

Factor Model Fit and Simple Structure Diagnostics

The GPArotation Package

Author: Coen A. Bernaards

1 Introduction

Evaluating an exploratory factor analysis solution involves two distinct questions. First, does the k -factor model adequately reproduce the observed correlations? Second, once a factor solution is accepted, does rotation produce clean simple structure with loading patterns that are easy to interpret?

This vignette covers both questions using the `GriffithMulaik` and `CCAI` datasets included in `GPArotation`. Model fit is assessed via RMSEA and SRMR. Simple structure quality is assessed via AUC, FSI, hyperplane counts, and the Hoffman, Gini, and Bentler (Bentler (1977)) indices, all of which are reported automatically by `summary()`.

2 Model Fit: How Well Does the Factor Model Reproduce the Data?

We use the Griffith and Mulaik (Griffith & Mulaik (1998)) interpersonal personality data (`GriffithMulaik`, $n = 523$, 24 variables, 6 hypothetical interpersonal factors) to illustrate the complete model evaluation workflow. The data are described in Mulaik (2018).

```
> library("GPArotation")
> data("GriffithMulaik", package = "GPArotation")
> n.obs <- 523
```

2.1 Choosing the Number of Factors

2.1.1 Fit Statistics

Note that `n.obs` must be specified in the `factanal` call for fit statistics to be available. It is stored automatically in the `GPArotation` object and used by `calc_fitstats` to compute RMSEA and SRMR.

```
> for (k in 3:8) {
  fa.k <- factanal(factors = k, covmat = GriffithMulaik,
                  n.obs = n.obs, rotation = "none")
  res.k <- quartimax(fa.k)
  fit.k <- GPArotation:::calc_fitstats(res.k)
  cat(sprintf("k = %d RMSEA = %.4f [%.4f, %.4f] SRMR = %.4f\n",
              k, fit.k$RMSEA, fit.k$RMSEA.l, fit.k$RMSEA.u,
              fit.k$SRMR))
}
```

```
k = 3 RMSEA = 0.0729 [0.0676, 0.0785] SRMR = 0.0479
k = 4 RMSEA = 0.0600 [0.0542, 0.0661] SRMR = 0.0327
k = 5 RMSEA = 0.0516 [0.0452, 0.0582] SRMR = 0.0269
k = 6 RMSEA = 0.0415 [0.0341, 0.0490] SRMR = 0.0238
k = 7 RMSEA = 0.0339 [0.0251, 0.0424] SRMR = 0.0218
k = 8 RMSEA = 0.0266 [0.0150, 0.0366] SRMR = 0.0169
```

RMSEA values below 0.05 indicate close fit and below 0.08 acceptable fit (Hu & Bentler (1999)). SRMR below 0.08 is generally considered acceptable. For these data $k = 6$ achieves RMSEA below 0.05 and SRMR below 0.025, consistent with Mulaik's theoretical prediction of six interpersonal factors.

2.2 Residual Analysis

Global fit indices summarize overall model adequacy but can mask localized problems. A residual correlation matrix inspection identifies which specific item pairs are poorly reproduced by the factor model.

The residuals here are *correlation residuals*. The difference between the observed correlation r_{ij} and the model-implied correlation $\hat{r}_{ij}$:

$$e_{ij} = r_{ij} - \hat{r}_{ij}, \quad \hat{R} = L\Phi L^T$$

A **positive residual** means the model underestimates the relationship between two items. They share more variance than the factors account for. This may indicate a missing factor, shared method variance, or item redundancy. A **negative residual** means the model overestimates the relationship. Residuals near zero indicate the factor model reproduces that pair well.

As a rough guide:

- $|e_{ij}| < 0.05$ — excellent local fit
- $0.05 \leq |e_{ij}| < 0.10$ — acceptable
- $|e_{ij}| \geq 0.10$ — worth investigating
- $|e_{ij}| \geq 0.20$ — serious local misfit

Patterns in the residuals are informative. Clustered large residuals around a particular item suggest that item may need its own factor or has method variance not captured by the model. Large residuals between items from different factors suggest those factors may be more correlated than the model captures.

