique contributions.

Choosing a Rotation Method

- Orthogonal or Oblique?
  - How correlated are the factors?
  - What are the goals of the analysis?
- Adequacy of rotation
  - Compare patterns of correlations
    - Are patterns represented in the rotated solution?
    - Do correlated variables tend to load on same factor?
    - Do specific variables load on obvious factors?
- Simple Structure – several variables correlate with each factor and only one factor correlates highly with each variable
- Plotting distance, clustering and direction of points relative to factor axes

Number of Factors?

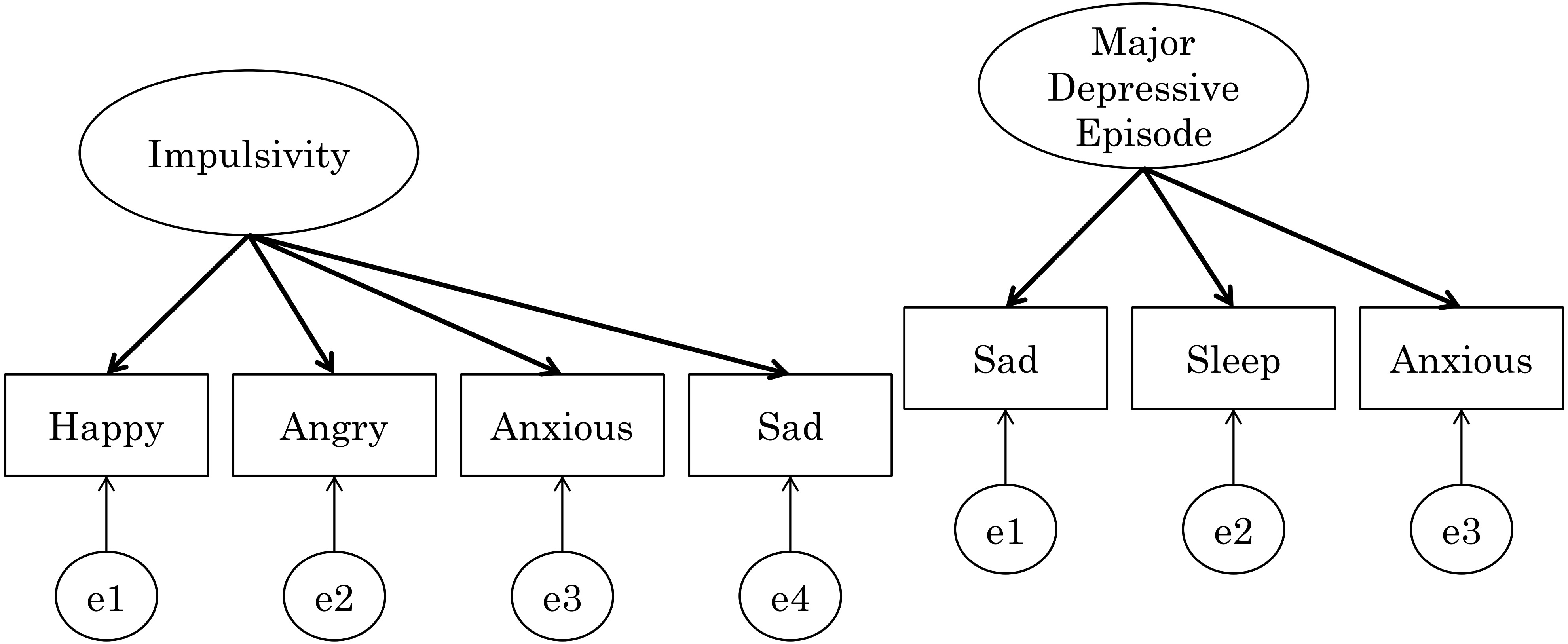
- *Comprehensibility*.
- *Kaiser criterion:* drop all components with eigenvalues under 1.0;
- *Scree plot:* plots the factors as the X axis and the corresponding eigenvalues as the Y axis. Cattell's scree test says to drop all further components after the one starting the elbow.
- *Other considerations:*
  - Percent variance explained (> 60%)
  - Factor loadings (greater than .4)
  - No cross-loadings

Approaches to Measurement Modeling

- Exploratory
  - Start with large number of items and very large sample
  - Use random split-half to "validate" an initial measurement model using EFA, then "replicate" in second split-half with second EFA
- Confirmatory
  - Theory-based or conducted after initial EFA yields interpretable model that is consistent with theory
  - Ideally conduct random split-half with validation and replication samples with CFA

Naming Fallacy and Reification

- Just because a factor is named – does not mean that it is understood or correctly labeled (fallacy) or that it corresponds to a real thing (reification)…

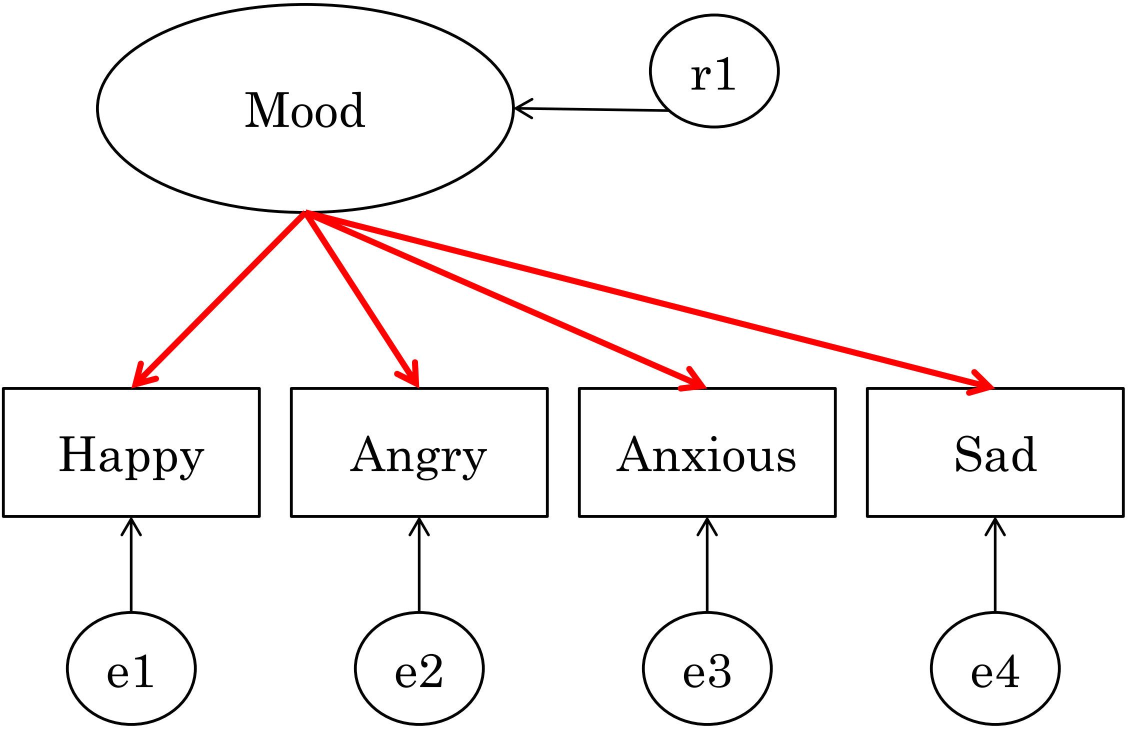


New Mplus code “by” statement

- To create a latent variable use the following code:
- F1 by x1 x2 x3 x4;
- In case its not obvious, you can name your latent variable anything you want, e.g.,
- Mood by happy anxious angry sad;

Interpretation of Estimates in CFA

Factor loadings interpreted as regression coefficients (e.g., an increase in 1 point on "mood" is associated with a 1.135 decrease in angry, a 1.402 decrease in anxious, and 1.563 decrease in sad)



Covariances

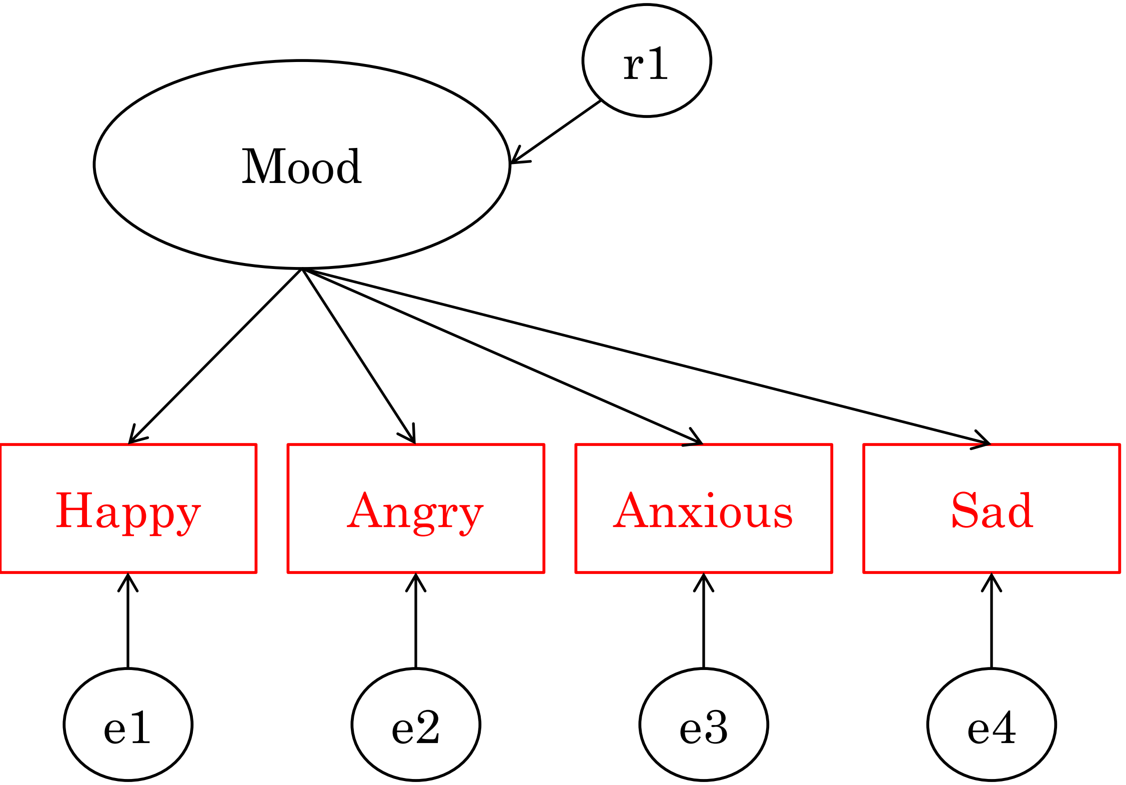
	HAPPY	ANGRY	ANXIOUS	SAD
HAPPY	0.461			
ANGRY	-0.206	0.495		
ANXIOUS	-0.230	0.287	0.865	
SAD	-0.279	0.307	0.392	0.676

MODEL RESULTS

	Estimate	S.E.	Est./S.E.	P-Value
MOOD BY				
HAPPY	**1.000**	0.000	999.000	999.000
ANGRY	**-1.135**	0.063	-18.086	0.000
ANXIOUS	**-1.402**	0.082	-17.020	0.000
SAD	**-1.563**	0.082	-19.167	0.000
Intercepts				
HAPPY	2.747	0.019	144.621	0.000
ANGRY	1.143	0.020	58.079	0.000
ANXIOUS	1.310	0.026	50.352	0.000
SAD	1.077	0.023	46.800	0.000
Variances				
MOOD	0.176	0.016	10.885	0.000
Residual Variances				
HAPPY	0.285	0.014	21.020	0.000
ANGRY	0.268	0.014	19.021	0.000
ANXIOUS	0.518	0.025	20.677	0.000
SAD	0.246	0.019	13.111	0.000

Interpretation of Estimates in CFA

Intercepts interpreted as the intercept of the regression model (e.g., mean on each item when “mood” = 0, so happiness mean = 2.747, angry = 1.143, anxious = 1.310, sad = 1.077)



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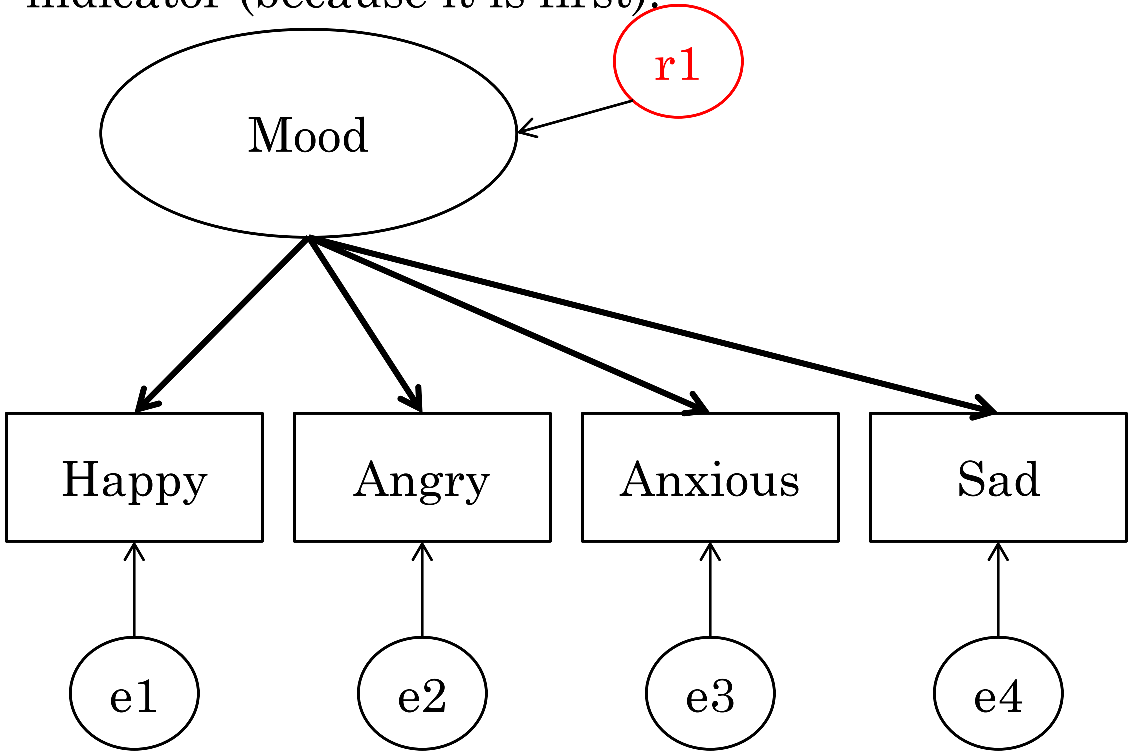
Interpretation of Estimates in CFA

Variance of the latent factor – variability in "mood" as scaled by the happy indicator (because it is first).



