

More adventures

Steps of analysis

I. Initial data entry as a spreadsheet

II. descriptive stats

III. preliminary correlational structure

IV. EFA

V. CFA/SEM

VI. Theoretical interpretation

Initial data entry

```
> megan <- read.clipboard()
> describe(megan)
```

	var	n	mean	sd	median	trimmed	mad	min	max	range	skew	kurtosis	se
adult11	1	302	-29.52	179.71	4	3.69	1.48	-999	5	1004	-5.19	25.05	10.34
adult21	2	302	-29.17	179.77	4	4.05	1.48	-999	5	1004	-5.19	25.05	10.34
adult31	3	302	-35.78	196.26	4	4.07	1.48	-999	5	1004	-4.69	20.05	11.29
revadult41	4	302	-39.21	203.90	4	4.00	1.48	-999	5	1004	-4.48	18.13	11.73
revadult51	5	302	-39.53	203.84	4	3.64	1.48	-999	5	1004	-4.48	18.13	11.73
revadult61	6	302	-36.06	196.21	4	3.82	1.48	-999	5	1004	-4.69	20.05	11.29
adult71	7	302	-32.42	188.24	4	4.13	0.00	-999	5	1004	-4.92	22.32	10.83
adult81	8	302	-35.58	196.31	4	4.31	1.48	-999	5	1004	-4.69	20.05	11.30
adult91	9	302	-32.42	188.24	4	4.14	1.48	-999	5	1004	-4.92	22.32	10.83
adult101	10	302	-52.47	231.56	4	3.95	1.48	-999	5	1004	-3.83	12.72	13.32
adult111	11	302	-52.57	231.53	4	3.87	1.48	-999	5	1004	-3.83	12.72	13.32
revadult121	12	302	-52.68	231.51	4	3.76	1.48	-999	5	1004	-3.83	12.72	13.32
adult131	13	302	-56.17	237.76	4	3.54	1.48	-999	5	1004	-3.70	11.74	13.68

```
>
```

Clearly, a missing value code of -999 was used

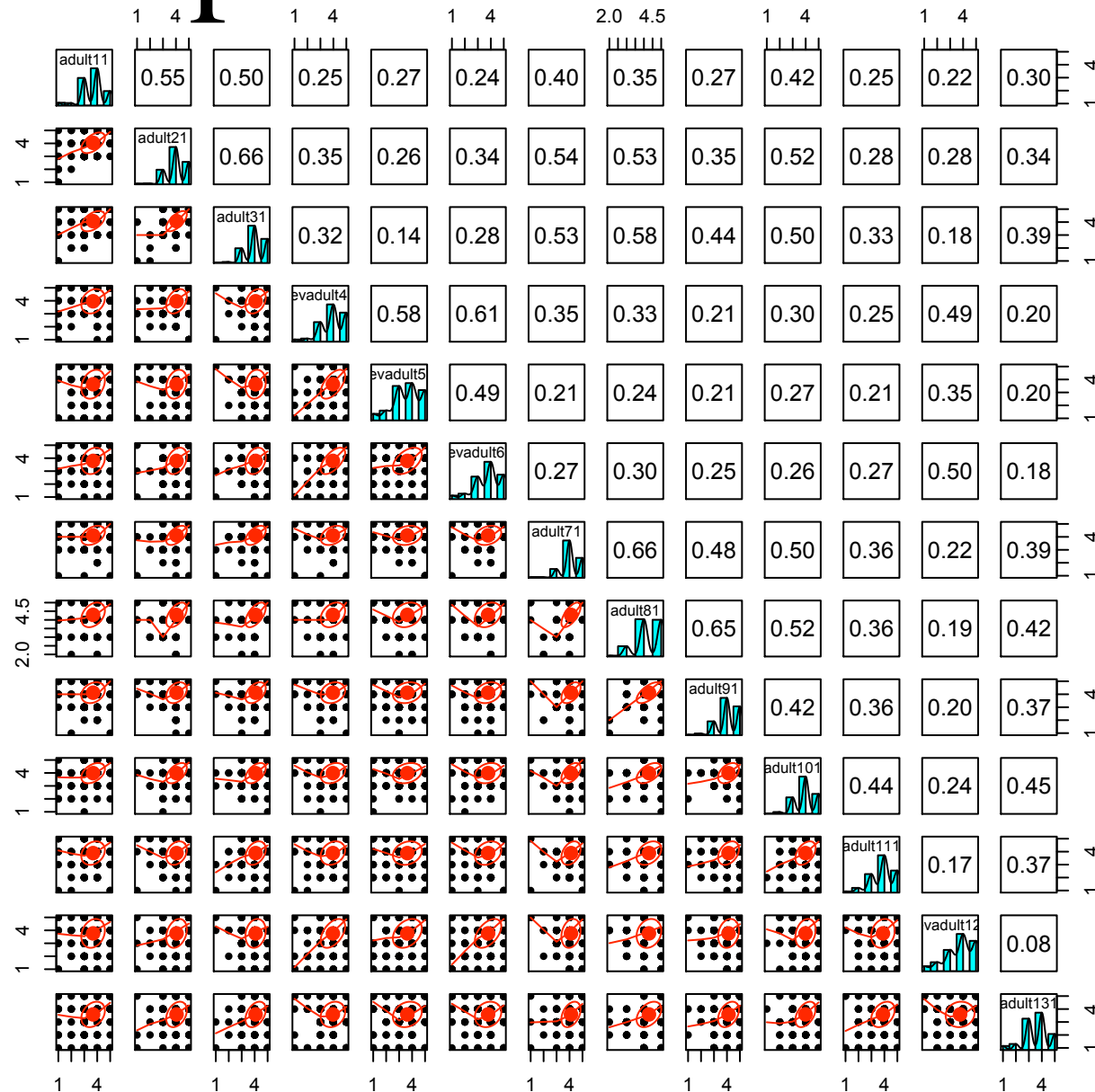
Minor data correction

```
> megan[megan == -999] <- NA
```

```
> describe(megan)
```

