Using R Series

Advanced Statistics Using R

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Preface

The book was developed from the teaching materials used for the Advanced Statistics taught by Drs. Zhiyong Zhang and Lijuan Wang at the University of Notre Dame started in Fall 2010. Advanced Statistics is a second course in statistics, which is intended to help students have a broader and deeper understanding of some widely used statistical methods in psychological research, beyond what has been covered in the Introduction to Statistics class taught at Notre Dame. Topics include a review of basic statistical concepts, an introduction to R, statistical inference, multiple regression, repeated measures ANOVA, mediation, moderation, factor analysis, logistic regression analysis, and longitudinal data analysis. The emphasis is on developing skills for implementing statistical methods for psychological research.

The book was initially offered as an online book on our webiste https://advstats.psychstat.org/ supported by digital learning initiatives at the University of Notre Dame to provide affordable textbooks for students. With more and more demending, we decided to publish it as an E-book as you are reading.

We would like to thank all the students who took the class and motivated the development of the book.

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Contents

Chapter 1

R Basics

1.1 Introduction to R

1.1.1 What is R?

R is a statistical language and software for data analysis and graphing. It is an open-source implementation of the S language which was developed at Bell Laboratories (formerly AT&T, now Lucent Technologies) by John Chambers and colleagues. Therefore, much code written for S runs directly under R.

R is built through packages, including the base package and thousands of extended packages or extensions.The base package contains the basic functions which let R function as a language: arithmetic, input/output, basic programming support, etc. It also allows the creation of extension packages based on it. With the base package and the extensions, many statistical data analysis can be conducted and high quality statistical graphs can be produced.

R is available as Free Software under the terms of the Free Software Foundation's GNU General Public License in source code form. It compiles and runs on a wide variety of UNIX platforms and similar systems (including FreeBSD and Linux), Windows and Mac OS.

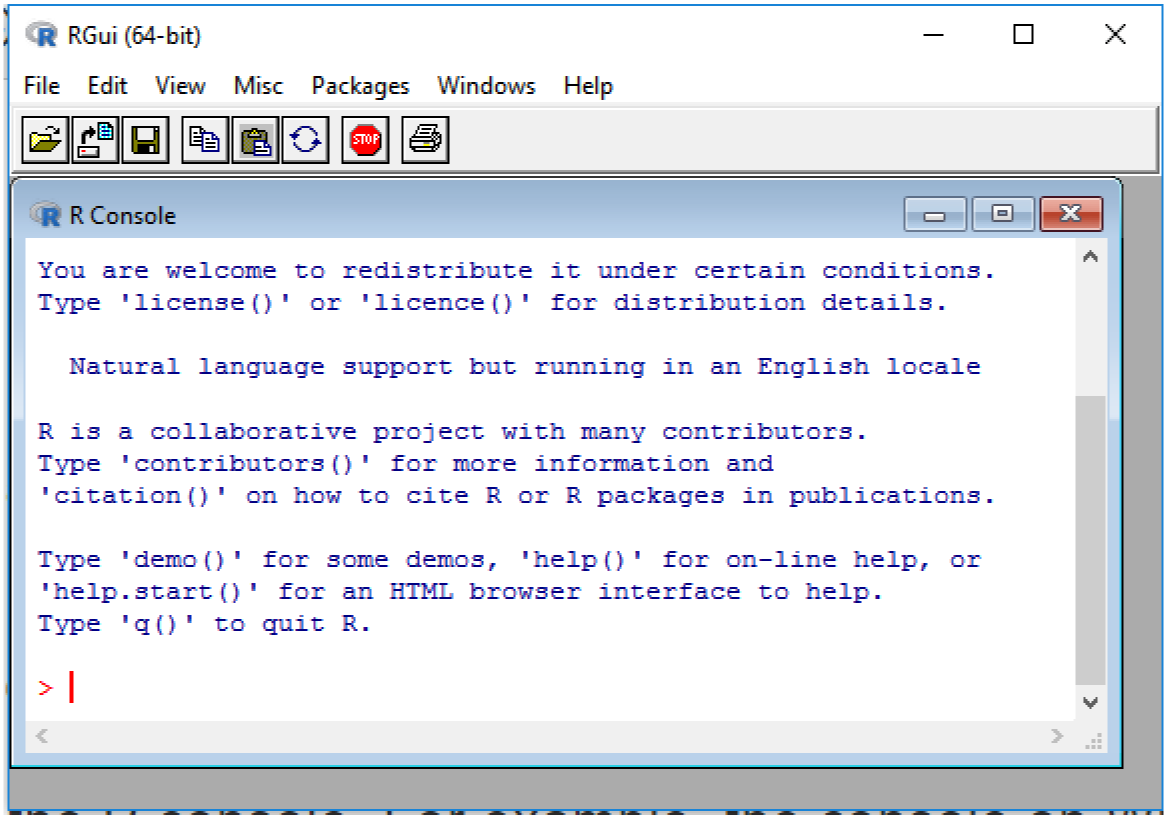
1.1.2 Why R?

R is now widely used by both statisticians and applied researchers for good reasons.

- R is free and open-source and can be used on Windows, Mac OS, Linux and even online.
- R is an integrated environment suitable for data manipulation, data analysis and graphical display.
- R is designed around a true computer language, and it allows users to write their own functions and packages for even the newestly developed statistical methods.
- R is supported by thousands of users around the world. Try out this link: https://www.r-project.org/help.html.

1.1.3 How to install R?

- R can be installed on different operating systems.
- For Windows PC
  1. Download the latest version of R from this url: https://cran.r-project.org/bin/windows/base/
  2. Double click the downloaded file for a Windows style installer. Select default options to proceed the installation.
- For Mac
  1. Download R from this url: https://cran.r-project.org/bin/macosx/
  2. Double click the downloaded file for installation.
  3. For Mac OS X 10.4 or earlier, please use this link http://cran.stat.ucla.edu/bin/macosx/old/R-2.9.2.dmg
- For Linux: See the instruction for Ubuntu, Redhat, SUSE and Debian at https://cran.r-project.org/bin/linux/
- Rstudio (the desktop version) is a free and open source integrated development environment (IDE) you may find useful. ### Start R R is most easily used in an interactive manner. You ask R a question and it gives you an answer. Questions are asked and answered on the command line. To start R, the following procedure can be used.
- On an operating system with Windows interface such as Windows and Mac OS X, double click the R icon R will open the R console. For example, the console on Windows looks like



```
You are welcome to redistribute it under certain conditions.
Type 'license()' or 'licence()' for distribution details.

  Natural language support but running in an English locale

R is a collaborative project with many contributors.
Type 'contributors()' for more information and
'citation()' on how to cite R or R packages in publications.

Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.

> 
```

- On machines without Windows interface such as Ubuntu server, one can start R by typing R and return in the terminal.

1.2 Basic operations in R

R can be first used as an advanced calculator. The code below shows the use of addition (+), subtraction (-), multiplication (*), division (/), logarithm (ln), exponential (exp).

```
2+3
## [1] 5
4-1
## [1] 3
2*3
## [1] 6
(2+3)/4
## [1] 1.25
log(10)
## [1] 2.302585
exp(2)
## [1] 7.389056
5^3
## [1] 125
```

Each value used in R can be given a name and the value can be referred using its name. For example, if we let a = 2, then a can be used anywhere to replace the value 2. Some example code is given below.

```
a = 2
b <- 3
4 -> d

a*b
## [1] 6
(a+b)/d
## [1] 1.25
d^2
## [1] 16
```

1.3 Vector

R is called a “vector language” because it can work on vectors directly. Vector is the most basic data structure in R. A vector is a collection of elements of the same data type. The data types can be logical, integer, double, character, complex or raw.

1.3.1 Create a vector

A vector can be created using the c() function, which combines its arguments or input to form a vector. Several examples are given below. As for the simple operations, names can be used for vectors. By typing its name, the content of a vector will be printed.

```
outcome <- c(1, 0, 0, 1, 0, 1)
gender <- c('F', 'F', 'M', 'F', 'M')
income <- c(100, 500, 900, 400, 700, 650, 320)

outcome
## [1] 1 0 0 1 0 1
gender
## [1] "F" "F" "M" "F" "M"
income
## [1] 100 500 900 400 700 650 320
```

1.3.2 Operating a vector

1.3.2.1 Subset of a vector

Since there are multiple elements in a vector, the elements can be taken our using their index. The index of an element is its position in the vector. For example, the first element has the index 1, the second element has the index 2, and so on. For example, suppose there is a vector called income with 7 values: 100, 500, 900, 400, 700, 650, 320. To take out the first value, one can use income[1] and to take out the last value, one can use income[7]. Note that the index is put into a set of brackets "[ ]". A vector of indexes can be provided as a vector to take out multiple elements. For example, income[c(1, 3, 7)].

```
income[1]
## [1] 100
income[7]
## [1] 320
income[c(1,3,7)]
## [1] 100 900 320
income[2:5]
## [1] 500 900 400 700
```

1.3.2.2 Vector operations

A vector can be operated like a scalar in R. Most operations for a scalar will operate on all elements in a vector. For example, 2*income will multiple each element in income by 2. income > 500 will check each element to see whether it is larger than 500. The outcome is called a logical vector that includes values FALSE or TRUE. Some other examples can be seen below.

```
2*income
## [1]  200 1000 1800  800 1400 1300  640
income > 500
## [1] FALSE FALSE  TRUE FALSE  TRUE  TRUE FALSE
income == 500
## [1] FALSE  TRUE FALSE FALSE FALSE FALSE FALSE
income + 500
## [1]  600 1000 1400  900 1200 1150  820
income/10
## [1] 10 50 90 40 70 65 32
```

1.3.2.3 Basic statistical function operating on vectors

Since a vector is a collection of values, statistical functions can be applied to it. For example, the function length() tells the sample size (the number of elements) of a vector. The function sum() adds all the values in the vector together. Other functions include min(), max(), median(), sd(), var(), and many others.

```
length(income)
## [1] 7
summary(income)
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##     100     360     500     510     675     900
min(income)
## [1] 100
max(income)
## [1] 900
median(income)
## [1] 500
sd(income)
## [1] 265.8947
var(income)
## [1] 70700
```

1.4 Array and Matrix

R saves a table of data in an array or a matrix. We usually deal with two-dimensional matrix but higher-dimensional matrix can also be used in R.

1.4.1 Create an array / matrix

Two functions can be used to create a matrix, array() or matrix(). We show how to create a 3 by 4 matrix.

The code below creates a matrix using the function array(). Note that 1:12 generates a sequence of values, 1, 2, . . . , 12. The sequence of valus are used to create the matrix. dim=c(3,4) tells there are 3 rows and 4 columns in the matrix. The function takes the 12 values and fills each column sequentially. For example, it first fills in the first column using 1, 2, and 3. Then it fills the second column using 4, 5, and 6.

To change the positions of the values in the matrix, one has to change the input values. See the difference in the creation of matrix y.

```
x <- array(1:12, dim=c(3,4))
x
##      [,1] [,2] [,3] [,4]
## [1,]    1    4    7   10
## [2,]    2    5    8   11
## [3,]    3    6    9   12
```

```
y <- array(c(1,5,9,2,6,10,3,7,11,4,8,12), dim=c(3,4))
y
##      [,1] [,2] [,3] [,4]
## [1,]    1    2    3    4
## [2,]    5    6    7    8
## [3,]    9   10   11   12
```

The function matrix() can control how to fill the values in a matrix. For example, setting byrow=TRUE, the values will be filled by rows instead of by columns. Note that to use the function, one needs to tell either the number of rows using nrow or the number of columns using ncol.

```
x <- matrix(1:12, nrow=3)
x
##      [,1] [,2] [,3] [,4]
## [1,]    1    4    7   10
## [2,]    2    5    8   11
## [3,]    3    6    9   12

y <- matrix(1:12, nrow=3, byrow=TRUE)
y
##      [,1] [,2] [,3] [,4]
## [1,]    1    2    3    4
## [2,]    5    6    7    8
## [3,]    9   10   11   12
```

1.4.2 Operating an array or matrix

We are often interested in taking out a subset of values in a matrix. x[i,j] takes out values according to the index i for the rows and j for the columns. Both i and j can be a single value or a vector. When i is replaced by blank, the whole column(s) is taken out and when j is replaced by blank, the whole row(s) is taken out. Some examples are given below.

Note that when a vector of values are taken out, by default, the sub-matrix will be converted to a vector and lose the matrix property. To keep the matrix property, add the option drop=FALSE.

```
x <- array(1:12, dim=c(3,4))
x
##      [,1] [,2] [,3] [,4]
## [1,]    1    4    7   10
## [2,]    2    5    8   11
## [3,]    3    6    9   12
```

```
x[2,3]
## [1] 8
x[1:2, 1:2]
##      [,1] [,2]
## [1,]    1    4
## [2,]    2    5
x[2, ]
## [1]  2  5  8 11
x[2, , drop=FALSE]
##      [,1] [,2] [,3] [,4]
## [1,]    2    5    8   11

x[, 3]
## [1] 7 8 9
x[, 3, drop=FALSE]
##      [,1]
## [1,]    7
## [2,]    8
## [3,]    9
```

1.5 List

A list is a collection of multiple objects which can be a scalar, a vector, a matrix, etc. Each object in a list can have its own name.

1.5.1 Create a list

To create a list, the function list() can be used as shown in the examples below.

```
x <- list('a'=3, 'b'=c(1,2), 'm'=array(1:6, dim=c(3,2)))
x
## $a
## [1] 3
##
## $b
## [1] 1 2
##
## $m
##      [,1] [,2]
## [1,]    1    4
## [2,]    2    5
## [3,]    3    6
```

```
a <- 3
b <- c(1,2)
m <- array(1:6, dim=c(3,2))

y <- list(a, b, m)
y
## [[1]]
## [1] 3
##
## [[2]]
## [1] 1 2
##
## [[3]]
##      [,1] [,2]
## [1,]    1    4
## [2,]    2    5
## [3,]    3    6
```

1.5.2 Access the object of a list

There are at least two ways to access the objects in a list. First, each object in the list has an index according to its order, which can be used to access that object. For example, x[[1]] will access the first object in the list. Note that [[ ]] instead of [ ] is used here. Second, the name of the object can be used to access it. For example, x$a will access a in the list. Note that a dollar sign $ is added between the name of the list and the name of the object.

```
x <- list('a'=3, 'b'=c(1,2), 'm'=array(1:6, dim=c(3,2)))

x[[3]]
##      [,1] [,2]
## [1,]    1    4
## [2,]    2    5
## [3,]    3    6

x$m
##      [,1] [,2]
## [1,]    1    4
## [2,]    2    5
## [3,]    3    6
```

1.6 Data Frame

A data frame is a special list in which every object has the same size.

1.6.1 Create a data frame

To create a data frame, the function data.frame() can be used as shown in the examples below. The data read from a file into R are often saved into a data frame.

```r
a <- 1:3
b <- 4:6
d <- 7:9
y <- data.frame(a,b,d)
y
##   a b d
## 1 1 4 7
## 2 2 5 8
## 3 3 6 9
```

1.6.2 Access the components of a data frame

The same methods for access the objects in a list can be used for a data frame. For example, y$a will access a in the data frame. The R function attach() can conveniently copy all objects in a data frame into R workspace so that they can be accessed using their names directly. To remove those objects, the function detach() can be used. Some examples are given below.

```r
y <- data.frame(a=1:4,b=5:8,d=9:12)
y
##   a b  d
## 1 1 5  9
## 2 2 6 10
## 3 3 7 11
## 4 4 8 12

y$a
## [1] 1 2 3 4

attach(y)
b
## [1] 4 5 6

detach(y)
```

Chapter 2

Data in R

2.1 Reading Data from Files

In practical data analysis, data are often stored in a data file. R can read different types of data files such as the free format text files, comma separated value files, Excel files, SPSS files, SAS files, and Stata files.

2.1.1 Read Data from a Free Format Text File

The most common way to get data into R is to save data as free format in a text file and then use read.table() function to read the data. For example, let's read the data in a file called gpa.txt which is available on the website. The content of the data file is shown below.

```
## GPA data
## 999 represents missing data
 id gender college   gpa weight
  1      f     yes   3.6    110
  2      m     yes   3.5    170
  3      m      no  99.0    165
  4      m      no 999.0    190
  5      f      no 999.0     95
  6      m     yes   3.7    200
  7      m     yes   3.6    150
  8      f     yes   3.8    100
  9      f     yes   3.0    130
 10      f      no 999.0    120
```

Note that the first two lines of the data file start with "#", which are clearly notes or comments about the data. The third line appears to be variable names. After that, there are 10 lines of data.

The function read.table() can load data from a local computer and from a remote location on Internet. Since the data file here is online, we first show how to get data in this way using the code below. Note that

- file provides the link to the data file on the Internet.
- header=TRUE tells there are variable names in the data file.
- na.string=“999” tells missing data are coded by 999. Multiple missing data strings can be provided in a vector such as na.string=c(“99”,“999”).
- comment.char = “#” lets R to skip lines starting with “#” in the file.

```
gpadata <- read.table(file='data/gpa.txt', header=TRUE,
                      na.string="999", comment.char = "#")

gpadata
##    id gender college gpa weight
## 1   1      f     yes 3.6    110
## 2   2      m     yes 3.5    170
## 3   3      m      no  NA    165
## 4   4      m      no  NA    190
## 5   5      f      no  NA     95
## 6   6      m     yes 3.7    200
## 7   7      m     yes 3.6    150
## 8   8      f     yes 3.8    100
## 9   9      f     yes 3.0    130
## 10 10      f      no  NA    120
```

2.1.2 Access data

Data that are read into R are generally saved as a data frame. Some useful operations.

- Type the name of the data to show all the data
- head and tail: show the first and last few rows of data
- names: list the variable names in the data set
- dim: show the number of rows (sample size) and columns (number of variables) of the data
- attach: copy the variables into R working memory
- detach: remove the variables from working memory
- dataset$varname: take out a variable in the data set
- dataset[i,j]: take out values according to index

```
head(gpadata)
##   id gender college gpa weight
## 1  1      f     yes 3.6    110
## 2  2      m     yes 3.5    170
## 3  3      m      no  NA    165
## 4  4      m      no  NA    190
## 5  5      f      no  NA     95
## 6  6      m     yes 3.7    200
tail(gpadata)
##    id gender college gpa weight
## 5   5      f      no  NA     95
## 6   6      m     yes 3.7    200
## 7   7      m     yes 3.6    150
## 8   8      f     yes 3.8    100
## 9   9      f     yes 3.0    130
## 10 10      f      no  NA    120
names(gpadata)
## [1] "id"      "gender"  "college" "gpa"     "weight"
dim(gpadata)
## [1] 10  5
gpadata$weight
##  [1] 110 170 165 190  95 200 150 100 130 120
gpadata[, 2]
##  [1] f m m m f m m f f f
## Levels: f m
gpadata[, 'gender']
##  [1] f m m m f m m f f f
## Levels: f m
attach(gpadata)
gender
## [1] "F" "F" "M" "F" "M"
detach(gpadata)
```

2.1.3 CSV (comma separated value) Data

The comma-separated value (comma delimited, csv) format data are often used to share data among different software since almost all statistical software can read and output this type of data. A comma-separated values (CSV) file stores tabular data (numbers and text) in plain text. Each line of the file is a data record. Each record consists of one or more fields, separated by commas. Such files often have an extension name “csv”. An example of csv file is available on our website with the following contents:

```
v1,v2
1,6
2,7
3,8
4,9
5,10
```

2.1.4 Read Data from a .csv File

The R function read.csv() function to read the csv data. The use of the function is similar to read.table(). By default, it assumes there are variable names in the data set. If not variable name is available, one should set header=FALSE.

```
csvdata<-read.csv("data/csvdata.csv")
csvdata
##   v1 v2
## 1  1  6
## 2  2  7
## 3  3  8
## 4  4  9
## 5  5 10
```

2.1.5 Save other types of data to csv format

2.1.5.1 Excel data

You can convert an Excel worksheet to a csv file by using the Save As command. Click the File tab, and then click Save As. In the Save as type box, choose the text file format as CSV (Comma delimited).

2.1.5.2 SPSS data

In File Menu, choose, “Save As…”, in the drop down menu in the dialog box that opens choose "Save as type: ’Comma delimited (*.csv)’)“, and underneath that select”Save value labels where defined instead of data values" (or hit “Alt-a”) and choose “Save”.

2.1.5.3 SAS data

The simplest method to save the SAS data to the csv is to use the DEXPORT statement. Below is an example assuming sasdata is the SAS data. After submitting the code, SAS will create a csv file specified.

```
dm "dexport sasdata 'pathtocsvfile\new.csv' ";
```

2.1.5.4 Stata data

To convert a Stata data to Excel, use the “outsheet” command as shown below. The command will create a comma-delimited file called “new.csv”.

```
outsheet using new.csv,c
```

2.2 Excel, SPSS, SAS, and Stata Data

Although there are packages and functions to read Excel, SPSS, SAS, and Stata data into R, the best way to use such kinds of data is to first convert them to csv data and then use the read.csv() function to read the csv data.

2.2.1 Excel data

Several R packages are available to read Excel data. Here we will use XLConnect. The package has to be installed first if not done yet. To install a package, use the function install.packages(). To load the package, use the function library(). An example is shown below. The sheet argument specifies which sheet you exactly want to import into R. Note that the function does not support reading remote data files. Therefore, an error is resulted.

```
library('XLConnect')
exceldata <- readWorksheetFromFile("data/csvdata.xlsx", sheet=1)
exceldata
##   v1 v2
## 1  1  6
## 2  2  7
## 3  3  8
## 4  4  9
## 5  5 10
```

2.2.2 SPSS, SAS, and Stata data

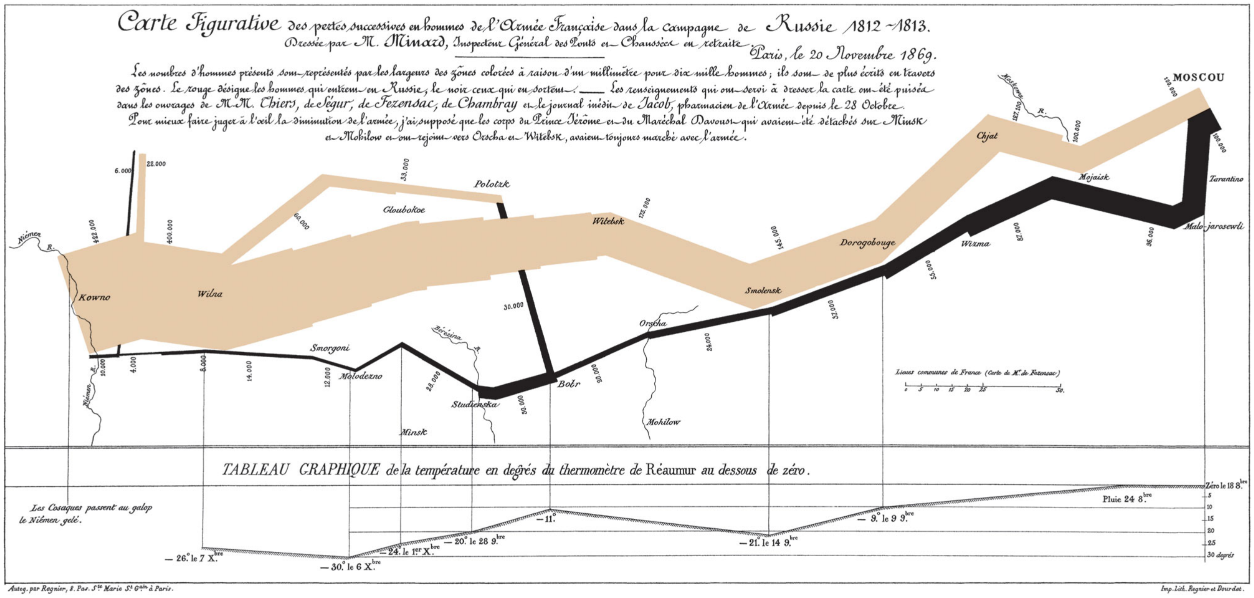
To read SPSS, SAS, and Stata data, we will use the R package haven. The package has the functions read_spss, read_sas, and read_dta. Some examples are given below.

```
library(haven)
spssdata <- read_spss("data/spssdata.sav")
spssdata
## # A tibble: 6 x 2
##    var1  var2
##   <dbl> <dbl>
## 1     1     7
## 2     2     8
## 3     3     9
## 4     4    10
## 5     5    11
## 6     6    12
```

Chapter 3

Statistical Graphs in R

A good graph can convey information more than words. The Napoleon's march to Moscow graph by Charles Minard is widely believed to be the most famous statistical graph.



Tufte (1983, p.40) described the graph as follows.

```
Beginning at the left on the Polish Russian border near the Nieman River, the thick band
```

3.1 Pie Chart

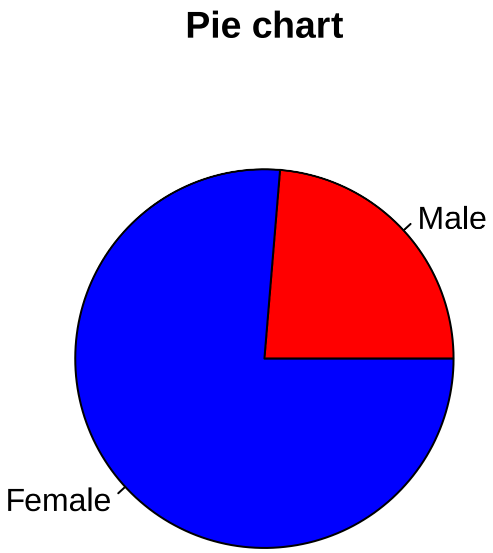
A pie chart (or a circle graph) is a circular chart divided into sectors, illustrating proportion. In a pie chart, the arc length of each sector (and consequently its central angle and area), is proportional to the quantity it represents. It is useful in comparing a slice with the whole pie but not effective to compare slices because our eyes are good at judging linear measures and bad at judging relative areas.

To generate a pie chart, the function pie() can be used. The function takes a vector of data. The most useful options include:

- labels: label the slices
- col: colors of the slices
- main: title of the plot

As an example, we compare the proportions of male and female participants in the ACTIVE study. The plot clearly showed there were more female participants than male participants in the sample. Note that the function table() calculates the number of male and female participants in the variable sex of the data set active. One can also "attach" the data and use the variable sex directly.

```
active <- read.csv("data/active.csv")
head(active)
##   site age edu group booster sex reason ufov hvltt hvltt2 hvltt3 hvltt4 mmse id
## 1    1  76  12     1       1   1     28   16    28     28     17     22   27  1
## 2    1  67  10     1       1   2     13   20    24     22     20     27   25  2
## 3    6  67  13     3       1   2     24   16    24     24     28     27   27  3
## 4    5  72  16     1       1   2     33   16    35     34     32     34   30  4
## 5    4  69  12     4       0   2     30   16    35     29     34     34   28  5
## 6    1  70  13     1       1   1     35   23    29     27     26     29   23  6
pie(table(active$sex), labels=c('Male','Female'),
    col=c('red','blue'), main='Pie chart')
```



3.2 Bar Graph

A bar plot or bar graph is a chart of rectangular bars with their lengths proportional to the values or proportions that they represent. It is good for displaying the distribution of a categorical variable. A bar plot is often preferred than a pie chart. In a bar plot, one doesn't need to include all the categories to make up a whole. To generate a bar plot, the function barplot() can be used.

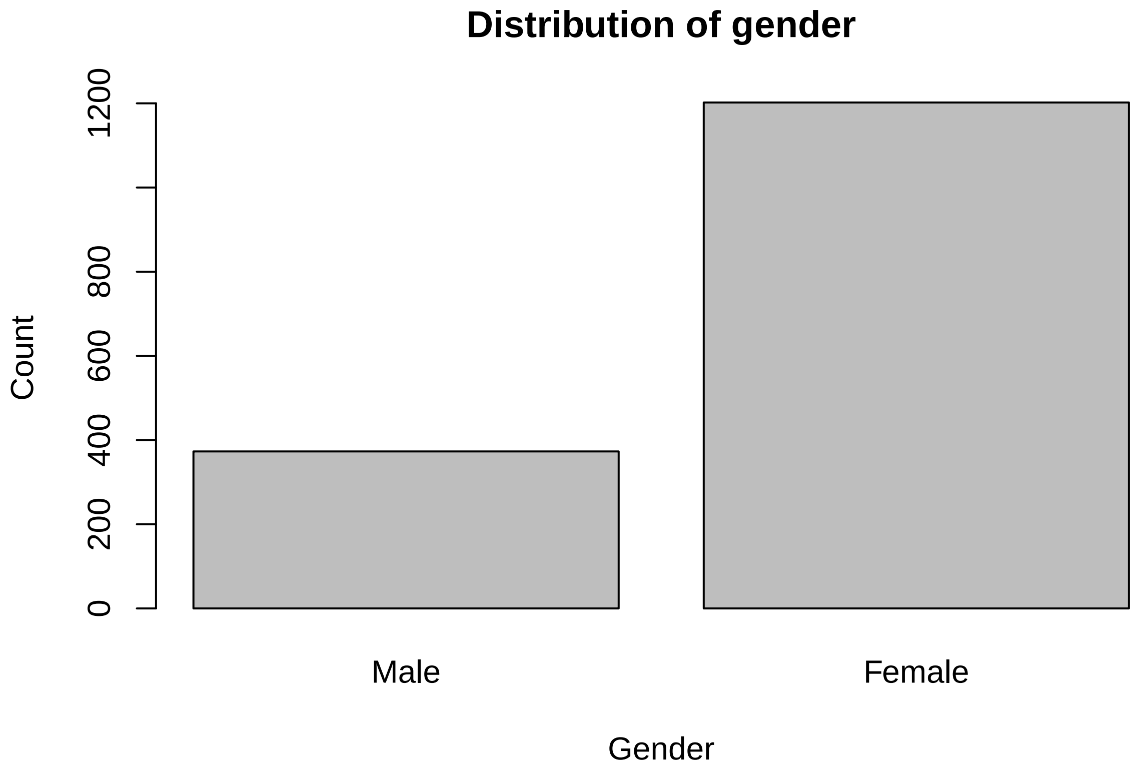
3.2.1 A simple bar plot

A simple bar plot can be generated for a vector of data as shown below. The plot shows the number of male and female participants in the ACTIVE study. Note that the function table() calculates the number of male and female participants in the variable sex of the data set active. One can also "attach" the data and use the variable sex directly.The most useful options include:

- names.arg: label the bars. The order should correspond to the data.
- xlab: label for x axis
- ylab: label for y axis

- main: title of the plot

```
attach(active)
gender.count<-table(sex)

barplot(gender.count, names.arg=c('Male','Female'),
        main='Distribution of gender', xlab='Gender', ylab='Count')
barplot(gender.count, names.arg=c('Male','Female'),
        main='Distribution of gender', xlab='Gender', ylab='Count')
```

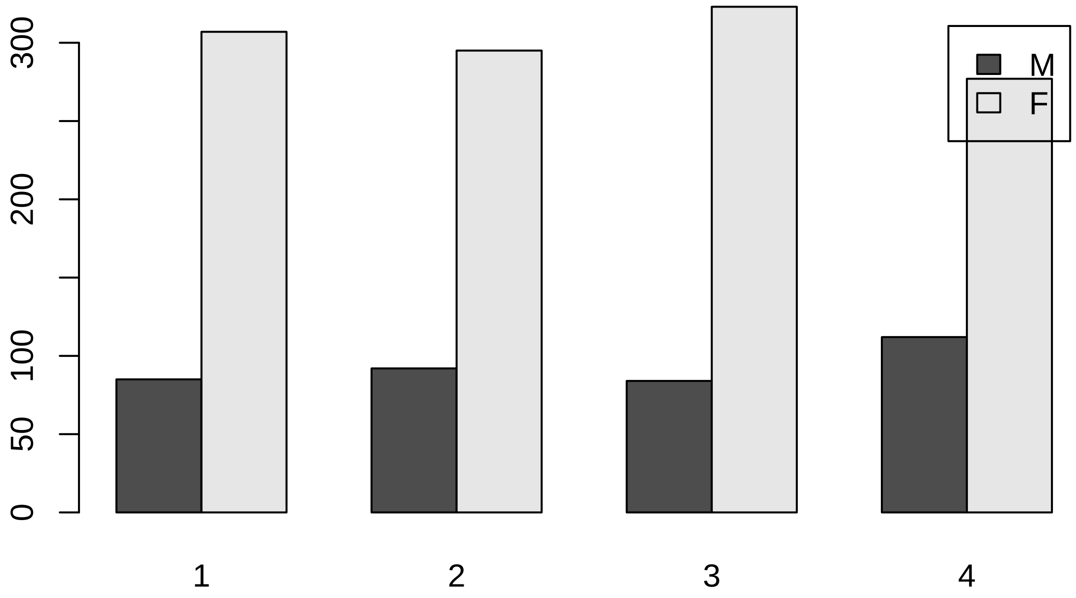


3.2.2 Clustered (side by side or stacked) bar plot

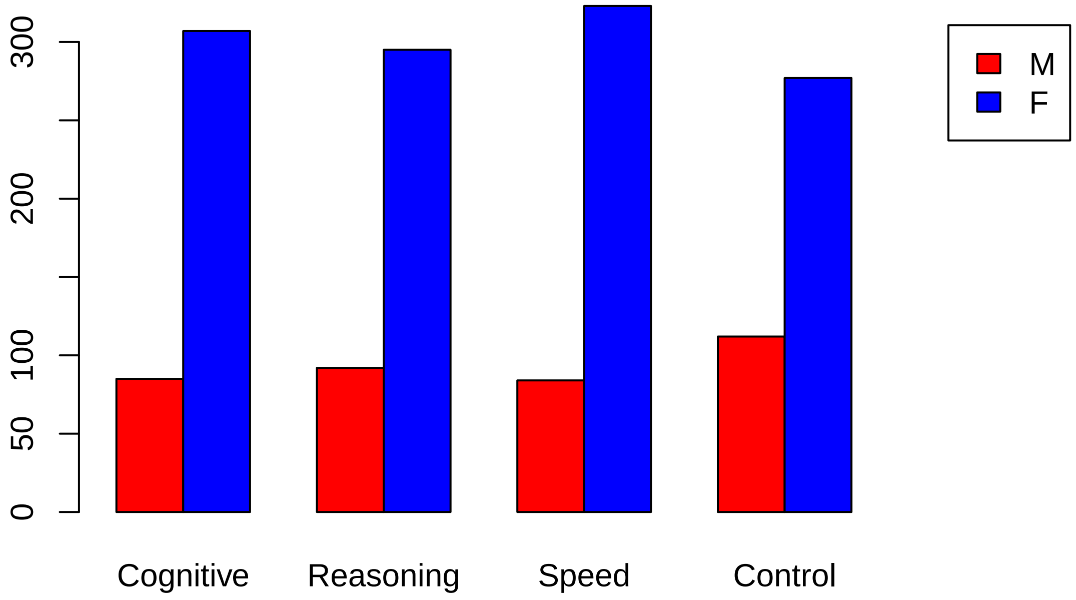
A clustered bar plot can be generated for a matrix of data. As an example, we compare the gender distribution across the 4 experimental groups (cognitive training, reasoning training, speed training and control) in the ACTIVE study. The most useful options include:

- names.arg: label the bar groups. The order should correspond to the data.
- col: color of the bars
- legend: legend within each group
- beside: put the bars side by side (TRUE), or stack them up (beside=FALSE)
- xlim and ylim: the minimum and maximum values of the x-axis and y-axis.

```
counts <- table(sex, group)
barplot(counts,beside=T,legend=c('M','F'))
```



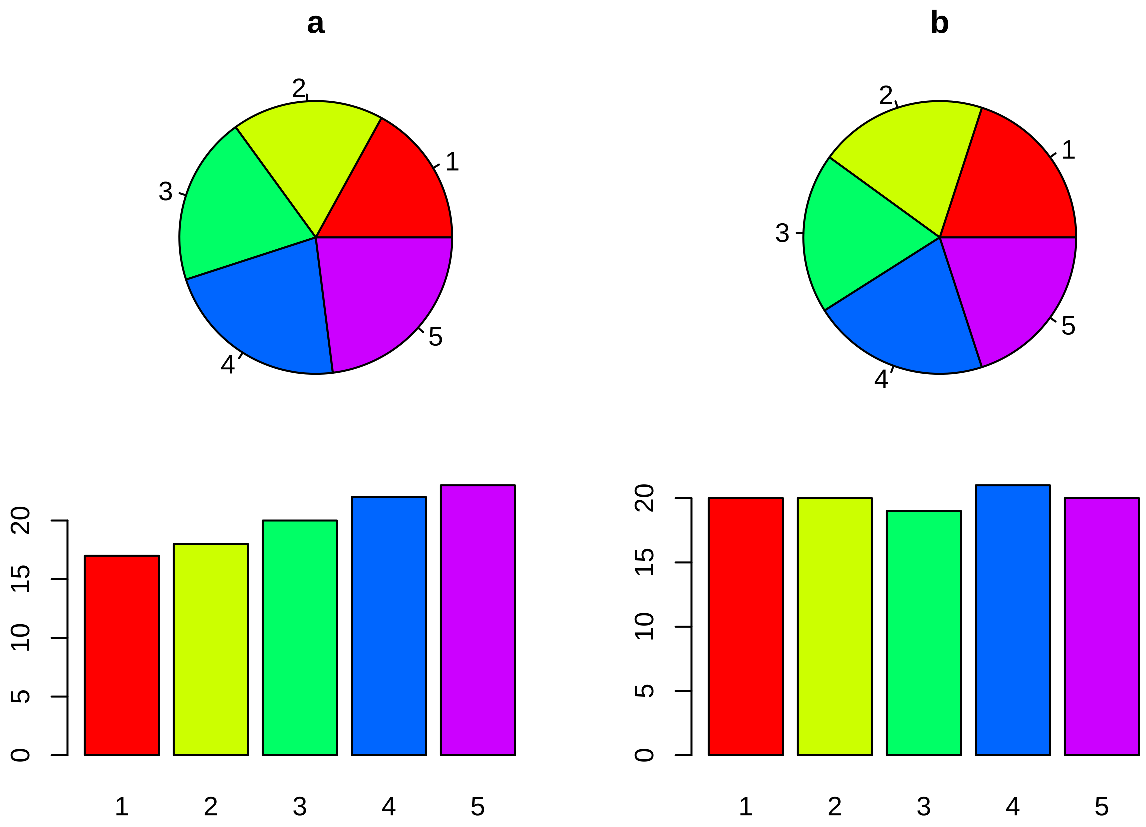
```
barplot(counts,col=c('red','blue'),
        names.arg=c('Cognitive', 'Reasoning', 'Speed', 'Control'),
        beside=T,legend=c('M','F'), xlim=c(1,15))
```



3.2.3 Compare a Pie chart to a Bar graph

When comparing groups, bar graph is easier to visualize the difference. See an example below.

```r
a<-c(17, 18, 20, 22, 23)

b<-c(20, 20, 19, 21, 20)

par(mfrow=c(2,2)) # plot figures in a 2 by 2 layout

par(mar=c(0,0,2,0)) # change the margins of the plots, bottom,left,upper,right

pie(a, main='a',col=rainbow(5))

pie(b, main='b',col=rainbow(5))

par(mar=c(3,2,2,3))

barplot(a,col=rainbow(5),names.arg=1:5)
barplot(b,col=rainbow(5),names.arg=1:5)
```



3.3 Boxplot

Both pie charts and bar graphs are for categorical variables. A categorical variable means that the variable only takes certain isolated/discrete values. Typically, we can use a not-too-long table to list all possible values for the variable. With a continuous variable that can take a large (e.g., infinite) number of values, it may not be informative to use pie charts or bar graphs.

A box plot or boxplot (also known as a box-and-whisker diagram or plot) is a convenient way of graphically displaying summaries of a variable. Often times, the five-number summary is used: the smallest observation, lower quartile (Q1), median (Q2), upper quartile (Q3), and largest observation.

Using a boxplot, we can describe data in a graphical way that readily conveys information about the location, spread, skewness, and longtailedness of a sample. Some advantages of boxplots include:

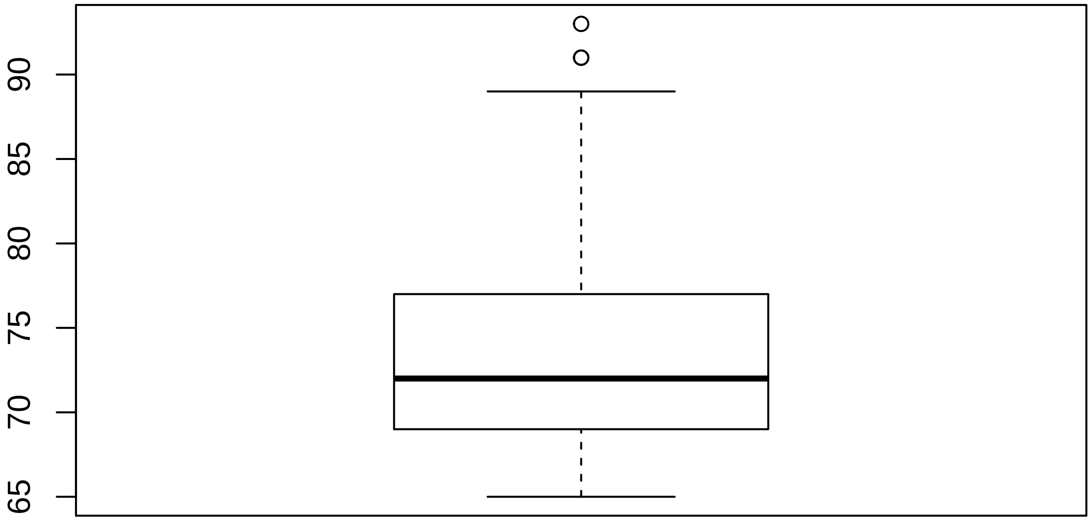
- A boxplot displays information about the observations in the tails, such as potential outliers.

