

# Using the psych package to generate and test structural models

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# 1 The psych package

## 1.1 Preface

The *psych* package (Revelle, 2010) 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](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 (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, *sem* is required for these examples. Although *Rgraphviz* had been used for the graphical displays, it has now been replaced with graphical functions within *psych*. 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.

The `sim` functions include:

**sim.structure** A function to combine a measurement and structural model into one data matrix. Useful for understanding structural equation models. Combined with `structure.diagram` to see the proposed structure.

**sim.congeneric** A function to create congeneric items/tests for demonstrating classical test theory. This is just a special case of `sim.structure`.

**sim.hierarchical** A function to create data with a hierarchical (bifactor) structure.

**sim.item** A function to create items that either have a simple structure or a circumplex structure.

**sim.circ** Create data with a circumplex structure.

**sim.dichot** Create dichotomous item data with a simple or circumplex structure.

**sim.minor** Create a factor structure for `nvar` variables defined by `nfact` major factors and  $\frac{nvar}{2}$  “minor” factors for `n` observations.

**sim.parallel** Create a number of simulated data sets using `sim.minor` to show how parallel analysis works.

**sim.rasch** Create IRT data following a Rasch model.

**sim.irt** Create a two parameter IRT logistic (2PL) model.

**sim.anova** Simulate a 3 way balanced ANOVA or linear model, with or without repeated measures.

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  $\tau$  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(.8,.8,.8,.8)) #population values
> tau.samp <- sim.congeneric(loads=c(.8,.8,.8,.8),N=100) # sample correlation matrix for 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(.8,.8,.8,.8),N=100, short=FALSE)
> tau.samp

Call: NULL

$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

> #plot.new()
> m1 <- structure.diagram(c("a","b","c","d"))
```

### Structural model

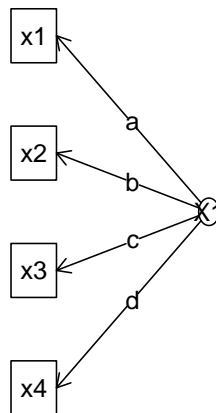


Figure 1: Tau equivalent tests are special cases of congeneric tests. Tau equivalence assumes  $a=b=c=d$

## 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 \(1937\)](#) (`holzinger`), a second is a nine variable problem adapted by [Bechtoldt \(1961\)](#) 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(.9,.8,.7),nrow=3)
> fload <- matrix(c(.9,.8,.7,rep(0,9)),.7,.6,.5,
+ rep(0,9),.6,.5,.4), ncol=3)
> fload #echo it to see the structure

      [,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 panel A) or *hierarchical* (Figure 2 Panel B) factor solution. The analysis was done with the `omega` function.

### 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 3

### 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

```

> 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))

```

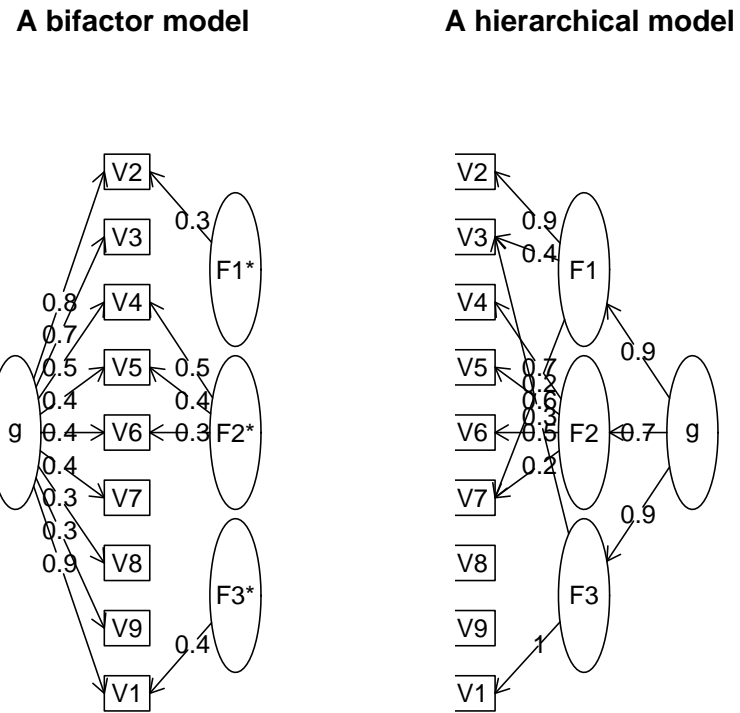


Figure 2: (Left panel) A bifactor solution represents each test in terms of a general factor and a residualized group factor. (Right Panel) A hierarchical factor solution has  $g$  as a second order factor accounting for the correlations between the first order factors

