Advanced Measurement Theory Course Notebook

William M. Murrah

2022-12-11

Contents

Introduction to the Course

Welcome! This is a notebook for ERMA 8350 Advanced Measurement Theory. The class will be using the textbook *Handbook of Educational Measurement and Psychometrics Using R* (Desjardins and Bulut, 2018), which will be the primary source for learning to use R for the methods covered in this course. I will use this notebook to make available additional readings to help you learn the theory behind these methods and to provide published examples of their use. It may include some examples from the textbook, with some elaborations, additional readings, and some more details about implementing the methods in R. These web-based notes will make it easy for you to use code, by allowing you to copy and paste code found within. Some of you will have experience with R and others not. So I will try to also point you to additional resources that may be helpful. For example, in this preface I will provide links to resources to help you setup R and RStudio. RStudio is a platform to make using R more productive. I will use it extensively in this course.

There are at least two way you can access the software needed for this course. You can use the virtual labs on campus. I know at least the education virtual labs have R and RStudio installed. IF you go this route you can watch the following video. Note you will need Duo setup for this to work.

Using Vlab to acces R/RStudio

A better option if you have a laptop, you can install both programs on your computer. They are both absolutely free and available on all major operating systems, so you will not have to worry about transferring information across computers, limited connection speeds, or other hassles inherent with the VLab route.

The following links take you to videos instructing you how to install them.

Installing R and RStudio

Organizing Projects in RStudio

Resources for Learning R

While such experience is certainly helpful, I do not assume you have prior knowledge of using R. I will demonstrate the use of R and provide (particularly in this notebook) the R code needed to use the methods we will learn. However, even if you have prior experience with R, you should plan to spend time learning to program in R. Some people find this intimidating initially, but most of you will grow to find R programming rewarding, and even fun by the end of the course. But, there will be frustration for sure.

Here are some good places to start learning R:

CRAN

R Packages

R is, among other paradigms, a functional programming language, which means is heavily utilizes functions. R's functions are stored in packages. While base R has a long list of very useful functions, to fully realize the power of R you will have to use additional packages. So, learning how to **install** packages (downloading from the web to your computer) and **loading** packages (making the package's functions accessible to your current R session) are important skills to master.

How To Use These Notes

Before going further, it may be helpful to watch the following video about how to use the code in this notebook with Rstudio:

How to Use RStudio with this Notebook

Chapter 1

Generalizability Theory

We describe our methods in this chapter.

Chapter 2

Factor Analysis

2.1 Correlation Coefficient

Pearson product-moment correlation:

$$r_{xy} = \frac{\Sigma_{n=1}^{n}(x_k - \bar{x})(y_i - \bar{y})}{\sqrt{\Sigma_{n=1}^{n}(x_i - \bar{x})^2}\sqrt{\Sigma_{n=1}^{n}(y_i - \bar{y})^2}} = \frac{s_{xy}}{s_x s_y}.$$

The equation looks very daunting, until you see that it is just the covariance of x and y divided by the product of their standard deviations.

```
library("MPsychoR")
data("YouthDep")
item1 <- YouthDep[, 1]
levels(item1) <- c("0", "1", "1")
item2 <- YouthDep[, 14]
levels(item2) <- c("0", "1", "1")
table(item1, item2)
```

```
     item2
item1    0    1
    0 1353  656
    1  115  166
```

```
## ------ correlation coefficients
library("psych")
tetcor <- tetrachoric(cbind(item1, item2))
```

```
tetcor
```

