

Using the psych package to generate and test structural models

William Revelle

March 26, 2009

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1 The psych package

1.1 Preface

The *psych* package (Revelle, 2009) has been developed to include those functions most useful for teaching and learning basic psychometrics and personality theory. Functions have been developed for many parts of the analysis of test data, including basic descriptive statistics (`describe` and `pairs.panels`), dimensionality analysis (`ICLUST`, `VSS`, `principal`, `factor.pa`), reliability analysis (`omega`, `guttman`) and eventual scale construction (`cluster.cor`, `score.items`). The use of these and other functions is described in more detail in the accompanying vignette (`overview.pdf`) as well as in the complete user's manual and the relevant help pages. (These vignettes are also available at <http://personality-project.org/r/overview.pdf>) and http://personality-project.org/r/psych_for_sem.pdf) .

This vignette is concerned with the problem of modeling structural data and using the *psych* package as a front end for the much more powerful *sem* package of John Fox (2006, 2009). The first section discusses how to simulate particular latent variable structures. The second considers several Exploratory Factor Analysis (EFA) solutions to these problems. The third section considers how to do confirmatory factor analysis and structural equation modeling using the *sem* package but with the input prepared using functions in the *psych* package.

1.2 Creating and modeling structural relations

One common application of *psych* is the creation of simulated data matrices with particular structures to use as examples for principal components analysis, factor analysis, cluster analysis, and structural equation modeling. This vignette describes some of the functions used for creating, analyzing, and displaying such data sets. The examples use two other packages: *Rgraphviz* and *sem*. Although not required to use the *psych* package, these two libraries are required for these examples. *Rgraphviz* is used for the graphical displays, but the analyses themselves require only the *sem* package to do the structural modeling.

2 Functions for generating correlational matrices with a particular structure

The `sim` family of functions create data sets with particular structure. Most of these functions have default values that will produce useful examples. Although graphical summaries

of these structures will be shown here, some of the options of the graphical displays will be discussed in a later section.

To make these examples replicable for readers, all simulations are prefaced by setting the random seed to a fixed (and for some, memorable) number (Adams, 1980). For normal use of the simulations, this is not necessary.

2.1 `sim.congeneric`

Classical test theory considers tests to be *tau* equivalent if they have the same covariance with a vector of latent true scores, but perhaps different error variances. Tests are considered *congeneric* if they each have the same true score component (perhaps to a different degree) and independent error components. The `sim.congeneric` function may be used to generate either structure.

The first example considers four tests with equal loadings on a latent factor (that is, a τ equivalent model). If the number of subjects is not specified, a population correlation matrix will be generated. If `N` is specified, then the sample correlation matrix is returned. If the “short” option is `FALSE`, then the population matrix, sample matrix, and sample data are all returned as elements of a list.

```
> library(psych)
> set.seed(42)
> tau <- sim.congeneric(loads = c(0.8, 0.8, 0.8, 0.8))
> tau.samp <- sim.congeneric(loads = c(0.8, 0.8, 0.8, 0.8), N = 100)
> round(tau.samp, 2)

      V1  V2  V3  V4
V1 1.00 0.68 0.72 0.66
V2 0.68 1.00 0.65 0.67
V3 0.72 0.65 1.00 0.76
V4 0.66 0.67 0.76 1.00

> tau.samp <- sim.congeneric(loads = c(0.8, 0.8, 0.8, 0.8), N = 100,
+   short = FALSE)
> tau.samp

$model (Population correlation matrix)
      V1  V2  V3  V4
V1 1.00 0.64 0.64 0.64
V2 0.64 1.00 0.64 0.64
V3 0.64 0.64 1.00 0.64
V4 0.64 0.64 0.64 1.00
```

```

$r (Sample correlation matrix for sample size = 100 )
      V1  V2  V3  V4
V1 1.00 0.70 0.62 0.58
V2 0.70 1.00 0.65 0.64
V3 0.62 0.65 1.00 0.59
V4 0.58 0.64 0.59 1.00

> dim(tau.samp$observed)

[1] 100  4

```

In this last case, the generated data are retrieved from `tau.samp$observed`. Congeneric data are created by specifying unequal loading values. The default values are loadings of `c(.8,.7,.6,.5)`. As seen in Figure 1, tau equivalence is the special case where all paths are equal.

```

> cong <- sim.congeneric(N = 100)
> round(cong, 2)

      V1  V2  V3  V4
V1 1.00 0.57 0.53 0.46
V2 0.57 1.00 0.35 0.41
V3 0.53 0.35 1.00 0.43
V4 0.46 0.41 0.43 1.00

```

2.2 sim.hierarchical

The previous function, `sim.congeneric`, is used when one factor accounts for the pattern of correlations. A slightly more complicated model is when one broad factor and several narrower factors are observed. An example of this structure might be the structure of mental abilities, where there is a broad factor of general ability and several narrower factors (e.g., spatial ability, verbal ability, working memory capacity). Another example is in the measure of psychopathology where a broad general factor of neuroticism is seen along with more specific anxiety, depression, and aggression factors. This kind of structure may be simulated with `sim.hierarchical` specifying the loadings of each sub factor on a general factor (the g-loadings) as well as the loadings of individual items on the lower order factors (the f-loadings). An early paper describing a *bifactor* structure was by Holzinger and Swineford (1937). A helpful description of what makes a good general factor is that of Jensen and Weng (1994).

For those who prefer real data to simulated data, six data sets are included in the `bifactor` data set. One is the original 14 variable problem of Holzinger and Swineford (1937)

Structural model

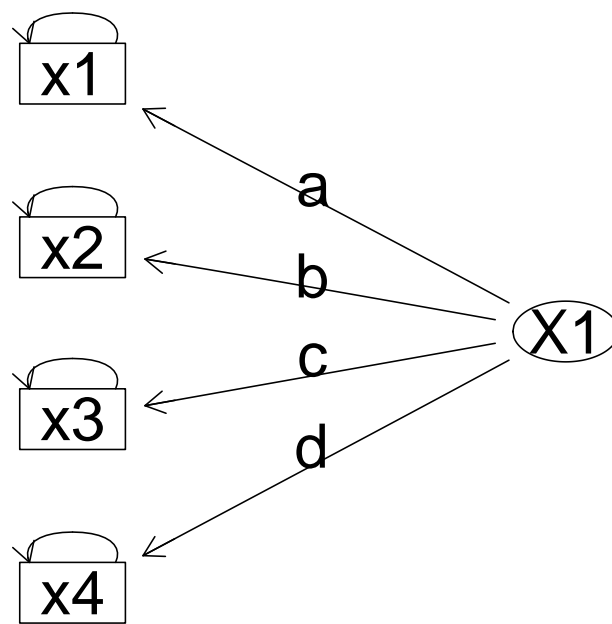


Figure 1: Tau equivalent tests are special cases of congeneric tests. Tau equivalence assumes $a=b=c=d$

(holzinger), a second is a nine variable problem adapted by ? from Thurstone and Thurstone (1941) (the data set is used as an example in the SAS manual and discussed in great detail by McDonald (1999)), a third is from a recent paper by Reise et al. (2007) with 16 measures of patient reports of interactions with their health care provider.

```
> set.seed(42)
> gload = matrix(c(0.9, 0.8, 0.7), nrow = 3)
> fload <- matrix(c(0.9, 0.8, 0.7, rep(0, 9), 0.7, 0.6, 0.5, rep(0,
+      9), 0.6, 0.5, 0.4), ncol = 3)
> fload

      [,1] [,2] [,3]
[1,]  0.9  0.0  0.0
[2,]  0.8  0.0  0.0
[3,]  0.7  0.0  0.0
[4,]  0.0  0.7  0.0
[5,]  0.0  0.6  0.0
[6,]  0.0  0.5  0.0
[7,]  0.0  0.0  0.6
[8,]  0.0  0.0  0.5
[9,]  0.0  0.0  0.4

> bifact <- sim.hierarchical(gload = gload, fload = fload)
> round(bifact, 2)

      V1  V2  V3  V4  V5  V6  V7  V8  V9
V1 1.00 0.72 0.63 0.45 0.39 0.32 0.34 0.28 0.23
V2 0.72 1.00 0.56 0.40 0.35 0.29 0.30 0.25 0.20
V3 0.63 0.56 1.00 0.35 0.30 0.25 0.26 0.22 0.18
V4 0.45 0.40 0.35 1.00 0.42 0.35 0.24 0.20 0.16
V5 0.39 0.35 0.30 0.42 1.00 0.30 0.20 0.17 0.13
V6 0.32 0.29 0.25 0.35 0.30 1.00 0.17 0.14 0.11
V7 0.34 0.30 0.26 0.24 0.20 0.17 1.00 0.30 0.24
V8 0.28 0.25 0.22 0.20 0.17 0.14 0.30 1.00 0.20
V9 0.23 0.20 0.18 0.16 0.13 0.11 0.24 0.20 1.00
```

These data can be represented as either a *bifactor* (Figure 2) or *hierarchical* (Figure ??) factor solution. The analysis was done with the **omega** function. The graphs require the *Rgraphviz* package.

```

> op <- par(mfrow = c(1, 2))
> m.bi <- omega(bifact, title = "A bifactor model")
> m.hi <- omega(bifact, sl = FALSE, title = "A hierarchical model")
> op <- par(mfrow = c(1, 1))

```

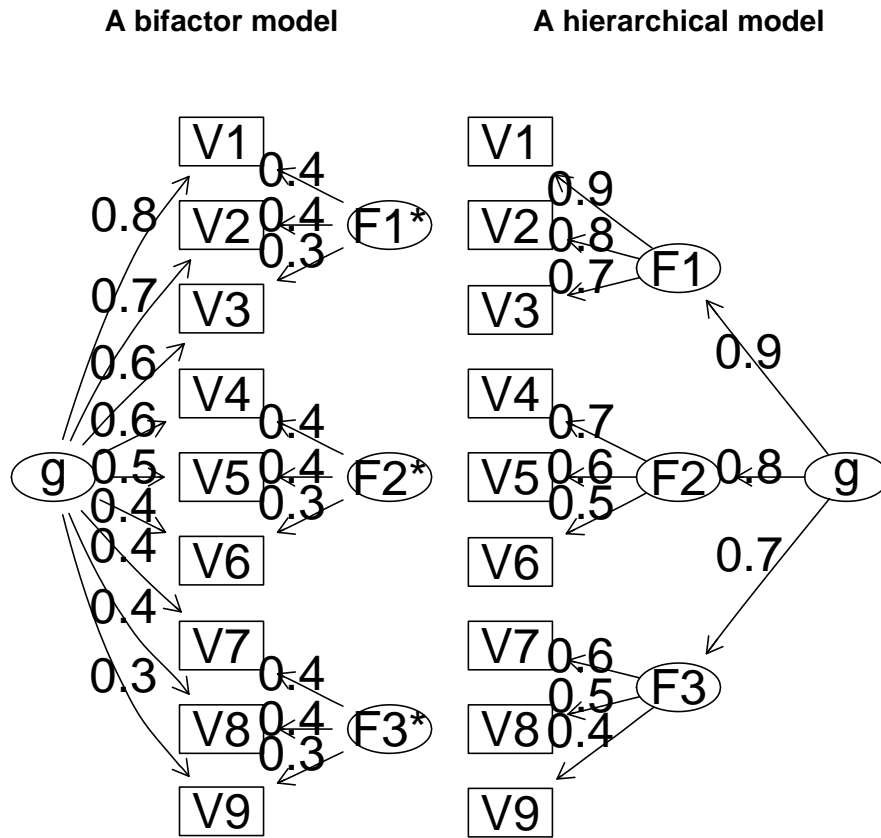


Figure 2: (Left panel) A bifactor solution represents each test in terms of a general factor and a residualized group factor. (Right Panel) A hierarchical factor solution has g as a second order factor accounting for the correlations between the first order factors

2.3 sim.item and sim.circ

Many personality questionnaires are thought to represent multiple, independent factors. A particularly interesting case is when there are two factors and the items either have *simple structure* or *circumplex structure*. Examples of such items with a circumplex structure are measures of emotion (Rafaeli and Revelle, 2006) where many different emotion terms can be arranged in a two dimensional space, but where there is no obvious clustering of items. Typical personality scales are constructed to have simple structure, where items load on one and only one factor.