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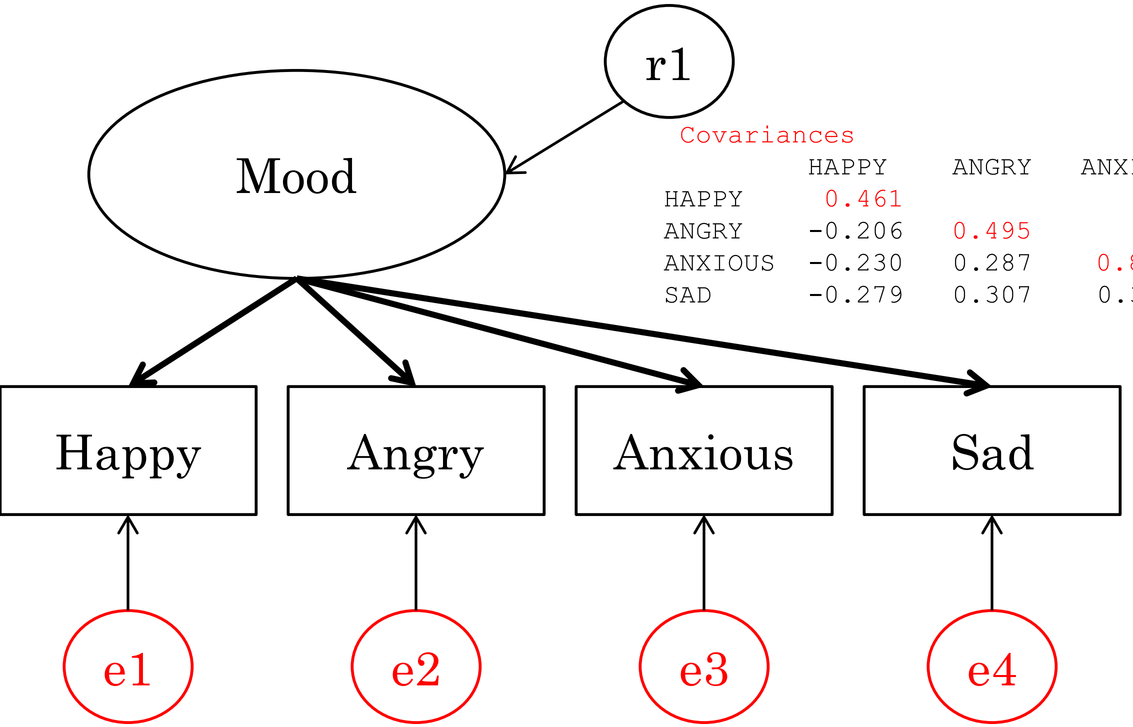
Interpretation of Estimates in CFA

<u>Residual variances</u> – ratio of unstandardized measure variance over the observed variance of the indicator = proportion of unexplained variance (1-this ratio = proportion of explained variance).... For Happy this ratio is 0.285/0.461 = 0.618, thus the R^2 for Happy = 1-.618 = .382. Angry 0.268/0.495 = .541, R^2 for Angry = 1-0.541 = .459. Anxious 0.518/0.865 = .599, R^2 = 1-.599 = .401. Sad 0.246/0.676 = .363, R^2 =.637



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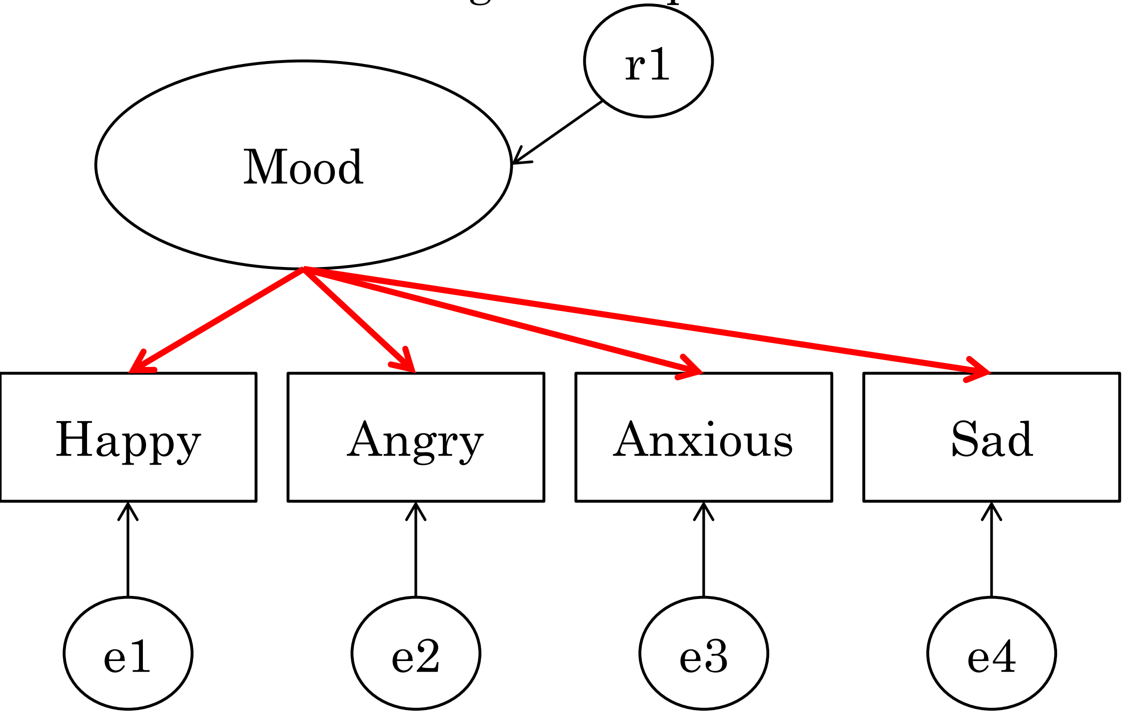
Interpretation of Estimates in CFA

Standardized factor loadings are estimated correlations between indicator and factor (when indicator loads on only 1 factor) this can be squared to indicate R^2 for each indicator. When indicator loads on multiple factors then standardized loading is interpreted as ß



STDYX Standardization

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MOOD BY				
HAPPY	0.618	0.022	28.449	0.000
ANGRY	-0.677	0.021	-33.011	0.000
ANXIOUS	-0.633	0.021	-29.681	0.000
SAD	-0.798	0.018	-44.369	0.000

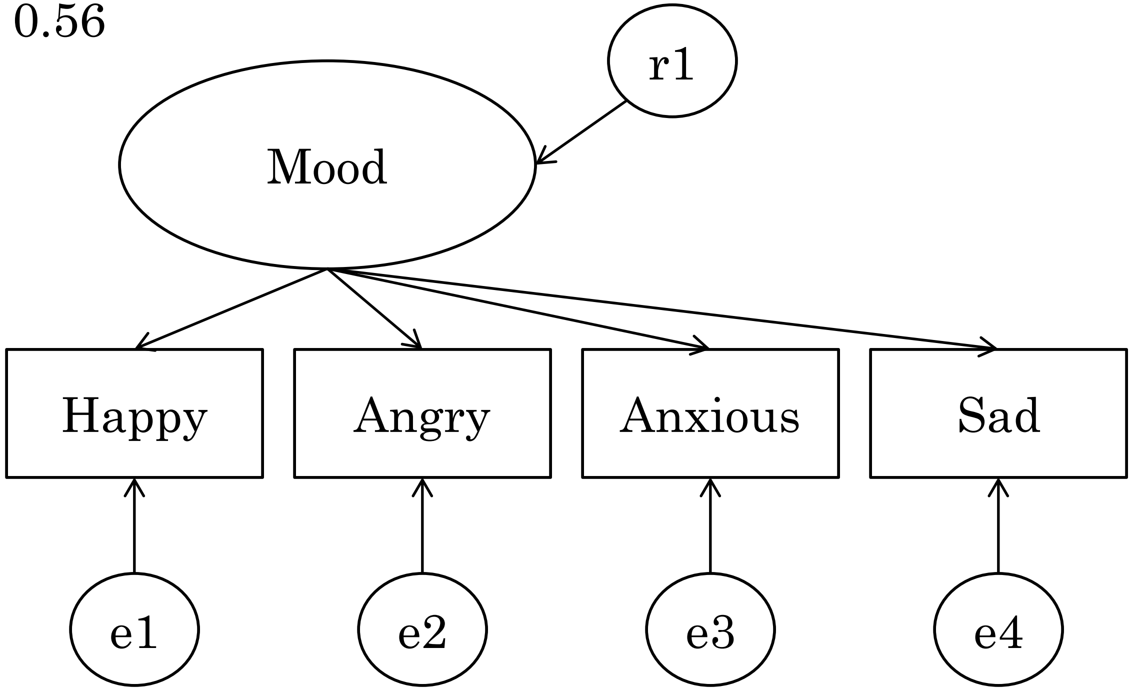
R-SQUARE

	Estimate	S.E.	Est./S.E.	P-Value
HAPPY	0.382	0.027	14.224	0.000
ANGRY	0.459	0.028	16.505	0.000
ANXIOUS	0.401	0.027	14.841	0.000
SAD	0.637	0.029	22.185	0.000

Interpretation of Estimates in CFA

Reliability of the factor (factor rho coefficient) is the ratio of explained variance over total variance $\hat{\rho} = \frac{(\Sigma\hat{\lambda}_i)^2\hat{\Phi}}{(\Sigma\hat{\lambda}_i)^2\hat{\Phi}+\Sigma\hat{\theta}_{ii}}$ where $\Sigma\hat{\lambda}_i$ is the sum of unstandardized factor loadings, $\hat{\Phi}$ is the estimated factor variance, and $\Sigma\hat{\theta}_{ii}$ is the sum of the unstandardized error variances…

$(1\text{-}1.135\text{-}1.402\text{-}1.563)^2(.176)/(1\text{-}1.135\text{-}1.402\text{-}1.563)^2(.176)+(.285+.268+.518+.246) = 1.69136/3.00836 = 0.56$



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Problems that can occur in CFA

1. Failed convergence due to poor start values (mountain climbers)
2. Inadmissible solutions
   a. Negative variance estimates
   b. Estimated correlations greater than 1.0
3. Small sample sizes
   a. Only include indicators with high reliabilities and high factor loadings
   b. Consider standardizing items and then imposing equality constraints
   c. Consider using item parcels
4. Nonpositive definite parameter matrices
   a. Small sample or few indicators per factor
   b. Over-parameterized – try to simplify
   c. Outliers and non-normal distributions
   d. Empirical underidentification (often due to factor covariances)
   e. Misspecification

Evaluating Model Fit

- Nice overview: http://davidakenny.net/cm/fit.htm
- $\chi 2$ goodness of fit – want this to be non-significant (fit of hypothesized model with observed data is not significantly different from zero)
- Incremental fit indices > .95 is good, < .90 poor
  - Comparative fit index (CFI)
  - Tucker Lewis index (TLI)
  - Normed fit index (NFI)
- Absolute fit indices < .05 is good, < .08 is marginal, > .10 bad
  - Root mean square error of approximation (RMSEA)
  - Standardized root mean square residual (SRMR)
- Comparative fit indices –used to compare 2+ models, closer to 0 is better
  - Akaike information criteria (AIC)
  - Bayesian information criteria (BIC)

Jackson et al (2009) Recommendations

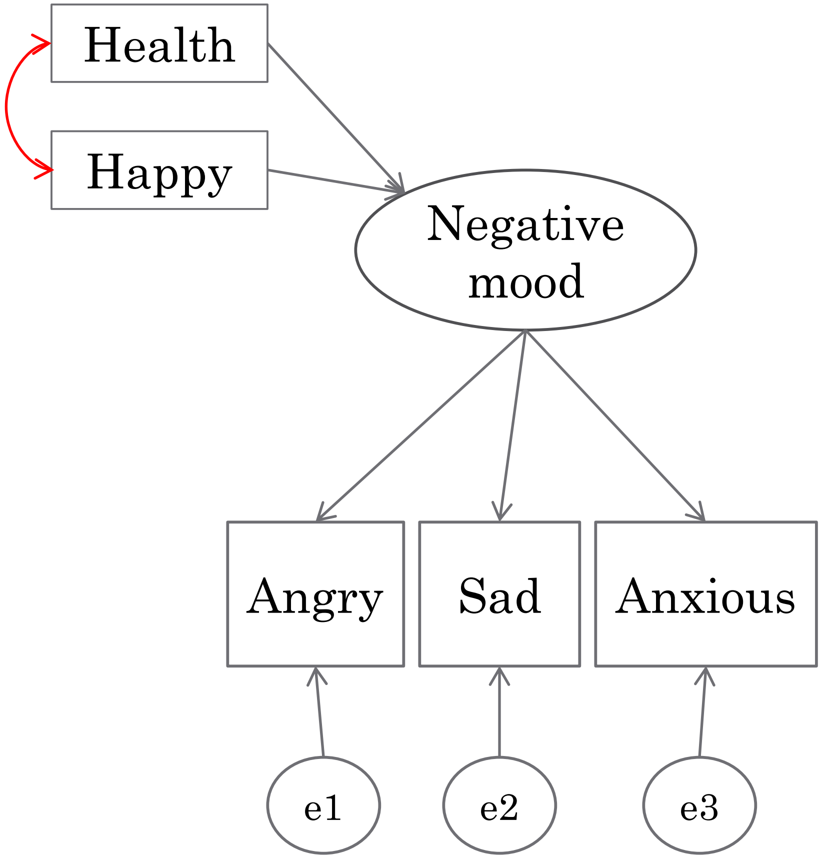
1. Pre-specify the cutoff values for fit measures
2. Report chi-square, degrees of freedom, and p-value for chi-square test
3. Report all parameter estimates that are necessary to interpret the results
4. One measure of incremental fit (TLI, CFI)
5. One measure of residualized fit (RMSEA and confidence interval, SRMR)

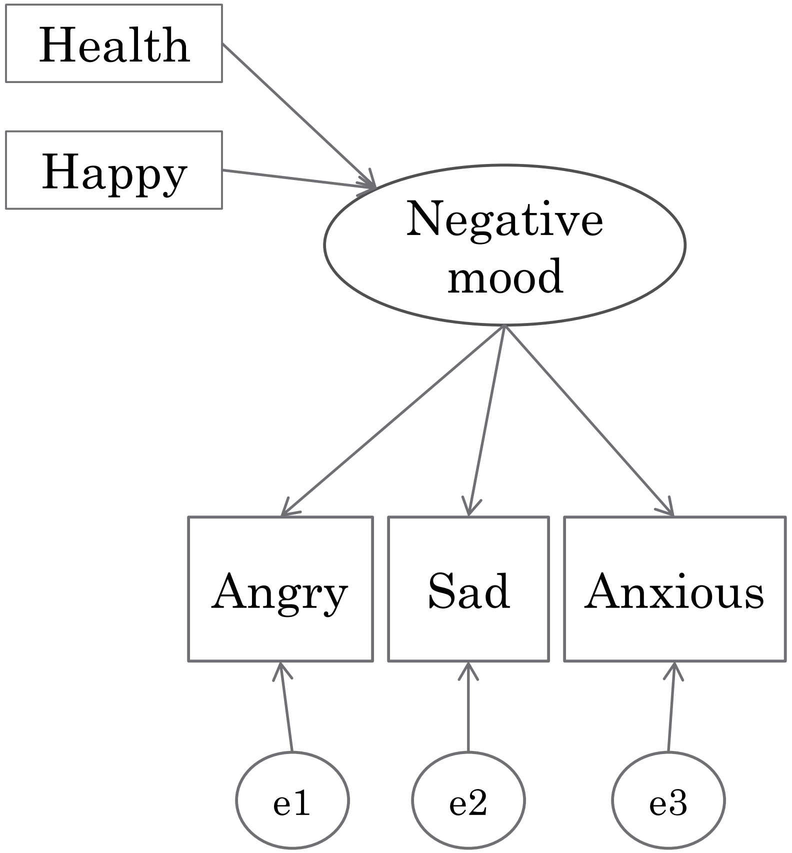
Testing Comparison Models

- Hierarchical or nested models
  - Chi-square difference test
    - Decrement in model fit as free parameters are eliminated (trimming)
    - Improvement in model fit as free parameters are added (building)
  - Information criteria – relative fit
    - AIC = $\chi^2_M + k(k+1) - 2df$
    - BIC = $\chi^2_M + \ln(N)[(k(k+1)/2 - df)$

      Where k = number of model parameters, ln(N) is the natural log of the number of cases in the sample

Examples of nested models





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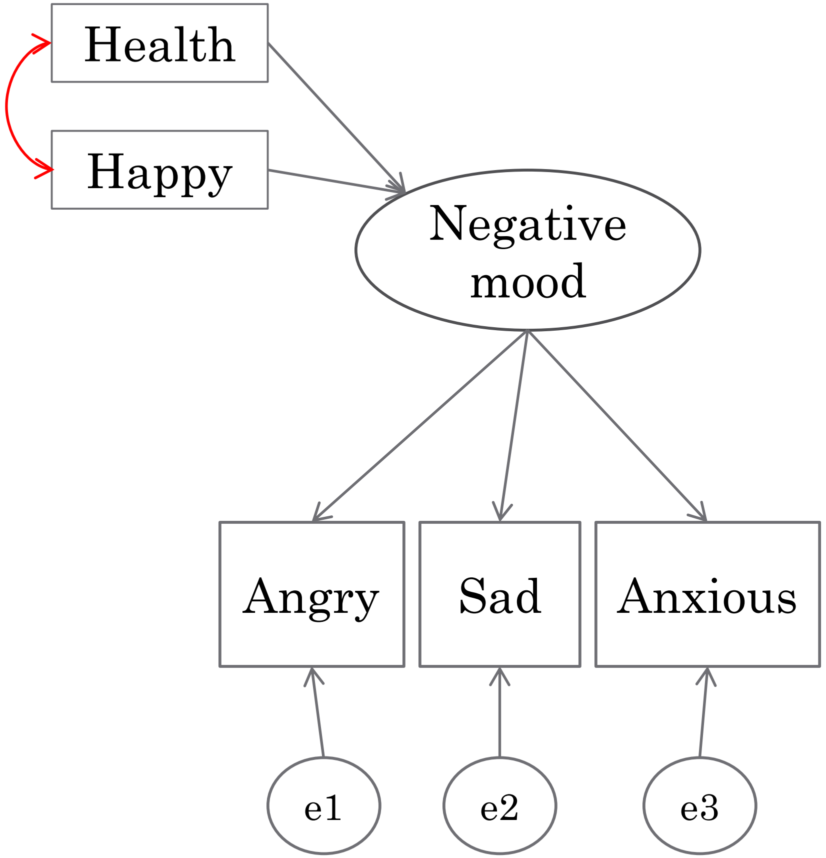
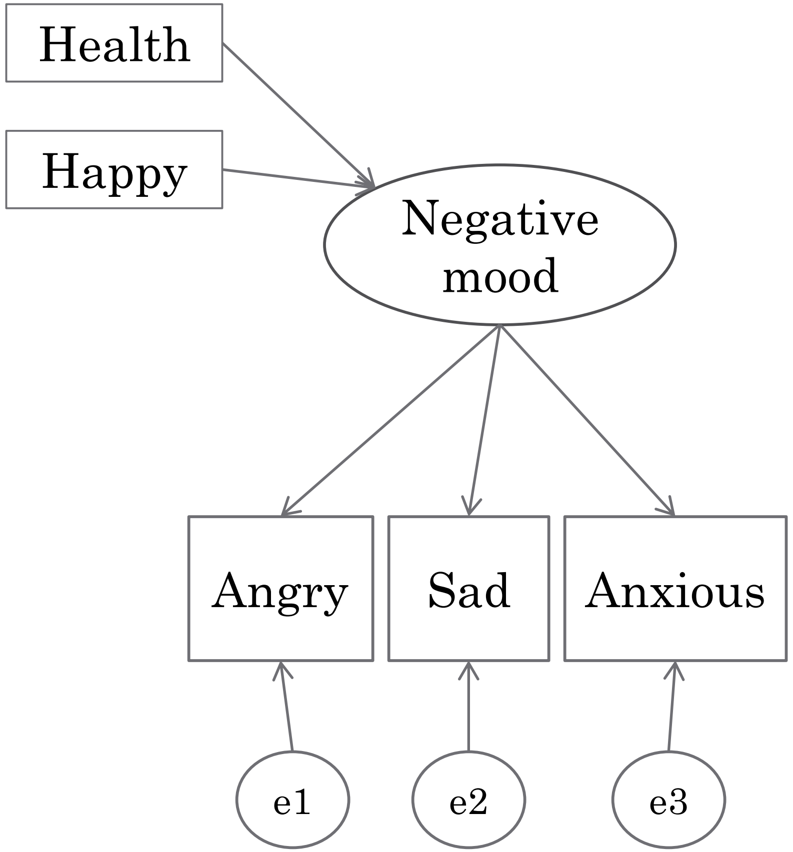


$\chi 2$ (4) = 8.449, p = 0.076
RMSEA = 0.03 (0.00, 0.058), p = .87
CFI = .997; TLI = .993; SRMR = 0.01



$\chi 2$ (5) = 160.351, $p < 0.0001$
RMSEA = 0.16 (0.14, 0.18), $p < .001$
CFI = .884; TLI = .792; SRMR = 0.09

χ^2_D (1) = 160.351-8.449 = 151.902

Equivalent and Near-Equivalent Models

- For every model there are almost always alternative models that are mathematically equivalent with identical fit
  - e.g., a saturated model with six latent variables has at least 33,925 equivalent models! (MacCallum et al., 1993)

Measurement Invariance in CFA

- Measurement invariance – psychometric properties of the observed indicators regressed on the latent factor(s) generalize across groups or over time
  - Are we measuring the same construct in the same way across groups or over time?
  - Differences between groups or over time reflect TRUE differences in amount or variability of the construct, do not reflect measurement change.