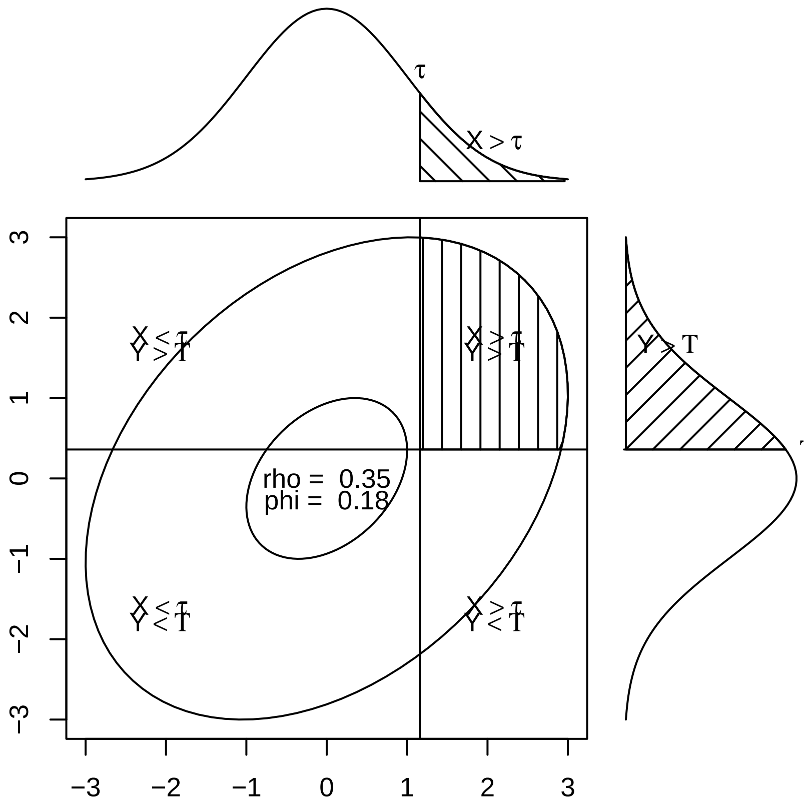
```
Call: tetrachoric(x = cbind(item1, item2))
tetrachoric correlation
```

```
      item1 item2
item1 1.00
item2 0.35  1.00

 with tau of
item1 item2
 1.16  0.36
```

```
item1 <- YouthDep[, 1]
item2 <- YouthDep[, 14]
polcor <- polychoric(cbind(item1, item2))
polcor
```

```
Call: polychoric(x = cbind(item1, item2))
Polychoric correlations
      item1 item2
item1 1.00
item2 0.33  1.00

 with tau of
         1   2
item1 1.16 2.3
item2 0.36 1.2
```

```
draw.tetra(r = .35, t1 = 1.16, t2 = .36)
```



```
DepItems <- YouthDep[,1:26]
Depnum <- data.matrix(DepItems) - 1  ## convert to numeric
Rdep <- polychoric(Depnum)
```

2.2 Think about these situations

What do you do when you have a large number of variables you are considering as predictors of a dependent variable?

- Often, subsets of these variables are measuring the same, or very similar things.
- We might like to reduce the variables to a smaller number of predictors.

What if you are developing a measurement scale and have a large number of items you think measure the same construct

- You might want to see how strongly the items are related to the construct.

2.3 Solutions

1. Principal Components Analysis
   - transforming the original variables into a new set of linear combinations (pricipal components).
2. Factor Analysis
   - setting up a mathematical model to estimate the number or factors

2.4 Principal Components Analysis

- Concerned with explaining variance-covariance structure of a set of variables.
- PCA attempts to explain as much of the total variance among the observed variables as possible with a smaller number of components.
- Because the variables are standardized prior to analysis, the total amount of variance available is the number of variables.
- The goal is **data reduction** for subsequent analysis.
- Variables *cause* components.
- Components are not representative of any underlying theory.

2.5 Factor Analysis

- The goal is understanding underlying constructs.
- Uses a modified correlation matrix (reduced matrix)
- factors *cause* the variables.
- Factors represent theoretical constructs.
- Focuses on the common variance of the variables, and purges the unique variance.

2.6 Components

The principal components partition the total variance (the sum of the variances of the original variables) by finding the linear combination of the variables that account for the maximum amount of variance:

$$PC1 = a_{11}x_1 + a_{12}x_2 ... a_{1p}x_p,$$

This is repeated as many time as there are variables.

2.7 PC Extraction

draw pretty pictures on the board

2.8 Eigenvalues

Eigenvalues represent the variance in the variables explained by the success components.

2.9 Determining the Number of Factors

1. Kaiser criterion: Retain only factors with eigenvalues > 1. (generally accurate)
2. Scree plot: plot eigenvalues and drop factors after leveling off.
3. Parallel analysis: compare observed eigenvalues to parallel set of data from randomly generated data. Retain factors in original if eigenvalue is greater than random eigenvalue.
4. Factor meaningfulness is also very important to consider.

2.10 Example data

```
lower <- "
1.00
0.70 1.00
0.65 0.66 1.00
0.62 0.63 0.60 1.00
"
cormat <- getCov(lower, names = c("d1", "d2", "d3", "d4"))

cormat
```

```
     d1   d2   d3   d4
d1 1.00 0.70 0.65 0.62
d2 0.70 1.00 0.66 0.63
d3 0.65 0.66 1.00 0.60
d4 0.62 0.63 0.60 1.00
```

