

Model identification

In general it is possible that there exists $\Theta_1 \neq \Theta_2$ such that $\Sigma(\Theta_1) = \Sigma(\Theta_2)$. This is a problem because it means that there is not just one unique solution to the discrepancy function. A name for this is “under-identification”. In EFA this is directly related to the issue of rotation. In CFA it is usually not a matter of rotation but of some parameters not being separable or simply trying to estimate more parameters than you have pieces of information to do so.

General Principles of identification)

- **Model under-identification or “non-identified” models** - Theoretically no matter how much data you have, there will not be a unique solution for the parameters in a non-identified model. This is always true when the number of parameters is greater than the number of unique elements in S , i.e. $p(p + 1)/2$. But a model can also be non-identified even if the degrees of freedom are > 0 , in this case we often rely on software to tell us the model is non-identified which it does by showing an error somewhere.
- **Empirical under-identification** - This occurs when, for a particular data set, it is not possible to uniquely estimate the parameters due to the some anomaly in the data, e.g. a correlation between two variables is very high and thus it is not possible to distinguish them from each other, or in a model where it is necessary for factors be correlated (in order that the model be identified), if the empirical correlation between them is very small, the model may have problems with empirical under-identification.
- **Identified or “over-identified”** - This means that each parameter is uniquely estimable. In other words it is possible to estimate all the parameters in the model. A special kind of identified model is the “just identified model” or “saturated model”, here the number of parameters equals the number of observations, i.e. the degrees of freedom equal zero. The model fits the data perfectly. Note there can be more than one saturated model.

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Identifiability in the CFA model Kline Section 7.5, 203-207 Table 7.1.

- Necessary conditions:
 - 1 The d.f. must be greater than zero. That is $p(p + 1)/2$ - the number of parameters being estimated must be greater than zero.
 - 2 Every factor must have a scale. This can be accomplished in one of two ways. Either the variance of the factor is fixed to be 1, or the loading of one unique observed variable for each factor is fixed to 1.
- Both methods of fixing the scale produce the exact same fit (Chi-square) value.
- If you fix a factor loading equal to 1 then the results are “unstandardized”, the scale (and thus variance) of the factor is similar to that of the variable it was identified with, i.e. a one unit increase in the factor results in a one unit increase in the observed variable.
- In AMOS and Mplus no matter which observed variable has loading fixed to 1, the “standardized estimates” created from the unstandardized estimates will be the same. Note, though that the unstandardized estimates will change depending on which loading is fixed to 1.

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Identifiability in the CFA model - continued

- The standardized estimates are also obtained when the factors have had their variance fixed to 1, thus a 1 standard deviation increase in the factor results in a λ_1^s standard deviation increase in the observed variable.
- Commonly the direction given is to use unstandardized estimates when making comparisons across groups (so that way the factor variance can be allowed to vary) but otherwise interpreting standardized estimates is usually simpler.
- See Table 7.1 in Kline for some sufficient conditions for identifiability in CFA models

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Example of a just-identified model

The 1 factor model measured by 3 variables...Note that first loading is fixed to 1 (so that the the factor has a scale).

$$\begin{aligned}x_1 &= f + \epsilon_1 \\x_2 &= \lambda_2 f + \epsilon_2 \\x_3 &= \lambda_3 f + \epsilon_3\end{aligned}$$

$$\Sigma = Var(\mathbf{x}) = \begin{pmatrix} \phi + \psi_1 & \lambda_2\phi & \lambda_3\phi \\ \lambda_2\phi & \lambda_2^2\phi + \psi_2 & \lambda_2\lambda_3\phi \\ \lambda_3\phi & \lambda_3\lambda_2\phi & \lambda_3^2\phi + \psi_3 \end{pmatrix}$$