Multiple levels of invariance

- Configural invariance – does the factor structure hold (i.e., same number of factors)?
- Metric (“weak”) invariance – do the groups have the same factor loadings?
- Scalar (“strong”) invariance – do the groups have the same loadings and intercepts?
- Residual variance (“strict”) invariance – do the groups have the same loadings, intercepts, and residual variances?

Multiple levels of invariance

- Interpreting tests of invariance
  - Witkiewitz, personal communication
- If the test is *non-significant* then that level of invariance is met (e.g., the more constrained model does not fit significantly worse than the less constrained model).
- You won't generally find that a more constrained model (e.g., scalar) fits better than a less constrained model (e.g., configural).
- The question is whether you can apply the constraints and the fit doesn't get *significantly* worse.

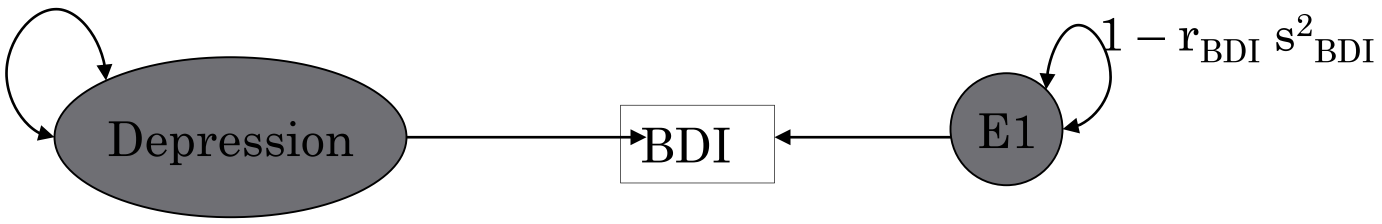
Building models

- Take a break?

- Let’s build a model and then do some invariance testing

Single Indicators in SR Models

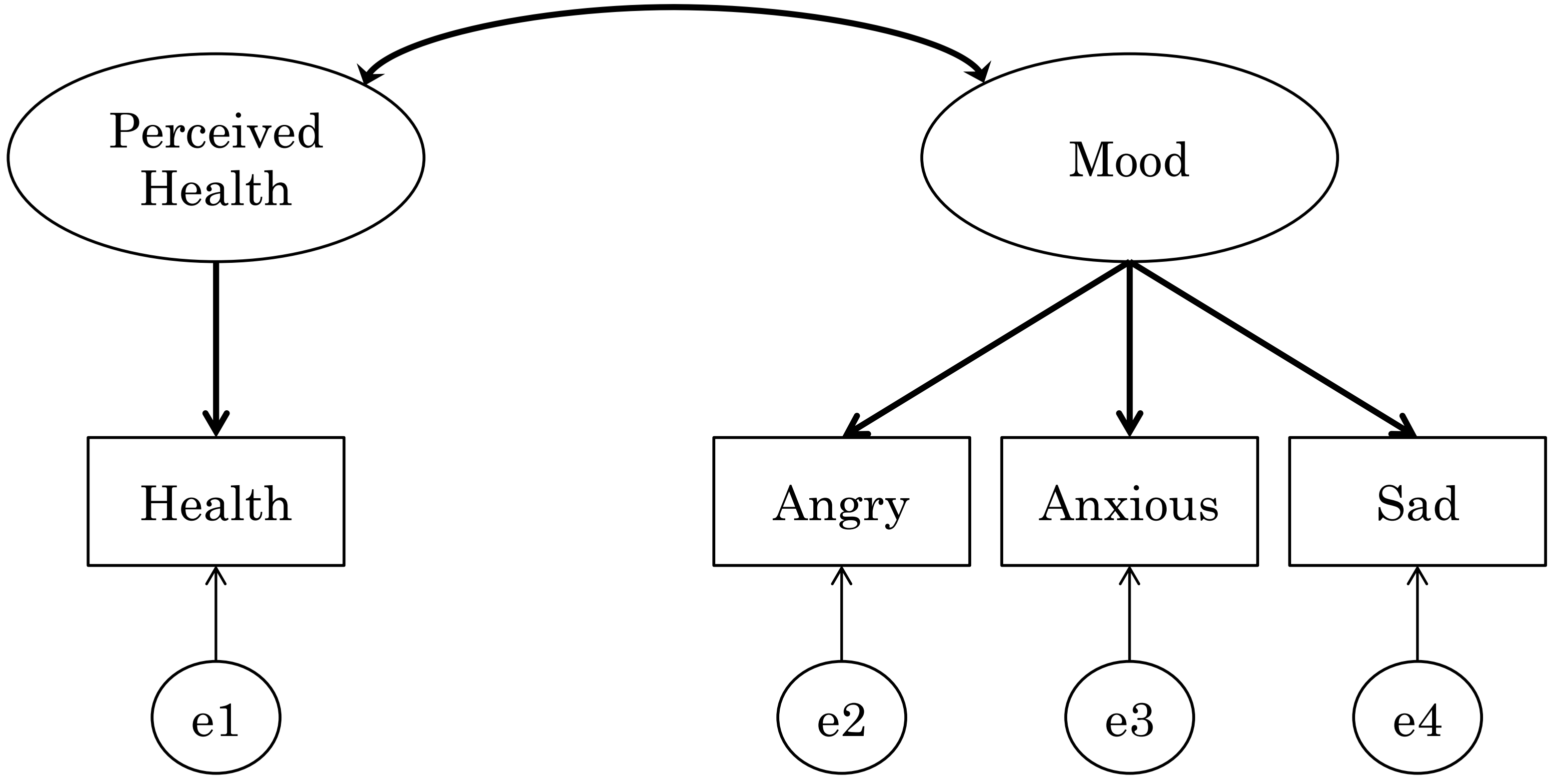
- Useful when you have only one measure of some construct
- Requires *a priori* estimate of the measurement error (i.e., Reliability)
  - Use prior experience or previous studies
    - If no prior research, can use 1 perfect reliability or .7 acceptable reliability as a starting point.
- $1 - r_{xx}$ = proportion of observed variance due to measurement error multiplied by observed variance



Single Indicator Model Example

In general, would you say your health is...
0 (poor) through 4 (excellent)

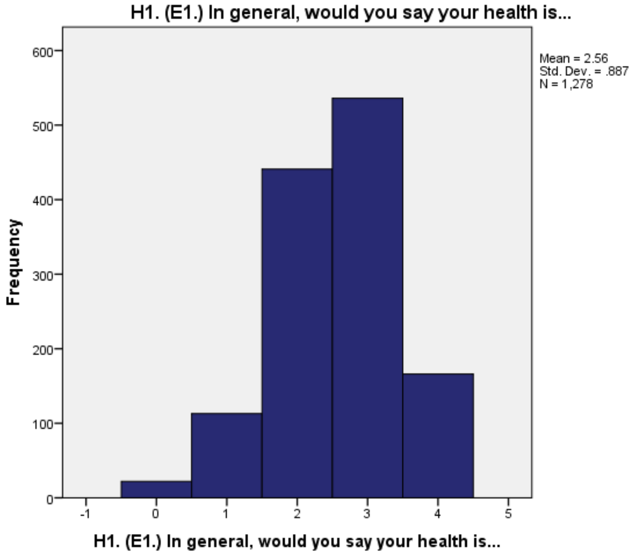
In the past 30 days, how often have you felt… Angry? Anxious? Sad?
0 (None of the time) to 4 (All of the time)

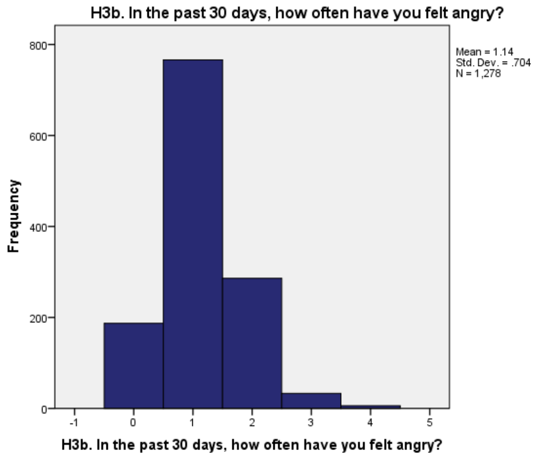


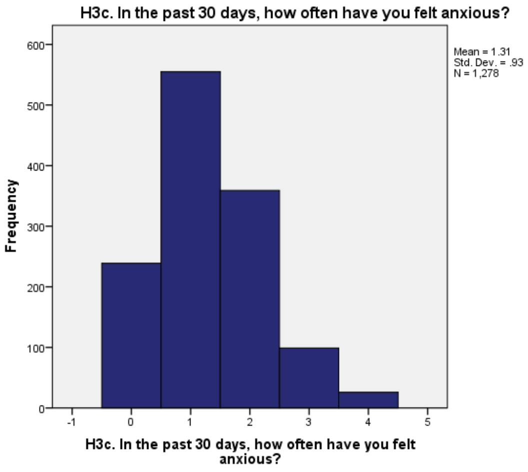
Single Indicator Model Example: Variable Distributions

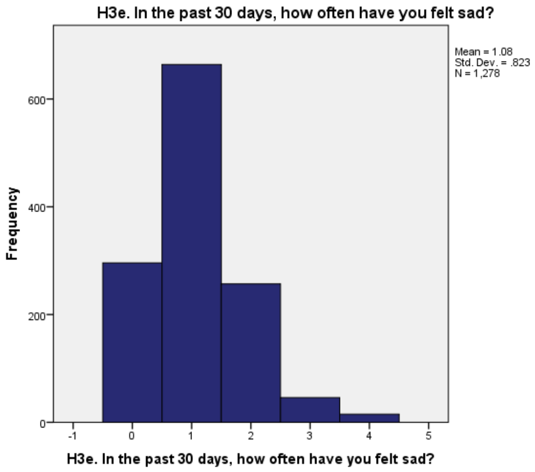
Statistics

		Health H1. (E1.) In general, would you say your health is...	Angry H3b. In the past 30 days, how often have you felt angry?	Anxious H3c. In the past 30 days, how often have you felt anxious?	Sad H3e. In the past 30 days, how often have you felt sad?
N	Valid	1278	1278	1278	1278
	Missing	0	0	0	0
Mean		2.56	1.14	1.31	1.08
Std. Deviation		.887	.704	.930	.823
Variance		.787	.496	.866	.677
Skewness		-.363	.561	.534	.753
Std. Error of Skewness		.068	.068	.068	.068
Kurtosis		.022	1.049	.101	.958
Std. Error of Kurtosis		.137	.137	.137	.137









Single Indicator Model Example

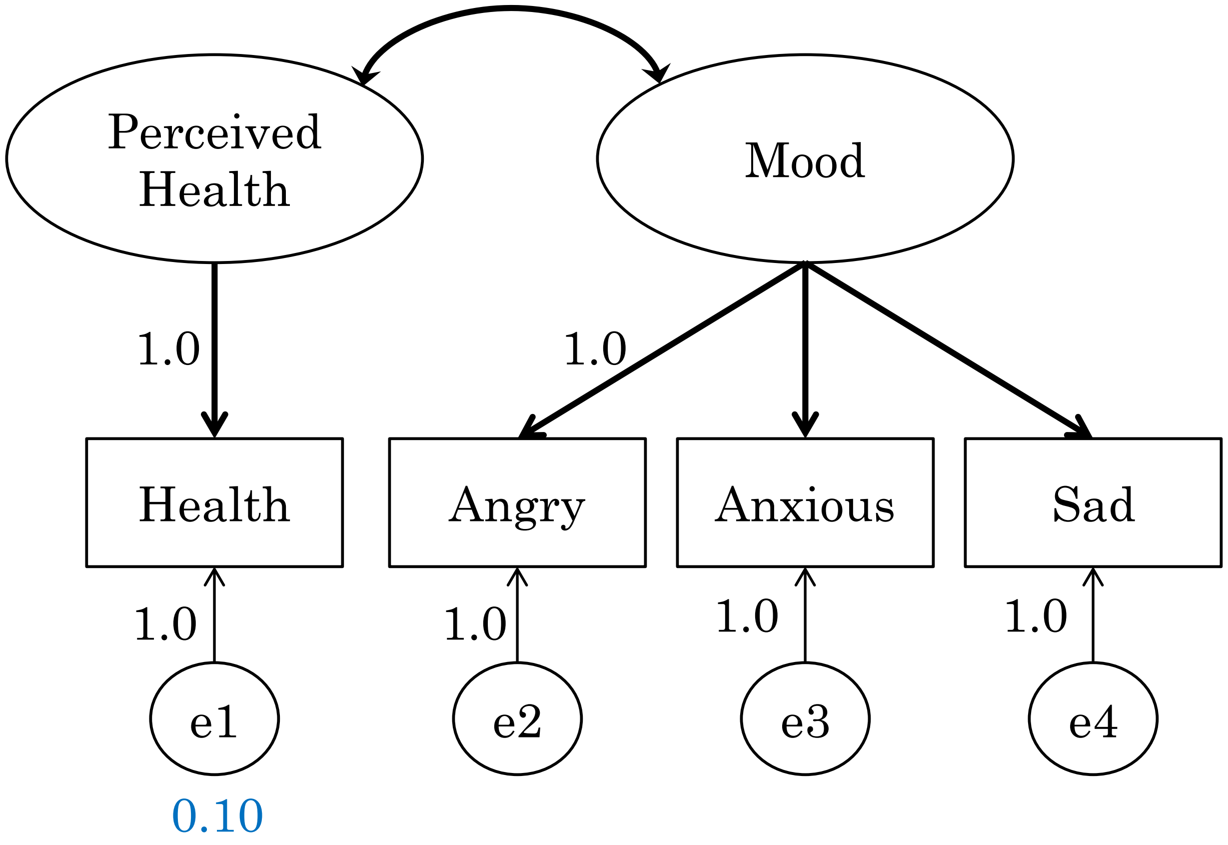
$1 - r_{health}\ s^2_{health}$

r_{health} estimated at .87 (from prior research)

1- r_{health} estimated at .13 (math)

$s^2_{health} = .787$ (from descriptives)

$1 - r_{health}\ s^2_{health} = .13 * .787 = 0.10$



Single Indicator Example

DATA:
FILE is hints.csv;
VARIABLE:
NAMES ARE Angry Anxious Sad Health;
USEVARIABLES ARE Angry Anxious Sad Health;

MODEL:
!Factor model for negative mood
mood BY Angry Anxious Sad;

!Factor model for healthy
healthy BY Health@1;

!Constrain (residual) variance of Health at 0.10
Health@.1;

!Allow mood to covary with latent health
mood WITH healthy;

OUTPUT:
SAMPSTAT RESIDUAL STDYX CINTERVAL TECH1 TECH4;