2.11 Kaiser

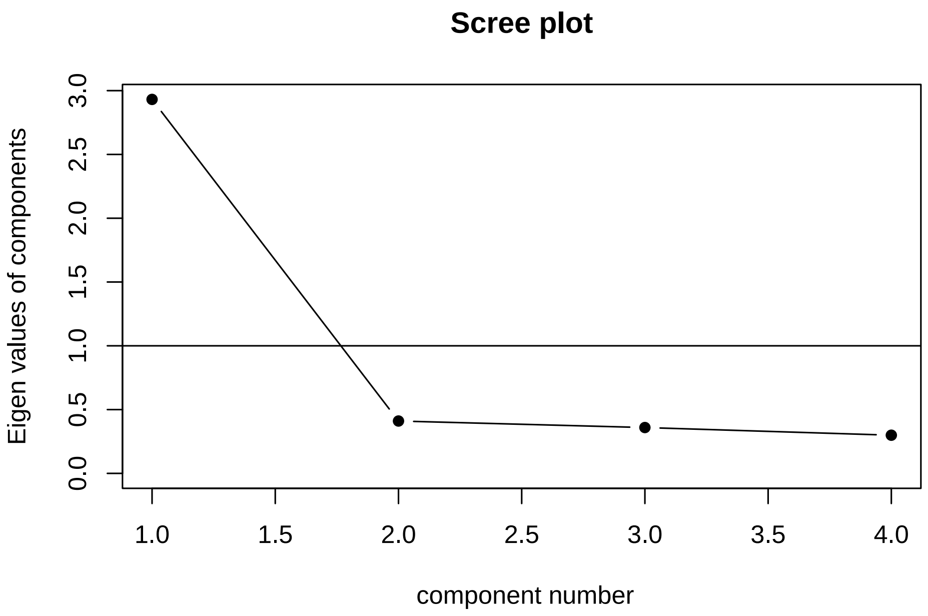
Retain factors with eigenvalues greater than 1

```
eigen(cormat)$values
```

```
[1] 2.9311792 0.4103921 0.3592372 0.2991916
```

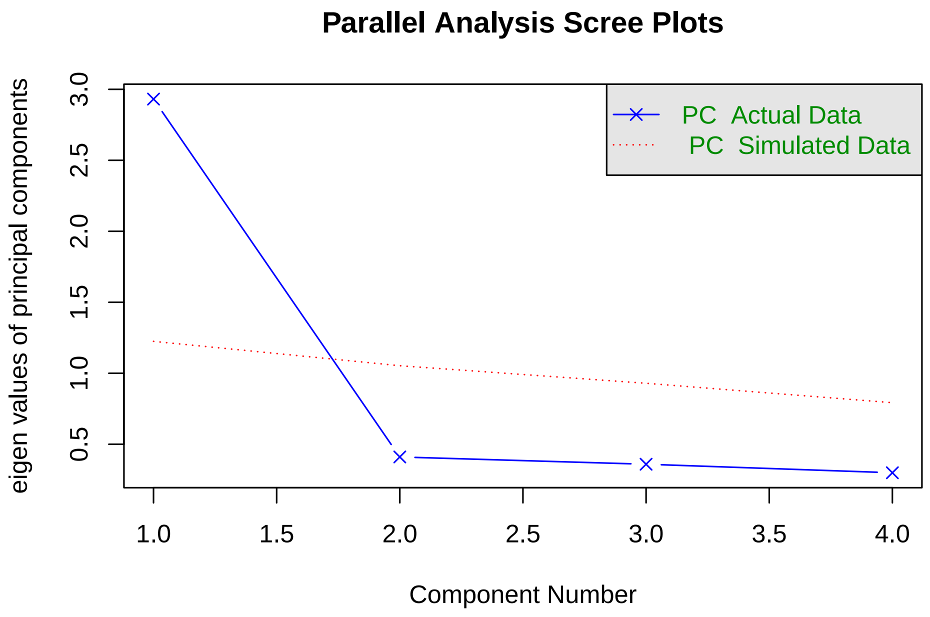
```
scree(cormat, factors = FALSE)
```

2.12 Scree Plot



```
fa.parallel(cormat, fa = "pc")
```

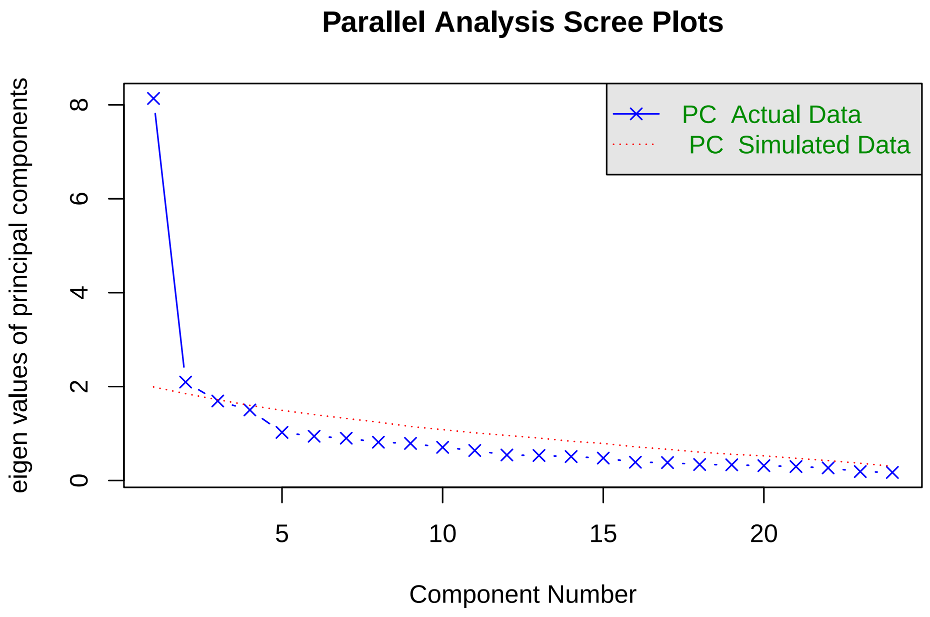
2.13 Horn's Parallel Analysis



```
Parallel analysis suggests that the number of factors =  NA  and the number of components =  1
```

