Confirmatory Factor Analysis

Statsomat.com

07 January 2021

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
case2.csv

Your selection for the encoding: Auto
Your selection for the decimal character: Auto
Observations (rows with at least one non-missing value): 500
Variables (columns with at least one non-missing value): 8
Variables considered continuous: 6

Variables considered continuous
ACTIV
SOMA
SOCF
VITAL
GENHLTH
AGE

Numerical variables considered binary or ordinal: 2

Numerical variables considered binary or ordinal
PAIN
MENTH

Warning: Based on an analysis of the variables considered continuous, we suspect outliers in the data. If observations are erroneous, you could drop them and restart the app. Outliers may affect negatively the execution or the results of the CFA. These are the suspected row numbers:

Table 4: Rows With Suspected Outliers

	ACTIV	SOMA	SOCF	VITAL	GENHLTH	AGE
477	14	44	30	49	29	19

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
PHYSF	=~	ACTIV	1	0
PHYSF	=~	SOMA	1	1
PHYSF	=~	PAIN	1	2
MENTF	=~	MENTH	1	0
MENTF	=~	SOCF	1	3
MENTF	=~	VITAL	1	4
GWB	=~	GENHLTH	1	0
AGEF	=~	AGE	1	0
GENHLTH	~~	GENHLTH	1	0
AGE	~~	AGE	1	0
ACTIV	~~	SOMA	1	5
ACTIV	~~	ACTIV	0	6
SOMA	~~	SOMA	0	7
PAIN	~~	PAIN	0	8
MENTH	~~	MENTH	0	9
SOCF	~~	SOCF	0	10
VITAL	~~	VITAL	0	11
PHYSF	~~	PHYSF	0	12
MENTF	~~	MENTF	0	13
GWB	~~	GWB	0	14
AGEF	~~	AGEF	0	15
PHYSF	~~	MENTF	0	16
PHYSF	~~	GWB	0	17
PHYSF	~~	AGEF	0	18
MENTF	~~	GWB	0	19
MENTF	~~	AGEF	0	20
GWB	~~	AGEF	0	21

Assumptions

Open issue

Model Settings

Outputs

Model Fit Summary

```
lavaan 0.6-7 ended normally after 235 iterations

  Estimator                                         ML
  Optimization method                           NLMINB
  Number of free parameters                         21

  Number of observations                           500

Model Test User Model:

  Test statistic                                45.009
  Degrees of freedom                                15
  P-value (Chi-square)                           0.000

Model Test Baseline Model:

  Test statistic                              1942.397
  Degrees of freedom                                28
  P-value                                        0.000

User Model versus Baseline Model:

  Comparative Fit Index (CFI)                    0.984
  Tucker-Lewis Index (TLI)                       0.971

Loglikelihood and Information Criteria:

  Loglikelihood user model (H0)             -13787.363
  Loglikelihood unrestricted model (H1)     -13764.859

  Akaike (AIC)                               27616.726
  Bayesian (BIC)                             27705.233
  Sample-size adjusted Bayesian (BIC)        27638.578

Root Mean Square Error of Approximation:

  RMSEA                                          0.063
  90 Percent confidence interval - lower         0.043
  90 Percent confidence interval - upper         0.085
  P-value RMSEA <= 0.05                          0.137
```

```
Standardized Root Mean Square Residual:

  SRMR                                           0.028

Parameter Estimates:

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

Latent Variables:
                   Estimate  Std.Err  z-value  P(>|z|)
  PHYSF =~
    ACTIV             1.000
    SOMA              0.868    0.049   17.631    0.000
    PAIN              0.150    0.018    8.566    0.000
  MENTF =~
    MENTH             1.000
    SOCF              1.850    0.072   25.787    0.000
    VITAL             2.357    0.109   21.599    0.000
  GWB =~
    GENHLTH           1.000
  AGEF =~
    AGE               1.000

Covariances:
                   Estimate  Std.Err  z-value  P(>|z|)
 .ACTIV ~~
   .SOMA             87.987   17.716    4.967    0.000
  PHYSF ~~
    MENTF            28.370    4.215    6.731    0.000
    GWB              69.057    7.881    8.763    0.000
    AGEF            -30.305    9.033   -3.355    0.001
  MENTF ~~
    GWB              25.179    2.283   11.027    0.000
    AGEF             -5.290    2.622   -2.018    0.044
  GWB ~~
    AGEF             -9.664    4.502   -2.147    0.032

Variances:
                   Estimate  Std.Err  z-value  P(>|z|)
   .GENHLTH           7.861
   .AGE               0.000
   .ACTIV           215.497   24.525    8.787    0.000
   .SOMA            113.524   15.653    7.253    0.000
   .PAIN              6.567    0.581   11.310    0.000
   .MENTH             8.548    0.751   11.384    0.000
   .SOCF             11.779    1.874    6.286    0.000
```

```
   .VITAL            68.148    5.263   12.948    0.000
    PHYSF           182.151   29.368    6.202    0.000
    MENTF            22.140    1.936   11.439    0.000
    GWB              63.601    4.520   14.072    0.000
    AGEF            140.490    8.885   15.811    0.000
```