Number of observations 1278

χ^2 (2) = 1.544, p = .462

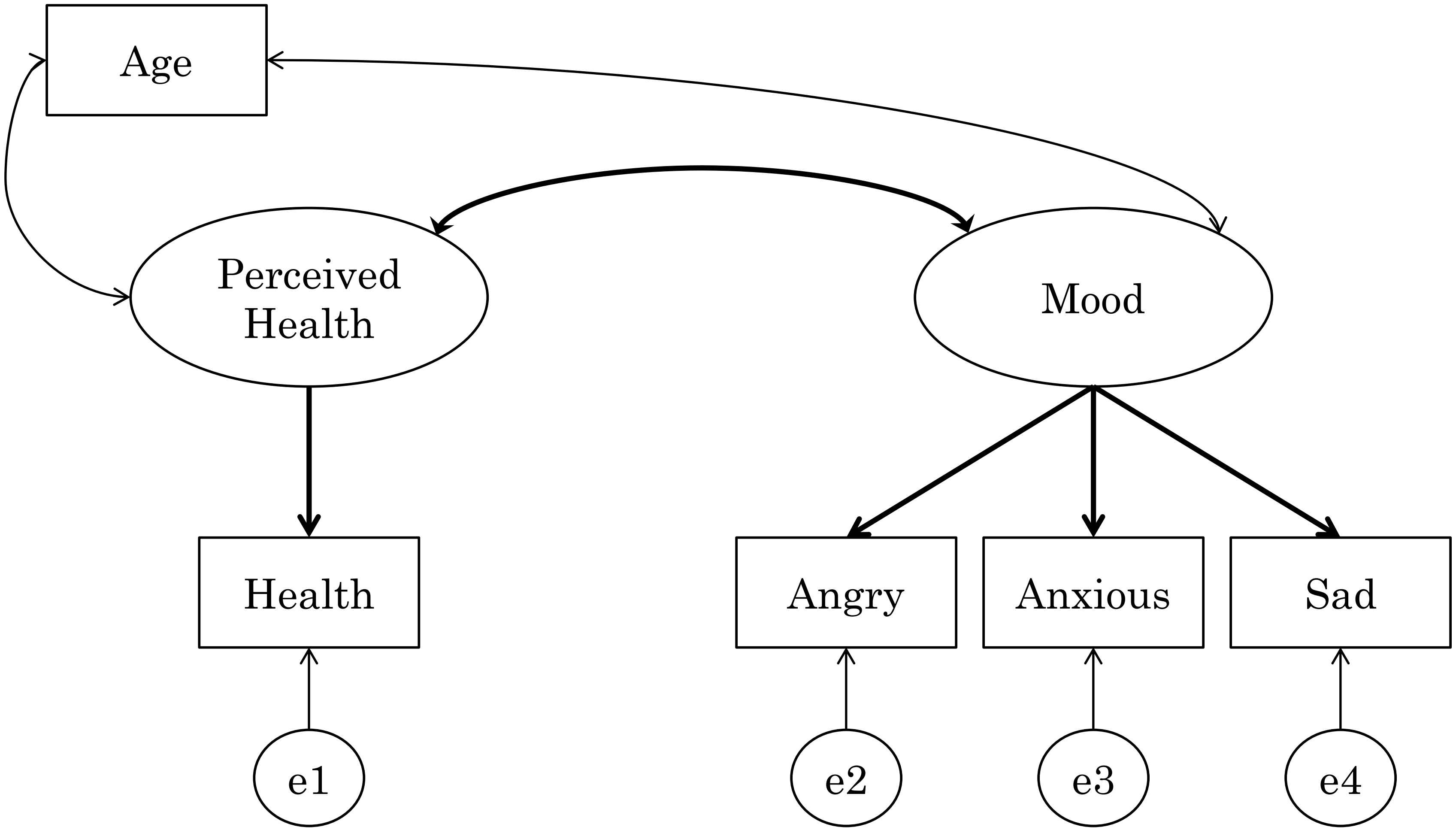
RMSEA = 0.00 (90% CI 0.00, 0.05), p = .943

CFI=1.000

SRMR=0.006

	Estimate	S.E.	Est./S.E.	P-Value
MOOD BY				
ANGRY	1.000	0.000	999.000	999.000
ANXIOUS	1.292	0.073	17.803	0.000
SAD	1.376	0.076	18.151	0.000
HEALTHY BY				
HEALTH	1.000	0.000	999.000	999.000
MOOD WITH				
HEALTHY	-0.138	0.015	-9.338	0.000
Intercepts				
ANGRY	1.143	0.020	58.079	0.000
ANXIOUS	1.310	0.026	50.352	0.000
SAD	1.077	0.023	46.799	0.000
HEALTH	2.556	0.025	103.032	0.000
Variances				
MOOD	0.222	0.019	11.449	0.000
HEALTHY	0.687	0.031	22.065	0.000
Residual Variances				
ANGRY	0.273	0.015	18.212	0.000
ANXIOUS	0.495	0.026	18.681	0.000
SAD	0.257	0.022	11.715	0.000
HEALTH	**0.100**	**0.000**	**999.000**	**999.000**
STDYX Standardization				
MOOD BY				
ANGRY	0.669	0.022	30.375	0.000
ANXIOUS	0.654	0.022	29.123	0.000
SAD	0.788	0.021	37.342	0.000
HEALTHY BY				
HEALTH	0.934	0.003	347.190	0.000
MOOD WITH				
HEALTHY	-0.353	0.031	-11.388	0.000

Adding “Age” To Health and Mood CFA



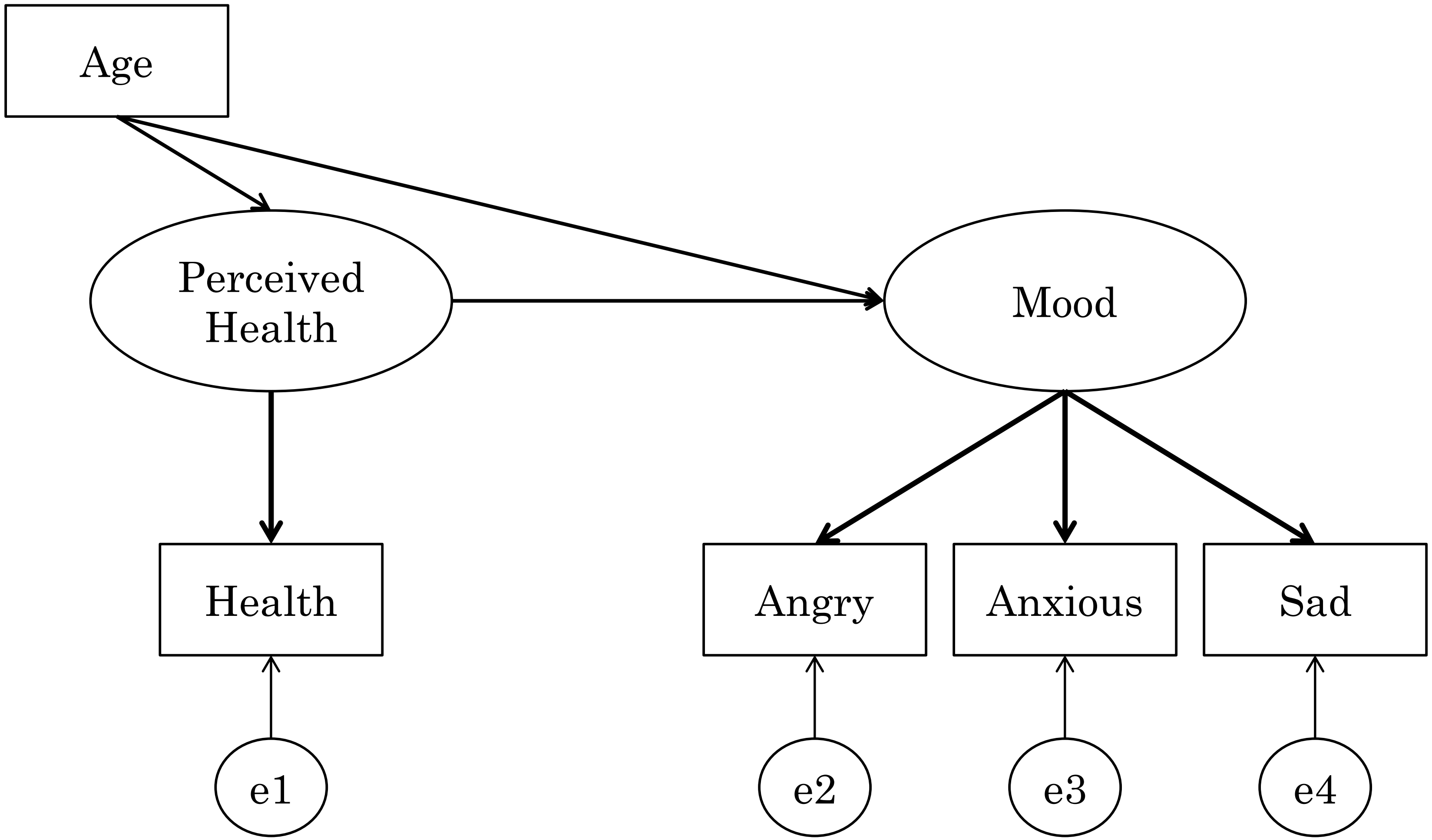
SR Step 1 Example

```
DATA:
FILE is hints.csv;
VARIABLE:
NAMES ARE  Angry Anxious Sad Health
Age;
USEVARIABLES ARE Angry Anxious
Sad Health Age;

MODEL:
!Factor model for negative mood
mood BY Angry Anxious Sad;

!Factor model for healthy
healthy BY Health@1;

!Constrain variance of Health at 0.10
Health@.1;

!Allow  covariances for mood, healthy,
and age
mood WITH healthy age;
healthy WITH age;

OUTPUT:
SAMPSTAT RESIDUAL STDYX
CINTERVAL TECH1 TECH4;
```

$\chi 2$ (4) = 5.210, p = .266
RMSEA = 0.015 (90% CI 0.00, 0.047), p = .966
CFI=0.999 ; SRMR=0.01

	Estimate	S.E.	Est./S.E.	P-Value
MOOD BY				
ANGRY	1.000	0.000	999.000	999.000
ANXIOUS	1.288	0.072	17.853	0.000
SAD	1.353	0.073	18.488	0.000
HEALTHY BY				
HEALTH	1.000	0.000	999.000	999.000
MOOD WITH				
HEALTHY	-0.139	0.015	-9.375	0.000
AGE	-1.028	0.255	-4.032	0.000
HEALTHY WITH				
AGE	-1.962	0.409	-4.798	0.000
Intercepts				
ANGRY	1.143	0.020	58.079	0.000
ANXIOUS	1.310	0.026	50.352	0.000
SAD	1.077	0.023	46.799	0.000
HEALTH	2.556	0.025	103.032	0.000
Variances				
AGE	266.586	10.546	25.278	0.000
MOOD	0.225	0.019	11.593	0.000
HEALTHY	0.687	0.031	22.065	0.000
Residual Variances				
ANGRY	0.270	0.015	18.136	0.000
ANXIOUS	0.492	0.026	18.767	0.000
SAD	0.264	0.021	12.415	0.000
HEALTH	0.100	0.000	999.000	999.000
STDYX Standardization				
MOOD BY				
ANGRY	0.674	0.022	30.974	0.000
ANXIOUS	0.657	0.022	29.644	0.000
SAD	0.781	0.021	37.755	0.000
HEALTHY BY				
HEALTH	0.934	0.003	347.191	0.000
MOOD WITH				
HEALTHY	-0.353	0.031	-11.390	0.000
AGE	-0.133	0.032	-4.183	0.000
HEALTHY WITH				
AGE	-0.145	0.029	-4.939	0.000

Structural Regression Model



SR Step 2 Example

DATA:
FILE is hints.csv;
VARIABLE:
NAMES ARE Angry Anxious Sad Health Age;
USEVARIABLES ARE Angry Anxious Sad Health Age;

MODEL:
!Factor model for negative mood
mood BY Angry Anxious Sad;

!Factor model for healthy
healthy BY Health@1;

!Constrain variance of Health at 0.10
Health@.1;

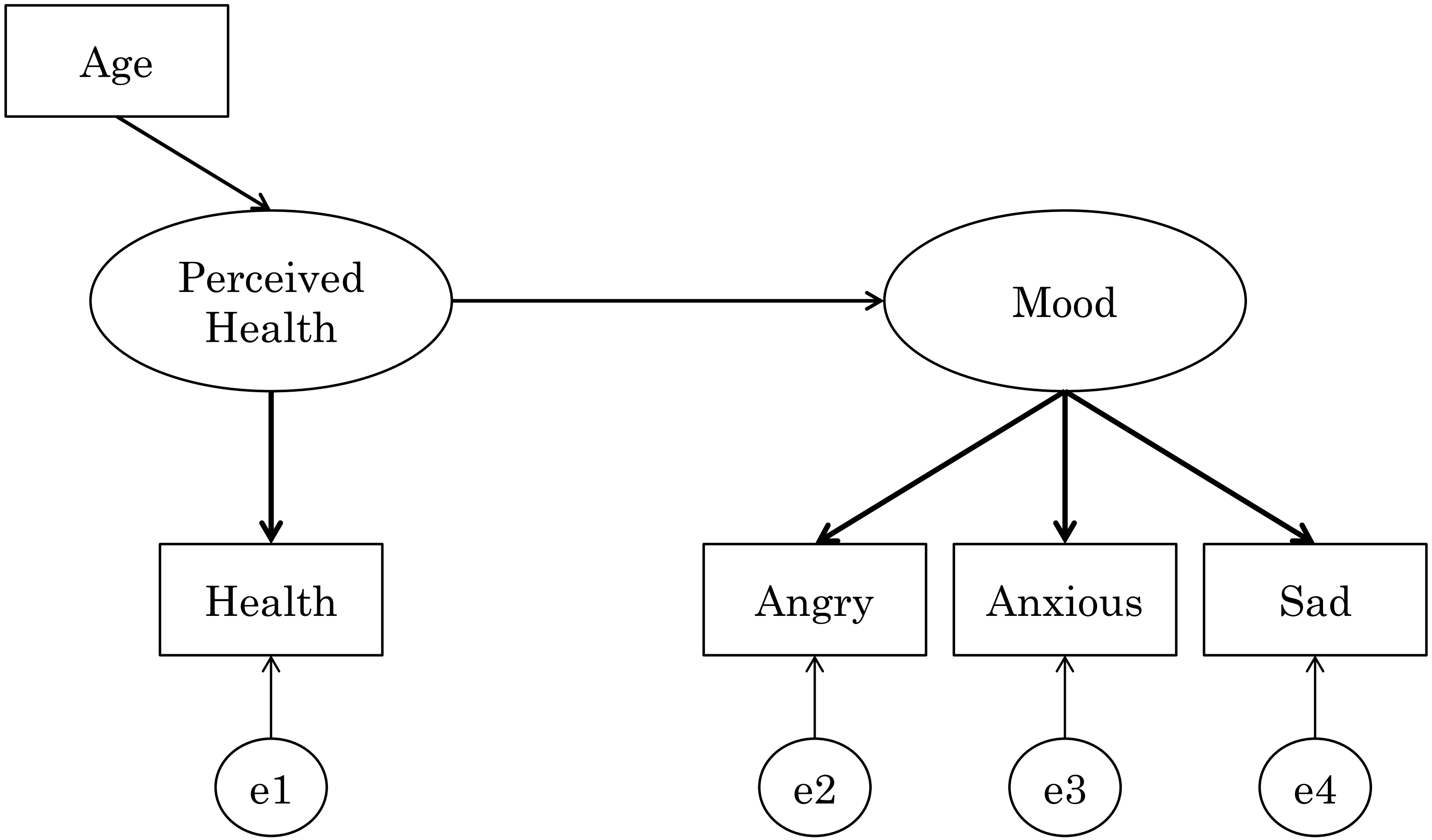
!Change covariances to regression terms
mood ON healthy age;
healthy ON age;

OUTPUT:
SAMPSTAT RESIDUAL STDYX CINTERVAL TECH1 TECH4;

$\chi 2$ (4) = 5.210, p = .266
RMSEA = 0.015 (90% CI 0.00, 0.047), p = .966
CFI=0.999 ; SRMR=0.01

	Estimate	S.E.	Est./S.E.	P-Value
MOOD BY				
ANGRY	1.000	0.000	999.000	999.000
ANXIOUS	1.288	0.072	17.853	0.000
SAD	1.353	0.073	18.488	0.000
HEALTHY BY				
HEALTH	1.000	0.000	999.000	999.000
MOOD ON				
HEALTHY	-0.218	0.020	-10.739	0.000
AGE	-0.005	0.001	-5.910	0.000
HEALTHY ON				
AGE	-0.007	0.002	-4.887	0.000
Intercepts				
ANGRY	1.350	0.054	24.857	0.000
ANXIOUS	1.576	0.070	22.496	0.000
SAD	1.357	0.071	19.057	0.000
HEALTH	2.951	0.084	34.951	0.000
Variances				
AGE	266.586	10.546	25.278	0.000
MOOD	0.225	0.019	11.593	0.000
HEALTHY	0.687	0.031	22.065	0.000
Residual Variances				
ANGRY	0.270	0.015	18.136	0.000
ANXIOUS	0.492	0.026	18.767	0.000
SAD	0.264	0.021	12.415	0.000
HEALTH	0.100	0.000	999.000	999.000
MOOD	0.189	0.017	11.335	0.000
HEALTHY	0.672	0.031	22.005	0.000
STDYX Standardization				
MOOD ON				
HEALTHY	-0.381	0.031	-12.358	0.000
MOOD ON				
AGE	-0.188	0.030	-6.173	0.000
HEALTHY ON				
AGE	-0.145	0.029	-4.939	0.000