fit this to the data

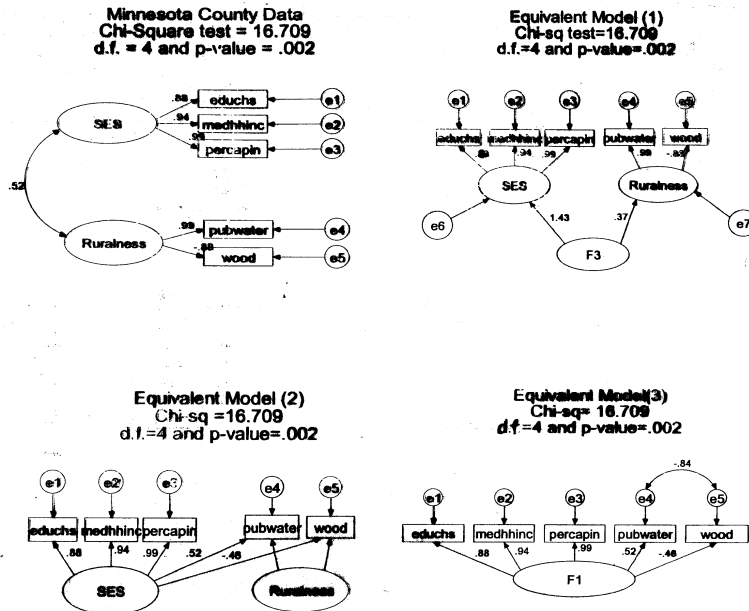
$$\mathbf{S} = \begin{pmatrix} s_1^2 & s_{12} & s_{13} \\ s_{12} & s_2^2 & s_{23} \\ s_{13} & s_{23} & s_3^2 \end{pmatrix}$$

Possible to algebraically solve for each parameter. 6 equations - 6 unknowns.

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Equivalent models

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Nested Models In addition to Chapter 7 some mention is given on pages 132-135 in Kline

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- Models are nested whenever one model is the same as the other model except that it has some parameters constrained. In other words, if you unconstrained some parameters in one model, you would get the other.
- Examples
 - Testing for redundancy - A one factor model is nested within a two factor simple structure CFA (constrains correlation between factors to equal 1)
 - Testing for orthogonality - an orthogonal factor structure is nested within an oblique structure
 - Testing for tau equivalence - a model with factor loadings constrained to be equal is nested within one that lets all loadings be different.
- When models are nested, we can perform a **Chi-square difference test** to compare them.

Nested Models - Chi square difference test

- H_0 : More restrictive model (the one with some parameters constrained)
- H_A : Less restrictive model

Chi-square test to compare these models = Chi-square test value for More restrictive model - Chi-square test value for Less restrictive model

Compare this test stat to a chi-squared distribution with d.f. = (d.f. for More restrictive model) - (d.f. for Less restrictive model)

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Nested Models - Chi square difference test

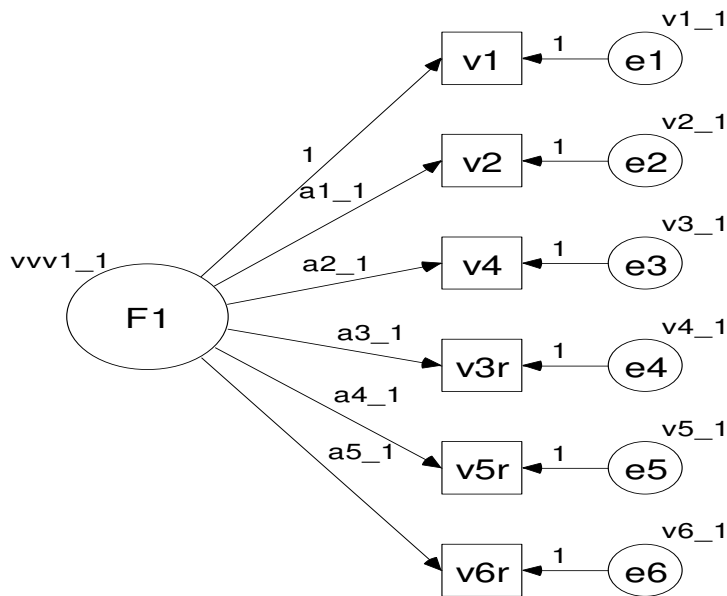
Example testing tau equivalence of Self-Esteem from Project EAT (see model on next page)

- H_0 : Tau-equivalent model vs H_A : Congeneric model
- H_0 : $1 = a_{1_1} = a_{2_1} = a_{3_1} = a_{4_1} = a_{5_1}$
vs H_A : all factor loadings can be different
- Chi-square test value for Congeneric model = 238.5 with 9 degrees of freedom
- Chi-square test value for Tau-equivalent model = 263.8 with 14 degrees of freedom
- Chi-square difference test for hypothesis above = $263.8 - 238.5 = 25.3$
with $14 - 9 = 5$ d.f.
- The p-value associated with this test is $< .0001$, so we reject the Null hypothesis in favor of the alternative.
- Thus the Tau-equivalent model (more restrictive model) does not fit as well as the Congeneric model (less restrictive model).
- NOTE: This does not mean the Congeneric model fits well, for this we should consider how it compares to the saturated model or look at other Goodness of Fit tests.