- Boxplots can be displayed side-by-side to compare the distribution of several variables.
- A boxplot is easy to construct.
- A boxplot is easily understood by users of statistics.

3.3.1 A simple boxplot

A boxplot can be generated for a variable simply using the function boxplot(). The plot shows the extreme of the lower whisker, the lower hinge, the median, the upper hinge and the extreme of the upper whisker. It also shows any data points which lie beyond the extremes of the whiskers. For example, the code below generates a boxplot for the age variable in the ACTIVE study.

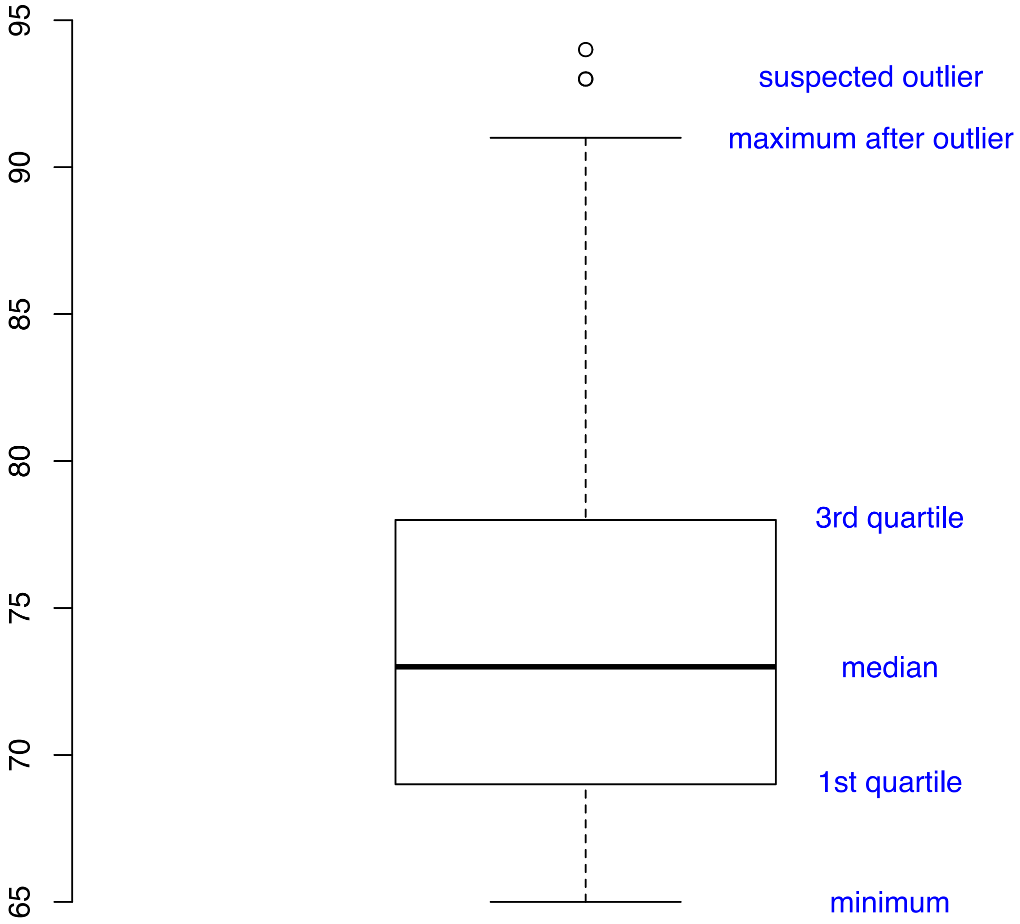
```r
boxplot(age)
```



3.3.1.1 Values plotted in a boxplot (five numbers and outliers)

In a boxplot, the following 5 values are plotted, median, 1st quartile, and 3rd quartile from all data as well as minimum and maximum after removing suspected outliers. The suspected outliers are determined in the following way. First, the interquartile range (IQR) is calculated as the difference between the 3rd quartile and the 1st quartile. Then, if a value is smaller than (inner fence = 1st quartile - 1.5*IQR) or greater than (inner fence = 3rd quartile + 1.5*IQR), it is identified as suspected outlier. For some boxplot, the inner fence is plotted if outliers are identified.

One boxplot with annotated information is shown below.



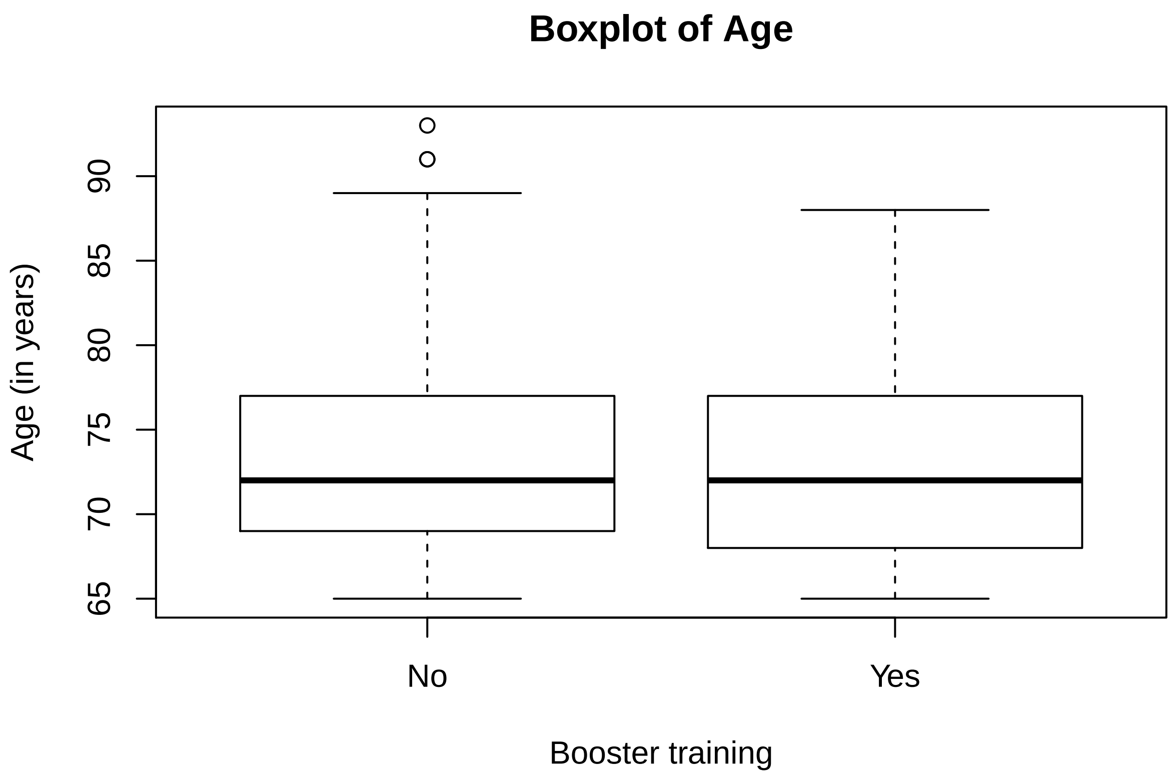
3.3.2 Compare multiple groups

Multiple boxplots can be put together for group comparison. To do so, a formula is often used as input, such as y ~ group, where y is a numeric vector of data values to be split into groups according to the grouping variable group. For example, the code below is used to compare the distribution of age for booster training group and control group in the ACTIVE study.

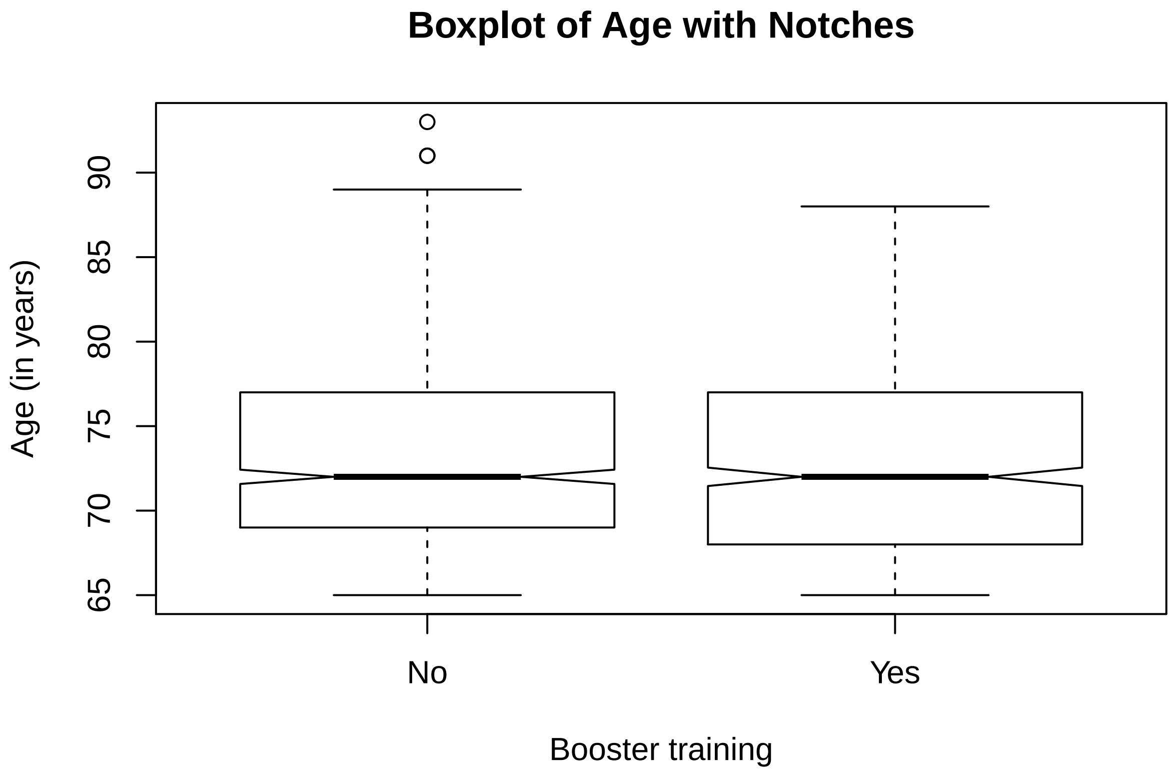
It can be useful to include the confidence interval for the median for comparison purpose in boxplot by setting the notch option to be TRUE to draw a notch in each side of the boxes. If the notches of two plots do not overlap, this is €~strong evidence€™ that the two medians differ (Chambers et al, 1983, p. 62).

For the current example, one question can be used is: If on average, the booster training group had a higher cognitive ability than the control group, was that due to the training or age differences?

```
boxplot(age~booster, main='Boxplot of Age', ylab='Age (in years)',
        xlab='Booster training', names=c('No','Yes'))
```



```
boxplot(age~booster, main='Boxplot of Age with Notches',
        ylab='Age (in years)', xlab='Booster training',
        names=c('No','Yes'), notch=T)
```



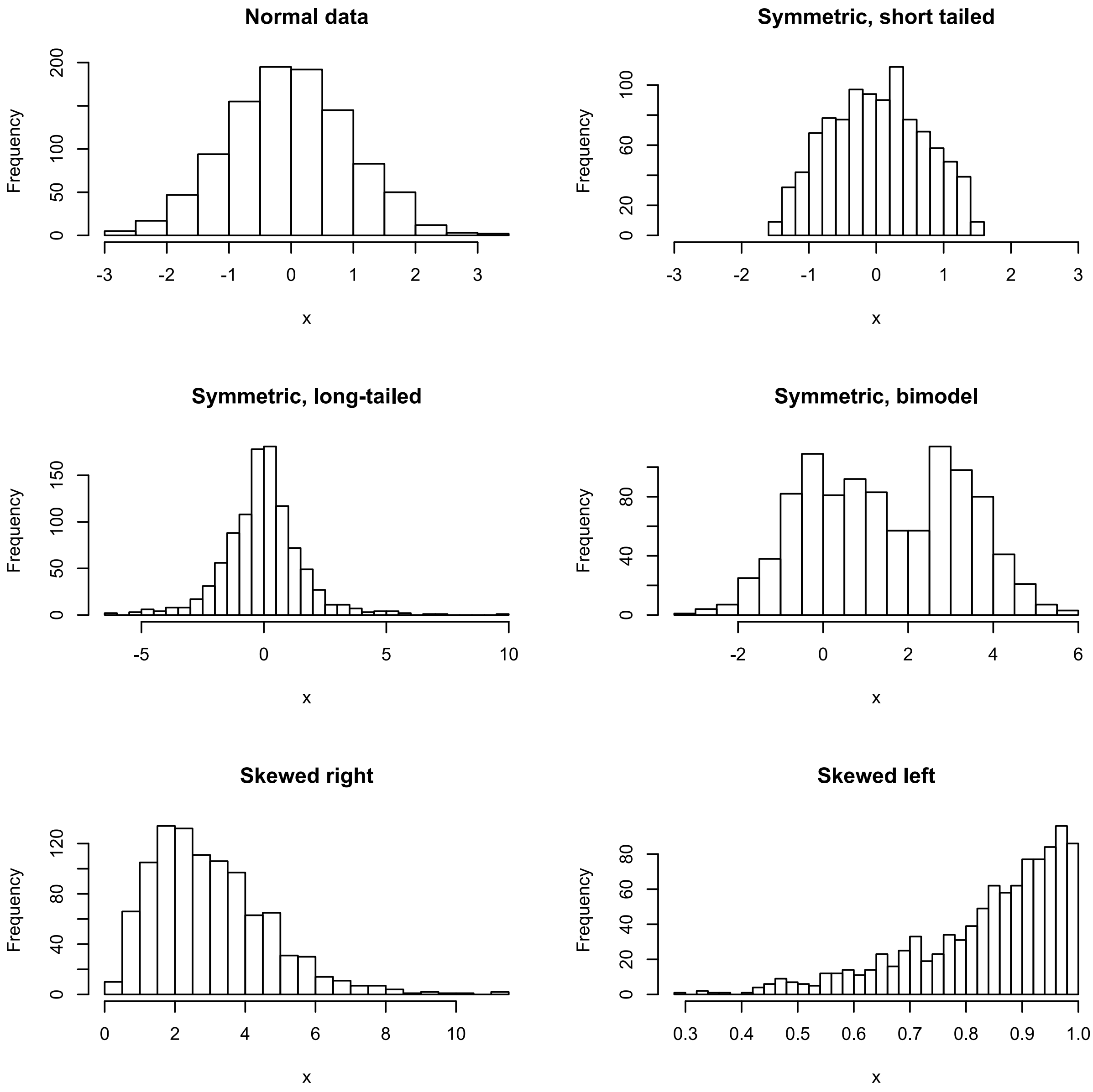
3.4 Histogram

A histogram is a graphical display of frequencies over a set of continuous intervals for a continuous variable. The range of a variable is divided into a list of equal intervals. Within each interval, the number of participants, frequency, is counted. Then, the frequencies can be plotted with attached bars. Heights of the bars stand for frequencies or relative frequencies.

The purpose of a histogram is often to graphically summarize the distribution of a variable such as

- center (i.e., the location) of the data
- spread (i.e., the scale) of the data
- skewness of the data
- presence of outliers
- presence of multiple modes in the data.

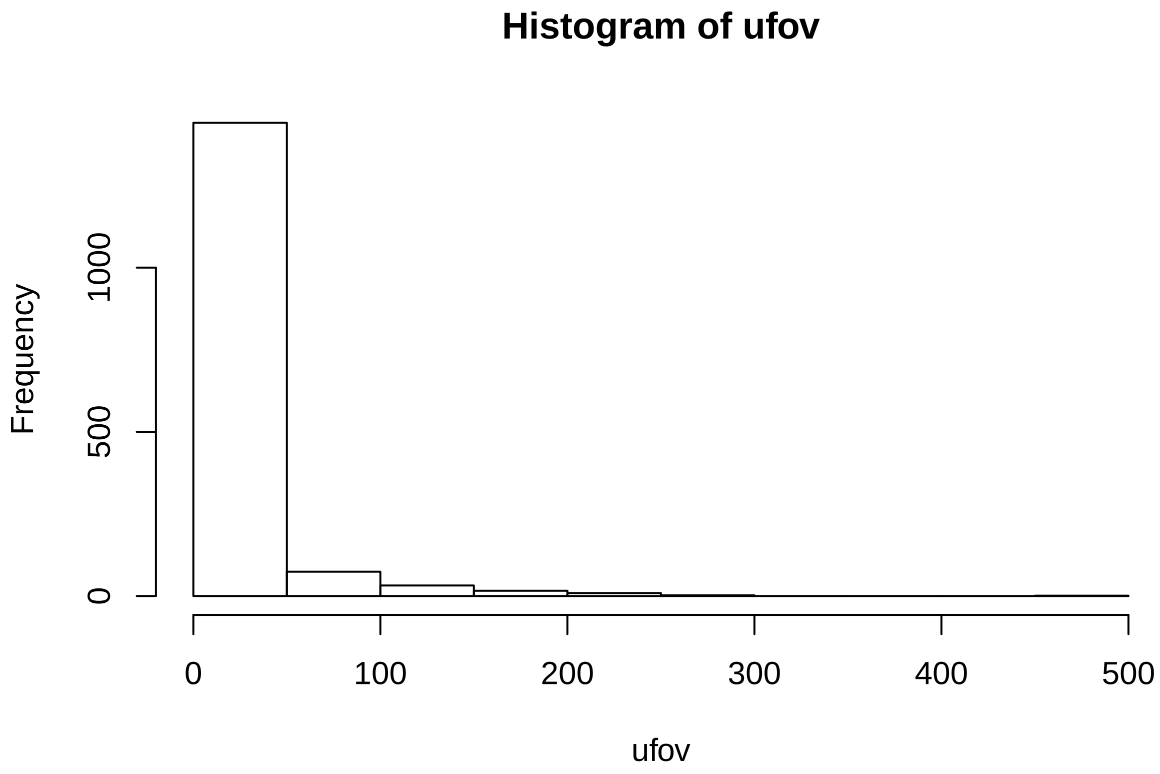
Some examples of histogram are given below.



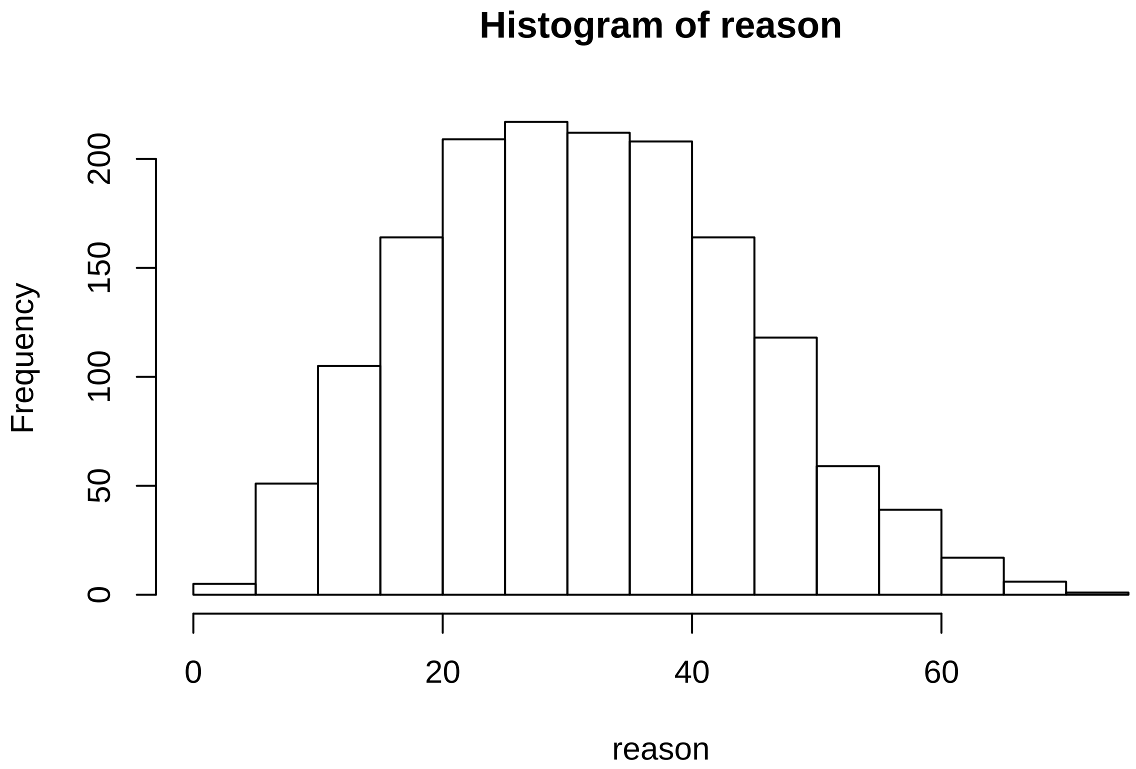
3.4.1 Examples

To generate a histogram, the function hist() can be used. In the following, we have histogram for the ufov (useful field of view) variable and the reason (reasoning ability) variable of the ACTIVE study. Clearly, the distribution of ufov is highly skewed while the distribution of reason is more normal.

```
hist(ufov)
```



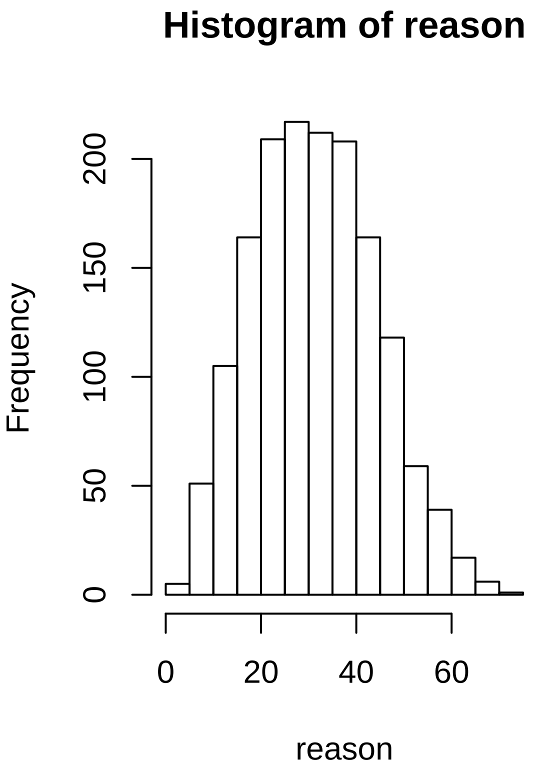
```
hist(reason)
```

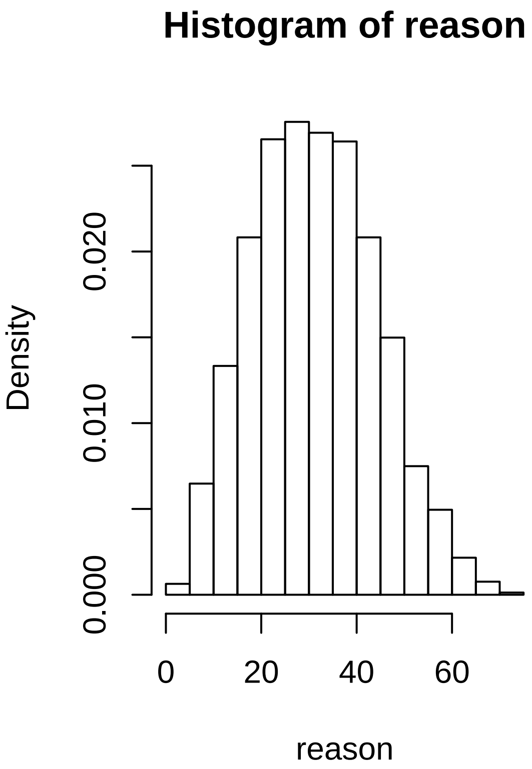


3.4.2 Probability density vs. frequency

By default, the histogram graphic is a representation of frequencies, the counts within each interval of a variable. If we set the option prob=TRUE, the probability densities are plotted (so that the histogram has a total area of one).

```r
par(mfrow=c(1,2))

hist(reason)
hist(reason, prob=T)
```





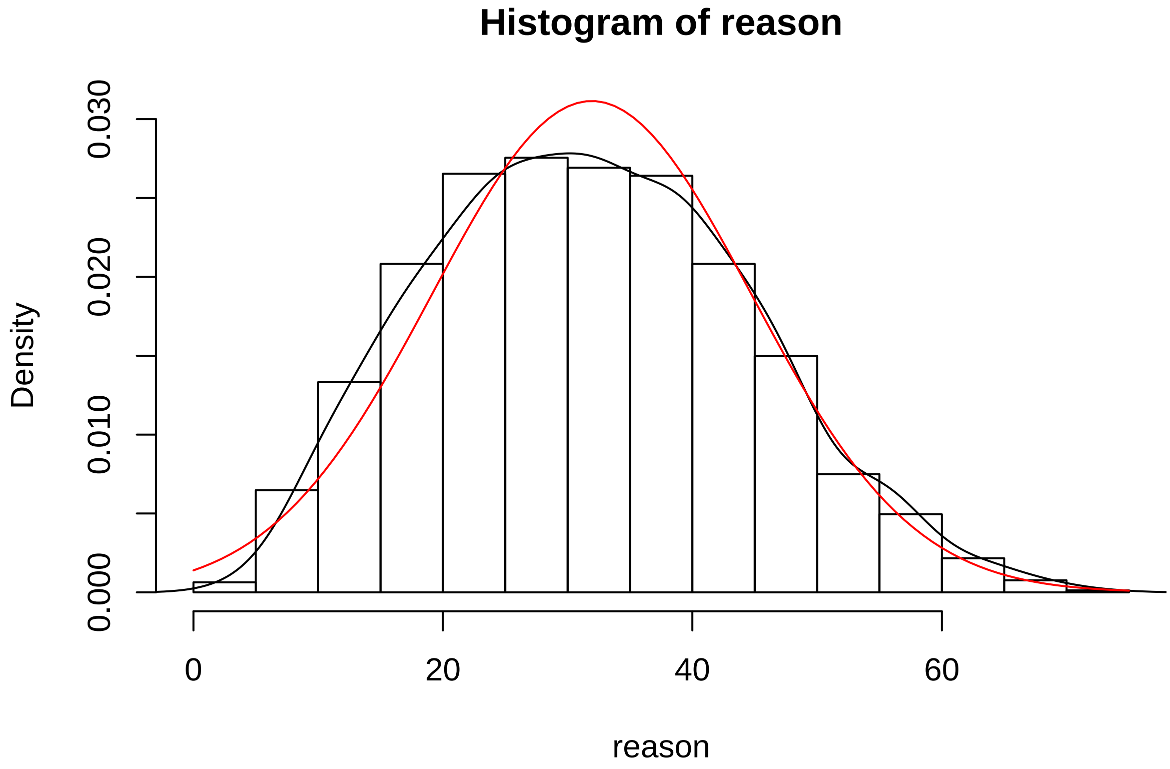
3.4.3 Add an estimated density curve and a normal curve

Often times, we are interested in whether the distribution of a variable is close to normal distribution. We can visually compare them by adding a normal curve to the histogram. In addition, a smoothed density curve can be added to approximate the distribution represented by the histogram for better comparison. In R, the smoothed density can be estimated using the density() function and the normal curve can be generated using the dnorm() function.

In the example below, we add an estimated density curve and a normal curve to the histogram of the reason variable. Some comments about the code used:

- The histogram has to be plotted using the density instead of the frequency.
- na.rm=T or na.rm=TRUE will remove the missing data (represented by NA in R) before applying a function.
- lines() function will add a line to an existing figure. Therefore, a figure has to be there before the use of this function.
- curve() can generate a new plot or add to an existing plot. To add to an existing plot, use the option add=T (or TRUE).
- dnorm(x,mean=mean(reason,na.rm=T), sd=sd(reason,na.rm=T)) generates a curve with the same mean and standard deviation as the reason variable.
- Oftentimes, one has to change ylim to make the plot fit.

```
hist(reason, prob=T, ylim=c(0, .03))
lines(density(reason,na.rm=T))
curve(dnorm(x,mean=mean(reason,na.rm=T),
            sd=sd(reason,na.rm=T)), add=T, col='red')
```



3.5 Scatter plot

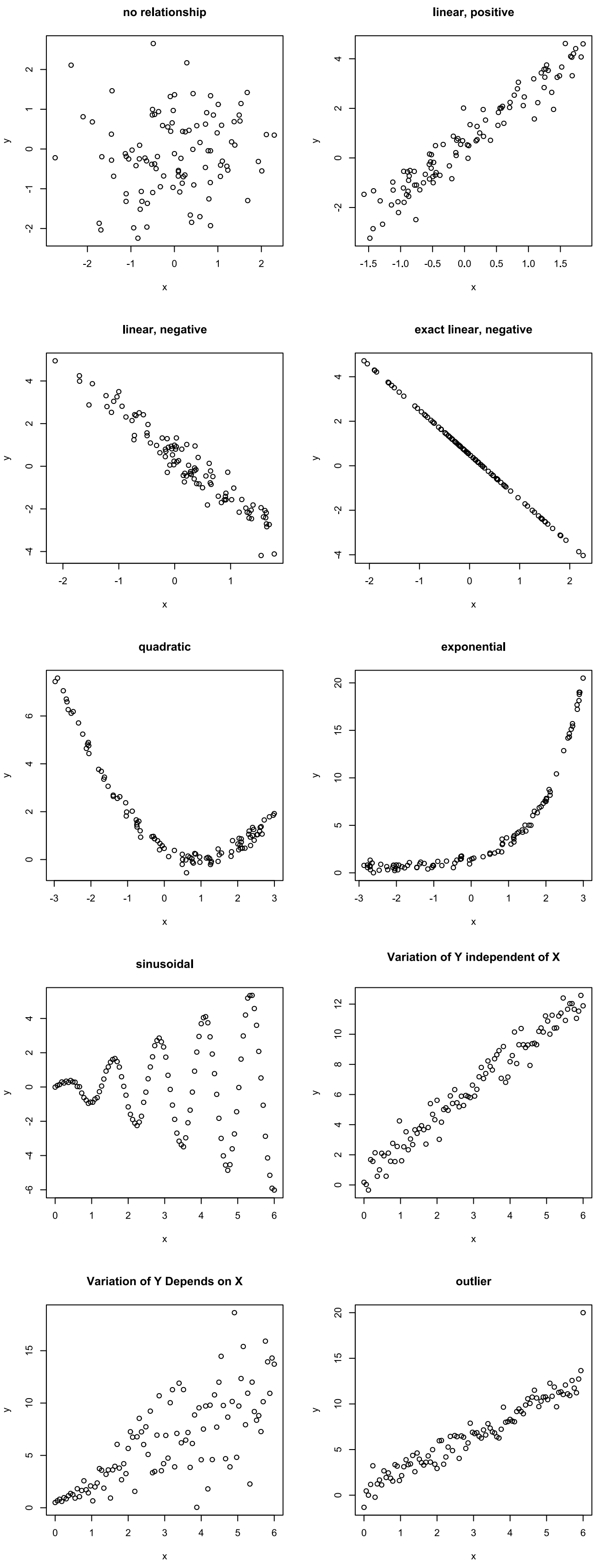
A scatter plot (also called a scatter graph, scatter chart, scattergram, or scatter diagram) is a plot to display the relation between two variables. The data is displayed as a collection of points, each having the value of one variable determining the position on the horizontal axis (X-axis) and the value of the other variable determining the position on the vertical axis (Y-axis). Typically, the response/outcome/dependent variable is on the Y-axis, and the variable we suspect may be related to the y-axis variable, predictor/explanatory/independent variable is on the X-axis.

A scatter plot reveals the relationship or association between two variables (form, direction, strength) such as

- Are variables X and Y related?
- Are variables X and Y linearly related?

- Are variables X and Y non-linearly related?
- Are changes in Y related to changes in X?
- Are there any outliers?

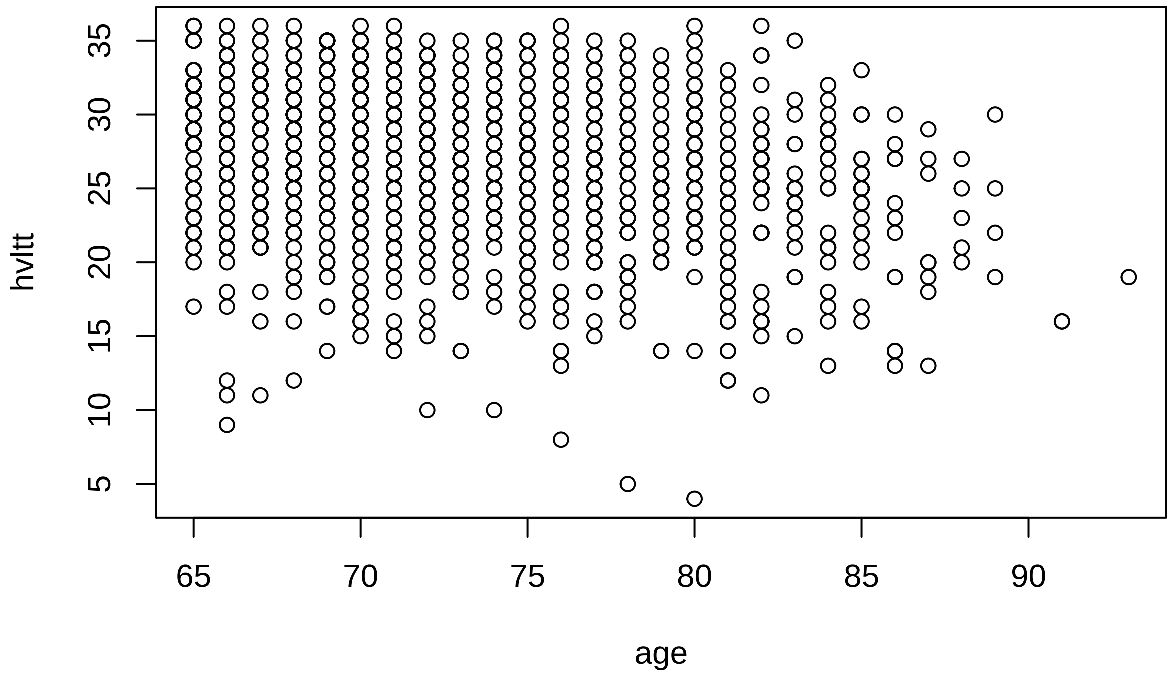
Some examples of scatter plots are given below.


no relationship
linear, positive
linear, negative
exact linear, negative
quadratic
exponential
sinusoidal
Variation of Y independent of X
Variation of Y Depends on X
outlier
x
y

3.5.1 Examples

To generate a scatter plot, the function plot() can be used. In the following, we plot the relationship between the age (in years) variable and the hvltt (verbal ability) variable of the ACTIVE study. The relationship of the two variable is not clear although tending to be negative.

```r
plot(age, hvltt)
```



3.5.2 Add regression line and a smoothing curve

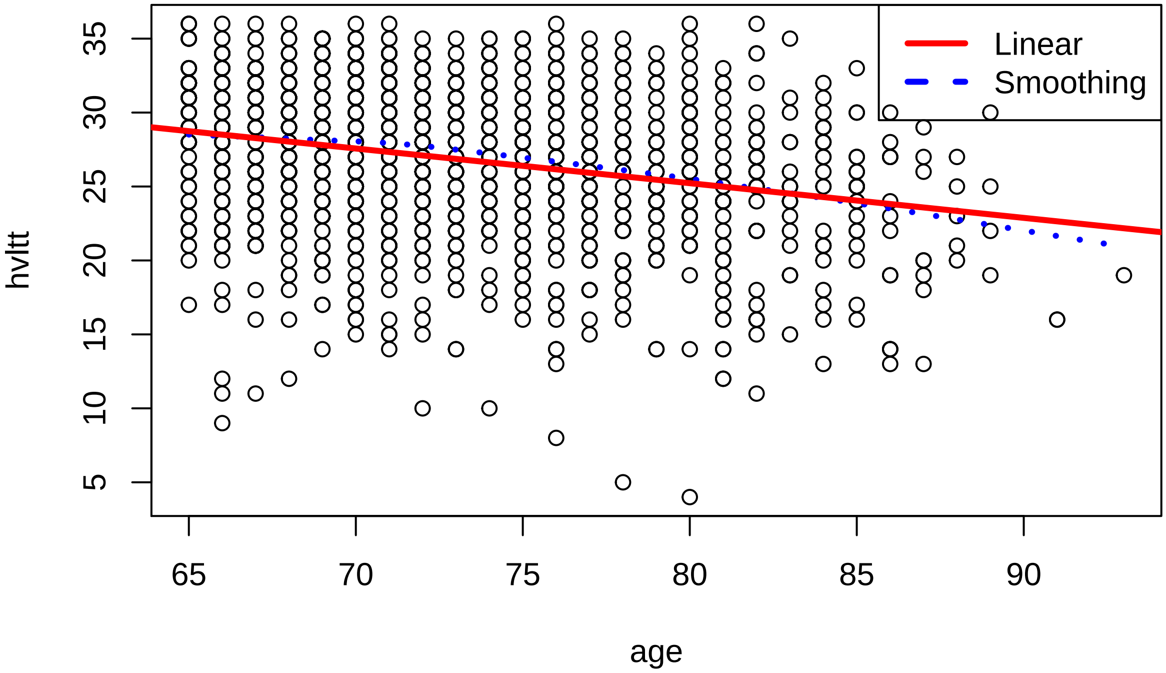
Often times, we are interested in whether two variables are linearly or nonlinearly related. We can better visualize the relationship by adding a straight regression line (linear) or a smoothed curve to the scatter plot. In R, the smoothed curve can be estimated using the loess.smooth() function or we can generate the plot using the scatter.smooth() function directly.

In the example below, we add both a regression line and a smoothed line to the scatter plot between age and hvltt variable. Note that their relationship appears to be nonlinear. Some comments about the code used:

- lm() function fits a linear regression model.

- abline() function will add a line with given intercept and slope to an existing figure.
- lwd option sets the width of lines.
- lty option sets the width of lines.
- legend() function adds a legend to the existing figure.

```
scatter.smooth(age, hvltt, lpars = list(col = "blue", lwd = 3, lty = 3))
abline(lm(hvltt~age), col='red',lwd=3)
legend('topright', c('Linear','Smoothing'),
       lty=c(1,2), lwd=c(3,3), col=c('red','blue'))
```



3.6 Line plot

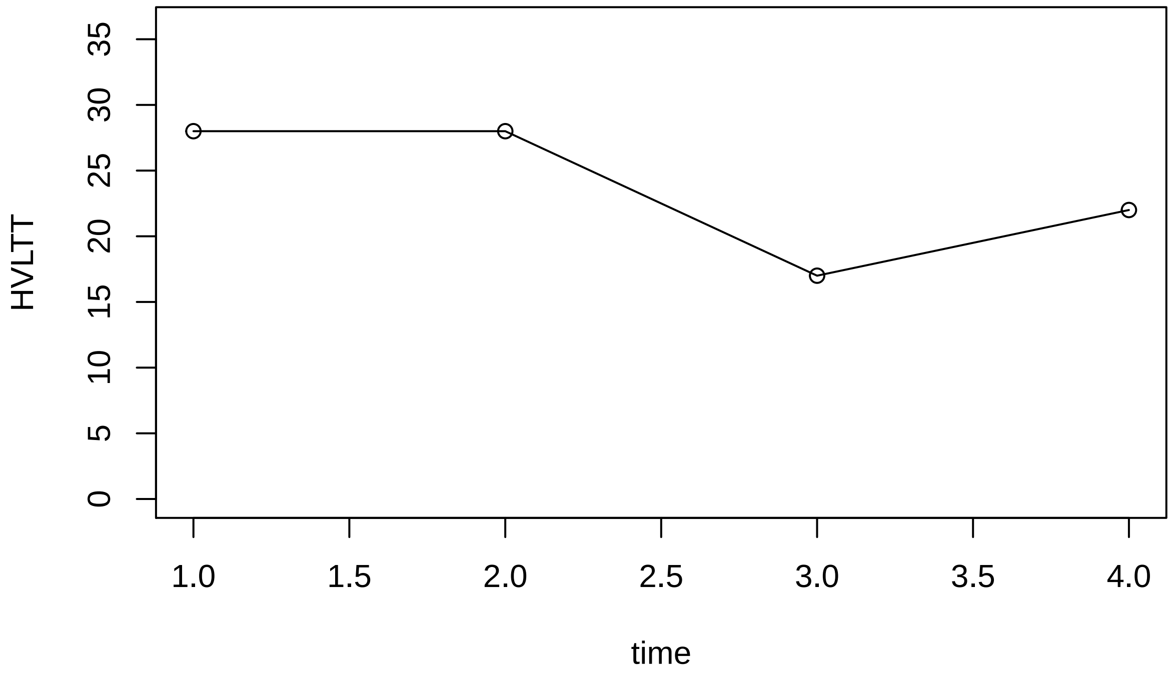
In a line plot, or line chart, a series of data points from the same individual/subject are connected by lines. This kind of plot is most widely used in longitudinal or time series data. It can be used to investigate how a variable changes over time within an individual. To generate a line plot in R, the function plot() can be used with the option type='l'. Setting type='o' will generate a line plot together with the points.

In the ACTIVE study, participants were followed over time. For example, the Hopkins Verbal Learning Test (hvltt) was administrated 4 times in the current data set. Therefore, we can plot the test score for an individual over time.