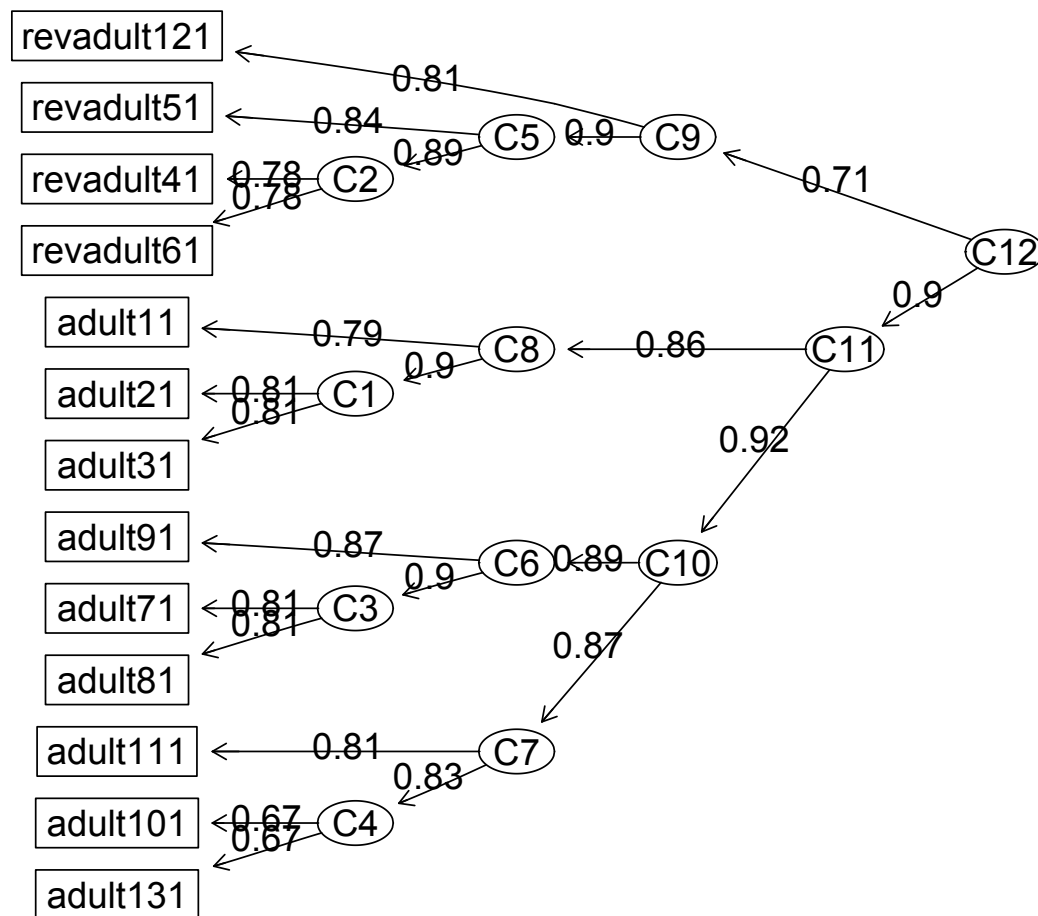
	var	n	mean	sd	median	trimmed	mad	min	max	range	skew	kurtosis	se
adult11	1	292	3.68	0.91	4	3.73	1.48	1	5	4	-0.67	0.79	0.05
adult21	2	292	4.04	0.80	4	4.10	1.48	1	5	4	-0.73	0.97	0.05
adult31	3	290	4.07	0.78	4	4.12	1.48	1	5	4	-0.64	0.58	0.05
revadult41	4	289	3.96	0.94	4	4.06	1.48	1	5	4	-0.86	0.69	0.06
revadult51	5	289	3.63	1.12	4	3.73	1.48	1	5	4	-0.56	-0.30	0.07
revadult61	6	290	3.79	1.02	4	3.91	1.48	1	5	4	-0.77	0.30	0.06
adult71	7	291	4.11	0.74	4	4.18	0.00	1	5	4	-0.94	2.17	0.04
adult81	8	290	4.29	0.71	4	4.38	1.48	2	5	3	-0.65	-0.20	0.04
adult91	9	291	4.12	0.81	4	4.19	1.48	1	5	4	-0.77	0.64	0.05
adult101	10	285	3.99	0.78	4	4.02	1.48	1	5	4	-0.46	0.05	0.05
adult111	11	285	3.89	0.91	4	3.97	1.48	1	5	4	-0.68	0.27	0.05
revadult121	12	285	3.76	1.12	4	3.89	1.48	1	5	4	-0.76	-0.10	0.07
adult131	13	284	3.58	0.98	4	3.66	1.48	1	5	4	-0.57	0.24	0.06

Graphics: SPLOM



Cluster structure

ICLUST



```
> ic.meg <- ICLUST(megan)
Loading required package: Rgraph
Loading required package: graph
Loading required package: grid
> ic.meg
ICLUST (Item Cluster Analysis)
Call: ICLUST(r.mat = megan)
Item by Cluster Structure matrix
```

```
[,1]
adult11 0.53
adult21 0.65
adult31 0.64
revadult41 0.56
revadult51 0.45
revadult61 0.52
adult71 0.65
adult81 0.67
adult91 0.55
adult101 0.63
adult111 0.48
revadult121 0.41
adult131 0.48
```

With eigenvalues of:

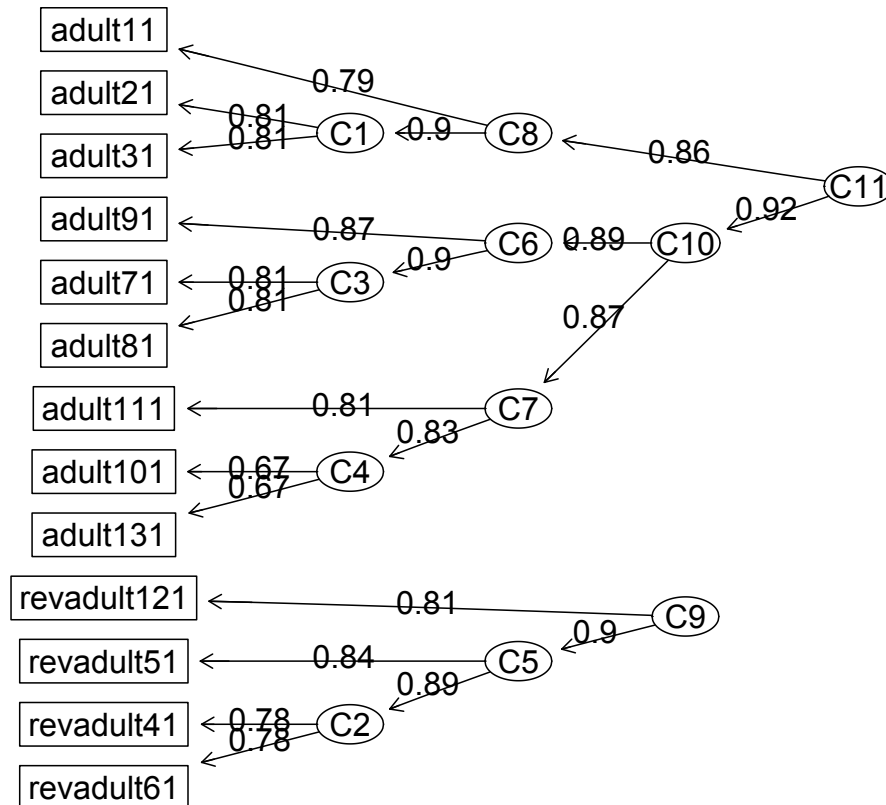
```
[1] 4.1
```

Purified scale intercorrelations
reliabilities on diagonal
correlations corrected for
attenuation above diagonal:

```
[,1]
[1,] 0.88
```

Theory says 2 clusters

ICLUST



```
> ic2
```

ICLUST (Item Cluster Analysis)

Call: ICLUST(r.mat = megan,

nclusters = 2)

Item by Cluster Structure matrix:

	C11	C9
adult11	0.54	0.31
adult21	0.66	0.39
adult31	0.70	0.29
revadult41	0.40	0.70
revadult51	0.32	0.59
revadult61	0.37	0.67
adult71	0.68	0.34
adult81	0.72	0.33
adult91	0.59	0.28
adult101	0.66	0.34
adult111	0.49	0.28
revadult121	0.28	0.56
adult131	0.53	0.21

With eigenvalues of:

C11	C9
4.0	2.5

Purified scale intercorrelations
reliabilities on diagonal
correlations corrected for
attenuation above diagonal:

	C11	C9
C11	0.88	0.52
C9	0.43	0.80

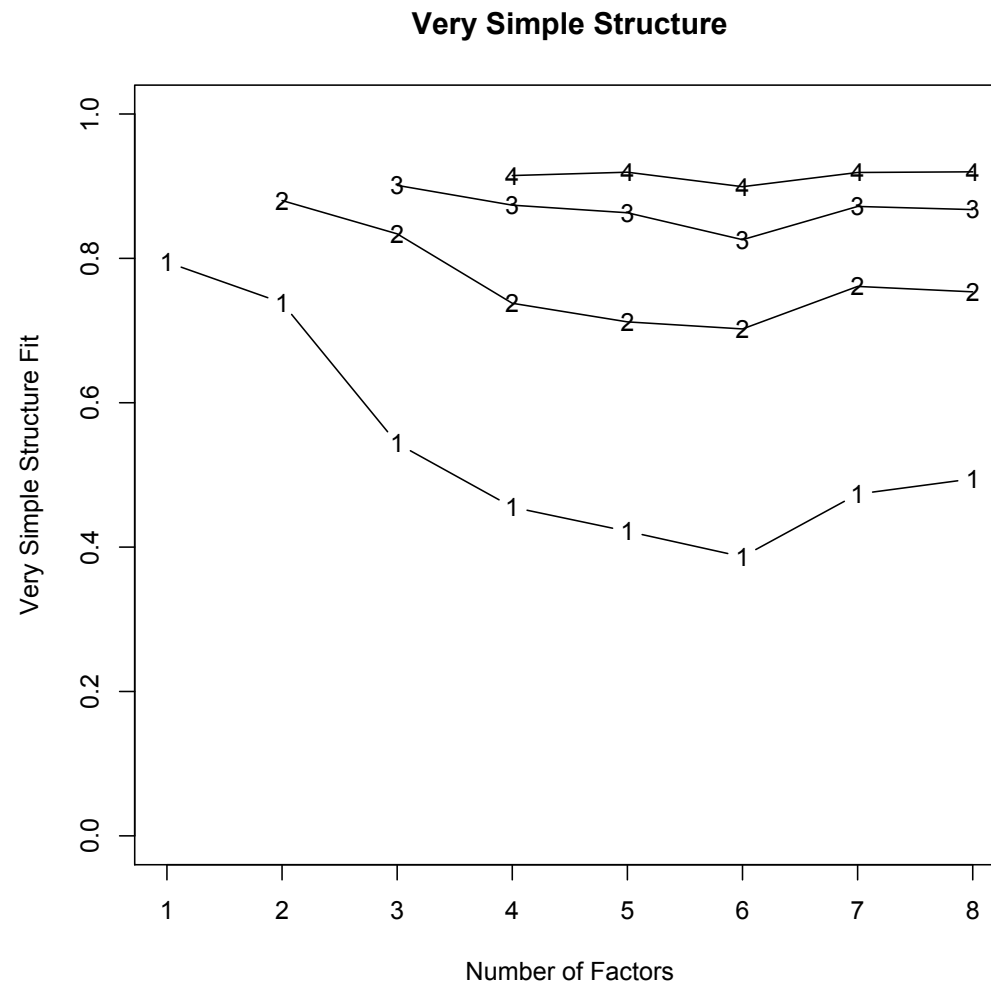
Sort the loadings

```
> ICLUST.sort(ic2)
```

```
$sorted
```

	item	content	cluster	C11	C9
adult81	8	adult81	1	0.72	0.33
adult31	3	adult31	1	0.70	0.29
adult71	7	adult71	1	0.68	0.34
adult21	2	adult21	1	0.66	0.39
adult101	10	adult101	1	0.66	0.34
adult91	9	adult91	1	0.59	0.28
adult11	1	adult11	1	0.54	0.31
adult131	13	adult131	1	0.53	0.21
adult111	11	adult111	1	0.49	0.28
revadult41	4	revadult41	2	0.40	0.70
revadult61	6	revadult61	2	0.37	0.67
revadult51	5	revadult51	2	0.32	0.59
revadult121	12	revadult121	2	0.28	0.56

VSS suggests 1 or 2



VSS says 1 or 2

```
> vss <- VSS(megan)
> vss
```

Very Simple Structure

Call: VSS(x = megan)

VSS complexity 1 achieves a maximum of 0.79 with 1 factors

VSS complexity 2 achieves a maximum of 0.88 with 2 factors

The Velicer MAP criterion achieves a minimum of 0.17 with 2 factors

Velicer MAP

```
[1] 0.04 0.03 0.03 0.04 0.06 0.09 0.12 0.17
```

Very Simple Structure Complexity 1

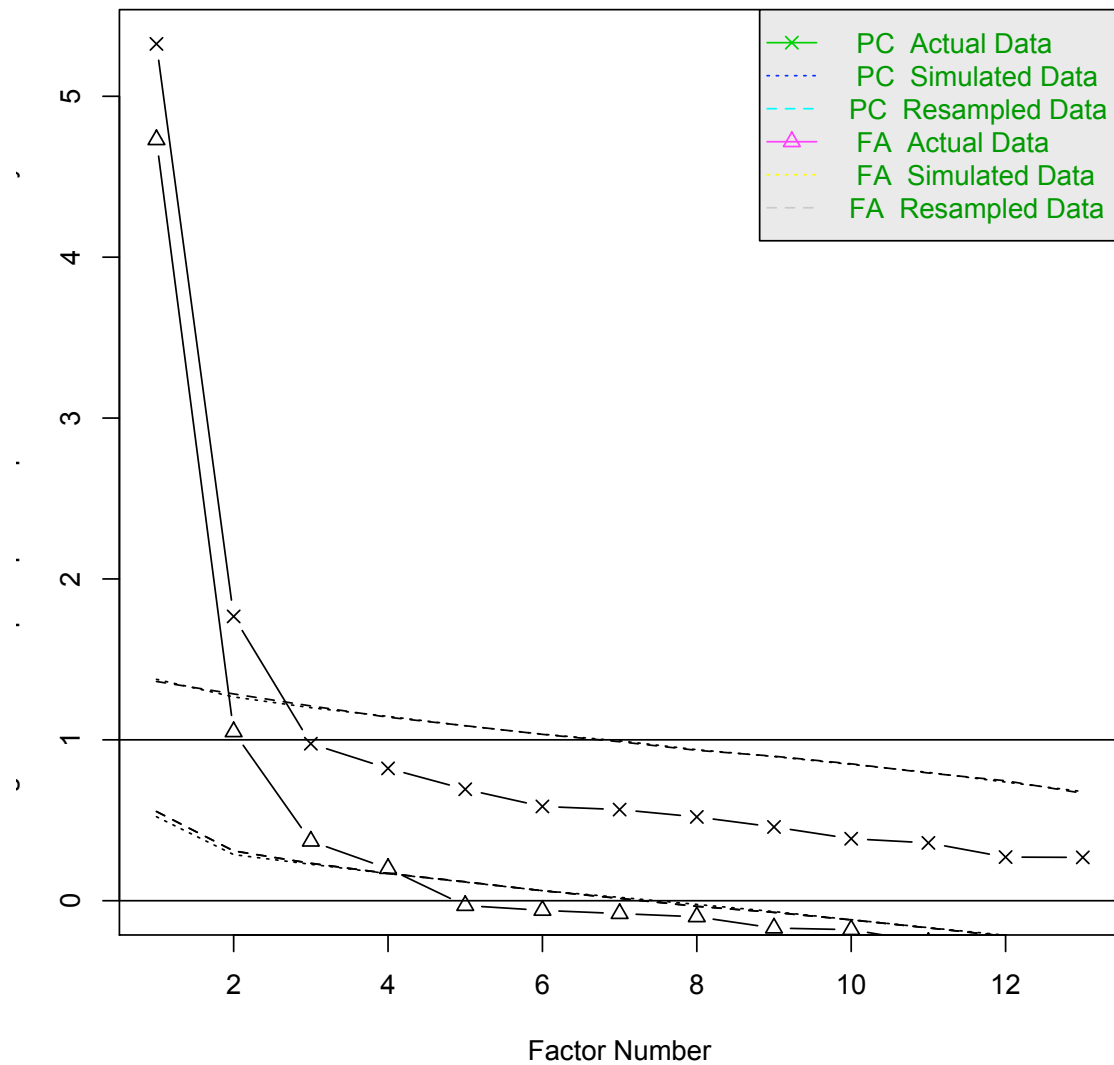
```
[1] 0.79 0.74 0.54 0.46 0.42 0.39 0.47 0.49
```