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Nested Models - Self esteem Project EAT

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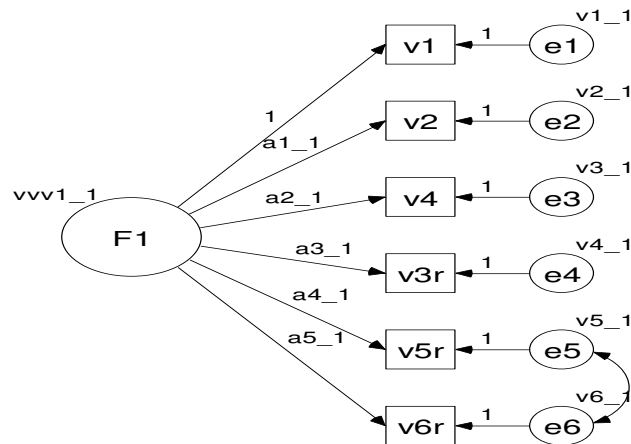


Modification Indices

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- Each path that has not been included in the model has an associated “modification index”.
- A modification index tells you how much the overall chi-square test statistic would change if that particular path was added to the model.
- Adding one new path will decrease the degrees of freedom by one. So, since the model without the path can be considered to be “nested” within the model with the path, we can consider the difference in the chi-square test as a test for whether the path is needed or not.
- Since 3.84 is the .05 cut-off value for a chi-square with 1 degree of freedom, modification indices greater than 3.84 suggest that a path should be added.
- AMOS has a default threshold of 4 for outputting modification indices. This can be changed in the output tab window under analysis properties.
- The ParChange found in the AMOS modification index output tells you what the unstandardized estimate of the path would be if it was added to the model.
- NOTE: modification indices should only be considered one at a time. If you add more than one path the change in overall chi-square will not necessarily equal the sum of the two modification indices.

Modification Indices - Self esteem Project EAT



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One of the Modification indices will test

H_0 : Model with $Corr(e5, e6) = 0$ (more restrictive since correlation forced to zero)

H_A : Model with $Corr(e5, e6) \neq 0$ (less restrictive since correlation is not fixed)

Modification Indices - Self esteem Project EAT

H_0 : Model with $Corr(e5, e6) = 0$ (more restrictive since correlation forced to zero)

H_A : Model with $Corr(e5, e6) \neq 0$ (less restrictive since correlation is not fixed)

The test is a chi-square difference test because the models are nested. That is, one model is just a restricted version of the other. So,

$$\chi^2_{\text{model w/o correlation}} - \chi^2_{\text{model with correlation}} = 238.5 - 129.9 = 108.6$$

and we compare this to a χ^2 distribution with $9 - 8 = 1$ d.f. This gives a p-value $< .0001$ suggesting we should reject the null in favor of the alternative suggesting that this added correlation greatly improves the model.

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Actual value given for modification index is different in AMOS and Mplus each is using a different approximation since it too computationally intensive to refit model over and over dropping each restriction. Mplus claims their approximation is a lower bound.

Sample Size and Normality Chi-squared test of model fit and standard errors for factor loadings are based on normality assumption for $\mathbf{x}|\mathbf{f}$ and \mathbf{f} and asymptotic theory

- How big should n be before we trust these numbers????
 - See “Literature on sample size fa.pdf” on class website, e.g. rule of thumb: $n > 15 * (\text{number of free parameters})$
- We should consider to what extent multivariate normality is violated
- How non-normal is non-normal??
 - Rules of thumb - examine univariate skew and kurtosis. West, Finch and Curran (1995) “Structural equation models with non-normal variables: Problems and remedies”. In R.H. Hoyle (Ed.) Structural equation modeling (pp. 56-75) Thousand Oaks, CA: Sage. This paper gives rule of thumb of skew > 2 and kurtosis > 7 to indicate problematic non-normal data.
 - Departures from normality cause the chi-square test to be larger than it should be and standard errors to be smaller than they should be.
 - If n is very large (i.e. rule of thumb $n > 1000$), do not need to worry about non-normality. Amemiya and Anderson (1988,1990)

<http://www.utexas.edu/cc/faqs/stat/general/gen33.html> <http://www.utexas.edu/cc/faqs/stat/amos/amos7.html>

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CFA invariance across groups

The question we want to answer is:

Does the factor structure differ across different subpopulations in terms of: numbers of factors, magnitude of loadings, overall means.