2.14 Another example

```
fa.parallel(Harman74.cor$cov, fa = "pc")
```



```
Parallel analysis suggests that the number of factors =  NA  and the number of componen
```

2.15 Rotation

- Principal components are derived to maximize the variance accounted for (data reduction).
- Rotation is done to make the factors more interpretable (i.e. meaningful).
- Two major classes of rotation:
  - Orthogonal - new factors are still uncorrelated, as were the initial factors.
  - Oblique - new factors are allowed to be correlated.

Essentially reallocates the loadings. The first factor may not be the one accounting for the most variance.

2.16 Orthogonal Rotation

1. **Quartimax** - idea is to clean up the *variables.* Rotation done so each variable loads mainly on one factor. Problematic if there is a general factor on which most or all variables load on (think IQ).

2. **Varimax** - to clean up *factors.* So each factor has high correlation with a smaller number of variables, low correlation with the other variables. Generally makes interpretation easier.

2.17 Oblique Rotation

- Often correlated factors are more reasonable.
- Therefore, oblique rotation is often preferred.
- But interpretation is more complicated.

2.18 Factor Matrices

1. Factor pattern matrix:
   - includes *pattern coefficients* analogous to standardized partial regression coefficients.
   - Indicated the unique importance of a factor to a variable, holding other factors constant.
2. Factor structure matrix:
   - includes *structure coefficients* which are simple correlations of the variables with the factors.

2.19 Which matrix should we interpret?

- When orthogonal rotation is used interpret *structural coefficients* (but they are the same as pattern coefficients).
- When oblique rotation is used pattern coefficients are preferred because they account for the correlation between the factors and they are parameters of the correlated factor model (which we will discuss next class).

2.20 Which variables should be used to interpret each factor?

- The idea is to use only those variables that have a strong association with the factor.
- Typical thresholds are $|.30|$ or $|.40|$.
- Content knowledge is critical.

2.21 Examples

Let's look at some examples

2.22 Steps in Factor Analysis

1. Choose extraction method
    - So far we've focused on PCA
2. Determine the number of components/factors
    - Kaiser method: eigenvalues > 1
    - Scree plot: All components before leveling off
    - Horn's parallel analysis: components/factors greater than simulated values from random numbers
3. Rotate Factors
    - Orthogonal
    - Oblique
4. Interpret Components/Factors

2.23 Tom Swift's Electric Factor Analysis Factory

"Little Jiffy" method of factor analysis

1. Extraction method : PCA
2. Number of factors: eigenvalues > 1
3. Rotation: orthogonal(varimax)

Table 2.1: Functional Definitions of Tom Swift's Original 11 Variables

Dimension	Derivation
Thickness	x
Width	y
Length	z
Volume	xyz
Density	d
Weight	xyzd
Surface area	2(xy + xz + yz)
Cross-section	yz
Edge length	4(x + y + z)
Diagonal length	(x^2)
Cost/lb	c

4. Interpretation

2.24 Metal Boxes

```
'data.frame':   63 obs. of  11 variables:
 $ thick   : num  1.362 2.385 3.101 0.934 0.845 ...
 $ width   : num  1.71 2.83 4.32 3.2 3.84 ...
 $ length  : num  2.93 5.01 5.99 4.15 4.09 ...
 $ volume  : num  6.02 30.2 72.01 11.78 16.1 ...
 $ density : int  10 7 16 22 11 16 11 21 6 13 ...
 $ weight  : num  60 210 1152 264 176 ...
 $ surface : num  22 62.1 108.2 38 48 ...
 $ crosssec: num  5.87 15.06 23.53 12.02 16.13 ...
 $ edge    : num  23.9 39.9 51.5 31.9 36.1 ...
 $ diagonal: num  196 1444 3721 676 1089 ...
 $ cost    : num  4.48 2.37 9.77 22.21 15.86 ...
```