3.6.1 A single line plot

In the example below, we plot the Hopkins Verbal Learning Test for the first participant in the data set.

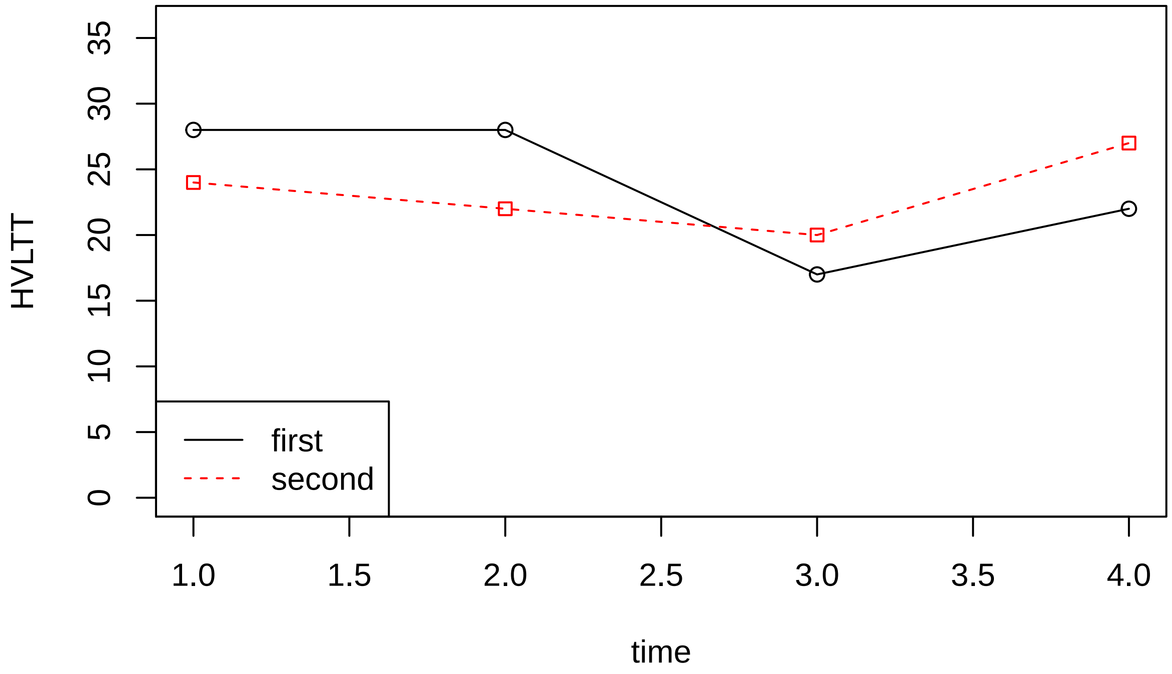
```
plot(1:4, active[1,9:12], type='o',
     xlab='time', ylab='HVLTT',ylim=c(0,36))
```



3.6.2 Compare the change trajectory of two participants

Two lines can be plotted together to compare changes for two subjects. Note that the second line can be added using the lines() function.

```
plot(1:4, active[1,9:12], type='o',
     xlab='time', ylab='HVLTT',ylim=c(0,36))
lines(1:4, active[2,9:12], type='o',
      pch=22, lty=2, col='red')
legend('bottomleft', c('first', 'second'),
       lty=c(1,2), col=c('black', 'red'))
```



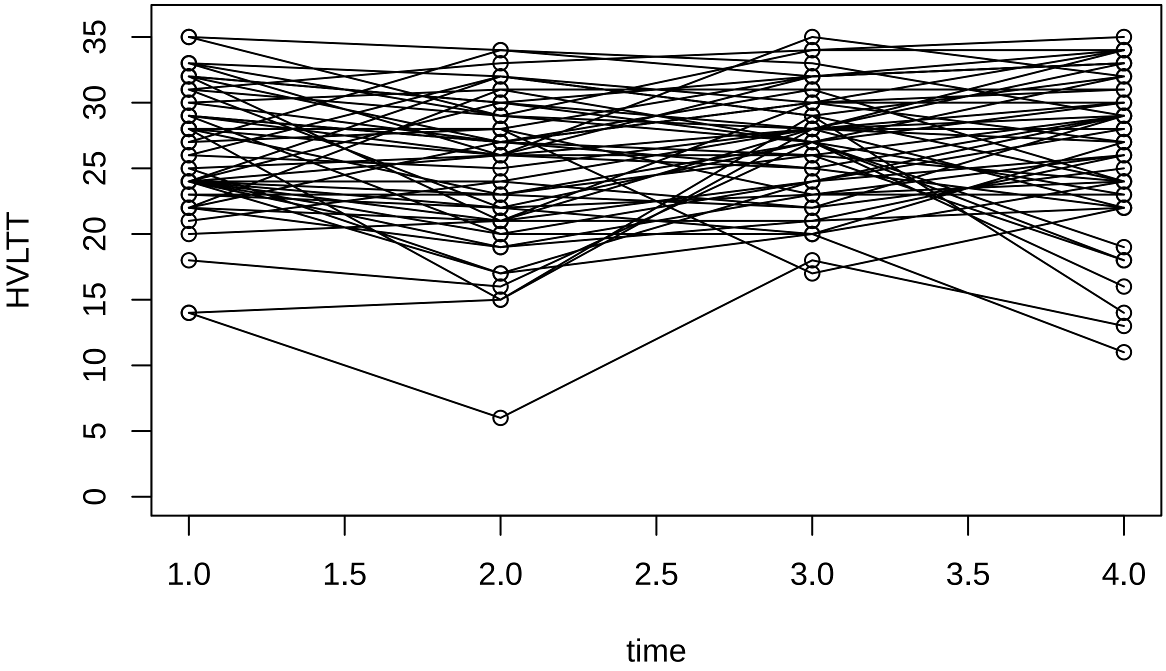
3.6.3 Plot more lines (use of for loop)

Each individual line can be added manually. Or this procedure can be automated using a for (){ } loop. A for loop repeats the same work within {}. More specifically, such a loop has a code format like for (var in sequence) { expression } where

- for and in are R keywords
- sequence is a vector of values, often time consecutive values such as 1:100.
- var is the name of a variable that takes a value sequently in sequence.
- expression is the R code to repeat
- note the use of () and {}

For example, the following code generates the line plot for the first 50 participants in the ACTIVE study.

```
plot(1:4, active[1,9:12], type='o',
     xlab='time', ylab='HVLTT',ylim=c(0,36))

for (i in 2:50){
  lines(1:4, active[i,9:12], type='o')
}
```


HVLTT
0
5
10
15
20
25
30
35
1.0
1.5
2.0
2.5
3.0
3.5
4.0
time

Chapter 4

Hypothesis testing

4.1 Null hypothesis testing

Null hypothesis testing is a procedure to evaluate the strength of evidence against a null hypothesis. Given/assuming the null hypothesis is true, we evaluate the likelihood of obtaining the observed evidence or more extreme, when the study is on a randomly-selected representative sample. The null hypothesis assumes no difference/relationship/effect in the population from which the sample is selected. The likelihood is measured by a p value. If the p value is small enough, we reject the null. In the significance testing approach of Ronald Fisher, a null hypothesis is rejected on the basis of data that are significantly unlikely if the null is true. However, the null hypothesis is never accepted or proved. This is analogous to a criminal trial: The defendant is assumed to be innocent (null is not rejected) until proven guilty (null is rejected) beyond a reasonable doubt (to a statistically significant degree).

To conduct a typical null hypothesis test, the following 7 steps can be followed:

1. State the research question
2. State the null and alternative hypotheses based on the research question
3. Select a value for significance level α
4. Collect or locate data
5. Calculate the test statistic and the p value
6. Make a decision on rejecting or failing to reject the hypothesis
7. Answer the research question

4.1.1 Step 1. State the research question

A hypothesis testing is used to answer a question. Therefore, the first step is to state a research question. For example, a research question could be “Does memory training improve participants’ performance on a memory test?” in the ACTIVE study.

4.1.2 Step 2. State the null and alternative hypotheses

Based on the research question, one then forms the null and the alternative hypotheses. For example, to answer the research question in Step 1, we would need to compare the memory test score for two groups of participants, those who receive training and those who do not. Let μ_1 and μ_2 be the population means of the two groups.

The **null** hypothesis H_0 should be a statement about parameter(s) and of “no effect” or “no difference”:

$$H_0: \ \mu_1 = \mu_2 \text{ or } \mu_1 - \mu_2 = 0.$$

The **alternative** hypothesis H_1 or H_a is the statement we hope or suspect is true. In this example, we hope the training group has a higher score than the control group, therefore, our alternative hypothesis would be

$$H_a: \ \mu_1 > \mu_2 \text{ or } \mu_1 - \mu_2 > 0$$

But note that it is cheating to first look at the data and then frame H_a to fit what the data show. If we do not have direction firmly in mind in advance, we must use a two-sided alternative (default) hypothesis such that

$$H_a: \ \mu_1 = \mu_2 \text{ or } \mu_1 - \mu_2 = 0.$$

4.1.3 Step 3. Set the significance level α

Hypothesis testing is a procedure to evaluate the strength of evidence against a null hypothesis. Given the null hypothesis is true, we calculate the probability of obtaining the observed evidence or more extreme, which is called p-value. If the p value is small enough, reject the null. In practice, a value 0.05 is considered as small but other values can be used. For example, recently a group of researchers recommended to use 0.005 instead (Benjamin et al., 2017). It is called the significance level, often denoted by α and should be decided before data analysis. If $p \leq \alpha$, we reject the null hypothesis and if $p > \alpha$, fail to reject the null and the evidence is insufficient to support a conclusion.

4.1.4 Step 4. Collect or locate data

In this step, we can conduct an experiment to collect data or we can use some existing data. Note that even data exist, we should not form our hypothesis by peeking into the data.

The ACTIVE study has data on memory training. Therefore, we use the data as an example. The following code gets the data for the training group and the control group. `hvltt2` has information on all 4 training groups (memory=1, reasoning=2, speed=3, control=4). Note that we use `hvltt2[group==1]` to select a subset of data from `hvltt2`. This means we want to get the data from `hvltt2` when the `group` value is equal to 1. Similarly, we select the data for the control group.

4.1.5 Step 5. Calculate the test statistic and the p value

When the null hypothesis is true, the population mean difference ($\mu_1 - \mu_2 = 0$) is zero. Based on our data, the observed mean difference for the two group is $\bar{x}_1 - \bar{x}_2 = 1.54$. To conduct a test, we would need to calculate the probability of drawing a random sample with the difference of 1.54 or more extreme when H_0 is true? That is

$$\Pr(\bar{x}_1 - \bar{x}_2 \geq 1.54 | \, \mu_1 - \mu_2 = 0) = ?$$

In obtaining the above probability, we need to know the sampling distribution of $\bar{x}_1 - \bar{x}_2$, which leads to the t distribution in a t test. We calculate a test statistic

$$t = \frac{\bar{x}_1 - \bar{x}_2}{s}$$

where s and the distribution of t need to be decided.

4.1.5.1 Welch's t test (unpooled two independent sample t test)

When the two population variances of the two groups are not equal (the two sample sizes may or may not be equal). The t statistic to test whether the population means are different is calculated as:

$$t = \frac{\bar{x}_1 - \bar{x}_2}{s_{\overline{\Delta}}}$$

where

$$s_{\overline{\Delta}} = \sqrt{\frac{s_1^2}{n_1} + \frac{s_2^2}{n_2}}.$$

Here, s_1^2 and s_2^2 are the unbiased estimators of the variances of the two samples with $n_k =$ number of participants in group $k = 1$ or 2. For use in significance testing, the distribution of the test statistic is approximated as an ordinary Student's t distribution with the degrees of freedom calculated as

$$\text{d.f.} = \frac{(s_1^2/n_1 + s_2^2/n_2)^2}{(s_1^2/n_1)^2/(n_1 - 1) + (s_2^2/n_2)^2/(n_2 - 1)}.$$

This is known as the Welch-Satterthwaite equation. The true distribution of the test statistic actually depends (slightly) on the two unknown population variances.

In R, the function `t.test()` can be used to conduct a t test. The following code conducts the Welch's t test. Note that `alternative = "greater"` sets the alternative hypothesis. The other options include `two.sided` and `less`.

```r
active <- read.csv("data/active.csv")
attach(active)

training <- hvltt2[group==1]
control <- hvltt2[group==4]

mean(training, na.rm=T)-mean(control, na.rm=T)
## [1] 1.970935

t.test(training, control, alternative = 'greater')
##
##  Welch Two Sample t-test
##
## data:  training and control
## t = 5.0416, df = 775.37, p-value = 2.876e-07
## alternative hypothesis: true difference in means is greater than 0
## 95 percent confidence interval:
##  1.327135      Inf
## sample estimates:
## mean of x mean of y
##  26.10204  24.13111
```

4.1.5.2 Pooled two independent sample t test

When the two groups have the same population variance.The t statistic can be calculated as follows:

$$t = \frac{\bar{x}_1 - \bar{x}_2}{s_p \cdot \sqrt{\frac{1}{n_1} + \frac{1}{n_2}}}$$

where

$$s_p = \sqrt{\frac{(n_1 - 1)s_1^2 + (n_2 - 1)s_2^2}{n_1 + n_2 - 2}}$$

is an estimator of the pooled standard deviation of the two samples. $n_k - 1$ is the degrees of freedom for each group, and the total sample size minus two $(n_1 + n_2 - 2)$ is the total number of degrees of freedom, which is used in significance testing.

The pooled two independent sample t test can also be conducted using the `t.test()` function by setting the option `var.equal=T` or `TRUE`.

```
training <- hvltt2[group==1]
control <- hvltt2[group==4]

t.test(training, control,
       alternative = 'greater', var.equal=T)
##
##  Two Sample t-test
##
## data:  training and control
## t = 5.0428, df = 779, p-value = 2.856e-07
## alternative hypothesis: true difference in means is greater than 0
## 95 percent confidence interval:
##  1.327289      Inf
## sample estimates:
## mean of x mean of y
##  26.10204  24.13111
```

4.1.6 Step 6. Make a decision

Based on the t test, we have a p-value about 2e-06. Since the p-value is smaller than the chosen significance level $\alpha = 0.05$, the null hypothesis is rejected.

4.1.7 Step 7. Answer the research question

Using the ACTIVE data, we tested whether the memory training can improve participants' performance on a memory test. Because we rejected the null hypothesis, we may conclude that the memory training statistically significantly increased the memory test performance.

4.1.8 Remarks on hypothesis testing

- Hypothesis testing is more of a confirmatory data analysis than exploratory data analysis method. Therefore, one starts with a hypothesis and then tests whether the collected data support the hypothesis.
- The logic of hypothesis testing is - Assuming that the null hypothesis is true, what is the probability of observing a value for the test statistic that is at least as extreme as the value that was actually observed?
- If the null hypothesis is true while one rejects the null hypothesis, one would make the Type I error. If the alternative hypothesis is true while one fails to reject the null

hypothesis, one would make the Type II error. Statistical power is when one would reject the null hypothesis when the alternative hypothesis is true.

Fail to reject H_0

Reject H_0

Null hypothesis H_0 is true

Correct decision

Type I error

Alternative hypothesis H_1 is true

Type II error

Power

- Statistical significance means that the results are unlikely to have occurred by chance, given that the null is true.
- Statistical significance does not imply practical importance. For example, in comparing two groups, the difference can still be statistically significant even if the difference is tiny.

4.2 Effect size

To measure the practical importance, effect size is often recommended to use. For example, for mean difference, the commonly used effect size measure is Cohen's "d" (Cohen, 1988). Cohen's d is defined as the difference between two means divided by a standard deviation.

$$d = \frac{\bar{x}_1 - \bar{x}_2}{s_p}$$

Cohen defined s_p, the pooled standard deviation, as

$$s_p = \sqrt{\frac{(n_1 - 1)s^2_{x_1} + (n_2 - 1)s^2_{x_2}}{n_1 + n_2 - 2}}$$

A Cohen's d with the value around 0.2 is considered small, .5, median, and $\geq$.8, large.

For example, the Cohen's d for the memory training example is 0.25, representing a small effect even though the p-value is small and indicates a statistical significance.

```
mean1=mean(training,na.rm=T)
mean2=mean(control,na.rm=T)
meandiff=mean1-mean2
```

```
n1=length(training)-sum(is.na(training))
n2=length(control)-sum(is.na(control))

v1=var(training,na.rm=T)
v2=var(control,na.rm=T)
s=sqrt(((n1-1)*v1+(n2-1)*v2)/(n1+n2-2))
s
## [1] 5.461292

cohend=meandiff
cohend
## [1] 1.970935
```

4.3 Criticisms of Null Hypothesis Testing and p-value

Let H_0 and H_a (or H_1) denote the null and alternative hypotheses, respectively. Let D denote the data observed. The hypothesis testing is based on the calculation of the probability that such a data set D and more extreme data can be observed given the hypothesis is true:

$$\Pr(D|H_0) = p,$$

which is often called p-value. In Fisher's formulation, a low p -value means either that the null hypothesis is true and a highly improbable event has occurred, or that the null hypothesis is false. If the probability p is smaller than, typically, 0.05, one would argue that there is a very small chance that the data set D (or more extreme data) can be observed. Thus, the null hypothesis should be rejected. Otherwise, one fails to reject the null hypothesis.

There have been criticisms since the use of the null hypothesis testing (NHT). We summarize the main criticisms below.

4.3.1 The focus of null hypothesis

In NHT, the null hypothesis is a statement of no effect, no difference, or no relation. However, researchers often believe the null hypothesis is false and are interested in finding certain effect. If the null hypothesis is always false, then what's the point to reject it? As Cohen put it:

The null hypothesis, taken literally (and that's the only way you can take it in formal hypothesis testing), is always false in the real world. It can only be true in the bowels of a computer processor running a Monte Carlo study (and even then a stray electron may make it false). If it is false, even to a tiny degree, it must be the case that a large enough sample will produce a significant result and lead to its rejection. So if the null is always false, what€™s the big deal about rejecting it? (Cohen, 1990, p. 1308).

Similarly, Meehl (1990) stated that everything is related to everything else. He argued that the “pairwise correlations of even arbitrarily chosen variables in most soft domains tend to run large enough to yield frequent pseudoconfirmations of unrelated substantive theories, given conventional levels of the statistical power function based on pilot studies” (p. 237). Tukey (1991) wrote that "It is foolish to ask ‘Are the effects of A and B different?’ They are always different - for some decimal place." (p. 100).

4.3.2 The test is done given that the null is true

In general, researchers choose to conduct a study because they believe there exists a significant effect. Therefore, they firmly believe that the null hypothesis is not true but the alternative hypothesis is true. However, the null hypothesis testing is conducted based on the null hypothesis. The whole rationale is “Assuming that the null hypothesis is true, what is the probability of observing a value for the test statistic that is at least as extreme as the value that was actually observed?”

4.3.3 The logic of NHST is flawed

In logic, contraposition means that a conditional statement is logically equivalent to its contrapositive. For example, given the statement that “if A is true, then B is true”, its equivalence is “if B is not true, then A is not true.”

In using NHST, one tends to reason in the following way. If the null hypothesis is correct, then the data can not be observed. However, since we have observed the current data, the null hypothesis is false. This is the contraposition and therefore logically correct.

However, the logic of NHST is not like this. Its logic is as follows. If the null hypothesis is correct, then the data are highly unlikely to observe. Now, these data have been observed. Therefore, the null hypothesis is highly unlikely to be correct. If this sounds right to you, consider the following example (Cohen, 1994):

If a person is an American, then he is probably not a member of Congress. This person is a member of Congress. Therefore, he is probably not an American.

Clearly, the conclusion of the example cannot be more wrong. Therefore, the logic of NHST is flawed.

4.3.4 NHST tells nothing about the probability of neither null hypothesis nor alternative hypothesis

Ultimately, a research is interested in $\Pr(H_1|D)$ or at least $\Pr(H_0|D)$. However, NHST only provides $\Pr(D|H_0)$. Generally speaking, $\Pr(H_0|D) \neq \Pr(D|H_0)$, meaning that rejecting the null hypothesis says nothing or very little about the likelihood that the null is true. Furthermore, $\Pr(H_1|D) \neq \Pr(D|H_0)$ or even $\Pr(H_0|D) \neq 1 - \Pr(D|H_0)$. Therefore, rejecting the null hypothesis in no means suggests the support of the alternative hypothesis. However, too many times, people incorrectly believe $\Pr(H_0|D) = \Pr(D|H_0)$ or even $\Pr(H_0|D) = 1 - \Pr(D|H_0)$. Doing so can be extremely dangerous.

Consider the following example. Suppose a crime has been committed and blood is found at the crime scene that is directly related to the crime in a city of 800,000 residents. Statistics shows that the type of blood is present in 1% of the population. Given a person is found to have this type of blood, one wants to infer whether the person is innocent (H_0) or not(H_1). Using the idea of NHST, we can get

$$\Pr(blood|H_0) = 0.01$$

Given it's smaller than 0.05, one may reject the null that the person is innocent. However, it does not suggest the person is actually innocent or guilt at all. Note that with 800,000 residents, there are 8,000 residents with this type of blood. If we assume everyone has the equal chance to commit the crime, a person only has a 1/8,000 probability to be guilt, close to 100% to be innocent.

4.3.5 NHST does not tell whether a result can be replicated

Too many times, researchers would wrongly believe that a significant result indicates the rejection of the null hypothesis in a replication study. The probability to replicate a study is related to power $\pi = \Pr(\text{reject } H_0|H_1)$. However, a p-value does not indicate much, if there is any, about replication. For example, for a one-tail one-sample t-test, its power is

$$\pi = 1 - \Phi(-\delta\sqrt{n} + c_{1-\alpha})$$

where

- Φ is the normal distribution function,
- δ is the effect size,
- n is the sample size,
- and c is the critical value for a standard normal distribution with probability $1 - \alpha$.

Suppose in a study, we observe a p-value 0.01 which is used as α in the above formular. Then if the effect size is 0.036, the power for a sample with size 100 is only about 0.1. This means that among 10 replication studies, there will be only one study to show significant results. Therefore, it never means there is a 99% (1-0.01) probability to have significant results.

4.3.6 p-value, effect size and sample size

p-value in NHST is at least related to effect size and sample size. A small p-value does not necessarily indicate large effect size. Therefore, a smaller p-value certainly does not mean more important findings. With a large enough sample size, one would always reject the null hypothesis no matter how small the observed difference is practically. Consider a two-sample t-test, the test statistic is

$$t = \frac{\bar{x}_1 - \bar{x}_2}{s.e.(\bar{x}_1 - \bar{x}_2)} = \frac{\bar{x}_1 - \bar{x}_2}{\sqrt{\frac{s_1^2}{n_1} + \frac{s_2^2}{n_2}}}.$$

If we have $\bar{x}_1 - \bar{x}_2 = 0.01$, $s_1^2 = 1$, $s_2^2 = 1$, $n_1 = n_2 = 80,000$, then we have $t = 2$ and $p - value = 0.0455$. Clearly, even though the two-sample difference is only 0.01, we would still reject the null hypothesis based on NHST using 0.05 as the significance level.

4.3.7 The choice of significance level at 0.05

The choice of significant level at 0.05 or other values has no foundation and is almost completely subjective.

To summarize, in using NHST, one should be very cautious in interpreting the p-value. Bear in mind that:

- The p-value is not the probability that the null hypothesis is true (not $\Pr(H_0|D)$), nor is it the probability that the alternative hypothesis is false (not $1 - \Pr(H_1|D)$) €“ it is not connected to either of these. In fact, frequentist statistics does not, and cannot, attach probabilities to hypotheses.
- The p-value is not the probability of falsely rejecting the null hypothesis. This error is a version of the so-called prosecutor's fallacy.
- The p-value is not the probability that a replicating experiment would not yield the same conclusion. Quantifying the replicability of an experiment was attempted through the concept of p-rep.
- The significance level of the test, such as 0.05, is not determined by the p-value.
- The p-value does not indicate the size or importance of the observed effect.

For a compilation of some commentaries on hypothesis testing, see http://www.indiana.edu/~stigtsts/.

4.4 Bayes' Theorem

We have shown the potential problems of NHST. One solution to the problems is to use the Bayesian method that is built on Bayes' theorem. The Bayes' theorem is stated mathematically as:

$$\Pr(A \mid B) = \frac{\Pr(B \mid A)\ \Pr(A)}{\Pr(B)},$$

where A and B are events and $\Pr(B) \neq 0$. For example, A can be a hypothesis and B can be data. In the formula,

- $\Pr(A)$ and $\Pr(B)$ are the probabilities of observing A and B without regard to each other.
- $\Pr(A|B)$, a conditional probability, is the probability of observing event A given that B is true.
- $\Pr(B|A)$ is the probability of observing event B given that A is true.

In terms of hypothesis testing, we are interested in $\Pr(H_0|D)$ and $\Pr(H_1|D)$, the probability of each hypothesis given data. Suppose there are only one null hypothesis and one alternative hypothesis. Then the probability that the null hypothesis is true given the observed data is

$$\Pr(H_0|D) = \frac{\Pr(D|H_0)\Pr(H_0)}{\Pr(D|H_1)\Pr(H_1) + \Pr(D|H_0)\Pr(H_0)},$$

and the probability that the alternative hypothesis is true given the observed data

$$\Pr(H_1|D) = \frac{\Pr(D|H_1)\Pr(H_1)}{\Pr(D|H_1)\Pr(H_1) + \Pr(D|H_0)\Pr(H_0)}.$$

Note that $\Pr(D) = \Pr(D|H_1)\Pr(H_1) + \Pr(D|H_0)\Pr(H_0)$ based on the law of total probability.

Clearly, Bayes' theorem provides a way to directly tangle the probability of the hypotheses, which is often the focus of a study. The Bayesian interpretation of the formula is as follows. $\Pr(H_0)$ is called prior that presents one's belief about the probability that the hypothesis H_0 is true before collection of data and/or conducting a study. With the collected data D, one can update the probability about the same hypothesis to get the posterior $\Pr(H_0|D)$.

4.4.1 An example

Suppose a crime has been committed and blood is found at the crime scene that is directly related to the crime. Statistics shows that the type of blood is present in 1% of the population.

The prosecutor may state: "There is a 1% chance that the defendant would have the crime blood type if he were innocent. Thus, there is a 99% chance that he is guilty."

However, the defender may argue: "The city of crime scene has 800,000 people. The blood type would be found in about 8,000 people. The defendant only has a chance of 1 in 8,000 to be guilty. Thus, the defendant is innocent."

There are problems in both of the statements. The first statement is known as the *prosecutor's fallacy* and the second one is known as the *defender's fallacy*.

In this example, the null hypothesis is that the defendant is innocent (I) and the alternative hypothesis is that the defendant is guilty (G). Now we want to know the probability that the defendant is guilty or innocent given the evidence of the found blood (E). From the statistics, we know that $p(E|I) = 1/100$. The prosecutor seems to believe $p(G|E) = 1 - p(I|E) =$

$1 - p(E|I) = 99/100$, which is not true. But note this is a typical mistake when employing NHST.

If there is no any evidence (or information) about who is the criminal, then everyone in the city has the equal probability to be guilty so that

$$p(I) = \frac{799,999}{800,000} \text{ and } p(G) = 1 - p(I) = \frac{1}{800,000}.$$

Those probabilities are prior probability in Bayesian terms. Now we need to find that conditional probability of I given the evidence E - $p(I|E)$. Based on the statistics, we know $p(E|G) = 1$ and $p(E|I) = 1/100$. This is because if the defendant committed the crime, the probability that his/her blood type would be found is 100%. However, even he/she is innocent, there is still a 1% chance that her/his blood type would be found.

Using Bayes' theorem, we know that

$$p(I|E) = \frac{p(E|I)p(I)}{p(E)} = \frac{p(E|I)p(I)}{p(E|I)p(I) + p(E|G)p(G)} = .999875.$$

Thus, the defendant is very likely to be innocent based on the current limited information. This is equivalent to the argument of the defender.

To investigate the two kinds of fallacies, we can also get

$$p(G|E) = \frac{p(E|G)p(G)}{p(E|G)p(G) + p(E|I)p(I)}.$$

Then we have

$$\frac{p(G|E)}{p(I|E)} = \frac{p(E|G)}{p(E|I)}\frac{p(G)}{p(I)} = 100 \times \frac{p(G)}{p(I)}.$$

Clearly, the odds of guilty to innocent conditionally on the evidence found falls back to the odds of prior probability - the probability without considering the current evident at all. The prosecutor believes that the defendant has equal chance (50%) to commit the crime. Thus, the prior odds is 1 and the posterior odds is 100. Then the prosecutor can conclude that the defendant has 99% chance to be guilty.

The defender assumes that the $p(G)/p(I) = 1/799,999$. Thus, the posterior odds is

$$100/799,999 \approx 1/8,000.$$

However, if the defender is arrested, there must be more evidence than the blood type only. Then, the prior odds could be much larger. As shown above, even the prior odds is 1, there is a 99% probablity for the defendant to be guilty.

Chapter 5

Confidence Interval

Psychological Science is a prestigious journal for psychological research. Its submission guidelines consist of specific guideline on the use of NHST:

Effective January 2014, Psychological Science recommends the use of the "new statistics" - effect sizes, confidence intervals, and meta-analysis - to avoid problems associated with null-hypothesis significance testing (NHST).

Confidence interval provides an alternative method to NHST, which some have argued provides more information on the NHST. A confidence interval (CI) is a type of interval estimate, instead of a point estimate, of a population parameter.

5.1 Formal definition

Let θ denote a population parameter (unknowns) and X denote a random variable (e.g., GPA) from which the data can be observed. Assume the observed outcome for X is x. We can calculate an interval $[l(x), u(x)]$ based on the observed data. More generally, we can define

$$\Pr(l(X) \leq \theta \leq u(X)) = 1 - \alpha = C$$

Then $[l(X), u(X)]$ is a confidence interval with confidence level $1 - \alpha = C$, or $100(1 - \alpha)\%$. $l(X)$ and $u(X)$ are called confidence limits (bounds), lower limit and upper limit, respectively.

5.1.1 Remarks

- A CI is an observed interval calculated based on a set of observed data. In general, it is different from sample to sample. Therefore, for two studies on the same topic, the CIs can be very different even following exactly the same study design.

- Different from the point estimate, a CI consists of a range of potential values as good estimates of the unknown population parameter.
- For a given CI, it either includes or does not include the population parameter value. Therefore, a CI does not necessarily cover the true parameter values at all.
- If we conduct many separate data analyses of repeated experiment and each time we calculate a CI, the proportion of such intervals that contain the true value of the parameter matches the confidence level C $(1-\alpha)$, This is called confidence level.
- When we say, "we are 99% confident that the true value of the parameter is in our confidence interval", we express that 99% of the observed confidence intervals will contain the true value of the parameter.
- The desired level of confidence is set by the researchers, not determined by data. If a corresponding hypothesis test is performed, the confidence level is the complement of respective level of significance, i.e. a 95% confidence interval reflects a significance level of 0.05.

5.2 How to obtain a confidence interval

The basic idea to get a CI is straightforward in theory but can be very difficult in practice. It involves three steps:

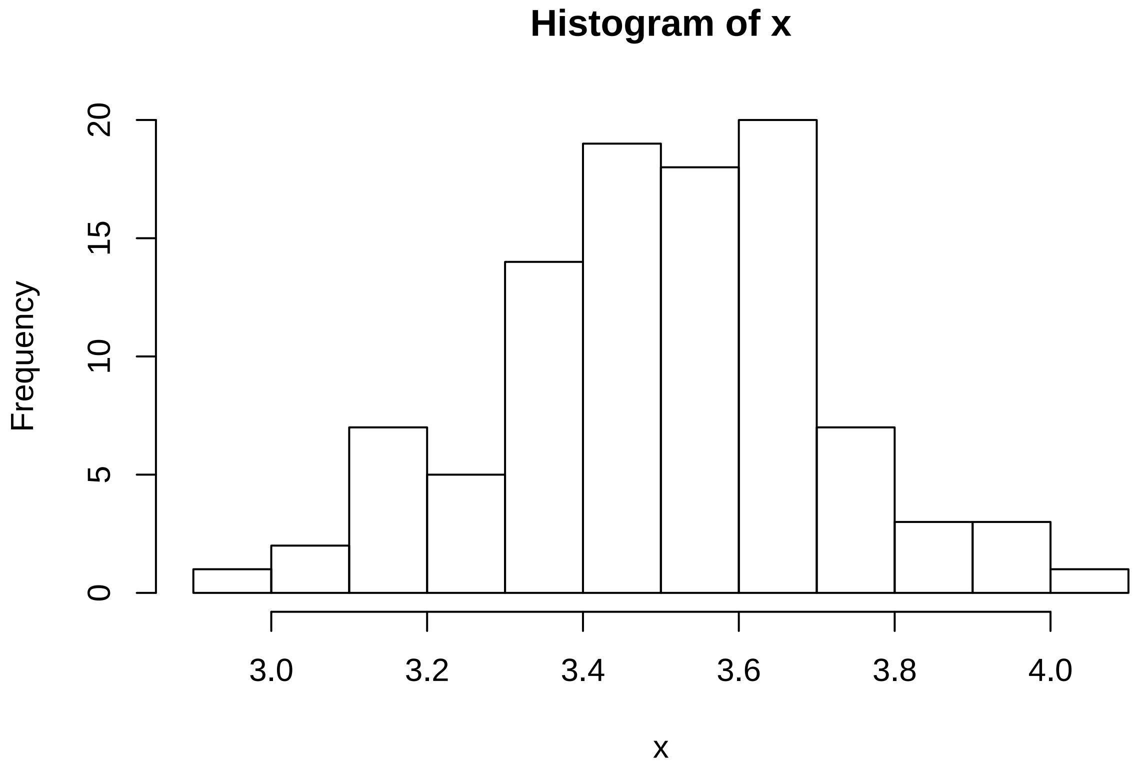
1. Obtain a point estimate $\hat{\theta}$ for θ. Note that $\hat{\theta}$ is a function of x or your data.
2. Find out the sampling distribution of $\hat{\theta}$.
3. An equal-tail confidence interval with 95% confidence level can be constructed using the 2.5th and 97.5th percentiles of the sampling distribution.

5.2.1 An example

Suppose we want to estimate and obtain the confidence interval estimate of the average GPA (μ) of all undergraduate students at University of Notre Dame. GPA typically follows a normal distribution $X \sim N(\mu, \sigma)$. Instead of going out to collect data from students, we will simulate (generate) some data for our example. To simulate data, we need to know the population mean and standard deviation of GPA. Here we assume the mean is $\mu = 3.5$ and the standard deviation $\sigma = .2$. Furthermore, we would like to generate a sample of data with the sample size 100.

In R, to generate random number from a normal distribution, the function `rnorm()` can be used. Specifically for this example, the code `x<-rnorm(100,3.5,0.2)` generates 100 values from a normal distribution with mean 3.5 and standard deviation 0.2. Therefore, in the function, the first number is the number of the values to generate, the second is the mean and the third is the standard deviation. The code below generates the values, prints them in the output, and displays the histogram of the generated data. Note that the histogram shows a bell shape.

```
x<-rnorm(100,3.5,0.2)
x ## show x
##   [1] 3.666912 3.505393 3.513702 3.350762 3.871895 3.283462 3.596087 3.684136
##   [9] 3.484478 3.449249 3.731040 3.517792 3.487425 3.502360 3.592607 3.698745
##  [17] 3.330702 3.247605 3.722761 3.576887 3.237014 3.394764 3.628747 3.516893
##  [25] 3.377679 3.655581 3.452306 3.532775 3.598987 3.498750 3.500586 3.364941
##  [33] 3.300062 3.354139 3.543074 3.774578 3.151708 3.556460 3.603588 3.751199
##  [41] 3.313614 3.553871 3.685358 3.522354 3.228461 3.628803 3.728081 3.574248
##  [49] 2.774994 3.741848 3.358530 3.381607 3.680215 3.451822 3.610234 3.559326
##  [57] 3.202037 3.540493 3.797942 3.442803 3.515349 3.493575 3.692337 3.690732
##  [65] 3.364037 3.584569 3.623174 3.490238 3.787200 3.587465 3.548139 3.440446
##  [73] 3.428566 4.060038 3.669719 3.533509 3.580912 3.644130 3.374645 3.584907
##  [81] 3.524748 3.330325 3.099236 3.543366 3.117910 3.542406 3.549324 3.676061
##  [89] 3.669131 3.411652 3.248079 3.628749 3.380642 3.304864 3.613016 3.760375
##  [97] 3.504437 3.424153 3.227398 3.429180
hist(x) ## histogram
```



With the simulated data for 100 students, an estimate of the average GPA (θ) is

$$\bar{x} = \frac{1}{100}\sum_{i=1}^{100} x_i.$$

Based on the central limit theorem, if the population variance σ is known, regardless of the shape of the population distribution, $\bar{x}$ is at least approximately normally distributed with mean (μ) and standard deviation (standard error of the mean)

$$s.e.(\bar{x}) = \sqrt{\frac{1}{n}\sigma^2} = .1\sigma.$$

Now we the point estimate is $\hat{\theta} = \bar{x}$ and its sampling distribution is a normal distribution. Then a 95% equal-tail confidence interval can be constructed using the 2.5% and 97.5% percentile of the normal distribution as $[\Phi^{-1}(0.025), \Phi^{-1}(0.975)]$ where Φ is the normal distribution function. The whole procedure to calculate a CI for a set of simulated data is shown below.

```
x <- rnorm(100,3.5,0.2)
xbar <- mean(x)
s.e. <- 0.2/10
qnorm(c(.025, .975), xbar, s.e.)
## [1] 3.445282 3.523681
```

Now, try run the code above one more time. Do you get the same confidence interval?

5.3 An experiment for CI interpretation

A CI changes each time with a study. If we repeat the same study again and again, $100(1-\alpha)\%$ of the time the obtained confidence intervals would cover the true population parameter value. This can be shown through a simulation study or experiment. Using the GPA example, we can conduct an experiment using the following steps:

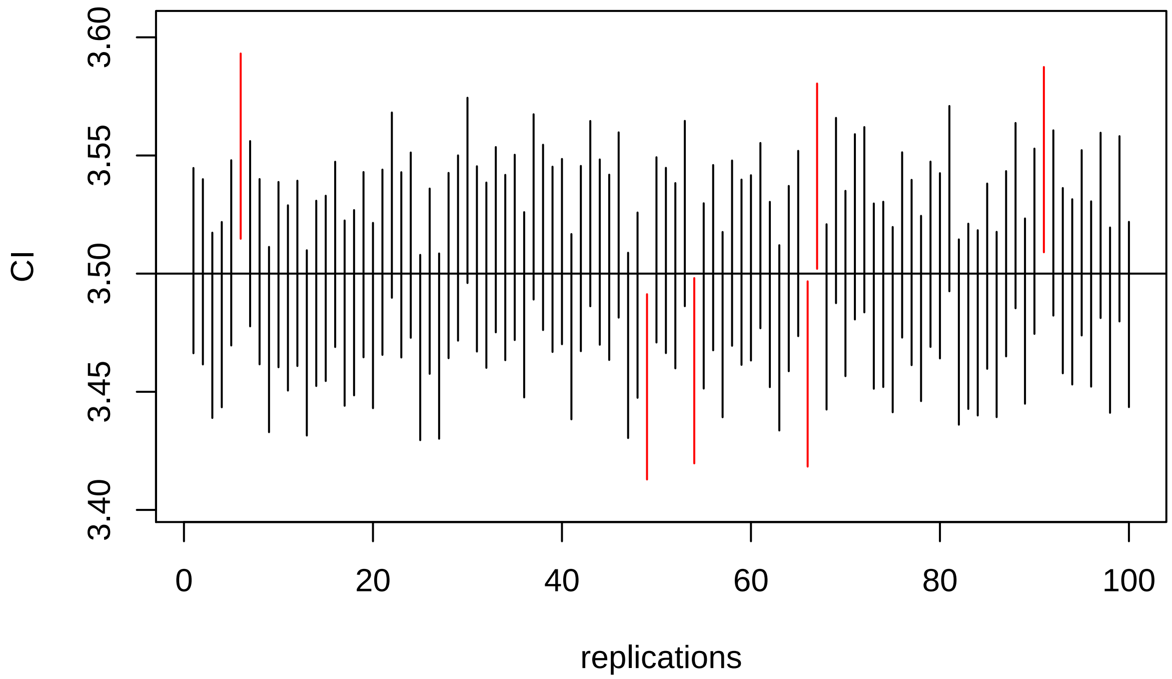
1. Generate a set of GPA data with 100 students from the population
2. Calculate the observed sample mean of GPA and the standard error of x bar
3. Calculate the confidence interval
4. Check whether the confidence interval covers the population parameter value
5. Repeat (1)-(4) 1000 times and count the total number of times that the confidence intervals cover the population value.
6. For a 95% CI, one would expect about 950 times the CIs cover the population value.