Very Simple Structure Complexity 2

```
[1] 0.00 0.88 0.83 0.74 0.71 0.70 0.76 0.75
```

Parallel Analysis

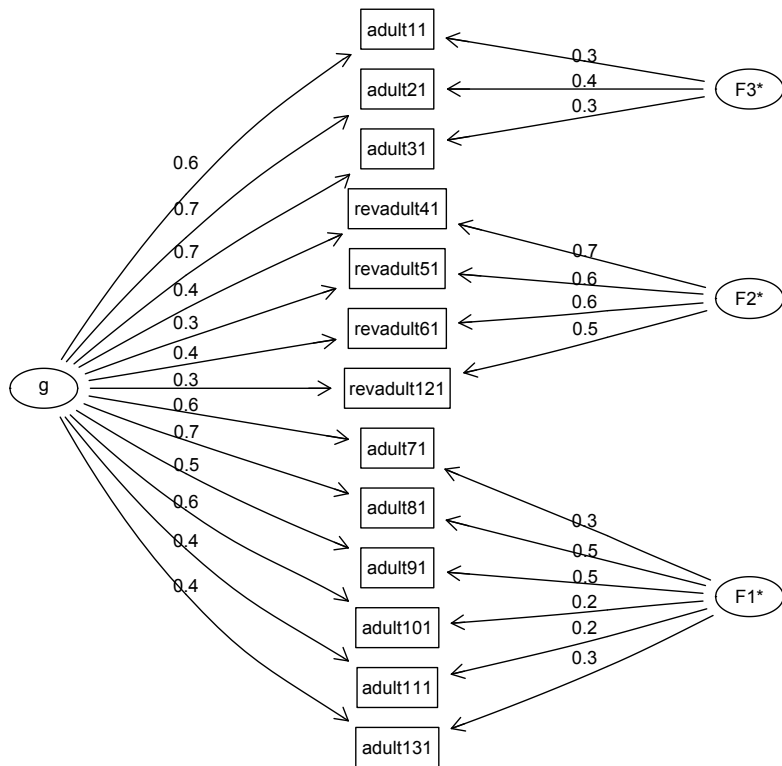
Parallel Analysis Scree Plots



2 PCs
3-4 Factors

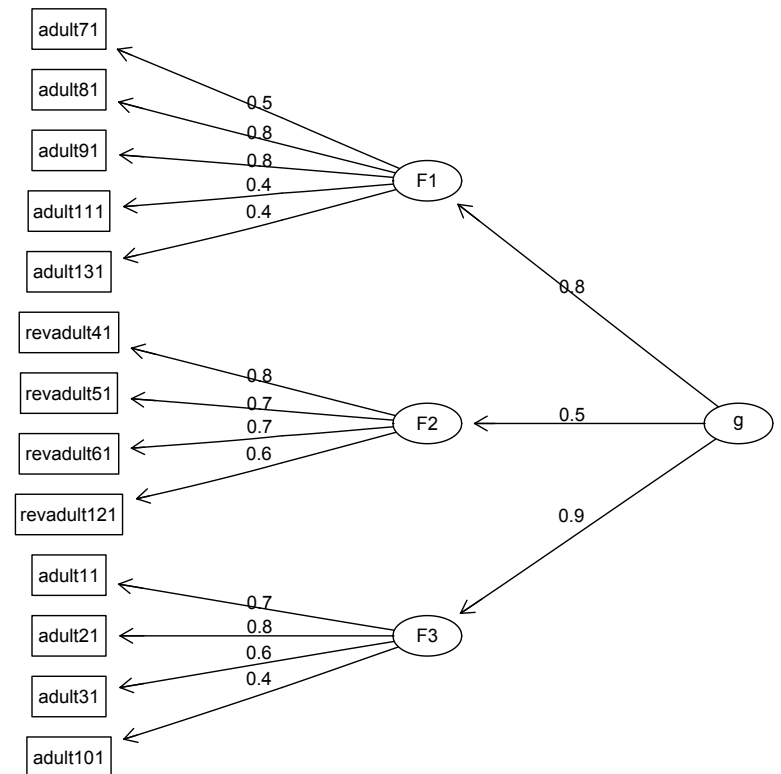
Omega

Omega



```
om <- omega(megan)
```

Omega



```
om.h <- omega(megan,sl=FALSE)
```

Omega fits, but badly

```
> om
Omega
Call: omega(m = megan)
Alpha: 0.88
G.6: 0.9
Omega Hierarchical: 0.69
Omega Total 0.91
Schmid Leiman Factor loadings greater than 0.2
```

	g	F1*	F2*	F3*	h2	u2
adult11	0.55			0.33	0.42	0.58
adult21	0.74			0.42	0.72	0.28
adult31	0.71			0.32	0.63	0.37
revadult41	0.45		0.69		0.67	0.33
revadult51	0.33		0.59		0.45	0.55
revadult61	0.41		0.63		0.56	0.44
adult71	0.65	0.34			0.56	0.44
adult81	0.69	0.52			0.74	0.26
adult91	0.53	0.53			0.56	0.44
adult101	0.61	0.23			0.46	0.54
adult111	0.41	0.25			0.25	0.75
revadult121	0.32		0.51		0.37	0.63
adult131	0.45	0.27			0.28	0.72

The degrees of freedom for
the model is 42 and the
fit was 0.3

The number of observations
was 302 with Chi Square
= 86.79 with prob <
5.9e-05

```
With eigenvalues of:
```

	g	F1*	F2*	F3*
	3.86	0.88	1.51	0.45
general/max	2.56			
max/min =				3.34

```
>
```

sem of bifactor

```
> mod1 <- sem(om$model,cov(megan,use="pairwise"),285)
> summary(mod1,digits=2)
```

```
Model Chisquare = 83    Df = 52 Pr(>Chisq) = 0.0042
Chisquare (null model) = 1554    Df = 78
Goodness-of-fit index = 0.96
Adjusted goodness-of-fit index = 0.93
RMSEA index = 0.046    90% CI: (0.026, 0.064)
Bentler-Bonnett NFI = 0.95
Tucker-Lewis NNFI = 0.97
Bentler CFI = 0.98
SRMR = 0.037
BIC = -211
```

Normalized Residuals

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
-1.4e+00	-2.7e-01	3.9e-06	6.0e-02	3.8e-01	1.9e+00