```

> circ <- sim.circ(16)
> f2 <- fa(circ,2)
> plot(f2,title="16 simulated variables in a circumplex pattern")

```

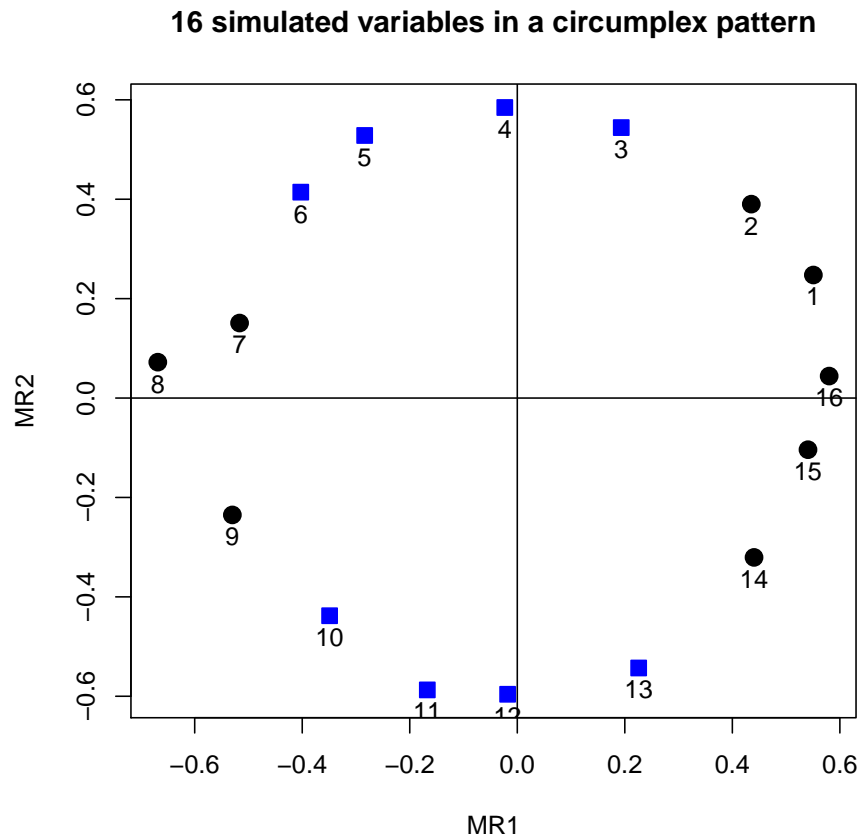


Figure 3: Emotion items or interpersonal items frequently show a circumplex structure. Data generated by `sim.circ` and factor loadings found by the principal axis algorithm using `factor.pa`.

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(.9,.8,.7,.6)
> cong1 <- sim.structure(fx)
> cong1
```

Call: sim.structure(fx = fx)

```
$model (Population correlation matrix)
      V1  V2  V3  V4
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(.9,.8,.7,rep(0,9),.7,.6,.5,rep(0,9),.6,.5,.4), ncol=3)
> three.fact <- sim.structure(fx)
> three.fact
```

Call: sim.structure(fx = fx)

```
$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
```

### Structural model

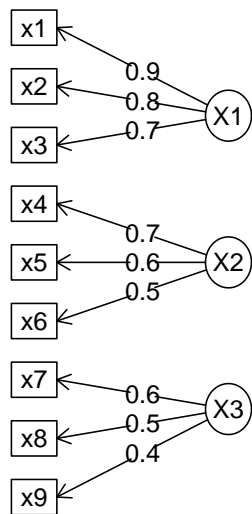


Figure 4: Three uncorrelated factors generated using the `sim.structure` function and drawn using `structure.diagram`.

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

```
> Phi = matrix(c(1,.5,.3,.5,1,.2,.3,.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
[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

Call: sim.structure(fx = fx, Phi = Phi)

$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 to 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 #show the matrix
```

```
      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"
```

```
> Phis #show this one as well
```

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

The `structure.list` and `phi.list` functions allow 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 `fa` (Principal axis or minimum residual (minres) 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(fa(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(.9,.8,.7,rep(0,9),.7,.6,.5,rep(0,9),.6,.5,.4), ncol=3)
```

```

> #plot.new()
> corf3.mod <- structure.diagram(fxs,Phis)

```

### Structural model

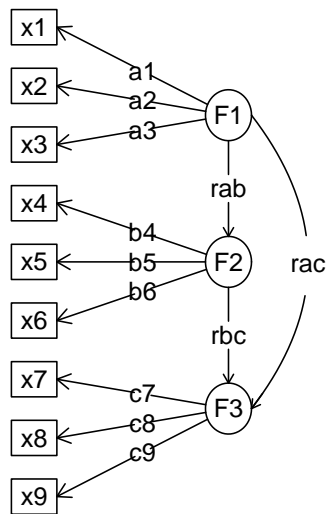


Figure 5: Three correlated factors with symbolic paths. Created using `structure.diagram` and `structure.list` and `phi.list` for ease of input.

```

> #plot.new()
> mod.f3p <- structure.diagram(f3.p,cut=.2)

```

### Structural model

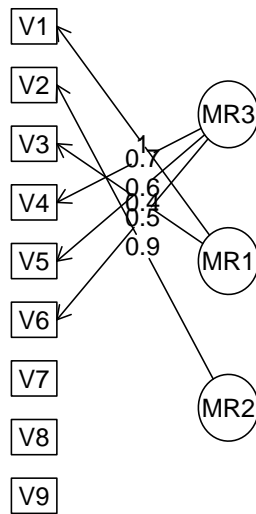


Figure 6: The empirically fitted structural model. Paths less than cut (.2 in this case, the default is .3) are not shown.

```

> fy <- c(.6,.5,.4)
> Phi <- matrix(c(1,.48,.32,.4,.48,1,.32,.3,.32,.32,1,.2,.4,.3,.2,1), ncol=4)
> 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.diagram` 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

```

> #plot.new()
> sg3 <- structure.diagram(fxs,phi,fyx)

```

### Structural model

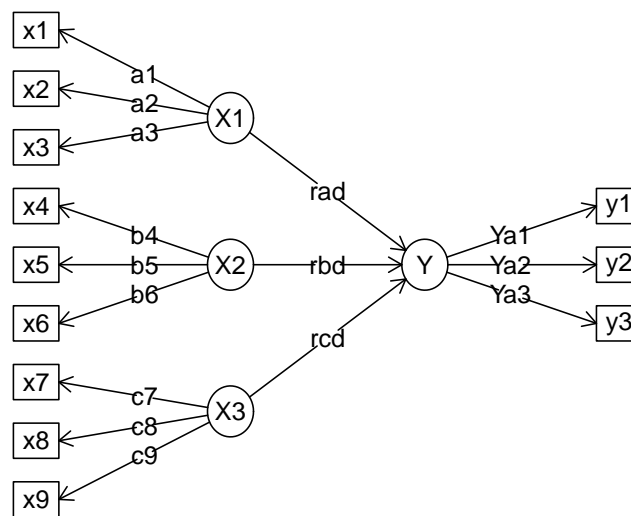


Figure 7: A symbolic structural model. Three independent latent variables are regressed on a latent Y.

```

> fxh <- structure.list(9,list(X1=c(1:3),X2=c(4:6),X3=c(7:9),g=NULL))
> fy <- structure.list(3,list(Y=c(1,2,3)))
> Phi <- diag(1,5,5)
> Phi[4,c(1:3)] <- letters[1:3]
> Phi[5,4] <- "r"
> #plot.new()
> hi.mod <-structure.diagram(fxh,Phi, fy)

