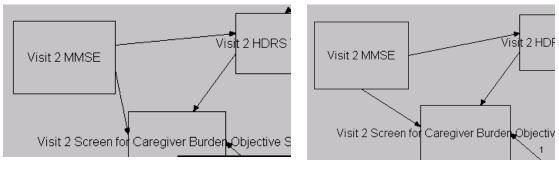
Amos User's Guide Part II

Jeannie-Marie Sheppard (2002), edited (2006)

This handout will include discussion of some more useful features. First, if you look at the button bar to the left, you notice that the top stripe is grey. If you click on it, it will turn blue. When that bar is blue, it means that the button bar is selected. When the button bar is selected, if you let the mouse hang out for a bit over a button, a caption will pop up saying what it is. In referencing the buttons' positions, I will use row-column notation, i.e., TITLE is in the (3,1) position.

Drawing a tidy picture is key.

This guy is cool. So suppose your diagram looks like this:

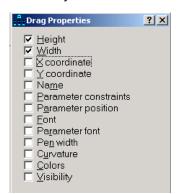


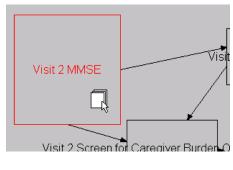
Clicking on the touch up wand and selecting V2 MMSE will tidy things up a bit... This wasn't an major change but it is quick. It works well on errors.

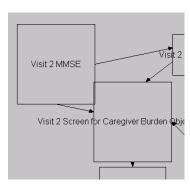
One way to make your boxes and ovals all the same size is to use the copy machine. Suppose you didn't do that, you could use the following tool: (10,2) Drag Properties

This button will drag properties from one object to another. So if you wanted to make two boxes be the same height and width, click on this box and height and

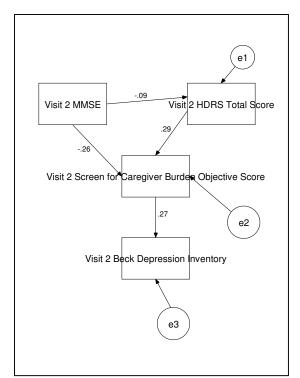
width. Note, don't close the drag Properties option box before you do it, but you may have to move it out of the way.







There are probably a tonne of ways to use this, another useful one is to line things up. If you want them to be at the same level, etc, you can drag X and Y coordinates.



Now, after you run your model, much to your chagrin, you have to tidy it up all over again. Not to worry.

The move parameter values button will help you move the numbers around. Unfortunately, there doesn't seem to be a way to move the estimate on top of the object, but you can rearrange things.

When you're in the output window, you can click on either the estimate itself, or the box or arrow to which it is related (they'll both turn red) and you can move things around, (just like the moving truck)



The change the shape of objects (6,1) does just that, and works intuitively.

Check out the other buttons, some of them are real time savers.

This is a toy example using a bit of data from the DIADS study concerning Alzheimer patient and caregiver depression. First I want to give this project a title (look at part 1 for this) If you use the title button on the button bar (3,1) this titles the picture, not the analysis. Use the title tab in the analysis properties

I run the model now. Part of the point of this example is to help you decide which elements of the output you should include in your homework. Including all the input a) kills trees b)doesn't give you the opportunity to show that you understand which parts of the output are relevant to a particular question.

Amos

Deviously trash. Don't include this.

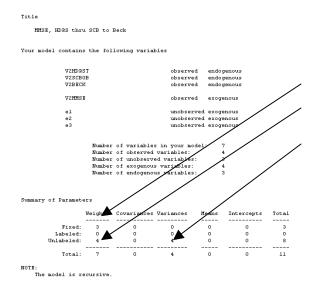
Amos

by James L. Arbuckle

Version 4.01

Copyright 1994-1999 SmallWaters Corporation
1807 E. 83rd Street - #452
Chicago, IL 60618 USA
773-667-6635
Fai: 773-955-6252
http://www.smallwaters.com

Looking here will help you make sure that you put the right variables in, and that they are doing the things that you thought they were doing (i.e., observed, exogenous, whatever)