- MIMC (Multiple indicator multiple cause) or CFA with covariates
- Multiple Group CFA

The difference between these is analogous to either including a covariate into a regression directly or instead stratifying by the covariate and analyzing the different groups.

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MIMIC example

See hard copy handout of NELS DATA example in Mplus

Multi-group analysis - Examples

Examples

- from Kline p.224-226. Kaufman Assessment Battery for Children.
- Self esteem paper from Homework 1 where they wanted to see if positive and negative factors showed up similarly for individuals with different grade achievement in school and different generational immigrants
- Project EAT self-esteem data comparing boys and girls (see lab exercise MultipleGroupCFAinAMOS.pdf on class website)

Multitrait Multimethod MTMM Confirmatory factor analysis approach used with specially designed survey implementation to investigate the validity of measuring latent variables (traits) with different instruments (methods). Common variance shared by traits is separated from common variance shared by method effect.

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Multi-group analysis (6.10 and 7.8 in Kline)

From the Help in AMOS

“When you have data from multiple groups, you often start by asking if it is necessary to draw a separate path diagram for each group, or if the same path diagram will do for all groups. If you conclude that all the groups share the same path diagram, you can proceed to ask whether parameter values are invariant across groups. For example, if you are studying boys and girls, you might want to know whether boys and girls have the same regression weights, or if only certain regression weights are the same for boys and girls. Of course there are also variances and covariances as well as regression weights to consider. Because of the large number of possible cross-group constraints, it is necessary to have a strategy for deciding which cross-group constraints are worth testing and in what order to test them. Bollen (1989), Kline (1998), and others discuss such strategies. Amos 5 implements an automatic procedure for generating a nested hierarchy of models in which cross-group constraints are introduced incrementally in a pre-chosen order.

No automatic procedure can anticipate the purpose of an individual study. If necessary, you can modify Amos automatically generated cross-group constraints to suit the needs of an individual study. However, no such customization will be necessary in most cases. You also have the option of performing multiple-group analyses by imposing cross-group constraints manually, just as in Amos 4.”

Multi-group analysis (6.10 and 7.8 in Kline)

Commonly used to see whether a measurement instrument exhibits same structure (dimensions and communalities) in different populations.

- We want to test if the latent variables defined the same way in each group
- Recall that to make a CFA identified, we either had to fix a loading to 1 or the variance of the factor to 1.
- For multiple group comparisons, it makes sense to fix the loading to 1 so that way the variance can be different in each group
- Kline tries to make an issue of concern about the fact that the loading fixed to 1 cannot be tested across groups, I'm not sure this is important because we should be testing all the indicators of a particular factor at once.
- Must analyze covariance matrices because there may be differences in variability across groups and if a correlation matrix is used (all variables are standardized) this info about differences in variances is lost.

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Multi-group analysis (6.10 and 7.8 in Kline)

If there are two groups

$$\mathbf{x} = \begin{pmatrix} \mathbf{x}^{group1} \\ \mathbf{x}^{group2} \end{pmatrix}$$

The groups are assumed to be independent, thus

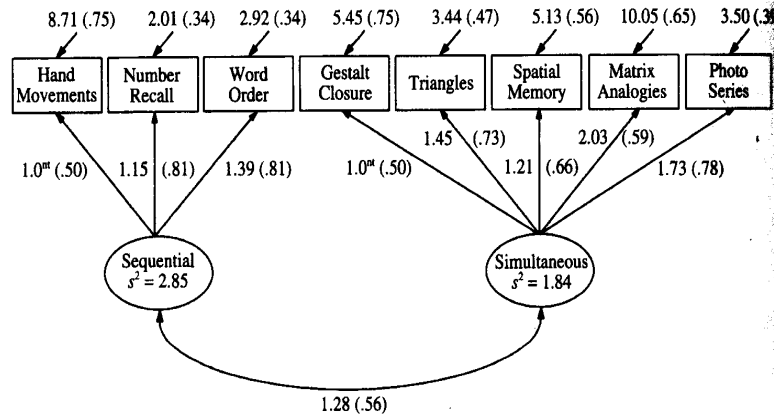
$$Var(\mathbf{x}) = \Sigma = \begin{pmatrix} \Sigma_{group1} & 0 \\ 0 & \Sigma_{group2} \end{pmatrix}$$

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The unconstrained multiple group model places no restrictions on the relationship between Σ_{group1} and Σ_{group2} , hence the chi-square and d.f. of the multigroup analysis equals the sum of the chi-square and d.f. of the separate group analysis.