```

### Structural model

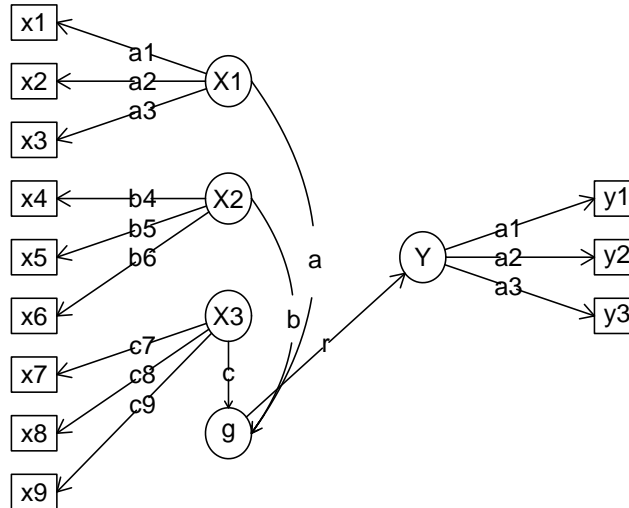


Figure 8: A symbolic structural model with a general factor and three group factors. The general factor is regressed on the latent  $Y$  variable.

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)
```

```
Principal Components Analysis
```

```
Call: principal(r = cong1$model)
```

```
Standardized loadings based upon correlation matrix
```

	PC1	h2	u2
1	0.89	0.80	0.20
2	0.85	0.73	0.27
3	0.80	0.64	0.36
4	0.73	0.53	0.47

	PC1
SS loadings	2.69
Proportion Var	0.67

```
Test of the hypothesis that 1 factor is sufficient.
```

```
The degrees of freedom for the null model are 6 and the objective function was 1.65  
The degrees of freedom for the model are 2 and the objective function was 0.14
```

```
Fit based upon off diagonal values = 0.96
```

```
> fa(cong1$model)
```

```
Factor Analysis using method = minres
```

```
Call: fac(r = r, nfactors = nfactors, n.obs = n.obs, rotate = rotate,  
  scores = scores, residuals = residuals, SMC = SMC, missing = FALSE,  
  impute = impute, min.err = min.err, max.iter = max.iter,  
  symmetric = symmetric, warnings = warnings, fm = fm, alpha = alpha)
```

```
Standardized loadings based upon correlation matrix
```

	MR1	h2	u2
V1	0.9	0.81	0.19
V2	0.8	0.64	0.36
V3	0.7	0.49	0.51
V4	0.6	0.36	0.64

	MR1
SS loadings	2.30
Proportion Var	0.57

Test of the hypothesis that 1 factor is sufficient.

The degrees of freedom for the null model are 6 and the objective function was 1.65  
 The degrees of freedom for the model are 2 and the objective function was 0

The root mean square of the residuals is 0  
 The df corrected root mean square of the residuals is 0

Fit based upon off diagonal values = 1  
 Measures of factor score adequacy

	MR1
Correlation of scores with factors	0.94
Multiple R square of scores with factors	0.88
Minimum correlation of possible factor scores	0.77

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 or minimum residual (minres) 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  $\chi^2$  value. The `factor.congruence` function reports the cosine of the angle between the factors.

```
> pc3 <- principal(bifact,3)
> pa3 <- fa(bifact,3,fm="pa")
> ml3 <- fa(bifact,3,fm="ml")
> pc3
```

Principal Components Analysis

Call: `principal(r = bifact, nfactors = 3)`

Standardized loadings based upon correlation matrix

	RC1	RC3	RC2	h2	u2
V1	0.82	0.29	0.22	0.80	0.20

```

V2 0.82 0.23 0.18 0.75 0.25
V3 0.82 0.15 0.12 0.71 0.29
V4 0.32 0.68 0.13 0.58 0.42
V5 0.22 0.70 0.10 0.56 0.44
V6 0.08 0.77 0.08 0.60 0.40
V7 0.24 0.12 0.66 0.51 0.49
V8 0.16 0.08 0.68 0.50 0.50
V9 0.03 0.08 0.71 0.51 0.49

```

```

          RC1  RC3  RC2
SS loadings    2.25 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 null model are 36 and the objective function was 2.37  
The degrees of freedom for the model are 12 and the objective function was 0.71

Fit based upon off diagonal values = 0.9

> pa3

Factor Analysis using method = pa

```

Call: fac(r = r, nfactors = nfactors, n.obs = n.obs, rotate = rotate,
  scores = scores, residuals = residuals, SMC = SMC, missing = FALSE,
  impute = impute, min.err = min.err, max.iter = max.iter,
  symmetric = symmetric, warnings = warnings, fm = fm, alpha = alpha)

```

Standardized loadings based upon correlation matrix

```

  PA1 PA3 PA2  h2  u2
V1 0.9 0.0 0.00 0.81 0.19
V2 0.8 0.0 0.00 0.64 0.36
V3 0.7 0.0 0.00 0.49 0.51
V4 0.0 0.7 0.00 0.49 0.51
V5 0.0 0.6 0.00 0.36 0.64
V6 0.0 0.5 0.00 0.25 0.75
V7 0.0 0.0 0.59 0.36 0.64
V8 0.0 0.0 0.50 0.25 0.75
V9 0.0 0.0 0.40 0.16 0.84

```

```

          PA1  PA3  PA2
SS loadings    1.94 1.10 0.77

```

Proportion Var 0.22 0.12 0.09  
Cumulative Var 0.22 0.34 0.42

With factor correlations of  
PA1 PA3 PA2  
PA1 1.00 0.72 0.63  
PA3 0.72 1.00 0.56  
PA2 0.63 0.56 1.00

Test of the hypothesis that 3 factors are sufficient.