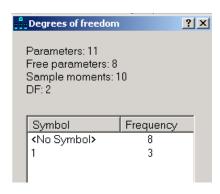
This says how many parameters you have and what they are. First there are 3 fixed weights (these are the ones between the errors and your endogenous weights)

There are 4 unlabeled weights (each arrow between observed variables)

There are 4 variances (for each of your observed variables)

If you asked it to estimate means and intercepts, (you would have to do this if you have any missing data) then there would be:

1 mean (1 for each exogenous variable) 3 intercepts (1 for predicting each endogenous variable)



Sample size: 41

At this point you may recall having clicked the DF (13,1) button and gotten the following information, which doesn't seem to match with the above.

Sample moments are correlations between observed variables, and their variances. n(n+1)/2 = 10

Total parameters is equal to variances for every box, and each arrow.

Now, you have 7 arrows, however, 3 (these are for the errors) are fixed so you are estimated 4 direct effects, and 4 correlations. This means there are 8 parameters that are free to be estimated.

	variances					
		V2HDRST				
VZMMSK	41.684					
VZHDRST		35.640				
72SCBOB	-9.430	9.534	25.378			
VZBECK	3.766	7.435	6.996	27	7.079	
Eigenvalu	ues of Samaj	ole Covar	iances			
1.542∈	+001 2.:	273e+001	4.019e+	001	5.144e+001	
Condition	number o	f Sample	Covarianc	es =	3.335068e+00	00
Sample Co	rrelation:	5				
		V2HDRST				
72MMSE	1.000					
	0.105	1.000				
VZHDRST	-0.107					
72SCBOB	-0.290	0.317	1.000			
V2SCB0B	-0.107 -0.290 0.112	0.317	1.000		000	
V2SCBOB V2BECK	-0.290	0.317 0.239	1.000 0.267		1.000	
V2SCBOB V2BECK Eigenvalu	-0.290 0.112 ues of Sam	0.317 0.239 ole Corre	1.000 0.267 lations	1	1.609e+000	
V2SCBOB V2BBCK Bigenvalu 5.435e	-0.290 0.112 ues of Sam	0.317 0.239 ole Corre	1.000 0.267 lations 1.127e+	000		000
Eigenvalu 5.435e Condition	-0.290 0.112 les of Samp 001 7.3	0.317 0.239 ple Corre. 201e-001 f Sample	1.000 0.267 lations 1.127e+ Correlati	000 ons =	1.609e+000	
V2SCB0B V2BBCK Bigenvalu 5.435e Condition	-0.290 0.112 les of Samp 001 7.3	0.317 0.239 ole Corre. 201e-001 f Sample	1.000 0.267 lations 1.127e+ Correlati	000 ons =	1.609e+000 2.961101e+0	
V2SCB0B V2BBCK Bigenvalu 5.435e Condition	-0.290 0.112 les of Samy -001 7.3 number o	0.317 0.239 ole Corre. 201e-001 f Sample	1.000 0.267 lations 1.127e+ Correlati	000 ons =	1.609e+000 2.961101e+0	
V2SCBOB V2BECK Eigenvalv 5.435e Condition Determins	-0.290 0.112 les of Samy -001 7.3 number o	0.317 0.239 ole Corre. 201e-001 & Sample (1.000 0.267 lations 1.127e+ Correlati iance mat	000 ons =	1.609e+000 2.961101e+0	

So, if in analysis properties you selected "sample moments" it will show you the covariance and correlation matrices of your observed variables.

Now for the eigenvalues: If you haven't studied linear algebra, just ignore them. Basically, this is making sure you really did give the computer 10 *different* pieces of information, and not any duplicates. If two rows of the variance-covariance matrix are equal, the determinant will be 0, and you won't be able to invert the matrix, which will make it impossible to calculate standard errors. The condition number is the largest eigenvalue divided by the smallest eigenvalue. The closer it is to 1, the better. You don't need to include this in your homework.

We already talked about computing degrees of freedom.