An additional challenge to measurement with emotion or personality items is that the items can be highly skewed and are assessed with a small number of discrete categories (do not agree, somewhat agree, strongly agree).

The more general `sim.item` function, and the more specific, `sim.circ` functions simulate items with a two dimensional structure, with or without skew, and varying the number of categories for the items. An example of a circumplex structure is shown in Figure ??

2.4 sim.structure

A more general case is to consider three matrices, $\vec{f}_x, \vec{\phi}_{xy}, \vec{f}_y$ which describe, in turn, a measurement model of x variables, \vec{f}_x , a measurement model of y variables, \vec{f}_y , and a covariance matrix between and within the two sets of factors. If \vec{f}_x is a vector and \vec{f}_y and $\vec{\phi}_{xy}$ are NULL, then this is just the congeneric model. If \vec{f}_x is a matrix of loadings with n rows and c columns, then this is a measurement model for n variables across c factors. If $\vec{\phi}_{xy}$ is not null, but \vec{f}_y is NULL, then the factors in \vec{f}_x are correlated. Finally, if all three matrices are not NULL, then the data show the standard linear structural relations (LISREL) structure.

Consider the following examples:

2.4.1 \vec{f}_x is a vector implies a congeneric model

```
> set.seed(42)
> fx <- c(0.9, 0.8, 0.7, 0.6)
> cong1 <- sim.structure(fx)
> cong1

$model (Population correlation matrix)
      V1  V2  V3  V4
V1  1.00 0.80 0.70 0.60
V2  0.80 1.00 0.60 0.50
V3  0.70 0.60 1.00 0.40
V4  0.60 0.50 0.40 1.00
```

```

> circ <- sim.circ(16)
> f2 <- factor.pa(circ, 2)
> plot(f2, main = "16 simulated variables in a circumplex pattern")
Use ICLUST.graph to see the hierarchical structure

```

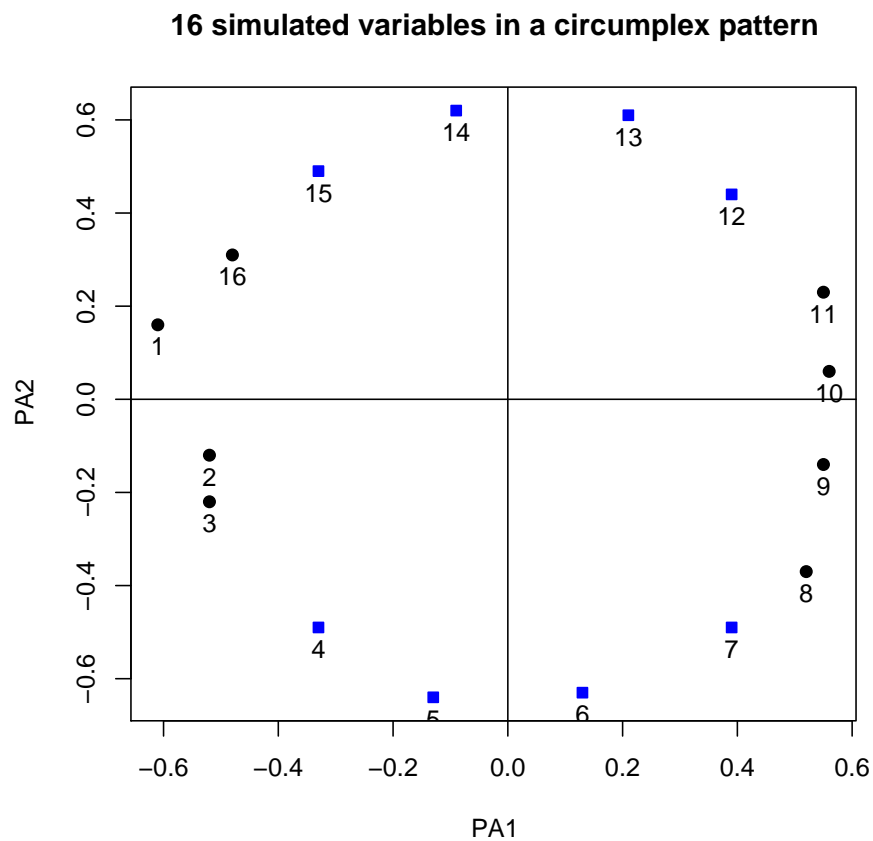


Figure 3: Emotion items or interpersonal items frequently show a circumplex structure. Data generated by `sim.circ` and factor loadings found by the principal axis algorithm using `factor.pa`.

```
V1 1.00 0.72 0.63 0.54
V2 0.72 1.00 0.56 0.48
V3 0.63 0.56 1.00 0.42
V4 0.54 0.48 0.42 1.00
```

```
$reliability (population reliability)
[1] 0.81 0.64 0.49 0.36
```

2.4.2 \vec{f}_x is a matrix implies an independent factors model:

```
> set.seed(42)
> fx <- matrix(c(0.9, 0.8, 0.7, rep(0, 9), 0.7, 0.6, 0.5, rep(0,
+ 9), 0.6, 0.5, 0.4), ncol = 3)
> three.fact <- sim.structure(fx)
> three.fact
```

```
$model (Population correlation matrix)
      V1  V2  V3  V4  V5  V6  V7  V8  V9
V1 1.00 0.72 0.63 0.00 0.00 0.00 0.00 0.0 0.00
V2 0.72 1.00 0.56 0.00 0.00 0.00 0.00 0.0 0.00
V3 0.63 0.56 1.00 0.00 0.00 0.00 0.00 0.0 0.00
V4 0.00 0.00 0.00 1.00 0.42 0.35 0.00 0.0 0.00
V5 0.00 0.00 0.00 0.42 1.00 0.30 0.00 0.0 0.00
V6 0.00 0.00 0.00 0.35 0.30 1.00 0.00 0.0 0.00
V7 0.00 0.00 0.00 0.00 0.00 0.00 1.00 0.3 0.24
V8 0.00 0.00 0.00 0.00 0.00 0.00 0.30 1.0 0.20
V9 0.00 0.00 0.00 0.00 0.00 0.00 0.24 0.2 1.00
```

```
$reliability (population reliability)
[1] 0.81 0.64 0.49 0.49 0.36 0.25 0.36 0.25 0.16
```

2.4.3 \vec{f}_x is a matrix and $\Phi \neq I$ is a correlated factors model

```
> Phi = matrix(c(1, 0.5, 0.3, 0.5, 1, 0.2, 0.3, 0.2, 1), ncol = 3)
> cor.f3 <- sim.structure(fx, Phi)
> fx
```

```
      [,1] [,2] [,3]
[1,]  0.9  0.0  0.0
[2,]  0.8  0.0  0.0
```

Structural model

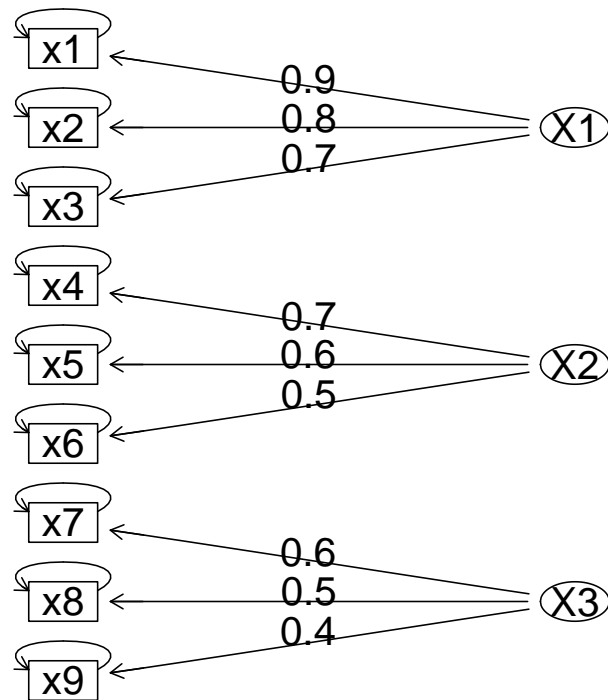


Figure 4: Three uncorrelated factors generated using the `sim.structure` function and drawn using `structure.graph`.

```

[3,] 0.7 0.0 0.0
[4,] 0.0 0.7 0.0
[5,] 0.0 0.6 0.0
[6,] 0.0 0.5 0.0
[7,] 0.0 0.0 0.6
[8,] 0.0 0.0 0.5
[9,] 0.0 0.0 0.4

> Phi

      [,1] [,2] [,3]
[1,] 1.0 0.5 0.3
[2,] 0.5 1.0 0.2
[3,] 0.3 0.2 1.0

> cor.f3

$model (Population correlation matrix)
      V1    V2    V3    V4    V5    V6    V7    V8    V9
V1 1.00 0.720 0.630 0.315 0.270 0.23 0.162 0.14 0.108
V2 0.72 1.000 0.560 0.280 0.240 0.20 0.144 0.12 0.096
V3 0.63 0.560 1.000 0.245 0.210 0.17 0.126 0.10 0.084
V4 0.32 0.280 0.245 1.000 0.420 0.35 0.084 0.07 0.056
V5 0.27 0.240 0.210 0.420 1.000 0.30 0.072 0.06 0.048
V6 0.23 0.200 0.175 0.350 0.300 1.00 0.060 0.05 0.040
V7 0.16 0.144 0.126 0.084 0.072 0.06 1.000 0.30 0.240
V8 0.14 0.120 0.105 0.070 0.060 0.05 0.300 1.00 0.200
V9 0.11 0.096 0.084 0.056 0.048 0.04 0.240 0.20 1.000

$reliability (population reliability)
[1] 0.81 0.64 0.49 0.49 0.36 0.25 0.36 0.25 0.16

```

Using symbolic loadings and path coefficients For some purposes, it is helpful not specify particular values for the paths, but rather to think of them symbolically. This can be shown with symbolic loadings and path coefficients by using the `structure.list` and `phi.list` functions to create the `fx` and `Phi` matrices (Figure 5).

```

> fxs <- structure.list(9, list(F1 = c(1, 2, 3), F2 = c(4, 5, 6),
+   F3 = c(7, 8, 9)))
> Phis <- phi.list(3, list(F1 = c(2, 3), F2 = c(1, 3), F3 = c(1,
+   2)))
> fxs

```

```

      F1  F2  F3
[1,] "a1" "0" "0"
[2,] "a2" "0" "0"
[3,] "a3" "0" "0"
[4,] "0"  "b4" "0"
[5,] "0"  "b5" "0"
[6,] "0"  "b6" "0"
[7,] "0"  "0"  "c7"
[8,] "0"  "0"  "c8"
[9,] "0"  "0"  "c9"

> Phi

```

```

      F1  F2  F3
F1 "1"  "rba" "rca"
F2 "rab" "1"  "rcb"
F3 "rac" "rbc" "1"

```

The `structure.list` and `phi.list` functions allow for for creation of `fx`, `Phi`, and `fy` matrices in a very compact form, just by specifying the relevant variables.