The degrees of freedom for the null model are 36 and the objective function was 2.37  
The degrees of freedom for the model are 12 and the objective function was 0

The root mean square of the residuals is 0  
The df corrected root mean square of the residuals is 0

Fit based upon off diagonal values = 1  
Measures of factor score adequacy

	PA1	PA3	PA2
Correlation of scores with factors	0.94	0.86	0.79
Multiple R square of scores with factors	0.88	0.73	0.63
Minimum correlation of possible factor scores	0.77	0.47	0.25

> ml3

Factor Analysis using method = ml  
Call: fac(r = r, nfactors = nfactors, n.obs = n.obs, rotate = rotate,  
scores = scores, residuals = residuals, SMC = SMC, missing = FALSE,  
impute = impute, min.err = min.err, max.iter = max.iter,  
symmetric = symmetric, warnings = warnings, fm = fm, alpha = alpha)

Standardized loadings based upon correlation matrix

	ML1	ML2	ML3	h2	u2
V1	0.9	0.0	0.0	0.81	0.19
V2	0.8	0.0	0.0	0.64	0.36
V3	0.7	0.0	0.0	0.49	0.51
V4	0.0	0.7	0.0	0.49	0.51
V5	0.0	0.6	0.0	0.36	0.64
V6	0.0	0.5	0.0	0.25	0.75
V7	0.0	0.0	0.6	0.36	0.64
V8	0.0	0.0	0.5	0.25	0.75
V9	0.0	0.0	0.4	0.16	0.84

	ML1	ML2	ML3
SS loadings	1.94	1.10	0.77
Proportion Var	0.22	0.12	0.09
Cumulative Var	0.22	0.34	0.42

With factor correlations of

	ML1	ML2	ML3
ML1	1.00	0.72	0.63
ML2	0.72	1.00	0.56
ML3	0.63	0.56	1.00

Test of the hypothesis that 3 factors are sufficient.

The degrees of freedom for the null model are 36 and the objective function was 2.37  
 The degrees of freedom for the model are 12 and the objective function was 0

The root mean square of the residuals is 0

The df corrected root mean square of the residuals is 0

Fit based upon off diagonal values = 1

Measures of factor score adequacy

	ML1	ML2	ML3
Correlation of scores with factors	0.94	0.86	0.79
Multiple R square of scores with factors	0.89	0.73	0.63
Minimum correlation of possible factor scores	0.77	0.47	0.25

> factor.congruence(list(pc3,pa3,ml3))

	RC1	RC3	RC2	PA1	PA3	PA2	ML1	ML2	ML3
RC1	1.00	0.52	0.42	0.94	0.25	0.18	0.94	0.25	0.18
RC3	0.52	1.00	0.33	0.30	0.93	0.12	0.30	0.93	0.12
RC2	0.42	0.33	1.00	0.24	0.15	0.94	0.24	0.15	0.94
PA1	0.94	0.30	0.24	1.00	0.00	0.00	1.00	0.00	0.00
PA3	0.25	0.93	0.15	0.00	1.00	0.00	0.00	1.00	0.00
PA2	0.18	0.12	0.94	0.00	0.00	1.00	0.00	0.00	1.00
ML1	0.94	0.30	0.24	1.00	0.00	0.00	1.00	0.00	0.00
ML2	0.25	0.93	0.15	0.00	1.00	0.00	0.00	1.00	0.00
ML3	0.18	0.12	0.94	0.00	0.00	1.00	0.00	0.00	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
```

Call: NULL

Standardized loadings based upon correlation matrix

	ML1	ML2	ML3	h2	u2
V1	0.9	0.0	0.0	0.81	0.19
V2	0.8	0.0	0.0	0.64	0.36
V3	0.7	0.0	0.0	0.49	0.51
V4	0.0	0.7	0.0	0.49	0.51
V5	0.0	0.6	0.0	0.36	0.64
V6	0.0	0.5	0.0	0.25	0.75
V7	0.0	0.0	0.6	0.36	0.64
V8	0.0	0.0	0.5	0.25	0.75
V9	0.0	0.0	0.4	0.16	0.84

	ML1	ML2	ML3
SS loadings	1.94	1.10	0.77
Proportion Var	0.22	0.12	0.09
Cumulative Var	0.22	0.34	0.42

With factor correlations of

	ML1	ML2	ML3
ML1	1	0	0
ML2	0	1	0
ML3	0	0	1

## 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)
```

