

# 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
case16.csv

Your selection for the encoding: Auto

Your selection for the decimal character: Auto

Observations (rows with at least one non-missing value): 300

Variables (columns with at least one non-missing value): 6

Variables considered continuous: 0

Numerical variables considered binary or ordinal: 6

Numerical variables considered binary or ordinal
BIO
GEO
CHEM
ALG
CALC
STAT

## 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
AFFINITY	=~	BIO	1	0
AFFINITY	=~	GEO	1	1
AFFINITY	=~	CHEM	1	2
AFFINITY	=~	ALG	1	3
AFFINITY	=~	CALC	1	4
AFFINITY	=~	STAT	1	5
BIO	~~	BIO	0	6
GEO	~~	GEO	0	7
CHEM	~~	CHEM	0	8
ALG	~~	ALG	0	9
CALC	~~	CALC	0	10
STAT	~~	STAT	0	11
AFFINITY	~~	AFFINITY	0	12

## Assumptions

Open issue

## Model Settings

## Outputs

### Model Fit Summary

lavaan 0.6-7 ended normally after 21 iterations

Estimator	ML
Optimization method	NLMINB
Number of free parameters	12
Number of observations	300

Model Test User Model:

Test statistic	350.589
Degrees of freedom	9
P-value (Chi-square)	0.000

Model Test Baseline Model:

Test statistic	860.205
Degrees of freedom	15
P-value	0.000

User Model versus Baseline Model:

Comparative Fit Index (CFI)	0.596
Tucker-Lewis Index (TLI)	0.326

Loglikelihood and Information Criteria:

Loglikelihood user model (H0)	-2645.288
Loglikelihood unrestricted model (H1)	-2469.994
Akaike (AIC)	5314.577
Bayesian (BIC)	5359.022
Sample-size adjusted Bayesian (BIC)	5320.965

Root Mean Square Error of Approximation:

RMSEA	0.356
90 Percent confidence interval - lower	0.324
90 Percent confidence interval - upper	0.388
P-value RMSEA <= 0.05	0.000

Standardized Root Mean Square Residual:

SRMR	0.204
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Parameter Estimates:

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

Latent Variables:

	Estimate	Std.Err	z-value	P(> z )
AFFINITY =~				
BIO	1.000			
GEO	0.918	0.059	15.571	0.000
CHEM	1.015	0.061	16.587	0.000
ALG	0.187	0.067	2.787	0.005
CALC	0.267	0.064	4.179	0.000
STAT	0.305	0.071	4.284	0.000

Variances:

	Estimate	Std.Err	z-value	P(> z )
.BIO	0.371	0.055	6.725	0.000
.GEO	0.555	0.060	9.226	0.000
.CHEM	0.448	0.060	7.457	0.000
.ALG	1.335	0.109	12.199	0.000
.CALC	1.185	0.098	12.137	0.000
.STAT	1.474	0.121	12.131	0.000
AFFINITY	1.131	0.127	8.872	0.000

### Completely Standardized Parameter Estimates

Latent Variables:

	est.std	Std.Err	z-value	P(> z )	ci.lower	ci.upper
AFFINITY =~						
BIO	0.868	0.023	38.182	0.000	0.823	0.912
GEO	0.795	0.027	29.540	0.000	0.742	0.848
CHEM	0.850	0.024	35.933	0.000	0.803	0.896
ALG	0.170	0.060	2.841	0.004	0.053	0.287
CALC	0.252	0.058	4.364	0.000	0.139	0.366
STAT	0.258	0.058	4.484	0.000	0.145	0.371

Variances:

	est.std	Std.Err	z-value	P(> z )	ci.lower	ci.upper
.BIO	0.247	0.039	6.264	0.000	0.170	0.324
.GEO	0.368	0.043	8.605	0.000	0.284	0.452
.CHEM	0.278	0.040	6.910	0.000	0.199	0.357
.ALG	0.971	0.020	47.788	0.000	0.931	1.011
.CALC	0.936	0.029	32.084	0.000	0.879	0.994
.STAT	0.933	0.030	31.317	0.000	0.875	0.992
AFFINITY	1.000				1.000	1.000