Standardized coefficients

```
> std.coef(mod1,digits=2)
```

		Std. Estimate	
adult11	adult11	0.502	adult11 <--- g
adult21	adult21	0.666	adult21 <--- g
adult31	adult31	0.699	adult31 <--- g
revadult41	revadult41	0.428	revadult41 <--- g
revadult51	revadult51	0.324	revadult51 <--- g
revadult61	revadult61	0.384	revadult61 <--- g
adult71	adult71	0.727	adult71 <--- g
adult81	adult81	0.802	adult81 <--- g
adult91	adult91	0.622	adult91 <--- g
adult101	adult101	0.748	adult101 <--- g
adult111	adult111	0.541	adult111 <--- g
revadult121	revadult121	0.284	revadult121 <--- g
adult131	adult131	0.574	adult131 <--- g
F3*adult11	F3*adult11	0.407	adult11 <--- F3*
F3*adult21	F3*adult21	0.520	adult21 <--- F3*
F3*adult31	F3*adult31	0.374	adult31 <--- F3*
F2*revadult41	F2*revadult41	0.712	revadult41 <--- F2*
F2*revadult51	F2*revadult51	0.570	revadult51 <--- F2*
F2*revadult61	F2*revadult61	0.633	revadult61 <--- F2*
F1*adult71	F1*adult71	-0.140	adult71 <--- F1*
F1*adult81	F1*adult81	-0.544	adult81 <--- F1*
F1*adult91	F1*adult91	-0.271	adult91 <--- F1*
F1*adult101	F1*adult101	0.148	adult101 <--- F1*
F1*adult111	F1*adult111	0.125	adult111 <--- F1*
F2*revadult121	F2*revadult121	0.533	revadult121 <--- F2*
F1*adult131	F1*adult131	0.077	adult131 <--- F1*

Hierarchical solution

```
> mod.h <- sem(om.h$model,cov(megan,use="pairwise"),285)
> summary(mod.h,digits=2)
```

```
Model Chisquare = 130    Df = 62 Pr(>Chisq) = 9.2e-07
Chisquare (null model) = 1554    Df = 78
Goodness-of-fit index = 0.93
Adjusted goodness-of-fit index = 0.9
RMSEA index = 0.062    90% CI: (0.047, 0.077)
Bentler-Bonnett NFI = 0.92
Tucker-Lewis NNFI = 0.94
Bentler CFI = 0.95
SRMR = 0.046
BIC = -220
```

Normalized Residuals

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
-1.960	-0.268	0.035	0.081	0.461	2.660

Standardized coefficients for hierarchical model

```
> std.coef(mod.h,digits=2)
```

		Std. Estimate	
gF1	gF1	0.89	F1 <--- g
gF2	gF2	0.53	F2 <--- g
gF3	gF3	0.94	F3 <--- g
F3adult11	F3adult11	0.62	adult11 <--- F3
F3adult21	F3adult21	0.80	adult21 <--- F3
F3adult31	F3adult31	0.80	adult31 <--- F3
F2revadult41	F2revadult41	0.83	revadult41 <--- F2
F2revadult51	F2revadult51	0.65	revadult51 <--- F2
F2revadult61	F2revadult61	0.74	revadult61 <--- F2
F1adult71	F1adult71	0.77	adult71 <--- F1
F1adult81	F1adult81	0.85	adult81 <--- F1
F1adult91	F1adult91	0.69	adult91 <--- F1
F3adult101	F3adult101	0.68	adult101 <--- F3
F1adult111	F1adult111	0.49	adult111 <--- F1
F2revadult121	F2revadult121	0.60	revadult121 <--- F2
F1adult131	F1adult131	0.53	adult131 <--- F1

Predicting delinquency

I. Wave 1 data, children are 12-13

II. Wave 2 data, children are 18-19

III. First do simple models, then do the panel wave data

Delinquency

```
> lindsay <- read.clipboard(sep="\t")
```

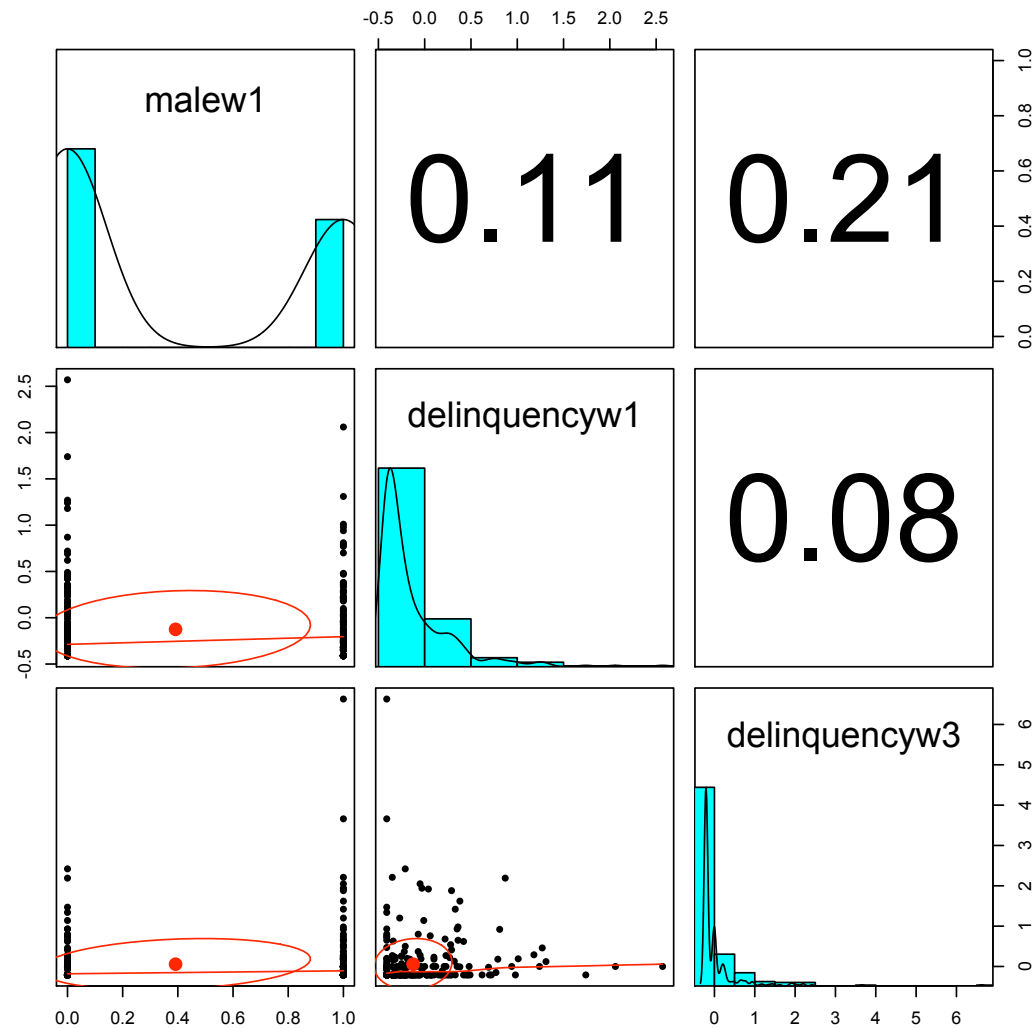
```
> dim(lindsay)
```

```
[1] 291  17
```

```
> describe(lindsay)
```