Drawing path models from Exploratory Factor Analysis solutions Alternatively, this result can represent the estimated factor loadings and oblique correlations found using `factanal` (Maximum Likelihood factoring) or `factor.pa` (Principal axis factoring) followed by a promax rotation using the `Promax` function (Figure 6. Comparing this figure with the previous one (Figure 5), it will be seen that one path was dropped because it was less than the arbitrary “cut” value of .2.

```
> f3.p <- Promax(factor.pa(cor.f3$model, 3))
```

2.4.4 \vec{f}_x and \vec{f}_y are matrices, and $\mathbf{Phi} \neq I$ represents their correlations

A more complicated model is when there is a \vec{f}_y vector or matrix representing a set of Y latent variables that are associated with the a set of y variables. In this case, the `Phi` matrix is a set of correlations within the X set and between the X and Y set.

```

> set.seed(42)
> fx <- matrix(c(0.9, 0.8, 0.7, rep(0, 9), 0.7, 0.6, 0.5, rep(0,
+ 9), 0.6, 0.5, 0.4), ncol = 3)
> fy <- c(0.6, 0.5, 0.4)
> Phi <- matrix(c(1, 0.48, 0.32, 0.4, 0.48, 1, 0.32, 0.3, 0.32,
+ 0.32, 1, 0.2, 0.4, 0.3, 0.2, 1), ncol = 4)

```

```
> corf3.mod <- structure.graph(fxs, Phis)
```

Structural model

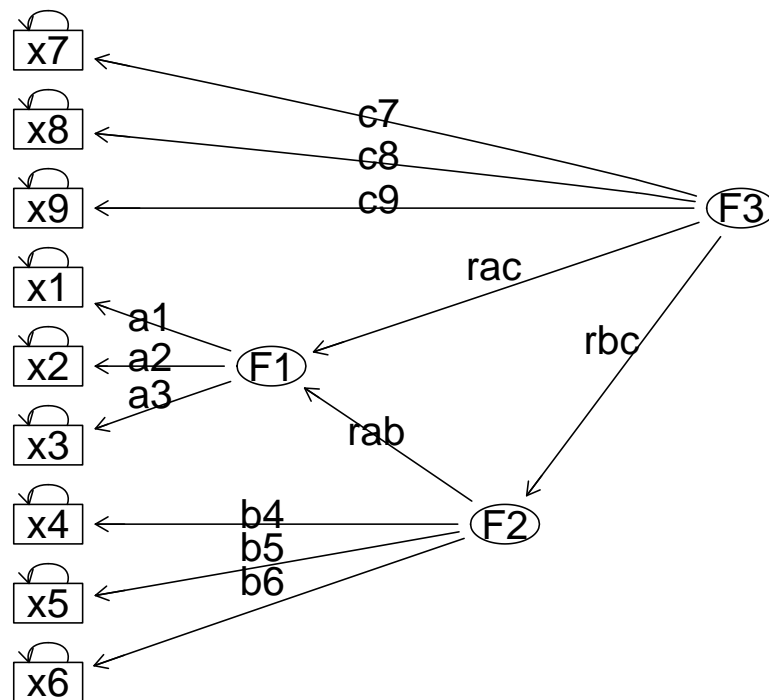


Figure 5: Three correlated factors with symbolic paths. Created using `structure.graph` and `structure.list` and `phi.list` for ease of input.

```
> mod.f3p <- structure.graph(f3.p, cut = 0.2)
```

Structural model

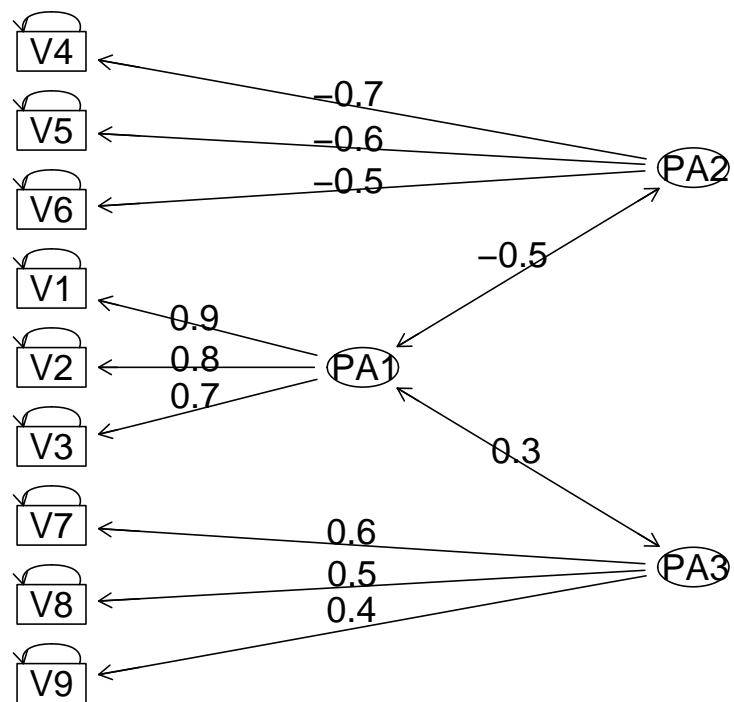


Figure 6: The empirically fitted structural model. Paths less than cut (.2 in this case, the default is .3) are not shown.


```

> twelveV <- sim.structure(fx, Phi, fy)$model
> colnames(twelveV) <- rownames(twelveV) <- c(paste("x", 1:9, sep = ""),
+       paste("y", 1:3, sep = ""))
> round(twelveV, 2)

```

	x1	x2	x3	x4	x5	x6	x7	x8	x9	y1	y2	y3
x1	1.00	0.72	0.63	0.30	0.26	0.22	0.17	0.14	0.12	0.22	0.18	0.14
x2	0.72	1.00	0.56	0.27	0.23	0.19	0.15	0.13	0.10	0.19	0.16	0.13
x3	0.63	0.56	1.00	0.24	0.20	0.17	0.13	0.11	0.09	0.17	0.14	0.11
x4	0.30	0.27	0.24	1.00	0.42	0.35	0.13	0.11	0.09	0.13	0.10	0.08
x5	0.26	0.23	0.20	0.42	1.00	0.30	0.12	0.10	0.08	0.11	0.09	0.07
x6	0.22	0.19	0.17	0.35	0.30	1.00	0.10	0.08	0.06	0.09	0.08	0.06
x7	0.17	0.15	0.13	0.13	0.12	0.10	1.00	0.30	0.24	0.07	0.06	0.05
x8	0.14	0.13	0.11	0.11	0.10	0.08	0.30	1.00	0.20	0.06	0.05	0.04
x9	0.12	0.10	0.09	0.09	0.08	0.06	0.24	0.20	1.00	0.05	0.04	0.03
y1	0.22	0.19	0.17	0.13	0.11	0.09	0.07	0.06	0.05	1.00	0.30	0.24
y2	0.18	0.16	0.14	0.10	0.09	0.08	0.06	0.05	0.04	0.30	1.00	0.20
y3	0.14	0.13	0.11	0.08	0.07	0.06	0.05	0.04	0.03	0.24	0.20	1.00

Data with this structure may be created using the `sim.structure` function, and shown either with the numeric values or symbolically using the `structure.graph` function (Figure 7).

```

> fxs <- structure.list(9, list(X1 = c(1, 2, 3), X2 = c(4, 5, 6),
+       X3 = c(7, 8, 9)))
> phi <- phi.list(4, list(F1 = c(4), F2 = c(4), F3 = c(4), F4 = c(1,
+       2, 3)))
> fyx <- structure.list(3, list(Y = c(1, 2, 3)), "Y")

```

2.4.5 A hierarchical structure among the latent predictors.

Measures of intelligence and psychopathology frequently have a general factor as well as multiple group factors. The general factor then is thought to predict some dependent latent variable. Compare this with the previous model (see Figure 7).

These two models can be compared using structural modeling procedures (see below).

3 Exploratory functions for analyzing structure

Given correlation matrices such as those seen above for congeneric or bifactor models, the question becomes how best to estimate the underlying structure. Because these data sets

```
> sg3 <- structure.graph(fxs, phi, fyx)
```

Structural model

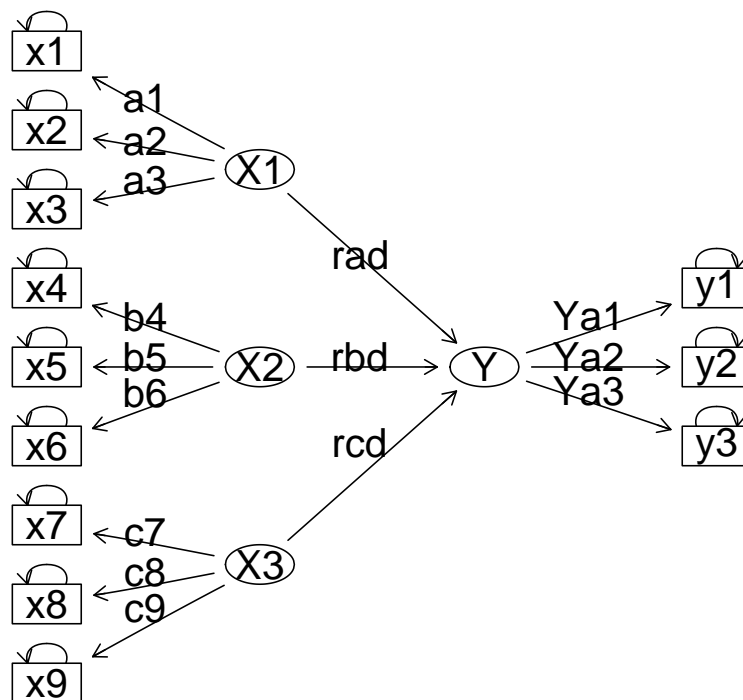


Figure 7: A symbolic structural model. Three independent latent variables are regressed on a latent Y.