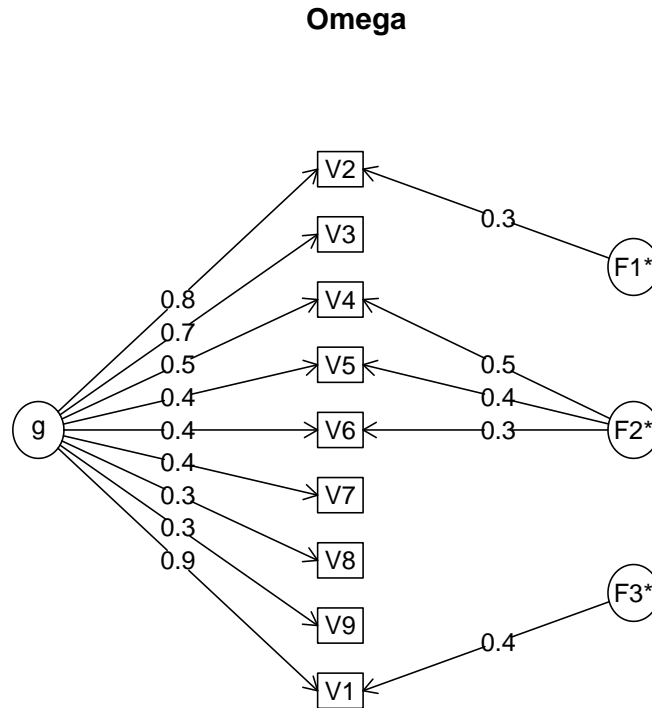


Figure 9: An exploratory bifactor solution to the nine variable problem

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)
```

### Omega

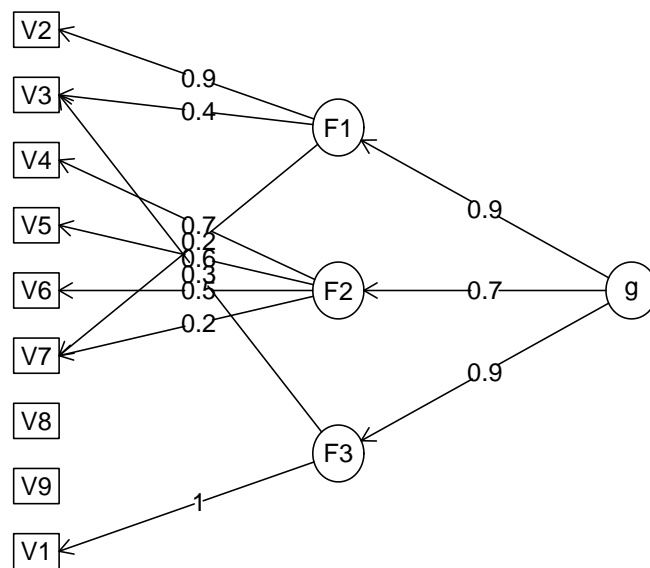


Figure 10: An exploratory hierarchical solution to the nine variable problem.

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: omegah(m = m, nfactors = nfactors, fm = fm, key = key, flip = flip,
  digits = digits, title = title, sl = sl, labels = labels,
  plot = plot, n.obs = n.obs, rotate = rotate, Phi = Phi, option = option)
```

```
Alpha: 0.79
```

```
G.6: 0.79
```

```
Omega Hierarchical: 0.69
```

```
Omega H asymptotic: 0.84
```

```
Omega Total 0.82
```

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

	g	F1*	F2*	F3*	h2	u2	p2
V1	0.90			0.40	0.98	0.02	0.84
V2	0.80	0.32			0.73	0.27	0.86
V3	0.65				0.46	0.54	0.93
V4	0.50		0.47		0.47	0.53	0.53
V5	0.43		0.42		0.36	0.64	0.51
V6	0.36		0.35		0.25	0.75	0.51
V7	0.37				0.17	0.83	0.82
V8	0.32				0.12	0.88	0.81
V9	0.25				0.08	0.92	0.80

```
With eigenvalues of:
```

	g	F1*	F2*	F3*
	2.74	0.13	0.58	0.17

```
general/max 4.73 max/min = 4.32
```

```
mean percent general = 0.73 with sd = 0.17 and cv of 0.23
```

```
The degrees of freedom are 12 and the fit is 0.07
```

```
The root mean square of the residuals is 0.03
```

```
The df corrected root mean square of the residuals is 0.07
```

```
Compare this with the adequacy of just a general factor and no group factors
```

The degrees of freedom for just the general factor are 27 and the fit is 0.21

The root mean square of the residuals is 0.05

The df corrected root mean square of the residuals is 0.08

Measures of factor score adequacy

	g	F1*	F2*	F3*
Correlation of scores with factors	0.94	0.47	0.67	0.62
Multiple R square of scores with factors	0.88	0.22	0.45	0.39
Minimum correlation of factor score estimates	0.75	-0.55	-0.11	-0.22

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  $\chi^2$  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 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.diagram`, `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.diagram`, `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 model is one with equal factor loadings. Tests for these may be done by creating the appropriate structures. The `structure.graph` function which requires

### Hierarchical cluster analysis of bifact data

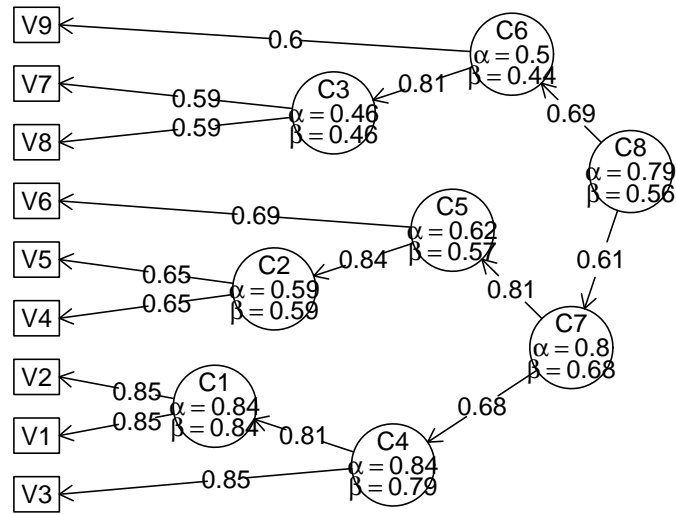


Figure 11: A hierarchical cluster analysis of the bifact data set using ICLUST

Rgraphviz, or `structure.diagram` or the `structure.sem` functions which do 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.sem(c("a","a","a","a"),labels=paste("V",1:4,sep=""))
> mod.tau #show it
```

	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.
	-1.03	-0.44	-0.25	-0.08	0.53	0.89

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 #show the model

```

```

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 = 0.99
SRMR = 0.03
BIC = -6.3

```

Normalized Residuals

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
-0.57	-0.07	0.03	0.01	0.16	0.54

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) #test the difference between the two models
```

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  $\chi^2$  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 #show the model
```

	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,bifact,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, 0.04)
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.
-0.27  -0.18   0.00   0.14   0.12   1.61

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 `fa` factor analysis function (using the *minimum residual* algorithm) is used to detect the structure. Alternatively, the `factanal` could have been used.