### Communality

Table 4: Communality

Variable	Communality
ALG	0.03
BIO	0.75
CALC	0.06
CHEM	0.72
GEO	0.63
STAT	0.07

### Factor Reliability

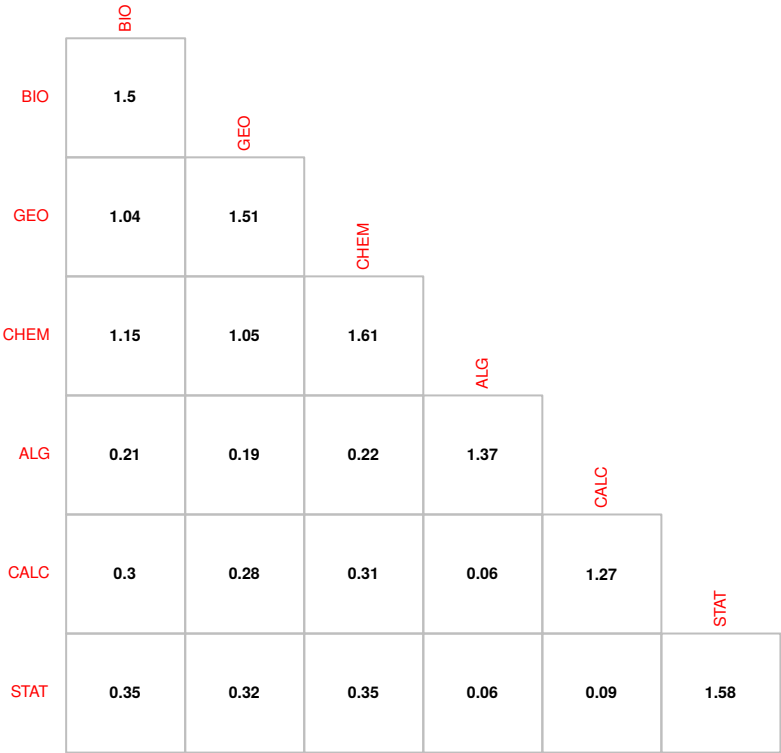
Table 5: Factor Reliability

	AFFINITY
Omega (Bentler)	0.74
Omega (McDonald)	0.63
AVE	0.39

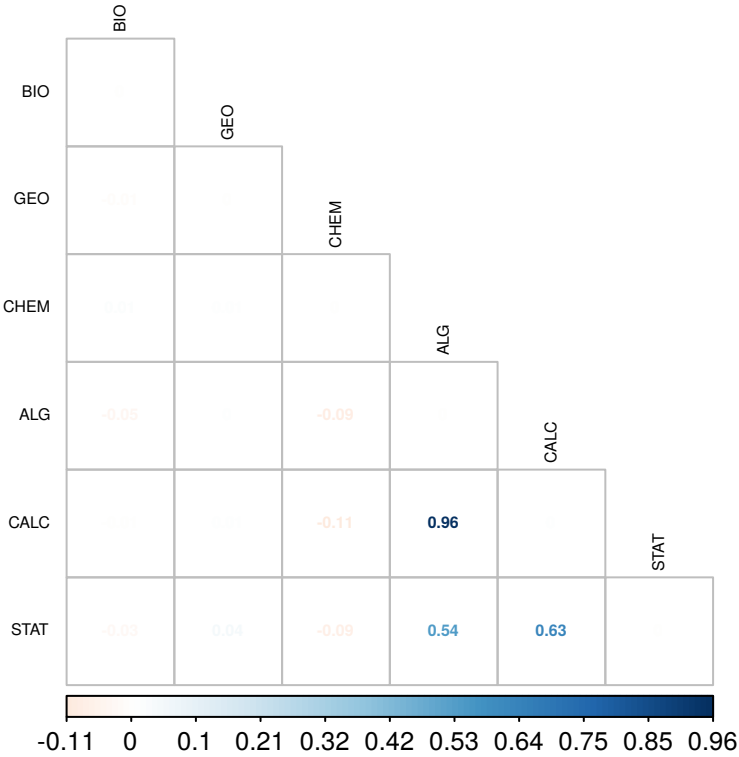
### Observed Covariance Matrix

BIO	1.5					
	GEO	1.03	1.51			
		CHEM	1.16	1.06	1.61	
			ALG	0.17	0.19	0.12
				CALC	1.37	
					STAT	0.29
						1.27
						0.31
						0.36
						0.26
						0.6
						0.72
						1.58