Then, what is of interest is to test certain restrictions relating Σ_{group1} and Σ_{group2} , the most restrictive being that $\Sigma_{group1} = \Sigma_{group2}$ which would mean that Λ , Φ , and Ψ are the same in both groups. This would then be a nested model within the unconstrained model and a chi-squared difference test could be used to test it. See the AMOS lab MultipleGroupCFAinAMOS.pdf for more examples of the kinds of multigroup restrictions that can be tested.

Multi-group Example Kline Chapter 7



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FIGURE 7.4. Two-factor model of the K-ABC with the unstandardized and standardized solutions. All unstandardized estimates are significant at the .01 level except those designated "nt," which means not tested. Standardized estimates are reported in parentheses. The standardized values for the measurement error terms are proportions of unexplained variance.

Multi-group Example Kline Chapter 7

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TABLE 7.6. Multiple Group CFA of a Two-Factor Model of the Kaufman Assessment Battery for Children

Correlations, means, and standard deviations (Naglieri & Jensen, 1987; elementary school students, $N = 86$ white [below diagonal], $N = 86$ African-American [above diagonal])

Variable	Sequential			Simultaneous				African-American		
	1	2	3	4	5	6	7	8	M	
Sequential Processing scale tasks										
1. Hand Movements	—	.19	.26	.13	.19	.26	.22	.28	12.00	4.1
2. Number Recall	.35	—	.40	.06	.22	.24	.18	.09	10.93	1.5
3. Word Order	.36	.59	—	.08	.10	.32	.30	.11	12.86	1.5
Simultaneous Processing scale tasks										
4. Gestalt Closure	.00	-.08	-.06	—	.50	.34	.27	.21	18.36	2.7
5. Triangles	.31	.25	.31	.07	—	.41	.48	.28	13.28	2.6
6. Matrix Analogies	.39	.21	.25	.17	.44	—	.41	.35	11.91	3.4
7. Spatial Memory	.30	.09	.25	.17	.39	.29	—	.38	13.81	2.3
8. Photo Series	.33	-.02	.10	.32	.31	.14	.29	—	12.38	2.4
White M	12.65	11.01	13.03	18.72	14.48	13.00	14.87	12.80		
SD	2.73	2.06	2.04	2.45	2.28	3.36	12.80	2.12		
Goodness of fit summary										
Model	χ^2	df	χ^2/df	Contrast with baseline model		CFI				
Single-sample analyses										
White only	34.90*	19	1.84	—	—	.87				
African-American only	22.46	19	1.18	—	—	.97				
Multiple group analyses										
Baseline (no constraints)	57.36*	38	1.51	—	—	.92				
Factor loadings invariant	63.83*	44	1.45	6.47	6	.91				

Note. CFI, Bentler Comparative Fit Index.
* $p < .05$.

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Multi-group Example Kline Chapter 7

Notice that the chi-square test for the Multiple group analysis - Baseline (no constraints) is $34.90 + 22.46 = 57.36$ with $19 + 19 = 38$ d.f. This is a model that allows Σ_{group1} to be estimated completely independently from Σ_{group2} hence it results in a chi-square and d.f. equal to the sum of the stratified analysis.

Then we see that the multigroup model with the factor loadings to be constrained to be the same across the groups (nested within the no constraints model) has a chi-square of 63.83 and 44 d.f. The reason it has 44 d.f. is because 6 parameters (loadings) have been constrained, thus $38 + 6 = 44$.

So the chi-square difference test

$H_0 : \Lambda_1 = \Lambda_2$ (restricted model)

$H_A : \Sigma_1 \neq \Sigma_2$ (unconstrained model)

is given by $63.83 - 57.36 = 6.47$ on 6 d.f.