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

Model Chisquare = 38 Df = 27 Pr(>Chisq) = 0.071  
 Chisquare (null model) = 235 Df = 36  
 Goodness-of-fit index = 0.9  
 Adjusted goodness-of-fit index = 0.84  
 RMSEA index = 0.065 90% CI: (NA, 0.11)  
 Bentler-Bonnett NFI = 0.84  
 Tucker-Lewis NNFI = 0.92  
 Bentler CFI = 0.94  
 SRMR = 0.15  
 BIC = -86

### Normalized Residuals

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
0.0	0.0	1.1	1.1	2.0	3.4

### Parameter Estimates

	Estimate	Std Error	z value	Pr(> z )	
F2V1	1.02	NaN	NaN	NaN	V1 <--- MR1
F3V2	0.80	0.091	8.8	0.0e+00	V2 <--- MR3
F3V3	0.70	0.094	7.5	7.1e-14	V3 <--- MR3
F1V4	0.70	0.110	6.4	1.7e-10	V4 <--- MR2

```

F1V5    0.60    0.110    5.5    4.3e-08    V5 <--- MR2
F1V6    0.50    0.111    4.5    7.2e-06    V6 <--- MR2
x1e     -0.04     NaN     NaN         NaN    V1 <--> V1
x2e      0.36    0.080    4.5    7.1e-06    V2 <--> V2
x3e      0.51    0.087    5.9    3.8e-09    V3 <--> V3
x4e      0.51    0.118    4.3    1.5e-05    V4 <--> V4
x5e      0.64    0.117    5.5    4.3e-08    V5 <--> V5
x6e      0.75    0.122    6.1    8.6e-10    V6 <--> V6
x7e      1.00    0.142    7.0    2.0e-12    V7 <--> V7
x8e      1.00    0.142    7.0    2.0e-12    V8 <--> V8
x9e      1.00    0.142    7.0    2.0e-12    V9 <--> V9
rF2F1   0.64     NaN     NaN         NaN    MR2 <--> MR1
rF3F1   0.72    0.104    6.9    5.1e-12    MR2 <--> MR3
rF3F2   0.88     NaN     NaN         NaN    MR1 <--> MR3

```

```
Iterations = 18
```

```
Aliased parameters: F2V1 x1e rF2F1 rF3F2
```

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

```

      V1  V2  V3  V4  V5  V6  V7  V8  V9
V1 0.00 0.00 0.00 0.00 0.00 0.00 0.34 0.28 0.23
V2 0.00 0.00 0.00 0.00 0.00 0.00 0.30 0.25 0.20
V3 0.00 0.00 0.00 0.00 0.00 0.00 0.26 0.22 0.18
V4 0.00 0.00 0.00 0.00 0.00 0.00 0.24 0.20 0.16
V5 0.00 0.00 0.00 0.00 0.00 0.00 0.20 0.17 0.13
V6 0.00 0.00 0.00 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 0.30 0.24
V8 0.28 0.25 0.22 0.20 0.17 0.14 0.30 0.00 0.20
V9 0.23 0.20 0.18 0.16 0.13 0.11 0.24 0.20 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() #create the data, use the sample correlation matrix
> f3 <- fa(bifact.s,3)          #extract three factors and do an oblique rotation
> mod.f3p <- structure.sem(f3.p) #create the sem model
> mod.f3p    #show it

```

	Path	Parameter	StartValue
1	MR1->V1	F2V1	
2	MR2->V2	F3V2	
3	MR1->V3	F2V3	
4	MR3->V4	F1V4	
5	MR3->V5	F1V5	
6	MR3->V6	F1V6	
7	V1<->V1	x1e	
8	V2<->V2	x2e	
9	V3<->V3	x3e	
10	V4<->V4	x4e	
11	V5<->V5	x5e	
12	V6<->V6	x6e	
13	V7<->V7	x7e	
14	V8<->V8	x8e	
15	V9<->V9	x9e	
16	MR3<->MR3	<fixed>	1
17	MR1<->MR1	<fixed>	1
18	MR2<->MR2	<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, bifactor, 100)
> summary(sem.f3p.adjusted, digits=2)

```

```

Model Chisquare = 111 Df = 32 Pr(>Chisq) = 1.2e-10
Chisquare (null model) = 169 Df = 36
Goodness-of-fit index = 0.75
Adjusted goodness-of-fit index = 0.65
RMSEA index = 0.16 90% CI: (NA, NA)
Bentler-Bonnett NFI = 0.34
Tucker-Lewis NNFI = 0.33
Bentler CFI = 0.41
SRMR = 0.22
BIC = -36

```

#### Normalized Residuals

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
-0.5	1.3	2.0	1.9	2.6	5.6

#### Parameter Estimates

	Estimate	Std Error	z value	Pr(> z )	
F3V2	1.0e+00	5.03	2.0e-01	8.4e-01	V2 <--- MR2
F2V3	4.8e-01	0.11	4.3e+00	1.7e-05	V3 <--- MR1
F1V5	4.6e-01	0.13	3.5e+00	4.4e-04	V5 <--- MR3
F1V6	3.8e-01	0.13	3.0e+00	2.5e-03	V6 <--- MR3
x1e	1.3e-06	0.14	8.9e-06	1.0e+00	V1 <--> V1
x2e	6.1e-07	10.06	6.0e-08	1.0e+00	V2 <--> V2
x3e	7.7e-01	0.11	6.7e+00	1.6e-11	V3 <--> V3
x4e	8.0e-02	0.17	4.6e-01	6.5e-01	V4 <--> V4
x5e	8.0e-01	0.13	6.4e+00	1.5e-10	V5 <--> V5
x6e	8.6e-01	0.13	6.7e+00	2.7e-11	V6 <--> V6
x7e	1.0e+00	0.14	7.0e+00	2.0e-12	V7 <--> V7
x8e	1.0e+00	0.14	7.0e+00	2.0e-12	V8 <--> V8
x9e	1.0e+00	0.14	7.0e+00	2.0e-12	V9 <--> V9

Iterations = 21

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

**Structural model**

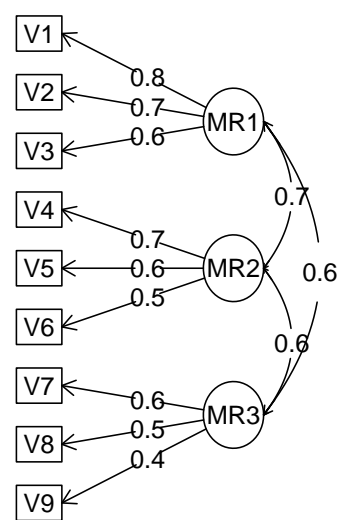


Figure 12: A three factor, oblique solution.

## 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.

### 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).