Structural model

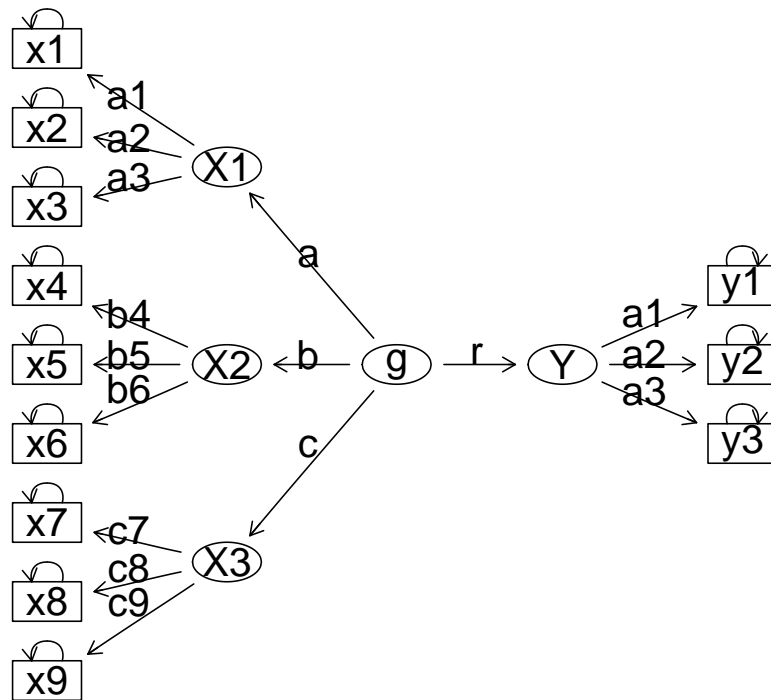


Figure 8: A symbolic structural model with a general factor and three group factors. The general factor is regressed on the latent Y variable.

were generated from a known model, the question becomes how well does a particular model recover the underlying structure.

3.1 Exploratory simple structure models

The technique of *principal components* provides a set of weighted linear composites that best approximates a particular correlation or covariance matrix. If these are then *rotated* to provide a more interpretable solution, the components are no longer the *principal* components. The `principal` function will extract the first `n` principal components (default value is 1) and if `n>1`, rotate to *simple structure* using a `varimax`, `quartimin`, or `Promax` criterion.

```
> principal(cong1$model)
```

```
  V  PA1
1 1 0.89
2 2 0.85
3 3 0.80
4 4 0.73
```

```

                PA1
SS loadings    2.69
Proportion Var 0.67
```

Test of the hypothesis that 1 factor is sufficient.

The degrees of freedom for the model is 2 and the fit was 0.14

```
> factor.pa(cong1$model)
```

```
  V  PA1
1 1 0.9
2 2 0.8
3 3 0.7
4 4 0.6
```

```

                PA1
SS loadings    2.30
Proportion Var 0.58
```

Test of the hypothesis that 1 factor is sufficient.

The degrees of freedom for the model is 2 and the fit was 0

It is important to note that although the `principal` components function does not exactly reproduce the model parameters, the `factor.pa` function, implementing principal axes factor analysis, does.

Consider the case of three underlying factors as seen in the bifactor example above. Because the number of observations is not specified, there is no associated χ^2 value. The `factor.congruence` function reports the cosine of the angle between the factors.

```
> pc3 <- principal(bifact, 3)
> pa3 <- factor.pa(bifact, 3)
> ml3 <- factanal(covmat = bifact, factors = 3)
> pc3
```

	V	PC1	PC3	PC2
V1	1	0.82		
V2	2	0.82		
V3	3	0.82		
V4	4	0.32	0.68	
V5	5		0.70	
V6	6		0.77	
V7	7			0.66
V8	8			0.68
V9	9			0.71

		PC1	PC3	PC2
SS loadings		2.26	1.73	1.53
Proportion Var		0.25	0.19	0.17
Cumulative Var		0.25	0.44	0.61

Test of the hypothesis that 3 factors are sufficient.

The degrees of freedom for the model is 12 and the fit was 0.71

```
> pa3
```

	V	PA1	PA3	PA2
V1	1	0.78	-0.34	
V2	2	0.70	-0.30	
V3	3	0.61		
V4	4		-0.63	
V5	5		-0.54	

V6	6	-0.45
V7	7	0.55
V8	8	0.47
V9	9	0.37

	PA1	PA3	PA2
SS loadings	1.66	1.21	0.93
Proportion Var	0.18	0.13	0.10
Cumulative Var	0.18	0.32	0.42

Test of the hypothesis that 3 factors are sufficient.

The degrees of freedom for the model is 12 and the fit was 0

> ml3

Call:

factanal(factors = 3, covmat = bifact)

Uniquenesses:

V1	V2	V3	V4	V5	V6	V7	V8	V9
0.19	0.36	0.51	0.51	0.64	0.75	0.64	0.75	0.84

Loadings:

	Factor1	Factor2	Factor3
V1	0.785	0.336	0.286
V2	0.697	0.298	0.254
V3	0.610	0.261	0.222
V4	0.242	0.631	0.182
V5	0.207	0.541	0.156
V6	0.173	0.451	0.130
V7	0.167	0.148	0.557
V8	0.139	0.124	0.464
V9	0.112		0.371

	Factor1	Factor2	Factor3
SS loadings	1.666	1.212	0.933
Proportion Var	0.185	0.135	0.104
Cumulative Var	0.185	0.320	0.423

The degrees of freedom for the model is 12 and the fit was 0

```
> factor.congruence(pc3, pa3)
```

	PA1	PA3	PA2
PC1	0.99	-0.70	0.65
PC3	0.57	-0.96	0.51
PC2	0.45	-0.43	0.95

```
> factor.congruence(pa3, ml3)
```

	Factor1	Factor2	Factor3
PA1	1.00	0.72	0.67
PA3	-0.72	-1.00	-0.63
PA2	0.67	0.63	1.00

By default, all three of these procedures use the varimax rotation criterion. Perhaps it is useful to apply an oblique transformation such as **Promax** or **oblimin** to the results. The **Promax** function in *psych* differs slightly from the standard **promax** in that it reports the factor intercorrelations.

```
> ml3p <- Promax(ml3)
```

```
> ml3p
```

	V	Factor1	Factor2	Factor3
V1	1	0.8329		
V2	2	0.7403		
V3	3	0.6478		
V4	4		0.6913	
V5	5		0.5925	
V6	6		0.4938	
V7	7			0.598
V8	8			0.498
V9	9			0.399

	Factor1	Factor2	Factor3
SS loadings	1.66	1.08	0.77
Proportion Var	0.18	0.12	0.09
Cumulative Var	0.18	0.30	0.39

With factor correlations of

	Factor1	Factor2	Factor3
Factor1	1.00	0.67	0.59
Factor2	0.67	1.00	0.55
Factor3	0.59	0.55	1.00

3.2 Exploratory hierarchical models

In addition to the conventional oblique factor model, an alternative model is to consider the correlations between the factors to represent a higher order factor. This can be shown either as a *bifactor* solution Holzinger and Swineford (1937); Schmid and Leiman (1957) with a general factor for all variables and a set of residualized group factors, or as a hierarchical structure. An exploratory hierarchical model can be applied to this kind of data structure using the `omega` function. Graphic options include drawing a Schmid - Leiman bifactor solution (Figure 9) or drawing a hierarchical factor solution f(Figure 10).

3.2.1 A bifactor solution

```
> om.bi <- omega(bifact)
```

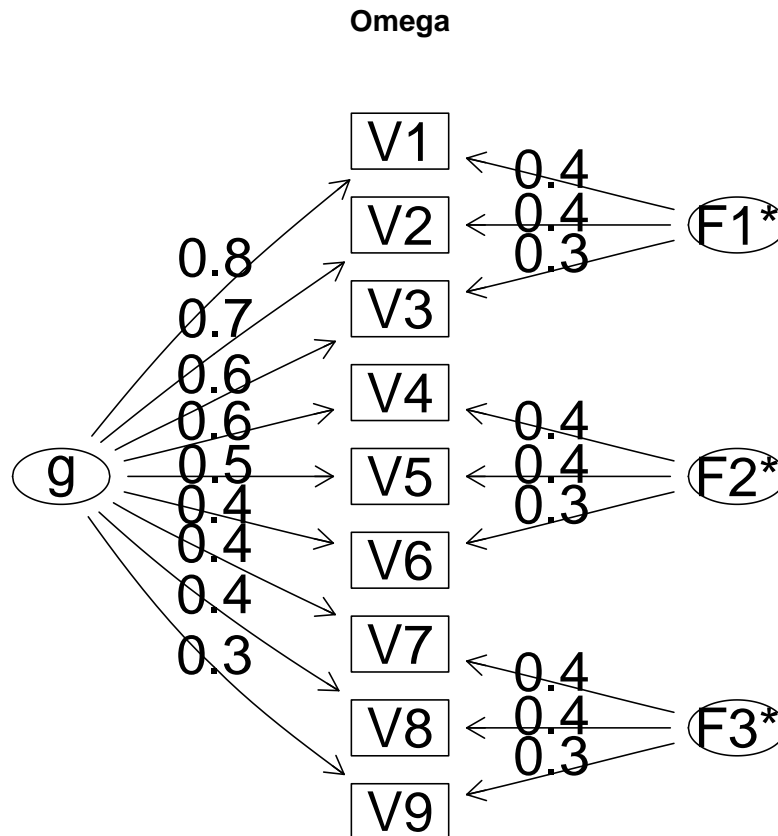


Figure 9: An exploratory bifactor solution to the nine variable problem

The *bifactor* solution has a general factor loading for each variable as well as a set of residual group factors. This approach has been used extensively in the measurement of ability and has more recently been used in the measure of psychopathology (Reise et al., 2007). Data sets included in the `bifactor` data include the original (Holzinger and Swineford, 1937) data set (`holzinger`) as well as a set from Reise et al. (2007) (`reise`) and a nine variable problem from Thurstone.