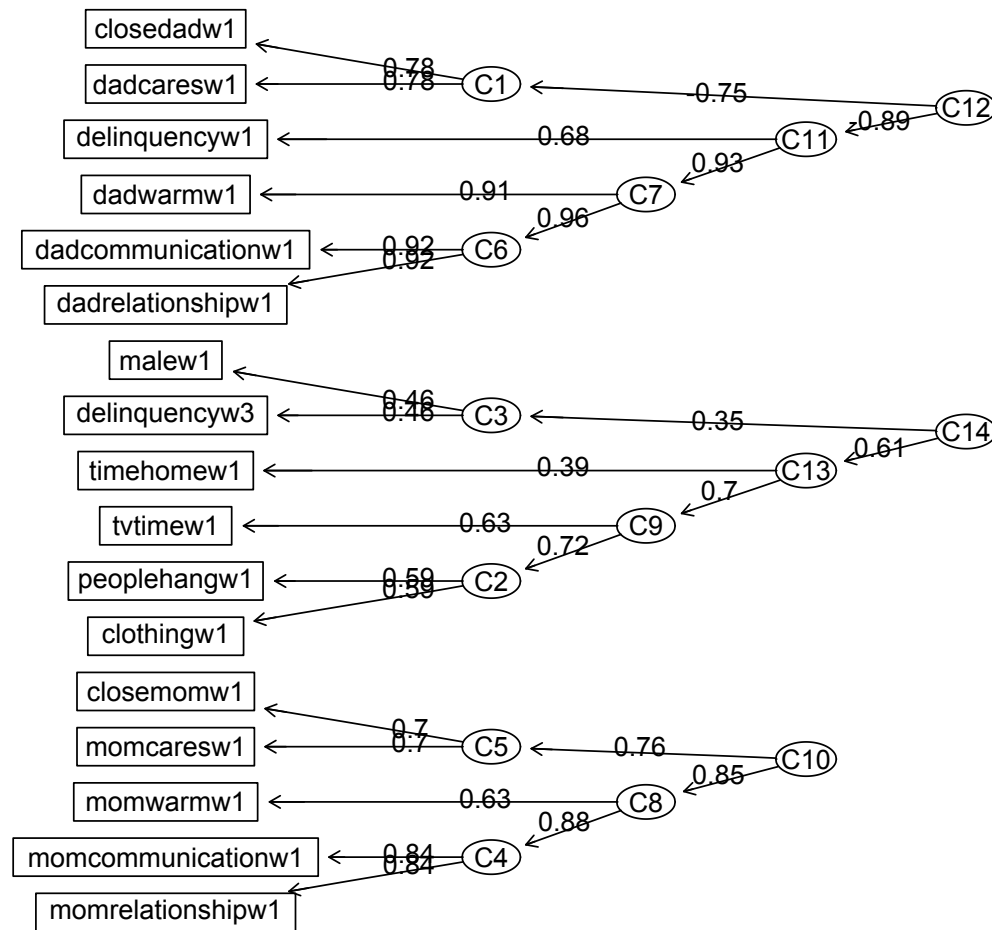
	var	n	mean	sd	median	trimmed	mad	min	max	range	skew	kurtosis	se
malew1	1	291	0.39	0.49	0.00	0.36	0.00	0.00	1.00	1.00	0.44	-1.81	0.03
momwarmw1	2	291	3.58	0.69	4.00	3.71	0.00	0.00	4.00	4.00	-1.75	3.30	0.04
momcommunicationw1	3	282	3.40	0.77	4.00	3.53	0.00	0.00	4.00	4.00	-1.75	4.42	0.05
momrelationshipw1	4	282	3.62	0.65	4.00	3.73	0.00	0.00	4.00	4.00	-2.16	6.14	0.04
dadwarmw1	5	291	3.42	0.62	3.48	3.48	0.77	1.00	4.00	3.00	-0.96	1.54	0.04
dadcommunicationw1	6	216	3.37	0.85	4.00	3.53	0.00	0.00	4.00	4.00	-1.65	3.05	0.06
dadrelationshipw1	7	216	3.50	0.71	4.00	3.60	0.00	0.00	4.00	4.00	-1.90	5.40	0.05
timehomew1	8	291	0.21	0.40	0.00	0.13	0.00	0.00	1.00	1.00	1.44	0.08	0.02
peoplehangw1	9	291	0.83	0.38	1.00	0.91	0.00	0.00	1.00	1.00	-1.73	1.00	0.02
clothingw1	10	291	0.87	0.33	1.00	0.97	0.00	0.00	1.00	1.00	-2.22	2.96	0.02
tvtimew1	11	291	0.66	0.48	1.00	0.69	0.00	0.00	1.00	1.00	-0.65	-1.58	0.03
closemomw1	12	291	4.78	0.50	5.00	4.90	0.00	2.00	5.00	3.00	-2.84	9.61	0.03
closedadw1	13	291	4.76	0.64	5.00	4.89	0.00	2.00	5.19	3.19	-2.24	4.81	0.04
momcaresw1	14	291	4.93	0.33	5.00	5.00	0.00	2.00	5.01	3.01	-5.75	36.06	0.02
dadcaresw1	15	291	5.02	0.42	5.00	5.08	0.00	2.00	5.46	3.46	-3.21	14.94	0.02
delinquencyw1	16	291	-0.13	0.42	-0.27	-0.21	0.21	-0.41	2.57	2.98	2.66	9.61	0.02
delinquencyw3	17	291	0.06	0.64	-0.21	-0.09	0.00	-0.21	6.63	6.84	5.45	42.96	0.04

Hard to predict criterion



Simple models

ICLUST



	C12	C10	C14
C12	0.83	-0.55	0.00
C10	-0.42	0.70	0.03
C14	0.00	0.02	0.44

ICLUST

stats

```
> ic.lind
ICLUST (Item Cluster Analysis)
Call: ICLUST(r.mat = lindsay)
Item by Cluster Structure matrix:

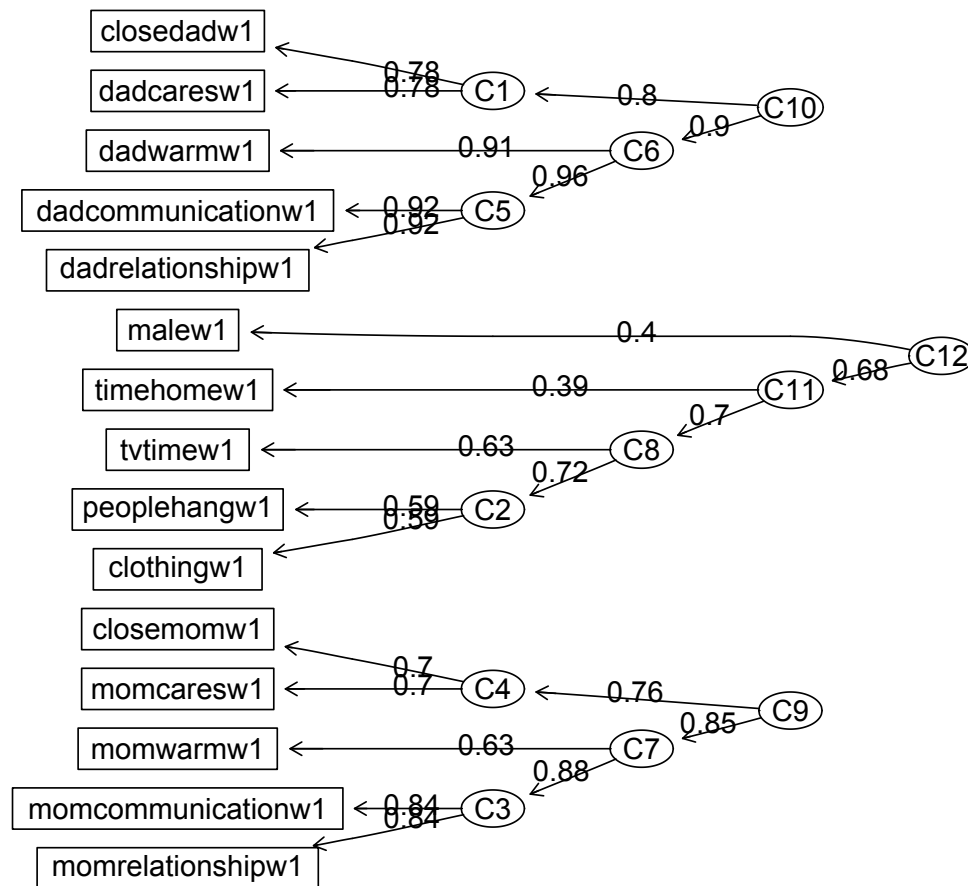
      C10   C12   C14
malew1 -0.03  0.03  0.11
momwarmw1 0.45 -0.34 -0.01
momcommunicationw1 0.57 -0.37  0.07
momrelationshipw1 0.63 -0.42  0.00
dadwarmw1 0.31 -0.51  0.04
dadcommunicationw1 0.40 -0.67  0.04
dadrelationshipw1 0.42 -0.68  0.02
timehomew1 -0.03  0.05 -0.13
peoplehangw1 0.08 -0.03 -0.25
clothingw1 -0.01 -0.06 -0.30
tvtimew1 -0.11  0.07 -0.21
closemomw1 0.50 -0.27  0.02
closedadw1 0.26 -0.47 -0.04
momcaresw1 0.43 -0.15  0.02
dadcaresw1 0.16 -0.44 -0.06
delinquencyw1 -0.27  0.32  0.00
delinquencyw3 -0.07  0.02  0.03
With eigenvalues of:
  C10  C12  C14
1.98 2.23 0.24
```