Maximum Li	kelihood Estimates					
Regression	Weights:	Estimate	S.E.	C.R.	Label	
		-0.099		-0.681		
	V2SCBOB < V2HDRST	0.244	0.122	1.993	par-1	
		-0.202				
	V2BECK < V2SCB0B	0.276	0.157	1.751	par-2	
	- A D	Kstimate				
	ed Regression Weights:	ESTIMATE				
	V2HDRST < V2MMSE	-0.107				
	V2HDRST < V2MMSE V2SCBOB < V2HDRST	-0.107 0.289				
	V2HDRST < V2MMSE V2SCBOB < V2HDRST V2SCBOB < V2MMSE	-0.107 0.289 -0.259				
	V2HDRST < V2MMSE V2SCBOB < V2HDRST	-0.107 0.289				
Variances:	V2HDRST < V2MMSE V2SCBOB < V2HDRST V2SCBOB < V2MMSE	-0.107 0.289 -0.259 0.267		C.R.		
	V2HDRST < V2MMSE V2SCBOB < V2HDRST V2SCBOB < V2MMSE	-0.107 0.289 -0.259 0.267	S.E.	C.R.		
√ariances:	V2HDRST < V2HMSE V2SCBOB < V2HDRST V2SCBOB < V2HMSE V2BECK < V2SCBOB	-0.107 0.289 -0.259 0.267				
√ariances:	V2HDRST < V2HMSE V2SCBOB < V2HDRST V2SCBOB < V2HMSE V2BECK < V2SCBOB	-0.107 0.289 -0.259 0.267	9.321		par-5	
Variances:	V2HDRST < V2HMSE V2SCB08 < V2HDRST V2SCB08 < V2HDRST V2SEBCK < V2SCB0B	-0.107 0.289 -0.259 0.267	9.321 7.878	4.472 4.472	par-5	

Here's the real meat of the output. CR (Critical Ratio) is like a z-value. The arrows are the same as the arrows on your picture.

This is stuff you would want to include.

Total Effects

V2MMSE	VZHDRST	V2SCB0B
-0.099	0.000	0.000
-0.226	0.244	0.000
-0.062	0.067	0.276
	-0.099 -0.226	-0.099 0.000 -0.226 0.244

Standardized Total Effects

	VZMMSE	V2HDRST	V2SCBOB
V2HDRST	-0.107	0.000	0.000
V2SCB0B	-0.290	0.289	0.000
V2BECK	-0.077	0.077	0.267

Direct Effects

	V2MMSE	V2HDRST	V2SCB0B
V2HDRST	-0.099	0.000	0.000
V2SCB0B	-0.202	0.244	0.000
V2BECK	0.000	0.000	0.276
			0.00

Standardized Direct Effects

	V2MMSE	V2HDRST	V2SCB0B
V2HDRST	-0.107	0.000	0.000
V2SCB0B	-0.259	0.289	0.000
V2BECK	0.000	0.000	0.267

Indirect	Effects		
		V2HDRST	
V2HDRST	0.0000		
V2SCB0B	-0.0242	0.0000	0.0000
V2BECK	-0.0624	0.0673	0.0000
Standardi	ized Indir	ect Effect	s
	VZMMSE	V2HDRST	V2SCB0B
V2HDRST	0.0000	0.0000	0.0000
	-0.0310		
V2BECK	-0.0774	0.0772	0.0000

You'll get these if you select "indirect, direct, and total effects in analysis properties. In your homework though, you must calculate them by hand to show you understand the path rules.

Summary of models					
Model	NPAR	CMIN	DF	p	CMIN/DE
MMSE, HDRS thru SCB	8	2.990	2	0.224	1.495
Saturated model	10	0.000	0		
Independence model	4	13.706	6	0.033	2.284
Model		RMR	GFI	AGFI	PGF
MMSE, HDRS thru SCB	2	. 522	0.965	0.826	0.193
Saturated model		0.000	1.000		
Independence model		5.615	0.856	0.760	0.51

Here's some more meat. I named my model, but if you didn't you would want to look at "Default Model". The saturated model is when you estimate all possible parameters (i.e., draw arrows between everything) It will always have perfect fit, because you have tailored the model perfectly to the data. The independence model assumes all your variables are uncorrelated.