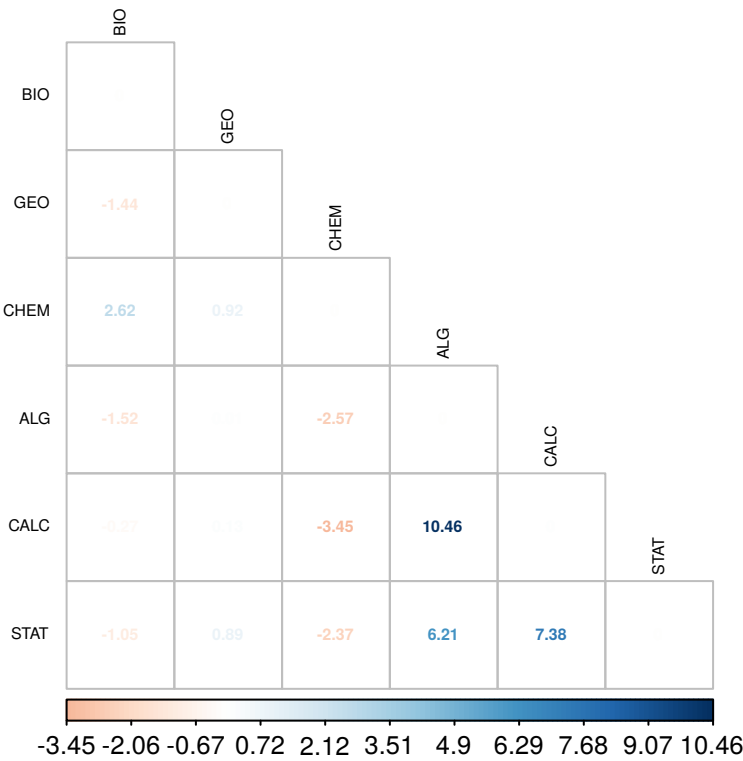
Model-Implied Covariance Matrix



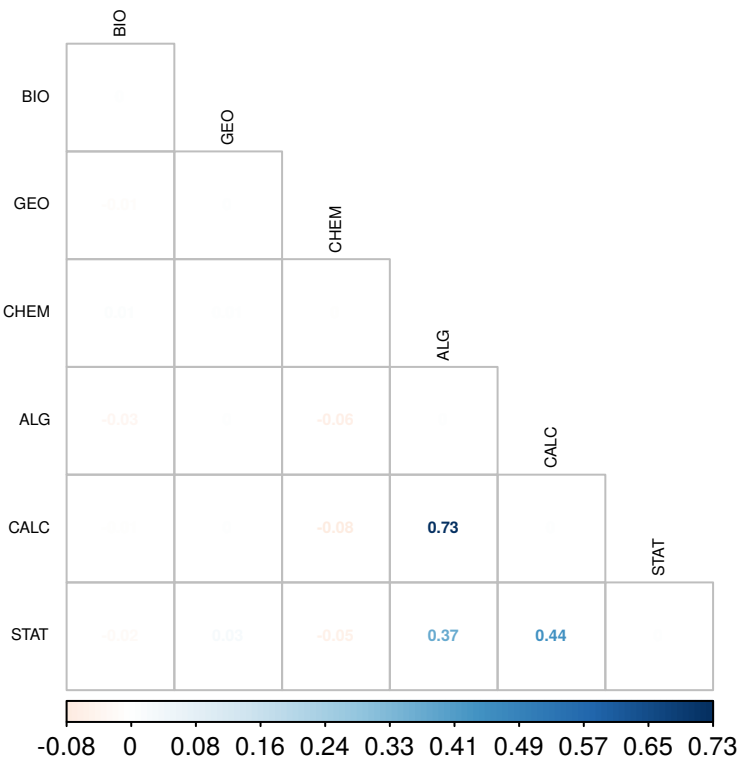
Residual Covariance Matrix



Standardized Residual Matrix



Residual Correlation Matrix



## Modification Indices

Table 6: Modification Indices With Respect To Error Covariances

Left	Operator	Right	Modification Index	Expected Parameter Change	Delta	Power	Decision
ALG	~~	CALC	177.201	0.973	0.1	0.277	** (m) **
CALC	~~	STAT	68.389	0.637	0.1	0.255	** (m) **
ALG	~~	STAT	44.835	0.546	0.1	0.232	** (m) **
BIO	~~	CHEM	14.868	0.552	0.1	0.108	** (m) **
CHEM	~~	CALC	11.128	-0.177	0.1	0.471	** (m) **
CHEM	~~	ALG	6.330	-0.140	0.1	0.436	** (m) **
CHEM	~~	STAT	5.294	-0.136	0.1	0.394	** (m) **
BIO	~~	GEO	3.731	-0.226	0.1	0.137	(i)
BIO	~~	ALG	2.204	-0.079	0.1	0.469	(i)
GEO	~~	CHEM	1.665	0.149	0.1	0.139	(i)

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:  $21 - 12 = 9$ . The 9 degrees of freedom indicate an over-identified model, fact which basically enables further analysis and interpretation.

The test statistic with the value 350.589 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 0.01 then the test is not statistically significant at 1 % 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 860.205 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 0.356. The upper bound of the 90% confidence interval of the RMSEA is 0.388 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 value is 0.2 which is greater or equal than the threshold value 0.08 suggesting a poor 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 0.596 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 0.326 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 7: Pair(s) with Underestimated Covariance

Pair 1	ALG	CALC
Pair 2	ALG	STAT
Pair 3	CALC	STAT
Pair 4	STAT	CALC

Following variable pairs have 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]. In these cases, the covariance relationship between the involved variables is probably overestimated:

Table 8: Pair(s) with Overestimated Covariance

Pair 1	CHEM	CALC