Purified scale
intercorrelations
reliabilities on diagonal
correlations corrected for
attenuation above diagonal:

	C12	C10	C14
C12	0.83	-0.55	0.00
C10	-0.42	0.70	0.03
C14	0.00	0.02	0.44

Drop criterion

ICLUST



	C10	C9	C12
C10	0.86	0.51	0.00
C9	0.41	0.76	0.04
C12	0.00	0.03	0.44

```
> ic.lind1 <- ICLUST(lindsay[1:15])
```

```
> ic.lind1
```

```
ICLUST (Item Cluster Analysis)
```

```
Call: ICLUST(r.mat = lindsay[1:15])
```

ICLUST stats

Item by Cluster Structure matrix:

	C10	C9	C12
malew1	-0.01	0.03	0.11
momwarmw1	0.33	0.46	-0.01
momcommunicationw1	0.36	0.60	0.07
momrelationshipw1	0.41	0.68	0.00
dadwarmw1	0.61	0.33	0.04
dadcommunicationw1	0.82	0.43	0.04
dadrelationshipw1	0.83	0.45	0.02
timehomew1	-0.03	-0.02	-0.13
peoplehangw1	0.02	0.09	-0.25
clothingw1	0.07	0.00	-0.30
tvtimew1	-0.06	-0.11	-0.21
closemomw1	0.26	0.56	0.02
closedadw1	0.60	0.27	-0.04
momcaresw1	0.12	0.44	0.02
dadcaresw1	0.57	0.16	-0.06

With eigenvalues of:

C10	C9	C12
2.92	2.16	0.24

Purified scale
intercorrelations
reliabilities on diagonal
correlations corrected for
attenuation above diagonal:

	C10	C9	C12
C10	0.86	0.51	0.00
C9	0.41	0.76	0.04
C12	0.00	0.03	0.44


```

> lind.keys <-
make.keys(17,list(mom=c(2,3,4,12,14),dad=c(5,6,7,13,15),
rec=c(7:10),del=c(16,17)))
> rownames(lind.keys) <- colnames(lindsay)
> lind.keys

```

	mom	dad	rec	del
malew1	0	0	0	0
momwarmw1	1	0	0	0
momcommunicationw1	1	0	0	0
momrelationshipw1	1	0	0	0
dadwarmw1	0	1	0	0
dadcommunicationw1	0	1	0	0
dadrelationshipw1	0	1	1	0
timehomew1	0	0	1	0
peoplehangw1	0	0	1	0
clothingw1	0	0	1	0
tvtimew1	0	0	0	0
closemomw1	1	0	0	0
closedadw1	0	1	0	0
momcaresw1	1	0	0	0
dadcaresw1	0	1	0	0
delinquencyw1	0	0	0	1
delinquencyw3	0	0	0	1

```

> lind <- score.items(lind.keys,lindsay)

```

sum
scores

scales

```
> lind
```

```
Alpha:
```

```
      mom  dad  rec  del
[1,] 0.73 0.85 0.22 0.14
```

```
Average item correlation:
```

```
      mom  dad  rec  del
[1,] 0.35 0.53 0.07 0.08
```

```
Scale intercorrelations:
```

```
      mom  dad  rec  del
mom  1.00  0.42  0.29 -0.20
dad  0.42  1.00  0.61 -0.12
rec  0.29  0.61  1.00 -0.01
del -0.20 -0.12 -0.01  1.00
```

```
Scale intercorrelations corrected for
attenuation
```

```
raw correlations below the diagonal,
alpha on the diagonal
corrected correlations above the
diagonal:
```

```
      mom  dad  rec  del
mom  0.73  0.53  0.73 -0.61
dad  0.42  0.85  1.41 -0.36
rec  0.29  0.61  0.22 -0.05
del -0.20 -0.12 -0.01  0.14
```

```
Item by scale correlations:
```

```
      mom  dad  rec  del
malew1      0.04  0.00 -0.05  0.23
momwarmw1    0.62  0.31  0.25 -0.19
momcommunicationw1 0.80  0.33  0.20 -0.15
momrelationshipw1 0.84  0.38  0.29 -0.13
dadwarmw1    0.36  0.65  0.34 -0.17
dadcommunicationw1 0.40  0.92  0.55 -0.09
dadrelationshipw1 0.42  0.92  0.66 -0.08
timehomew1   -0.02 -0.02  0.46  0.07
peoplehangw1 0.09  0.02  0.55  0.00
clothingw1   0.00  0.07  0.54  0.03
tvtimew1     -0.12 -0.07  0.17  0.04
closemomw1   0.68  0.26  0.20 -0.07
closedadw1   0.28  0.75  0.45 -0.09
momcaresw1   0.53  0.12  0.04 -0.16
dadcaresw1   0.16  0.71  0.42 -0.07
delinquencyw1 -0.25 -0.24 -0.12  0.60
delinquencyw3 -0.08  0.01  0.06  0.85
```

more scales

```
> lind.keys1 <- make.keys(17,list(mom=c(2,3,4,12,14),dad=c(5,6,7,13,15),
rec=c(7:10),del=c(16,17),del1=c(16),del2=c(17)))
> lind1 <- score.items(lind.keys1,lindsay)
> lind1
```

Alpha:

	mom	dad	rec	del	del1	del2
[1,]	0.73	0.85	0.22	0.14	1	1

Average item correlation:

	mom	dad	rec	del	del1	del2
[1,]	0.35	0.53	0.07	0.08	1	1

Scale intercorrelations:

	mom	dad	rec	del	del1	del2
mom	1.00	0.42	0.29	-0.20	-0.25	-0.08
dad	0.42	1.00	0.61	-0.12	-0.24	0.01
rec	0.29	0.61	1.00	-0.01	-0.12	0.06
del	-0.20	-0.12	-0.01	1.00	0.60	0.85
del1	-0.25	-0.24	-0.12	0.60	1.00	0.08
del2	-0.08	0.01	0.06	0.85	0.08	1.00