3.2.2 A hierarchical solution

```
> om.hi <- omega(bifact, sl = FALSE)
```

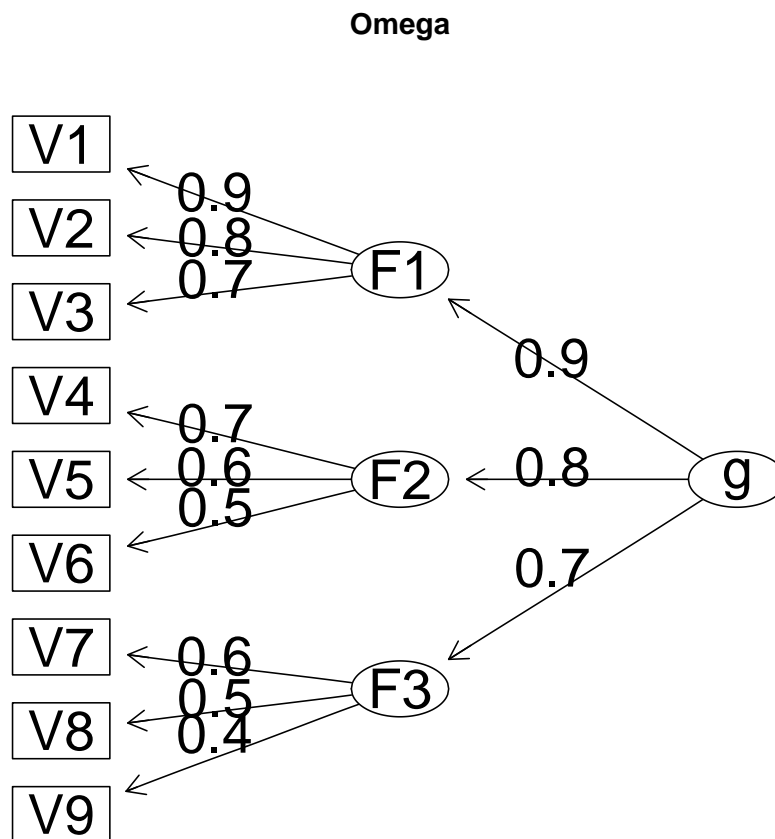


Figure 10: An exploratory hierarchical solution to the nine variable problem.

Both of these graphical representations are reflected in the output of the `omega` function. The first was done using a Schmid-Leiman transformation, the second was not. As will be

seen later, the objects returned from these two analyses may be used as models for a `sem` analysis. It is also useful to examine the estimates of reliability reported by `omega`.

```
> om.bi
```

```
Omega
Call: omega(m = bifact)
Alpha: 0.79
G.6: 0.79
Omega Hierarchical: 0.72
Omega Total 0.83
```

```
Schmid Leiman Factor loadings greater than 0.2
```

	g	F1*	F2*	F3*	h2	u2
V1	0.81	0.39			0.81	
V2	0.72	0.35			0.64	0.36
V3	0.63	0.31			0.49	0.51
V4	0.56		0.42		0.49	0.51
V5	0.48		0.36		0.36	0.64
V6	0.40		0.30		0.25	0.75
V7	0.42			0.43	0.36	0.64
V8	0.35			0.36	0.25	0.75
V9	0.28			0.29		0.84

```
With eigenvalues of:
```

	g	F1*	F2*	F3*
	2.65	0.37	0.40	0.40

```
general/max 6.66 max/min = 1.08
```

```
The degrees of freedom for the model is 12 and the fit was 0
```

Yet one more way to treat the hierarchical structure of a data set is to consider hierarchical cluster analysis using the ICLUST algorithm (Figure 11). ICLUST is most appropriate for forming item composites.

4 Confirmatory models

Although the exploratory models shown above do estimate the goodness of fit of the model and compare the residual matrix to a zero matrix using a χ^2 statistic, they estimate more parameters than are necessary if there is indeed a simple structure, and they do not allow for tests of competing models. The `sem` function in the `sem` package by John Fox allows

Hierarchical cluster analysis of bifact data

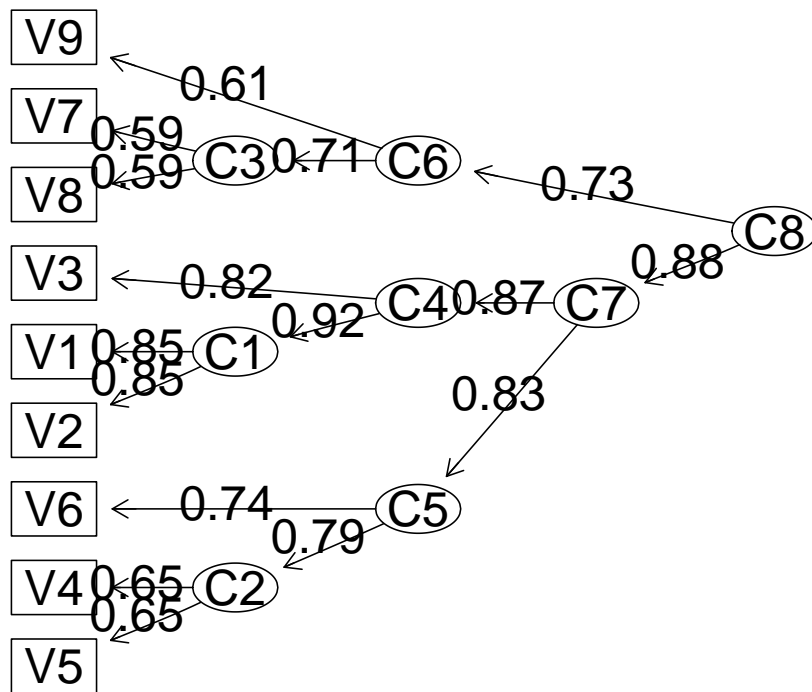


Figure 11: A hierarchical cluster analysis of the bifact data set using ICLUST

for confirmatory tests. The interested reader is referred to the *sem* manual for more detail (Fox, 2009).

4.1 Using psych as a front end for the sem package

Because preparation of the **sem** commands is a bit tedious, several of the *psych* package functions have been designed to provide the appropriate commands. That is, the functions **structure.list**, **phi.list**, **structure.graph**, **structure.sem**, and **omega.graph** may be used as a front end to **sem**. Usually with no modification, but sometimes with just slight modification, the model output from the **structure.graph**, **structure.sem**, and **omega.graph** functions is meant to provide the appropriate commands for **sem**.

4.2 Testing a congeneric model versus a tau equivalent model

The congeneric model is a one factor model with possibly unequal factor loadings. The tau equivalent model is one with equal factor loadings. Tests for these may be done by creating the appropriate structures. Either the **structure.graph** function which requires **Rgraphviz** or the **structure.sem** function which does not may be used.

The following example tests the hypothesis (which is actually false) that the correlations found in the cong data set (see 2.1) are tau equivalent. Because the variable labels in that data set were V1 ... V4, we specify the labels to match those.

```
> library(sem)
> mod.tau <- structure.graph(c("a", "a", "a", "a"), labels = paste("V",
+ 1:4, sep = ""))
> mod.tau
```

	Path	Parameter	StartValue
1	X1->V1	a	
2	X1->V2	a	
3	X1->V3	a	
4	X1->V4	a	
5	V1<->V1	x1e	
6	V2<->V2	x2e	
7	V3<->V3	x3e	
8	V4<->V4	x4e	
9	X1<->X1	<fixed>	1

```
> sem.tau <- sem(mod.tau, cong, 100)
> summary(sem.tau, digits = 2)
```

```

Model Chisquare = 6.6 Df = 5 Pr(>Chisq) = 0.25
Chisquare (null model) = 105 Df = 6
Goodness-of-fit index = 0.97
Adjusted goodness-of-fit index = 0.94
RMSEA index = 0.057 90% CI: (NA, 0.16)
Bentler-Bonnett NFI = 0.94
Tucker-Lewis NNFI = 0.98
Bentler CFI = 0.98
SRMR = 0.07
BIC = -16

```

Normalized Residuals

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
-1.030	-0.442	-0.250	-0.079	0.527	0.888

Parameter Estimates

	Estimate	Std Error	z value	Pr(> z)	
a	0.69	0.064	10.8	0.0e+00	V1 <--- X1
x1e	0.43	0.082	5.2	1.8e-07	V1 <--> V1
x2e	0.56	0.098	5.7	1.5e-08	V2 <--> V2
x3e	0.58	0.101	5.7	1.1e-08	V3 <--> V3
x4e	0.59	0.103	5.8	8.3e-09	V4 <--> V4

```
Iterations = 10
```

Test whether the data are congeneric. That is, whether a one factor model fits. Compare this to the prior model using the `anova` function.

```

> mod.cong <- structure.sem(c("a", "b", "c", "d"), labels = paste("V",
+ 1:4, sep = ""))
> mod.cong

```

	Path	Parameter	StartValue
1	X1->V1	a	
2	X1->V2	b	
3	X1->V3	c	
4	X1->V4	d	
5	V1<->V1	x1e	
6	V2<->V2	x2e	
7	V3<->V3	x3e	
8	V4<->V4	x4e	
9	X1<->X1	<fixed>	1

```
> sem.cong <- sem(mod.cong, cong, 100)
> summary(sem.cong, digits = 2)

Model Chisquare = 2.9 Df = 2 Pr(>Chisq) = 0.23
Chisquare (null model) = 105 Df = 6
Goodness-of-fit index = 0.99
Adjusted goodness-of-fit index = 0.93
RMSEA index = 0.069 90% CI: (NA, 0.22)
Bentler-Bonnett NFI = 0.97
Tucker-Lewis NNFI = 0.97
Bentler CFI = 1
SRMR = 0.03
BIC = -6.3
```

Normalized Residuals

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
-0.574	-0.070	0.034	0.011	0.160	0.541

Parameter Estimates

	Estimate	Std Error	z value	Pr(> z)	
a	0.83	0.098	8.4	0.0e+00	V1 <--- X1
b	0.66	0.100	6.6	3.4e-11	V2 <--- X1
c	0.63	0.102	6.2	6.4e-10	V3 <--- X1
d	0.59	0.105	5.7	1.5e-08	V4 <--- X1
x1e	0.31	0.101	3.1	2.1e-03	V1 <--> V1
x2e	0.56	0.100	5.6	2.1e-08	V2 <--> V2
x3e	0.61	0.104	5.8	6.5e-09	V3 <--> V3
x4e	0.65	0.111	5.9	4.7e-09	V4 <--> V4

Iterations = 12

```
> anova(sem.cong, sem.tau)
```

LR Test for Difference Between Models

	Model	Df	Model	Chisq	Df	LR	Chisq	Pr(>Chisq)
Model 1	2	2.9417						
Model 2	5	6.5935	3	3.6518			0.3016	

The anova comparison of the congeneric versus tau equivalent model shows that the change in χ^2 is significant given the change in degrees of freedom.

4.3 Testing the dimensionality of a hierarchical data set by creating the model

The bifactor correlation matrix was created to represent a hierarchical structure. Various confirmatory models can be applied to this matrix.