Structural Regression Model - Nested



SR Step 2 Example

DATA:
FILE is hints.csv;
VARIABLE:
NAMES ARE Angry Anxious Sad Health Age;
USEVARIABLES ARE Angry Anxious Sad Health Age;

MODEL:
!Factor model for negative mood
mood BY Angry Anxious Sad;

!Factor model for healthy
healthy BY Health@1;

!Constrain variance of Health at 0.10
Health@.1;

!Regress mood on healthy
mood ON healthy;

!Regress healthy on age;
healthy ON age;
OUTPUT:
SAMPSTAT RESIDUAL STDYX CINTERVAL TECH1 TECH4;

$\chi 2$ (5) = 41.875, p < .000
RMSEA = 0.076 (90% CI 0.045, 0.098), p = .019 CFI=0.965 ; SRMR=0.05

	Estimate	S.E.	Est./S.E.	P-Value
MOOD BY				
ANGRY	1.000	0.000	999.000	999.000
ANXIOUS	1.292	0.073	17.798	0.000
SAD	1.376	0.076	18.128	0.000
HEALTHY BY				
HEALTH	1.000	0.000	999.000	999.000
MOOD ON				
HEALTHY	-0.198	0.020	-9.932	0.000
HEALTHY ON				
AGE	-0.007	0.002	-4.887	0.000
Intercepts				
ANGRY	1.069	0.026	40.611	0.000
ANXIOUS	1.214	0.034	35.199	0.000
SAD	0.975	0.033	29.364	0.000
HEALTH	2.930	0.084	34.678	0.000
Residual Variances				
ANGRY	0.273	0.015	18.206	0.000
ANXIOUS	0.495	0.026	18.676	0.000
SAD	0.256	0.022	11.681	0.000
HEALTH	0.100	0.000	999.000	999.000
MOOD	0.195	0.017	11.228	0.000
HEALTHY	0.674	0.031	22.020	0.000
STDYX Standardization				
MOOD BY				
ANGRY	0.669	0.022	30.344	0.000
ANXIOUS	0.654	0.022	29.095	0.000
SAD	0.788	0.021	37.299	0.000
HEALTHY BY				
HEALTH	0.934	0.003	347.312	0.000
MOOD ON				
HEALTHY	-0.349	0.031	-11.243	0.000
HEALTHY ON				
AGE	-0.137	0.029	-4.670	0.000

Measurement Invariance in CFA

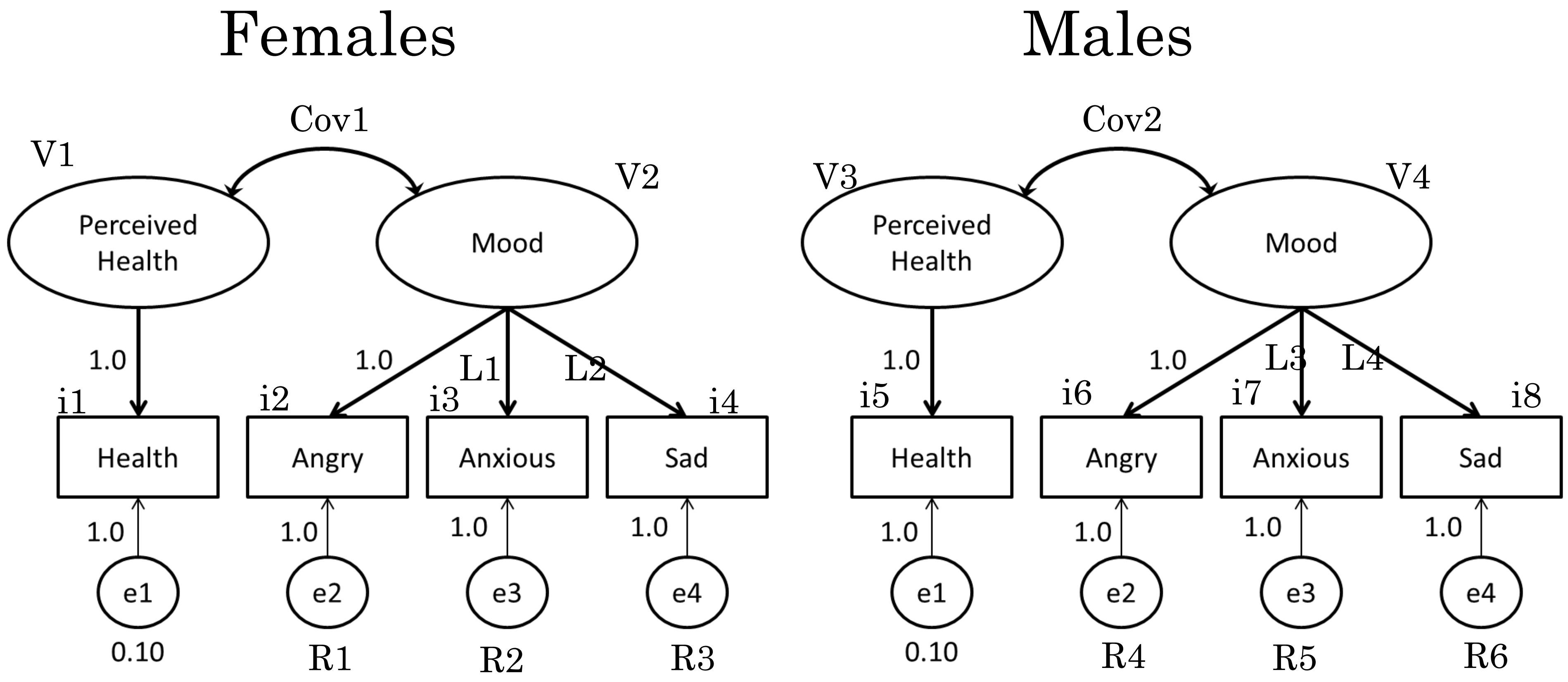
- Measurement invariance – psychometric properties of the observed indicators regressed on the latent factor(s) generalize across groups or over time
  - Are we measuring the same construct in the same way across groups or over time?
  - Differences between groups or over time reflect TRUE differences in amount or variability of the construct, do not reflect measurement change.
    - Can only make this claim if invariance holds.

Multiple levels of invariance

(its good to hear this a couple times)

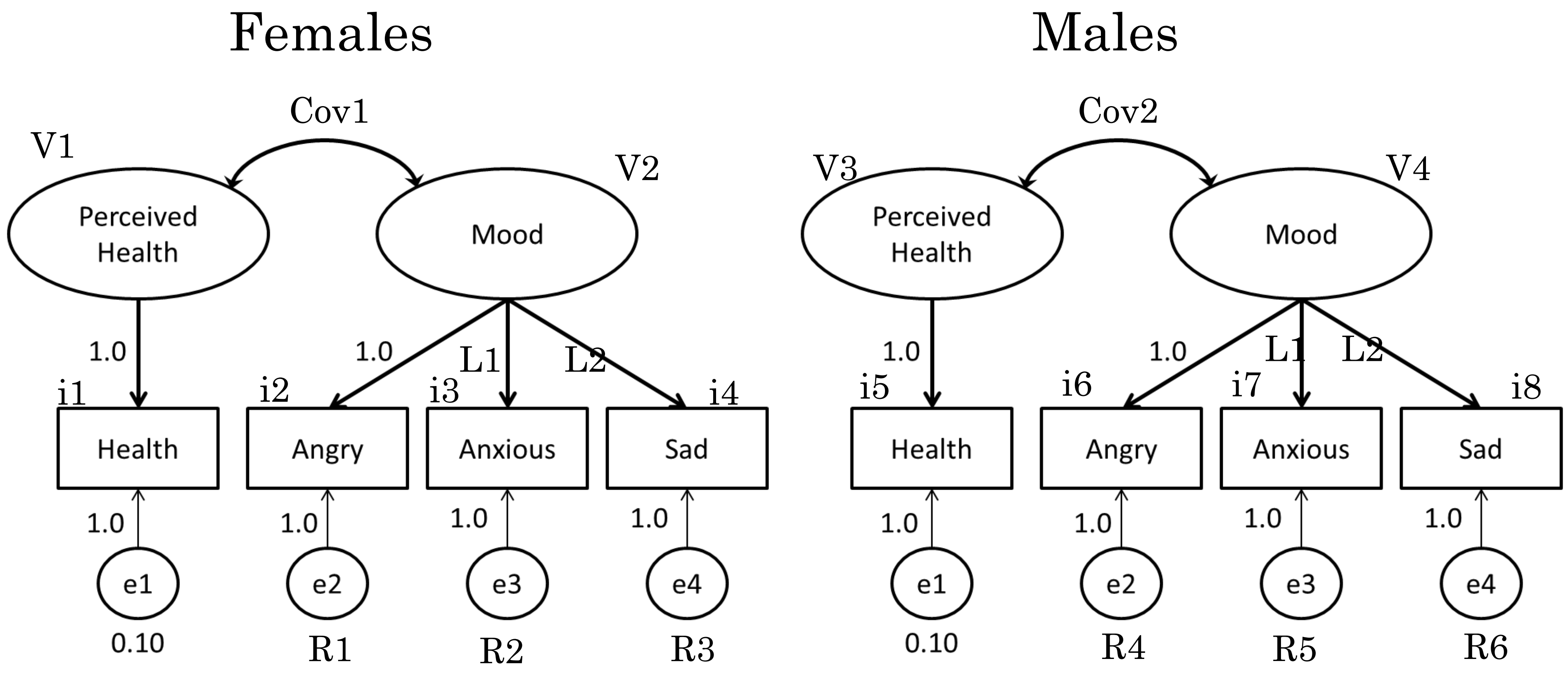
- Configural invariance – does the factor structure hold (i.e., same number of factors)?
- Metric (“weak”) invariance – do the groups have the same factor loadings?
- Scalar (“strong”) invariance – do the groups have the same loadings and intercepts?
- Residual variance (“strict”) invariance – do the groups have the same loadings, intercepts, and residual variances?

Configural Invariance



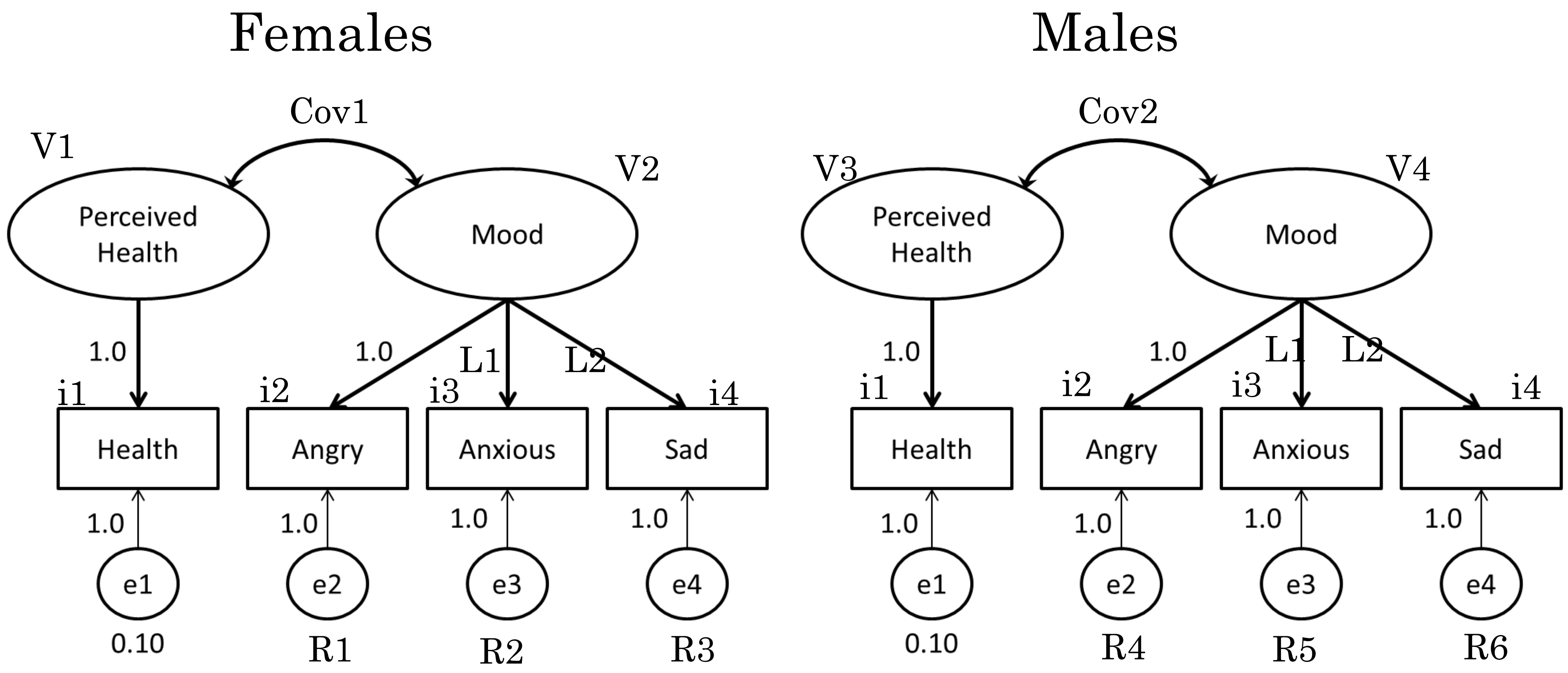
Females, Mood: Factor Loadings: 1, L1, L2, Intercepts: i1, i2, i3, i4, Residuals: R1, R2, R3, Cov1
Males, Mood: Factor Loadings: 1, L3, L4, Intercepts: i5, i6, i7, i8, Residuals: R4, R5, R6, Cov2
*looking for same number of factors

Metric (Weak) Invariance: Loadings Constrained to be Equal (i.e., Invariant) across Groups



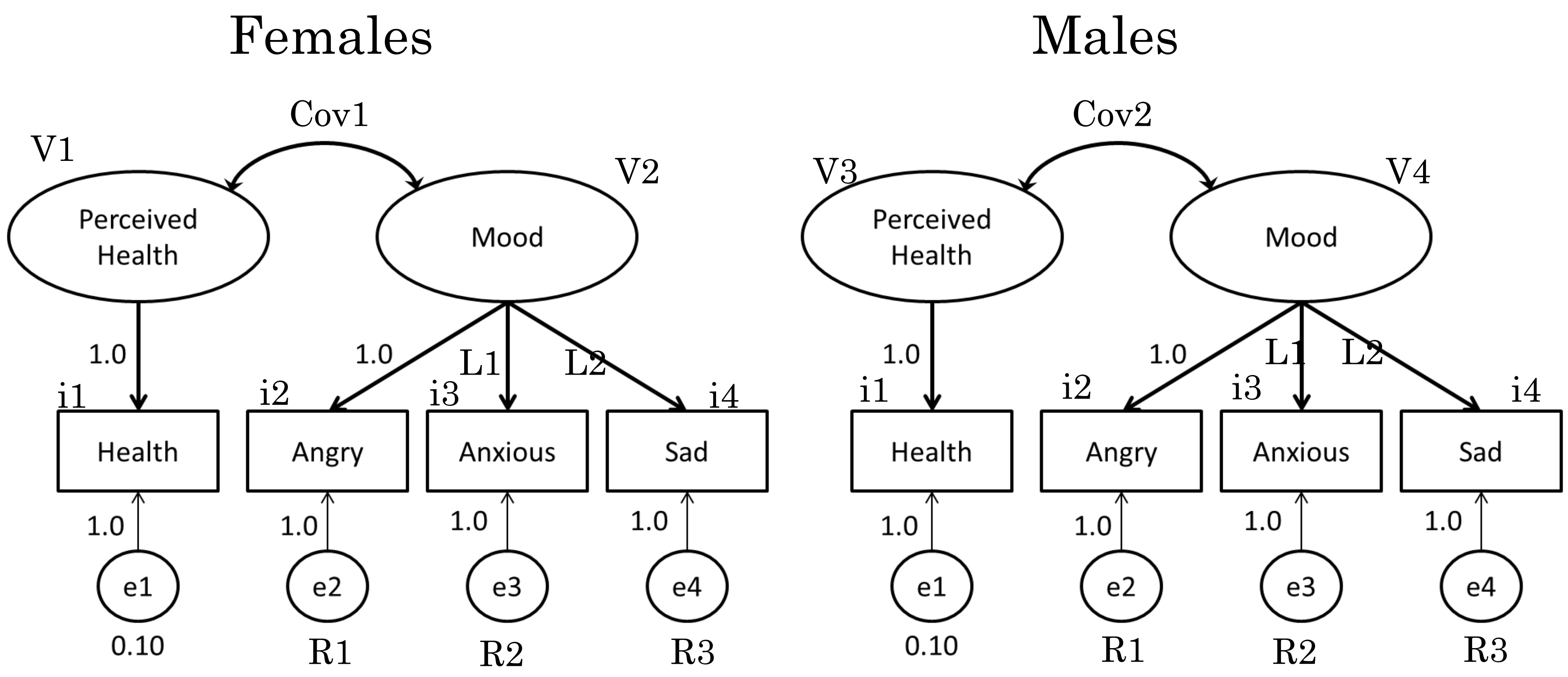
Females, Mood: Factor Loadings: 1, L1, L2, Intercepts: i1, i2, i3, i4, Residuals: R1, R2, R3, Cov1
Males, Mood: Factor Loadings: 1, L1, L2, Intercepts: i5, i6, i7, i8, Residuals: R4, R5, R6, Cov2
*Looking for the same factor loadings