This has a p-value = .373, so we DO NOT REJECT the null hypothesis, suggesting that the model with the factor loadings the same in the two groups is not significantly different from the more complicated model (model with more parameters) which says the loadings are different in the two groups. Hence, we choose the more parsimonious model with $\Lambda_1 = \Lambda_2$

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Multi-group Example Genetic Testing Concern

The question is does the 2-factor structure found for Questions C8 C18 C19 and C9 C11 C14 fit the same in the group of women who have insurance versus those who do not.

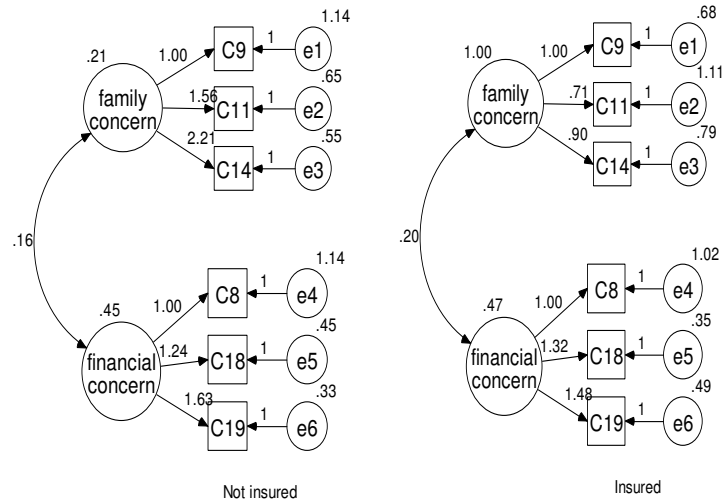
A two-group analysis is performed in AMOS and a confirmatory factor analysis with the covariate insurance status is performed in Mplus.

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Multi-group Example Genetic Testing Concern

Unstandardized estimates in Unconstrained model for the two groups

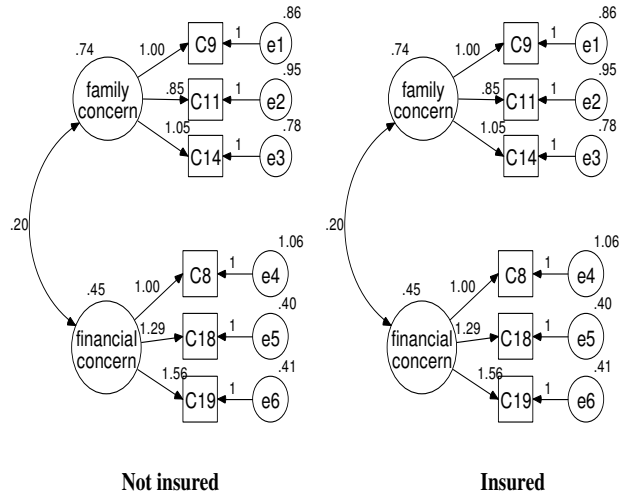
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Multi-group Example Genetic Testing Concern

Unstandardized estimates for the Model where loadings, factor variance and covariance, and error variances are fixed to be equal (called Measurement residuals in AMOS output)

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Multi-group Example Genetic Testing Concern

Model Fit Summary

CMIN

Model	NP	DF	CMIN	P	CMIN/DF
Unconstrained	26	16	38.84619	.00114	2.42789
Measurement weights	22	20	44.31363	.00137	2.21568
Structural covariances	19	23	45.93968	.00304	1.99738
Measurement residuals	13	29	52.02953	.00541	1.79412
Saturated model	42	0	.00000		
Independence model	12	30	361.49472	.00000	12.04982

RMSEA

Model	RMSEA	LO 90	HI 90	PCLOSE
Unconstrained	.08387	.05052	.11782	.04772
Measurement weights	.07739	.04652	.10824	.06930
Structural covariances	.07009	.03982	.09952	.12452
Measurement residuals	.06255	.03370	.08955	.21103

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Multi-group Example Genetic Testing Concern

Nested Model Comparisons

Assuming model Unconstrained to be correct:

Model	DF	CMIN	P	NFI Delta-1	IFI Delta-2	RFI rho-1	TLI rho2
Measurement weights	4	5.46743	.24261	.01512	.01582	-.01761	-.01920
Structural covariances	7	7.09349	.41921	.01962	.02053	-.03573	-.03896
Measurement residuals	13	13.18334	.43375	.03647	.03816	-.05260	-.05736

Assuming model Measurement weights to be correct:

Model	DF	CMIN	P	NFI Delta-1	IFI Delta-2	RFI rho-1	TLI rho2
Structural covariances	3	1.62605	.65350	.00450	.00476	-.01812	-.01976
Measurement residuals	9	7.71590	.56301	.02134	.02259	-.03498	-.03815

Assuming model Structural covariances to be correct:

Model	DF	CMIN	P	NFI Delta-1	IFI Delta-2	RFI rho-1	TLI rho2
Measurement residuals	6	6.08985	.41320	.01685	.01799	-.01687	-.01839

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Multi-group Example Genetic Testing Concern Mplus - results from two-factor model with no mention of groups

```

TESTS OF MODEL FIT
Chi-Square Test of Model Fit
    Value                30.453
    Degrees of Freedom      8
    P-Value                0.0002

Chi-Square Test of Model Fit for the Baseline Model
    Value                347.568
    Degrees of Freedom    15
    P-Value                0.0000

CFI/TLI
    CFI                0.932
    TLI                0.873

Loglikelihood
    H0 Value            -1826.043
    H1 Value            -1810.816

Information Criteria
    Number of Free Parameters    13
    Akaike (AIC)                 3678.086
    Bayesian (BIC)               3721.285
    Sample-Size Adjusted BIC     3680.096
    (n* = (n + 2) / 24)

RMSEA (Root Mean Square Error Of Approximation)
    Estimate                0.117
    90 Percent C.I.        0.075 0.162
    Probability RMSEA <= .05 0.006

SRMR (Standardized Root Mean Square Residual)
    Value                0.069
    
```

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Multi-group Example Genetic Testing Concern

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MODEL RESULTS
      Estimates      S.E.  Est./S.E.  Std  StdYX
FINANCE BY
  C8      1.000    0.000    0.000    0.673    0.547
  C18     1.293    0.178    7.258    0.870    0.809
  C19     1.554    0.217    7.151    1.046    0.850
FAMILY BY
  C9      1.000    0.000    0.000    0.871    0.685
  C11     0.851    0.137    6.216    0.741    0.604
  C14     1.044    0.165    6.342    0.909    0.717
FAMILY WITH
  FINANCE 0.202    0.062    3.240    0.345    0.345
Variances
  FINANCE 0.453    0.117    3.877    1.000    1.000
  FAMILY  0.758    0.172    4.402    1.000    1.000
Residual Variances
  C8      1.061    0.115    9.215    1.061    0.701
  C18     0.400    0.084    4.768    0.400    0.346
  C19     0.420    0.114    3.674    0.420    0.278
  C9      0.856    0.136    6.286    0.856    0.530
  C11     0.954    0.123    7.741    0.954    0.635
  C14     0.780    0.139    5.613    0.780    0.486
R-SQUARE Observed
Variable  R-Square
  C8      0.299
  C18     0.654
  C19     0.722
  C9      0.470
  C11     0.365
  C14     0.514
    
```

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Multi-group Example Genetic Testing Concern Program to include insurance status as a covariate influencing the factors.

```

TITLE:

DATA:
  FILE IS "C:\Mplus\ph5482\genetictestingrawdatanomiss.csv";

VARIABLE:
  NAMES ARE
  c1-c20 age race marital educ insure
  ;

USEVARIABLES ARE
  c8 c18 c19 c9 c11 c14 insure
  ;

missing are .;

MODEL:
  finance by c8 c18 c19;
  family by c9 c11 c14;
  finance on insure;
  family on insure;

c8 c18 c19 c9 c11 c14 on insure @0;

output: modindices(4.00) sampstat standardized;

```

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Multi-group Example Genetic Testing Concern

```

TESTS OF MODEL FIT

Chi-Square Test of Model Fit
  Value                31.832
  Degrees of Freedom    12
  P-Value               0.0015

Chi-Square Test of Model Fit for the Baseline Model
  Value                351.391
  Degrees of Freedom    21
  P-Value               0.0000

CFI/TLI
  CFI                  0.940
  TLI                  0.895

Loglikelihood
  H0 Value             -1946.389
  H1 Value             -1930.473

Information Criteria
  Number of Free Parameters    15
  Akaike (AIC)                 3922.778
  Bayesian (BIC)               3972.623
  Sample-Size Adjusted BIC     3925.098
  (n* = (n + 2) / 24)