The first example creates the model directly, the next several create models based upon exploratory factor analyses. `mod.one` is a congeneric model of one factor accounting for the relationships between the nine variables. Although not correct, with 100 subjects, this model can not be rejected. However, an examination of the residuals suggests serious problems with the model.

```
> mod.one <- structure.sem(letters[1:9], labels = paste("V", 1:9,
+      sep = ""))
> mod.one
```

	Path	Parameter	StartValue
1	X1->V1	a	
2	X1->V2	b	
3	X1->V3	c	
4	X1->V4	d	
5	X1->V5	e	
6	X1->V6	f	
7	X1->V7	g	
8	X1->V8	h	
9	X1->V9	i	
10	V1<->V1	x1e	
11	V2<->V2	x2e	
12	V3<->V3	x3e	
13	V4<->V4	x4e	
14	V5<->V5	x5e	
15	V6<->V6	x6e	
16	V7<->V7	x7e	
17	V8<->V8	x8e	
18	V9<->V9	x9e	
19	X1<->X1	<fixed>	1

```
> sem.one <- sem(mod.one, bifactor, 100)
> summary(sem.one, digits = 2)
```

```
Model Chisquare = 19   Df = 27 Pr(>Chisq) = 0.88
Chisquare (null model) = 235   Df = 36
Goodness-of-fit index = 0.96
```

Adjusted goodness-of-fit index = 0.93
 RMSEA index = 0 90% CI: (NA, 0.040)
 Bentler-Bonnett NFI = 0.92
 Tucker-Lewis NNFI = 1.1
 Bentler CFI = 1
 SRMR = 0.053
 BIC = -106

Normalized Residuals

	Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
	-2.7e-01	-1.8e-01	-1.4e-06	1.4e-01	1.2e-01	1.6e+00

Parameter Estimates

	Estimate	Std Error	z value	Pr(> z)	
a	0.88	0.084	10.5	0.0e+00	V1 <--- X1
b	0.80	0.088	9.1	0.0e+00	V2 <--- X1
c	0.70	0.092	7.6	3.8e-14	V3 <--- X1
d	0.54	0.099	5.5	4.9e-08	V4 <--- X1
e	0.47	0.101	4.6	3.5e-06	V5 <--- X1
f	0.39	0.103	3.8	1.3e-04	V6 <--- X1
g	0.40	0.103	3.9	8.3e-05	V7 <--- X1
h	0.34	0.104	3.3	1.1e-03	V8 <--- X1
i	0.27	0.105	2.6	9.1e-03	V9 <--- X1
x1e	0.23	0.061	3.7	2.4e-04	V1 <--> V1
x2e	0.36	0.069	5.3	1.1e-07	V2 <--> V2
x3e	0.51	0.084	6.1	1.0e-09	V3 <--> V3
x4e	0.71	0.107	6.6	4.1e-11	V4 <--> V4
x5e	0.78	0.116	6.7	1.6e-11	V5 <--> V5
x6e	0.84	0.123	6.8	7.5e-12	V6 <--> V6
x7e	0.84	0.122	6.8	7.9e-12	V7 <--> V7
x8e	0.88	0.128	6.9	5.0e-12	V8 <--> V8
x9e	0.92	0.133	7.0	3.5e-12	V9 <--> V9

Iterations = 14

> round(residuals(sem.one), 2)

	V1	V2	V3	V4	V5	V6	V7	V8	V9
V1	0.00	0.02	0.02	-0.02	-0.02	-0.02	-0.02	-0.02	-0.01
V2	0.02	0.00	0.00	-0.03	-0.03	-0.03	-0.02	-0.02	-0.02
V3	0.02	0.00	0.00	-0.02	-0.03	-0.02	-0.02	-0.02	-0.02
V4	-0.02	-0.03	-0.02	0.00	0.17	0.14	0.02	0.01	0.01


```

V5 -0.02 -0.03 -0.03  0.17  0.00  0.11  0.01  0.01  0.01
V6 -0.02 -0.03 -0.02  0.14  0.11  0.00  0.01  0.01  0.00
V7 -0.02 -0.02 -0.02  0.02  0.01  0.01  0.00  0.16  0.13
V8 -0.02 -0.02 -0.02  0.01  0.01  0.01  0.16  0.00  0.11
V9 -0.01 -0.02 -0.02  0.01  0.01  0.00  0.13  0.11  0.00

```

4.4 Testing the dimensionality based upon an exploratory analysis

Alternatively, the output from an exploratory factor analysis can be used as input to the `structure.sem` function.

```

> f1 <- factanal(covmat = bifact, factors = 1)
> mod.f1 <- structure.sem(f1)
> sem.f1 <- sem(mod.f1, bifact, 100)
> sem.f1

Model Chisquare = 18.72871 Df = 27

      V1      V2      V3      V4      V5      V6      V7      V8
0.8801449 0.7978613 0.6986695 0.5401625 0.4691098 0.3944311 0.4036073 0.3400459
      V9      x1e      x2e      x3e      x4e      x5e      x6e      x7e
0.2742160 0.2253461 0.3634188 0.5118600 0.7082243 0.7799344 0.8444243 0.8371012
      x8e      x9e
0.8843691 0.9248059

Iterations = 14

```

The answers are, of course, identical.

4.5 Specifying a three factor model

An alternative model is to extract three factors and try this solution. The `factor.pa` factor analysis function is used to detect the structure. Alternatively, the `factanal` could have been used.

```

> f3 <- factor.pa(bifact, 3)
> mod.f3 <- structure.sem(f3)
> sem.f3 <- sem(mod.f3, bifact, 100)
> summary(sem.f3, digits = 2)

Model Chisquare = 49 Df = 26 Pr(>Chisq) = 0.0037
Chisquare (null model) = 235 Df = 36

```

Goodness-of-fit index = 0.9
 Adjusted goodness-of-fit index = 0.82
 RMSEA index = 0.095 90% CI: (0.053, 0.14)
 Bentler-Bonnett NFI = 0.79
 Tucker-Lewis NNFI = 0.84
 Bentler CFI = 0.88
 SRMR = 0.20
 BIC = -70

Normalized Residuals

	Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
	-2.0e-05	1.9e-05	1.8e+00	1.7e+00	2.6e+00	4.0e+00

Parameter Estimates

	Estimate	Std Error	z value	Pr(> z)	
F1V1	0.79	0.094	8.4	0.0e+00	V1 <--- PA1
F2V1	0.23	0.089	2.6	1.0e-02	V1 <--- PA3
F1V2	0.80	0.093	8.6	0.0e+00	V2 <--- PA1
F1V3	0.70	0.095	7.4	1.7e-13	V3 <--- PA1
F2V4	0.70	0.129	5.4	6.1e-08	V4 <--- PA3
F2V5	0.60	0.124	4.8	1.2e-06	V5 <--- PA3
F2V6	0.50	0.120	4.2	3.1e-05	V6 <--- PA3
F3V7	0.60	0.190	3.2	1.5e-03	V7 <--- PA2
F3V8	0.50	0.167	3.0	2.8e-03	V8 <--- PA2
F3V9	0.40	0.147	2.7	6.5e-03	V9 <--- PA2
x1e	0.19	0.074	2.6	8.5e-03	V1 <--> V1
x2e	0.36	0.085	4.2	2.5e-05	V2 <--> V2
x3e	0.51	0.089	5.7	1.2e-08	V3 <--> V3
x4e	0.51	0.152	3.4	7.8e-04	V4 <--> V4
x5e	0.64	0.136	4.7	2.4e-06	V5 <--> V5
x6e	0.75	0.130	5.8	8.3e-09	V6 <--> V6
x7e	0.64	0.219	2.9	3.5e-03	V7 <--> V7
x8e	0.75	0.175	4.3	1.8e-05	V8 <--> V8
x9e	0.84	0.149	5.6	1.6e-08	V9 <--> V9

Iterations = 34

> round(residuals(sem.f3), 2)

	V1	V2	V3	V4	V5	V6	V7	V8	V9
V1	0.13	0.09	0.08	0.29	0.25	0.21	0.34	0.28	0.23
V2	0.09	0.00	0.00	0.40	0.35	0.29	0.30	0.25	0.20

```

V3 0.08 0.00 0.00 0.35 0.30 0.25 0.26 0.22 0.18
V4 0.29 0.40 0.35 0.00 0.00 0.00 0.24 0.20 0.16
V5 0.25 0.35 0.30 0.00 0.00 0.00 0.20 0.17 0.13
V6 0.21 0.29 0.25 0.00 0.00 0.00 0.17 0.14 0.11
V7 0.34 0.30 0.26 0.24 0.20 0.17 0.00 0.00 0.00
V8 0.28 0.25 0.22 0.20 0.17 0.14 0.00 0.00 0.00
V9 0.23 0.20 0.18 0.16 0.13 0.11 0.00 0.00 0.00

```

The residuals show serious problems with this model. Although the residuals within each of the three factors are zero, the residuals between groups are much too large.

4.6 Allowing for an oblique solution

That solution is clearly very bad. What would happen if the exploratory solution were allowed to have correlated (oblique) factors? This analysis is done on a sample of size 100 with the bifactor structure created by `sim.hierarchical`.

```

> set.seed(42)
> bifact.s <- sim.hierarchical()
> f3 <- factor.pa(bifact.s, 3)
> f3.p <- Promax(f3)
> mod.f3p <- structure.sem(f3.p)
> mod.f3p

```

	Path	Parameter	StartValue
1	PA1->V1	F1V1	
2	PA1->V2	F1V2	
3	PA1->V3	F1V3	
4	PA3->V4	F2V4	
5	PA3->V5	F2V5	
6	PA3->V6	F2V6	
7	PA2->V7	F3V7	
8	PA2->V8	F3V8	
9	PA2->V9	F3V9	
10	V1<->V1	x1e	
11	V2<->V2	x2e	
12	V3<->V3	x3e	
13	V4<->V4	x4e	
14	V5<->V5	x5e	
15	V6<->V6	x6e	
16	V7<->V7	x7e	

```

17 V8<->V8    x8e
18 V9<->V9    x9e
19 PA3<->PA1  rF2F1
20 PA2<->PA1  rF3F1
21 PA2<->PA3  rF3F2
22 PA1<->PA1  <fixed>    1
23 PA3<->PA3  <fixed>    1
24 PA2<->PA2  <fixed>    1

```

Unfortunately, the model as created automatically by `structure.sem` is not identified and would fail to converge if run. The problem is that the covariances between items on different factors is a product of the factor loadings and the between factor covariance. Multiplying the factor loadings by a constant can be compensated for by dividing the between factor covariances by the same constant. Thus, one of these paths must be fixed to provide a scale for the solution. That is, it is necessary to fix some of the paths to set values in order to properly identify the model. This can be done using the `edit` function and hand modification of particular paths. Set one path for each latent variable to be fixed.

e.g.,

```
mod.adjusted <- edit(mod.f3p)
```

Alternatively, the model can be adjusted by specifying the changes directly.