The R code below carries out the experiment. The output shows that the among the 1000 sets of CIs calculated based on the 1000 sets of simulated data, 949 of them cover the population value 3.5.

```
count<-0

for (i in 1:1000){
  x<-rnorm(100, 3.5, .2)
  xbar<-mean(x)
  s.e.<-.2/10
  l<-qnorm(.025, xbar, s.e.)
  u<-qnorm(.975, xbar, s.e.)
  if (l<3.5 & u>3.5){
    count<-count+1
  }
}
count
## [1] 943
```

For a given CI, it either covers the population value or not. This can be best demonstrated by plotting the CIs. The R code and output are given below. In the code, we generate 100 CIs, among which 97 cover the population value and 3 do not.

```
count<-0
all.l<-all.u<-NULL
for (i in 1:100){
  x<-rnorm(100, 3.5, .2)
  xbar<-mean(x)
  s.e.<-.2/10
  l<-qnorm(.025, xbar, s.e.)
  u<-qnorm(.975, xbar, s.e.)
  if (l<3.5 & u>3.5){
    count<-count+1
  }
  all.l<-c(all.l, l)
  all.u<-c(all.u, u)
}
count
## [1] 95

## generate a plot
plot(c(1,1), c(all.l[1], all.u[1]), type='l',
     ylim=c(min(all.l)-.01, max(all.u)+.01),
     xlim=c(1,100), xlab='replications',
     ylab='CI')
abline(h=3.5)
for (i in 2:100){
  if (all.l[i]<3.5 & all.u[i]>3.5){
    lines(c(i,i), c(all.l[i], all.u[i]))
  }else{
    lines(c(i,i),c(all.l[i], all.u[i]),col='red')
  }
}
```



5.4 Confidence interval and hypothesis testing

Confidence intervals do not require a-priori hypotheses, nor do they test trivial hypotheses. A confidence interval provides information on both the effect and its precision. A smaller interval usually suggests the estimate is more precise. For example, [3.3, 3.7] is more precise than [3,4].

A confidence interval can be used for hypothesis testing. For example, given the null hypothesis

$$\theta = \theta_0$$

for any value of θ_0. If a confidence interval with confidence level $C = 1 - \alpha$ contains θ_0, we fail to reject the corresponding null hypothesis at the significance level α. Otherwise, we reject the null hypothesis at the significance level α.

For example, suppose we are interested in testing whether a training intervention method is effective or not. Based on a pre- and post-test design, we find the confidence interval for the change after training is [0.7, 1.5] with the confidence level 0.95. Since this CI does not include 0, we would reject the null hypothesis that the change is 0 at the alpha level 0.05.

Using CI for hypothesis testing does not provide the exact p-value. However, a CI can be used to test multiple hypotheses. For example, for any null hypothesis that the change score is less than 0.7, one would reject it.

CI kinds of focuses on the alternative hypothesis, the effect of interest. It provides a range of plausible values to estimate the effect of interest.

Reichardt and Gollob (1997) discussed conditions that NHST and CI can be useful. NHST is shown generally to be more informative than confidence intervals when assessing (1) the probability that a parameter equals a pre-specified value; (2) the direction of a parameter relative to a pre-specified value (e.g., 0); and (3) the probability that a parameter lies within a pre-specified range.

On the other hand, confidence intervals are shown generally to be more informative than NHST when assessing the size of a parameter (1) without reference to a pre-specified value or range of values; (2) with reference to many pre-specified values or ranges of values. Hagen (1997) pointed out: “We cannot escape the logic of NHST [null hypothesis statistical testing] by turning to point estimates and confidence intervals” (p. 22). In addition, Schmidt and Hunter (1997) suggested: “The assumption underlying this objection is that because confidence intervals can be interpreted as significance tests, they must be so interpreted. But this is a false assumption” (p. 50).

5.5 Bootstrap

Obtaining a CI is not an easy, most times an extremely difficult, task. For example, even for the most widely used correlation coefficient, it is already difficult to get the confidence interval. For bivariate normal data, one can get the exact distribution of the sample correlation coefficient r as

$$f(r) = \frac{(n-2)\,\mathbf{\Gamma}(n-1)(1-\rho^2)^{\frac{n-1}{2}}(1-r^2)^{\frac{n-4}{2}}}{\sqrt{2\pi}\,\mathbf{\Gamma}\left(n-\frac{1}{2}\right)(1-\rho r)^{n-\frac{3}{2}}}\,{}_{\mathbf{2}}\mathbf{F}_{\mathbf{1}}\left(\frac{1}{2},\frac{1}{2};\frac{2n-1}{2};\frac{\rho r+1}{2}\right).$$

With the sampling distribution, theoretically, one can get an exact CI for the correlation coefficient ρ. However, because the computational difficulty, many ways have been proposed to approximate it instead (see https://arxiv.org/pdf/1410.8165.pdf). The most widely used method is based on Fisher’s z-transformation. For a sample correlation r, its Fisher’s transformation is

$$Z = \frac{1}{2}\ln\frac{1+r}{1-r}.$$

After transformation, Z approximately follows a normal distribution with mean

$$\frac{1}{2}\ln\frac{1+\phi}{1-\phi}$$

and variance $\phi = 1/(\phi - 3)$.

To get the CI for ρ, we first construct a CI for

$$\frac{1}{2}\ln\frac{1+\rho}{1-\rho}$$

as

$$\left[\frac{1}{2}\ln\frac{1+r}{1-r}-\frac{z_{1-\alpha/2}}{\sqrt{n-3}},\frac{1}{2}\ln\frac{1+r}{1-r}+\frac{z_{1-\alpha/2}}{\sqrt{n-3}}\right]$$

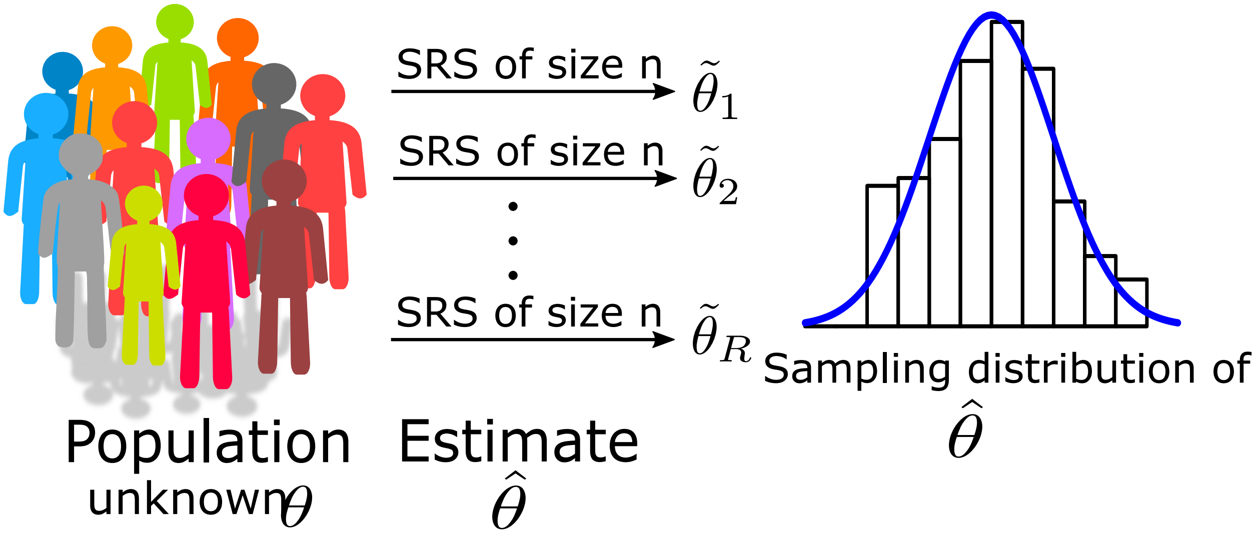
With Z_α denoting the $100\alpha\%$ percentile of the standard normal distribution. Then, we can solve this for the the CI of ρ.

Bootstrap provides a useful procedure that can be used to construct a CI. Bootstrap method is computationally intensive but can be used to get the distribution of a quantity of interest especially when the theoretical distribution of a statistic is complicated or unknown and / or the sample size is insufficient for straightforward statistical inference.

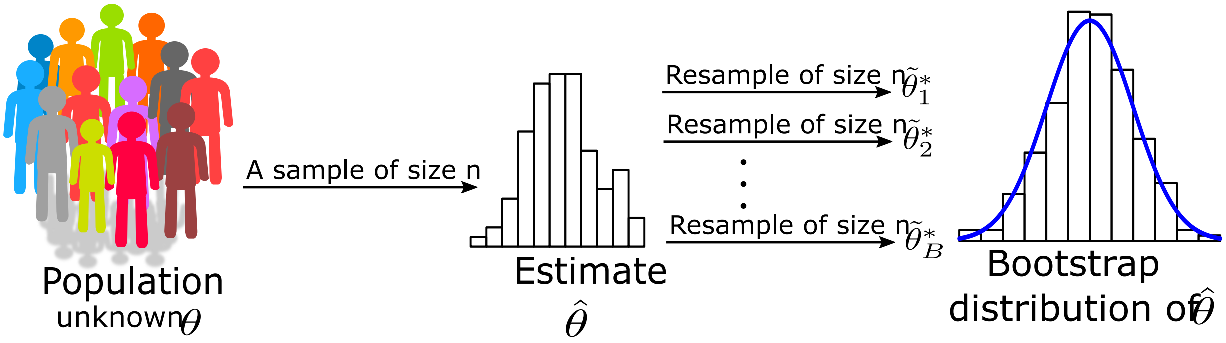
5.5.1 Basic idea

The basic idea of the bootstrap method is to circumvent the difficulty to get the sampling distribution of a statistic. Sometimes, one can get the theoretical distribution of such a statistic through derivation. But the underlying idea can be understood through a simple example.

Suppose we are interested in estimating a parameter called θ, such as average GPA of students at University of Notre Dame. To do so, we can get a sample with sample size 100 and then use the average GPA as an estimate of θ, denoted as $\hat{\theta}$. To make inference, we would need to get the sampling distribution of $\hat{\theta}$, which is the distribution of the statistic for *all possible samples from the same population* (students at Notre Dame) of a given size (100). Although generally it is not feasible to get all possible samples, we assume we can repeatedly get R samples each with sample size 100. For each sample, we can get the average GPA as $\tilde{\theta}_i, i = 1, \ldots, R$. Then, the R average GPA will form a distribution, which can be viewed as an approximation of the sampling distribution. If R is equal to the number of all possible samples, then it would be the exact sampling distribution. This procedure is illustrated in the figure below.



Bootstrap is analogous to the procedure to get the sampling distribution. First, from a population, we can get a random sample with size n. Using the sample, we can obtain an estimate of θ, denoted as $\hat{\theta}$. Second, using the random sample as a "population", we can randomly sample the subjects to form new samples with the same size. In doing so, we allow the subjects in the original sample to appear more than once in the new, bootstrapping samples. Each time we get a bootstrapping sample, we can calculate the statistic we are interested in, denoted by $\tilde{\theta}$. By repeating the procedure for B times, we can get a set of $\tilde{\theta}_j, j = 1, \dots, B$. With the set of values, we can get an empirical distribution, e.g., as a histogram, for $\hat{\theta}$. Inference about the parameter can be conducted by viewing the bootstrap distribution as the "sampling" distribution. This procedure is illustrated in the figure below.



5.5.2 Bootstrap standard error and confidence intervals

The bootstrap method is often used to obtain bootstrap standard error or confidence intervals for statistics of interest. The bootstrap standard error of the parameter estimate $\hat{\theta}$ can be calculated as

$$s.e.(\hat{\theta}_p) = \sqrt{\sum_{j=1}^{B} (\tilde{\theta}_j - \bar{\tilde{\theta}}_j)^2/(B-1)}$$

with

$$\bar{\tilde{\theta}} = \sum_{j=1}^{B} \tilde{\theta}_j/B.$$

One way to construct a confidence interval is based on the standard error by assuming a normal distribution. Specially, a normal based $1-2\alpha$ CI can be constructed as

$$[\hat{\theta} - z_{1-\alpha} s.e.(\hat{\theta}), \hat{\theta}_p + z_{1-\alpha} s.e.(\hat{\theta})].$$

A widely used CI is called the percentile bootstrap CI that is constructed by

$$[\tilde{\theta}(\alpha), \tilde{\theta}(1-\alpha)]$$

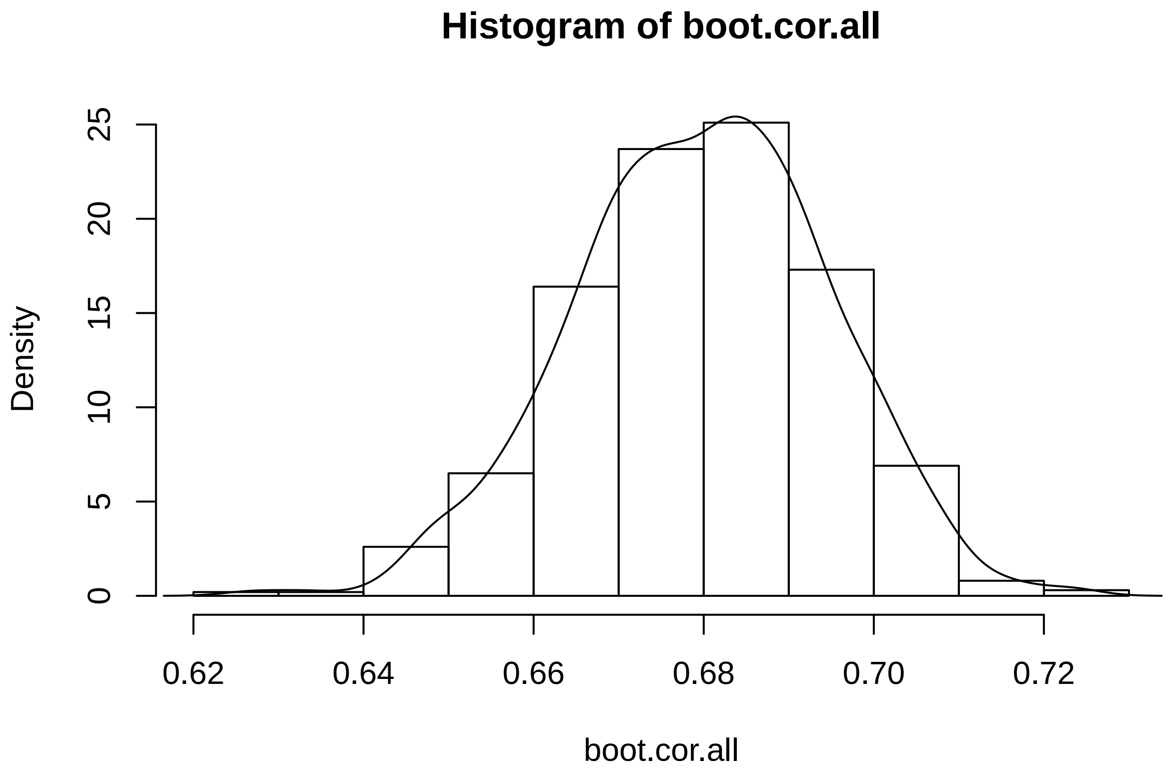
with $\tilde{\theta}(\alpha)$ denoting the 100αth percentile of the B bootstrap estimates. Practically, this is constructed by ordering all the bootstrap estimates $\tilde{\theta}$ and then select the pair of values that are at the 100αth percentile and the $100(1-\alpha)$th percentile.

5.5.3 Example for correlation coefficient

As an example, we obtain the bootstrap standard error and confidence interval for the correlation between the verbal test scores at time 1 and time 2. The complete R code is given below.

```r
active <- read.csv("data/active.csv")
attach(active)

## calculate correlation for the sample

orig.cor <- cor(hvltt, hvltt2)
orig.cor
## [1] 0.6793641

## calculate the sample size
n<-length(hvltt)

## Bootstrap for 1000 times
```

```
B<-1000
boot.cor.all<-NULL

for (i in 1:B){
  index<-sample(1:n, replace=T)
  boot.hvltt2<-hvltt2[index]
  boot.hvltt<-hvltt[index]
  boot.cor<-cor(boot.hvltt2, boot.hvltt)
  boot.cor.all<-c(boot.cor.all, boot.cor)
}

## plot the bootstrap distribution
hist(boot.cor.all,prob=T)
lines(density(boot.cor.all))
```



```
## Bootstrap standard error
sd(boot.cor.all)
## [1] 0.01527072

## percentile bootstrap CI
quantile(boot.cor.all, prob=c(0.025, 0.975))
```

```
##      2.5%     97.5%
## 0.6497606 0.7081108
```

We now explain the code line by line.

- `usedata('active')` is used to set the data set “active.csv” to be used in this example. We use `attach(active)` to attach the dataframe so that the variables in the data can be accessed directly.
- The correlation for the two variables hvltt and hvltt2 is calculated using `orig.cor <- cor(hvltt, hvltt2)`, where `cor()` is the R function to calculate a correlation.
- To use bootstrap, the data have to be sampled with replacement. Thus, the same datum can appear more than once in the bootstrap sample. `sample()` is a function to sample data randomly from an input vector. To sample with replacement, the option `replace=T` should be supplied. `1:n`, where `n` is the sample size, is a vector that represents the index of each subject in the data. Therefore, `index<-sample(1:n, replace=T)` will generate a set of values with the length `n`.
- `hvltt[index]` and `hvltt2[index]` will obtain the values in the two variables using the index from above. Therefore, each time, a new set of values for hvltt and hvltt2 are obtained and saved into `boot.hvltt` and `boot.hvltt2`, respectively.
- The correlation based on the newly sampled data is calculated and called `boot.cor`.
- `for ()` is a control function for loop. Using this function, the same statements, for example, the procedure for resampling and correlation calculation, can be repeated. The statements to be repeated are put into a pair of braces. `(i in 1:B)` tell R that `i` is the index for the repetition.
- At each time, we can get a bootstrapping correlation. We can combine all the correlations together using the R function `c()`. After running the `for` loop, the correlations are saved as `boot.cor.all`. Note that we define `boot.cor.all` as `NULL`, meaning there is no value inside initially. Since `B<-1000`, there will be 1000 values in `boot.cor.all` after the analysis.
- With the bootstrapping information in `boot.cor.all`, we can plot the histogram, calculate bootstrap standard error and percentile CI (using `quantile()` function).

Chapter 6

t-test

A t-test is a family of statistical hypothesis tests in which the test statistic follows a Student's t-distribution under the null hypothesis. The most widely used t-tests include the one-sample t-test, t-test for paired samples and independent two-sample t-test.

6.1 One-sample t-test

The one-sample t-test is used to test the null hypothesis the population mean μ is equal to a specified value μ_0, which is often 0. Therefore, the null hypothesis is

$$H_0 : \mu = \mu_0.$$

Depending on the alternative hypothesis, we can carry out either a one-tailed or two-tailed test. If the sign for the difference between μ and μ_0 is not known, a two-tailed test should be used and the alternative hypothesis is

$$H_1 : \mu \neq \mu_0$$

Otherwise, a one-tailed test is used and the alternative hypothesis is

$$H_a : \mu > \mu_0$$

if it is expected the population mean is greater than μ_0, or

$$H_a : \mu < \mu_0$$

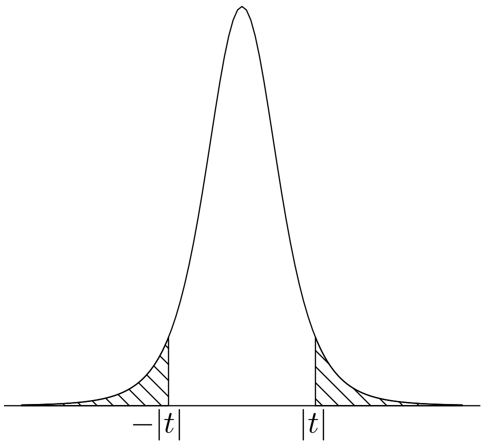
if it is expected the population mean is less than μ_0.

6.1.1 Test statistic

For one-sample t-test, the statistic

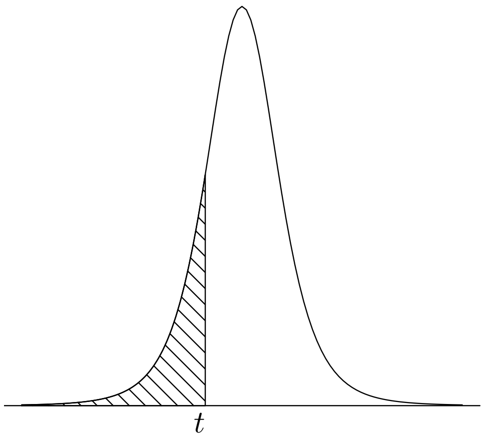
$$t = \frac{\overline{x} - \mu_0}{s/\sqrt{n}}$$

where $\overline{x}$ is the sample mean, s is the sample standard deviation of the sample and n is the sample size. This is also called the t-statistics, which follows a $t-$distribution with the degrees of freedom $n\hat{}'1$, under the assumption that the data follow a normal distribution. With the $t-$distribution, the calculation of a p-value is illustrated in the figure below.



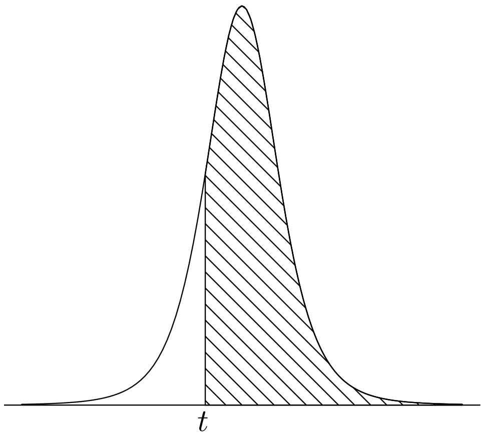
$H_1 : \mu \neq \mu_0$

$p = \Pr(T \leq -|t|) + \Pr(T \geq |t|)$



$H_1 : \mu < \mu_0$

$p = \Pr(T \leq t)$



$H_1 : \mu > \mu_0$

$p = \Pr(T \geq t)$

Using the ACTIVE data, we want to test whether the education level of people older than 65 years is above high school (years of education is greater than 13). From the t-test output, we have t-value 2.465. Comparing that with a t-distribution with degrees of freedom 2801, we get the p-value $= 0.007$. We therefore reject the null hypothesis.

```
active <- read.csv("data/active.csv")
attach(active)

t.test(edu, mu=12, alternative = "greater" )
##
##  One Sample t-test
##
## data:  edu
## t = 3.7234, df = 1574, p-value = 0.0001017
## alternative hypothesis: true mean is greater than 12
## 95 percent confidence interval:
##  13.30691      Inf
## sample estimates:
## mean of x
##  14.34222
```

6.1.2 Effect size

For the one-sample t-test, the effect size is defined as

$$\delta = \frac{\mu - \mu_0}{\delta},$$

where δ is the population standard deviation. The sample effect size

$$d = \frac{\overline{x} - \mu_0}{s}.$$

Whether an effect size should be interpreted small, medium, or large depends on its substantive context and its operational definition. Some guidelines were provided in the literature as shown in the table below. However, they should be used with extraordinary caution.

Effect size

d

Very small

0.01

Small

0.20

Medium

0.50

Large

0.80

Very large

1.20

Huge

2.0

For the ACTIVE example, the estimated effect size $d = 0.047$, indicating a small effect. Note that even though the result based on the t-test was significant, the difference was actually quite small in practice.

```
(14.23233 - 13)/sd(edu)
## [1] 0.04936283
```

6.2 t-test for paired samples

This test is used when we have paired samples where two samples can be matched or "paired". A common example is pre- and post-test design or repeated measures. For example, suppose we want to assess of an intervention method to reduce depression. We can enroll 100 participants and measure each participant's depression level. Then all the participants are given the intervention, after which their depression levels are measured again. Our interest is in whether the intervention has any effect on mean depression levels.

To answer the question, we can first calculate the difference in depression level before and after intervention: $d_i = y_{i2} - y_{i1}$. Then d_i can be analyzed using the one-sample t-test.

$$t = \frac{\overline{d} - \mu_0}{s_d/\sqrt{(n)}},$$

where $\overline{d}$ is the average and s_d is the standard deviation of the differences. Under the null hypothesis $H_0 : \mu = \mu_0$, the t-statistic follows a t-distribution with the degree of freedom used is $n - 1$, where n represents the number of pairs.

Note that although the mean difference is the same for the paired and unpaired samples, their statistical significance levels can be very different. This is because the variance of d is

$$\text{var}(d) = \text{var}(y_2 - y_1) = \text{var}(y_1) + \text{var}(y_2) - 2\rho\text{var}(y_1)\text{var}(y_2)$$

where ρ is the correlation before and after the treatment. Since the correlation is often positive, the variance for the paired samples is often smaller than unpaired samples.

In the ACTIVE data, we have measures on verbal test for 4 times. As an example, we want to test if there is any difference in the score between the first time and the last time. The input and output can be seen below. Note that the same `t.test()` function is used but the option `paired=TRUE` is used.

```
t.test(hvltt, hvltt4, paired=TRUE)
## 
##  Paired t-test
## 
## data:  hvltt and hvltt4
## t = -1.6266, df = 1574, p-value = 0.104
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -0.41456609  0.03869307
## sample estimates:
## mean of the differences
##              -0.1879365
```

6.3 Independent two-sample t-test

The independent samples t-test is used when two separate sets of independent and identically distributed samples are obtained, one from each of the two populations being compared. For example, in evaluating the effect of an intervention, we enroll 100 participants and randomly assign 50 to the treatment group and the other 50 to the control group. In this case, we have two independent samples and should use the independent two-sample t-test.

6.3.1 Welch's t test (unpooled two independent sample t test)

When the two population variances of the two groups are not equal (the two sample sizes may or may not be equal). The t statistic to test whether the population means are different is calculated as:

$$t = \frac{\bar{x}_1 - \bar{x}_2}{s_{\overline{\Delta}}}$$

where

$$s_{\overline{\Delta}} = \sqrt{\frac{s_1^2}{n_1} + \frac{s_2^2}{n_2}}.$$

Here, s_1^2 and s_2^2 are the unbiased estimators of the variances of the two samples with $n_k =$ number of participants in group $k = 1$ or 2. For use in significance testing, the distribution of the test statistic is approximated as an ordinary Student's t distribution with the degrees of freedom calculated as

$$\text{d.f.} = \frac{(s_1^2/n_1 + s_2^2/n_2)^2}{(s_1^2/n_1)^2/(n_1-1) + (s_2^2/n_2)^2/(n_2-1)}$$

This is known as the Welch-Satterthwaite equation. The true distribution of the test statistic actually depends (slightly) on the two unknown population variances.

In R, the function `t.test()` can be used to conduct a t test. The following code conducts the Welch's t test. Note that `alternative = "greater"` sets the alternative hypothesis. The other options include `two.sided` and `less`.

```
training<-hvltt2[group==1]
control<-hvltt2[group==4]

mean(training, na.rm=T)-mean(control, na.rm=T)
## [1] 1.970935

t.test(training, control, alternative = 'greater')
##
##  Welch Two Sample t-test
##
## data:  training and control
## t = 5.0416, df = 775.37, p-value = 2.876e-07
## alternative hypothesis: true difference in means is greater than 0
## 95 percent confidence interval:
##  1.327135      Inf
## sample estimates:
## mean of x mean of y
##  26.10204  24.13111
```

6.3.2 Pooled two independent sample t test

When the two samples have the same population variance.The t statistic can be calculated as follows:

$$t = \frac{\bar{x}_1 - \bar{x}_2}{s_p \cdot \sqrt{\frac{1}{n_1} + \frac{1}{n_2}}}$$

where

$$s_p = \sqrt{\frac{(n_1-1)s_1^2 + (n_2-1)s_2^2}{n_1+n_2-2}}$$

is an estimator of the pooled standard deviation of the two samples. $n_k - 1$ is the degrees of freedom for each group, and the total sample size minus two $(n_1 + n_2 - 2)$ is the total number of degrees of freedom, which is used in significance testing.

The pooled two independent sample t test can also be conducted using the `t.test()` function by setting the option `var.equal=T` or `TRUE`.

```
training<-hvltt2[group==1]
control<-hvltt2[group==4]

t.test(training, control, var.equal=T, alternative = 'greater')
##
##  Two Sample t-test
##
## data:  training and control
## t = 5.0428, df = 779, p-value = 2.856e-07
## alternative hypothesis: true difference in means is greater than 0
## 95 percent confidence interval:
##  1.327289      Inf
## sample estimates:
## mean of x mean of y
##  26.10204  24.13111
```

6.3.3 Effect size

For the two-sample t-test, Cohen's d is defined as the difference between two means divided by a standard deviation.

$$d = \frac{\bar{x}_1 - \bar{x}_2}{s_p}$$

Cohen defined s_p, the pooled standard deviation, as

$$s_p = \sqrt{\frac{(n_1-1)s_{x_1}^2 + (n_2-1)s_{x_2}^2}{n_1+n_2-2}}$$

For the ACTIVE data analysis example, the effect size is calculated as below.

```
training<-hvltt2[group==1]
control<-hvltt2[group==4]

mean1=mean(training,na.rm=T)
```

```
mean2=mean(control,na.rm=T)
meandiff=mean1-mean2

n1=length(training)-sum(is.na(training))
n2=length(control)-sum(is.na(control))

v1=var(training,na.rm=T)
v2=var(control,na.rm=T)
s=sqrt(((n1-1)*v1+(n2-1)*v2)/(n1+n2-2))
s
## [1] 5.461292

cohend=meandiff
cohend
## [1] 1.970935
```

Chapter 7

Analysis of variance

Analysis of variance (ANOVA) is a collection of statistical models used to analyze the differences between group means, developed by R.A. Fisher (Fisher, 1925). In ANOVA, the observed variance in a particular variable, usually an outcome variable, is partitioned into components attributable to different sources of variation: typically the between-group variation and the within-group variation. Simply speaking, ANOVA provides a statistical test of whether or not the means of several groups are equal, and therefore generalizes the t-test to more than two groups.

7.1 One-way ANOVA

One-way ANOVA typically evaluates whether there is difference in means of three or more groups, although it also works for two-group analysis. In other words, it investigates the effect a grouping variable on the outcome variable.

In the ACTIVE data, we have 4 groups: one control group and three training groups - memory, reasoning, and speed training groups. As an example, we test whether there is any difference in the four groups in terms of memory performance measured by the *Hopkins Verbal Learning Test*, denoted by the `hvltt2` variable in the data set. Then, one-way ANOVA can be used.

Specifically for this example, the null and alternative hypotheses

$$H_0: \mu_1 = \mu_2 = \mu_3 = \mu_4$$

$$H_a: H_0 \text{ is not true or at least two groups have different means.}$$

For the hypothesis testing, an F-test is used. The basic idea is to decompose the total variation of the outcome variance into the variation because of the difference between groups and the variation within groups. The variation is measured by the sum of squares. For one-way ANOVA, we have

$$SST = SSB + SSW$$

- SST is the total sum of squares.
- SSB is the between-group sum of squares.
- SSW is the within-group sum of squares.

Then the F-statistic is

$$F = \frac{SSB/df_B}{SSW/df_W} = \frac{MSB}{MSW}$$

- df_B is the between-group degrees of freedom, which is equal to the number of groups - 1. For the ACTIVE example, it is $4 - 1 = 3$.
- df_W is the within-group degrees of freedom, which is equal to the total sample size - the number of groups. Since the sample size is 1575, $df_W = 1575 - 4 = 1571$.

If the null hypothesis is true, the F-statistic should follow an F distribution with degrees of freedom df_B and df_W under certain condition. The R code below conducts the one-way ANOVA for the ACTIVE data.

- ANOVA in R is based on the linear regression. Therefore, the model is fitted using the function `lm()`. Then the function `anova()` is used to construct the ANOVA source of variation table. In the table, the sum of squares (Sum Sq), mean sum of squares (Mean Sq), degrees of freedom (Df), F value and p-value (Pr(>F)) are included.
- In the data set, the group variable is coded using numeric values. To conduct ANOVA, one needs to first change it to a grouping variable, which is done using the function `factor()`.
- Specifically for this example, we have F=10.051. Comparing it to an F distribution with degrees of freedom (3, 1571), we obtain the p-value = 1.466e-06. Therefore, one would reject the null hypothesis. The memory performance significantly differed across the 4 groups.

```
active <- read.csv("data/active.csv")
attach(active)

model<-lm(hvltt~factor(group))
anova(model)
## Analysis of Variance Table
##
## Response: hvltt
##                  Df Sum Sq Mean Sq F value Pr(>F)
## factor(group)    3    130  43.251  1.7464 0.1556
## Residuals     1571  38907  24.766
```

7.1.1 Post-hoc multiple comparison

In the one-way ANOVA, we have found at least two groups are different in memory performance. We can further investigate which two groups are different. In R, the function `pairwise.t.test()` can be used to conduct a t-test for any two groups to see if they are significantly different. For example, the code below shows how to conduct such analysis.

```
pairwise.t.test(hvltt2, group, p.adj = "none")
##
##  Pairwise comparisons using t tests with pooled SD
##
## data:  hvltt2 and group
##
##   1       2      3
## 2 2.9e-05 -      -
## 3 0.0014  0.2995 -
## 4 2.8e-07 0.3375 0.0445
##
## P value adjustment method: none
```

From the output, we might "naively" conclude that group 1 is statistically different from groups 2, 3, and 4 as well as group 3 different from group 4. However, in doing so, we run into the multiple comparison problem – when conducting a group of more than one hypothesis testing simultaneously, hypothesis tests are more likely to incorrectly reject the null hypothesis. To demonstrate this, consider two hypotheses:

$$H_{01} : \text{group } 1 = \text{group } 2$$

and

$$H_{02} : \text{group } 3 = \text{group } 4.$$

If for each individual hypothesis, the type I error rate is controlled at 0.05, meaning there is 5% probability to reject the hypothesis even it is true. Then, the type I error rate to reject either or both of the two hypotheses is $1-(1-.05)*(1-0.05)=0.0975$, which is about two times of the nominal level 0.05. This indicates to control the type I error rate, one should use a smaller significance level. Such a significance level can be calculated. Suppose we have k simultaneous hypotheses to test and we want to keep the overall type I error rate to be 0.05. Let α^* is the significance level to use. Then we have

$$1-(1-\alpha^*)^k = 0.05$$

Solving this equation leads to

$$\alpha^* = 1-0.95^{1/k} \approx 0.05/k.$$

For the one-way ANOVA post-hoc comparison, we conducted a total of 6 hypotheses tests. Therefore, the corrected significance level should be $0.05/6 = 0.008$. Therefore, only a p-value smaller than this can be considered significant. In this case, the difference between group 3 and group 4 is not statistically significant anymore. Another way to solve the problem is to multiply the obtained p-value by the number of tests and then compare it with 0.05 all the time. The way to adjust the p-value is called Bonferroni correction (Dunn, 1961). This can be done easily in R as shown below.

```
pairwise.t.test(hvltt2, group, p.adj = "bonf")
##
##  Pairwise comparisons using t tests with pooled SD
##
## data:  hvltt2 and group
##
##   1       2       3
## 2 0.00017 -       -
## 3 0.00828 1.00000 -
## 4 1.7e-06 1.00000 0.26720
##
## P value adjustment method: bonferroni
```

7.1.2 Barplot with standard error or confidence interval

With a fairly large sample size, it can be useful to make a barplot to show the group information. The height of each bar is proportional to the mean of each group. In addition, the standard error or the confidence interval for the mean of each group can be added to the bars. Such a plot can be generated using the R package ggplot2. To generate a such a plot, we need a data frame with the following information: the grouping variable, the mean of each group and the standard error. For the ACTIVE data, the information is given in the following table.

group

mean

se

1

26.1

0.27

2

24.5

0.27

3

24.9

0.25

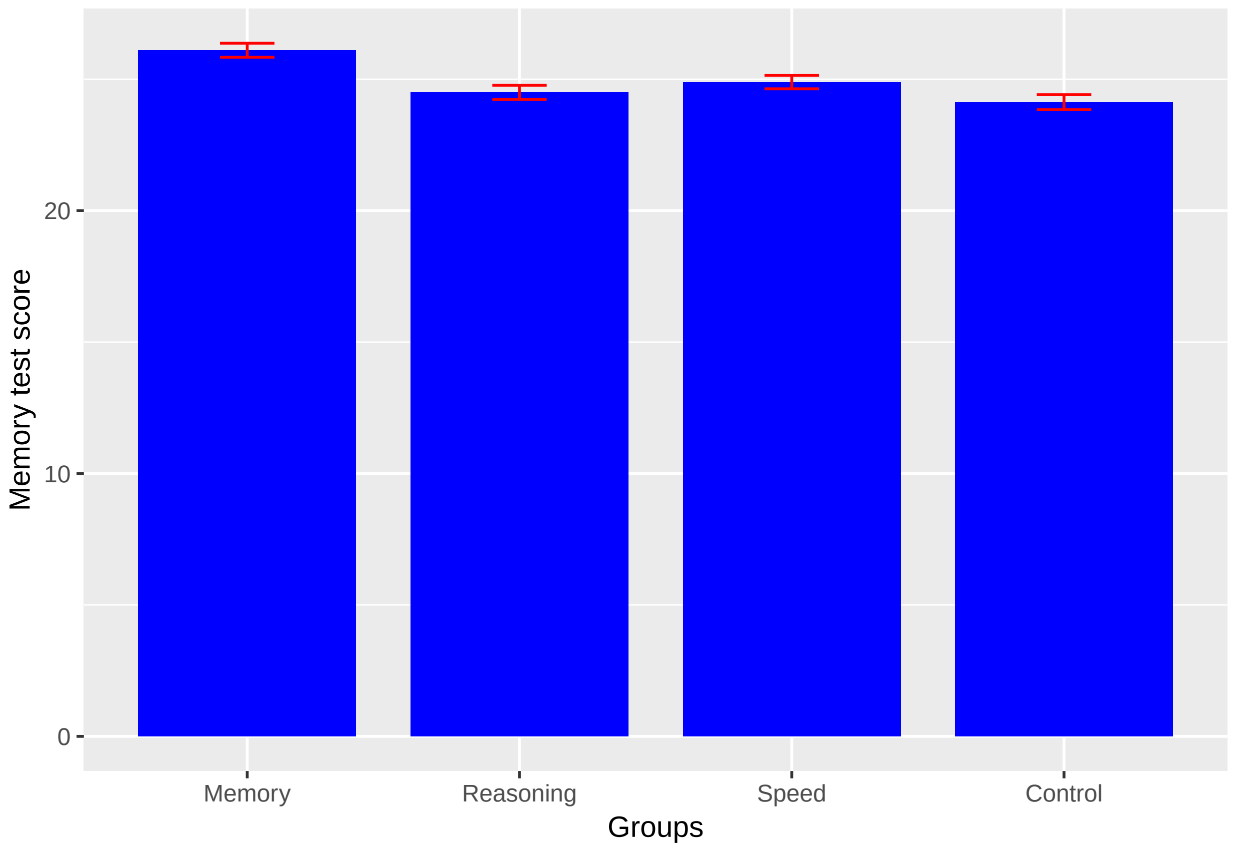
4

24.1

0.29

The R code below calculates the information in the table and generates a bar plot as shown in the output. We now explain each line of the R code.

```
library(Rmisc)
library(ggplot2)

stats <- summarySE(active, measurevar="hvltt2", groupvars=c("group"))
stats
##   group   N   hvltt2       sd        se        ci
## 1     1 392 26.10204 5.293416 0.2673579 0.5256389
## 2     2 387 24.49871 5.307817 0.2698115 0.5304842
## 3     3 407 24.89189 5.116197 0.2536005 0.4985340
## 4     4 389 24.13111 5.625401 0.2852192 0.5607685

ggplot(stats, aes(x=factor(group), y=hvltt2)) +
    geom_bar(stat="identity", fill="blue", width=0.8) +
    geom_errorbar(aes(ymin=hvltt2-se, ymax=hvltt2+se),
                  width=.2, colour='red') +
    xlab("Groups") +
    ylab("Memory test score") +
    scale_x_discrete(breaks=c("1", "2", "3", "4"),
        labels=c("Memory", "Reasoning", "Speed", "Control"))
```



- To generate the plot, two R packages `Rmisc` and ggplot2 are used.
- The function `summarySE()` from `Rmisc` is first used to obtain the needed information that includes the mean and se of hvltt2 for each groups the four groups.
  - For the `summarySE()` function, (1) the first input the name of the `dataframe` to be used, (2) `measurevar` tells the target variable to be analyzed, and (3) `groupvars` tells the grouping variable to be used.

To generate the plot, the `ggplot()` function from the ggplot2 package is used.

- `ggplot()` can generate all kinds of plot and allow the use of difference options. Note that the different options (layers) are connected using the symbol "+".
- Line 8 provides the basic information for a plot. It says the data set stats are used here. `aes()` function provides some other information. For example, here it tells the variable on the x-axis should be "group" variable in the data using `x=group`. Similarly, on the y-axis, the group mean should be plotted.
- `geom_bar` tells that a bar plot is used. `stat="identify"` tells the bar should be proportional to the data value in the data set. `fill="blue"` specifies the color to fill the bar, blue in this example. `width=0.8` tells the width of the bar.
- `geom_errorbar()` tells to add error bar to the plot. `aes(ymin=mean-se, ymax=mean+se)` specifies the lower and upper values for the bar. In the barplot with error bars, the lower value is the mean minus one standard error and the upper value is the mean plus one standard error. `width=.2` tells the width and `colour='red'` tells

the color of the error bars.
- `xlab` and `ylab` add the labels for the x-axis and y-axis.
- `scale_x_discrete` can be used to customize the labels for each group. In the original data, the 4 groups are represented by 1, 2, 3, and 4. `breaks` tells the position of the original data and `labels` provides the new labels for each group.

7.2 Two-way ANOVA

Two-way analysis of variance (two-way ANOVA) is an extension of the one-way ANOVA to examine the influence of two different categorical independent variables on one continuous dependent variable. The two-way ANOVA can evaluate not only the main effect of each independent variable but also the potential interaction between them. For example, for the ACTIVE data, we can test whether the four training groups and gender are related to the memory test performance.