Now, the CMIN, look in appendix B of AMOS help if you want the formula.

Depending on your method of estimation it will take on a different value, it compares your model to the saturated model, if it is significant, than your model has significantly worse fit that the saturated (perfect) model.

Model	RMR	GFI	AGFI	PGFI
MMSE, HDRS thru SCB	2.522	0.965	0.826	0.193
Saturated model	0.000	1.000		
Independence model	5.615	0.856	0.760	0.513

You could also include these: RMR -root mean square residual. Compares estimated variances and covariances to observed variances and covariances. Smaller is better.

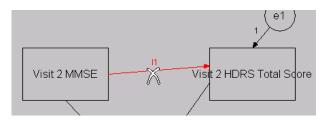
GFI ranges from 0-1, 1 is good.

Model	AIC	BCC	BIC	CAIC
MMSE, HDRS thru SCB	18.990	21.276	43.789	40.699
Saturated model	20.000	22.857	50.999	47.136
Independence model	21.706	22.849	34.105	32.560

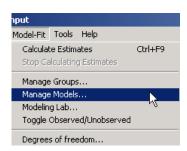
You could include these as well.

Everything else is trash.

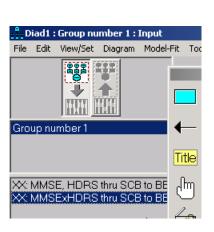
Dr.. David Garson is a full professor at NCSU and teaches a class using AMOS at NCSU http://www2.chass.ncsu.edu/garson/pa765/semAMOS1.htm He goes into detail about the other fit measures if you are interested. His website is awesome, it's where I go with all my questions, and other parts of the website will be included as weblinks for some of the lectures.

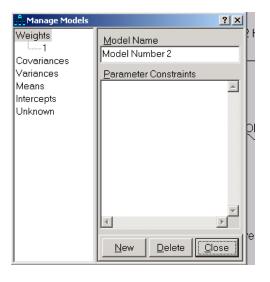


Now suppose I want to fit another model, you decide that you want to take out the link between MMSE and HDRS. I could just fit to separate models and compare the output, but I wanted to set it up so that it ran them both in one go, so that the estimates would be right next to each other, to make comparison easier.



If you already see Model Number 2 in the window, just rename the new model and click close, otherwise, click new, rename model number 2, then close.







Notice you now have two model in the window on the left. Go to the second one, and opposite click on the arrow between mmse and hdrs.

Select object properties, then parameters, then type a name in the regression weight space.

Note, in manage models you will get sent to the model you

were in on the outside. So, I set that covariance (arrow) to

I was a little concerned if this would work right or not, i.e., is

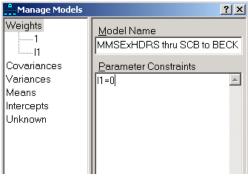
setting I1 to 0 the same thing as erasing the arrow. It seems

constrained model by pressing the DF key (1,13), it still says I have the same degrees of freedom as the unconstrained, however, when I run the two models, in the output I have the proper degrees of freedom for each model, and the same

equal 0 in the second model (thus erasing the arrow)

that it is. When you look at degrees of freedom for the

Now, go back to manage models



estimates as if I deleted the arrow.

Now, run the two models...

Summary of models

CMIN/DF	P	DF	CMIN	NPAR	Model
1.495 1.150 2.284	0.224 0.327 0.033	2 3 0 6	2.990 3.450 0.000 13.706	8 7 10 4	MMSE, HDRS thru SCB MMSExHDRS thru SCB t Saturated model Independence model
PGFI	AGFI	GFI	RMR		Model
0.193 0.289	0.826 0.878	0.965 0.963 1.000	2.852	2	MMSE, HDRS thru SCB MMSExHDRS thru SCB t Saturated model
0.513	0.760	0.856	5.615	.5	Independence model