When this is done

```

> mod.f3p.adjusted <- mod.f3p
> mod.f3p.adjusted[c(1, 4), 2] <- NA
> mod.f3p.adjusted[c(1, 4), 3] <- "1"
> sem.f3p.adjusted <- sem(mod.f3p.adjusted, bifact.s, 100)
> summary(sem.f3p.adjusted, digits = 2)

```

```

Model Chisquare =  7.1   Df =  26 Pr(>Chisq) = 1
Chisquare (null model) = 235   Df =  36
Goodness-of-fit index =  0.99
Adjusted goodness-of-fit index =  0.98
RMSEA index =  0   90% CI: (NA, NA)
Bentler-Bonnett NFI =  0.97
Tucker-Lewis NNFI =  1.1
Bentler CFI =  1
SRMR =  0.12
BIC =  -113

```

Normalized Residuals

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
-1.97	-0.79	-0.51	-0.67	-0.34	-0.11

Parameter Estimates

	Estimate	Std Error	z value	Pr(> z)	
F1V2	0.87	0.089	9.8	0.0e+00	V2 <--- PA1
F1V3	0.76	0.094	8.1	6.7e-16	V3 <--- PA1
F2V5	0.65	0.124	5.2	1.7e-07	V5 <--- PA3
F2V6	0.55	0.126	4.4	1.4e-05	V6 <--- PA3
F3V7	0.63	0.134	4.7	2.5e-06	V7 <--- PA2
F3V8	0.52	0.131	4.0	5.9e-05	V8 <--- PA2
F3V9	0.42	0.131	3.2	1.3e-03	V9 <--- PA2
x1e	0.18	0.063	2.8	4.7e-03	V1 <--> V1
x2e	0.37	0.071	5.1	3.0e-07	V2 <--> V2
x3e	0.51	0.084	6.1	1.1e-09	V3 <--> V3
x4e	0.39	0.125	3.1	1.8e-03	V4 <--> V4
x5e	0.67	0.117	5.8	7.2e-09	V5 <--> V5
x6e	0.77	0.122	6.3	2.8e-10	V6 <--> V6
x7e	0.64	0.143	4.5	7.8e-06	V7 <--> V7
x8e	0.75	0.135	5.6	2.7e-08	V8 <--> V8
x9e	0.84	0.135	6.2	5.3e-10	V9 <--> V9
rF2F1	0.73	0.081	9.0	0.0e+00	PA1 <--> PA3
rF3F1	0.67	0.113	5.9	3.1e-09	PA1 <--> PA2
rF3F2	0.58	0.144	4.1	4.7e-05	PA3 <--> PA2

Iterations = 21

The structure being tested may be seen using `structure.graph`

4.7 Extract a bifactor solution using omega and then test that model using sem

A bifactor solution has previously been shown (Figure 9). The output from the `omega` function includes the sem commands for the analysis. As an example of doing this with real rather than simulated data, consider 9 variables from Thurstone. For completeness, the `std.coef` from `sem` is used as well as the `summary` function.

Structural model

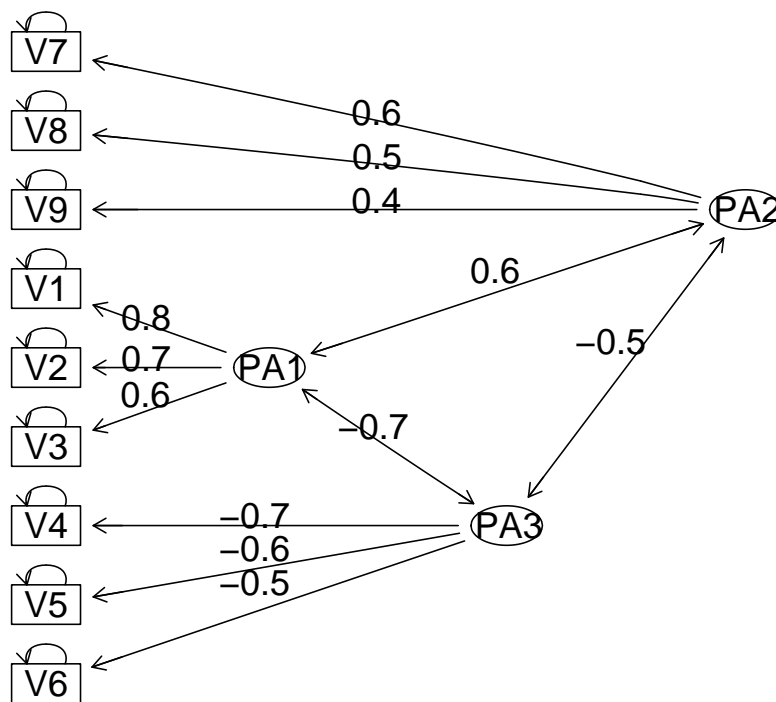


Figure 12: A three factor, oblique solution.

4.7.1 sem of Thurstone 9 variable problem

The sem manual includes an example of a hierarchical solution to 9 mental abilities originally reported by Thurstone and used in the SAS manual for PROC CALIS and discussed in detail by McDonald (1999). The data matrix, as reported by Fox may be found in the **bifactor** data set. Using the commands just shown, it is possible to analyze this data set using a bifactor solution (Figure 13).

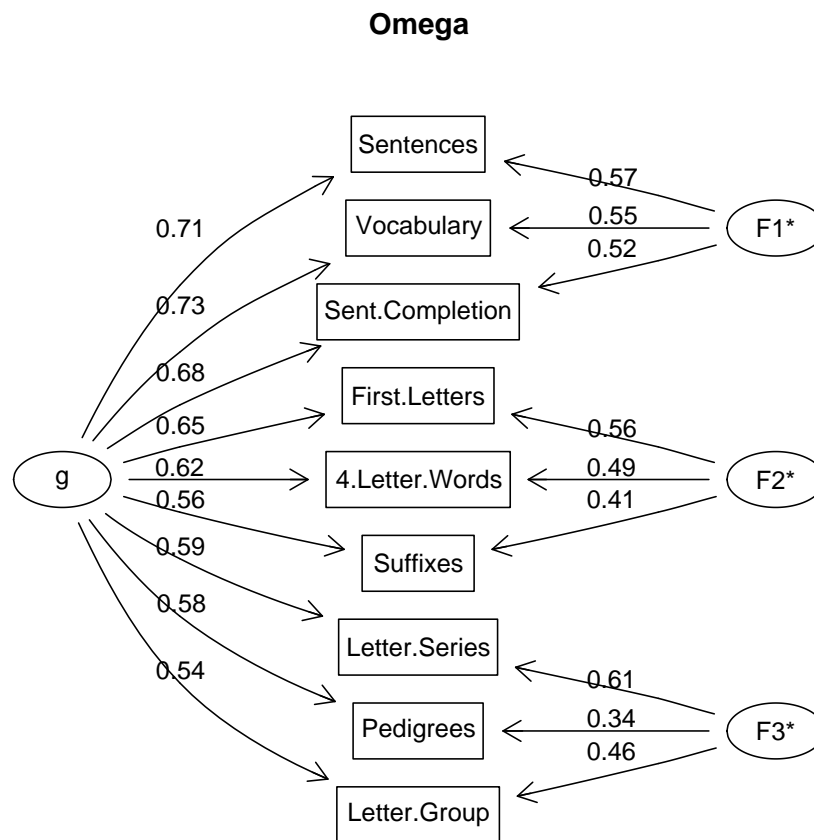


Figure 13: A bifactor solution to the Thurstone 9 variable problem. All items load on a general factor of ability, the residual factors account for the correlations between items within groups.

```
> sem.bi <- sem(om.th.bi$model, Thurstone, 213)
> summary(sem.bi, digits = 2)
```

Model Chisquare = 24 Df = 18 Pr(>Chisq) = 0.15
 Chisquare (null model) = 1102 Df = 36
 Goodness-of-fit index = 0.98
 Adjusted goodness-of-fit index = 0.94
 RMSEA index = 0.04 90% CI: (NA, 0.078)
 Bentler-Bonnett NFI = 0.98
 Tucker-Lewis NNFI = 0.99
 Bentler CFI = 1
 SRMR = 0.035
 BIC = -72

Normalized Residuals

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
-8.2e-01	-3.3e-01	-8.9e-07	2.8e-02	1.6e-01	1.8e+00

Parameter Estimates

	Estimate	Std Error	z value	Pr(> z)
Sentences	0.77	0.073	10.57	0.0e+00
Vocabulary	0.79	0.072	10.92	0.0e+00
Sent.Completion	0.75	0.073	10.27	0.0e+00
First.Letters	0.61	0.072	8.43	0.0e+00
4.Letter.Words	0.60	0.074	8.09	6.7e-16
Suffixes	0.57	0.071	8.00	1.3e-15
Letter.Series	0.57	0.074	7.63	2.3e-14
Pedigrees	0.66	0.069	9.55	0.0e+00
Letter.Group	0.53	0.079	6.71	2.0e-11
F1*Sentences	0.49	0.085	5.71	1.1e-08
F1*Vocabulary	0.45	0.090	5.00	5.7e-07
F1*Sent.Completion	0.40	0.093	4.33	1.5e-05
F2*First.Letters	0.61	0.086	7.16	8.2e-13
F2*4.Letter.Words	0.51	0.085	5.96	2.5e-09
F2*Suffixes	0.39	0.078	5.04	4.7e-07
F3*Letter.Series	0.73	0.159	4.56	5.1e-06
F3*Pedigrees	0.25	0.089	2.77	5.6e-03
F3*Letter.Group	0.41	0.122	3.35	8.1e-04
e1	0.17	0.034	5.05	4.4e-07
e2	0.17	0.030	5.65	1.6e-08
e3	0.27	0.033	8.09	6.7e-16
e4	0.25	0.079	3.18	1.5e-03
e5	0.39	0.063	6.13	8.8e-10
e6	0.52	0.060	8.68	0.0e+00

e7	0.15	0.223	0.67	5.0e-01
e8	0.50	0.060	8.39	0.0e+00
e9	0.55	0.085	6.51	7.4e-11

Sentences	Sentences <--- g
Vocabulary	Vocabulary <--- g
Sent.Completion	Sent.Completion <--- g
First.Letters	First.Letters <--- g
4.Letter.Words	4.Letter.Words <--- g
Suffixes	Suffixes <--- g
Letter.Series	Letter.Series <--- g
Pedigrees	Pedigrees <--- g
Letter.Group	Letter.Group <--- g
F1*Sentences	Sentences <--- F1*
F1*Vocabulary	Vocabulary <--- F1*
F1*Sent.Completion	Sent.Completion <--- F1*
F2*First.Letters	First.Letters <--- F2*
F2*4.Letter.Words	4.Letter.Words <--- F2*
F2*Suffixes	Suffixes <--- F2*
F3*Letter.Series	Letter.Series <--- F3*
F3*Pedigrees	Pedigrees <--- F3*
F3*Letter.Group	Letter.Group <--- F3*
e1	Sentences <--> Sentences
e2	Vocabulary <--> Vocabulary
e3	Sent.Completion <--> Sent.Completion
e4	First.Letters <--> First.Letters
e5	4.Letter.Words <--> 4.Letter.Words
e6	Suffixes <--> Suffixes
e7	Letter.Series <--> Letter.Series
e8	Pedigrees <--> Pedigrees
e9	Letter.Group <--> Letter.Group