7.2.1 Type of effects and hypotheses

In two-way ANOVA with two factors (independent variables) A and B, we can test two main effects and one interaction effect:

- Main effect of A: whether the population means are the same for different levels (groups) of A?
  - The null hypothesis: the population means are the same for different levels of A.
- Main effect of A: whether the population means are the same for different levels (groups) of A?
  - The null hypothesis: the population means are the same for different levels of A.
- The interaction effect of A and B: whether the difference in the population means for difference level of A depends on the level of B or vice visa?
  - The null hypothesis: the effect of A or B on the outcome does not depend on B or A.

7.2.2 Two-way ANOVA F tests

Like in one-way ANOVA, F test is used in hypothesis testing. The test is constructed based on the decomposition of the sum of squares of the outcome variables. Specifically, we have

$$SS_T = SS_A + SS_B + SS_{A\times B} + SS_W$$

- SS_T or SS_{total} is the sum of squares for the outcome variable.
- SS_A is the sum of squares attributes to the factor A.
- SS_B is the sum of squares attributes to the factor B.
- $SS_{A\times B}$ is the sum of squares attributes to the joint effect of A and B.

- SS_W or SS_{within} is the residual sum of squares that cannot be explain by A, B or their interaction.

Let N be the sample size, J is the number of levels in factor A, and K is the number of levels in factor B. With the information, we can construct a source of variance table below:

Source

Sum of squares

Degree of freedom

Mean square

F statistic

Factor A

SS_A

$J-1$

$MS_A = \frac{SS_A}{J-1}$

$F_A = \frac{MS_A}{MS_W}$

Factor B

SS_B

$K-1$

$MS_B = \frac{SS_B}{K-1}$

$F_B = \frac{MS_B}{MS_W}$

Interaction A*B

$SS_{A\times B}$

$(J-1)*(K-1)$

$MS_{A\times B} = \frac{SS_{A\times B}}{(J-1)\times(K-1)}$

$F_{A\times B} = \frac{MS_{A\times B}}{MS_W}$

Within

SS_W

$N-(J\times K)$

$MS_W = \frac{SS_W}{N-(J\times K)}$

Total

SS_T

$N - 1$

It is easy to see that $SS_T = SS_A + SS_B + SS_{A\times B} + SS_W$. For testing the effect of Factor A, we compare the statistic F_A to an F distribution with degrees of freedom $J - 1$ and $N - (J \times K)$. For testing the effect of Factor B, we compare the statistic F_B to an F distribution with degrees of freedom $K - 1$ and $N - (J \times K)$. To test the interaction effect of Factor A and Factor B, we compare the statistic $F_{A\times B}$ to an F distribution with degrees of freedom $(J - 1) * (K - 1)$ and $N - (J \times K)$.

7.2.3 Example: Effects of training and gender on the memory test performance

As an example, we test the effect of training and gender on the memory test performance using the ACTIVE data. We want to answer the following questions:

1. At the population level, are there any difference in memory test performance for the 4 training groups?
2. At the population level, are there any difference in memory test performance for male and female participants?
3. Do the effects of training on the memory test performance differ across the two gender groups?

The R code below carries out the two-way ANOVA to answer the above questions.

```
model<-lm(hvltt2~factor(group)*factor(sex), data=active)
anova(model)
## Analysis of Variance Table
##
## Response: hvltt2
##                              Df Sum Sq Mean Sq F value    Pr(>F)
## factor(group)                 3    859  286.20 10.2434 1.114e-06 ***
## factor(sex)                   1    919  919.28 32.9013 1.161e-08 ***
## factor(group):factor(sex)     3     34   11.46  0.4102    0.7457
## Residuals                  1567  43783   27.94
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

7.2.3.1 Main effect of training group

From the output, the F-statistic for testing the main effect of training group is 10.2434. Based on the F distribution with degrees of freedom 3 and 1567, the corresponding p-value is 1.114e-06, which indicates a significant main effect for training group. Therefore, one may conclude there is significant difference in memory performance among the four groups.

7.2.3.2 Main effect of sex

From the output, the F-statistic for testing the main effect of sex is 32.9013. Based on the F distribution with degrees of freedom 1 and 1567, the corresponding p-value is 1.161e-08, which indicates a significant main effect sex. Therefore, one may conclude there is significant difference in memory performance between the male and female participants.

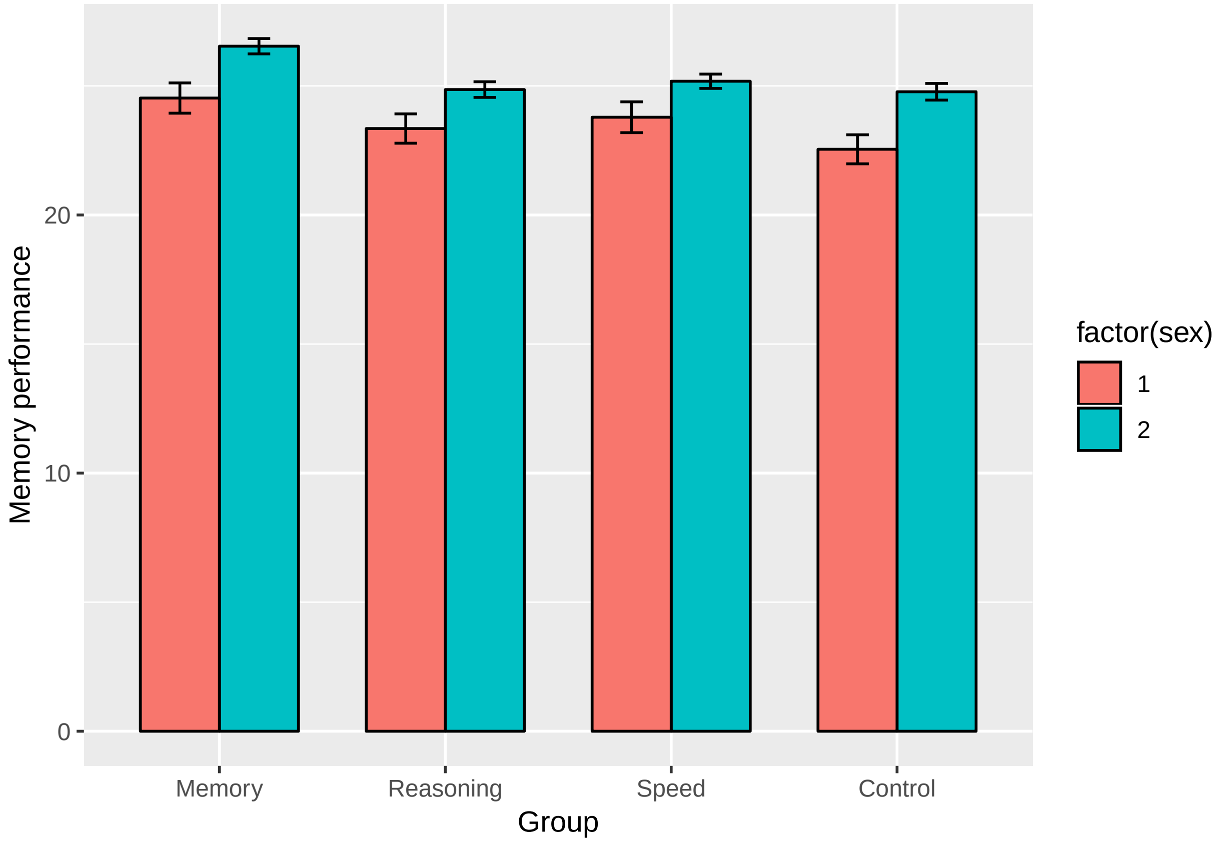
7.2.3.3 Interaction effect between training group and sex

From the output, the F-statistic for testing the interaction effect [`factor(group):factor(sex)`] is 0.41. Based on the F distribution with degrees of freedom 3 and 1567, the corresponding p-value is 0.7457, which indicates an insignificant interaction effect. Therefore, one may conclude the difference in memory performance among the four training group does not depend on sex.

7.2.4 Plot data

As in one-way ANOVA, we can also plot data with two factors with error bars. The code below can be used.

```
stats <- summarySE(active, measurevar="hvltt2", groupvars=c("group","sex"))
stats
##   group sex   N   hvltt2       sd        se        ci
## 1     1   1  85 24.52941 5.412922 0.5871138 1.1675401
## 2     1   2 307 26.53746 5.184920 0.2959190 0.5822937
## 3     2   1  92 23.34783 5.453973 0.5686160 1.1294858
## 4     2   2 295 24.85763 5.219019 0.3038631 0.5980225
## 5     3   1  84 23.78571 5.477383 0.5976314 1.1886649
## 6     3   2 323 25.17957 4.986810 0.2774735 0.5458900
## 7     4   1 112 22.54464 5.950075 0.5622293 1.1140948
## 8     4   2 277 24.77256 5.367870 0.3225240 0.6349197

ggplot(stats,
   aes(x = factor(group), y = hvltt2, fill = factor(sex),
       ymax=hvltt2+se, ymin=hvltt2-se))  +
       geom_bar(stat="identity", position = "dodge", width = 0.7) +
       geom_bar(stat="identity", position = "dodge",
                colour = "black", width = 0.7)  +
       geom_errorbar(position=position_dodge(width=0.7),
                     width=0.2, size=0.5, color="black")  +
       labs(x = "Group",
            y = "Memory performance")  +
      scale_x_discrete(breaks=c("1", "2", "3", "4"),
        labels=c("Memory", "Reasoning", "Speed", "Control"))
```



7.3 Repeated-measures ANOVA

Repeated-measures designs are often used in psychology in which the same participants are measured multiple times. One popular example is the longitudinal design in which the same participants are followed and measured over time. Another example is the cross-over study in which participants receive a sequence of different treatments. To analyze such data, repeated-measures ANOVA can be used.

7.3.1 An example

The ACITVE study has measures on verbal ability through the Hopkins Verbal Learning Test for 4 times. The data are apparently repeated measures. Using the data as an example, we try to answer the following questions:

- Whether there is any difference in verbal ability among the 4 times of measures. In this case, time is a within-subject factor.

- Whether there is any difference between male and female participants. In this case, sex is a between-subject factor.
- Whether there is an interaction effect between time and sex.

7.3.2 Long format of data

For repeated-measures ANOVA in R, it requires the long format of data. The current data are in wide format in which the `hvltt` data at each time are included as a separated variable on one column in the data frame. For the long format, we would need to stack the data from each individual into a vector. To reshape the data, the function `melt()` from the R package `reshape2` can be used. Specially, for the ACITVE data, the following code can be used.

```
library(reshape2)
head(active)
##   site age edu group booster sex reason ufov hvltt hvltt2 hvltt3 hvltt4 mmse id
## 1    1  76  12     1       1   1     28   16    28     28     17     22   27  1
## 2    1  67  10     1       1   2     13   20    24     22     20     27   25  2
## 3    6  67  13     3       1   2     24   16    24     24     28     27   27  3
## 4    5  72  16     1       1   2     33   16    35     34     32     34   30  4
## 5    4  69  12     4       0   2     30   16    35     29     34     34   28  5
## 6    1  70  13     1       1   1     35   23    29     27     26     29   23  6

active_long <- melt(active,
    id.vars=c("id", "sex"),
    measure.vars=c("hvltt", "hvltt2", "hvltt3", "hvltt4"),
    variable.name="time",
    value.name="hvltt"
)

head(active_long)
##   id sex  time hvltt
## 1  1   1 hvltt    28
## 2  2   2 hvltt    24
## 3  3   2 hvltt    24
## 4  4   2 hvltt    35
## 5  5   2 hvltt    35
## 6  6   1 hvltt    29
```

Note that in the `melt()` function,

- The first input is the data set name.
- `id.vars` provides a vector of variables that will be repeated (not stacked) in the new long format data set.
- `measure.vars` tells the variables in the wide-format to be stacked in the long format.
- `variable.name` gives the name for the variable created by the columns in the wide

format.
- `value.name` gives the name for the variable created by the data in the long format. In this example, that is hvltt data.

7.3.3 One within-subject factor

We first consider just one within-subject factor, time, to evaluate whether there is any difference in verbal ability across the 4 times of data. To answer the question, the following analysis can be conducted.

```
ex1<-aov(hvltt~time+Error(id/time), data=active_long)
summary(ex1)
##
## Error: id
##           Df Sum Sq Mean Sq F value Pr(>F)
## Residuals  1 0.3716  0.3716
##
## Error: id:time
##      Df Sum Sq Mean Sq
## time  3   3800    1267
##
## Error: Within
##             Df Sum Sq Mean Sq F value   Pr(>F)
## time         3   1112   370.7   13.12 1.54e-08 ***
## Residuals 6292 177742    28.2
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

To look at the effect of “time”, we check the output in the “`Error: Within`” section. For the F value 13.12 with the degrees of freedom 3 and 6292, we have p-value 1.54e-08. Therefore, there is a significant difference among the 4 times of data.

Note that to conduct the repeated-measures ANOVA, the R function `aov()` is used. The function uses the regular expression to represent the model. In this case, the outcome is `hvltt` and the predictor is `time`. `Error(id/time)` is used to divide the error variance into 4 different clusters, which therefore takes into account of the repeated measures.

7.3.4 One within-subject factor and one between-subject factor

As an example, we consider an additional between-subject factor, sex. With the two factors, we can also test the interaction effect between time and sex. The code below can be used to conduct the analysis. Based on the output, we have significant time and sex effects but no interaction effect.

```
ex2<-aov(hvltt~time*sex+Error(id/(time*sex)), data=active_long)
summary(ex2)
##
## Error: id
##     Df Sum Sq Mean Sq
## sex  1 0.3716  0.3716
##
## Error: id:time
##      Df Sum Sq Mean Sq
## time  3   3800    1267
##
## Error: id:sex
##     Df Sum Sq Mean Sq
## sex  1   5020    5020
##
## Error: id:time:sex
##      Df Sum Sq Mean Sq
## time  3  204.9   68.29
##
## Error: Within
##              Df Sum Sq Mean Sq F value   Pr(>F)
## time          3   1091   363.8  13.383 1.05e-08 ***
## sex           1   1592  1592.1  58.564 2.26e-14 ***
## time:sex      3    116    38.6   1.419    0.235
## Residuals 6284 170830    27.2
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Chapter 8

Simple Linear Regression

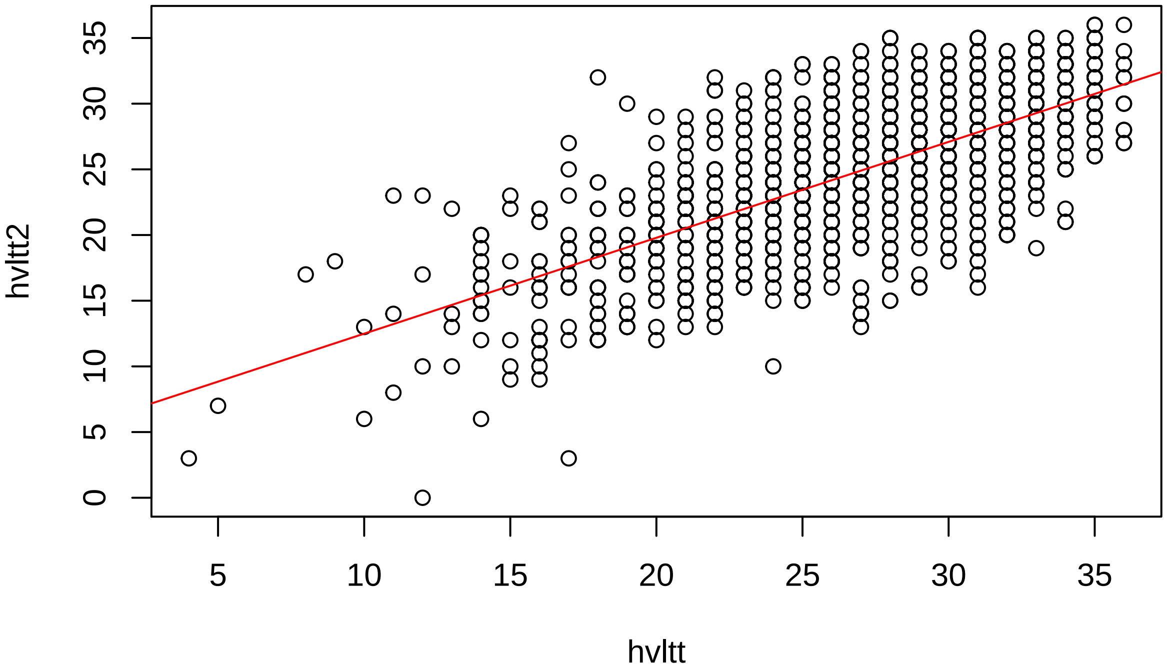
In the ACTIVE study, we have data on verbal ability at two times (hvltt and hvltt2). To investigate the relationship between them, we can generate a scatterplot using hvltt and hvltt2 as shown below. From the plot, it is easy to observe that those with a higher score on hvltt tend to have a higher score on hvltt2. Certainly, it is not difficult to find two people where the one with higher score on hvltt has a lower score on hvltt2. But in general hvltt and hvltt2 tend to go up and down together.

Furthermore, the association between hvltt and hvltt2 seems to be able to be described by a straight line. The red line in the figure is one that run across the points in the scatter plot. The straight line can be expressed using

$$hvltt2 = 5.19 + 0.73 * hvltt$$

It says multiplying one's test score (hvltt) at the first occasion by 0.73 and adding 5.19 predict his/her test score (hvltt2) at the second occasion.

```r
active <- read.csv("data/active.csv")
attach(active)

plot(hvltt, hvltt2)
abline(5.19, 0.73, col='red')
```



8.1 Simple regression model

A regression model / regression analysis can be used to predict the value of one variable (the dependent or outcome variable) on the basis of other variables (the independent and predictor variables). Typically, we use y to denote the dependent variable and x to denote an independent variable.

The simple linear regression model for the population can be written as

$$y = \beta_0 + \beta_1 x + \epsilon$$

where

- β_0 is called the intercept, which is also the average value of y when $x = 0$.
- β_1 is called the slope, which is the change in y given the unit change in x. Therefore, it is also called rate of change.
- ϵ is a normal error that is often assumed to have a normal distribution with mean 0 and unknown variance σ^2. This term represents the part of information in y that cannot be explained by x.

8.2 Parameter estimation

In practice, the population parameters β_0 and β_1 are unknown. However, with a set of sample data, they can be estimated. One often used estimation method for regression analysis is called least squares estimation method. We explain the method here.

Let the model below represent the estimated regression model:

$$y = b_0 + b_1 x + e$$

where

- b_0 is an estimate of the population intercept β_0
- b_1 is an estimate of the population slope β_1
- e is the residual, which estimate ϵ.

Assume we already get the estimates b_0 and b_1, then we can make a prediction of the value of y based on the value of x. For example, for the ith participant, if his/her score on the independent variable is x_i, then the corresponding predicted outcome $\hat{y}_i$ based on the regression model is

$$\hat{y}_i = b_0 + b_1 x_i.$$

The difference between the predicted value and the observed data for this participant, also called the prediction error, is

$e_i = y_i - \hat{y}_i$.

The parameter b_0 and b_1 potentially can take any values. A good choice could be those that make the errors smallest, which leads to the least squares estimation.

8.2.1 Least squares estimation

The least squares estimation obtains b_0 and b_1 by minimizing the sum of the squared prediction errors. Therefore, such a set of parameters makes $\hat{y}_i$ closest to y_i on average. Specifically, one minimizes SSE as

$SSE = \sum_{i=1}^{n} e_i^2 = \sum_{i=1}^{n}(y_i - \hat{y}_i)^2 = \sum_{i=1}^{n}(y_i - b_0 - b_1 x_i)^2$.

The values of b0 and b1 that minimize SSE can be calculated by

$$b_1 = \frac{S_{xy}}{S_x^2} = \frac{\sum_{i=1}^{n}(x_i - \bar{x})(y_i - \bar{y})}{\sum_{i=1}^{n}(x_i - \bar{x})^2}$$

and

$$b_0 = \bar{y} - b_1\bar{x}$$

where $\bar{x} = \sum_{i=1}^{n} x_i/n$ and $\bar{y} = \sum_{i=1}^{n} y_i/n$.

8.2.2 Hypothesis testing

If no linear relationship exists between the two variables, we would expect the regression line to be horizontal, that is, to have a slope of zero. Therefore, we can test whether the hypothesis that the population regression slope is 0. More specifically, we have the null hypothesis

$$H_0 : \beta_1 = 0.$$

And the alternative hypothesis is

$$H_1 : \beta_1 \neq 0.$$

To conduct the hypothesis testing, we calculate a t test statistic

$$t = \frac{b_1 - \beta_1}{s_{b_1}}$$

where s_{b_1} is the standard error of b_1.

If $\beta_1 = 0$ in the population, then the statistic t follows a t-distribution with degrees of freedom $n - 2$.

8.2.3 Regression in R

Both the parameter estimates and the t test can be conducted using an R function `lm()`.

8.3 An example

To show how to conduct a simple linear regression, we analyze the relationship between hvltt and hvltt2 from the ACTIVE study. The R input and output for the regression analysis is given below.

- Within the function `lm()`, the first required input is a "formula" to specify the model. A model is usually formed by the "~" operator. For a regression, we use `y ~ x`, which is interpreted as the outcome variable y is modelled by a linear predictor x. Therefore, for the regression analysis in this specific example, we use `hvltt2 ~ hvltt`.

- The regression results are saved into an R object called `regmodel`. To show the basic results including the estimated regression intercept and slope, one can type the name of the object directly in the R console.
- For more detailed results, the `summary` function can be applied to the regression object.
  - The estimated intercept is `5.1853` and the estimated slope is `0.7342`. Their corresponding standard errors are `0.5463` and `0.200`, respectively.
  - For testing the hypothesis that the slope is 0 – $H_0 : \beta_1 = 0$. The t-statistic is `36.719`. Based on the t distribution with the degrees of freedom `1573`, we have the p-value $<$ 2e-16. Therefore, one would reject the null hypothesis if the signifance level 0.05 is used.
  - Similarly, for testing the hypothesis that the intercept is 0 – $H_0 : \beta_0 = 0$. The t-statistic is 9.492. Based on the t distribution with the degrees of freedom 1573, we have the p-value $<$ 2e-16. Therefore, one would reject the null hypothesis.
  - The residual standard error is 3.951 and therefore, the estimated variance of the residual is $\hat{\sigma}^2 = 3.951^2 = 15.61$.

```
regmodel<-lm(hvltt2~hvltt, data=active)
regmodel
##
## Call:
## lm(formula = hvltt2 ~ hvltt, data = active)
##
## Coefficients:
## (Intercept)        hvltt
##      5.1854       0.7342

summary(regmodel)
##
## Call:
## lm(formula = hvltt2 ~ hvltt, data = active)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -14.6671  -2.5408   0.2565   2.7250  13.5987
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)   5.1853     0.5463   9.492   <2e-16 ***
## hvltt         0.7342     0.0200  36.719   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.951 on 1573 degrees of freedom
## Multiple R-squared:  0.4615, Adjusted R-squared:  0.4612
## F-statistic:  1348 on 1 and 1573 DF,  p-value: < 2.2e-16
```

8.4 Coefficient of Determination (Multiple R-squared)

Significant tests show ***if*** a linear relationship exists but not the ***strength of the relationship***. The coefficient of determination, R^2, is a descriptive measure of the strength of the regression relationship, a measure on how well the regression line fits the data. In general the higher the value of R^2, the better the model fits the data.

- $R^2 = 1$: Perfect match between the line and the data points.
- $R^2 = 0$: There are no linear relationship between x and y.

R^2 is an effect size measure. Cohen (1988) defined some standards for interpreting R^2.

- $R^2 = .01$: Small effect
- $R^2 = .06$: Medium effect
- $R^2 = .15$: Large effect.

For the regression example, the $R^2 = 0.4615$, representing a large effect.

8.4.1 Calculation and interpretation of R^2

Simply speaking, the R^2 tells the percentage of variance in y that can be explained by the regression model or by x.

The variance of y is

$$Var(y) = \sum_{i=1}^{n}(y_i - \bar{y})^2$$

With some simple re-arrangement, we have

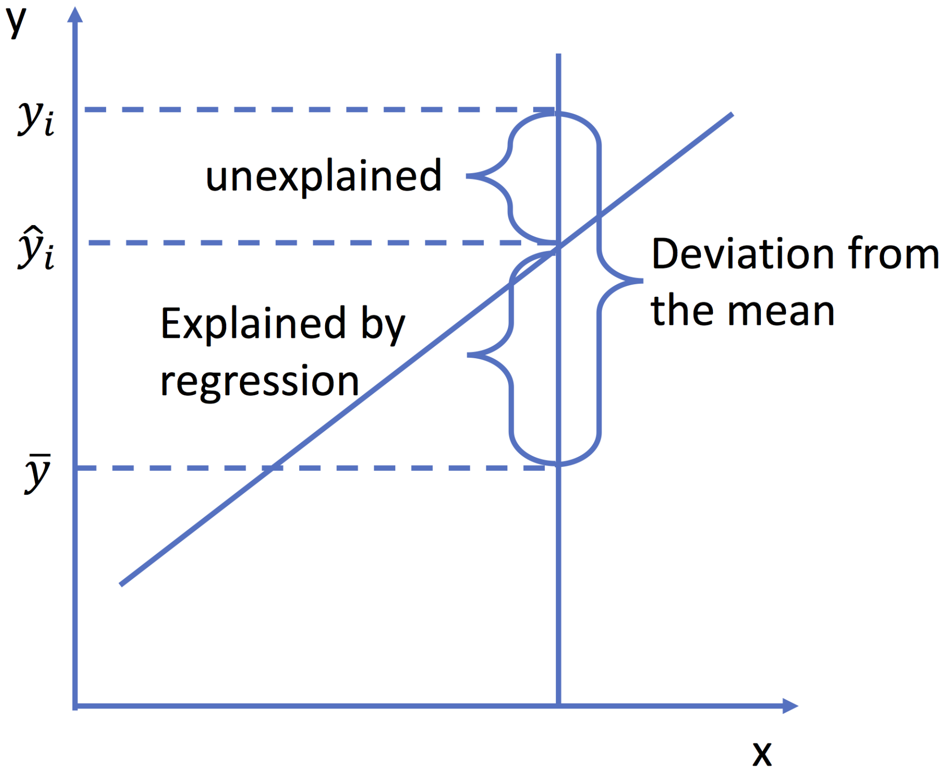
$$\begin{aligned} Var(y) &= \sum_{i=1}^{n}(y_i - \bar{y})^2 \\ &= \sum_{i=1}^{n}(y_i - \hat{y}_i + \hat{y}_i - \bar{y})^2 \\ &= \sum_{i=1}^{n}(y_i - \hat{y}_i)^2 + \sum_{i=1}^{n}(\hat{y}_i - \bar{y})^2 \\ &= \text{Residual variance} + \text{Variance explained by regression.} \end{aligned}$$

And the R^2 is

$$R^2 = \frac{\sum_{i=1}^{n}(\hat{y}_i - \bar{y})^2}{Var(y)} = 1 - \frac{\sum_{i=1}^{n}(y_i - \hat{y}_i)^2}{Var(y)}.$$

This can be illustrated using the figure below.

$$y_i - \bar{y} = y_i - \hat{y}_i + \hat{y}_i - \bar{y}$$



Chapter 9

Multiple Linear Regression

9.1 Multiple Regression Analysis

The general purpose of multiple regression (the term was first used by Pearson, 1908), as a generalization of simple linear regression, is to learn about how several independent variables or predictors (IVs) together predict a dependent variable (DV). Multiple regression analysis often focuses on understanding (1) how much variance in a DV a set of IVs explain and (2) the relative predictive importance of IVs in predicting a DV.

In the social and natural sciences, multiple regression analysis is very widely used in research. Multiple regression allows a researcher to ask (and hopefully answer) the general question "what is the best predictor of … ". For example, educational researchers might want to learn what the best predictors of success in college are. Psychologists may want to determine which personality dimensions best predicts social adjustment.

9.1.1 Multiple regression model

A general multiple linear regression model at the population level can be written as

$$y_i = \beta_0 + \beta_1 x_{1i} + \beta_2 x_{2i} + \ldots + \beta_k x_{ki} + \varepsilon_i$$

- y_i: the observed score of individual i on the DV.
- $x_1, x_2, \ldots, x_k$: a set of predictors.
- x_{1i}: the observed score of individual i on IV 1; x_{ki}: observed score of individual i on IV k.
- β_0: the intercept at the population level, representing the predicted y score when all the independent variables have their values at 0.
- $\beta_1, \ldots, \beta_k$: regression coefficients at the population level; β_1: representing the amount predicted y changes when x_1 changes in 1 unit while holding the other IVs constant; β_k:

representing the amount predicted y changes when x_k changes in 1 unit while holding the other IVs constant.

- ε: unobserved errors with mean 0 and variance σ^2.

9.1.2 Parameter estimation

The least squares method used for the simple linear regression analysis can also be used to estimate the parameters in a multiple regression model. The basic idea is to minimize the sum of squared residuals or errors. Let $b_0, b_1, \ldots, b_k$ represent the estimated regression coefficients.The individual i's residual e_i is the difference between the observed y_i and the predicted y_i

$$e_i = y_i - \hat{y}_i = y_i - b_0 - b_1 x_{1i} - \ldots - b_k x_{ki}.$$

The sum of squared residuals is

$$SSE = \sum_{i=1}^{n} e_i^2 = \sum_{i=1}^{n} (y_i - \hat{y}_i)^2.$$

By minimizing SSE, the regression coefficient estimates can be obtained as

$$\boldsymbol{b} = (\boldsymbol{X}'\boldsymbol{X})^{-1}\boldsymbol{X}'\boldsymbol{y} = (\sum \boldsymbol{x}_i \boldsymbol{x}_i')^{-1}(\sum \boldsymbol{x}_i \boldsymbol{y}_i).$$

9.1.3 R^2

How well the multiple regression model fits the data can be assessed using the R^2. Its calculation is the same as for the simple regression

$$\begin{aligned} R^2 = & \quad 1 - \frac{\sum e_i^2}{\sum_{i=1}^{n} (y_i - \bar{y})^2} \\ = & \quad \frac{\text{Variation explained by IVs}}{\text{Total variation}} \end{aligned}.$$

In multiple regression, R^2 is the total proportion of variation in y explained by the multiple predictors.

The R^2 increases or at least is the same with the inclusion of more predictors. However, with more predators, the model becomes more complex and potentially more difficult to interpret. In order to take into consideration of the model complexity, the adjusted R^2 has been defined, which is calculated as

$$aR^2 = 1 - (1 - R^2)\frac{n - 1}{n - k - 1}.$$

9.1.4 Hypothesis testing of regression coefficient(s)

With the estimates of regression coefficients and their standard errors estimates, we can conduct hypothesis testing for one, a subset, or all regression coefficients.

9.1.4.1 Testing a single regression coefficient

At first, we can test the significance of the coefficient for a single predictor. In this situation, the null and alternative hypotheses are

$$H_0 : \beta_j = 0 \text{ vs } H_1 : \beta_j \neq 0$$

with β_j denoting the regression coefficient of x_j at the population level.

As in the simple regression, we use a test statistic

$$t_j = \frac{b_j - \beta j}{s.e.(b_j)}$$

where b_j is the estimated regression coefficient of x_j using data from a sample. If the null hypothesis is true and $\beta_j = 0$, the test statistic follows a t-distribution with degrees of freedom $n - k - 1$ where k is the number of predictors.

One can also test the significance of β_j by constructing a confidence interval for it. Based on a t distribution, the $100(1 - \alpha)\%$ confidence interval is

$$[b_j + t_{n-k-1}(\alpha/2) * s.e.(b_j),\ b_j + t_{n-k-1}(1 - \alpha/2) * s.e.(b_j)]$$

where $t_{n-k-1}(\alpha/2)$ is the $\alpha/2$ percentile of the t distribution. As previously discussed, if the confidence interval includes 0, the regression coefficient is not statistically significant at the significance level α.

9.1.4.2 Testing all the regression coefficients together (overall model fit)

Given the multiple predictors, we can also test whether all of the regression coefficients are 0 at the same time. This is equivalent to test whether all predictors combined can explained a significant portion of the variance of the outcome variable. Since R^2 is a measure of the variance explained, this test is naturally related to it.

For this hypothesis testing, the null and alternative hypothesis are

$$H_0 : \beta_1 = \beta_2 = \ldots = \beta_k = 0$$

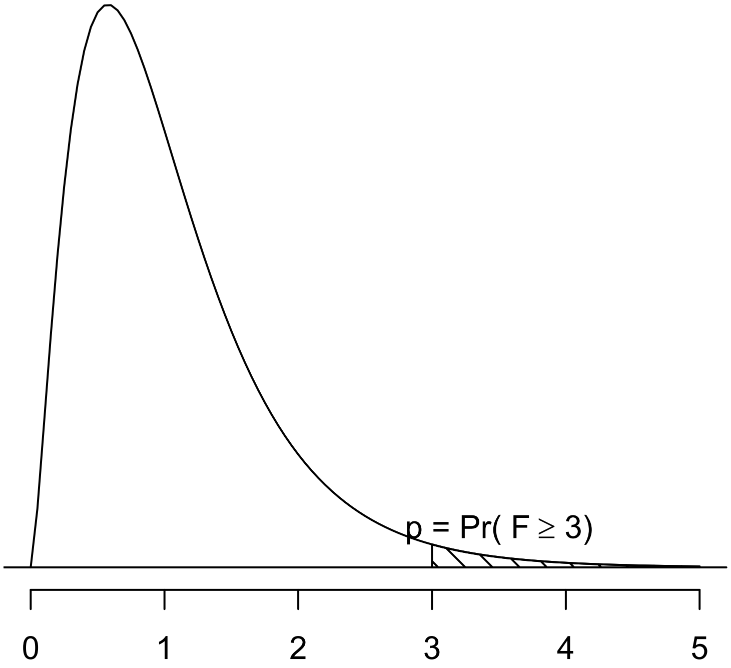
vs.

$$H_1: \text{ at least one of the regression coefficients is different from 0.}$$

In this kind of test, an F test is used. The F-statistic is defined as

$$F = \frac{n-k-1}{k}\frac{R^2}{1-R^2}.$$

It follows an F-distribution with degrees of freedom k and $n-k-1$ when the null hypothesis is true. Given an F statistic, its corresponding p-value can be calculated from the F distribution as shown below. Note that we only look at one side of the distribution because the extreme values should be on the large value side.



9.1.4.3 Testing a subset of the regression coefficients

We can also test whether a subset of p regression coefficients, e.g., p from 1 to the total number coefficients k, are equal to zero. For convenience, we can rearrange all the p regression coefficients to be the first p coefficients. Therefore, the null hypothesis should be

$$H_0 : \beta_1 = \beta_2 = \ldots = \beta_p = 0$$

and the alternative hypothesis is that at least one of them is not equal to 0.

As for testing the overall model fit, an F test can be used here. In this situation, the F statistic can be calculated as

$$F = \frac{n-k-1}{p}\frac{R^2 - R_0^2}{1-R^2},$$

which follows an F-distribution with degrees of freedom p and $n-k-1$. R^2 is for the regression model with all the predictors and R_0^2 is from the regression model without the first p predictors $x_1, x_2, \ldots, x_p$ but with the rest predictors $x_{p+1}, x_{p+2}, \ldots, x_k$.

Intuitively, this test determine whether the variance explained by the first p predictors above and beyond the $k-p$ predictors is significance or not. That is also the increase in R-squared.

9.1.5 An example

As an example, suppose that we wanted to predict student success in college. Why might we want to do this? There's an ongoing debate in college and university admission offices (and in the courts) regarding what factors should be considered important in deciding which applicants to admit. Should admissions officers pay most attention to more easily quantifiable measures such as high school GPA and SAT scores? Or should they give more weight to more subjective measures such as the quality of letters of recommendation? What are the pros and cons of the approaches? Of course, how we define college success is also an open question. For the sake of this example, let's measure college success using college GPA.

In this example, we use a set of simulated data (generated by us). The data are saved in the file gpa.csv. As shown below, the sample size is 100 and there are 4 variables: college GPA (c.gpa), high school GPA (h.gpa), SAT, and quality of recommendation letters (recommd).

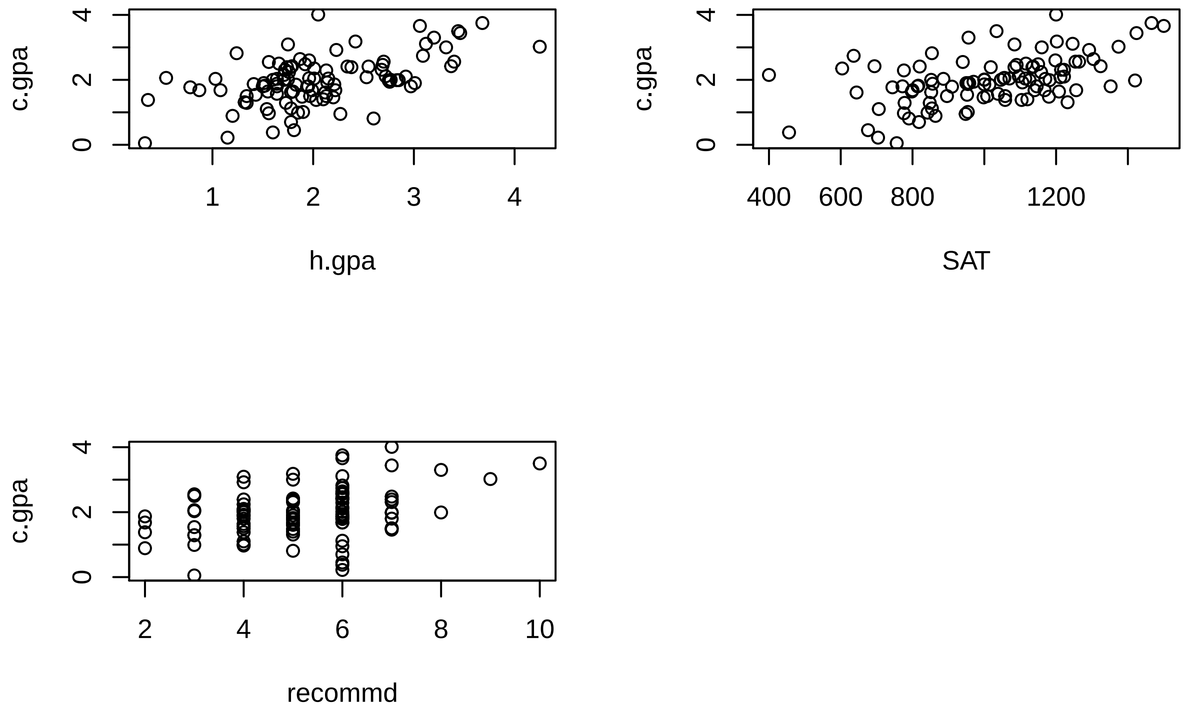
```
gpa <- read.table("data/gpa.regression.txt")
names(gpa) <- c("c.gpa", "h.gpa",  "SAT", "recommd")

dim(gpa)
## [1] 100   4
head(gpa)
##   c.gpa h.gpa  SAT recommd
## 1  2.04  2.01 1070       5
## 2  2.56  3.40 1254       6
## 3  3.75  3.68 1466       6
## 4  1.10  1.54  706       4
## 5  3.00  3.32 1160       5
## 6  0.05  0.33  756       3
```

9.1.5.1 Graph the data

Before fitting a regression model, we should check the relationship between college GPA and each predictor through a scatterplot. A scatterplot can tell us the form of relationship, e.g., linear, nonlinear, or no relationship, the direction of relationship, e.g., positive or negative, and the strength of relationship, e.g., strong, moderate, or weak. It can also identify potential outliers.

The scatterplots between college GPA and the three potential predictors are given below. From the plots, we can roughly see all three predictors are positively related to the college GPA. The relationship is close to linear and the relationship seems to be stronger for high school GPA and SAT than for the quality of recommendation letters.

```r
attach(gpa)

par(mfrow=c(2,2))
plot(h.gpa, c.gpa)
plot(SAT, c.gpa)
plot(recommd, c.gpa)
```



9.1.5.2 Descriptive statistics

Next, we can calculate some summary statistics to explore our data further. For each variable, we calculate 6 numbers: minimum, 1st quartile, median, mean, 3rd quartile, and maximum. Those numbers can be obtained using the `summary()` function. To look at the relationship among the variables, we can calculate the correlation matrix using the correlation function `cor()`.

Based on the correlation matrix, the correlation between college GPA and high school GPA is about 0.545, which is larger than that (0.523) between college GPA and SAT, in turn larger than that (0.35) between college GPA and quality of recommendation letters.