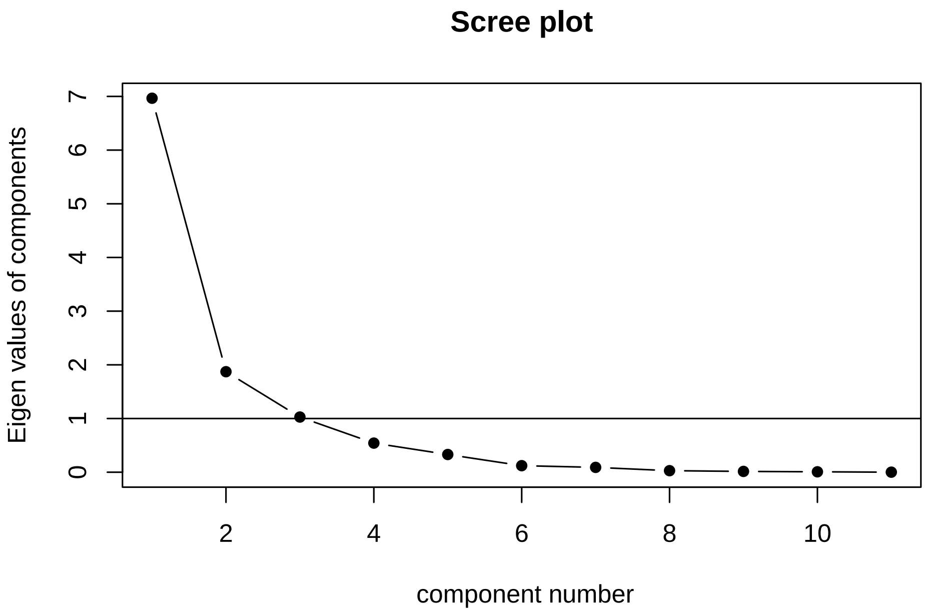
Dimension	Derivation
Thickness	x
Width	y
Length	z
Volume	xyz
Density	d
Weight	$xyzd$
Total surface area	$2(xy + xz +_y z)$
Cross-sectional area	yz
Total edge length	$4(x + y + z)$
Internal diagonal length	$(x^2 + y^2 + z^2)^2$
Cost per pound	c

Table 2.2: Correlations between dimensions

	thick	width	length	volume	density	weight	surface	crosssec	edge	diagonal	cost
thick	1.00	0.49	0.24	0.84	-0.13	0.59	0.74	0.46	0.61	0.51	-0.02
width	0.49	1.00	0.61	0.77	-0.15	0.55	0.87	0.92	0.88	0.78	0.03
length	0.24	0.61	1.00	0.58	-0.02	0.45	0.72	0.83	0.84	0.86	-0.02
volume	0.84	0.77	0.58	1.00	-0.22	0.65	0.97	0.81	0.87	0.85	-0.11
density	-0.13	-0.15	-0.02	-0.22	1.00	0.44	-0.20	-0.15	-0.15	-0.18	0.62
weight	0.59	0.55	0.45	0.65	0.44	1.00	0.65	0.56	0.61	0.57	0.24
surface	0.74	0.87	0.72	0.97	-0.20	0.65	1.00	0.92	0.97	0.91	-0.07
crosssec	0.46	0.92	0.83	0.81	-0.15	0.56	0.92	1.00	0.96	0.93	-0.03
edge	0.61	0.88	0.84	0.87	-0.15	0.61	0.97	0.96	1.00	0.92	-0.04
diagonal	0.51	0.78	0.86	0.85	-0.18	0.57	0.91	0.93	0.92	1.00	-0.12
cost	-0.02	0.03	-0.02	-0.11	0.62	0.24	-0.07	-0.03	-0.04	-0.12	1.00

2.25 Correlations

2.26 Eigenvalues > 1



2.27 Orthogonal Rotation

```
Loadings:
         RC1    RC3    RC2    RC5    RC4
thick           0.968
width                         0.734
length   0.986
volume          0.754
density                0.864
weight
surface  0.703
crosssec 0.829
edge     0.819
diagonal 0.875
cost                                 0.955

                 RC1   RC3   RC2   RC5   RC4
SS loadings    4.425 2.662 1.318 1.225 1.106
Proportion Var 0.402 0.242 0.120 0.111 0.101
Cumulative Var 0.402 0.644 0.764 0.876 0.976
```

2.28 Orthogonal Rotation with Loadings > .70

```
Loadings:
         RC1    RC3    RC2
```

```
thick           0.947
width     0.801
length    0.936
volume          0.744
density                0.930
weight
surface   0.792
crosssec  0.942
edge      0.892
diagonal  0.905
cost                   0.841

                 RC1   RC3   RC2
SS loadings    5.298 2.699 1.868
Proportion Var 0.482 0.245 0.170
Cumulative Var 0.482 0.727 0.897
```

