Confirmatory Factor Analysis

Statsomat.com

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Warning: The automatic computation and interpretation delivered by the Statsomat should not completely replace the classical, made by humans graphical exploratory data analysis and statistical analysis. There may be data cases for which the Statsomat does not deliver the most optimal solution or output interpretation.

Basic Information

Automatic statistics for the file:

File case20.csv

Your selection for the encoding: Auto

Your selection for the decimal character: Auto

Observations (rows with at least one non-missing value): 250 Variables (columns with at least one non-missing value): 8

Variables considered continuous: 8

Variables considered continuous
A1
B1
C1
D1
A2
B2
C2
D2

Model Syntax

The following table describes the applied model equations in lavaan model syntax, either as entered by you in the text area (denoted by User=1) or established internally (User=0). The last column numbers the free parameters which are estimated.

Left hand side	Operator	Right hand side	User	Free parameter
SATIS1	=~	A1	1	0
SATIS1	=~	B1	1	1
SATIS1	=~	C1	1	2
SATIS1	=~	D1	1	3
SATIS2	=~	A2	1	0
SATIS2	=~	B2	1	4
SATIS2	=~	C2	1	5
SATIS2	=~	D2	1	6
A1	~~	A1	0	7
B1	~~	B1	0	8
C1	~~	C1	0	9
D1	~~	D1	0	10
A2	~~	A2	0	11
B2	~~	B2	0	12
C2	~~	C2	0	13
D2	~~	D2	0	14
SATIS1	~~	SATIS1	0	15
SATIS2	~~	SATIS2	0	16
SATIS1	~~	SATIS2	0	17

Assumptions

Open issue

Model Settings

Outputs

Model Fit Summary

lavaan 0.6-7 ended normally after 34 iterations

Estimator	ML
Optimization method	NLMINB
Number of free parameters	17
Number of observations	250

Model Test User Model:

Test statistic	349.385
Degrees of freedom	19
P-value (Chi-square)	0.000

Model Test Baseline Model:

Test statistic	1823.749
Degrees of freedom	28
P-value	0.000

User Model versus Baseline Model:

Comparative Fit Index (CFI)	0.816
Tucker-Lewis Index (TLI)	0.729

${\tt Loglikelihood\ and\ Information\ Criteria:}$

Loglikelihood user model (HO)	-3747.218
Loglikelihood unrestricted model (H1)	-3572.526
Akaike (AIC)	7528.437
Bayesian (BIC)	7588.301
Sample-size adjusted Bayesian (BIC)	7534.410

Root Mean Square Error of Approximation:

RMSEA	0.264
90 Percent confidence interval - lower	0.240
90 Percent confidence interval - upper	0.288
P-value RMSEA <= 0.05	0.000

Standardized Root Mean Square Residual:

SRMR	0.051

Parameter Estimates:

Standard errors	Standard
Information	Expected
Information saturated (h1) model	Structured

Latent Variables:

Estimate Std.Err z-value P(>|z|)

SATIS1 =~

A1 1.000

B1	0.938	0.055	17.032	0.000
C1	0.944	0.056	16.933	0.000
D1	0.965	0.052	18.683	0.000
SATIS2 =~				
A2	1.000			
B2	0.912	0.054	16.836	0.000
C2	0.903	0.052	17.358	0.000
D2	0.911	0.050	18.189	0.000
Covariances:				
	Estimate	Std.Err	z-value	P(> z)
SATIS1 ~~				
SATIS2	2.991	0.358	8.348	0.000
Variances:				
	Estimate	Std.Err	z-value	P(> z)
.A1	0.672	0.100	6.715	0.000
.B1	1.400	0.150	9.305	0.000
.C1	1.445	0.155	9.341	0.000
.D1	1.078	0.126	8.555	0.000
.A2	1.241	0.183	6.774	0.000
.B2	2.438	0.262	9.322	0.000
.C2	2.164	0.237	9.120	0.000
.D2	1.874	0.215	8.734	0.000
SATIS1				
211122	3.077	0.339	9.066	0.000