```
summary(gpa)
##      c.gpa           h.gpa             SAT          recommd
##  Min.   :0.050   Min.   :0.330   Min.   : 400   Min.   : 2.00
##  1st Qu.:1.562   1st Qu.:1.640   1st Qu.: 852   1st Qu.: 4.00
##  Median :1.985   Median :1.930   Median :1036   Median : 5.00
##  Mean   :1.980   Mean   :2.049   Mean   :1015   Mean   : 5.19
##  3rd Qu.:2.410   3rd Qu.:2.535   3rd Qu.:1168   3rd Qu.: 6.00
##  Max.   :4.010   Max.   :4.250   Max.   :1500   Max.   :10.00
cor(gpa)
##             c.gpa     h.gpa       SAT   recommd
## c.gpa   1.0000000 0.5451980 0.5227546 0.3500768
## h.gpa   0.5451980 1.0000000 0.4326248 0.6265836
## SAT     0.5227546 0.4326248 1.0000000 0.2175928
## recommd 0.3500768 0.6265836 0.2175928 1.0000000
```

9.1.5.3 Fit a multiple regression model

As for the simple linear regression, The multiple regression analysis can be carried out using the `lm()` function in R. From the output, we can write out the regression model as

$$c.gpa = -0.153 + 0.376 \times h.gpa + 0.00122 \times SAT + 0.023 \times recommd$$

9.1.5.4 Interpret the results / output

From the output, we see the intercept is -0.153. Its immediate meaning is that when all predictors' values are 0, the predicted college GPA is -0.15. This clearly does not make much sense because one would never get a negative GPA, which results from the unrealistic presumption that the predictors can take the value of 0.

The regression coefficient for the predictor high school GPA (h.gpa) is 0.376. This can be interpreted as ***keeping SAT and recommd scores constant***, the predicted college GPA would increase 0.376 with a unit increase in high school GPA.This is again might be problematic because it might be impossible to increase high school GPA while keeping the other two predictors unchanged. The other two regression coefficients can be interpreted in the same way.

From the output, we can also see that the multiple R-squared (R^2) is 0.3997. Therefore, about 40% of the variation in college GPA can be explained by the multiple linear regression with h.GPA, SAT, and recommd as the predictors. The adjusted R^2 is slightly smaller because of the consideration of the number of predictors. In fact,

$$\begin{aligned} aR^2 &= 1-(1-R^2)\frac{n-1}{n-k-1} \\ &= 1-(1-.3997)\frac{100-1}{100-3-1} \\ &= .3809 \end{aligned}$$

9.1.5.5 Hypothesis testing

9.1.5.5.1 Testing Individual Regression Coefficient

For any regression coefficients for the three predictors (also the intercept), a t test can be conducted. For example, for high school GPA, the estimated coefficient is 0.376 with the standard error 0.114. Therefore, the corresponding t statistic is $t = 0.376/0.114 = 3.294$. Since the statistic follows a t distribution with the degrees of freedom $df = n-k-1 = 100-3-1 = 96$, we can obtain the p-value as $p = 2*(1-pt(3.294, 96)) = 0.0013$. Since the p-value is less than 0.05, we conclude the coefficient is statistically significant. Note the t value and p-value are directly provided in the output.

```
t <- 0.376/0.114
t
## [1] 3.298246
2*(1-pt(t, 96))
## [1] 0.001365401
```

9.1.5.5.2 Overall model fit (testing all coefficients together)

To test all coefficients together or the overall model fit, we use the F test. Given the R^2, the F statistic is

$$\begin{aligned} F &= \frac{n-k-1}{k}\frac{R^2}{1-R^2} \\ &= \left(\frac{100-3-1}{3}\right)\times\left(\frac{0.3997}{1-.3997}\right) = 21.307 \end{aligned}$$

which follows the F distribution with degrees of freedom $df1 = k = 3$ and $df2 = n-k-1 = 96$. The corresponding p-value is 1.160e-10. Note that this information is directly shown in the output as "`F-statistic: 21.31 on 3 and 96 DF, p-value: 1.160e-10`".

Therefore, at least one of the regression coefficients is statistically significantly different from 0. Overall, the three predictors explained a significant portion of the variance in college GPA. The regression model with the 3 predictors is significantly better than the regression model with intercept only (i.e., predict c.gpa by the mean of c.gpa).

```
F <- (100 - 3 -1)/3*0.3997/(1-0.3997)
F
## [1] 21.30668
1 - pf(F, 3, 96)
## [1] 1.162797e-10
```

9.1.5.5.3 Testing a subset of regression coefficients

Suppose we are interested in testing whether the regression coefficients of high school GPA and SAT together are significant or not. Alternative, we want to see above and beyond the quality of recommendation letters, whether the two predictors can explain a significant portion of variance in college GPA. To conduct the test, we need to fit two models:

- A full model: which consists of all the predictors to predict c.gpa by intercept, h.gpa, SAT, and recommd.
- A reduced model: obtained by removing the predictors to be tested in the full model.

From the full model, we can get the $R^2 = 0.3997$ with all three predictors and from the reduced model, we can get the $R_0^2 = 0.1226$ with only quality of recommendation letters. Then the F statistic is constructed as

$$F = \frac{n-k-1}{p}\frac{R^2 - R_0^2}{1-R^2} = \left(\frac{100-3-1}{2}\right) \times \frac{.3997 - .1226}{1 - .3997} = 22.157.$$

Using the F distribution with the degrees of freedom $p = 2$ (the number of coefficients to be tested) and $n-k-1 = 96$, we can get the p-value close to 0 ($p = 1.22e - 08$).

```
model.reduce <- lm(c.gpa~recommd, data=gpa)
summary(model.reduce)
##
## Call:
## lm(formula = c.gpa ~ recommd, data = gpa)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.90257 -0.33372  0.01973  0.43457  1.71204
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  1.07020    0.25596   4.181 6.31e-05 ***
## recommd      0.17539    0.04741   3.700 0.000356 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.7054 on 98 degrees of freedom
## Multiple R-squared:  0.1226, Adjusted R-squared:  0.1136
## F-statistic: 13.69 on 1 and 98 DF,  p-value: 0.0003564

F <- (100 - 3 -1)/2*(0.3997-0.1226)/(1-0.3997)
F
## [1] 22.15692
1 - pf(F, 2, 96)
## [1] 1.225164e-08
```

Note that the test conducted here is based on the comparison of two models. In R, if there are two models, they can be compared conveniently using the R function `anova()`. As shown below, we obtain the same F statistic and p-value.

```
model.full <- lm(c.gpa~h.gpa+SAT+recommd, data=gpa)
model.reduce <- lm(c.gpa~recommd, data=gpa)
anova(model.reduce, model.full)
## Analysis of Variance Table
##
## Model 1: c.gpa ~ recommd
## Model 2: c.gpa ~ h.gpa + SAT + recommd
##   Res.Df    RSS Df Sum of Sq      F    Pr(>F)
## 1     98 48.762
## 2     96 33.358  2    15.404 22.165 1.219e-08 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

9.2 Centering and Standardization

In the GPA example, we already showed that the intercept didn't make much sense in practice. If we further look at the coefficients for the three predictors, they are 0.376, 0.0012, and 0.022. They clearly cannot be compared directly because 1 unit change in GPA means very differently than 1 unit change in SAT. In order to improve interpretability of the regression, we can conduct centering and standardization.

9.2.1 Centering

First, we can make the intercept more interpretable by centering the predictors. For the GPA example, we can create the centered predictors by subtracting their corresponding means. Therefore, we have

$$\begin{aligned} h.gpa^c &= \quad h.gpa - \overline{h.gpa} \\ SAT^c &= \quad SAT - \overline{SAT}. \\ recommd^c &= \quad recommd - \overline{recommd} \end{aligned}$$

Then the centered predictors can be used in the regression analysis. In R, the function `[scale()](https://stat.ethz.ch/R-manual/R-devel/library/base/html/scale.html)` can be used to center a variable around its mean. This function can be used in the regression function `lm()` directly. Note that after centering, the intercept becomes 1.98. Since when all three predictors are at their average values, the centered variables are 0. Therefore, the intercept can be interpreted as the predicted y value when the predictors are at their average values. Specifically, the college GAP would be 1.98 for a student with average high school GPA, average SAT score, and average quality of recommendation letter. Furthermore, we can see that centering does not change the regression coefficient estimates for the predictors.

```
gpa.model.c<-lm(c.gpa~ scale(h.gpa,scale=F) + scale(SAT,scale=F)
                + scale(recommd,scale=F), data=gpa)
summary(gpa.model.c)
##
## Call:
## lm(formula = c.gpa ~ scale(h.gpa, scale = F) + scale(SAT, scale = F) +
##     scale(recommd, scale = F), data = gpa)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -1.0979 -0.4407 -0.0094  0.3859  1.7606
##
## Coefficients:
##                           Estimate Std. Error t value Pr(>|t|)
## (Intercept)               1.980500   0.058948  33.598  < 2e-16 ***
## scale(h.gpa, scale = F)   8.338782   2.531682   3.294 0.001385 **
## scale(SAT, scale = F)     0.027185   0.006718   4.046 0.000105 ***
## scale(recommd, scale = F) 0.502613   1.129597   0.445 0.657358
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.5895 on 96 degrees of freedom
## Multiple R-squared:  0.3997, Adjusted R-squared:  0.381
## F-statistic: 21.31 on 3 and 96 DF,  p-value: 1.16e-10
```

9.2.1.1 Relationship between coefficients before and after centering

For a regression model before centering, we have

$$y_i = \beta_0 + \beta_1 x_{1i} + \beta_2 x_{2i} + \ldots + \beta_k x_{ki} + \varepsilon_i.$$

After centering, we would have

$$\begin{aligned} y_i = & \quad \beta_0 + \beta_1 x_{1i} + \beta_2 x_{2i} + \ldots + \beta_k x_{ki} + \varepsilon_i \\ = & \quad \beta_0 + \beta_1 (x_{1i} - \bar{x}_1) + \beta_2 (x_{2i} - \bar{x}_2) + \ldots + \beta_k (x_{ki} - \bar{x}_k) + \varepsilon_i. \\ = & \quad (\beta_0 - \beta_1 * \bar{x}_1 - \beta_2 * \bar{x}_2 - \ldots - \beta_k * \bar{x}_k) + \beta_1 x_{1i} + \beta_2 x_{2i} + \ldots + \beta_k x_{ki} + \varepsilon_i \end{aligned}$$

Comparing the two models, only the intercepts are different.

9.2.2 Standardization

The estimated regression coefficients are not comparable when the IVs originally have very different scales (e.g., SAT, h.GPA, and recommd) even after centering. Through standardization, however, we can remove the scales of the predictors and therefore make the coefficients relatively more comparable. We can standardize predictors only or both predictors and the outcome variable.

After standardization, the variable means are all 0 and variances are all 1. The estimated standardized regression coefficient, also called beta coefficient, tells us how many standard deviations the predicted DV changes given one standard deviation change in the IV when the other IVs are held constant. For example, If an IV has an estimated standardized regression coefficient at .5, this means that when other IVs are held constant, the predicted DV value will increase by half a standard deviation if the IV increases by 1 standard deviation. Now the estimated standardized regression coefficients are comparable even when the IVs originally have different scales. Some researchers argue in this case, the one with larger beta coefficient can predict the outcome better. However, other researchers also pointed out that a change of one standard deviation in one variable has no reason to be equivalent to 1 standard deviation change in another predictor.

For the GPA example, the estimated beta coefficients are 0.363, 0.360 and 0.045 respectively. From them, we might say high school GPA and SAT are better predictors than the quality of recommendation letters. However, this might not be reliable when the predictors are correlated. Note that when both x and y are standardized, there is no need to estimate the intercept since it should automatically be 0.

In R, `[scale()](https://stat.ethz.ch/R-manual/R-devel/library/base/html/scale.html)` can also be used for standardization. Note that to skip the estimation of the intercept, one can add `-1` in the regression model formular.

```
gpa.model.s<-lm(scale(c.gpa) ~ scale(h.gpa)
                + scale(SAT) + scale(recommd)-1, data=gpa)
summary(gpa.model.s)
##
## Call:
## lm(formula = scale(c.gpa) ~ scale(h.gpa) + scale(SAT) + scale(recommd) -
##     1, data = gpa)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.46544 -0.58820 -0.01254  0.51510  2.34994
##
## Coefficients:
##                Estimate Std. Error t value Pr(>|t|)
## scale(h.gpa)    0.36285    0.10959   3.311  0.00131 **
## scale(SAT)      0.35593    0.08751   4.067 9.68e-05 ***
## scale(recommd)  0.04528    0.10123   0.447  0.65568
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.7827 on 97 degrees of freedom
## Multiple R-squared:  0.3997, Adjusted R-squared:  0.3812
## F-statistic: 21.53 on 3 and 97 DF,  p-value: 9.028e-11
```

9.3 Relative Importance of Predictors

With multiple predictors, a natural question is which predictor is more important or useful to predict the outcome variable. Correlation can be used to tell the relationship between two variables. However, it would fall short with multiple predictors. In the regression framework, the standardized regression coefficients can be compared. But as mentioned earlier, even after standardization, the predictors might not be directly compared. In addition, with correlated predictors, the standardardized coefficients might not tell which predictor is more important. One alternative way that has been recommended is to calculate the "relative importance" of the predictors. There are different ways to estimate the relative importance of predictors, among which the method developed by Lindemann, Merenda and Gold (lmg; 1980) is often recommended. lmg calculates the relative contribution of each predictor to the R square with the consideration of the sequence of predictors appearing in the model.

9.3.1 Basic idea of lmg

R^2 represents the proportion of variance explained by a set of predictors. If one can estimate the proportion of the R^2 contributed by each individual predictor, the one with larger R^2 would be more important to explain the outcome variable. However, the difficulty lies in how to get the R^2 for each predictor.

The most intuitive way to decompose the total R^2 is to add the predictors to the regression model sequentially. Then, the increased R^2 can be considered as the contribution by the predictor just added. However, this method depends on the sequence the predictors are added if the predictors are correlated.

The lmg approach is based on sequential R^2 but takes care of the dependence on orderings by averaging over orderings. For example, for a model with 4 predictors, there are a total of 24 orderings. For each ordering, the contributed R^2 can be calculated. lmg is the average of the R^2 across the 24 orderings.

9.3.2 R package relaimpo

The R package `relaimpo` developed by Groemping (2007) includes the method lmg and 7 other methods to calculate the relative importance of predictors.

9.3.3 An example

We now calculate the relative importance of the three predictors: high school GPA, SAT and quality of recommendation letters in the GPA example. To do that, the function `calc.relimp()` is used. Before using the function, we have to fit the regression model first.

From the output, we can see that the total proportion of variance explained by the model with all three predictors is 39.97%. For the three predictors, high school GPA contributed to 0.172, SAT 0.177 and recommd 0.051. Note that the three numbers add to 0.3997. We can also get the proportion of contribution of each predictor to the overall R^2 by adding the option `rela=TRUE` in the function. Clearly, the relative importance of high school GPA and SAT is similar whereas the relative importance of the quality of recommendation letters is lower.

```
library('relaimpo')

gpa.model<-lm(c.gpa~h.gpa+SAT+recommd, data=gpa)
calc.relimp(gpa.model)
## Response variable: c.gpa
## Total response variance: 0.5613402
## Analysis based on 100 observations
##
## 3 Regressors:
```

```
## h.gpa SAT recommd
## Proportion of variance explained by model: 39.97%
## Metrics are not normalized (rela=FALSE).
##
## Relative importance metrics:
##
##                lmg
## h.gpa   0.17169723
## SAT     0.17698341
## recommd 0.05105477
##
## Average coefficients for different model sizes:
##
##                 1X         2Xs        3Xs
## h.gpa   0.56549057 0.481773394 0.37635109
## SAT     0.00180201 0.001416298 0.00122693
## recommd 0.17539410 0.065635789 0.02268425
calc.relimp(gpa.model, rela=TRUE)
## Response variable: c.gpa
## Total response variance: 0.5613402
## Analysis based on 100 observations
##
## 3 Regressors:
## h.gpa SAT recommd
## Proportion of variance explained by model: 39.97%
## Metrics are normalized to sum to 100% (rela=TRUE).
##
## Relative importance metrics:
##
##               lmg
## h.gpa   0.4295272
## SAT     0.4427514
## recommd 0.1277214
##
## Average coefficients for different model sizes:
##
##                 1X         2Xs        3Xs
## h.gpa   0.56549057 0.481773394 0.37635109
## SAT     0.00180201 0.001416298 0.00122693
## recommd 0.17539410 0.065635789 0.02268425
```

9.3.4 Bootstrap relative importance

For two predictors, after we get their relative importance measured by R^2, we might want to test whether one predictor is significantly more important than the other. However, unlike t-test, it is rather difficult to find an analytical test statistic for a test. Instead, bootstrap can be used. The package `relaimpo` includes two functions – `boot.relimp()` and `booteval.relimp()` – for the task. The first function conducts the bootstrap and the second one gets the confidence intervals.

From the output, we can see that the lower and upper bounds for the $R^2 = 0.1717$ of high school GPA is 0.0852 and 0.2837. For SAT, it's [0.069, 0.3223] and for recommd, it's [0.0146, 0.1355]. Using the CIs, we can conduct a test. For example, since the interval for h.gpa covers the R^2 of SAT, there is no difference in terms of relative importance for the two predictors. On the other hand, both CIs for h.gpa and SAT do not cover the $R^2 = 0.0511$ of recommd. Therefore, the two predictors are statistically more important than the predictor the quality of recommendation letters.

The output also includes the CIs for the differences in the R^2 of any two predictors. For example, the difference in R^2 between h.gpa and SAT is -0.0053 with a CI [-0.1827, 0.1605]. Since the CI covers 0, the difference is insignificant. Similarly, the difference between h.gpa and recommd is statistically significant.

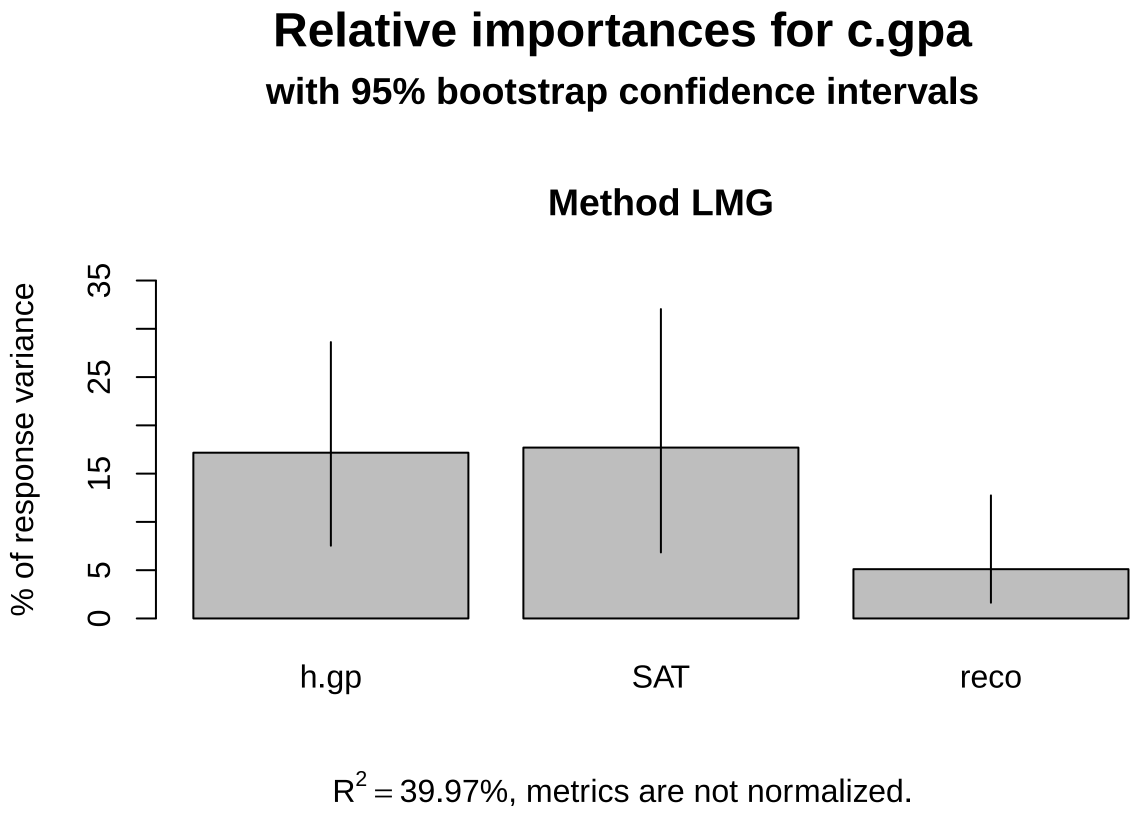
Note that the two ways for conducting the test may not necessarily lead to the same conclusion.

```
gpa.model<-lm(c.gpa~h.gpa+SAT+recommd, data=gpa)
bootresults<-boot.relimp(gpa.model, b=1000)
ci<-booteval.relimp(bootresults, norank=T)
ci
## Response variable: c.gpa
## Total response variance: 0.5613402
## Analysis based on 100 observations
##
## 3 Regressors:
## h.gpa SAT recommd
## Proportion of variance explained by model: 39.97%
## Metrics are not normalized (rela=FALSE).
##
## Relative importance metrics:
##
##                lmg
## h.gpa   0.17169723
## SAT     0.17698341
## recommd 0.05105477
##
## Average coefficients for different model sizes:
##
```

```
##                 1X         2Xs        3Xs
## h.gpa   0.56549057 0.481773394 0.37635109
## SAT     0.00180201 0.001416298 0.00122693
## recommd 0.17539410 0.065635789 0.02268425
##
##
##  Confidence interval information ( 1000 bootstrap replicates, bty= perc ):
## Relative Contributions with confidence intervals:
##
##                        Lower  Upper
##             percentage 0.95   0.95
## h.gpa.lmg   0.1717     0.0812 0.2866
## SAT.lmg     0.1770     0.0678 0.3233
## recommd.lmg 0.0511     0.0164 0.1303
##
## CAUTION: Bootstrap confidence intervals can be somewhat liberal.
##
##
##  Differences between Relative Contributions:
##
##                                   Lower   Upper
##                   difference 0.95 0.95    0.95
## h.gpa-SAT.lmg     -0.0053         -0.1868  0.1700
## h.gpa-recommd.lmg  0.1206     *    0.0013  0.2275
## SAT-recommd.lmg    0.1259         -0.0351  0.2901
##
## * indicates that CI for difference does not include 0.
## CAUTION: Bootstrap confidence intervals can be somewhat liberal.
```

The relative importance with CI can also be plotted conveniently in R. The bars are the bootstrap CIs.

```
plot(ci)
```



9.4 Variable Selection

Variable selection in regression is arguably the hardest part of model building. The purpose of variable selection in regression is to identify the best subset of predictors among many variables to include in a model. The issue is how to find the necessary variables among the complete set of variables by deleting both irrelevant variables (variables not affecting the dependent variable), and redundant variables (variables not adding anything to the dependent variable). Many variable selection methods exist. Each provides a solution to one of the most important problems in statistics.

The general theme of the variable selection is to examine certain subsets and select the best subset, which either maximizes or minimizes an appropriate criterion. More specifically, a model selection method usually should include the following three components:

1. Select a test statistic
2. Select a criterion for the selected test statistic
3. Make a decision on removing / keeping a variable.

9.4.1 Statistics/criteria for variable selection

In the literature, many statistics have been used for the variable selection purpose. Before we discuss them, bear in mind that *different statistics/criteria may lead to very different choices of variables.*

9.4.1.1 t-test for a single predictor at a time

We have learned how to use t-test for significance test of a single predictor. It is often used as a way to select predictors. The general rule is that if a predictor is significant, it can be included in a regression model.

9.4.1.2 F-test for the whole model or for comparing two nested models

As for the F-test, it can be used to test the significance of one or more than one predictors. Therefore, it can also be used for variable selection. For example, for a subset of predictors in a model, if its overall F-test is not significant, then one might simply remove them from the regression model.

9.4.1.3 R^2 and Adjusted R^2

R^2 can be used to measure the practical importance of a predictor. If a predictor can contribute significantly to the overall R^2 or adjusted R^2, it should be considered to be included in the model.

9.4.1.4 Mallows' C_p

Mallows' C_p is widely used in variable selection. It compares a model with p predictors vs. all k predictors ($k > p$) using a C_p statistic:

$$C_p = \frac{SSE_p}{MSE_k} - N + 2(p+1)$$

where SSE_p is the sum of squared errors for the model with p predictors and MSE_k is the mean squared residuals for the model with all k predictors. The expectation of C_p is $p+1$. Intuitively, if the model with p predictors fits as well as the model with k predictors – the simple model fits as well as a more complex model, the mean squared error should be the same. Therefore, we would expect $SSE_p/MSE_k = N - p - 1$. Therefore, $C_p = p + 1$. In variable selection, we therefore should look for a subset of variables with C_p around $p+1$ ($C_p \approx p+1$) or smaller ($C_p < p+1$) than $p+1$. On the other hand, a model with bad fit would have a C_p much bigger than p+1.

9.4.1.5 Information criteria

Information criteria such as AIC (Akaike information criterion) and BIC (Bayesian information criterion) are often used in variable selection. AIC and BIC are define as

$$\begin{aligned} AIC &= n\ln(SSE/n) + 2p \\ BIC &= n\ln(SSE/n) + p\ln(n) \end{aligned}.$$

Note that AIC and BIC are trade-off between goodness of model fit and model complexity. With more predictors in a regression model, SSE typically would become smaller or at least the same and therefore the first part of AIC and BIC becomes smaller. However, with model predictors, the model would become more complex and therefore the second part of AIC and BIC becomes bigger. *An information criterion tries to identify the model with the smallest AIC and BIC* that balance the model fit and model complexity.

9.4.2 An example

Through an example, we introduce different variable selection methods and illustrate their use. The data here were collected from 189 infants and mothers at the Baystate Medical Center, Springfield, Mass in 1986 on the following variables.

- low: indicator of birth weight less than 2.5 kg.
- age: mother's age in years.
- lwt: mother's weight in pounds at last menstrual period.
- race: mother's race (1 = white, 2 = black, 3 = other).
- smoke: smoking status during pregnancy.
- ptl: number of previous premature labors.
- ht: history of hypertension.
- ui: presence of uterine irritability.
- ftv: number of physician visits during the first trimester.
- bwt: birth weight in grams.

A subset of the data is shown below. Note that the data are included with the R package `MASS`. Therefore, once the package is loaded, one can access the data using `data(birthwt)`.

```
library(MASS)
data(birthwt)
head(birthwt)
##    low age lwt race smoke ptl ht ui ftv  bwt
## 85   0  19 182    2     0   0  0  1   0 2523
## 86   0  33 155    3     0   0  0  0   3 2551
## 87   0  20 105    1     1   0  0  0   1 2557
## 88   0  21 108    1     1   0  0  1   2 2594
## 89   0  18 107    1     1   0  0  1   0 2600
## 91   0  21 124    3     0   0  0  0   0 2622
```

The purpose of the study is to identify possible risk factors associated with low infant birth weight. Using the study and the data, we introduce four methods for variable selection: (1) all possible subsets (best subsets) analysis, (2) backward elimination, (3) forward selection, and (4) Stepwise selection/regression.

9.4.3 All possible (best) subsets

The basic idea of the all possible subsets approach is to run every possible combination of the predictors to find the best subset to meet some pre-defined objective criteria such as C_p and adjusted R^2. It is hoped that that one ends up with a reasonable and useful regression model. Manually, we can fit each possible model one by one using `lm()` and compare the model fits. To automatically run the procedure, we can use the `regsubsets()` function in the R package `leaps`.

Using the birth weight data, we can run the analysis as shown below. In the function `regsubsets()`,

- The regular formula can be used to specify the model with all the predictors to be studied. In this example, it is `bwt~lwt+race+smoke+ptl+ht+ui+ftv`. One can also provides the outcome variable as a vector and the predictors in a matrix.
- `data` tells the data set to be used.
- `nbest` is the number of the best subsets of each size to save. If `nbest=1`, only the best model will be saved for each number of predictors. If `nbest=2`, the best two models with be saved given the number of predictors.
- `nvmax` is the maximum size of subsets of predictors to examine. It specifies the maximum number of predictors you want to include in the final regression model. For example, if you have 7 predictors but set `nvmax=5`, then the most complex model to be evaluated will have only 5 predictors. Using this option will largely reduce computing time if a large number of predictors are evaluated.

```
library(leaps)
all<-regsubsets(bwt~lwt+race+smoke+ptl+ht+ui+ftv,
                data=birthwt,
                nbest=1, nvmax=7)
all
## Subset selection object
## Call: regsubsets.formula(bwt ~ lwt + race + smoke + ptl + ht + ui +
##     ftv, data = birthwt, nbest = 1, nvmax = 7)
## 7 Variables  (and intercept)
##       Forced in Forced out
## lwt       FALSE      FALSE
## race      FALSE      FALSE
## smoke     FALSE      FALSE
## ptl       FALSE      FALSE
## ht        FALSE      FALSE
## ui         FALSE      FALSE
## ftv        FALSE      FALSE
## 1 subsets of each size up to 7
## Selection Algorithm: exhaustive
```

The immediate output of the function `regsubsets()` does not provide much information. To extract more useful information, the function `summary()` can be applied. This will include the following objects that can be printed.

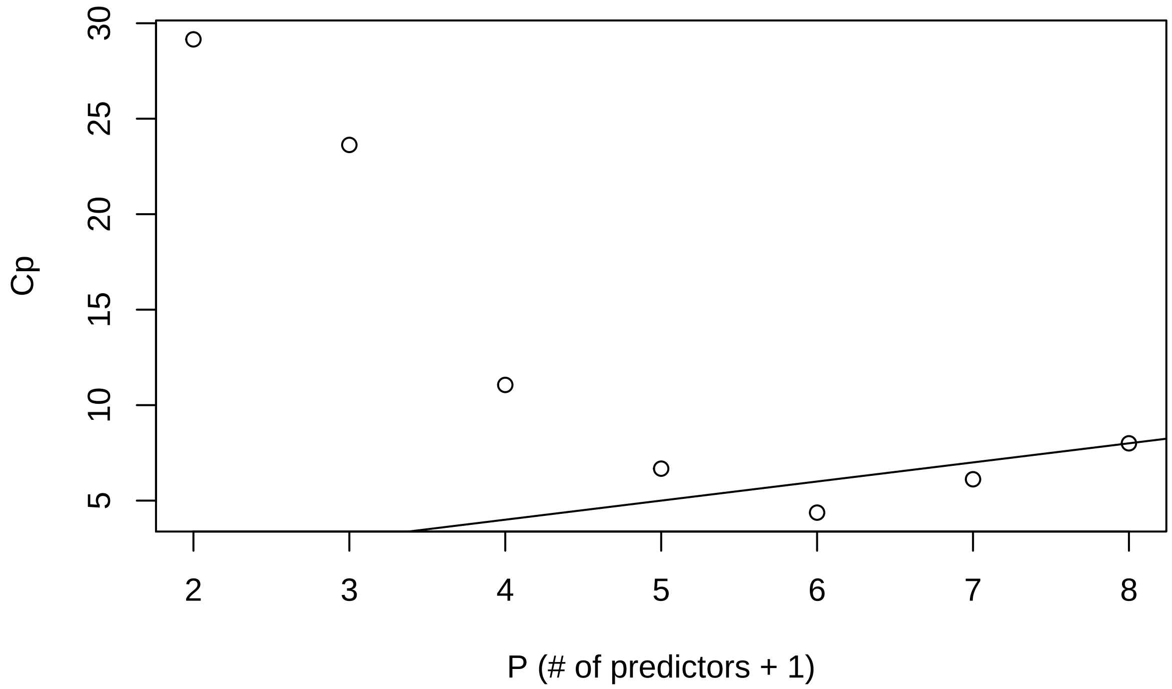
- `which`: A logical matrix indicating which predictors are in each model. 1 indicates a variable is included and 0 not.
- `rsq`: The r-squared for each model (higher, better)
- `adjr2`: Adjusted r-squared (higher, better)
- `cp`: Mallows' Cp (smaller, better)
- `bic`: Schwartz's Bayesian information criterion, BIC (lower, better)
- `rss`: Residual sum of squares for each model (lower, better)

Note that from the output below, we have R^2, adjusted R^2, Mallows' cp, BIC and RSS for the best models with 1 predictor till 7 predictors. We can then select the best model among the 7 best models. For example, based on adjusted R^2, we would say the model with 6 predictors is best because it has the largest adjusted R^2. But based on BIC, the model with the 5 predictors is the best since is has the smallest BIC. Obviously, different criterion might lead to different best models.

```
info <- summary(all)
cbind(info$which, round(cbind(rsq=info$rsq,
          adjr2=info$adjr2, cp=info$cp,
          bic=info$bic, rss=info$rss), 3))
##   (Intercept) lwt race smoke ptl ht ui ftv   rsq adjr2     cp     bic      rss
## 1           1   0    0     0   0  0  1   0 0.081 0.076 29.155  -5.402 91910625
## 2           1   0    1     0   0  0  1   0 0.113 0.103 23.629  -6.922 88680498
## 3           1   0    1     1   0  0  1   0 0.175 0.162 11.058 -15.501 82427257
## 4           1   0    1     1   0  1  1   0 0.203 0.186  6.674 -16.648 79687294
## 5           1   1    1     1   0  1  1   0 0.221 0.200  4.371 -15.838 77840556
## 6           1   1    1     1   1  1  1   0 0.222 0.197  6.117 -10.861 77731620
## 7           1   1    1     1   1  1  1   1 0.223 0.193  8.000  -5.742 77681278
```

We can also plot the different statistics to visually inspect the best models. Mallow's Cp plot is one popular plot to use. In such a plot, Mallows' Cp is plotted along the number of predictors. As mentioned early, for a good model, $C_p \approx p$. Therefore, the models are on or below the line of x=y can be considered as acceptable models. In this example, both the model with 5 predictors and the one with 6 predictors are good models.

```
plot(2:8, info$cp, xlab='P (# of predictors + 1)', ylab='Cp')
abline(a=0,b=1)
```



9.4.3.1 Remarks

Using the all possible subsets method, one would select a model with a larger adjusted R-square, smaller Cp, smaller rsq, and smaller BIC. The different criteria quantify different aspects of the regression model, and therefore often yield different choices for the best set of predictors. That's okay €" as long as we don't misuse best subsets regression by claiming that it yields the best model. Rather, we should use best subsets regression as a screening tool €" that is, as a way to reduce the large number of possible regression models to just a handful of models that we can evaluate further before arriving at one final model. If there are two competing models, one can select the one with fewer predictors or the one with practical or theoretical sense.

With many predictors, for example, more than 40 predictors, the number of possible subsets can be huge. Often, there are several good models, although some are unstable. The best subset may be no better than a subset of some randomly selected variables, if the sample size is relatively small to the number of predictors. The regression fit statistics and regression coefficient estimates can also be biased. In addition, all-possible-subsets selection can yield models that are too small. Generally speaking, one should not blindly trust the results. The data analyst knows more than the computer and failure to use human knowledge produces inadequate data analysis.

9.4.4 Backward elimination

Backward elimination begins with a model which includes all candidate variables. Variables are then deleted from the model one by one until all the variables remaining in the model are significant and exceed certain criteria. At each step, the variable showing the smallest improvement to the model is deleted. Once a variable is deleted, it cannot come back to the model.

The R package `MASS` has a function `stepAIC()` that can be used to conduct backward elimination. To use the function, one first needs to define a null model and a full model. The null model is typically a model without any predictors (the intercept only model) and the full model is often the one with all the candidate predictors included. For the birth weight example, the R code is shown below. Note that backward elimination is based on AIC. It stops when the AIC would increase after removing a predictor.

```
null<-lm(bwt~ 1, data=birthwt) # 1 here means the intercept
full<-lm(bwt~ lwt+race+smoke+ptl+ht+ui+ftv, data=birthwt)

stepAIC(full, scope=list(lower=null, upper=full),
          data=birthwt, direction='backward')
## Start:  AIC=2459.09
## bwt ~ lwt + race + smoke + ptl + ht + ui + ftv
##
##         Df Sum of Sq      RSS    AIC
## - ftv    1     50343 77731620 2457.2
## - ptl    1    110047 77791325 2457.3
## <none>               77681278 2459.1
## - lwt    1   1789656 79470934 2461.4
## - ht     1   3731126 81412404 2465.9
## - race   1   4707970 82389248 2468.2
## - smoke  1   4843734 82525012 2468.5
## - ui     1   5749594 83430871 2470.6
##
## Step:  AIC=2457.21
## bwt ~ lwt + race + smoke + ptl + ht + ui
##
##         Df Sum of Sq      RSS    AIC
## - ptl    1    108936 77840556 2455.5
## <none>               77731620 2457.2
## - lwt    1   1741198 79472818 2459.4
## - ht     1   3681167 81412788 2463.9
## - race   1   4660187 82391807 2466.2
## - smoke  1   4810582 82542203 2466.6
## - ui     1   5716074 83447695 2468.6
##
```

```
## Step:  AIC=2455.47
## bwt ~ lwt + race + smoke + ht + ui
##
##         Df Sum of Sq      RSS    AIC
## <none>                77840556 2455.5
## - lwt    1   1846738 79687294 2457.9
## - ht     1   3718531 81559088 2462.3
## - race   1   4727071 82567628 2464.6
## - smoke  1   5237430 83077987 2465.8
## - ui     1   6302771 84143327 2468.2
##
## Call:
## lm(formula = bwt ~ lwt + race + smoke + ht + ui, data = birthwt)
##
## Coefficients:
## (Intercept)          lwt         race        smoke           ht           ui
##    3104.438        3.434     -187.849     -366.135     -595.820     -523.419
```

9.4.5 Forward selection

Forward selection begins with a model which includes no predictors (the intercept only model). Variables are then added to the model one by one until no remaining variables improve the model by a certain criterion. At each step, the variable showing the biggest improvement to the model is added. Once a variable is in the model, it remains there.

The function `stepAIC()` can also be used to conduct forward selection. For the birth weight example, the R code is shown below. Note that forward selection stops when the AIC would decrease after adding a predictor.

```
stepAIC(null, scope=list(lower=null, upper=full),
          data=birthwt, direction='forward')
## Start:  AIC=2492.76
## bwt ~ 1
##
##         Df Sum of Sq      RSS    AIC
## + ui     1   8059031 91910625 2478.9
## + race   1   3790184 96179472 2487.5
## + smoke  1   3625946 96343710 2487.8
## + lwt    1   3448639 96521017 2488.1
## + ptl    1   2391041 97578614 2490.2
## + ht     1   2130425 97839231 2490.7
## <none>                99969656 2492.8
## + ftv    1    339993 99629663 2494.1
##
```

```
## Step:  AIC=2478.88
## bwt ~ ui
## 
##          Df Sum of Sq      RSS    AIC
## + race   1   3230127 88680498 2474.1
## + ht     1   3162595 88748030 2474.3
## + smoke  1   2996636 88913988 2474.6
## + lwt    1   2074421 89836203 2476.6
## <none>               91910625 2478.9
## + ptl    1    854664 91055961 2479.1
## + ftv    1    172098 91738526 2480.5
## 
## Step:  AIC=2474.11
## bwt ~ ui + race
## 
##          Df Sum of Sq      RSS    AIC
## + smoke  1   6253241 82427257 2462.3
## + ht     1   3000965 85679533 2469.6
## + lwt    1   1367676 87312822 2473.2
## <none>               88680498 2474.1
## + ptl    1    869259 87811239 2474.2
## + ftv    1     59737 88620761 2476.0
## 
## Step:  AIC=2462.29
## bwt ~ ui + race + smoke
## 
##        Df Sum of Sq      RSS    AIC
## + ht    1   2739963 79687294 2457.9
## + lwt   1    868170 81559088 2462.3
## <none>              82427257 2462.3
## + ptl   1    220563 82206694 2463.8
## + ftv   1      8390 82418867 2464.3
## 
## Step:  AIC=2457.9
## bwt ~ ui + race + smoke + ht
## 
##        Df Sum of Sq      RSS    AIC
## + lwt   1   1846738 77840556 2455.5
## <none>              79687294 2457.9
## + ptl   1    214476 79472818 2459.4
## + ftv   1      1134 79686160 2459.9
## 
## Step:  AIC=2455.47
## bwt ~ ui + race + smoke + ht + lwt
```

```
##
##        Df Sum of Sq      RSS    AIC
## <none>              77840556 2455.5
## + ptl   1    108936 77731620 2457.2
## + ftv   1     49231 77791325 2457.3
##
## Call:
## lm(formula = bwt ~ ui + race + smoke + ht + lwt, data = birthwt)
##
## Coefficients:
## (Intercept)           ui         race        smoke           ht          lwt
##    3104.438     -523.419     -187.849     -366.135     -595.820        3.434
```

9.4.6 Stepwise regression

Stepwise regression is a combination of both backward elimination and forward selection methods. Stepwise method is a modification of the forward selection approach and differs in that variables already in the model do not necessarily stay. As in forward selection, stepwise regression adds one variable to the model at a time. After a variable is added, however, stepwise regression checks all the variables already included again to see whether there is a need to delete any variable that does not provide an improvement to the model based on a certain criterion.