2.3 Residuals Are a Property of the Extraction, Not the Rotation

An important property of factor rotation is that it does not change the model-implied correlation matrix $\hat{R}$. For orthogonal rotation, $\Phi = I$ and T is orthogonal ($TT' = I$), so:

$$\hat{R} = LT(LT)' = LTT'L' = LL' = AA'$$

For oblique rotation, $\Phi = T'T$, so:

$$\hat{R} = AT^{-T} \cdot T'T \cdot T^{-1}A' = AA'$$

Both reduce to AA' , the model-implied correlation matrix that depends only on the unrotated loadings A , not on the rotation matrix T . This means the residual matrix $R - \hat{R}$ and all derived fit statistics (SRMR, RMSEA) are identical across all rotation methods applied to the same unrotated solution.

```
> fa.un <- factanal(factors = 6, covmat = GriffithMulaik,
                    n.obs = n.obs, rotation = "none")
> res.vm <- Varimax(fa.un)
> res.ob <- oblimin(fa.un, randomStarts = 100)
> res.t1 <- tandemI(fa.un)
> fit.vm <- GPArotation:::calc_fitstats(res.vm)
> fit.ob <- GPArotation:::calc_fitstats(res.ob)
> fit.t1 <- GPArotation:::calc_fitstats(res.t1)
> cat(sprintf("Varimax  SRMR = %.4f  RMSEA = %.4f\n",
              fit.vm$SRMR, fit.vm$RMSEA))
```

```
Varimax  SRMR = 0.0238  RMSEA = 0.0415
```

```
> cat(sprintf("Oblimin  SRMR = %.4f  RMSEA = %.4f\n",
              fit.ob$SRMR, fit.ob$RMSEA))
```

```
Oblimin  SRMR = 0.0238  RMSEA = 0.0415
```

```
> cat(sprintf("TandemI  SRMR = %.4f  RMSEA = %.4f\n",
              fit.t1$SRMR, fit.t1$RMSEA))
```

```
TandemI  SRMR = 0.0238  RMSEA = 0.0415
```

All three produce identical SRMR and RMSEA values. Fit statistics therefore inform the choice of *how many* factors to extract, not *how* to rotate them. To compare rotation methods, use the criterion-free simple structure measures (AUC, FSI, and hyperplane counts) which do vary across rotation methods and are reported automatically by `print()` and `summary()`.

```
> GPArotation:::audit_residuais(res.ob)
```

SRMR: 0.0238

Mean absolute residual per item:

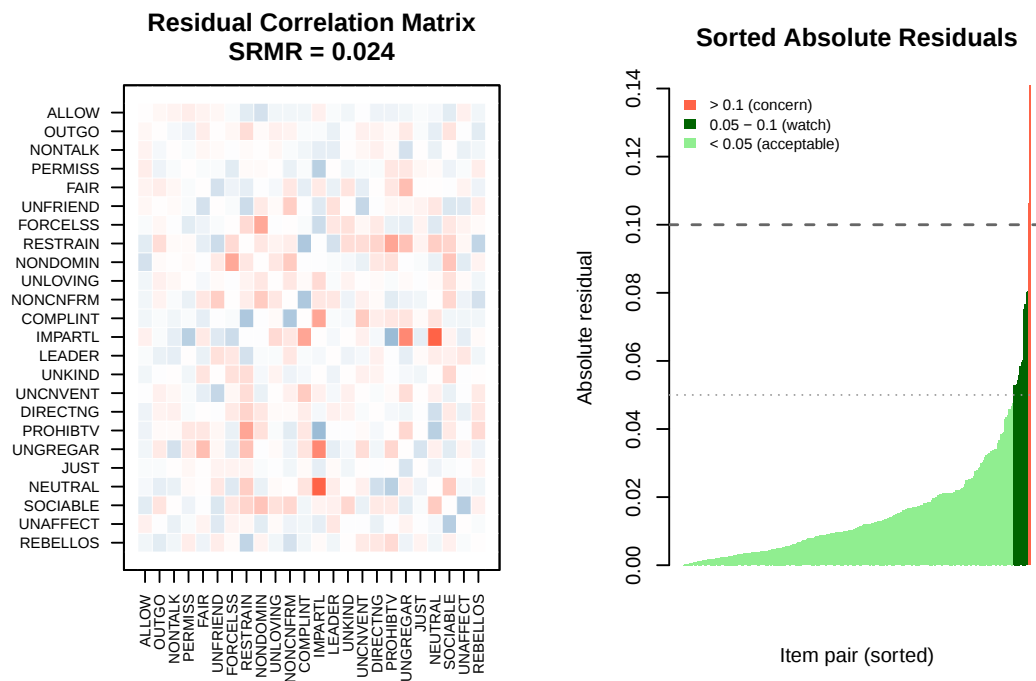
IMPARTL	RESTRAIN	UNGREGAR	NEUTRAL	SOCIABLE	PROHIBTV	NONCNFRM	COMPLINT
0.0296	0.0278	0.0230	0.0221	0.0219	0.0198	0.0183	0.0179
NONDOMIN	FORCELSS	UNFRIEND	REBELLOS	FAIR	UNCNVENT	LEADER	DIRECTNG
0.0168	0.0161	0.0154	0.0138	0.0137	0.0132	0.0123	0.0119
UNAFFECT	ALLOW	OUTGO	PERMISS	UNKIND	UNLOVING	NONTALK	JUST
0.0112	0.0106	0.0105	0.0102	0.0097	0.0087	0.0084	0.0065