Scalar (Strong) Invariance: Loadings and Intercepts Constrained to be Equal (i.e., Invariant) across Groups



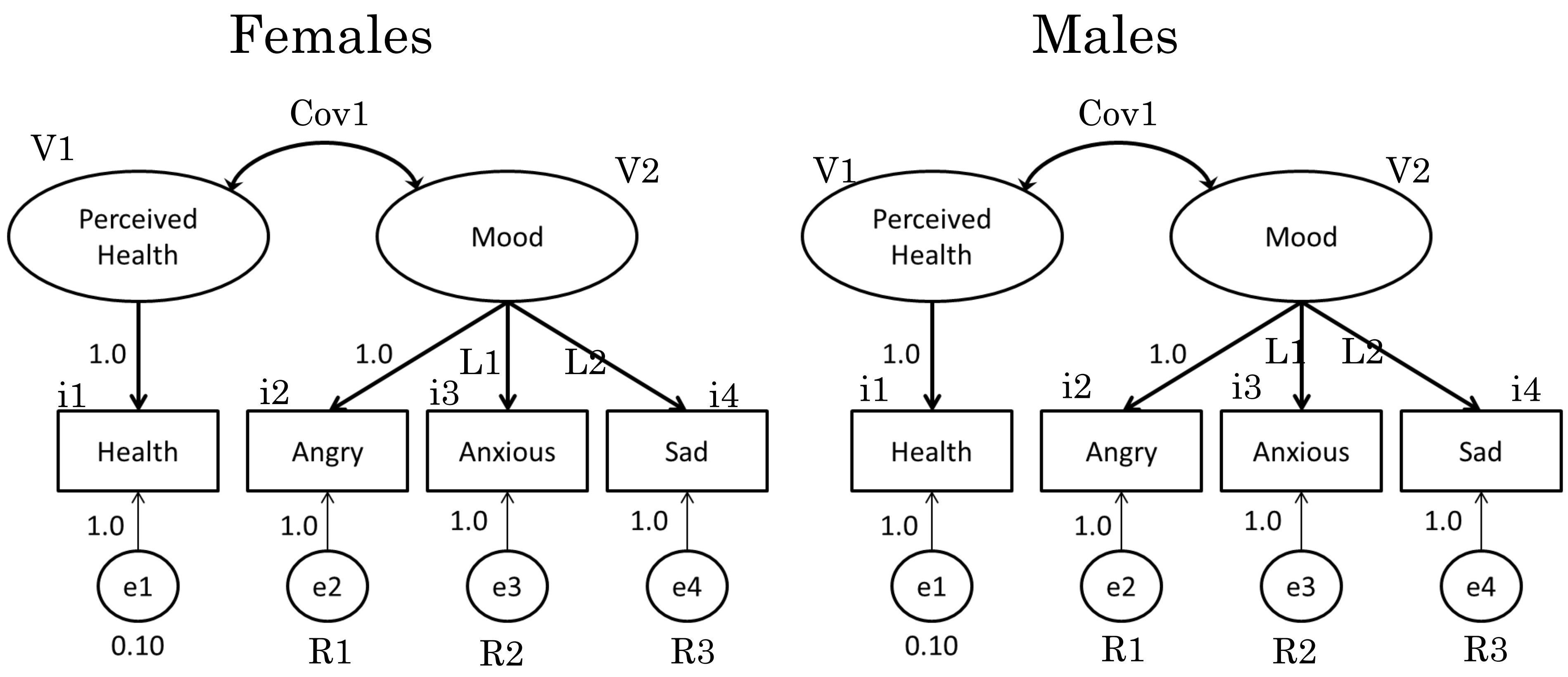
Females, Mood: Factor Loadings: 1, L1, L2, Intercepts: i1, i2, i3, i4, Residuals: R1, R2, R3, Cov1
Males, Mood: Factor Loadings: 1, L1, L2, Intercepts: i1, i2, i3, i4, Residuals: R4, R5, R6, Cov2
*Looking for the same factor loadings and intercepts

Residual (Strict) Invariance: Loadings, Intercepts, and Residual Variances Constrained to be Equal



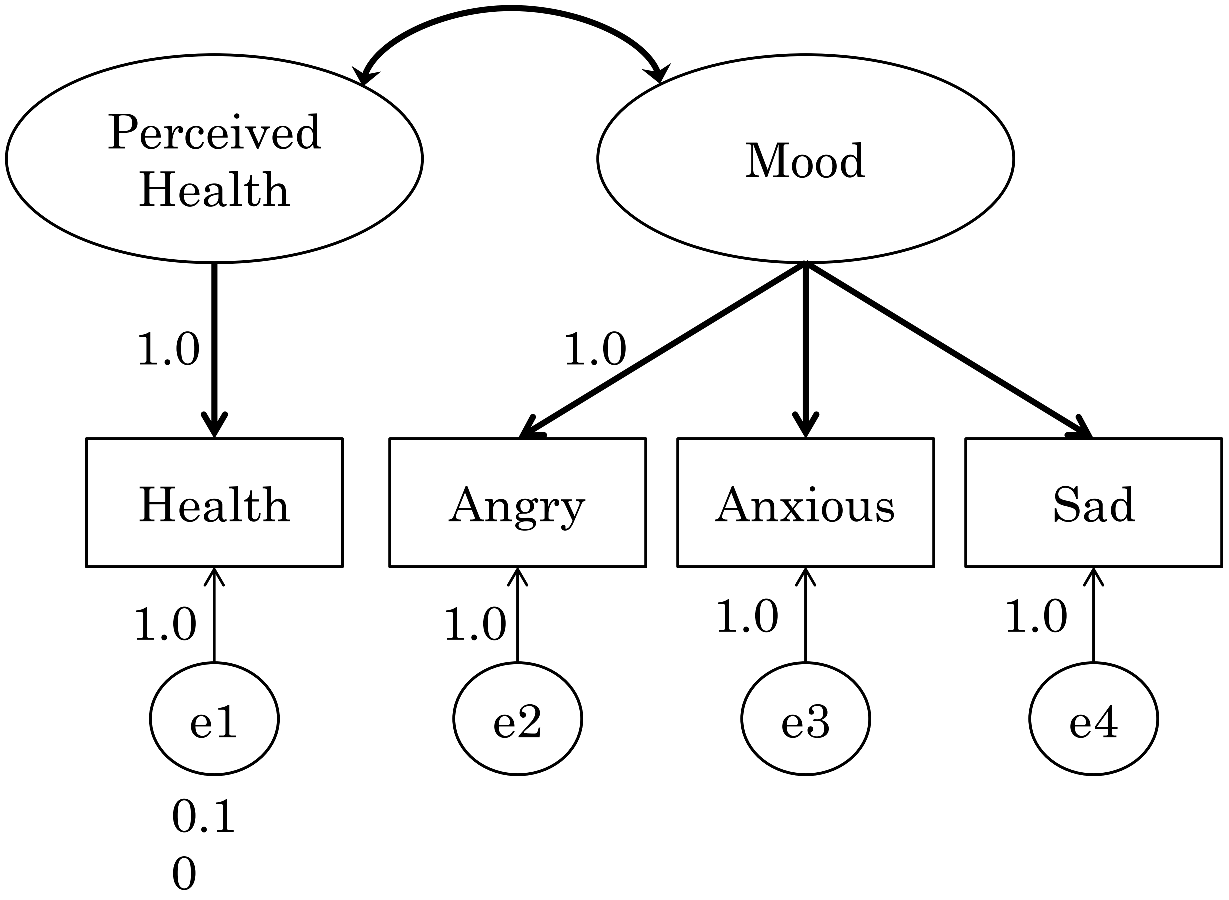
Females, Mood: Factor Loadings: 1, L1, L2, Intercepts: i1, i2, i3, i4, Residuals: R1, R2, R3, Cov1
Males, Mood: Factor Loadings: 1, L1, L2, Intercepts: i1, i2, i3, i4, Residuals: R1, R2, R3, Cov2
*Looking for the same factor loadings, intercepts, and residuals

Factor Variance Invariance: Loadings, Intercepts, Residual Variances and Factor Variances/Covariances



Females, Mood: Factor Loadings: 1, L1, L2, Intercepts: i1, i2, i3, i4, Residuals: R1, R2, R3, Cov1
Males, Mood: Factor Loadings: 1, L1, L2, Intercepts: i1, i2, i3, i4, Residuals: R1, R2, R3, Cov1
*Looking for the same factor loadings, intercepts, residuals, and variances/covariances

Measurement invariance testing…



Multiple levels of invariance

(its good to hear this a couple of times)

- Interpreting tests of invariance
  - Witkiewitz, personal communication
- If the test is *non-significant* then that level of invariance is met (e.g., the more constrained model does not fit significantly worse than the less constrained model).
- You won't generally find that a more constrained model (e.g., scalar) fits better than a less constrained model (e.g., configural).
- The question is whether you can apply the constraints and the fit doesn't get *significantly* worse.

Invariance testing the easy way…

```
DATA:
FILE is hints.csv;
VARIABLE:
NAMES ARE  Angry Anxious Sad Health gender;
USEVARIABLES ARE Angry Anxious Sad Health;

GROUPING IS gender (0=female 1=male);

ANALYSIS:
MODEL = CONFIGURAL METRIC SCALAR;

MODEL:
!Factor model for negative mood
mood BY Angry Anxious Sad;
!Factor model for healthy
healthy BY Health@1;
!Constrain variance of Health at 0.10
Health@.1;
!Allow  mood to covary with health
mood WITH healthy;

OUTPUT:
SAMPSTAT RESIDUAL CINTERVAL TECH1 TECH4;
```

```
Number of observations
   Group FEMALE                                                        751
   Group MALE                                                          527
   Total sample size                                                  1278

MODEL FIT INFORMATION

Invariance Testing

                      Number of                      Degrees of
     Model            Parameters         Chi-square    Freedom        P-value

     Configural            24               7.752           4         0.1011
     Metric                22               8.694           6         0.1915
     Scalar                20              25.448           8         0.0013

                                                     Degrees of
     Models Compared                     Chi-square    Freedom        P-value

     Metric against Configural              0.942           2         0.6243
     Scalar against Configural             17.697           4         0.0014
     Scalar against Metric                 16.754           2         0.0002


*in this example we have Metric invariance
```

Step-by-Step: Step 1a, Run CFA by groups to check model fit

```
USEOBSERVATIONS ARE GENDER EQ 0;

MODEL:
negmood BY Angry@1 Anxious Sad;
  healthy BY Health@1;
  Health@.10;
  healthy WITH negmood;
```

THEN RUN A SECOND MODEL…

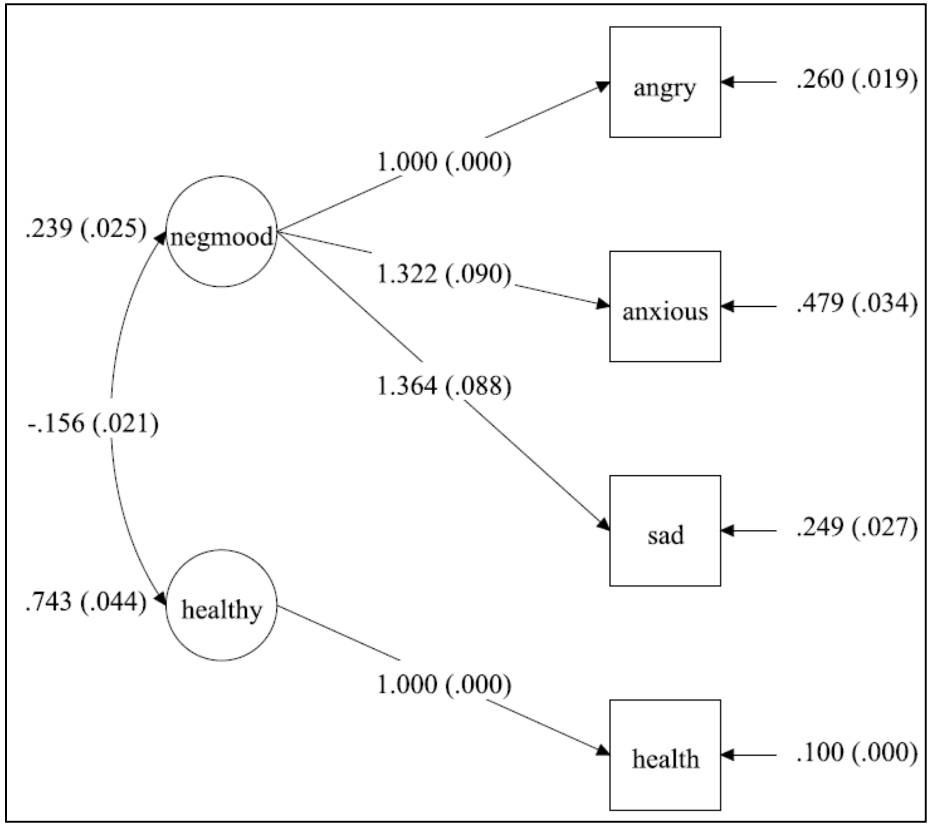
```
USEOBSERVATIONS ARE GENDER EQ 1;

MODEL:
negmood BY Angry@1 Anxious Sad;
  healthy BY Health@1;
  Health@.10;
  healthy WITH negmood;
```

Step 1b - Configural Invariance (no equality constraints)

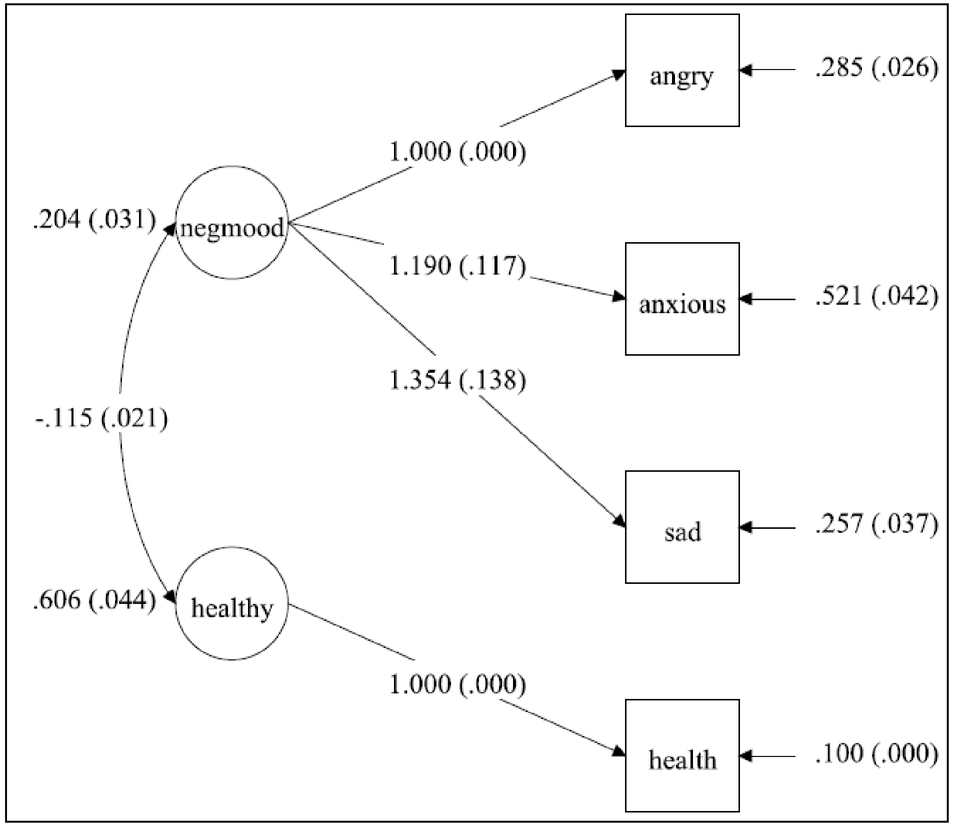
```
USEVARIABLES ARE Angry Anxious Sad Health;
GROUPING IS GENDER (0=FEMALE 1=MALE);
MODEL:
!specify factor model for default group (female)
negmood BY Angry@1 Anxious Sad;
healthy BY Health@1;
Health@.10;
healthy WITH negmood;
!Constrain factor means to 0 for identification
[negmood@0 healthy@0];
!specify intercepts
[angry anxious sad health];
!specify variances
negmood healthy angry anxious sad;

!specify factor model for males
MODEL MALE:
negmood BY Angry@1 Anxious Sad;
healthy BY Health@1;
Health@.10;
healthy WITH negmood;
!Constrain factor means to 0 for identification
[negmood@0 healthy@0];
!specify intercepts
[angry anxious sad health];
!specify variances
negmood healthy angry anxious sad;
```