Iterations = 72

> std.coef(sem.bi, digits = 2)

		Std. Estimate	
Sentences	Sentences	0.77	Sentences <--- g
Vocabulary	Vocabulary	0.79	Vocabulary <--- g
Sent.Completion	Sent.Completion	0.75	Sent.Completion <--- g
First.Letters	First.Letters	0.61	First.Letters <--- g
4.Letter.Words	4.Letter.Words	0.60	4.Letter.Words <--- g

Suffixes	Suffixes	0.57	Suffixes <--- g
Letter.Series	Letter.Series	0.57	Letter.Series <--- g
Pedigrees	Pedigrees	0.66	Pedigrees <--- g
Letter.Group	Letter.Group	0.53	Letter.Group <--- g
F1*Sentences	F1*Sentences	0.49	Sentences <--- F1*
F1*Vocabulary	F1*Vocabulary	0.45	Vocabulary <--- F1*
F1*Sent.Completion	F1*Sent.Completion	0.40	Sent.Completion <--- F1*
F2*First.Letters	F2*First.Letters	0.61	First.Letters <--- F2*
F2*4.Letter.Words	F2*4.Letter.Words	0.51	4.Letter.Words <--- F2*
F2*Suffixes	F2*Suffixes	0.39	Suffixes <--- F2*
F3*Letter.Series	F3*Letter.Series	0.73	Letter.Series <--- F3*
F3*Pedigrees	F3*Pedigrees	0.25	Pedigrees <--- F3*
F3*Letter.Group	F3*Letter.Group	0.41	Letter.Group <--- F3*

Compare this solution to the one reported below, and to the sem manual.

4.8 Examining a hierarchical solution

A hierarchical solution to this data set was previously found by the `omega` function (Figure 10). The output of that analysis can be used as a model for a `sem` analysis. Once again, the `std.coef` function helps see the structure. Alternatively, using the `omega` function on the Thurstone data (in the `bifactor` data set) will create the model for this particular data set.

```
> sem.hi <- sem(om.hi$model, Thurstone, 213)
> summary(sem.hi, digits = 2)

Model Chisquare = 38   Df = 24 Pr(>Chisq) = 0.033
Chisquare (null model) = 1102   Df = 36
Goodness-of-fit index = 0.96
Adjusted goodness-of-fit index = 0.92
RMSEA index = 0.053   90% CI: (0.015, 0.083)
Bentler-Bonnett NFI = 0.97
Tucker-Lewis NNFI = 0.98
Bentler CFI = 0.99
SRMR = 0.044
BIC = -90

Normalized Residuals
      Min.  1st Qu.   Median     Mean  3rd Qu.    Max.
-9.7e-01 -4.2e-01 -1.3e-06  4.0e-02  9.4e-02  1.6e+00
```

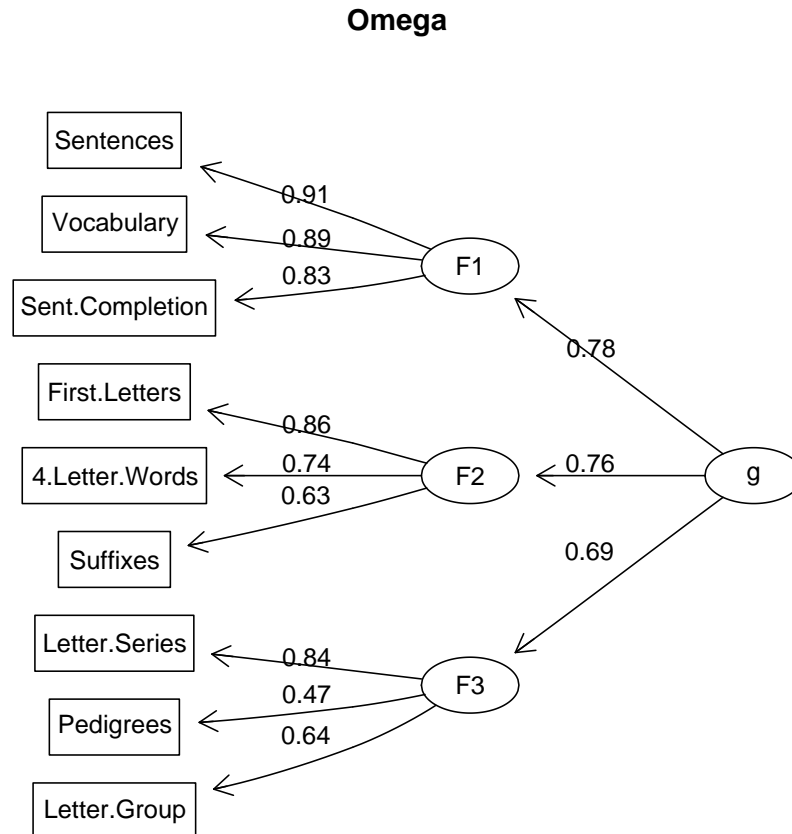


Figure 14: Hierarchical analysis of the Thurstone 9 variable problem using an exploratory algorithm can provide the appropriate sem code for analysis using the sem package.

Parameter Estimates

	Estimate	Std Error	z value	Pr(> z)
gF1	1.44	0.264	5.5	4.6e-08
gF2	1.25	0.217	5.8	7.1e-09
gF3	1.41	0.279	5.0	4.8e-07
F1Sentences	0.52	0.065	7.9	2.2e-15
F1Vocabulary	0.52	0.065	8.0	1.3e-15
F1Sent.Completion	0.49	0.062	7.8	5.8e-15
F2First.Letters	0.52	0.063	8.3	2.2e-16
F24.Letter.Words	0.50	0.060	8.3	0.0e+00
F2Suffixes	0.44	0.056	7.8	8.7e-15
F3Letter.Series	0.45	0.071	6.3	2.3e-10
F3Pedigrees	0.42	0.061	6.8	8.1e-12
F3Letter.Group	0.41	0.065	6.3	2.7e-10
e1	0.18	0.028	6.4	1.7e-10
e2	0.16	0.028	5.9	3.0e-09
e3	0.27	0.033	8.0	1.6e-15
e4	0.30	0.051	5.9	2.7e-09
e5	0.36	0.052	7.0	3.4e-12
e6	0.51	0.060	8.4	0.0e+00
e7	0.39	0.062	6.3	2.3e-10
e8	0.48	0.065	7.4	1.8e-13
e9	0.51	0.065	7.7	9.5e-15

gF1	F1 <--- g
gF2	F2 <--- g
gF3	F3 <--- g
F1Sentences	Sentences <--- F1
F1Vocabulary	Vocabulary <--- F1
F1Sent.Completion	Sent.Completion <--- F1
F2First.Letters	First.Letters <--- F2
F24.Letter.Words	4.Letter.Words <--- F2
F2Suffixes	Suffixes <--- F2
F3Letter.Series	Letter.Series <--- F3
F3Pedigrees	Pedigrees <--- F3
F3Letter.Group	Letter.Group <--- F3
e1	Sentences <--> Sentences
e2	Vocabulary <--> Vocabulary
e3	Sent.Completion <--> Sent.Completion
e4	First.Letters <--> First.Letters

```
e5          4.Letter.Words <--> 4.Letter.Words
e6          Suffixes <--> Suffixes
e7          Letter.Series <--> Letter.Series
e8          Pedigrees <--> Pedigrees
e9          Letter.Group <--> Letter.Group
```

```
Iterations = 53
```

```
> std.coef(sem.hi, digits = 2)
```

		Std. Estimate	
gF1	gF1	0.82	F1 <--- g
gF2	gF2	0.78	F2 <--- g
gF3	gF3	0.82	F3 <--- g
F1Sentences	F1Sentences	0.90	Sentences <--- F1
F1Vocabulary	F1Vocabulary	0.91	Vocabulary <--- F1
F1Sent.Completion	F1Sent.Completion	0.86	Sent.Completion <--- F1
F2First.Letters	F2First.Letters	0.84	First.Letters <--- F2
F24.Letter.Words	F24.Letter.Words	0.80	4.Letter.Words <--- F2
F2Suffixes	F2Suffixes	0.70	Suffixes <--- F2
F3Letter.Series	F3Letter.Series	0.78	Letter.Series <--- F3
F3Pedigrees	F3Pedigrees	0.72	Pedigrees <--- F3
F3Letter.Group	F3Letter.Group	0.70	Letter.Group <--- F3

```
> anova(sem.hi, sem.bi)
```

```
LR Test for Difference Between Models
```

	Model	Df	Model	Chisq	Df	LR	Chisq	Pr(>Chisq)
Model 1	24	38.196						
Model 2	18	24.216	6	13.980	0.02986	*		

```
---
```

```
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Using the Thurstone data set, we see what happens when a hierarchical model is applied to real data. The exploratory structure derived from the `omega` function (Figure 14) provides estimates in close approximation to those found using `sem`. The model definition created by using `omega` is the same hierarchical model discussed in the `sem` help page. The *bifactor* model, with 6 more parameters does provide a better fit to the data than the hierarchical model.

Similar analyses can be done with other data that are organized hierarchically. Examples of these analyses are analyzing the 14 variables of `holzinger` and the 16 variables of `reise`. The output from the following analyses has been limited to just the comparison between

the bifactor and hierarchical solutions.

```
> data(bifactor)
> om.holz.bi <- omega(Holzinger, 4)
> sem.holz.bi <- sem(om.holz.bi$model, Holzinger, 355)
> om.holz.hi <- omega(Holzinger, 4, sl = FALSE)
> sem.holz.hi <- sem(om.holz.hi$model, Holzinger, 355)
> anova(sem.holz.bi, sem.holz.hi)
```

LR Test for Difference Between Models

	Model	Df	Model	Chisq	Df	LR	Chisq	Pr(>Chisq)
Model 1		63		147.179				
Model 2		73		183.047	10	35.868	8.868e-05	***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1								

5 Summary and conclusion

The use of exploratory and confirmatory models for understanding real data structures is an important advance in psychological research. To understand these approaches it is helpful to try them first on “baby” data sets. To the extent that the models we use can be tested on simple, artificial examples, it is perhaps easier to practice their application. The *psych* tools for simulating structural models and for specifying models are a useful supplement to the power of packages such as *sem*. The techniques that can be used on simulated data set can also be applied to real data sets.

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