Item pairs with absolute residual exceeding 0.1 :

Item_A	Item_B	Residual
NEUTRAL	IMPARTL	0.1409
UNGREGAR	IMPARTL	0.1063

Items with high mean absolute residuals may cross-load on an additional factor or have method variance not captured by the model. For the GriffithMulaik data, IMPARTL is flagged with two pairs exceeding 0.10. It loads weakly on multiple factors, suggesting it does not discriminate cleanly between the six interpersonal dimensions.

```
> plot(res.ob, "residuals")
```



The heatmap shows the full residual matrix. Blue cells indicate the model overestimates the correlation, red cells indicate underestimation. The sorted bar chart shows the distribution of all off-diagonal absolute residuals.

3 Simple Structure: How Clean Is the Rotated Solution?

Once an adequate model is accepted, rotation is evaluated by how well it achieves simple structure. GPArotation reports five criterion-free simple structure measures automatically via `print()` and `summary()`.

3.1 Per-Factor Measures: AUC and FSI

`print()` reports AUC (Liu et al. (2023)) and FSI (Lorenzo-Seva (2003)) for each factor. AUC measures how rapidly a factor's variance accumulates when loadings are sorted by size. AUC values near 1 indicate one or two dominant loadings with the rest near zero. FSI measures the kurtosis of the squared loadings. FSI values near 1 indicate a sharp contrast between large and small loadings.

```
> print(res.ob)
```

Oblique rotation method Oblimin Quartimin converged at lowest minimum.

Of 100 random starts 100% converged, 100% at the same lowest minimum.

Loadings at lowest minimum:

	Factor1	Factor2	Factor3	Factor4	Factor5	Factor6
ALLOW				0.755		
OUTGO		0.138	-0.684			
NONTALK			0.759			
PERMISS				0.793		
FAIR	-0.134				0.678	
UNFRIEND	0.390		0.305	-0.153	-0.159	
FORCELESS	-0.138	-0.455	0.190	0.349		
RESTRAIN		0.252	0.367	-0.115		-0.126
NONDOMIN	-0.164	-0.526	0.179	0.260		
UNLOVING	0.854					
NONCNFRM	-0.113	0.100	0.106	-0.128	0.116	0.622
COMPLINT					0.109	-0.454
IMPARTL			0.198	0.107	0.313	
LEADER		0.753				
UNKIND	0.525		0.136		-0.272	
UNCNVENT				0.112		0.686
DIRECTNG		0.858				
PROHIBTV		0.129		-0.346		-0.143
UNGREGAR			0.357			
JUST					0.923	
NEUTRAL	-0.120		0.160	0.195	0.282	-0.115
SOCIABLE	-0.167	0.178	-0.500	0.170		-0.111
UNAFFECT	0.618		0.148			
REBELLOS	0.278		-0.184			0.587

	Factor1	Factor2	Factor3	Factor4	Factor5	Factor6
SS loadings	2.265	2.208	2.085	2.053	2.011	1.594
AUC	0.926	0.941	0.898	0.922	0.947	0.935
FSI	0.216	0.227	0.151	0.231	0.316	0.205

Phi:

	Factor1	Factor2	Factor3	Factor4	Factor5	Factor6
Factor1	1.000	0.036	0.327	-0.439	-0.610	0.273
Factor2	0.036	1.000	-0.369	-0.471	0.099	0.026
Factor3	0.327	-0.369	1.000	-0.066	-0.175	-0.031
Factor4	-0.439	-0.471	-0.066	1.000	0.321	-0.123
Factor5	-0.610	0.099	-0.175	0.321	1.000	-0.374
Factor6	0.273	0.026	-0.031	-0.123	-0.374	1.000

3.2 Overall Solution Measures

`summary()` adds three overall measures (Hoffman, Gini, Bentler), the hyperplane count, and the structure matrix for oblique solutions.

```
> summary(res.ob)
```

Oblique rotation method Oblimin Quartimin converged in 46 iterations.
 Algorithm: bb | fwindow: 10 | Iterations:
 Of 100 random starts 100% converged, 100% at the same lowest minimum.
 Pattern (loadings) - see Structure (correlations) below:

Loadings:

	Factor1	Factor2	Factor3	Factor4	Factor5	Factor6
ALLOW				0.755		
OUTGO		0.138	-0.684			
NONTALK			0.759			
PERMISS				0.793		
FAIR	-0.134				0.678	
UNFRIEND	0.390		0.305	-0.153	-0.159	
FORCELSS	-0.138	-0.455	0.190	0.349		
RESTRAIN		0.252	0.367	-0.115		-0.126
NONDOMIN	-0.164	-0.526	0.179	0.260		
UNLOVING	0.854					
NONCNFRM	-0.113	0.100	0.106	-0.128	0.116	0.622
COMPLINT					0.109	-0.454
IMPARTL			0.198	0.107	0.313	
LEADER		0.753				
UNKIND	0.525		0.136		-0.272	
UNCNVENT				0.112		0.686
DIRECTNG		0.858				
PROHIBTV		0.129		-0.346		-0.143
UNGREGAR			0.357			
JUST					0.923	
NEUTRAL	-0.120		0.160	0.195	0.282	-0.115
SOCIABLE	-0.167	0.178	-0.500	0.170		-0.111
UNAFFECT	0.618		0.148			
REBELLOS	0.278		-0.184			0.587

	Factor1	Factor2	Factor3	Factor4	Factor5	Factor6
SS loadings	2.265	2.208	2.085	2.053	2.011	1.594
AUC	0.926	0.941	0.898	0.922	0.947	0.935
FSI	0.216	0.227	0.151	0.231	0.316	0.205

Correlations:

	Factor1	Factor2	Factor3	Factor4	Factor5	Factor6
ALLOW	-0.402	-0.423		0.817	0.261	
OUTGO	-0.376	0.353	-0.772	0.124	0.290	
NONTALK	0.257	-0.287	0.764			
PERMISS	-0.306	-0.327		0.758	0.259	-0.104
FAIR	-0.545	0.113	-0.148	0.282	0.769	-0.274
UNFRIEND	0.666		0.471	-0.399	-0.517	0.219
FORCELSS	-0.287	-0.691	0.284	0.632	0.181	-0.170
RESTRAIN		0.172	0.256	-0.197		-0.156
NONDOMIN	-0.278	-0.719	0.298	0.587	0.160	-0.178
UNLOVING	0.847		0.296	-0.347	-0.518	0.221
NONCNFRM		0.145		-0.171		0.563
COMPLINT	-0.248			0.181	0.322	-0.514
IMPARTL	-0.153	-0.117	0.148	0.197	0.290	
LEADER	-0.134	0.771	-0.386	-0.258	0.237	
UNKIND	0.780		0.341	-0.410	-0.655	0.315
UNCNVENT	0.144				-0.285	0.687
DIRECTNG		0.828	-0.257	-0.409		
PROHIBTV	0.276	0.259		-0.458	-0.187	

UNGREGAR	0.114	-0.195	0.359		-0.129	
JUST	-0.530		-0.165	0.276	0.901	-0.354
NEUTRAL	-0.358	-0.176		0.363	0.428	-0.283
SOCIABLE	-0.459	0.279	-0.636	0.222	0.352	-0.176
UNAFFECT	0.727		0.352	-0.383	-0.466	0.208
REBELLOS	0.374			-0.126	-0.374	0.673