Configural Invariance

Females



Males



Step 2 - Metric Invariance (equality constraints of loadings)

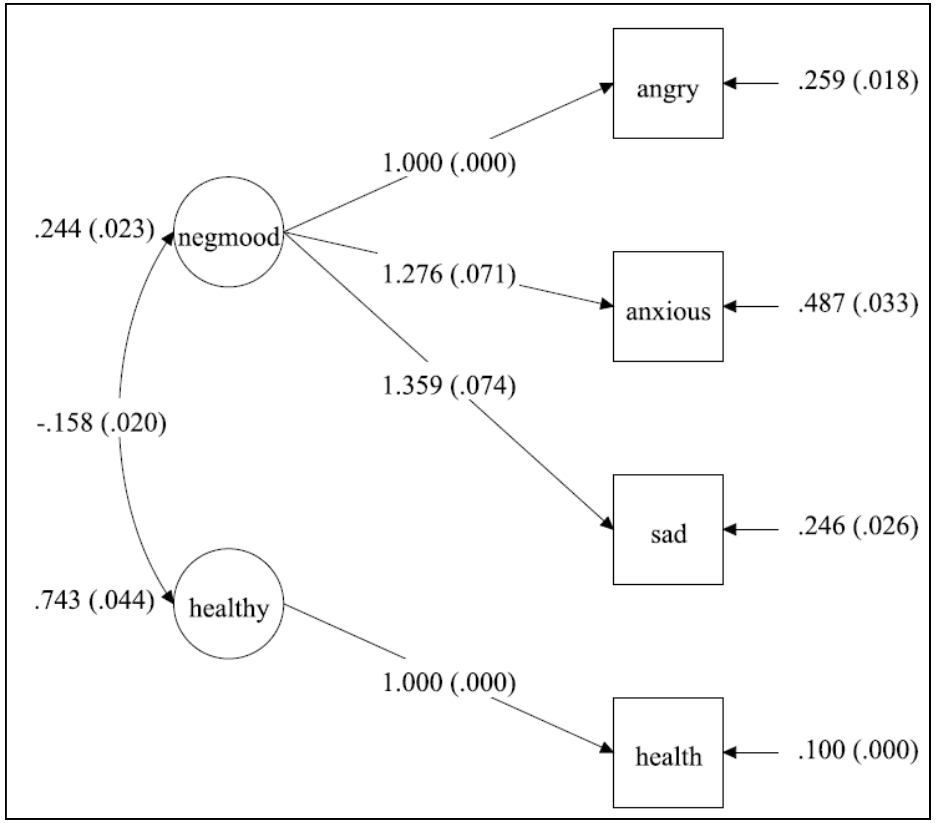
```
 USEVARIABLES ARE
 Angry Anxious Sad Health;
 GROUPING IS GENDER (0=FEMALE 1=MALE);

MODEL:
 !specify factor model for default group (female)
negmood BY Angry@1 Anxious Sad;
 healthy BY Health@1;
 Health@.10;
 healthy WITH negmood;

!Constrain factor means to 0 for identification
 [negmood@0 healthy@0];
 !specify intercepts
 [angry anxious sad health];
 !specify variances
 negmood healthy angry anxious sad;

 !DO NOT Re-specify factor model for males
MODEL MALE:
!Constrain factor means to 0 for identification
 [negmood@0 healthy@0];

 !specify intercepts
 [angry anxious sad health];

 !specify variances
 negmood healthy angry anxious sad;
```

Metric Invariance

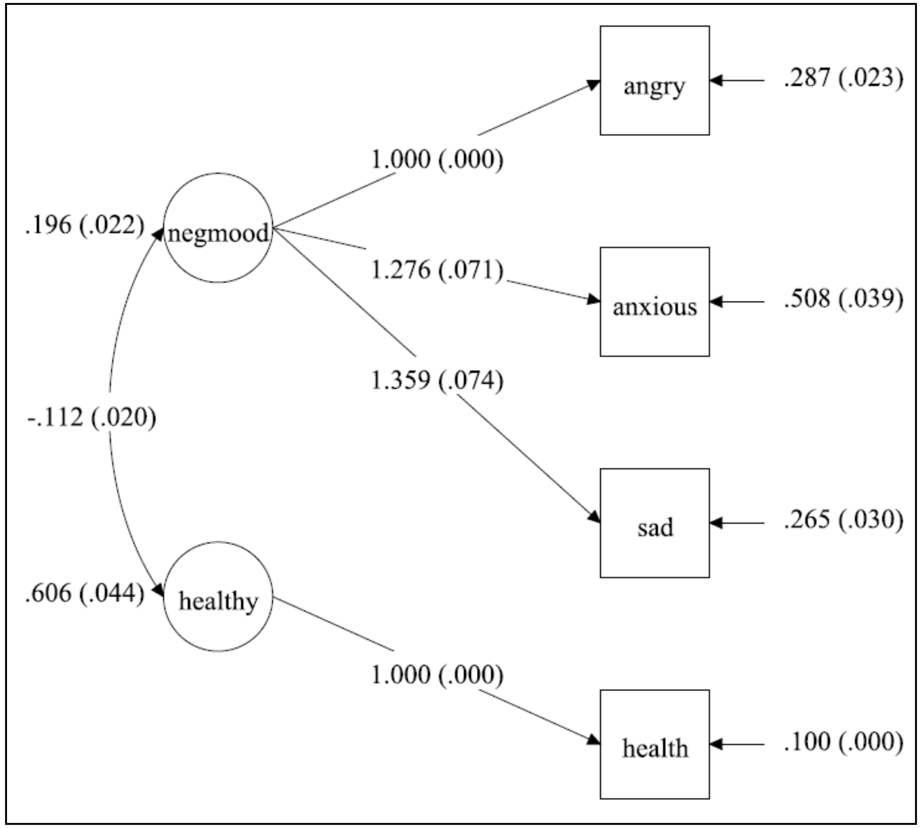
```
Measurement invariance tests:
Model 1: configural invariance:
    chisq        df     pvalue        cfi      rmsea        bic
    7.752     4.000      0.101      0.996      0.038  11762.831
Model 2: weak invariance (equal loadings):
    chisq        df     pvalue        cfi      rmsea        bic
    8.694     6.000      0.192      0.997      0.027  11749.467
```

```
[Model 1 versus model 2]
  delta.chisq       delta.df  delta.p.value       delta.cfi
        0.942          2.000          0.624          -0.001
```

Females



Males



Step 3 - Scalar Invariance (equality constraints of loadings/intercepts)

```
USEVARIABLES ARE
Angry Anxious Sad Health;
GROUPING IS GENDER (0=FEMALE 1=MALE);

MODEL:
 !specify factor model for default group (female)
negmood BY Angry@1 Anxious Sad;
 healthy BY Health@1;
 Health@.10;
 healthy WITH negmood;

!Constrain factor means to 0 for identification
 [negmood@0 healthy@0];

!specify intercepts
 [angry anxious sad health];

 !specify variances
 negmood healthy angry anxious sad;

!DO NOT Re-specify factor model or intercept  for males
MODEL MALE:
!Constrain factor means to 0 for identification
 [negmood@0 healthy@0];

!specify variances
 negmood healthy angry anxious sad;
```

Scalar Invariance

Model 3: strong invariance (equal loadings + intercepts):

chisq	df	pvalue	cfi	rmsea	bic
25.448	8.000	0.001	0.982	0.058	11751.915

[Model 1 versus model 3]

delta.chisq	delta.df	delta.p.value	delta.cfi
17.697	4.000	0.001	0.014

[Model 2 versus model 3]

delta.chisq	delta.df	delta.p.value	delta.cfi
16.754	2.000	0.000	0.015

Females

	Estimate	S.E.	Est./S.E.	P-Value
NEGMOOD BY				
ANGRY	1.000	0.000	999.000	999.000
ANXIOUS	1.295	0.073	17.857	0.000
SAD	1.376	0.075	18.314	0.000
HEALTHY BY				
HEALTH	1.000	0.000	999.000	999.000
HEALTHY WITH				
NEGMOOD	-0.156	0.020	-7.682	0.000
Means				
NEGMOOD	0.000	0.000	999.000	999.000
HEALTHY	0.000	0.000	999.000	999.000
Intercepts				
ANGRY	1.138	0.020	57.390	0.000
ANXIOUS	1.306	0.026	50.050	0.000
SAD	1.074	0.023	46.234	0.000
HEALTH	2.558	0.025	103.127	0.000
Variances				
NEGMOOD	0.241	0.023	10.409	0.000
HEALTHY	0.743	0.044	17.080	0.000
Residual Variances				
ANGRY	0.261	0.018	14.353	0.000
ANXIOUS	0.485	0.033	14.700	0.000
SAD	0.247	0.026	9.545	0.000
HEALTH	0.100	0.000	999.000	999.000

Males

	Estimate	S.E.	Est./S.E.	P-Value
NEGMOOD BY				
ANGRY	1.000	0.000	999.000	999.000
ANXIOUS	1.295	0.073	17.857	0.000
SAD	1.376	0.075	18.314	0.000
HEALTHY BY				
HEALTH	1.000	0.000	999.000	999.000
HEALTHY WITH				
NEGMOOD	-0.111	0.020	-5.577	0.000
Means				
NEGMOOD	0.000	0.000	999.000	999.000
HEALTHY	0.000	0.000	999.000	999.000
Intercepts				
ANGRY	1.138	0.020	57.390	0.000
ANXIOUS	1.306	0.026	50.050	0.000
SAD	1.074	0.023	46.234	0.000
HEALTH	2.558	0.025	103.127	0.000
Variances				
NEGMOOD	0.194	0.022	8.941	0.000
HEALTHY	0.606	0.044	13.934	0.000
Residual Variances				
ANGRY	0.291	0.023	12.639	0.000
ANXIOUS	0.506	0.039	12.833	0.000
SAD	0.271	0.030	8.915	0.000
HEALTH	0.100	0.000	999.000	999.000

Step 4 - Residual Invariance (equality constraints of loadings/intercepts/residuals)

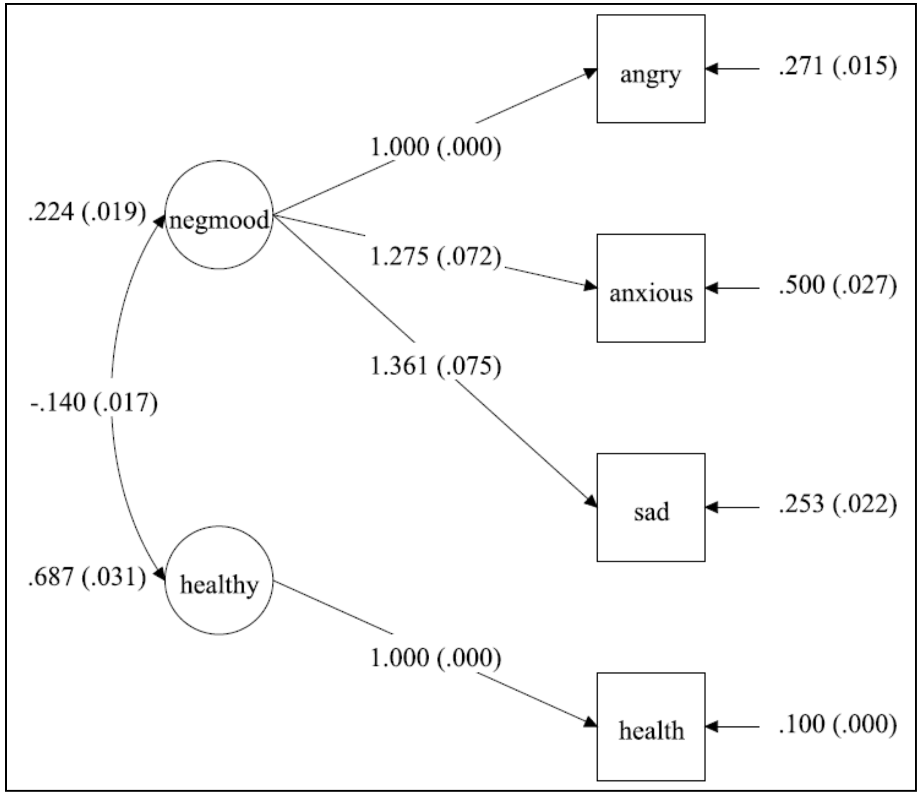
```
 USEVARIABLES ARE
 Angry Anxious Sad Health;
 GROUPING IS GENDER (0=FEMALE 1=MALE);

MODEL:
 !specify factor model for default group (female)
negmood BY Angry@1 Anxious Sad;
 healthy BY Health@1;
 Health@.10;
 healthy WITH negmood;

!Constrain factor means to 0 for identification
 [negmood@0 healthy@0];

!specify intercepts
 [angry anxious sad health];

!specify variances
!(r1-r5) names the residual variances r1 through r5
negmood healthy angry anxious sad (r1-r5);


 MODEL MALE:
!specify variances
!Naming r1-r5 constrain the 5 residuals to be equal
 negmood healthy angry anxious sad (r1-r5);
!Specify a unique intercept for "sad" in males
[sad];
```

Residual Invariance

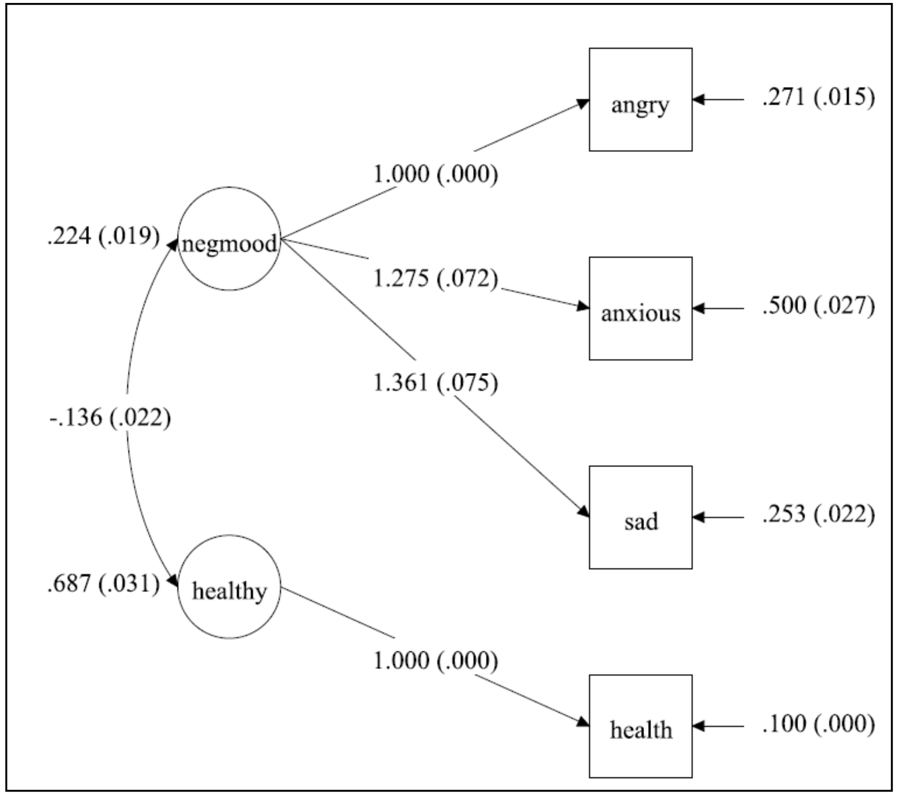
```
Measurement invariance tests:
Model 3: Partial strong invariance (equal loadings +
intercepts):
    chisq        df     pvalue        cfi      rmsea
    17.059      9.00    0.0478      0.992      0.037
Model 4: Residual invariance:
    chisq        df     pvalue        cfi      rmsea
    26.520     14.00    0.0222      0.987      0.037
```

```
[Model 3 partial versus model 4]
  delta.chisq      delta.df  delta.p.value     delta.cfi
        9.461         5.000          0.092         0.005
```

Females



Males



Latent factor variance invariance (constrain factor variance/covariance)

```
 USEVARIABLES ARE Angry Anxious Sad Health;
 GROUPING IS GENDER (0=FEMALE 1=MALE);
 MODEL:
negmood BY Angry@1 Anxious Sad;
 healthy BY Health@1;
 Health@.10;
!specify and label factor covariance
 healthy WITH negmood (cov);
 !Constrain factor means to 0 for identification
 [negmood@0 healthy@0];
!Specify factor variances, fixed at 1.0
 negmood@1 healthy@1;
!specify intercepts
 [angry anxious sad health];
 !specify variances
 !(r1-r5) names the residual variances r1 through r5
 negmood healthy angry anxious sad (r1-r5);
 MODEL MALE:
 !specify variances
negmood healthy angry anxious sad (r1-r5);
!specify and label factor covariance
 healthy WITH negmood (cov);
!Allow means to vary
[negmood* healthy*];
!Specify factor variances, fixed at 1.0
 negmood@1 healthy@1;
!Estimate "Sad" for partial invariance
 [sad];
```