The function `stepAIC()` can also be used to conduct forward selection. For the birth weight example, the R code is shown below.

```
stepAIC(null, scope=list(lower=null, upper=full),
          data=birthwt, direction='both')
## Start:  AIC=2492.76
## bwt ~ 1
##
##          Df Sum of Sq      RSS    AIC
## + ui      1   8059031 91910625 2478.9
## + race    1   3790184 96179472 2487.5
## + smoke   1   3625946 96343710 2487.8
## + lwt     1   3448639 96521017 2488.1
## + ptl     1   2391041 97578614 2490.2
## + ht      1   2130425 97839231 2490.7
## <none>                99969656 2492.8
## + ftv     1    339993 99629663 2494.1
##
## Step:  AIC=2478.88
## bwt ~ ui
##
```

```
##         Df Sum of Sq      RSS    AIC
## + race   1   3230127 88680498 2474.1
## + ht     1   3162595 88748030 2474.3
## + smoke  1   2996636 88913988 2474.6
## + lwt    1   2074421 89836203 2476.6
## <none>               91910625 2478.9
## + ptl    1    854664 91055961 2479.1
## + ftv    1    172098 91738526 2480.5
## - ui     1   8059031 99969656 2492.8
##
## Step:  AIC=2474.11
## bwt ~ ui + race
##
##         Df Sum of Sq      RSS    AIC
## + smoke  1   6253241 82427257 2462.3
## + ht     1   3000965 85679533 2469.6
## + lwt    1   1367676 87312822 2473.2
## <none>               88680498 2474.1
## + ptl    1    869259 87811239 2474.2
## + ftv    1     59737 88620761 2476.0
## - race   1   3230127 91910625 2478.9
## - ui     1   7498974 96179472 2487.5
##
## Step:  AIC=2462.29
## bwt ~ ui + race + smoke
##
##         Df Sum of Sq      RSS    AIC
## + ht     1   2739963 79687294 2457.9
## + lwt    1    868170 81559088 2462.3
## <none>               82427257 2462.3
## + ptl    1    220563 82206694 2463.8
## + ftv    1      8390 82418867 2464.3
## - smoke  1   6253241 88680498 2474.1
## - ui     1   6323012 88750270 2474.3
## - race   1   6486731 88913988 2474.6
##
## Step:  AIC=2457.9
## bwt ~ ui + race + smoke + ht
##
##         Df Sum of Sq      RSS    AIC
## + lwt    1   1846738 77840556 2455.5
## <none>               79687294 2457.9
## + ptl    1    214476 79472818 2459.4
## + ftv    1      1134 79686160 2459.9
## - ht     1   2739963 82427257 2462.3
## - smoke  1   5992239 85679533 2469.6
## - race   1   6186692 85873986 2470.0
## - ui     1   7205312 86892607 2472.3
##
## Step:  AIC=2455.47
## bwt ~ ui + race + smoke + ht + lwt
##
##         Df Sum of Sq      RSS    AIC
## <none>                77840556 2455.5
## + ptl    1    108936 77731620 2457.2
## + ftv    1     49231 77791325 2457.3
## - lwt    1   1846738 79687294 2457.9
## - ht     1   3718531 81559088 2462.3
## - race   1   4727071 82567628 2464.6
## - smoke  1   5237430 83077987 2465.8
## - ui     1   6302771 84143327 2468.2
##
## Call:
## lm(formula = bwt ~ ui + race + smoke + ht + lwt, data = birthwt)
##
## Coefficients:
## (Intercept)           ui         race        smoke           ht          lwt
##    3104.438     -523.419     -187.849     -366.135     -595.820        3.434
```

9.4.7 Remarks

9.4.7.1 Forward or backward?

If you have a very large set of candidate predictors from which you wish to extract a few€“i.e., if you're on a fishing expedition€“you should generally go forward. If, on the other hand, if you have a modest-sized set of potential variables from which you wish to eliminate a few€“i.e., if you're fine-tuning some prior selection of variables€“you should generally go backward. If you're on a fishing expedition, you should still be careful not to cast too wide a net, selecting variables that are only accidentally related to your dependent variable.

9.4.7.2 Stepwise regression

Stepwise regression can yield R-squared values that are badly biased high. The method can also yield confidence intervals for effects and predicted values that are falsely narrow. It gives biased regression coefficients that need shrinkage e.g., the coefficients for remaining variables are too large. It also has severe problems in the presence of collinearity and increasing the sample size doesn't help very much.

9.4.7.3 Stepwise or all-possible-subsets?

Stepwise regression often works reasonably well as an automatic variable selection method, but this is not guaranteed. If the number of candidate predictors is large compared to the number of observations in your data set (say, more than 1 variable for every 10 observations), or if there is excessive multicollinearity (predictors are highly correlated), then the stepwise algorithms may go crazy and end up throwing nearly all the variables into the model, especially if you used a low threshold on a criterion like F statistic.

All-possible-subsets goes beyond stepwise regression and literally tests all possible subsets of the set of potential independent variables. But it carries all the caveats of stepwise regression.

9.4.7.4 Use your knowledge

A model selected by automatic methods can only find the "best" combination from among the set of variables you start with: if you omit some important variables, no amount of searching will compensate! Remember that the computer is not necessarily right in its choice of a model during the automatic phase of the search. Don't accept a model just because the computer gave it its blessing. Use your own judgment and intuition about your data to try to fine-tune whatever the computer comes up with.

9.5 Regression with Categorical Predictors

In the variable selection example, we have a predictor – race, which has three categories: 1 = white, 2 = black, 3 = other. In the previous example, we blindly treated it as continuous by taking the numbers literally. This can cause problems. For example, when we interpret the regression slope, we say how much change in the outcome for one unit change the predictor. Although numerically it is fine to say the change from 1 to 2 is the same as the change from 2 to 3, it does not make sense at all to compare the change in the actual race categories. Therefore, although the categories are coded using numerical values, they should be treated as discrete values. This kind variables is called nominal variables. A typical example is ANOVA where the different levels of a factor should be treated as discrete values. In regression, such variables need special treatment for valid statistical inference. We show how to conduct such regression analysis through an example.

9.5.1 An example

In this example, we study the mid-career median salary of college graduates. The data set `college.csv` includes the information on salary and college backgrounds. Specifically, there are 6 variables in the data set: id, name of the college, mid-career median salary of graduates, cost of study, whether the college is public (1) or private (0), and the location of the college: 1, Southern colleges; 2, Midwestern; 3, Northeastern; and 4, Western. A subset of the data as well as some summary information are given below. In total, there are 85 colleges in the data and 50 of them are private colleges. Clearly, the variables public and location in the data set should be treated as categorical variables. Using this example, we study the factors related to median salary.

```
college <- read.csv("data/college.csv")

head(college)
##   id                                        name salary   cost public location
## 1  1 Massachusetts Institute of Technology (MIT) 119000 189300      0        3
## 2  2                          Harvard University 121000 189600      0        3
## 3  3                           Dartmouth College 123000 188400      0        3
## 4  4                        Princeton University 123000 188700      0        3
## 5  5                             Yale University 110000 194200      0        3
## 6  6                    University of Notre Dame 112000 181900      0        2
attach(college)
table(public)
## public
##  0  1
## 50 35
table(location)
## location
##  1  2  3  4
## 20 19 25 21
```

9.5.2 A naive analysis

Suppose we simply treat the variables public and location and fit a multiple regression model to directly. Then, we would get the results as shown below. Then the regression model is

$$salary = 105.48 - 11.679 * public - 1.869 * location.$$

Using the typical way to interpret the regression coefficients, we would say (1) when public=0 and location=0, the average salary is 105.48; (2) when public changes from 0 to 1, the salary would reduce 11.679; and (3) when location increases 1, the salary decreases 1.869. Clearly, (1) and (3) do not make sense at all even though (2) seems to be ok.

By fitting the above regression model, we assume that each predictor has equal interval in their values. For example, for the location variable, the change from Southern to Midwestern is the same as the change from Midwestern to Northeastern. This assumption is certainly questionable for variables with distinct, non-numerical categories. The location variable here is a categorical variable, not a continuous one. The use of numerical values in the data file for categorical variables is for convenience of data input and storage and should be viewed as discrete instead of continuous values. For example, for the "public" variable, 0 should read as private and 1 should read as public. Similarly, for the "location" variable, 1 means Southern, 2 means Midwestern, etc. To deal with such variables, we need recode the categorical variables.

9.5.3 Regression with categorical predictors

9.5.3.1 Code categorical numerical values to avoid confusion

To avoid mistakenly treating the categorical data as continuous, we can code the numerical values as discrete values, or better yet, more descriptive strings. In R, this can be done easily using the function `factor()`. For example, the following R code changes the value 0 to `Private` and 1 to `Public` and for location variable, the values 1 to 4 are recoded as `S`, `MW`, `NE`, and `W`, respectively. Note that each category of a variable is called a level. So, for the `public` variable, there are two levels and for the location variables, there are 4 levels.

```
public<-factor(public, c(0,1), labels=c('Private', 'Public'))
public
##  [1] Private Private Private Private Private Private Private Private Private
## [10] Private Private Private Private Private Private Private Private Public
## [19] Private Private Public  Private Private Private Public  Private Private
## [28] Private Private Private Private Public  Private Private Public  Public
## [37] Private Private Public  Private Public  Private Private Private Public
## [46] Public  Public  Private Private Private Public  Private Private Public
## [55] Public  Public  Public  Private Public  Public  Public  Private Public
## [64] Private Public  Private Public  Public  Public  Public  Private Public
## [73] Private Public  Public  Public  Public  Public  Private Public  Public
## [82] Public  Private Public  Private
## Levels: Private Public

location<-factor(location, c(1,2,3,4), labels=c('S', 'MW','NE', 'W'))
location
##  [1] NE NE NE NE NE MW NE S  NE NE NE NE NE NE S  NE S  W  NE NE S  NE MW NE S
## [26] NE MW S  NE S  NE S  S  MW MW MW MW MW S  MW S  S  W  S  NE S  MW MW S  S
## [51] MW S  MW S  S  NE MW S  MW W  NE W  W  MW NE W  W  MW NE W  W  MW W  W  W
## [76] W  W  W  W  MW W  W  W  W  W
## Levels: S MW NE W
```

9.5.3.2 Dummy coding

Dummy coding provides a way of using categorical predictor variables in regression or other statistical analysis. Dummy coding uses only ones and zeros to convey all of the necessary information on categories or groups. In general, a categorical variable with k levels / categories will be transformed into $k-1$ dummy variables. Regression model can be fitted using the dummy variables as the predictors.

In R using `lm()` for regression analysis, if the predictor is set as a categorical variable, then the dummy coding procedure is automatic. However, we need to figure out how the coding is done. In R, the dummy coding scheme of a categorical variable can be seen using the function `contrasts()`. For example, for the public variable, we need one dummy variable, in which 0 means a Private school and 1 means a public score. In regression analysis, a new variable is then created using the original variable name plus the category shown in the output. In this case, it will be `publicPlublic`.

For the location variable, since it has 4 categories, we would need three dummy variables. In the output of `contrasts(location)`, there are three columns, representing the three variables. The variables in the regression will be represented as `locationMW`, `locationNE`, and `locationW`. Note that with the three dummy variables, the four categories can be uniquely determined. For example, `locationMW = locationNE = locationW = 0` indicates the college is from the south. `locationMW = 1` and `locationNE = locationW = 0` indicate the college is from the Midwest.

```
contrasts(public)
##         Public
## Private      0
## Public       1
contrasts(location)
##    MW NE W
## S   0  0 0
## MW  1  0 0
## NE  0  1 0
## W   0  0 1
```

9.5.4 lm() for data analysis

Conducting regression analysis with categorical predictors is actually not difficult. The same function for multiple regression analysis can be applied. We use several examples to illustrate this.

9.5.4.1 Example 1. A predictor with two categories (one-way ANOVA)

Suppose we want to see if there is a difference in salary for private and public colleges. Then, we use the `public` variable as a predictor, which has two categories. The input and output for the analysis are given below.

```
salary <- salary / 1000

summary(lm(salary ~ public))
##
## Call:
## lm(formula = salary ~ public)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -25.944  -7.134   0.156   5.156  24.166
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   100.844      1.473  68.478  < 2e-16 ***
## publicPublic  -12.010      2.295  -5.233 1.23e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 10.41 on 83 degrees of freedom
## Multiple R-squared:  0.2481, Adjusted R-squared:  0.239
## F-statistic: 27.39 on 1 and 83 DF,  p-value: 1.231e-06
```

First, note that the same formula as for the regular regression analysis is used. However, now the `public` variable is a categorical variable. Second, in the output, there is a variable called `publicPublic`, which was created by the R function automatically. It has two values, 0 and 1. From the output of `contrasts(public)`, we know that for a private college, it takes the value 0 and for a public college, it takes the value 1.

9.5.4.1.1 Write out the model

When using a categorical variable, it's best to write out the model for all the different categories.

$$\begin{aligned} salary &= & b_0 + b_1 * publicPublic \\ &= & 100.8 - 12 publicPublic \\ &= & \begin{cases} 100.8 & \text{For private colleges}(publicPublic = 0) \\ 88.8 & \text{For public colleges}(publicPublic = 1) \end{cases} \end{aligned}$$

9.5.4.1.2 Interpretation

First, note that the difference in the average salaries between the private colleges and the public colleges is equal to 12k, which is also the estimated regression coefficient for `publicPublic`. To test whether the difference is significantly different from 0, it is equivalent to testing the significance of the regression coefficient. In this case, it is significant given $t = -5.233$ and $p < .0011$. Note that this is just another way of doing the pooled two-independent sample t test!

9.5.4.2 Example 2. A predictor with four categories

Suppose we are interested in whether the location of college is related to the salary. For the `location` variable, there are four categories. As expected, three dummy variables are needed to conduct the regression analysis as shown below. The three dummy variable predictors are `locationMW, locationNE, locationW`.

```
summary(lm(salary ~ location))
##
## Call:
## lm(formula = salary ~ location)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -22.988  -4.010  -0.888   3.605  28.890
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)   96.635      1.913  50.514  < 2e-16 ***
## locationMW    -2.940      2.741  -1.073 0.286556
## locationNE    10.253      2.567   3.995 0.000142 ***
## locationW    -12.525      2.673  -4.686 1.11e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 8.555 on 81 degrees of freedom
## Multiple R-squared:  0.5047, Adjusted R-squared:  0.4863
## F-statistic: 27.51 on 3 and 81 DF,  p-value: 2.287e-12
```

Based on the output, we can write out the model for the predicted salaries as below.

$$\text{salary} = 96.6 - 2.94 * \text{locationMW} + 10.25 * \text{locationNE} - 12.53 * \text{locationW}$$

$$= \begin{cases} 96.6 & \text{locationMW=locationNE=locationW=0, South} \\ 96.6\text{-}2.94 & \text{locationMW=1, locationNE=locationW=0, Midwest} \\ 96.6\text{+}10.25 & \text{locationMW=0, locationNE=1, locationW=0, Northeast} \\ 96.6\text{-}12.53 & \text{locationMW=locationNE=0, locationW=1, West} \end{cases}$$

Based on the analysis, we can get the following information:

- The average salary of each area. The South area is the reference area, called reference group since the other groups can be directly compared with it.
- `-2.94` is the difference in the average salaries between South and Midwest. Whether this difference is significantly different from 0 can be tested, therefore, through testing the regression coefficient of `locationMW`. Since `t = -1.073, p = 0.287`, the difference is not signifcant at the 0.05 level.
- `10.25` is the difference in the average salaries between South and Northeast. Since `t = 3.995, p = .0001` for the parameter in the regression, the difference is significantly different from 0.
- `-12.53` is the difference in the average salaries between South and West. Since `t = -4.686, p = 1.11e-05` for the parameter in the regression, the difference is significantly different from 0.

9.5.4.2.1 Testing the significance of the predictor

To test the significance of a categorical predictor, one can check the overall model fit of the regression analysis based on the F-test. This is equivalent to test the significance of all the dummy variables together. For this specific example, we have `F=27.51` and `p-value=2.287e-12`. Therefore, the predictor is statistically significant.

9.5.4.3 Example 3. Two categorical predictors (two-way ANOVA)

Now let's consider the use of both predictors: public and location. With two categorical variables, we can dummy code each of them separately. Then, we should combine the dummy coded variables together to identify features based on the predictors for all possible subjects in the data. For example, for the current analysis, we have the following 4 dummy coded variables.

Sector

Location

MW

NE

W

Public

Public

South

0

0

0

1

Public

Midwest

1

0

0

1

Public

Northeast

0

1

0

1

Public

West

0

0

1

1

Private

South

0

0

0

0

Private

Midwest

1

0

0

0

Private

Northeast

0

1

0

0

Private

West

0

0

1

0

In fitting the model, we would expect the three dummy variables `locationMW`, `locationNE,` `locationW` for the categorical variable `location` and `publicPublic` for the categorical variable `public`. Note that when `locationMW=0`, `locationNE=0,` `locationW=0` and `publicPublic=1`, the college is a public college in the south. For the other colleges, they can be identified in the same way using the 4 dummy coded variables.

The R input and output for the analysis are given below.

```
summary(lm(salary~public+location))
##
## Call:
## lm(formula = salary ~ public + location)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -17.147  -4.754  -0.348   2.847  31.672
##
```

```
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    99.556      1.904  52.296  < 2e-16 ***
## publicPublic   -7.301      1.828  -3.994 0.000143 ***
## locationMW     -2.402      2.522  -0.953 0.343662
## locationNE      8.793      2.386   3.685 0.000415 ***
## locationW     -10.926      2.488  -4.391 3.42e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 7.86 on 80 degrees of freedom
## Multiple R-squared:  0.587,  Adjusted R-squared:  0.5664
## F-statistic: 28.43 on 4 and 80 DF,  p-value: 1.06e-14
```

Based on the output, we can calculate the expected salary for each type of college as below:

$$\text{salary} = 99.56 - 2.40 * \text{locationMW} + 8.79 * \text{locationNE} - 10.93 * \text{locationW} - 7.30 * \text{publicPublic}$$

$$= \begin{cases} 99.56 & \text{locationMW=locationNE=locationW=0, South \& publicPublic=0, Private} \\ 99.56\text{-}2.40 & \text{locationMW=1, locationNE=locationW=0, Midwest \& publicPublic=0, Private} \\ 99.56\text{+}8.79 & \text{locationMW=0, locationNE=1, locationW=0, Northeast \& publicPublic=0, Private} \\ 99.56\text{-}10.83 & \text{locationMW=locationNE=0, locationW=1, West \& publicPublic=0, Private} \\ 99.56\text{-}7.30 & \text{locationMW=locationNE=locationW=0, South \& publicPublic=1, Public} \\ 99.56\text{-}2.40\text{-}7.30 & \text{locationMW=1, locationNE=locationW=0, Midwest \& publicPublic=1, Public} \\ 99.56\text{+}8.79\text{-}7.30 & \text{locationMW=0, locationNE=1, locationW=0, Northeast \& publicPublic=1, Public} \\ 99.56\text{-}10.83\text{-}7.30 & \text{locationMW=locationNE=0, locationW=1, West \& publicPublic=1, Public} \end{cases}$$

With this, we can easily calculate the difference in salary between any two types of colleges.

9.5.4.3.1 Testing the significance of the predictor

Note to test the significance of `public` variable, we can directly look at the coefficient for `publicPublic` since there is only one dummy variable here. For this example, it is significant given `t=-3.994` with a `p-value=0.00014`.

For testing the significance of `location`, it is equivalent to test the significance of a subset of coefficients for the three dummy variables related to `location`. In the case, we can compare two models, one with both categorical predictors and the other with `public` predictor only. Then we can conduct a F-test for comparing the two models. From the comparison, we have an `F = 21.887` with a `p-value = 1.908e-10`. Therefore, `location` is significant above and beyond the predictor `public`.

```
m1 <- lm(salary~public+location)
m2 <- lm(salary~public)
anova(m2,m1)
## Analysis of Variance Table
```

```
##
## Model 1: salary ~ public
## Model 2: salary ~ public + location
##   Res.Df    RSS Df Sum of Sq      F    Pr(>F)
## 1     83 9000.1
## 2     80 4943.0  3    4057.1 21.887 1.908e-10 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

9.5.4.4 Example 4. Two categorical predictors with interaction

We can also look the interaction effects between two categorical predictors. In doing the analysis, we simply include the product of the two predictors. R automatically includes the interaction terms among the dummy coded variables. To investigate the significance of the interaction, we similarly can compare the models with and without the interaction term. For this particular example, we have an `F = 8.4569` with a `p-value = 6.316e-05`. Therefore, the interaction is significant.

```
m1 <- lm(salary~public+location)
m2 <- lm(salary~public*location)
anova(m1,m2)
## Analysis of Variance Table
##
## Model 1: salary ~ public + location
## Model 2: salary ~ public * location
##   Res.Df  RSS Df Sum of Sq      F    Pr(>F)
## 1     80 4943
## 2     77 3718  3      1225 8.4569 6.316e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Note that one can directly apply `anova()` function in the regression analysis as in ANOVA.

9.5.4.5 Example 4. Regression with one categorical and one continuous predictors (ANCOVA)

One might argue that the salary is related to the cost of education. Therefore, when looking at the salary difference across locations, one should first control the effect of the cost of eduction. Such analysis can be carried out conveniently as below. And from the output, we still observe significant location effect after controlling the cost of eduction.

```
cost <- cost/1000
summary(res<-lm(salary~cost + location))
##
```

```
## Call:
## lm(formula = salary ~ cost + location)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -20.2444  -4.9326  -0.5719   3.1620  29.9388
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  87.78906    3.09770  28.340  < 2e-16 ***
## cost          0.06052    0.01728   3.501  0.00076 ***
## locationMW   -2.80035    2.56841  -1.090  0.27885
## locationNE    9.23247    2.42247   3.811  0.00027 ***
## locationW   -10.52177    2.56915  -4.095  0.00010 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 8.016 on 80 degrees of freedom
## Multiple R-squared:  0.5705, Adjusted R-squared:  0.549
## F-statistic: 26.57 on 4 and 80 DF,  p-value: 4.956e-14
anova(res)
## Analysis of Variance Table
##
## Response: salary
##           Df Sum Sq Mean Sq F value    Pr(>F)
## cost       1 2757.0 2756.97  42.903 5.120e-09 ***
## location   3 4071.8 1357.26  21.121 3.571e-10 ***
## Residuals 80 5140.8   64.26
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

9.5.4.6 Post-hoc comparison

Given the above regression analysis, we can conclude that the location of a university and the private/public sector of the university are related to the average salary the students in the university earn. We can further compare, for example, a private midwest university with a public west university. To make such a comparison, we use the function `contrast()` in the package `contrast`. For example, based on the analysis below, students from public Western colleges earn significantly less than students from private Midwest colleges. Note that in using the function, we use a `list()` to tell the categories of each predictor in the comparison. Keep in mind that this kind of comparison can run into multiple comparison problem and therefore Bonferroni correction should be considered.

```
m1 <- lm(salary~public+location)

library(contrast)
contrast(m1, list(location='W', public='Public'),
             list(location='MW', public='Private'))
## lm model parameter contrast
##
##    Contrast    S.E.     Lower    Upper     t df Pr(>|t|)
## 1 -15.82522 2.93855 -21.67312 -9.97732 -5.39 80        0
```

Chapter 10

Logistic Regression

Logistic regression is widely used in social and behavioral research in analyzing the binary (dichotomous) outcome data. In logistic regression, the outcome can only take two values 0 and 1. Some examples that can utilize the logistic regression are given in the following.

- The election of Democratic or Republican president can depend on the factors such as the economic status, the amount of money spent on the campaign, as well as gender and income of the voters.
- Whether an assistant professor can be tenured may be predicted from the number of publications and teaching performance in the first three years.
- Whether or not someone has a heart attack may be related to age, gender and living habits.
- Whether a student is admitted may be predicted by her/his high school GPA, SAT score, and quality of recommendation letters.

We use an example to illustrate how to conduct logistic regression in R.

10.1 An example

In this example, the aim is to predict whether a woman is in compliance with mammography screening recommendations from four predictors, one reflecting medical input and three reflecting a woman's psychological status with regarding to screening.

- Outcome y: whether a woman is in compliance with mammography screening recommendations (1: in compliance; 0: not in compliance)
- Predictors:
  - x1: whether she has received a recommendation for screening from a physician;
  - x2: her knowledge about breast cancer and mammography screening;
  - x3: her perception of benefit of such a screening;
  - x4: her perception of the barriers to being screened.

```
mamm <- read.table("data/mamm.txt", header=TRUE)
head(mamm)
##   y x1   x2 x3 x4
## 1 1  1 0.22  4  3
## 2 0  0 0.56  1  1
## 3 1  0 0.44  4  3
## 4 0  0 0.33  3  0
## 5 1  1 0.44  5  0
## 6 0  1 0.56  5  0
```

10.2 Basic ideas

With a binary outcome, the linear regression does not work any more. Simply speaking, the predictors can take any value but the outcome cannot. Therefore, using a linear regression cannot predict the outcome well. In order to deal with the problem, we model the probability to observe an outcome 1 instead, that is $p = \Pr(y = 1)$. Using the mammography example, that'll be the probability for a woman to be in compliance with the screening recommendation.

Even directly modeling the probability would work better than predicting the 1/0 outcome, intuitively. A potential problem is that the probability is bound between 0 and 1 but the predicted values are generally not. To further deal with the problem, we conduct a transformation using

$$\eta = \log \frac{p}{1-p}.$$

After transformation, η can take any value from $-\infty$ when $p = 0$ to ∞ when $p = 1$. Such a transformation is called logit transformation, denoted by $\text{logit}(p)$. Note that $p_i/(1-p_i)$ is called odds, which is simply the ratio of the probability for the two possible outcomes. For example, if for one woman, the probability that she is in compliance is 0.8, then the odds is 0.8/(1-0.2)=4. Clearly, for equal probability of the outcome, the odds=1. If odds>1, there is a probability higher than 0.5 to observe the outcome 1. With the transformation, the η can be directly modeled.

Therefore, the logistic regression is

$$\text{logit}(p_i) = \log(\frac{p_i}{1-p_i}) = \eta_i = \beta_0 + \beta_1 x_{1i} + \ldots + \beta_k x_{ki}$$

where $p_i = \Pr(y_i = 1)$. Different from the regular linear regression, no residual is used in the model.

10.2.1 Why is this?

For a variable y with two and only two outcome values, it is often assumed it follows a Bernoulli or binomial distribution with the probability p for the outcome 1 and probability $1-p$ for 0. The density function is

$$p^y(1-p)^{1-y}.$$

Note that when $y=1$, $p^y(1-p)^{1-y}=p$ exactly.

Furthermore, we assume there is a continuous variable y^* underlying the observed binary variable. If the continuous variable takes a value larger than certain threshold, we would observe 1, otherwise 0. For logistic regression, we assume the continuous variable has a logistic distribution with the density function:

$$\frac{e^{-y^*}}{1+e^{-y^*}}.$$

The probability for observing 1 is therefore can be directly calculated using the logistic distribution as:

$$p=\frac{1}{1+e^{-y^*}},$$

which transforms to

$$\log\frac{p}{1-p}=y^*.$$

For y^*, since it is a continuous variable, it can be predicted as in a regular regression model.

10.3 Fitting a logistic regression model in R

In R, the model can be estimated using the `glm()` function. Logistic regression is one example of the generalized linear model (glm). Below gives the analysis of the mammography data.

- `glm` uses the model formula same as the linear regression model.
- `family =` tells the distribution of the outcome variable. For binary data, the binomial distribution is used.
- `link =` tell the transformation method. Here, the logit transformation is used.
- The output includes the regression coefficients and their z-statistics and p-values.
- The dispersion parameter is related to the variance of the response variable.

```
m1<-glm(y~x1+x2+x3+x4, family=binomial(link='logit'), data=mamm)
summary(m1)
##
## Call:
## glm(formula = y ~ x1 + x2 + x3 + x4, family = binomial(link = "logit"),
##     data = mamm)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -2.3941  -0.7660   0.3756   0.7881   1.6004
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  -1.4466     1.1257  -1.285 0.198754
## x1            1.7731     0.4841   3.663 0.000249 ***
## x2           -0.8694     1.1201  -0.776 0.437628
## x3            0.5935     0.2058   2.883 0.003933 **
## x4           -0.1527     0.1542  -0.990 0.321946
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 203.32  on 163  degrees of freedom
## Residual deviance: 155.48  on 159  degrees of freedom
## AIC: 165.48
##
## Number of Fisher Scoring iterations: 5
```

10.4 Interpret the results

We first focus on how to interpret the parameter estimates from the analysis. For the intercept, when all the predictors take the value 0, we have

$$\beta_0 = \log(\frac{p}{1-p}),$$

which is the log odds that the observed outcome is 1.

We now look at the coefficient for each predictor. For the mammography example, let's assume x_2, x_3, and x_4 are the same and look at x_1 only. If a woman has received a recommendation ($x_1 = 1$), then the odds is

$$\log(\frac{p}{1-p})|(x_1 = 1) = \beta_0 + \beta_1 + \beta_2 x_2 + \beta_3 x_3 + \beta_4 x_4.$$

If a woman has not received a recommendation ($x_1 = 0$), then the odds is

$$\log(\frac{p}{1-p})|(x_1 = 0) = \beta_0 + \beta_2 x_2 + \beta_3 x_3 + \beta_4 x_4.$$

The difference is

$$\log(\frac{p}{1-p})|(x_1 = 1) - \log(\frac{p}{1-p})|(x_1 = 0) = \beta_1.$$

Therefore, the logistic regression coefficient for a predictor is the difference in the log odds when the predictor changes 1 unit given other predictors unchanged.

This above equation is equivalent to

$$\log\left(\frac{\frac{p(x_1=1)}{1-p(x_1=1)}}{\frac{p(x_1=0)}{1-p(x_1=0)}}\right) = \beta_1.$$

More descriptively, we have

$$\log\left(\frac{\text{ODDS(received recommendation)}}{\text{ODDS(not received recommendation)}}\right) = \beta_1.$$

Therefore, the regression coefficients is the log odds ratio. By a simple transformation, we have

$$\frac{\text{ODDS(received recommendation)}}{\text{ODDS(not received recommendation)}} = \exp(\beta_1)$$

or

$$\text{ODDS(received recommendation)} = \exp(\beta_1) * \text{ODDS(not received recommendation)}.$$

Therefore, the exponential of a regression coefficient is the odds ratio. For the example, $exp(\beta_1)$=exp(1.7731)=5.9. Thus, the odds in compliance to screening for those who received recommendation is about 5.9 times of those who did not receive recommendation.

For continuous predictors, the regression coefficients can also be interpreted the same way. For example, we may say that if high school GPA increase one unit, the odds a student to be admitted can be increased to 6 times given other variables the same.

Although the output does not directly show odds ratio, they can be calculated easily in R as shown below.

```
exp(coef(m1))
## (Intercept)          x1          x2          x3          x4 
##   0.2353638   5.8892237   0.4192066   1.8103735   0.8583652
```

By using odds ratios, we can intercept the parameters in the following.

- For x1, if a woman receives a screening recommendation, the odds for her to be in compliance with screening is about 5.9 times of the odds of a woman who does not receive a recommendation given x2, x3, x4 the same. Alternatively (may be more intuitive), if a woman receives a screening recommendation, the odds for her to be in compliance with screening will increase 4.9 times (5.889 €“ 1 = 4.889 =4.9), given other variables the same.
- For x2, if a woman has one unit more knowledge on breast cancer and mammography screening, the odds for her to be in compliance with screening decreases 58.1% (.419-1=-58.1%, negative number means decrease), keeping other variables constant.
- For x3, if a woman's perception about the benefit increases one unit, the odds for her to be in compliance with screening increases 81% (1.81-1=81%, positive number means increase), keeping other variables constant.
- For x4, if a woman's perception about the barriers increases one unit, the odds for her to be in compliance with screening decreases 14.2% (.858-1=-14.2%, negative number means decrease), keeping other variables constant.

10.5 Statistical inference for logistic regression

Statistical inference for logistic regression is very similar to statistical inference for simple linear regression. We can (1) conduct significance testing for each parameter, (2) test the overall model, and (3) test the overall model.

10.5.1 Test a single coefficient (z-test and confidence interval)

For each regression coefficient of the predictors, we can use a z-test (note not the t-test). In the output, we have z-values and corresponding p-values. For x1 and x3, their coefficients are significant at the alpha level 0.05. But for x2 and x4, they are not. Note that some software outputs Wald statistic for testing significance. Wald statistic is the square of the z-statistic and thus Wald test gives the same conclusion as the z-test.

We can also conduct the hypothesis testing by constructing confidence intervals. With the model, the function `confint()` can be used to obtain the confidence interval. Since one is often interested in odds ratio, its confidence interval can also be obtained.

Note that if the CI for odds ratio includes 1, it means nonsignificance. If it does not include 1, the coefficient is significant. This is because for the original coefficient, we compare the CI with 0. For odds ratio, exp(0)=1.

If we were reporting the results in terms of the odds and its CI, we could say, €œThe odds of in compliance to screening increases by a factor of 5.9 if receiving screening recommendation (z=3.66, P = 0.0002; 95% CI = 2.38 to 16.23) given everything else the same.

```
confint(m1)
##                  2.5 %    97.5 %
## (Intercept) -3.7161449 0.7286948
## x1           0.8665475 2.7871626
## x2          -3.1466137 1.2831677
## x3           0.2023731 1.0134006
## x4          -0.4577415 0.1506678
exp(confint(m1))
##                  2.5 %    97.5 %
## (Intercept) 0.02432757  2.072374
## x1          2.37868419 16.234889
## x2          0.04299748  3.608051
## x3          1.22430472  2.754954
## x4          0.63271101  1.162610
```

10.5.2 Test the overall model

For the linear regression, we evaluate the overall model fit by looking at the variance explained by all the predictors. For the logistic regression, we cannot calculate a variance. However, we can define and evaluate the deviance instead. For a model without any predictor, we can calculate a null deviance, which is similar to variance for the normal outcome variable. After including the predictors, we have the residual deviance. The difference between the null deviance and the residual deviance tells how much the predictors help predict the outcome. If the difference is significant, then overall, the predictors are significant statistically.

The difference or the decease in deviance after including the predictors follows a chi-square (χ^2) distribution. The chi-square (χ^2) distribution is a widely used distribution in statistical inference. It has a close relationship to F distribution. For example, the ratio of two independent chi-square distributions is a F distribution. In addition, a chi-square distribution is the limiting distribution of an F distribution as the denominator degrees of freedom goes to infinity.

There are two ways to conduct the test. From the output, we can find the Null and Residual deviances and the corresponding degrees of freedom. Then we calculate the difference. For the mammography example, we first get the difference between the Null deviance and the Residual deviance, 203.32-155.48= 47.84. Then, we find the difference in the degrees of freedom 163-159=4. Then, the p-value can be calculated based on a chi-square distribution with the degree of freedom 4. Because the p-value is smaller than 0.05, the overall model is significant.

The test can be conducted simply in another way. We first fit a model without any predictor and another model with all the predictors. Then, we can use `anova()` to get the difference in deviance and the chi-square test result.

```
## method 1
d_chi <- 203.32 - 155.48
d_df <- 163 - 159

1 - pchisq(d_chi, d_df)
## [1] 1.019117e-09

## method 2
m0 <- glm(y~1, family=binomial(link='logit'), data=mamm)
anova(m0,m1)
## Analysis of Deviance Table
##
## Model 1: y ~ 1
## Model 2: y ~ x1 + x2 + x3 + x4
##   Resid. Df Resid. Dev Df Deviance
## 1       163     203.32
## 2       159     155.48  4   47.837
```

10.5.3 Test a subset of predictors

We can also test the significance of a subset of predictors. For example, whether x3 and x4 are significant above and beyond x1 and x2. This can also be done using the chi-square test based on the difference. In this case, we can compare a model with all predictors and a model without x3 and x4 to see if the change in the deviance is significant. In this example, the p-value is 0.002, indicating the change is signficant. Therefore, x3 and x4 are statistically significant above and beyond x1 and x2.

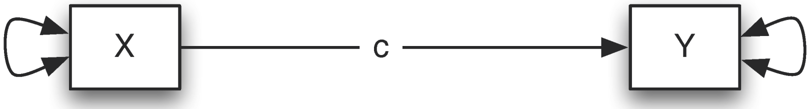
```
m1<-glm(y~x1+x2+x3+x4, family=binomial(link='logit'), data=mamm)
m2 <- glm(y~x1+x2, family=binomial(link='logit'), data=mamm)

anova(m2, m1)
## Analysis of Deviance Table
##
## Model 1: y ~ x1 + x2
## Model 2: y ~ x1 + x2 + x3 + x4
##   Resid. Df Resid. Dev Df Deviance
## 1       161     168.23
## 2       159     155.48  2   12.749

1 - pchisq(12.749, 2)
## [1] 0.001704472
```

Chapter 11

Moderation Analysis

11.1 What is a moderator?

To explain what is a moderator, we start with a bivariate relationship between an input variable X and an outcome variable Y. For example, X could be the number of training sessions (training intensity) and Y could be math test score. We can hypothesize that there is a relationship between them such that the number of training sessions predicts math test performance. Using a diagram, we can portray the relationship below.

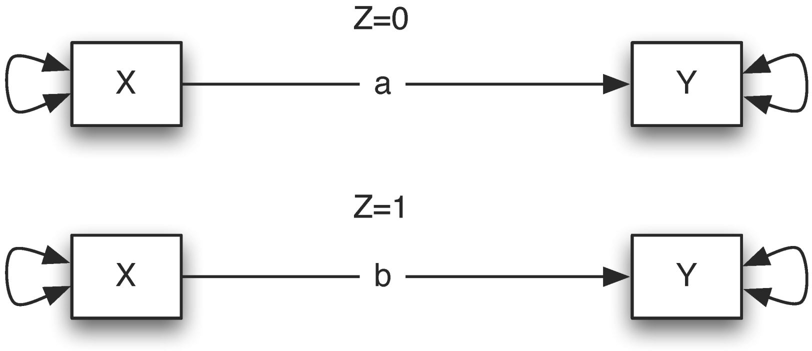


The above path diagram can be expressed using a regression model as

$$Y = \beta_0 + \beta_1 * X + \epsilon$$

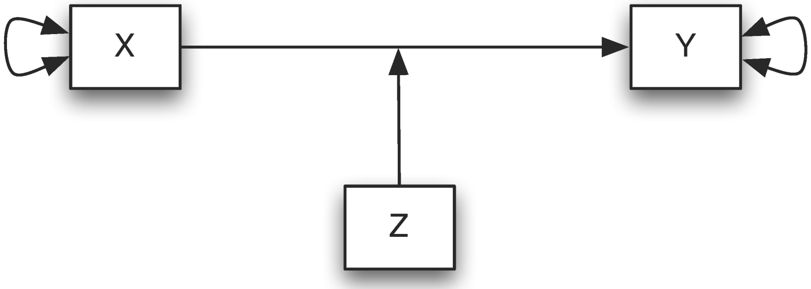
where β_0 is the intercept and β_1 is the slope.

A moderator variable Z is a variable that alters the strength of the relationship between X and Y. In other words, the effect of X on Y depends on the levels of the moderator Z. For instance, if male students ($Z = 0$) benefit more (or less) from training than female students ($Z = 1$), then gender can be considered as a moderator. Using the diagram, if the coefficient a is different b, there is a moderation effect.



To summarize, a moderator Z is a variable that alters the direction and/or strength of the relation between a predictor X and an outcome Y.

Questions involving moderators address **when** or **for whom** a variable most strongly predicts or causes an outcome variable. Using a path diagram, we can express the moderation effect as:



11.2 How to conduct moderation analysis?

Moderation analysis can be conducted by adding one or multiple interaction terms in a regression analysis. For example, if Z is a moderator for the relation between X and Y, we can fit a regression model

$$\begin{aligned} Y = & \beta_0 + \beta_1 * X + \beta_2 * Z + \beta_3 * X * Z + \epsilon \\ = & \quad \beta_0 + \beta_2 * Z + (\beta_1 + \beta_3 * Z) * X + \epsilon. \end{aligned}$$

Thus, if β_3 is not equal to 0, the relationship between X and Y depends on the value of Z, which indicates a moderation effect. In fact, from the regression model, we can get:

- If $z = 0$, the effect of X on Y is $\beta_1 + \beta_3 * 0 = \beta_1$.
- If $z = 2$, the effect of X on Y is $\beta_1 + \beta_3 * 2$.
- If $z = 4$, the effect of X on Y is $\beta_1 + \beta_3 * 4$.

If Z is a dichotomous/binary variable, for example, gender, the above equation can be written as

$$
\begin{aligned}
Y = & \quad \beta_0 + \beta_1 * X + \beta_2 * Z + \beta_3 * X * Z + \epsilon \\
= & \begin{cases} \beta_0 + \beta_1 * X + \epsilon & \text{For male students}(Z = 0) \\ \beta_0 + \beta_2 + (\beta_1 + \beta_3) * X + \epsilon & \text{For female students}(Z = 1) \end{cases}
\end{aligned}
$$

Thus, if β_3 is not equal to 0, the relationship between X and Y depends on the value of Z, which indicates a moderation effect. When $z = 0$, the effect of X on Y is $\beta_1 + \beta_3 * 0 = \beta_1$ and when $z = 1$, the effect of X on Y is $\beta_1 + \beta_3 * 1$ for female students.

11.2.1 Steps for moderation analysis

A moderation analysis typically consists of the following steps.

1. Compute the interaction term XZ=X*Z.
2. Fit a multiple regression model with X, Z, and XZ as predictors.
3. Test whether the regression coefficient for XZ is significant or not.
4. Interpret the moderation effect.
5. Display the moderation effect graphically.

11.2.2 An example

The data set `mathmod.csv` includes three variables: training intensity, gender, and math test score. Using the example, we investigate whether the effect of training intensity on math test performance depends on gender. Therefore, we evaluate whether gender is a moderator.

The R code for the analysis is given below.