RMSEA (Root Mean Square Error Of Approximation)
  Estimate                   0.090
  90 Percent C.I.           0.053 0.128
  Probability RMSEA <= .05  0.041

SRMR (Standardized Root Mean Square Residual)
  Value                      0.060

```

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Multi-group Example Genetic Testing Concern

MODEL RESULTS

	Estimates	S.E.	Est./S.E.	Std	StdYX
FINANCE BY					
C8	1.000	0.000	0.000	0.673	0.547
C18	1.291	0.178	7.259	0.869	0.807
C19	1.557	0.218	7.143	1.048	0.852
FAMILY BY					
C9	1.000	0.000	0.000	0.874	0.688
C11	0.851	0.136	6.252	0.744	0.607
C14	1.034	0.162	6.401	0.904	0.713
FINANCE ON					
INSURE	0.022	0.118	0.185	0.032	0.014
FAMILY ON					
INSURE	0.254	0.165	1.538	0.291	0.127
C8 ON					
INSURE	0.000	0.000	0.000	0.000	0.000
C18 ON					
INSURE	0.000	0.000	0.000	0.000	0.000
C19 ON					
INSURE	0.000	0.000	0.000	0.000	0.000
C9 ON					
INSURE	0.000	0.000	0.000	0.000	0.000
C11 ON					
INSURE	0.000	0.000	0.000	0.000	0.000
C14 ON					
INSURE	0.000	0.000	0.000	0.000	0.000
FAMILY WITH					
FINANCE	0.201	0.062	3.233	0.341	0.341

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Multi-group Example Genetic Testing Concern

Residual Variances

C8	1.061	0.115	9.216	1.061	0.701
C18	0.403	0.084	4.805	0.403	0.348
C19	0.416	0.115	3.626	0.416	0.275
C9	0.850	0.135	6.277	0.850	0.527
C11	0.949	0.123	7.728	0.949	0.632
C14	0.789	0.137	5.754	0.789	0.492
FINANCE	0.453	0.117	3.875	1.000	1.000
FAMILY	0.751	0.170	4.428	0.984	0.984

R-SQUARE

Observed

Variable	R-Square
C8	0.299
C18	0.652
C19	0.725
C9	0.473
C11	0.368
C14	0.508

Latent

Variable	R-Square
FINANCE	0.000
FAMILY	0.016

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Multi-group Example Genetic Testing Concern

MODEL MODIFICATION INDICES
 Minimum M.I. value for printing the modification index 4.000

	M.I.	E.P.C.	Std E.P.C.	StdYX E.P.C.
ON/BY Statements				
C8 ON FAMILY /				
FAMILY BY C8	6.698	-0.289	-0.253	-0.206
C14 ON FINANCE /				
FINANCE BY C14	9.062	0.462	0.311	0.245
ON Statements				
FINANCE ON C8	6.888	0.418	0.621	0.764
FINANCE ON C14	9.007	0.234	0.347	0.440
FAMILY ON C8	6.916	-0.186	-0.213	-0.262
FAMILY ON C14	6.999	-0.729	-0.834	-1.056
C8 ON C9	9.547	-0.190	-0.190	-0.196
C18 ON C19	6.894	-2.142	-2.142	-2.450
C18 ON C14	6.529	0.122	0.122	0.144
C19 ON C18	6.893	-2.213	-2.213	-1.935
C19 ON C9	5.580	0.129	0.129	0.133
C9 ON C8	8.100	-0.183	-0.183	-0.177
C9 ON C18	6.789	-0.210	-0.210	-0.178
C9 ON C11	7.002	0.499	0.499	0.481
C11 ON C9	7.001	0.557	0.557	0.577
C14 ON C18	14.603	0.310	0.310	0.263
WITH Statements				
C8 WITH FINANCE	6.889	0.443	0.659	0.535
C8 WITH FAMILY	6.916	-0.197	-0.226	-0.183
C19 WITH C18	6.892	-0.891	-0.891	-0.673
C9 WITH C8	6.486	-0.202	-0.202	-0.130
C9 WITH C18	7.571	-0.160	-0.160	-0.117
C9 WITH C19	8.191	0.188	0.188	0.121
C11 WITH C9	7.001	0.473	0.473	0.304
C14 WITH FINANCE	9.007	0.184	0.274	0.216
C14 WITH FAMILY	6.999	-0.575	-0.658	-0.519
C14 WITH C18	9.711	0.179	0.179	0.132

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