Completely Standardized Parameter Estimates

```
Latent Variables:
                    est.std  Std.Err  z-value  P(>|z|) ci.lower ci.upper
  PHYSF =~
    ACTIV             0.677    0.045   15.051    0.000    0.589    0.765
    SOMA              0.740    0.043   17.362    0.000    0.656    0.823
    PAIN              0.620    0.041   15.066    0.000    0.540    0.701
  MENTF =~
    MENTH             0.849    0.016   53.180    0.000    0.818    0.881
    SOCF              0.930    0.012   76.573    0.000    0.906    0.954
    VITAL             0.802    0.019   42.790    0.000    0.765    0.839
  GWB =~
    GENHLTH              NA       NA                          NA       NA
  AGEF =~
    AGE               1.000                                1.000    1.000

Covariances:
                    est.std  Std.Err  z-value  P(>|z|) ci.lower ci.upper
 .ACTIV ~~
   .SOMA              0.563    0.054   10.499    0.000    0.458    0.668
  PHYSF ~~
    MENTF             0.447    0.050    8.918    0.000    0.349    0.545
    GWB               0.231    0.020   11.506    0.000    0.191    0.270
    AGEF             -0.189    0.054   -3.536    0.000   -0.294   -0.084
  MENTF ~~
    GWB               0.241    0.017   14.466    0.000    0.209    0.274
    AGEF             -0.095    0.046   -2.047    0.041   -0.186   -0.004
  GWB ~~
    AGEF             -0.037    0.017   -2.159    0.031   -0.070   -0.003

Variances:
                    est.std  Std.Err  z-value  P(>|z|) ci.lower ci.upper
   .GENHLTH           7.877    0.498   15.811    0.000    6.900    8.853
   .AGE               0.000                                0.000    0.000
   .ACTIV             0.542    0.061    8.903    0.000    0.423    0.661
   .SOMA              0.453    0.063    7.181    0.000    0.329    0.576
   .PAIN              0.615    0.051   12.042    0.000    0.515    0.715
   .MENTH             0.279    0.027   10.266    0.000    0.225    0.332
   .SOCF              0.135    0.023    5.952    0.000    0.090    0.179
   .VITAL             0.357    0.030   11.858    0.000    0.298    0.416
```

```
PHYSF                 1.000                                 1.000    1.000
MENTF                 1.000                                 1.000    1.000
GWB                      NA        NA                          NA       NA
AGEF                  1.000                                 1.000    1.000
```

Communality

Table 6: Communality

Variable	Communality
ACTIV	0.46
AGE	1.00
GENHLTH	0.89
MENTH	0.72
PAIN	0.38
SOCF	0.87
SOMA	0.55
VITAL	0.64

Factor Discriminant Validity

Table 7: Factor Discriminant Validity Test at Cutoff 0.85

			Factor Correlation	Chisq diff	Df diff	P-Value
PHYSF	~~	MENTF	0.447	70.750	1	<0.001
PHYSF	~~	GWB	0.642	26.904	1	<0.001
PHYSF	~~	AGEF	-0.189	115.670	1	<0.001
MENTF	~~	GWB	0.671	64.020	1	<0.001
MENTF	~~	AGEF	-0.095	526.184	1	<0.001
GWB	~~	AGEF	-0.102	514.423	1	<0.001