```
> sem.bi <- sem(om.th.bi$model,Thurstone,213) #use the model created by omega
> 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 = 0.99
SRMR = 0.035
BIC = -72
```

#### Normalized Residuals

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
-0.82	-0.33	0.00	0.03	0.16	1.80

#### 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

## Omega

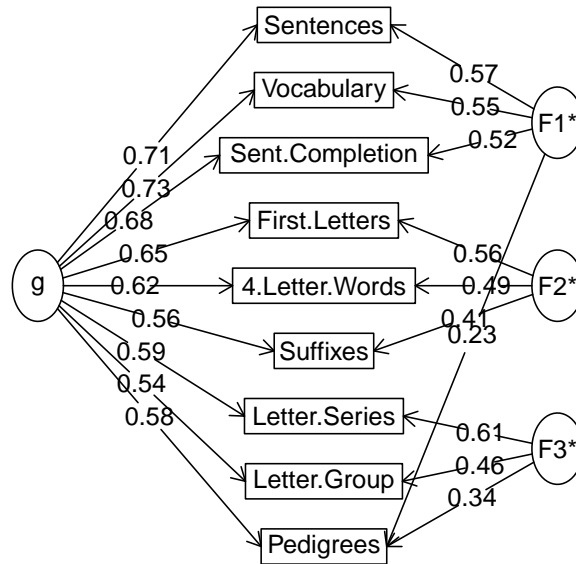


Figure 13: A bifactor solution to the Thurstone 9 variable problem. All items load on a general factor of ability, the residual factors account for the correlations between items within groups.

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	
1	Sentences	0.7678671	Sentences <--- g
2	Vocabulary	0.7909246	Vocabulary <--- g
3	Sent.Completion	0.7536211	Sent.Completion <--- g
4	First.Letters	0.6083814	First.Letters <--- g
5	4.Letter.Words	0.5973349	4.Letter.Words <--- g
6	Suffixes	0.5717900	Suffixes <--- g
7	Letter.Series	0.5668950	Letter.Series <--- g
8	Pedigrees	0.6623317	Pedigrees <--- g
9	Letter.Group	0.5299523	Letter.Group <--- g
10	F1*Sentences	0.4878697	Sentences <--- F1*
11	F1*Vocabulary	0.4523233	Vocabulary <--- F1*
12	F1*Sent.Completion	0.4044507	Sent.Completion <--- F1*
13	F2*First.Letters	0.6140531	First.Letters <--- F2*
14	F2*4.Letter.Words	0.5058063	4.Letter.Words <--- F2*
15	F2*Suffixes	0.3943206	Suffixes <--- F2*
16	F3*Letter.Series	0.7272957	Letter.Series <--- F3*
17	F3*Pedigrees	0.2468418	Pedigrees <--- F3*
18	F3*Letter.Group	0.4091494	Letter.Group <--- F3*
19	e1	0.1723633	Sentences <--> Sentences
20	e2	0.1698418	Vocabulary <--> Vocabulary
21	e3	0.2684748	Sent.Completion <--> Sent.Completion
22	e4	0.2528108	First.Letters <--> First.Letters
23	e5	0.3873510	4.Letter.Words <--> 4.Letter.Words
24	e6	0.5175675	Suffixes <--> Suffixes
25	e7	0.1496710	Letter.Series <--> Letter.Series
26	e8	0.5003859	Pedigrees <--> Pedigrees
27	e9	0.5517473	Letter.Group <--> Letter.Group

28	1.0000000	F1* <--> F1*
29	1.0000000	F2* <--> F2*
30	1.0000000	F3* <--> F3*
31	1.0000000	g <--> g

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.
-0.97	-0.42	0.00	0.04	0.09	1.63

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

## Omega

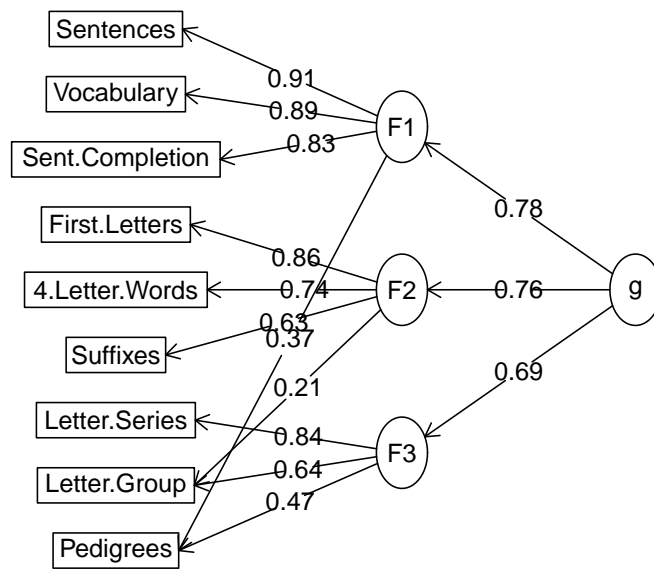


Figure 14: Hierarchical analysis of the Thurstone 9 variable problem using an exploratory algorithm can provide the appropriate sem code for analysis using the sem package.

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	
1	gF1	0.8220756	F1 <--- g
2	gF2	0.7817998	F2 <--- g
3	gF3	0.8150140	F3 <--- g
4	F1Sentences	0.9047110	Sentences <--- F1
5	F1Vocabulary	0.9138215	Vocabulary <--- F1
6	F1Sent.Completion	0.8560765	Sent.Completion <--- F1
7	F2First.Letters	0.8357616	First.Letters <--- F2
8	F24.Letter.Words	0.7971820	4.Letter.Words <--- F2
9	F2Suffixes	0.7025559	Suffixes <--- F2
10	F3Letter.Series	0.7808129	Letter.Series <--- F3
11	F3Pedigrees	0.7201599	Pedigrees <--- F3
12	F3Letter.Group	0.7034902	Letter.Group <--- F3
13	e1	0.1814980	Sentences <--> Sentences
14	e2	0.1649303	Vocabulary <--> Vocabulary
15	e3	0.2671331	Sent.Completion <--> Sent.Completion
16	e4	0.3015025	First.Letters <--> First.Letters
17	e5	0.3645009	4.Letter.Words <--> 4.Letter.Words
18	e6	0.5064152	Suffixes <--> Suffixes
19	e7	0.3903313	Letter.Series <--> Letter.Series
20	e8	0.4813697	Pedigrees <--> Pedigrees
21	e9	0.5051015	Letter.Group <--> Letter.Group
22		0.3241917	F1 <--> F1
23		0.3887891	F2 <--> F2
24		0.3357522	F3 <--> F3
25		1.0000000	g <--> g