Completely Standardized Parameter Estimates

Latent	Variables	:
--------	-----------	---

	est.std	Std.Err	z-value	P(> z)	ci.lower	ci.upper
SATIS1 =~						
A1	0.906	0.016	55.446	0.000	0.874	0.938
B1	0.812	0.025	32.551	0.000	0.763	0.861
C1	0.809	0.025	32.134	0.000	0.760	0.859
D1	0.852	0.021	40.446	0.000	0.811	0.894
SATIS2 =~						
A2	0.904	0.017	54.487	0.000	0.871	0.936
B2	0.809	0.025	31.987	0.000	0.759	0.858
C2	0.822	0.024	34.269	0.000	0.775	0.869
D2	0.843	0.022	38.276	0.000	0.800	0.886
Covariances:						
	est.std	Std.Err	z-value	P(> z)	ci.lower	ci.upper
SATIS1 ~~						
SATIS2	0.724	0.036	20.016	0.000	0.653	0.795

Variances:

	est.std	Std.Err	z-value	P(> z)	<pre>ci.lower</pre>	ci.upper
.A1	0.179	0.030	6.051	0.000	0.121	0.237
.B1	0.341	0.040	8.424	0.000	0.262	0.420
.C1	0.345	0.041	8.470	0.000	0.265	0.425
.D1	0.273	0.036	7.605	0.000	0.203	0.344
.A2	0.183	0.030	6.101	0.000	0.124	0.242
.B2	0.346	0.041	8.460	0.000	0.266	0.426
.C2	0.324	0.039	8.208	0.000	0.247	0.401
.D2	0.289	0.037	7.790	0.000	0.217	0.362
SATIS1	1.000				1.000	1.000
SATIS2	1.000				1.000	1.000

Communality

Table 4: Communality

Variable	Communality
A1	0.82
A2	0.82
B1	0.66
B2	0.65
C1	0.65
C2	0.68
D1	0.73
D2	0.71

Factor Discriminant Validity

Table 5: Factor Discriminant Validity Test at Cutoff 0.85

			Factor Correlation	Chisq diff	Df diff	P-Value
SATIS1	~~	SATIS2	0.724	19.058	1	<0.001

Factor Reliability

Table 6: Factor Reliability

	SATIS1	SATIS2	total
Omega (Bentler)	0.91	0.91	0.94
Omega (McDonald)	0.91	0.91	0.94
AVE	0.71	0.71	0.71

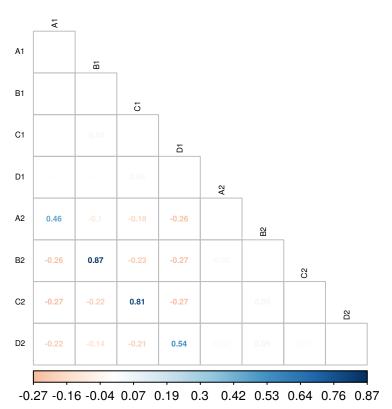
Observed Covariance Matrix

	A1							
A1	3.75	B1						
B1	2.89	4.1	-					
C1	2.9	2.69	4.19	10				
D1	2.96	2.79	2.84	3.94	A2			
A 2	3.45	2.7	2.64	2.63	6.78	B2		
B2	2.47	3.43	2.34	2.37	5.02	7.05	C2	
C2	2.43	2.31	3.36	2.34	5	4.61	6.68	D2
D2	2.5	2.42	2.36	3.17	5.03	4.65	4.57	6.48

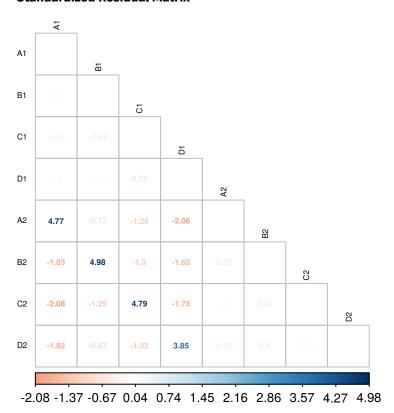
Model-Implied Covariance Matrix

	A1	1						
A1	3.75	B1						
B1	2.88	4.1	5					
C1	2.9	2.72	4.19	10				
D1	2.97	2.78	2.8	3.94	A2			
A2	2.99	2.8	2.82	2.89	6.78	B2		
B2	2.73	2.56	2.57	2.63	5.05	7.05	C2	
C2	2.7	2.53	2.55	2.61	5	4.56	6.68	D2
D2	2.73	2.56	2.57	2.63	5.05	4.61	4.56	6.48