Factor Reliability

Table 8: Factor Reliability

	PHYSF	MENTF	GWB	AGEF	total
Omega (Bentler)	0.59	0.87	0.89	1	0.80
Omega (McDonald)	0.59	0.87	0.89	1	0.81
AVE	0.49	0.71	0.89	1	0.63

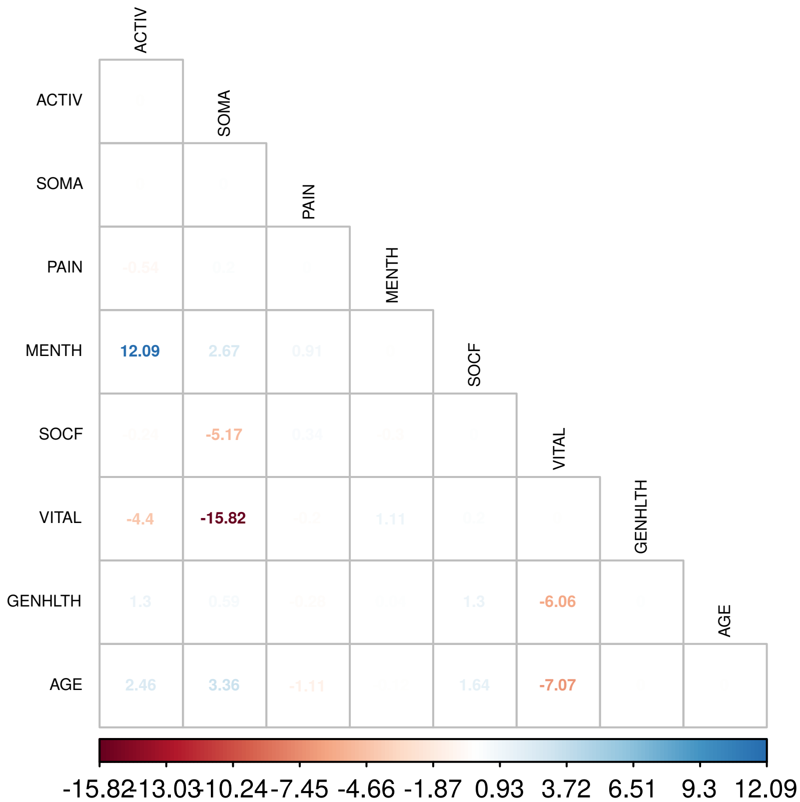
Observed Covariance Matrix

	ACTIV	SOMA	PAIN	MENTH	SOCF	VITAL	GENHLTH	AGE
ACTIV	397.65							
SOMA	246.09	250.76						
PAIN	26.82	23.95	10.68					
MENTH	40.46	27.3	5.17	30.69				
SOCF	52.25	40.38	8.22	40.66	87.55			
VITAL	62.45	42.21	9.84	53.29	96.73	191.11		
GENHLTH	70.36	60.53	10.09	25.22	47.88	53.28	71.46	
AGE	-27.85	-22.94	-5.66	-5.41	-8.14	-19.54	-9.66	140.49