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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  $\chi^2$  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 (i.e. p-value  $\leq 0.05$ ). Nevertheless, (some) completely standardized factor loadings are in absolute value smaller 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 <sup>1</sup>	P-Value	Significant? <sup>2</sup>	Relevance <sup>3</sup>	Sign <sup>4</sup>	Check
AFFINITY	BIO	0.87	<0.001	Yes	***	—	Ok
AFFINITY	GEO	0.79	<0.001	Yes	**	—	Ok
AFFINITY	CHEM	0.85	<0.001	Yes	***	—	Ok
AFFINITY	ALG	0.17	0.004	Yes	!	—	Uncertain <sup>7</sup>
AFFINITY	CALC	0.25	<0.001	Yes	!	—	Uncertain <sup>7</sup>
AFFINITY	STAT	0.26	<0.001	Yes	!	—	Uncertain <sup>7</sup>

Table 9: Check Completely Standardized Factor Loadings (continued)

Latent Variable	Observed Variable	Loading <sup>1</sup>	P-Value	Significant? <sup>2</sup>	Relevance <sup>3</sup>	Sign <sup>4</sup>	Check
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<sup>1</sup> The completely standardized factor loading can be interpreted as the correlation with the factor.

<sup>2</sup> Completely standardized factor loading significance at 5% type I error.

<sup>3</sup> Stars correspond to factor loadings cutoff-values: 0.4, 0.6, 0.8.

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

<sup>5</sup> \_\_\_\_\_

<sup>6</sup> \_\_\_\_\_

<sup>7</sup> Uncertain. Significant but small(er) effect size. Further analysis is recommended.

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).

### Error Variances

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

Table 10: Completely Standardized Error Variances and Communality

Observed Variable	Error Variance <sup>1</sup>	Communality <sup>23</sup>	P-Value	Significant Error Variance? <sup>4</sup>
ALG	0.97	0.03	<0.001	Yes
BIO	0.25	0.75	<0.001	Yes
CALC	0.94	0.06	<0.001	Yes
CHEM	0.28	0.72	<0.001	Yes
GEO	0.37	0.63	<0.001	Yes
STAT	0.93	0.07	<0.001	Yes

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

<sup>2</sup> Corresponds to the squared factor loading.