Scale intercorrelations corrected for attenuation

raw correlations below the diagonal, alpha on the diagonal

corrected correlations above the diagonal:

	mom	dad	rec	del	del1	del2
mom	0.73	0.53	0.73	-0.61	-0.29	-0.09
dad	0.42	0.85	1.41	-0.36	-0.26	0.01
rec	0.29	0.61	0.22	-0.05	-0.25	0.14
del	-0.20	-0.12	-0.01	0.14	1.59	2.26
del1	-0.25	-0.24	-0.12	0.60	1.00	0.08
del2	-0.08	0.01	0.06	0.85	0.08	1.00

item correlations

Item by scale correlations:

	mom	dad	rec	del	del1	del2
malew1	0.04	0.00	-0.05	0.23	0.11	0.21
momwarmw1	0.62	0.31	0.25	-0.19	-0.20	-0.10
momcommunicationw1	0.80	0.33	0.20	-0.15	-0.18	-0.06
momrelationshipw1	0.84	0.38	0.29	-0.13	-0.17	-0.04
dadwarmw1	0.36	0.65	0.34	-0.17	-0.31	0.00
dadcommunicationw1	0.40	0.92	0.55	-0.09	-0.21	0.02
dadrelationshipw1	0.42	0.92	0.66	-0.08	-0.19	0.03
timehomew1	-0.02	-0.02	0.46	0.07	0.07	0.04
peoplehangw1	0.09	0.02	0.55	0.00	-0.06	0.04
clothingw1	0.00	0.07	0.54	0.03	0.01	0.03
tvtimew1	-0.12	-0.07	0.17	0.04	0.09	0.00
closemomw1	0.68	0.26	0.20	-0.07	-0.18	0.03
closedadw1	0.28	0.75	0.45	-0.09	-0.14	-0.01
momcaresw1	0.53	0.12	0.04	-0.16	-0.16	-0.10
dadcaresw1	0.16	0.71	0.42	-0.07	-0.08	-0.04
delinquencyw1	-0.25	-0.24	-0.12	0.60	1.00	0.08
delinquencyw3	-0.08	0.01	0.06	0.85	0.08	1.00

```
>
mat.regress(lind1$cor,c(1:3),c(4:6))
$beta
```

	del	del1	del2
mom	-0.19	-0.18	-0.11
dad	-0.11	-0.19	0.00
rec	0.11	0.05	0.09

Multiple R

```
$R
```

	del	del1	del2
	0.22	0.29	0.12

```
$R2
```

	del	del1	del2
	0.05	0.09	0.01

Multiple stats

```
> mat.regress(lind1$cor,c(1:3),c(4:6),n.obs=291)
```

```
$beta
```

	del	del1	del2
mom	-0.19	-0.18	-0.11
dad	-0.11	-0.19	0.00
rec	0.11	0.05	0.09

```
$se
```

	del	del1	del2
mom	0.06	0.06	0.06
dad	0.08	0.08	0.08
rec	0.07	0.07	0.07

```
$t
```

	del	del1	del2
mom	-2.93	-2.94	-1.64
dad	-1.43	-2.59	-0.02
rec	1.52	0.73	1.24

```
$Probability
```

	del	del1	del2
mom	0.00	0.00	0.10
dad	0.16	0.01	0.99
rec	0.13	0.47	0.22

```
$R
```

	del	del1	del2
	0.22	0.29	0.12

```
$R2
```

	del	del1	del2
	0.05	0.09	0.01

```
$shrunkR2
```

	del	del1	del2
	0.04	0.08	0.00

```
$seR2
```

	del	del1	del2
	0.02	0.03	0.01

```
$F
```

	del	del1	del2
	4.96	9.04	1.35

```
$probF
```

	del	del1	del2
	0.002	0.000	0.257

```
$df
```

```
[1] 3 287
```

```

> lind.keys1 <-
make.keys(17,list(mom=c(2,3,4,12,14),dad=c(5,6,7,13,15),
rec=c(7:10),del=c(16,17),del1=c(16),del2=c(17),male=c(1)))
> lind1 <- score.items(lind.keys1,lindsay)
> lind1

```

Alpha:

	mom	dad	rec	del	del1	del2	male
[1,]	0.73	0.85	0.22	0.14	1	1	1

Average item correlation:

	mom	dad	rec	del	del1	del2	male
[1,]	0.35	0.53	0.07	0.08	1	1	1

Scale intercorrelations:

	mom	dad	rec	del	del1	del2	male
mom	1.00	0.42	0.29	-0.20	-0.25	-0.08	0.04
dad	0.42	1.00	0.61	-0.12	-0.24	0.01	0.00
rec	0.29	0.61	1.00	-0.01	-0.12	0.06	-0.05
del	-0.20	-0.12	-0.01	1.00	0.60	0.85	0.23
del1	-0.25	-0.24	-0.12	0.60	1.00	0.08	0.11
del2	-0.08	0.01	0.06	0.85	0.08	1.00	0.21
male	0.04	0.00	-0.05	0.23	0.11	0.21	1.00

Add gender

Multiple R with gender

```
> mat.regress(lind1$cor,c(1:3,7),c(4:6),n.obs=291)
```

```
$beta
```

	del	del1	del2
mom	-0.20	-0.19	-0.12
dad	-0.12	-0.20	-0.01
rec	0.13	0.06	0.11
male	0.24	0.12	0.22

```
$se
```

	del	del1	del2
mom	0.06	0.06	0.06
dad	0.07	0.07	0.08
rec	0.07	0.07	0.07
male	0.06	0.06	0.06

```
$t
```

	del	del1	del2
mom	-3.23	-3.06	-1.86
dad	-1.56	-2.65	-0.10
rec	1.85	0.87	1.51
male	4.37	2.15	3.83

```
$Probability
```

	del	del1	del2
mom	0.00	0.00	0.06
dad	0.12	0.01	0.92
rec	0.07	0.38	0.13
male	0.00	0.03	0.00

```
$R
```

	del	del1	del2
	0.33	0.32	0.25

```
$R2
```

	del	del1	del2
	0.11	0.10	0.06

```
$shrunkR2
```

	del	del1	del2
	0.10	0.09	0.05

```
$seR2
```

	del	del1	del2
	0.03	0.03	0.03

```
$F
```

	del	del1	del2
	8.72	8.01	4.74

```
$probF
```

	del	del1	del2
	0.000	0.000	0.001

```
$df
```

```
[1] 4 286
```


sem of delinquency

Final comments

I. Theory first

II. Measurement model

III. structural model

IV. Theory last

Theory first

I. What are the constructs of interest

II. How do we identify them

III. What are the observed variables

A. how well do they measure latent
constructs

IV. What is the presumed causal structure

Measurement model

- I. How many latent variables
- II. How well are they measured
- III. What are alternative models
 - A. factors versus components
 - B. simple structure, hierarchical structure, bifactor models, circumplex, simplex

Structural model

I. Direction of causality

II. Parsimony versus fit

III. Alternative structural models

A. equivalent models

B. nested models

Theory

- I. What have we learned that we did not know
- II. What do we know is wrong that we used to think was right