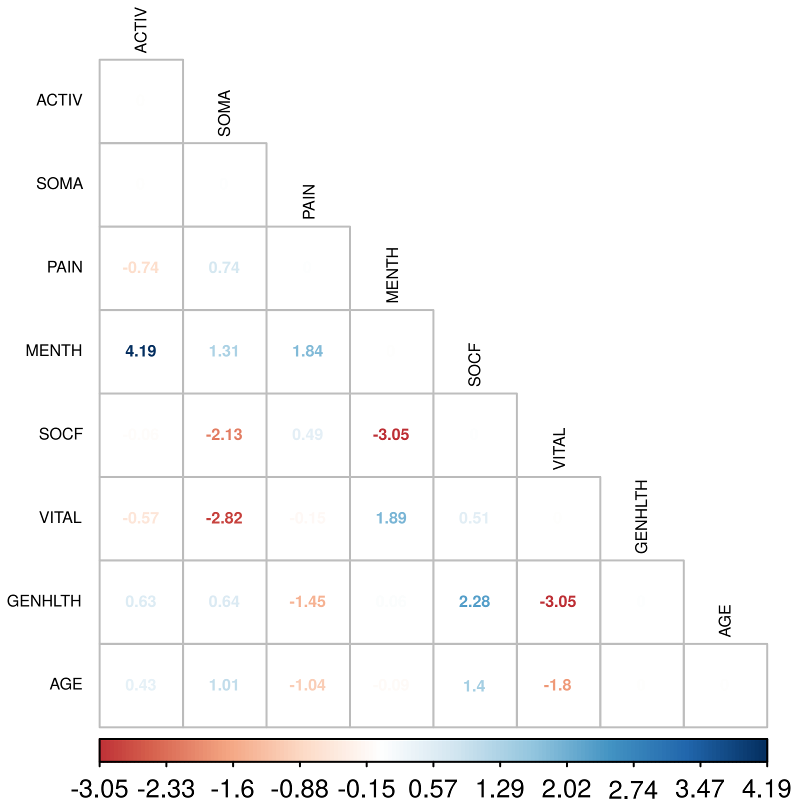
Model-Implied Covariance Matrix

	ACTIV	SOMA	PAIN	MENTH	SOCF	VITAL	GENHLTH	AGE
ACTIV	397.65							
SOMA	246.09	250.76						
PAIN	27.35	23.74	10.68					
MENTH	28.37	24.62	4.26	30.69				
SOCF	52.48	45.55	7.88	40.96	87.55			
VITAL	66.86	58.03	10.04	52.18	96.52	191.11		
GENHLTH	69.06	59.94	10.37	25.18	46.58	59.34	71.46	
AGE	-30.3	-26.3	-4.55	-5.29	-9.79	-12.47	-9.66	140.49

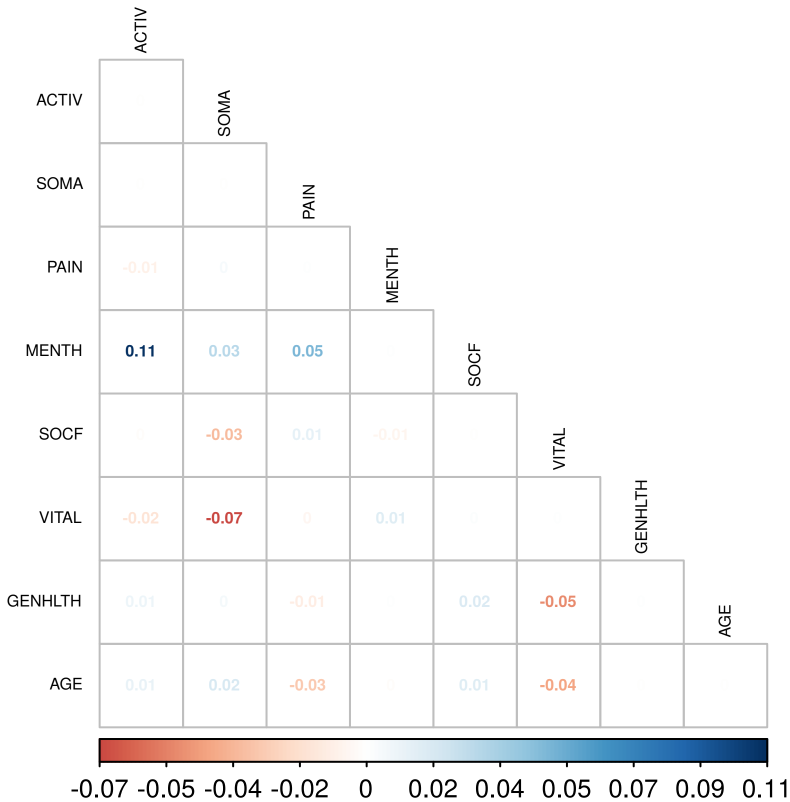
Residual Covariance Matrix



Standardized Residual Matrix



Residual Correlation Matrix



Modification Indices

Table 9: Modification Indices With Respect To Error Covariances

Left	Operator	Right	Modification Index	Expected Parameter Change	Delta	Power	Decision
ACTIV	~~	MENTH	14.761	6.982	0.1	0.05	**(m)**
SOCF	~~	GENHLTH	9.929	5.308	0.1	0.05	**(m)**
MENTH	~~	SOCF	8.687	-5.760	0.1	0.05	**(m)**
VITAL	~~	GENHLTH	5.425	-6.083	0.1	0.05	**(m)**
ACTIV	~~	SOCF	4.522	-5.811	0.1	0.05	**(m)**