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

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

### 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 interpretability of the reliability measures depend on the specific research context. Nevertheless, omega values below 0.6 or AVE values below 0.5 (at least one of these existent in your case) should be regarded with criticism. The factor reliability estimates are not further considered in the final summary.

### 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. Moreover, there exist localized areas of ill fit.

Please reconsider your data and the theory behind. Only if supported by theory, you could try to respecify the model and improve the goodness-of-fit by applying (one of the) following recommendations or call for actions.

There exist factor loadings which are uncertain. To decide upon the statistical significance and relevance, further statistical tests and/or power and sample size analysis, not covered by this app are recommended. Only if supported by theory and further statistical analysis, you could drop the uncertain parameter(s) from the model.

## Addings to the Model

### Factors

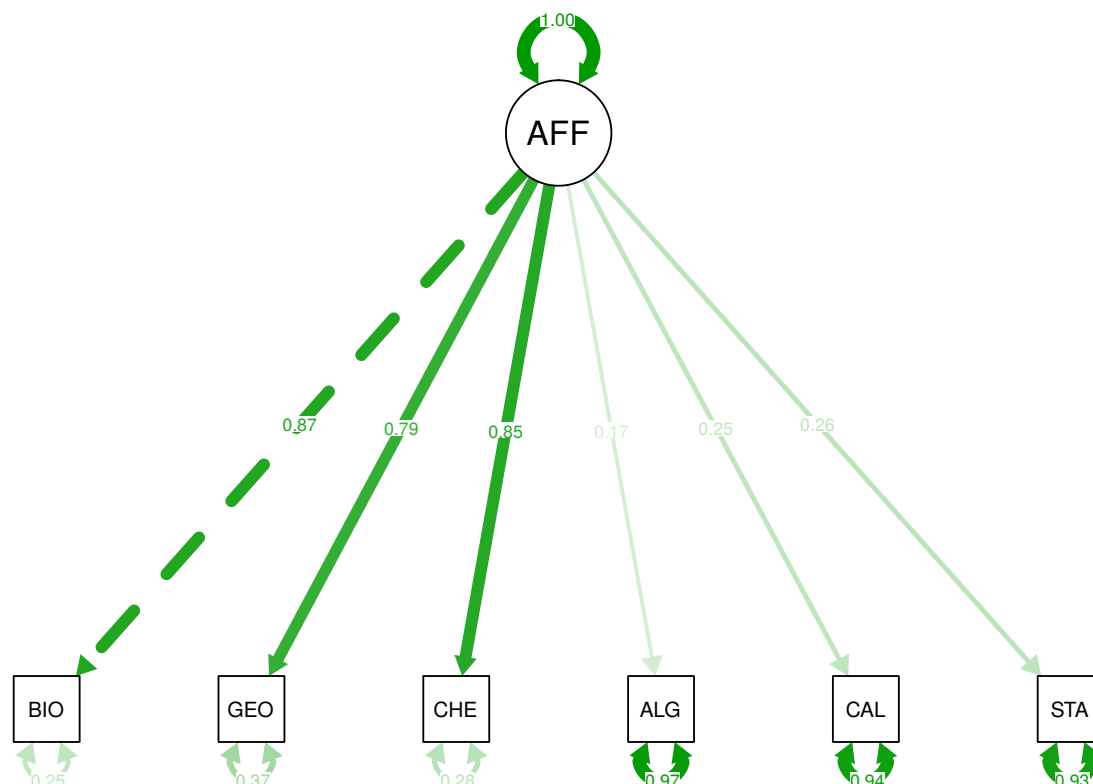
Following factors contain at least three completely standardized factor loadings smaller or equal than the chosen cutoff-value of 0.4. In some cases, this is an indicator of a model with too few factors. Only if supported by theory, you could try to split and increase the number of factors in the model:

Table 11: Factors to Split

AFFINITY

Final comments: Please consider that this summary depends on hard-coded cutoff-values which may be too liberal or too conservative for your research area. If you have sound theory-based reasons and decide to respecify the model, we strongly recommend the replication of the CFA in an independent sample.

## 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