```
> 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	13.98		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			147.66				
Model 2	73			178.79	10	31.129	0.0005587	***

---

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

## 4.9 Estimating Omega using EFA followed by CFA

The function `omegaSem` combines both an exploratory factor analysis using `omega`, then calls the appropriate `sem` functions and organizes the results as in a standard `omega` analysis.

An example is found from the Thurstone data set of 9 cognitive variables:

```
> data(bifactor)
[1] "bifactor"
> om.sem <- omegaSem(Thurstone,n.obs=213)
Call: omegaSem(m = Thurstone, n.obs = 213)
Omega
Call: omegah(m = m, nfactors = nfactors, fm = fm, key = key, flip = flip,
  digits = digits, title = title, sl = sl, labels = labels,
  plot = plot, n.obs = n.obs, rotate = rotate, Phi = Phi, option = option)
Alpha:          0.89
G.6:            0.91
Omega Hierarchical: 0.74
```

Omega H asymptotic: 0.79  
 Omega Total 0.93

Schmid Leiman Factor loadings greater than 0.2

	g	F1*	F2*	F3*	h2	u2	p2
Sentences	0.71	0.57			0.82	0.18	0.61
Vocabulary	0.73	0.55			0.84	0.16	0.63
Sent.Completion	0.68	0.52			0.73	0.27	0.63
First.Letters	0.65		0.56		0.73	0.27	0.57
4.Letter.Words	0.62		0.49		0.63	0.37	0.61
Suffixes	0.56		0.41		0.50	0.50	0.63
Letter.Series	0.59			0.61	0.72	0.28	0.48
Pedigrees	0.58	0.23		0.34	0.50	0.50	0.66
Letter.Group	0.54			0.46	0.53	0.47	0.56

With eigenvalues of:

	g	F1*	F2*	F3*
	3.58	0.96	0.74	0.71

general/max 3.71 max/min = 1.35  
 mean percent general = 0.6 with sd = 0.05 and cv of 0.09

The degrees of freedom are 12 and the fit is 0.01  
 The number of observations was 213 with Chi Square = 2.82 with prob < 1  
 The root mean square of the residuals is 0  
 The df corrected root mean square of the residuals is 0.01  
 RMSEA index = 0 and the 90 % confidence intervals are 0 0.023  
 BIC = -61.51

Compare this with the adequacy of just a general factor and no group factors  
 The degrees of freedom for just the general factor are 27 and the fit is 1.48  
 The number of observations was 213 with Chi Square = 307.1 with prob < 2.8e-49  
 The root mean square of the residuals is 0.1  
 The df corrected root mean square of the residuals is 0.16

RMSEA index = 0.224 and the 90 % confidence intervals are 0.223 0.226  
 BIC = 162.35

Measures of factor score adequacy

	g	F1*	F2*	F3*
Correlation of scores with factors	0.86	0.73	0.72	0.75

Multiple R square of scores with factors            0.74 0.54 0.52 0.56  
 Minimum correlation of factor score estimates 0.49 0.08 0.03 0.11

Omega Hierarchical from a confirmatory model using sem = 0.79

Omega Total from a confirmatory model using sem = 0.93

With loadings of

	g	F1*	F2*	F3*	h2	u2
Sentences	0.77	0.49			0.83	0.17
Vocabulary	0.79	0.45			0.83	0.17
Sent.Completion	0.75	0.40			0.73	0.27
First.Letters	0.61		0.61		0.75	0.25
4.Letter.Words	0.60		0.51		0.61	0.39
Suffixes	0.57		0.39		0.48	0.52
Letter.Series	0.57			0.73	0.85	0.15
Pedigrees	0.66			0.25	0.50	0.50
Letter.Group	0.53			0.41	0.45	0.55

With eigenvalues of:

	g	F1*	F2*	F3*
	3.88	0.61	0.79	0.76

Comparing the two models graphically (Figure 15 with Figure 13 shows that while not identical, they are very similar. The sem version is basically a forced simple structure. Notice that the values of  $\omega_h$  are not identical from the EFA and CFA models.

## 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.

### Omega from SEM

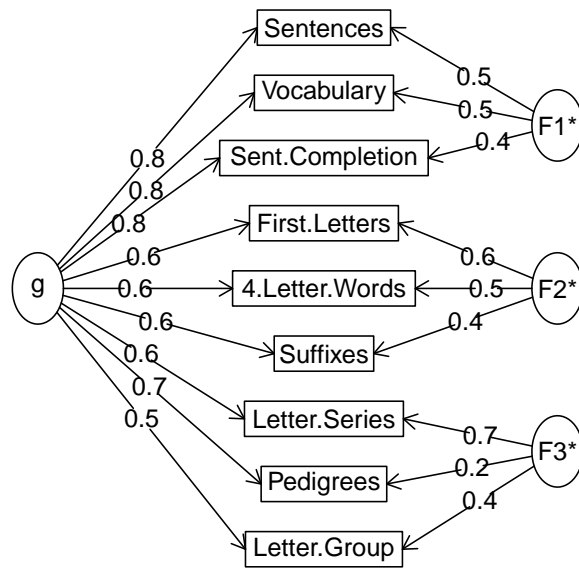


Figure 15: Confirmatory Omega structure using `omegaSem`

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