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

Table 10: Modification Indices With Respect To Factor Loadings

Left	Operator	Right	Modification Index	Expected Parameter Change	Delta	Power	Decision
PHYSF	=~	MENTH	9.314	0.049	0.4	1.000	epc:nm
GWB	=~	VITAL	9.278	-0.248	0.4	0.998	epc:nm
MENTF	=~	SOMA	5.317	-0.301	0.4	0.864	epc:nm
PHYSF	=~	VITAL	5.292	-0.099	0.4	1.000	epc:nm
GWB	=~	SOCF	4.805	0.118	0.4	1.000	epc:nm

Table 10: Modification Indices With Respect To Factor Loadings (continued)

Left	Operator	Right	Modification Index	Expected Parameter Change	Delta	Power	Decision

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 - 21 = 15 . The 15 degrees of freedom indicate an over-identified model, fact which basically enables further analysis and interpretation.

The test statistic with the value 45.009 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 1942.397 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 0.063. The upper bound of the 90% confidence interval of the RMSEA is 0.085 and smaller than the threshold value 0.1, suggesting an acceptable 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 0.03 which is smaller than the threshold value 0.06 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 0.984 which is greater or equal than the threshold value 0.95, suggesting a good 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 0.971 which is greater or equal than the threshold value 0.95, suggesting a good model fit.

Summary of the Goodness of Fit Indices

The TLI model fit index suggests an acceptable model fit. Moreover the SRMR and the RMSEA model fit indices. The Chi-square model fit index suggests a poor model fit. The Chi-square model fit index is based on a very stringent statistical hypothesis. Therefore, we ignor it and tentatively assume an acceptable model fit. We verify this assertion by considering further metrics.

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 11: Pair(s) with Underestimated Covariance

Pair 1	ACTIV	MENTH
Pair 2	GENHLTH	GENHLTH

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 12: Pair(s) with Overestimated Covariance

Pair 1	AGE	AGE
Pair 2	GENHLTH	VITAL
Pair 3	MENTH	SOCF
Pair 4	SOMA	VITAL
Pair 5	VITAL	GENHLTH

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 these conditions are not fulfilled for modification indices with respect to factor loadings. Therefore, there exist no significant and relevant 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 13: Check Completely Standardized Factor Loadings

Latent Variable	Observed Variable	Loading[1]	P-Value	Significant?[2]	Relevance[3]	Sign[4]	Check
PHYSF	ACTIV	0.68	<0.001	Yes	**	—	Ok
PHYSF	SOMA	0.74	<0.001	Yes	**	—	Ok
PHYSF	PAIN	0.62	<0.001	Yes	**	—	Ok
MENTF	MENTH	0.85	<0.001	Yes	***	—	Ok
MENTF	SOCF	0.93	<0.001	Yes	***	—	Ok
MENTF	VITAL	0.80	<0.001	Yes	***	—	Ok
GWB	GENHLTH					—	Ok
AGEF	AGE	1.00			***	—	Ok

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

Table 13: Check Completely Standardized Factor Loadings (continued)

Latent Variable	Observed Variable	Loading[1]	P-Value	Significant?[2]	Relevance[3]	Sign[4]	Check

[7] _____

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 14: Interpretation of Unstandardized Factor Loadings

Interpretation of Unstandardized Factor Loadings
A 1-unit increase in PHYSF leads to a 1.00 -unit increase in the ACTIV
A 1-unit increase in PHYSF leads to a 0.87 -unit increase in the SOMA
A 1-unit increase in PHYSF leads to a 0.15 -unit increase in the PAIN
A 1-unit increase in MENTF leads to a 1.00 -unit increase in the MENTH
A 1-unit increase in MENTF leads to a 1.85 -unit increase in the SOCF
A 1-unit increase in MENTF leads to a 2.36 -unit increase in the VITAL
A 1-unit increase in GWB leads to a 1.00 -unit increase in the GENHLTH
A 1-unit increase in AGEF leads to a 1.00 -unit increase in the AGE