2.29 R Code for Chapter 2

```
## ----------------------- Chapter 2: Factor Analysis ------------------
library("MPsychoR")
data("YouthDep")
item1 <- YouthDep[, 1]
levels(item1) <- c("0", "1", "1")
item2 <- YouthDep[, 14]
levels(item2) <- c("0", "1", "1")
table(item1, item2)

## ------ correlation coefficients
library("psych")
tetcor <- tetrachoric(cbind(item1, item2))
tetcor
item1 <- YouthDep[, 1]
item2 <- YouthDep[, 14]
polcor <- polychoric(cbind(item1, item2))
polcor

DepItems <- YouthDep[,1:26]
Depnum <- data.matrix(DepItems) - 1  ## convert to numeric
Rdep <- polychoric(Depnum)

data("Rmotivation")
vind <- grep("ext|int", colnames(Rmotivation))
Rmotivation1 <- Rmotivation[, vind]
Rmot1 <- tetrachoric(Rmotivation1, smooth = FALSE)
tail(round(eigen(Rmot1$rho)$values, 3))
Rmot <- tetrachoric(Rmotivation1)
tail(round(eigen(Rmot$rho)$values, 3))

## ----- exploratory factor analysis
motFA <- fa(Rmot$rho, nfactors = 2, rotate = "none", fm = "ml")
print(motFA$loadings, cutoff = 0.2)
round(motFA$communality, 2)

motFA2 <- fa(Rmot$rho, nfactors = 2, rotate = "varimax", fm = "ml")
plot(motFA$loadings, asp = 1, xlim = c(-0.2, 0.9), ylim = c(-0.5, 0.9), type = "n", xlab = "Factor 1", ylab = "Factor 2'
text(motFA$loadings, labels = rownames(motFA$loadings), cex = 0.8, col = "gray")
abline(h = 0, v = 0, col = "lightgray", lty = 2)
text(motFA2$loadings, labels = rownames(motFA2$loadings), col = 1, cex = 0.8)
legend("bottomleft", legend = c("rotated", "unrotated"), col = c("black", "gray"), pch = 19)

Rmot2 <- tetrachoric(Rmotivation[,1:36])
motFA3 <- fa(Rmot2$rho, nfactors = 3, rotate = "oblimin", fm = "ml")
motFA3$loadings
round(motFA3$Phi, 3)

motFA2 <- fa(Rmotivation1, nfactors = 2, rotate = "varimax", cor = "tet", fm = "ml", scores = "regression",
             missing = TRUE, impute = "median")
dim(motFA2$scores)

Rdep <- polychoric(Depnum)$rho
evals <- eigen(Rdep)$values
scree(Rdep, factors = FALSE)
(evals/sum(evals)*100)[1:2]

set.seed(123)
resPA <- fa.parallel(Depnum, fa = "pc", cor = "poly", fm = "ml")
resvss <- vss(Rdep, fm = "ml", n.obs = nrow(Depnum), plot = FALSE)
resvss

fadep <- fa(Depnum, 1, cor = "poly", fm = "ml")
summary(fadep)

resnf <- nfactors(Depnum, n = 8, fm = "ml", cor = "poly")
resnf

## ----- Bayesian exploratory factor analysis
library("MPsychoR")
library("corrplot")
library("BayesFM")
data("Privacy")
Privstd <- scale(Privacy)
corrplot(cor(Privstd))

Nid <- 2              ## minimum number of variables per factor
pmax <- trunc(ncol(Privstd)/Nid)   ## maximum number of factors
pmax

set.seed(123)
Rsim <- simul.R.prior(pmax, nu0 = pmax + c(1, 2, 5, 7, 10))
plot(Rsim)

Ksim <- simul.nfac.prior(nvar = ncol(Privstd), Nid = Nid, Kmax = pmax, kappa = c(.1, .2, .5, 1))
plot(Ksim)

set.seed(222)
fitbefa <- befa(Privstd, Nid = 2, Kmax = pmax, nu0 = 10, kappa = 0.2, kappa0 = 0.1, xi0 = 0.1,
                burnin = 5000, iter = 50000)
fitbefa <- post.column.switch(fitbefa)   ## column reordering
fitbefa <- post.sign.switch(fitbefa)     ## sign switching
sumbefa <- summary(fitbefa)

## ----- confirmatory factor analysis
```

```r
library("MPsychoR")
library("lavaan")
data("Rmotivation")
vind <- grep("ext|int", colnames(Rmotivation)) ## ext/int items
Rmot <- na.omit(Rmotivation[, vind])
mot_model <- '
  extrinsic  =~ ext1 + ext2 + ext3 + ext4 + ext5 + ext6 +
                ext7 + ext8 + ext9 + ext10 + ext11 + ext12