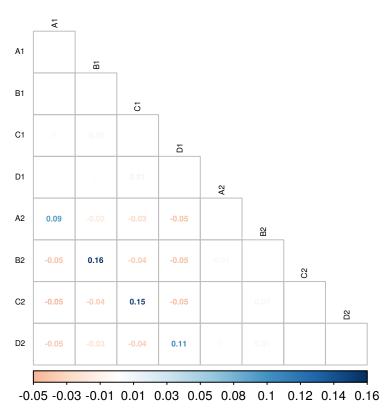
Residual Covariance Matrix



Standardized Residual Matrix



Residual Correlation Matrix



Modification Indices

Table 7: Modification Indices With Respect To Error Covariances

Left	Operator	Right	Modification Index	Expected Parameter Change	Delta	Power	Decision
A1	~~	A2	104.186	0.923	0.1	0.198	**(m)**
C1	~~	C2	84.389	1.218	0.1	0.117	**(m)**
B1	~~	B2	78.657	1.219	0.1	0.112	**(m)**
D1	~~	D2	74.105	0.969	0.1	0.144	**(m)**
D1	~~	A2	23.562	-0.498	0.1	0.164	**(m)**
A1	~~	D2	19.570	-0.438	0.1	0.173	**(m)**
A1	~~	C2	17.535	-0.437	0.1	0.160	**(m)**
A1	~~	B2	15.287	-0.429	0.1	0.149	**(m)**
C1	~~	A2	14.632	-0.437	0.1	0.141	**(m)**
B1	~~	A2	10.393	-0.363	0.1	0.144	**(m)**

Note:

Maximum 10 modification indices in descending order of their magnitude are listed.

Interpretation

Goodness of Fit Indices

We consider some of the model fit indices from the Model Fit Summary section to check the goodness-of-fit of the model. To decide for an acceptable or non-acceptable model, we apply thresholds considered in the References: [@brown], [@kline].

Model Test User Model

The degrees of freedom are calculated as the number of known parameters minus the number of free parameters: 36 - 17 = 19. The 19 degrees of freedom indicate an over-identified model, fact which basically enables further analysis and interpretation.

The test statistic with the value 349.385 is called the Chi-square model fit index and represents the difference between summaries of the model-implied covariance matrix and the observed covariance matrix which is hypothesized and desirable to be zero. In general, if the p-value is larger than 0.05 then the test is not statistically significant at 5 % error, the hypothesis cannot be rejected, which would be in favour of the model.

In our case, the p-value is <0.001 suggesting that the model may not be acceptable for the data. The Chi-square model fit index is based on a very stringent statistical hypothesis which may have no practical relevance. We will consider it only in connection with other model fit indices.

Model Test Baseline Model

The test statistic with the value 1823.749 represents the difference between summaries of the baseline model (an alternative model-implied covariance matrix having zero covariances, i.e. a worst fitting model assuming independent variables) and the observed covariance matrix. The p-value of the test of a zero difference is <0.001 suggesting that the baseline model does not fit good to the data. This result is used indirectly in the construction of other model fit indices.

Root Mean Square Error of Approximation:

The Root Mean Square Error of Approximation (RMSEA) is a fit index based on the chi-square test statistic, which corrects for parsimony, i.e. overly complex models are penalized. RMSEA can be greater or equal than zero, with values close to zero suggesting an acceptable model fit.

In our case, the RMSEA is 0.264. The upper bound of the 90% confidence interval of the RMSEA is 0.288 and greater or equal than the threshold value 0.1, suggesting a poor model fit.

Standardized Root Mean Square Residual:

The Standardized Root Mean Square Residual (SRMR) is a fit index derived from the residual correlation matrix with a range between zero and one with values close to zero suggesting an acceptable model fit.

In our case, the SRMR is 0.05 which is smaller than the threshold value 0.1 suggesting an acceptable model fit.

User Model versus Baseline Model

The Comparative Fit Index (CFI), evaluates the fit of the the model in relation to the worst-fitting baseline model described above. It ranges between zero and one, with values close to one suggesting good models (in the sense of departure from the baseline model).

In our case, the CFI is 0.816 which is smaller or equal than the threshold value 0.90, suggesting a poor model fit.

Similarly to the CFI, the Tucker-Lewis Index (TLI) evaluates the fit of the model in relation to the worst-fitting baseline model described above. Moreover, overly complex models are penalized. Values can range outside zero and one but the index is interpreted similarly to the CFI.