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 estimated factor intercorrelation within the section "Completely Standardized Parameter Estimates" is 0.45 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 15: Completely Standardized Error Variances and Communality

Observed Variable	Error Variance[1]	Communality[23]	P-Value	Significant Error Variance?[4]
ACTIV	0.54	0.46	<0.001	Yes
AGE	0.00	1.00		
GENHLTH	7.88	0.89	<0.001	Yes
MENTH	0.28	0.72	<0.001	Yes
PAIN	0.62	0.38	<0.001	Yes
SOCF	0.13	0.87	<0.001	Yes
SOMA	0.45	0.55	<0.001	Yes
VITAL	0.36	0.64	<0.001	Yes

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

[2] Corresponds to the squared factor loading.

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

Table 15: Completely Standardized Error Variances and Communality (continued)

Observed Variable	Error Variance[1]	Communality[23]	P-Value	Significant Error Variance?[4]

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

Error Covariances

By investigating the completely standardized parameter estimates, we remark that all error correlations are above 0.1 (in absolute value) and are statistically significant at 5% type I error. Therefore, we assume that they are well defined.

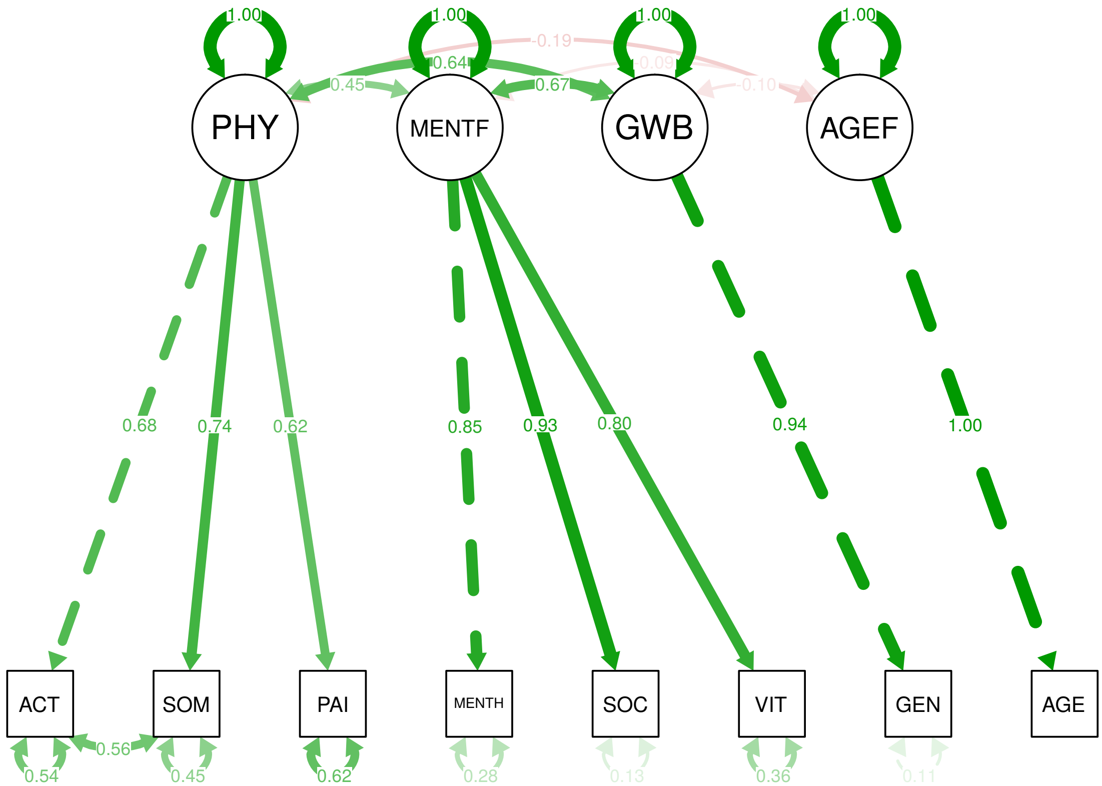
Factor Reliability

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 acceptable. Moreover, we cannot identify localized areas of ill fit. We conclude that the model is acceptable.

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