Hyperplane total: 83 of 120 (69.167 %) at cutoff 0.1

Post-Hoc Simplicity Suite (overall solution):

Hoffman Index: 0.839

Gini Coefficient: 0.577

Bentler Index: 0.131

Phi:

	Factor1	Factor2	Factor3	Factor4	Factor5	Factor6
Factor1	1.000	0.036	0.327	-0.439	-0.610	0.273
Factor2	0.036	1.000	-0.369	-0.471	0.099	0.026
Factor3	0.327	-0.369	1.000	-0.066	-0.175	-0.031
Factor4	-0.439	-0.471	-0.066	1.000	0.321	-0.123
Factor5	-0.610	0.099	-0.175	0.321	1.000	-0.374
Factor6	0.273	0.026	-0.031	-0.123	-0.374	1.000

The hyperplane count reports how many loadings fall below a cutoff of 0.10 in absolute value. For a perfectly simple solution with p items and k factors, the theoretical maximum is $p(k - 1)$.

3.3 Comparing Rotation Methods

These measures are criterion-free, so they can be used to compare simple structure quality across different rotation methods applied to the same unrotated solution.

```
> res.gm <- geominQ(fa.un, randomStarts = 100)
> auc.ob <- GPArotation:::calc_AUC(res.ob)$AUC_mean
> auc.vm <- GPArotation:::calc_AUC(res.vm)$AUC_mean
> auc.gm <- GPArotation:::calc_AUC(res.gm)$AUC_mean
> hp.ob <- GPArotation:::calc_hyperplane(res.ob)$HP_pct
> hp.vm <- GPArotation:::calc_hyperplane(res.vm)$HP_pct
> hp.gm <- GPArotation:::calc_hyperplane(res.gm)$HP_pct
> cat(sprintf("%-12s AUC = %.3f Hyperplane = %.1f pct\n",
              "Varimax", auc.vm, hp.vm))
```

```
Varimax      AUC = 0.883 Hyperplane = 43.3 pct
```

```
> cat(sprintf("%-12s AUC = %.3f Hyperplane = %.1f pct\n",
              "Oblimin", auc.ob, hp.ob))
```

```
Oblimin      AUC = 0.928 Hyperplane = 69.2 pct
```

```
> cat(sprintf("%-12s AUC = %.3f Hyperplane = %.1f pct\n",
              "GeominQ", auc.gm, hp.gm))
```

```
GeominQ      AUC = 0.929 Hyperplane = 68.3 pct
```

Oblique rotations achieve higher AUC and hyperplane counts than Varimax because the underlying interpersonal factors are correlated; an orthogonal constraint forces loadings to spread across factors.

3.4 Unrotated vs Rotated: Does Rotation Help?

Simple structure measures should always improve after rotation:

```

> sim.un <- GPArotation:::calc_simplicity(fa.un)
> sim.ob <- GPArotation:::calc_simplicity(res.ob)
> cat(sprintf("%-12s Hoffman = %.3f Gini = %.3f Bentler = %.3f\n",
              "Unrotated", sim.un$Hoffman, sim.un$Gini, sim.un$Bentler))

Unrotated      Hoffman = 0.767 Gini = 0.412 Bentler = 0.275

> cat(sprintf("%-12s Hoffman = %.3f Gini = %.3f Bentler = %.3f\n",
              "Oblimin", sim.ob$Hoffman, sim.ob$Gini, sim.ob$Bentler))

Oblimin        Hoffman = 0.839 Gini = 0.577 Bentler = 0.131

```

All three indices increase after rotation. If Bentler remains low despite high AUC and hyperplane counts, this typically indicates high factor intercorrelations rather than poor simple structure.

4 Summary

A complete EFA diagnostic workflow in GPArotation:

1. Extract a k -factor solution via `factanal`.
2. Compare scree plots from raw and reduced correlation matrices (Mulaik (2018)).
3. Check global fit via `GPArotation:::calc_fitstats` across a range of k .
4. Rotate with `randomStarts` to avoid local minima.
5. Inspect residuals via `audit_residuals` and `plot(..., "residuals")` for local misfit.
6. Compare rotation methods using AUC and hyperplane counts.
7. Use `summary()` for the full diagnostic scorecard.

References

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