In our case, the TLI is 0.729 which is smaller or equal than the threshold value 0.90, suggesting a poor model fit.

Summary of the Goodness of Fit Indices

At least the comparative fit indices CFI and TLI suggest a poor model fit. Therefore, we assume a poor model fit and proceed by diagnosing the sources of possible misspecification.

Residuals

We analyze the residual matrices from the Outputs chapter. The residual covariance matrix represents the difference between the observed covariance matrix and the fitted model-implied covariance matrix. Large absolute values indicate local areas of misfit. However, the residuals are affected by the raw metric and are difficult to interpret more precisely.

A better interpretation allows the standardized residual matrix (residuals divided by their estimated asymptotic standard error) and the residual correlation matrix.

Following variable pairs have standardized residuals which are larger or equal than the considered threshold 2.58 [@brown] or correlation residuals which are larger or equal than the considered threshold 0.1 [@kline]. In these cases, the covariance relationship between the involved variables is probably underestimated:

Table 8: Pair(s) with Underestimated Covariance

Pair 1	A1	A2
Pair 2	B1	B2
Pair 3	C1	C2
Pair 4	D1	D2

There are no variable pairs with standardized residuals which are smaller or equal than the considered threshold -2.58 [@brown] or correlation residuals which are smaller or equal than the considered threshold -0.1 [@kline]. Therefore, no relationships among the variables are substantially overestimated by the model. Depending on the sample size, the misspecification detected by the analysis of the residual covariance resp. correlation matrices can be statistically significant but not relevant and in practice negligible. This is matter of subject in the next section(s).

Modification Indices

In the interpretation of the modification indices table(s) we rely mostly on [@brown] and [@mi]. We cite from [@brown]: "The modification index reflects an approximation of how much the overall model Chi² will decrease if the fixed or constrained parameter is freely estimated." In other words, if adding a line with a high modification index to the model, i.e. if adding a parameter, the overall goodness-of-fit may be improved. Nevertheless, this should be done only under certain conditions, described in the sequel.

We consider only modification indices greater or equal than 3.84 (which are statistically significant at 5% type I error). Next, we search only for modification indices which achieve a power of minimum 75% in detecting a (relevant) misspecification of at least 0.1 for error or factor correlations, respectively 0.4 for factor loadings. These are characterized in the decision column by the label "epc:m". For more information with regard to the labels of the decision column, please consult the Appendix.

We remark that these conditions are not fulfilled for modification indices with respect to error covariances. Therefore, there exist no significant and relevant modification indices with respect to error covariances.

We remark that there exist no modification indices with respect to factor loadings.

We remark that there exist no modification indices with respect to factor covariances.

Parameter Estimates

Factor Loadings

We remark that the completely standardized factor loadings (section "Completely Standardized Parameter Estimates") are all statistically significant at 5% type I error. Moreover, in absolute value they are all greater than 0.4. This cutoff-value is considered in some CFA research areas a magnitude that is substantively meaningful [@brown]. Please consider also cutoff-values from your particular research area when interpreting the factor loadings. We summarize the interpretation of the completely standardized factor loadings in the next table:

Table 9: Check Completely Standardized Factor Loadings

Latent Variable	Observed Variable	Loading ¹	P-Value	Significant? ²	Relevance ³	Sign ⁴	Check
SATIS1	A1	0.91	<0.001	Yes	***	_	Ok
SATIS1	B1	0.81	<0.001	Yes	***	_	Ok
SATIS1	C1	0.81	<0.001	Yes	***	—	Ok
SATIS1	D1	0.85	<0.001	Yes	***	—	Ok
SATIS2	A2	0.90	<0.001	Yes	***	_	Ok
SATIS2	B2	0.81	<0.001	Yes	***	_	Ok
SATIS2	C2	0.82	<0.001	Yes	***	—	Ok
SATIS2	D2	0.84	<0.001	Yes	***	_	Ok

¹ The completely standardized factor loading can be interpreted as the correlation with the factor.

Moreover, we remark that the significance test results for the completely standardized factor loadings from above coincide to those of the unstandardized factor loadings (within section "Model Fit Summary", for non-marker variables).