  intrinsic =~  int1 + int2 + int3 + int4 + int5'
fitMot <- lavaan::cfa(mot_model, data = Rmot, ordered = names(Rmot))

library("semPlot")
semPaths(fitMot, what = "est", edge.label.cex = 0.7, edge.color = 1, esize = 1, sizeMan = 4.5, asize = 2.5,
         intercepts = FALSE, rotation = 4, thresholdColor = "red", mar = c(1, 5, 1.5, 5), fade = FALSE, nCharNodes = 4)

inspect(fitMot, what = "est")$theta
inspect(fitMot, what = "est")$lambda
inspect(fitMot, what = "std")$lambda
inspect(fitMot, what = "est")$psi
inspect(fitMot, what = "std")$psi

parameterEstimates(fitMot, standardized = TRUE)
summary(fitMot, standardized = TRUE, fit.measures = TRUE)
parameterEstimates(fitMot)[5,]

mot_model2 <- '
  extrinsic  =~ ext1 + ext2 + ext3 + ext4 + ext6 + ext7 +
                ext8 + ext9 + ext10 + ext11 + ext12
  intrinsic =~  int1 + int2 + int3 + int4 + int5'
fitMot2 <- lavaan::cfa(mot_model2, data = Rmot, ordered = names(Rmot)[-5])
vind <- c(1:4, 13:16, 32:35)
Rmot2 <- na.omit(Rmotivation[, vind])

mot_model3 <- '
  extrinsic  =~ ext1 + ext2 + ext3 + ext4
  hybrid =~ hyb1 + hyb2 + hyb3 + hyb4
  intrinsic =~  int1 + int2 + int3 + int4
  motivation =~ extrinsic + hybrid + intrinsic'
fitMot3 <- lavaan::cfa(mot_model3, data = Rmot2, ordered = names(Rmot2))

semPaths(fitMot3, what = "std", edge.label.cex = 0.7, edge.color = 1, esize = 1, sizeMan = 5, asize = 2.5,
         intercepts = FALSE, rotation = 4, thresholdColor = "red", mar = c(1, 5, 1.5, 5), fade = FALSE, nCharNodes = 4)

summary(fitMot3, standardized = TRUE, fit.measures = TRUE)

vind <- c(1:4, 13:16, 32:35, 39:41)
Rmot3 <- na.omit(Rmotivation[, vind])
mot_model4 <- '
  extrinsic  =~ ext1 + ext2 + ext3 + ext4
  hybrid =~ hyb1 + hyb2 + hyb3 + hyb4
  intrinsic =~  int1 + int2 + int3 + int4
  motivation =~ extrinsic + hybrid + intrinsic
  motivation ~ npkgs + phd'
fitMot4 <- lavaan::cfa(mot_model4, data = Rmot3, ordered = names(Rmot3[1:12]))

semPaths(fitMot4, what = "std", edge.label.cex = 0.7, edge.color = 1, esize = 1, sizeMan = 5, asize = 2.5,
         intercepts = FALSE, rotation = 4, thresholdColor = "red", mar = c(1, 5, 1.5, 5), fade = FALSE, nCharNodes = 4)
```

```
parameterEstimates(fitMot4)[16:17,]

library("semTools")
data("Bergh")
GP_model <- 'GP =~ EP + HP + DP + SP'
minvfit1 <- measEq.syntax(GP_model, data = Bergh, group = "gender", return.fit = TRUE)
minvfit2 <- measEq.syntax(GP_model, data = Bergh, group = "gender",
                          group.equal = c("loadings"), return.fit = TRUE)
minvfit3 <- measEq.syntax(GP_model, data = Bergh, group = "gender",
                          group.equal = c("loadings", "intercepts"), return.fit = TRUE)
minvfit4 <- measEq.syntax(GP_model, data = Bergh, group = "gender",
                          group.equal = c("loadings", "intercepts", "means"), return.fit = TRUE)
anova(minvfit1, minvfit2, minvfit3, minvfit4)

GP_model <- 'GP =~ c(v1,v1)*EP + c(v2,v2)*HP + c(v3,v3)*DP + SP'
fitBase <- lavaan::cfa(GP_model, data = Bergh, group = "gender", estimator = "MLR")

GP_model <- 'GP =~ EP + HP + DP + SP'
fitBase <- lavaan::cfa(GP_model, data = Bergh, group = "gender", group.equal = c("loadings"),
                       group.partial = c("GP=~ SP"), estimator = "MLR")

fitBase1 <- lavaan::cfa(GP_model, data = Bergh, group = "gender", group.equal = c("loadings", "intercepts")
                        group.partial = c("GP=~SP", "DP~1", "HP~1", "SP~1"), estimator = "MLR")