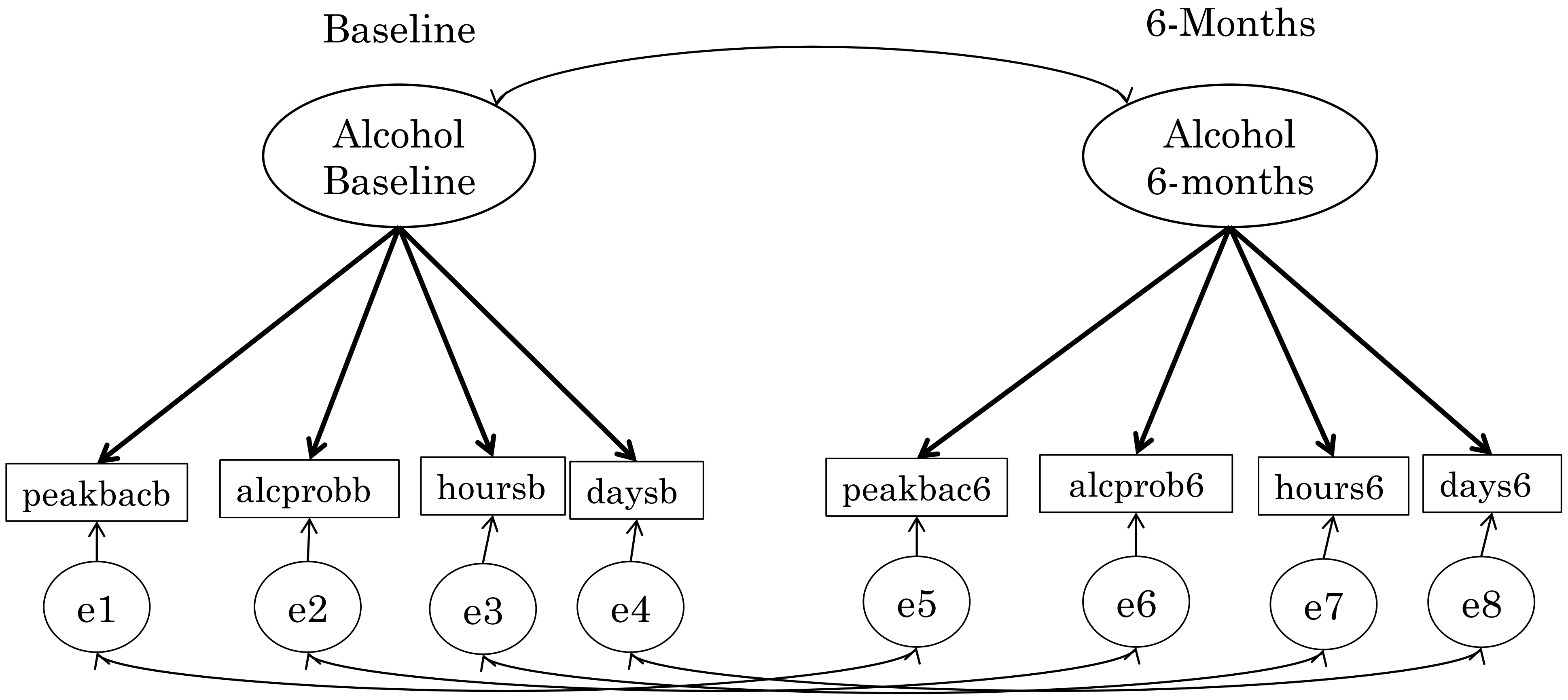
Latent factor variance invariance (constrain factor variance/covariance)

```
MODEL FIT INFORMATION

Chi-Square Test of Model Fit
          Value                              318.668
          Degrees of Freedom                      13
          P-Value                             0.0000

RMSEA (Root Mean Square Error Of Approximation)
          Estimate                             0.192
          90 Percent C.I.                      0.174  0.210
          Probability RMSEA <= .05             0.000

CFI/TLI
          CFI                                  0.692
          TLI                                  0.716

SRMR (Standardized Root Mean Square Residual)

          Value                                0.394
```

Longitudinal Invariance Testing

- Measuring change over time: For each construct of interest, we are measuring the same thing in the same metric at each occasion
- Same as multiple group measurement invariance testing with constraints placed on the same indicators across time (rather than across groups)

Example: Longitudinal Invariance Testing (n=3325)



Longitudinal Non-Invariance

```
MODEL:
 !correlated errors over time
 peakbacb WITH peakbac6;
 alcprobb WITH alcprob6;
 hoursb WITH hours6;  daysb  WITH days6;
 !factor structure baseline
 alc_b  by peakbacb* (L1)
 alcprobb            (L2)
 hoursb              (L3)
 daysb               (L4) ;
 !intercepts
 [peakbacb alcprobb hoursb daysb] (I1-I4);
!residual variances
 peakbacb           (r1);
 alcprobb           (r2);
 hoursb                     (r3);
 daysb                      (r4);
```

```
 !factor structure 6-month
 alc_6 by peakbac6* (L1) !constrain 1st loading
 alcprob6             (L6)
 hours6               (L7)
 days6                (L8) ;
 !intercepts
 [peakbac6](I1); !constrain 1st intercept
[alcprob6 hours6 days6]  (I6-I8);
 !residual variances
 peakbac6           (r5);
 alcprob6           (r6);
 hours6             (r7);
 days6              (r8);
!Constrain time 1 factor variance and mean
alc_b@1;  [alc_b@0];
!Estimate time 2 factor variance and mean
alc_6*; [alc_6*};
!Covary baseline and 6-month alcohol use
alc_6 WITH alc_b;
```

Longitudinal Non-Invariance

MODEL FIT INFORMATION

Chi-Square Test of Model Fit

Value	75.242
Degrees of Freedom	15
P-Value	0.0000

RMSEA

Estimate	0.035
90 Percent C.I.	0.027 0.043
Probability <= .05	0.999

CFI/TLI

CFI	0.993
TLI	0.986

SRMR

Value	0.019

	Estimate	S.E.	Est./S.E.	p
ALC_B BY				
PEAKBACB	0.096	0.002	46.807	0.000
ALCPROBB	0.180	0.006	32.052	0.000
HOURSB	2.032	0.044	45.821	0.000
DAYSB	1.481	0.032	46.555	0.000
ALC_6 BY				
PEAKBAC6	0.096	0.002	46.807	0.000
ALCPROB6	0.214	0.011	20.369	0.000
HOURS6	2.453	0.093	26.374	0.000
DAYS6	1.811	0.066	27.528	0.000
ALC_6 WITH				
ALC_B	0.749	0.026	29.201	0.000
PEAKBACB WITH				
PEAKBAC6	0.002	0.000	8.344	0.000
ALCPROBB WITH				
ALCPROB6	0.033	0.003	12.914	0.000
HOURSB WITH				
HOURS6	1.254	0.113	11.076	0.000
DAYSB WITH				
DAYS6	0.168	0.053	3.190	0.001

Longitudinal Non-Invariance

MODEL FIT INFORMATION

Chi-Square Test of Model Fit

Value	75.242
Degrees of Freedom	15
P-Value	0.0000

RMSEA

Estimate	0.035
90 Percent C.I.	0.027 0.043
Probability <= .05	0.999

CFI/TLI

CFI	0.993
TLI	0.986

SRMR

Value	0.019

	Estimate	S.E.	Est./S.E.	p
Means				
ALC_B	0.000	0.000	999.000	999.000
ALC_6	-0.076	0.025	-3.022	0.003
Intercepts				
PEAKBACB	0.113	0.002	51.021	0.000
ALCPROBB	0.200	0.006	35.993	0.000
HOURSB	2.649	0.048	55.759	0.000
DAYSB	1.765	0.034	52.025	0.000
PEAKBAC6	0.113	0.002	51.021	0.000
ALCPROB6	0.253	0.009	27.689	0.000
HOURS6	3.414	0.081	41.938	0.000
DAYS6	2.350	0.058	40.672	0.000
Variances				
ALC_B	1.000	0.000	999.000	999.000
ALC_6	0.857	0.051	16.880	0.000
Residual Variances				
PEAKBACB	0.006	0.000	26.561	0.000
ALCPROBB	0.068	0.002	35.680	0.000
HOURSB	3.129	0.110	28.389	0.000
DAYSB	1.601	0.058	27.737	0.000
PEAKBAC6	0.007	0.000	24.673	0.000
ALCPROB6	0.103	0.004	27.609	0.000
HOURS6	4.399	0.180	24.470	0.000
DAYS6	1.695	0.082	20.697	0.000

Longitudinal Metric (Weak) Invariance

```
MODEL:
 !correlated errors over time
 peakbacb WITH peakbac6;
 alcprobb WITH alcprob6;
 hoursb WITH hours6;  daysb  WITH days6;
 !factor structure baseline
 alc_b  by peakbacb* (L1)
 alcprobb            (L2)
 hoursb              (L3)
 daysb               (L4) ;
 !intercepts
 [peakbacb alcprobb hoursb daysb] (I1-I4);
!residual variances
 peakbacb         (r1);
 alcprobb         (r2);
 hoursb                    (r3);
 daysb                     (r4);

 !factor structure 6-month
 alc_6 by peakbac6* (L1)
 alcprob6            (L2)
 hours6              (L3)
 days6               (L4) ;

 !intercepts
 [peakbac6](I1); !constrain 1st intercept
[alcprob6 hours6 days6]  (I6-I8);
 !residual variances
 peakbac6          (r5);
 alcprob6          (r6);
 hours6            (r7);
 days6             (r8);
!Constrain time 1 factor variance and mean
alc_b@1; [alc_b@0];
!Estimate time 2 factor variance and mean
alc_6*; [alc_6*};
!Covary baseline and 6-month alcohol use
alc_6 WITH alc_b;
```

Longitudinal Metric Invariance

MODEL FIT INFORMATION

Chi-Square Test of Model Fit

Value	112.809
Degrees of Freedom	18
P-Value	0.0000

RMSEA

Estimate	0.040
90 Percent C.I.	0.033 0.047
Probability <= .05	0.991

CFI/TLI

CFI	0.989
TLI	0.982

SRMR

Value	0.026

Non-invariance Model :

$\chi 2$ (15)= 75.242, CFI = .993

Δ $\chi 2$ (Δ 3) = 37.567, $p < 0.0001$

Δ CFI = 0.004

MODEL RESULTS

	Estimate	S.E.	Est./S.E.	P
ALC_B BY				
PEAKBACB	0.091	0.002	47.606	0.000
ALCPROBB	0.182	0.005	34.622	0.000
HOURSB	2.063	0.042	49.047	0.000
DAYSB	1.520	0.029	52.091	0.000
ALC_6 BY				
PEAKBAC6	0.091	0.002	47.606	0.000
ALCPROB6	0.182	0.005	34.622	0.000
HOURS6	2.063	0.042	49.047	0.000
DAYS6	1.520	0.029	52.091	0.000

MODEL MODIFICATION INDICES

	M.I.	E.P.C.	Std	StdYX
BY Statements				
ALC_B BY PEAKBACB	35.369	0.005	0.005	0.040
ALC_B BY PEAKBAC6	22.099	-0.013	-0.013	-0.099
ALC_6 BY PEAKBACB	22.439	0.012	0.012	0.101
ALC_6 BY DAYSB	11.079	-0.135	-0.143	-0.073
ALC_6 BY PEAKBAC6	35.369	-0.012	-0.013	-0.099

Longitudinal Scalar (Strong) Invariance

```
MODEL:
 !correlated errors over time
 peakbacb WITH peakbac6;
 alcprobb WITH alcprob6;
 hoursb WITH hours6;  daysb  WITH days6;
 !factor structure baseline
 alc_b  by peakbacb* (L1)
 alcprobb            (L2)
 hoursb              (L3)
 daysb               (L4) ;
 !intercepts
 [peakbacb alcprobb hoursb daysb] (I1-I4);
!residual variances
 peakbacb          (r1);
 alcprobb          (r2);
 hoursb                    (r3);
 daysb                     (r4);
 !factor structure 6-month
 alc_6 by peakbac6* (L1)
 alcprob6           (L2)
 hours6             (L3)
 days6              (L4) ;
!Constrain intercepts
[peakbac6 alcprob6 hours6 days6]  (I1-I4);
 !residual variances
 peakbac6          (r5);
 alcprob6          (r6);
 hours6            (r7);
 days6             (r8);
!Constrain time 1 factor variance and mean
alc_b@1; [alc_b@0];
!Estimate time 2 factor variance and mean
alc_6*; [alc_6*};
!Covary baseline and 6-month alcohol use
alc_6 WITH alc_b;
```

Longitudinal Scalar Invariance

MODEL FIT INFORMATION

Chi-Square Test of Model Fit

Value	279.097
Degrees of Freedom	21
P-Value	0.0000

RMSEA

Estimate	0.061
90 Percent C.I.	0.055 0.067
Probability <= .05	0.002

CFI/TLI

CFI	0.969
TLI	0.958

SRMR

Value	0.031

Weak invariance Model :

$\chi 2$ (18)= 112.809, CFI = .989

$\Delta\ \chi 2\ (\Delta\ 3) = 166.288$, $p < 0.0001$

Δ CFI = 0.020

MODEL MODIFICATION INDICES

	M.I.	E.P.C.	Std	StdYX
BY Statements				
ALC_B BY PEAKBACB	47.701	0.006	0.006	0.049
ALC_B BY DAYSB	10.917	-0.044	-0.044	-0.022
ALC_6 BY PEAKBACB	58.194	0.018	0.019	0.160
ALC_6 BY DAYSB	20.380	-0.179	-0.191	-0.097
ALC_6 BY PEAKBAC6	47.700	-0.014	-0.014	-0.113
ALC_6 BY DAYS6	10.917	0.114	0.121	0.058
Means/Intercepts/Thresholds				
[PEAKBACB]	159.140	0.009	0.009	0.072
[HOURSB]	30.813	-0.060	-0.060	-0.022
[DAYSB]	38.855	-0.064	-0.064	-0.033
[PEAKBAC6]	159.139	-0.023	-0.023	-0.181
[HOURS6]	30.813	0.256	0.256	0.083
[DAYS6]	38.854	0.195	0.195	0.093

Fooling Yourself: Specification

- Specify model after data is collected
- Omit causes that are correlated with other variables
- Not enough indicators
- Measures with inadequate psychometrics
- Directionality?
- Feedback loops in structural models when directionality is unknown
- Overparameterization (lack of parsimony)
- Correlated disturbance or measurement errors without substantive reason
- Indicators loading on more than one factor without substantive reason

Fooling Yourself: Data Issues

- Data entry/coding errors
- Ignore patterns of missing data
- Ignore distributional characteristics
- Ignore outliers
- Assume linearity
- Ignore lack of independence among observations (e.g., repeated measures or clustering)

Fooling Yourself: Analysis

- Respecify model based on statistical criteria or MIs
- Accuracy of syntax? Check defaults
- Fail to inspect solution for illogical results
- Reporting only standardized estimates
- Analyze correlation matrix when inappropriate (longitudinal data, independent samples) or using inappropriate methods (ML assumes unstandardized variables
- Failure to inspect for constraint interaction
- Interpret unstable “nonadmissable” solutions

Fooling Yourself: Analysis ctd.

- Complex model with small sample
- Ignoring scaling and start values
- Not checking for uniqueness when identification is uncertain
- Ignoring empirical underidentification
- One-step modeling
- Looking at group mean differences without establishing measurement invariance

Fooling Yourself: Interpretation

- “Fit index tunnel vision” ignoring residuals and individual parameter estimates
- Assuming good fit = proven model
- Interpreting good fit as meaning the endogenous vars are strongly predicted
- Rely only on statistical criteria and cutoffs
- Interpreting standardized solution across multiple groups or over time
- Ignore equivalent or non-equivalent alternative models
- Naming fallacy
- Assume analysis covers up methodological flaws
- Interpret good fit as proof of causality

Revisiting Criticisms

- Cliff (1983): Data can never confirm a model; they can only fail to disconfirm it. If the data do not disconfirm a particular model, then there are other (alternative) models that are not disconfirmed either.
- Ling (1982): "Methods and techniques, developed and applied under that premise, for causal inference…are at best a form of statistical fantasy." SEM approaches are "a class of pseudo-black-magic methods." Ling's view is still held by many statisticians.
- Balance between overall model fit and significance of particular path coefficients.
- Post hoc model modification—It has been shown that it is difficult to modify misspecified models to move closer to "true" models.

How to write up results…

- Analysis plan
  - Start with describing your model
    - Make a path figure
    - Link the model to hypotheses
    - List the number of latent variables and the number of indicators for each
    - Describe your model building procedure
      - Measurement model
      - Invariance testing
      - Model fit decision
      - Modification indices?
    - Report any decisions you made to improve fit (i.e., re-specifications from a priori model)
- Results
  - Overall model fit
  - Measurement model summary
  - Parameter estimates