We proceed by interpreting the (unstandardized) factor loadings from the "Model Fit Summary" section:

Table 10: Interpretation of Unstandardized Factor Loadings

Interpretation of Unstandardized Factor Loadings						
A 1-unit increase in SATIS1 leads to a 1.00 -unit increase in the A1						
A 1-unit increase in SATIS1 leads to a 0.94 -unit increase in the B1						
A 1-unit increase in SATIS1 leads to a 0.94 -unit increase in the C1						
A 1-unit increase in SATIS1 leads to a 0.97 -unit increase in the D1						
A 1-unit increase in SATIS2 leads to a 1.00 -unit increase in the A2						
A 1-unit increase in SATIS2 leads to a 0.91 -unit increase in the B2						
A 1-unit increase in SATIS2 leads to a 0.90 -unit increase in the C2						
A 1-unit increase in SATIS2 leads to a 0.91 -unit increase in the D2						

² Completely standardized factor loading significance at 5% type I error.

³ Stars correspond to factor loadings cutoff-values: 0.4, 0.6, 0.8.

⁴ No (correct) information available. We assume the signs of the factor loadings correspond to your expectation.

⁵ ____

⁶ _____

⁷ ____

Factor Discriminant Validity

As noted by [@brown], "the interpretability of the size and statistical significance of factor intercorrelations depends on the specific research context." Though, the largest (absolute) estimated factor intercorrelation within the section "Completely Standardized Parameter Estimates" is 0.72 which we regard as a proof of a reasonable discriminant validity. Moreover, the statistical test(s) for factor discriminant validity are statistically significant at 5% type I error.

Error Variances

We summarize the interpretation of the error variances and communalities in the next table:

Table 11: Completely Standardized Error Variances and Communality

Observed Variable	Error Variance ¹	Communality ²³	P-Value	Significant Error Variance? ⁴
A1	0.18	0.82	<0.001	Yes
A2	0.18	0.82	<0.001	Yes
B1	0.34	0.66	<0.001	Yes
B2	0.35	0.65	<0.001	Yes
C1	0.35	0.65	<0.001	Yes
C2	0.32	0.68	<0.001	Yes
D1	0.27	0.73	<0.001	Yes
D2	0.29	0.71	<0.001	Yes

¹ Can be interpreted as proportion of unexplained variance by the latent factor(s) (%).

Factor Reliability

The table "Factor Reliability" contains the omega measures of factor reliability given by Bentler (Bentler, 1972, 2009) and McDonald (McDonald, 1999) and the average variance extracted (AVE). The interpretatibility of the reliability measures depend on the specific research context. In some fields of research, omega values greater or equal than 0.6 and AVE values greater or equal than 0.5 (fulfilled by and large in your case) could be sufficient.

Final Summary

In our final evaluation, we distinguish between following model quality categories: acceptable, non-acceptable or uncertain.

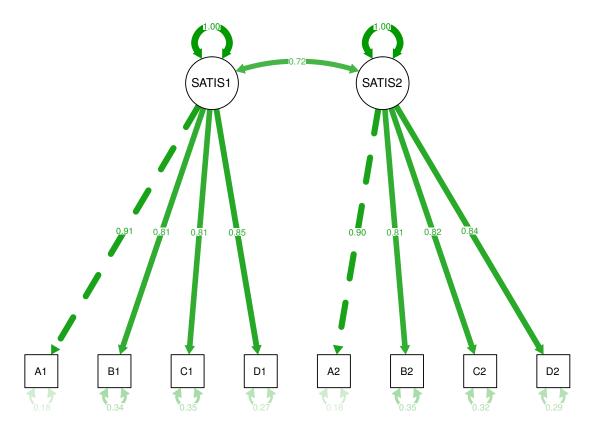
Considering the goodness-of-fit indices, the model is non-acceptable. Please reconsider your data and the theory behind.

² Corresponds to the squared factor loading.

³ Can be interpreted as proportion of explained variance by the latent factor(s) (%).

⁴ 5% type I error. Typically significant since a large portion of variance is not explained by the latent variable.

Path Diagram



APPENDIX

Decision Column of the Modification Indices Table

```
not mi.significant & not high.power := "(i)"
mi.significant & not high.power := "**(m)**"
not mi.significant & high.power := "(nm)"
mi.significant & high.power & not epc.high := "epc:nm"
mi.significant & high.power & epc.high := "*epc:m*"
```

References