GP_model2 <- 'GP =~ c(v1,v1)*EP + c(v2,v2)*HP + c(v3,v3)*DP + c(NA, 0)*SP'
fitIO <- lavaan::cfa(GP_model2, data = Bergh, group = "gender", group.equal = c("intercepts"),
                     group.partial = c("DP~1", "HP~1", "SP~1"), estimator = "MLR")

fitMarg <- lavaan::cfa(GP_model, data = Bergh, group = "gender", group.equal = c("loadings", "intercepts"),
                       group.partial = c("DP~1", "HP~1", "SP~1"), estimator = "MLR")

anova(fitMarg, fitBase1)

library("MPsychoR")
library("lavaan")
data("SDOwave")
model_sdo1 <- '
  SDO1996 =~ 1*I1.1996 + a2*I2.1996 + a3*I3.1996 + a4*I4.1996
  SDO1998 =~ 1*I1.1998 + a2*I2.1998 + a3*I3.1998 + a4*I4.1998
  SDO1996 ~~ SDO1998

  ## intercepts
  I1.1996 ~ int1*1; I1.1998 ~ int1*1
  I2.1996 ~ int2*1; I2.1998 ~ int2*1
  I3.1996 ~ int3*1; I3.1998 ~ int3*1
  I4.1996 ~ int4*1; I4.1998 ~ int4*1

  ## residual covariances
  I1.1996 ~~ I1.1998
  I2.1996 ~~ I2.1998
  I3.1996 ~~ I3.1998
  I4.1996 ~~ I4.1998

  ## latent means: 1996 as baseline
  SDO1996 ~ 0*1
  SDO1998 ~ 1'
fitsdo1 <- cfa(model_sdo1, data = SDOwave, estimator = "MLR")
```

```
parameterEstimates(fitsdo1)[22:23,]

model_sdo2 <- '
  ## 1st CFA level, constant loadings across time
  SDOD1996 =~ 1*I1.1996 + d1*I2.1996
  SDOD1998 =~ 1*I1.1998 + d1*I2.1998
  SDOD1999 =~ 1*I1.1999 + d1*I2.1999
  SDOE1996 =~ 1*I3.1996 + a1*I4.1996
  SDOE1998 =~ 1*I3.1998 + a1*I4.1998
  SDOE1999 =~ 1*I3.1999 + a1*I4.1999

  ## 2nd CFA level, constant loadings across time
  SDO1996 =~ 1*SDOD1996 + sd1*SDOE1996
  SDO1998 =~ 1*SDOD1998 + sd1*SDOE1998
  SDO1999 =~ 1*SDOD1999 + sd1*SDOE1999

  ## Constant 1st level intercepts
  I1.1996 ~ iI1*1; I1.1998 ~ iI1*1; I1.1999 ~ iI1*1
  I2.1996 ~ iI2*1; I2.1998 ~ iI2*1; I2.1999 ~ iI2*1
  I3.1996 ~ iI3*1; I3.1998 ~ iI3*1; I3.1999 ~ iI3*1
  I4.1996 ~ iI4*1; I4.1998 ~ iI4*1; I4.1999 ~ iI4*1

  ## residual covariances:
  I1.1999 ~~ I1.1998; I1.1996 ~~ I1.1998; I1.1999 ~~ I1.1996
  I2.1999 ~~ I2.1998; I2.1996 ~~ I2.1998; I2.1999 ~~ I2.1996
  I3.1999 ~~ I3.1998; I3.1996 ~~ I3.1998; I3.1999 ~~ I3.1996
  I4.1999 ~~ I4.1998; I4.1996 ~~ I4.1998; I4.1999 ~~ I4.1996

  ## latent means
  SDO1996 ~ 0*1    ## 1996 baseline year
  SDO1998 ~ 1      ## 1998 vs. 1996
  SDO1999 ~ 1      ## 1999 vs. 1996
'
fitsdo2 <- cfa(model_sdo2, data = SDOwave, estimator = "MLR")

semPaths(fitsdo2, what = "est", edge.label.cex = 0.7, edge.color = 1, esize = 1, sizeMan = 6, asize = 2.5,
         intercepts = FALSE, rotation = 4, thresholdColor = "red", mar = c(1, 5, 1.5, 5), fade = FALSE)
parameterEstimates(fitsdo2)[43:45,]

data("FamilyIQ")
modelIQ <- '
 level: 1
  numeric =~ wordlist + cards + matrices
  perception =~ figures + animals + occupation
 level: 2
  general =~ wordlist + cards +  matrices + figures + animals +
             occupation'
fitIQ <- cfa(modelIQ, data = FamilyIQ, cluster = "family", std.lv = TRUE)
fitIQ

## ----- bayesian confirmatory factor analysis
library("blavaan")
dpriors()[c("lambda", "itheta", "ipsi")]

library("MPsychoR")
data("Bergh")
GP_model <- 'GP =~ EP + HP + DP + SP'
```

```
set.seed(123)
fitBCFA <- bcfa(GP_model, data = Bergh, burnin = 2000, sample = 10000, n.chains = 2)

plot(fitBCFA, pars = 1:2, plot.type = "trace")
plot(fitBCFA, pars = 1:2, plot.type = "autocorr")
summary(fitBCFA)
```

Bibliography

Desjardins, C. D. and Bulut, O. (2018). *Handbook of educational measurement and psychometrics using R.* CRC Press.