```r
mathmod <- read.table("data/math.mod.txt", header = TRUE)
attach(mathmod)

# Computer the interaction term
xz<-training*gender
summary(lm(math~training+gender+xz))
##
## Call:
## lm(formula = math ~ training + gender + xz)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -2.6837 -0.5892 -0.1057  0.7811  2.2350
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  4.98999    0.27499  18.146  < 2e-16 ***
## training    -0.33943    0.05387  -6.301 8.70e-09 ***
## gender      -2.75688    0.37912  -7.272 9.14e-11 ***
## xz           0.50427    0.06845   7.367 5.80e-11 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.9532 on 97 degrees of freedom
## Multiple R-squared:  0.3799, Adjusted R-squared:  0.3607
## F-statistic: 19.81 on 3 and 97 DF,  p-value: 4.256e-10
```

Since the regression coefficient (`0.504`) for the interaction term XZ is significant at the alpha level 0.05 with a `p-value=5.8e-11`, there exists a significant moderation effect. In other words, the effect of training intensity on math performance significantly depends on gender.

When Z=0 (male students), the estimated effect of training intensity on math performance is $\hat{\beta}_1 = -.34$. When Z=1 (female students), the estimated effect of training intensity on math performance is $\hat{\beta}_1 + \hat{\beta}_3 = -.34 + .50 = .16$. The moderation analysis tells us that the effects of training intensity on math performance for males (`-.34`) and females (`.16`) are significantly different for this example.

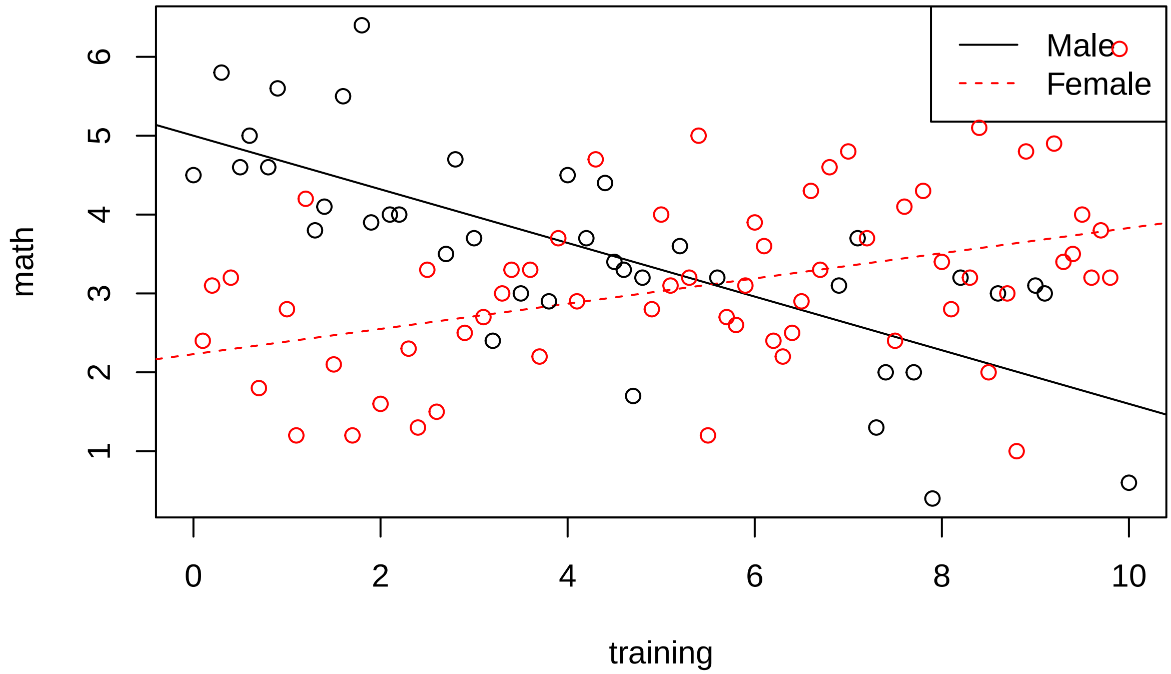
11.2.2.1 Interaction plot

A moderation effect indicates the regression slopes are different for different groups. Therefore, if we plot the regression line for each group, they should interact at certain point. Such a plot is called an interaction plot. To get the plot, we first calculate the intercept and slope for each level of the moderator. For this example, we have

$$
\begin{aligned}
Y = & \quad \beta_0 + \beta_1 * X + \beta_2 * Z + \beta_3 * X * Z && (11.1)\\
= & \begin{cases} \beta_0 + \beta_1 * X & \text{For male students}(Z = 0) \\ \beta_0 + \beta_2 + (\beta_1 + \beta_3) * X & \text{For female students}(Z = 1) \end{cases}. && (11.2)\\
= & \begin{cases} 5 - 0.34 * X & \text{For male students}(Z = 0) \\ 2.23 + 0.16 * X & \text{For female students}(Z = 1) \end{cases} && (11.3)
\end{aligned}
$$

With the information, we can generate a plot using the R code below. Note that the option `type='n'` generates a figure without actually plotting the data. In the function `abline()`, the first value is the intercept and the second is the slope. Note that the values for each level can also be added to the plot.

```
plot(training, math, type='n') ## create an empty frame
abline(5, -.34)  ## for male
abline(2.23, .16, lty=2, col='red')  ## for female
legend('topright', c('Male', 'Female'), lty=c(1,2),
       col=c('black', 'red'))

## add scatter plot
points(training[gender==0], math[gender==0])
points(training[gender==1], math[gender==1], col='red')
```



11.2.3 Another example - continuous moderator

The data set `depress.csv` includes three variables: Stress, Social support and Depression. Suppose we want to investigate whether social support is a moderator for the relation between stress and depression. That is, to study whether the effect of stress on depression depends on different levels of social support. Note that the potential moderator social support is a continuous variable.

The analysis is given below. The regression coefficient estimate of the interaction term is `-.39` with `t = -20.754, p <.001`. Therefore, social support is a significant moderator for the relation between stress and depression. The relation between stress and depression significantly depends on different levels of social support.

```
depress <- read.table("data/depress.txt", header = TRUE)
```

```r
# the interaction term
depress$inter<-depress$stress*depress$support
summary(lm(depress~stress+support+inter, data=depress))
##
## Call:
## lm(formula = depress ~ stress + support + inter, data = depress)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -3.7322 -0.9035 -0.1127  0.8542  3.6089
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  29.2583     0.6909  42.351   <2e-16 ***
## stress        1.9956     0.1161  17.185   <2e-16 ***
## support      -0.2356     0.1109  -2.125   0.0362 *
## inter        -0.3902     0.0188 -20.754   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.39 on 96 degrees of freedom
## Multiple R-squared:  0.9638, Adjusted R-squared:  0.9627
## F-statistic:   853 on 3 and 96 DF,  p-value: < 2.2e-16
```

Since social support is a continuous variable, there is no immediate levels to look at the relationship between stress and depression. However, we can choose several difference levels. One way is to use these three levels of a moderator: mean, one standard deviation below the mean and one standard deviation above the mean. For this example, the three values for social support are 5.37, 2.56 and 8.18. The fitted regression lines for the three values are

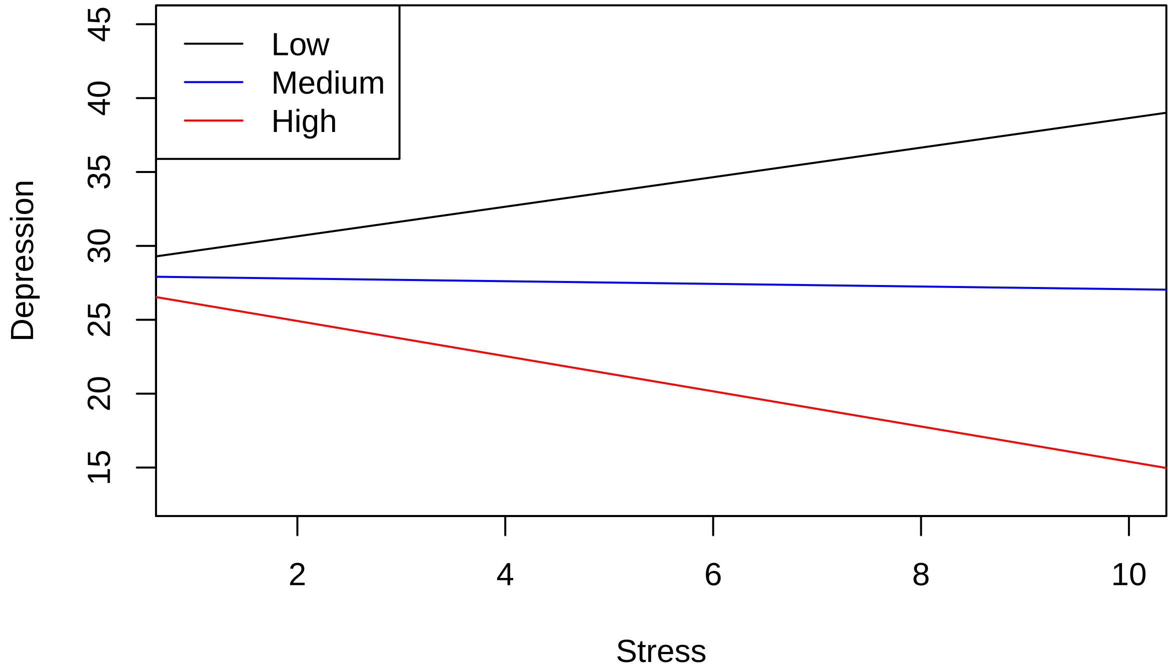
$$\hat{depress} = 29.26 + 2.00 * stress - .24 * support - .39 * stress * support \tag{11.4}$$

$$= \begin{cases} 28.65 + 1 * stress & support = 2.56 \\ 27.97 - .09 * stress & support = 5.37. \\ 27.30 - 1.19 * stress & support = 8.18 \end{cases} \tag{11.5}$$

From it, we can clearly see that with more social support, the relationship between depression and stress becomes negative from positive. This can also be seen from the interaction plot below.

```r
## create an empty frame
plot(depress$stress, depress$depress, type='n',
     xlab='Stress', ylab='Depression')
```

```
## abline(interceptvalue, linearslopevalue)
# for support = mean -1SD
abline(28.65, 1)
# for support = mean
abline(27.97, -.09, col='blue')
# for support = mean +1SD
abline(27.30, -1.19, col='red')

legend('topleft', c('Low', 'Medium', 'High'),
                  lty=c(1,1,1),
                  col=c('black','blue','red'))
```



Chapter 12

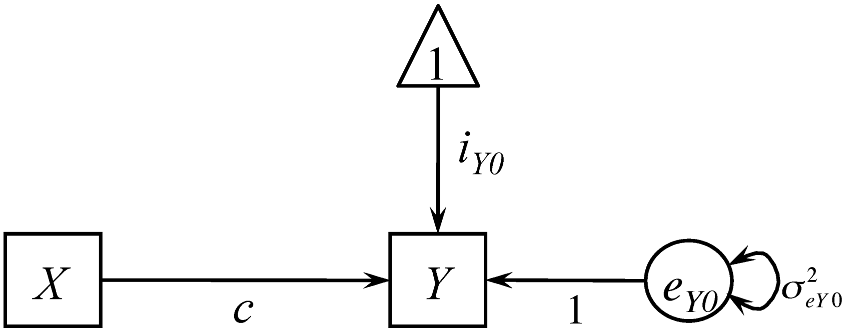
Mediation Analysis

12.1 Path diagrams

Consider a bivariate relationship between X and Y. If X is a predictor and Y is the outcome, we can fit a regression model

$$Y = i_{Y0} + cX + e_{Y0}$$

where c is the effect of X on Y, also called as the total effect of X on Y. The model can be expressed as a path diagram as shown below.



12.1.1 Rules to draw a path diagram

In a path diagram, there are three types of shapes: a rectangle, a circle, and a triangle, as well as two types of arrows: one-headed (single-headed) arrow and two-headed (double-headed) arrows.

A rectangle represents an observed variable, which is a variable in the dataset with known information from the subjects. A circle or elliptical represents an unobserved variable, which can be the residuals, errors, or factors. A triangle, typically with 1 in it, represents either an intercept or a mean.

A one-headed arrow means that the variable on the side without the arrow predicts the variable on the side with the arrow. If the two-headed arrow is on a single variable, it represents a variance. If the two-headed arrow is between two variables, it represents the covariance between the two variables.

12.1.2 How to draw path diagrams?

Many different software can be used to draw path diagrams such as Powerpoint, Word, OmniGaffle, ect. For the ease of use, we recommend the online program WebSEM (https://websem.psychstat.org), which allows researchers to do SEM online, even on a smart phone. In addition, the drawn path diagram can be estimated using the uploaded/provided data (WebSEM). A simpler version of such program can be found at http://semdiag.psychstat.org.

12.2 What is mediation or what is a mediator?

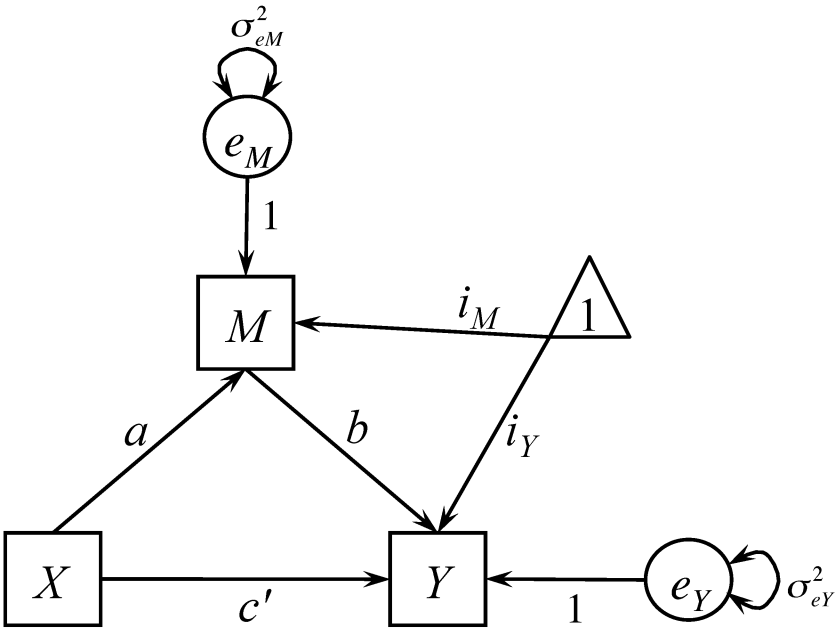
In the classic paper on mediation analysis, Baron and Kenny (1986, p.1176) defined a mediator as “In general, a given variable may be said to function as a mediator to the extent that it accounts for the relation between the predictor and the criterion.” Therefore, mediation analysis answers the question **why** X can predict Y.

Suppose the effect of X on Y may be mediated by a mediating variable M. Then, we can write a mediation model as two regression equations

$$M = i_M + aX + e_M \tag{12.1}$$

$$Y = i_Y + c'X + bM + e_Y. \tag{12.2}$$

This is the simplest but most popular mediation model. c' is called the direct effect of X on Y with the inclusion of variable M. The indirect effect or mediation effect is $a * b$, the effect of X on Y through M. The total effect of X on Y is $c = c\prime + a * b$. This simple mediation model can also be portrayed as a path diagram shown below.



Note that a mediation model is a directional model. For example, the mediator is presumed to cause the outcome and not vice versa. If the presumed model is not correct, the results from the mediation analysis are of little value. Mediation is not defined statistically; rather statistics can be used to evaluate a presumed mediation model.

12.3 Mediation effects

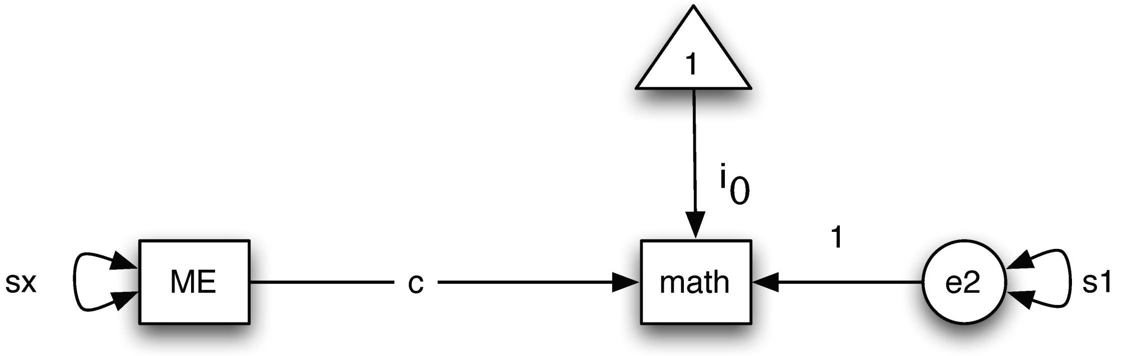
The amount of mediation, which is called the indirect effect, is defined as the reduction of the effect of the input variable on the outcome, $c - c'$. $c - c' = ab$ when (1) multiple regression (or structural equation modeling without latent variables) is used, (2) there are no missing data, and (3) the same covariates are in the equations if there are any covariates. However, the two are only approximately equal for multilevel models, logistic analysis and structural equation models with latent variables. In this case, we calculate the total effect via $c' + ab$ instead of c. For the simplest mediation model without missing data, $ab = c - c'$.

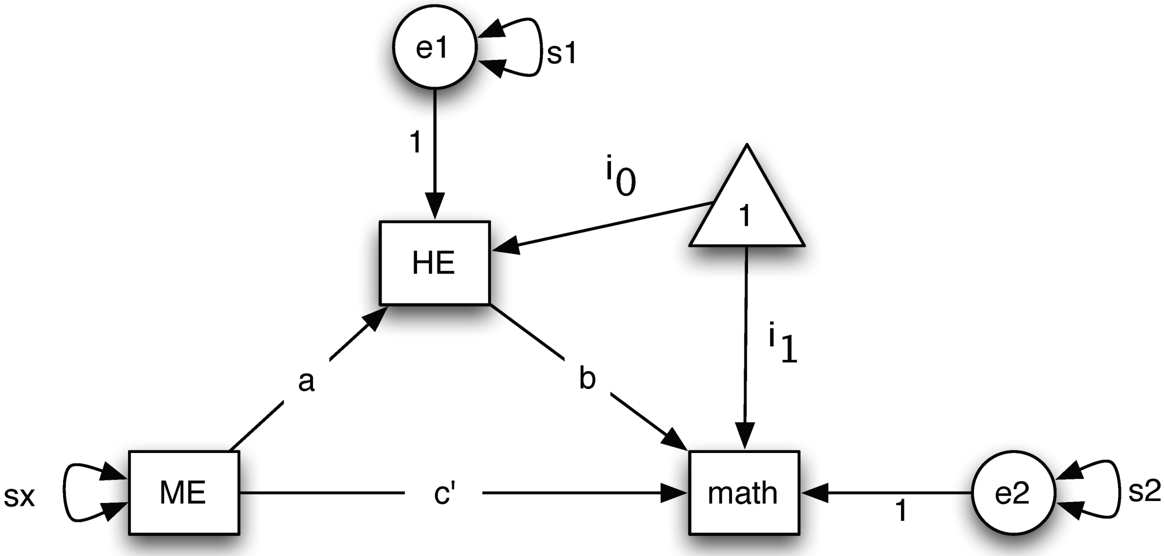
12.4 Testing mediation effects

12.4.1 An example

We use the following example to show how to conduct mediation analysis and test mediation effects.

Research has found that parents' education levels can influence adolescent mathematics achievement directly and indirectly. For example, Davis-Kean (2005) showed that parents' education levels are related to children's academic achievement through parents' beliefs and behaviors. To test a similar hypothesis, we investigate whether home environment is a mediator in the relation between mothers' education and children's mathematical achievement. Data used in this example are from the National Longitudinal Survey of Youth, the 1979 cohort (NLSY79, for Human Resource Research, 2006). Data were collected in 1986 from N=371 families on mothers' education level (ME), home environment (HE), and children's mathematical achievement (Math). For the mediation analysis, mothers' education is the input variable, home environment is the mediator, and children's mathematical achievement is the outcome variable. Using a path diagram, the involved mediation model is given below.





12.4.2 Baron and Kenny (1986) method

Baron and Kenny (1989) outlined a 4-step procedure to determine whether there is a mediation effect.

1. Show that X is correlated with Y. Regress Y on X to estimate and test the path *c*. This step establishes that there is an effect that may be mediated.

2. Show that X is correlated with M. Regress M on X to estimate and test path *a*. This step essentially involves treating the mediator as if it were an outcome variable.
3. Show that M affects Y. Regress Y on both X and M to estimate and test path *b*. Note that it is not sufficient just to correlate the mediator with the outcome; the mediator and the outcome may be correlated because they are both caused by the input variable X. Thus, the input variable X must be controlled in establishing the effect of the mediator on the outcome.
4. To establish that M *completely* mediates the X-Y relationship, the effect of X on Y controlling for M (path c') should be zero. The effects in both Steps 3 and 4 are estimated in the same equation.

If all four of these steps are met, then the data are consistent with the hypothesis that variable M *completely* mediates the X-Y relationship, and if the first three steps are met but the Step 4 is not, then *partial* mediation is indicated.

The R code for the 4-step method for the example data is shown below.

```
nlsy <- read.table("data/nlsy.med.comp.txt", header=TRUE)
attach(nlsy)

# Step 1
summary(lm(math~ME))
##
## Call:
## lm(formula = math ~ ME)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -14.6224  -2.9299  -0.4574   2.4876  29.4876
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)   6.1824     1.3709   4.510 8.73e-06 ***
## ME            0.5275     0.1199   4.398 1.43e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 4.618 on 369 degrees of freedom
## Multiple R-squared:  0.04981,    Adjusted R-squared:  0.04723
## F-statistic: 19.34 on 1 and 369 DF,  p-value: 1.432e-05

# Step 2
summary(lm(HE~ME))
##
## Call:
## lm(formula = HE ~ ME)
```

```
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -5.5020 -0.7805  0.2195  1.2195  3.3587
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  4.10944    0.49127   8.365 1.25e-15 ***
## ME           0.13926    0.04298   3.240   0.0013 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.655 on 369 degrees of freedom
## Multiple R-squared:  0.02766,    Adjusted R-squared:  0.02502
## F-statistic:  10.5 on 1 and 369 DF,  p-value: 0.001305

# Step 3 & 4
summary(lm(math~ME+HE))
##
## Call:
## lm(formula = math ~ ME + HE)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -14.9302  -3.0045  -0.2226   2.2386  29.3856
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)   4.2736     1.4764   2.895 0.004022 **
## ME            0.4628     0.1201   3.853 0.000137 ***
## HE            0.4645     0.1434   3.238 0.001311 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 4.559 on 368 degrees of freedom
## Multiple R-squared:  0.07613,    Adjusted R-squared:  0.07111
## F-statistic: 15.16 on 2 and 368 DF,  p-value: 4.7e-07
```

In Step 1, we fit a regression model using ME as the predictor and math as the outcome variable. Based on this analysis, we have $\hat{c}$ =.5275 `(t = 4.298, p <.001)` and thus ME is significantly related to math. Therefore, Step 1 is met: the input variable is correlated with the outcome.

In Step 2, we fit a regression model using ME as the predictor and HE as the outcome variable. From this analysis, we have $\hat{a}$ = `.139 (t = 3.24, p = .0013)` and thus ME is significantly related to HE. Therefore, Step 2 is met: the input variable is correlated with the mediator.

In Step 3, we fit a multiple regression model with ME and HE as predictors and math as the outcome variable. For the analysis, we have $\hat{b}$=`.4645 (t = 3.238, p =.0013).` Because both $\hat{a}$ and $\hat{b}$ are significant, we can say HE significantly mediates the relationship between ME and math. The mediation effect estimate is $\hat{ab} = .139 * .4645 = 0.065$.

Step 4, from the results in Step 3, we know that the direct effect c' ($\hat{c'}$=`.4628, t = 3.853, p = .00013`) is also significant. Thus, there exists a partial mediation.

12.4.3 Sobel test

Many researchers believe that the essential steps in establishing mediation are Steps 2 and 3. Step 4 does not have to be met unless the expectation is for complete mediation. In the opinion of most researchers, though not all, Step 1 is not required. However, note that a path from the input variable to the outcome is implied if Steps 2 and 3 are met. If c' were in the opposite sign to that of ab, then it could be the case that Step 1 would not be met, but there is still mediation. In this case the mediator acts like a suppressor variable. MacKinnon, Fairchild, and Fritz (2007) called it inconsistent mediation. For example, consider the relationship between stress and mood as mediated by coping. Presumably, the direct effect is negative: more stress, the worse the mood. However, likely the effect of stress on coping is positive (more stress, more coping) and the effect of coping on mood is positive (more coping, better mood), making the indirect effect positive. The total effect of stress on mood then is likely to be very small because the direct and indirect effects will tend to cancel each other out. Note that with inconsistent mediation, the direct effect is typically larger than the total effect.

It is therefore much more common and highly recommended to perform a single test of ab, than the two seperate tests of a and b. The test was first proposed by Sobel (1982) and thus is also called the Sobel test. The standard error estimate of $\hat{a}$ is denoted as $s_{\hat{a}}$ and the standard error estimate of $\hat{b}$ is denoted as $s_{\hat{b}}$. The Sobel test used the following standard error estimate of $\hat{ab}$

$$\sqrt{\hat{b}^2 s_{\hat{a}}^2 + \hat{a}^2 s_{\hat{b}}^2}.$$

The test of the indirect effect is given by dividing $\hat{ab}$ by the above standard error estimate and treating the ratio as a Z test:

$$z - score = \frac{\hat{ab}}{\sqrt{\hat{b}^2 s_{\hat{a}}^2 + \hat{a}^2 s_{\hat{b}}^2}}.$$

If a z-score is larger than 1.96 in absolute value, the mediation effect is significant at the .05 level.

From the example in the 4-step method, the mediation effect is $\widehat{ab}$=0.065 and its standard error is

$$\sqrt{\hat{b}^2 s_{\hat{a}}^2 + \hat{a}^2 s_{\hat{b}}^2} = \sqrt{.4645^2 * .043^2 + .139^2 * .1434^2} = .028.$$

Thus,

$$z - score = \frac{.065}{.028} = 2.32.$$

Because the z-score is greater than 1.96, the mediation effect is significant at the alpha level 0.05. Actually, the p-value is 0.02.

The Sobel test is easy to conduct but has many disadvantages. The derivation of the Sobel standard error estimate presumes that $\hat{a}$ and $\hat{b}$ are independent, something that may not be true. Furthermore, the Sobel test assumes $\widehat{ab}$ is normally distributed and might not work well for small sample sizes. The Sobel test has also been shown to be very conservative and thus the power of the test is low. One solution is to use the bootstrap method.

12.4.4 Bootstrapping for mediation analysis

The bootstrap method was first employed in the mediation analysis by Bollen and Stine (1990). This method has no distribution assumption on the indirect effect $\widehat{ab}$. Instead, it approximates the distribution of $\widehat{ab}$ using its bootstrap distribution. The bootstrap method was shown to be more appropriate for studies with sample sizes 20-80 than single sample methods. Currently, the bootstrap method of mediation is generally following the procedure used in Bollen and Stine (1990).

The method works in the following way. Using the original data set (Sample size = n) as the population, draw a bootstrap sample of n individuals with paired (Y, X, M) scores randomly from the data set with replacement. From the bootstrap sample, estimate ab through some method such as OLS based on a set of regression models. Repeat the two steps for a total of B times. B is called the number of bootstraps. The empirical distribution based on this bootstrap procedure can be viewed as the distribution of $\widehat{ab}$. The $(1-\alpha) * 100\%$ confidence interval of ab can be constructed using the $\alpha/2$ and $1-\alpha/2$ percentiles of the empirical distribution.

In R, mediation analysis based on both Sobel test and bootstrapping can be conducted using the R `bmem()` package. For example, the R code for Sobel test is given below.

```
library(bmem)

m1 <- "math = b*HE + cp*ME
HE = a*ME"
```

```
nlsy.model<-specifyEquations(text=m1, exog.variances=T)

effects<-c('a*b', 'cp+a*b')
nlsy.res<-bmem.sobel(nlsy, nlsy.model,effects)
##              Estimate       S.E.   z-score      p.value
## b          0.46450283 0.14304860  3.247168 1.165596e-03
## cp         0.46281480 0.11977862  3.863918 1.115825e-04
## a          0.13925694 0.04292438  3.244239 1.177650e-03
## V[HE]      2.73092635 0.20078170 13.601471 0.000000e+00
## V[math]   20.67659134 1.52017323 13.601471 0.000000e+00
## V[ME]      4.00590078 0.29451968 13.601471 0.000000e+00
## a*b        0.06468524 0.02818457  2.295059 2.172977e-02
## cp+a*b     0.52750005 0.11978162  4.403848 1.063474e-05
```

Note that to use the package, we need to specify the mediation model first. The mediation model can be provided using equations. For the simple mediation model, there need two regression equation: `math = b*HE + cp*ME` and `HE = a*ME`. Clearly, the outcome variable is on the left of the "=" sign. In addition, we should include the parameter labels in the model. For example, `a`, `b`, and `cp` represent the parameters in the model. The function to specify the model is `specifyEquations()`, which is a function of the R package `bmem()`, which `bmem()` was developed based on. In this function, we also use the option `exog.variances=T`, which is used to specify the variance parameters automatically.

In addition to the model, we also need to provide the indirect effects or any other effects of interest. Multiple effects can be provided using a vector. Each effect is a combination of multiple model parameters. For example, `a*b` is the mediation effect and `a*b + cp` is the total effect.

Finally, the function `bmem.sobel()` is used to conduct the Sobel test. The function requires at least three options: a data set, a model, and the effects of interest, in the order presented.

The output includes the parameter estimate, standard error, z-score and p-value for each parameter and effect under investigation. Note that the mediation effect is again 0.065 and is significant at the alpha level 0.05.

Conducting a bootstrap is similar to Sobel test. In this case, the function `bmem()` is used. In addition to provide a data set, a model, and the effects of interest, we can also specify how many bootstrap samples are used (the option `boot=`). The default is 1,000. In this example, we used 500.

The output includes the 95% bootstrap CIs. Using a CI, we can conduct a test. Based on the fact that the CI for ab [.0258, .1377] does not include 0, there is a significant mediation effect. In addition, because the CI for c' does not contain 0, c' is significantly different from 0. Thus, we have a partial mediation effect.

```
m2 <- "math = b*HE + cp*ME
HE = a*ME"
```

```
nlsy.model<-specifyEquations(text=m2, exog.variances=T)

effects<-c('a*b', 'cp+a*b')
nlsy.res<-bmem(nlsy, nlsy.model,effects, boot=500)
## The bootstrap confidence intervals for parameter estimates
##            estimate    se.boot        2.5%      97.5%
## b        0.46450283 0.12927150  0.23684369  0.7513838
## cp       0.46281480 0.12202802  0.19596233  0.6819319
## a        0.13925694 0.04049624  0.05960756  0.2205426
## V[HE]    2.72356536 0.20502992  2.34827521  3.1285073
## V[math] 20.62085929 3.00168098 16.33015136 28.4972467
## V[ME]    3.99510320 0.37598374  3.38286944  4.8439352
## a*b      0.06468524 0.02532558  0.02312769  0.1258055
## cp+a*b   0.52750005 0.12417868  0.26368381  0.7482335
##
## The bootstrap confidence intervals for model fit indices
##          estimate      se.boot 2.5%       97.5%
## chisq 3.28626e-13 2.940822e-13    0 6.57252e-13
## GFI            NA           NA   NA          NA
## AGFI           NA           NA   NA          NA
## RMSEA          NA           NA   NA          NA
## NFI            NA           NA   NA          NA
## NNFI           NA           NA   NA          NA
## CFI            NA           NA   NA          NA
## BIC   3.28626e-13 2.940822e-13    0 6.57252e-13
## SRMR           NA           NA   NA          NA
##
## The literature has suggested the use of Bollen-Stine bootstrap for model fit. To do s
```

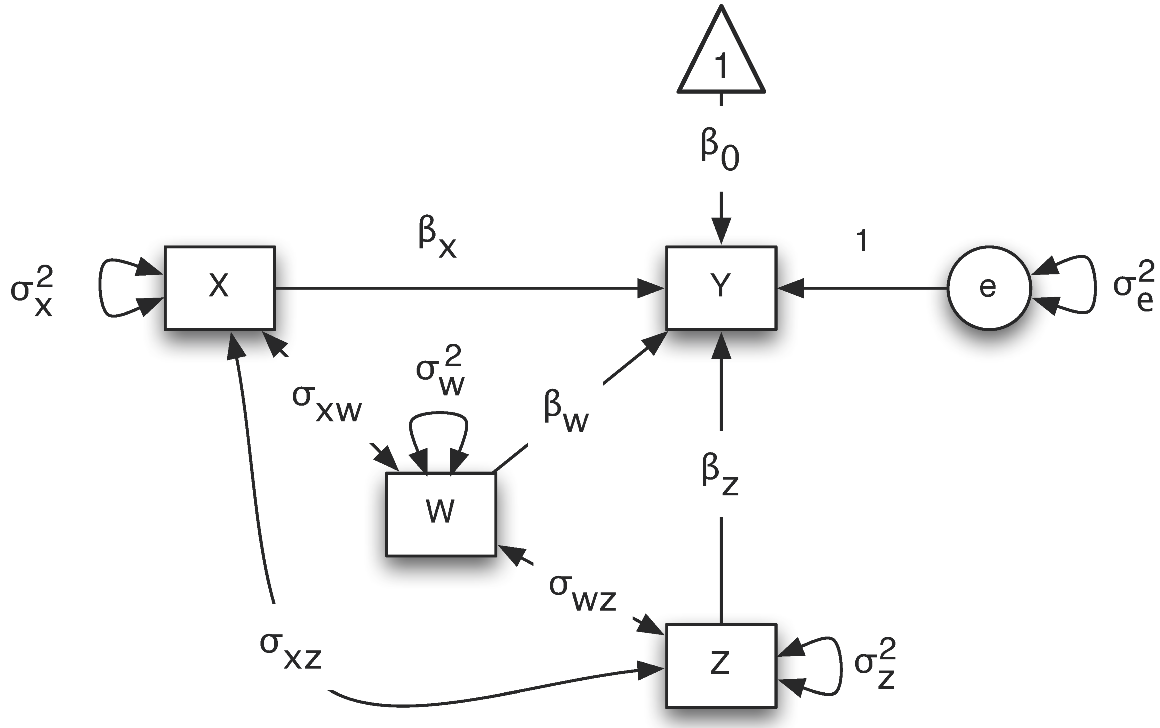
Chapter 13

Path Analysis

Path analysis is a type of statistical method to investigate the direct and indirect relationship among a set of exogenous (independent, predictor, input) and endogenous (dependent, output) variables. Path analysis can be viewed as generalization of regression and mediation analysis where multiple input, mediators, and output can be used. The purpose of path analysis is to study relationships among a set of observed variables, e.g., estimate and test direct and indirect effects in a system of regression equations and estimate and test theories about the absence of relationships

13.1 Path diagrams

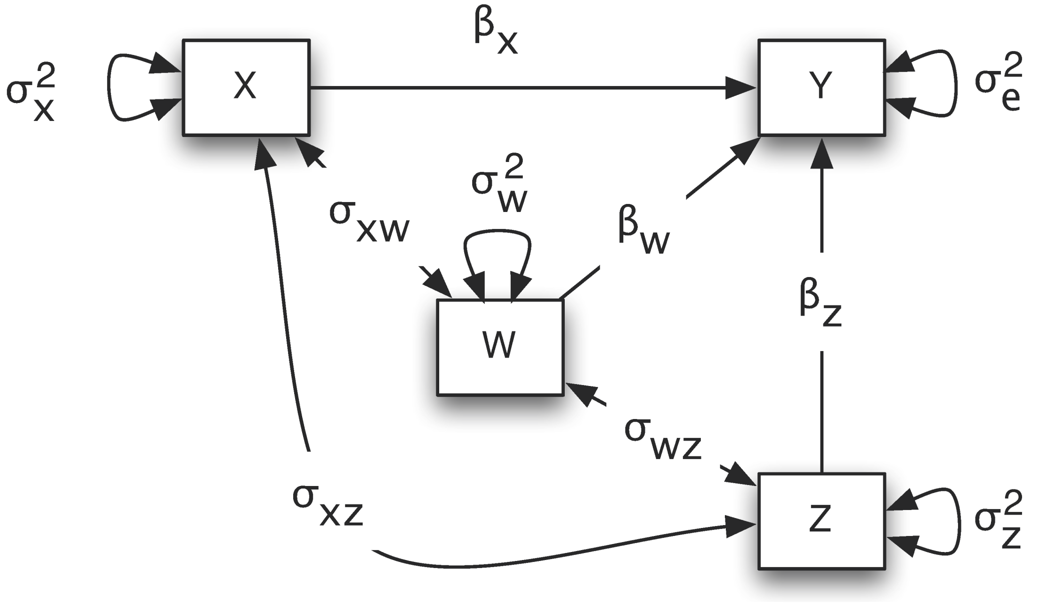
Path analysis is often conducted based on path diagrams. Path diagram represents a model using shapes and paths. For example, the diagram below portrays the multiple regression model $Y = \beta_0 + \beta_X X + \beta_W W + \beta_Z Z + e$.



In a path diagram, different shapes and paths have different meanings:

- Squares or rectangular boxes: observed or manifest variables
- Circles or ovals: errors, factors, latent variables
- Single-headed arrows: linear relationship between two variables. Starts from an independent variable and ends on a dependent variable.
- Double-headed arrows: variance of a variable or covariance between two variables
- Triangle: a constant variable, usually a vector of ones

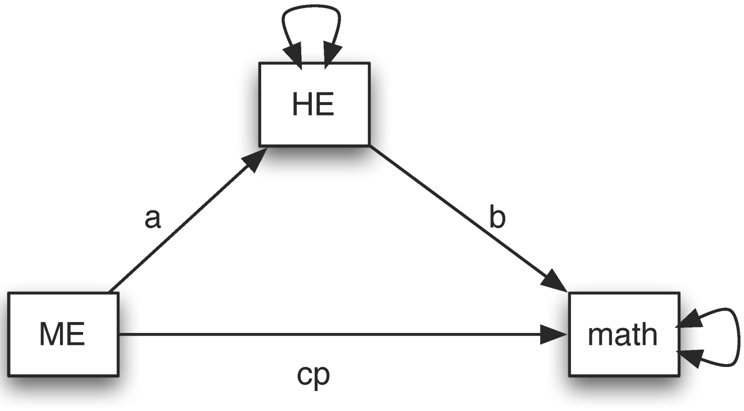
A simplified path diagram is often used in practice in which the intercept term is removed and the residual variances are directly put on the outcome variables. For example, for the regression example, the path diagram is shown below.



In R, path analysis can be conducted using R package `lavaan`. We now show how to conduct path analysis using several examples.

13.2 Example 1. Mediation analysis – Test the direct and indirect effects

The NLSY data include three variables €“ mother's education (ME), home environment (HE), and child's math score. Assume we want to test whether home environment is a mediator between mother€™s education and child's math score. The path diagram for the mediation model is:



To estimate the paths in the model, we use the R package `lavaan`. To specify the mediation model, we follow the rules below. First, a model is put into a pair of quotation marks. Second, to specify the regression relationship, we use a symbol `~`. The variable on the left is the outcome and the ones on the right are predictors or covariates. Third, parameter names can be used for paths in model specification such as a, b and cp. Fourth, we can define new parameters using the notation :=. On the left is the name of the new parameter and on the right is the formula to define the new parameter such as a*b that defines the mediation effect and a*b + cp that defines the total effect.

To estimate the model, the sem() function from lavaan can be used. To view the results, the summary() function is used. For example, for the mediation example, the output is given below. From the output, we can see

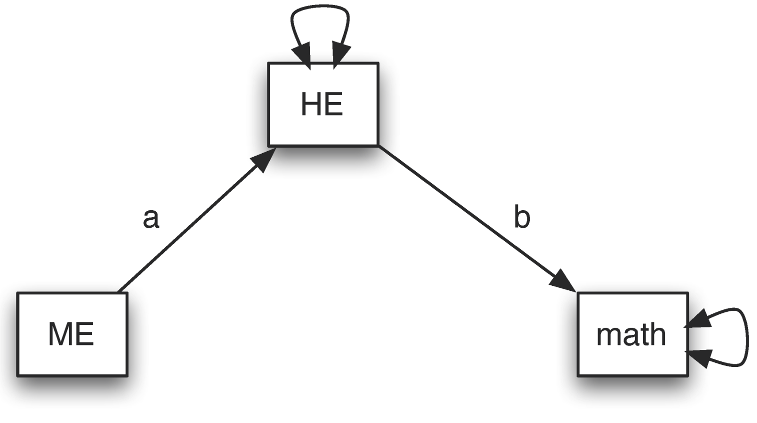
```
detach(package:bmem)
detach(package:sem)
```

```
library(lavaan)

nlsy <- read.table("data/nlsy.med.comp.txt", header=TRUE)

mediation<-'
math ~ b*HE + cp*ME
HE ~ a*ME
ab := a*b
total := a*b + cp
'

mediation.res<-sem(mediation, data=nlsy)
summary(mediation.res)
## lavaan 0.6-3 ended normally after 21 iterations
##
##   Optimization method                           NLMINB
##   Number of free parameters                          5
##
##   Number of observations                           371
##
##   Estimator                                         ML
##   Model Fit Test Statistic                       0.000
##   Degrees of freedom                                 0
##   Minimum Function Value               0.0000000000000
##
## Parameter Estimates:
##
##   Information                                 Expected
##   Information saturated (h1) model          Structured
##   Standard Errors                             Standard
##
## Regressions:
##                    Estimate  Std.Err  z-value  P(>|z|)
##   math ~
##     HE         (b)    0.465    0.143    3.252    0.001
##     ME        (cp)    0.463    0.120    3.869    0.000
##   HE ~
##     ME         (a)    0.139    0.043    3.249    0.001
##
## Variances:
##                    Estimate  Std.Err  z-value  P(>|z|)
##    .math             20.621    1.514   13.620    0.000
##    .HE                2.724    0.200   13.620    0.000
##
## Defined Parameters:
##                    Estimate  Std.Err  z-value  P(>|z|)
##     ab                0.065    0.028    2.298    0.022
##     total             0.528    0.120    4.410    0.000
```

- An individual path can be tested. For example, the coefficient from ME to HE is 0.139, which is significant based on the z-test.
- The residual variance parameters are also automatically estimated.
- The mediation effect is estimated and tested using the defined parameter. For example, the mediation effect here is 0.065 with the standard error 0.028. It is significant based on a z-test (Sobel test). Note that the result is the same as the mediation analysis before.

13.3 Example 2. Testing a theory of no direct effect

Assume we hypothesize that there is no direct effect from ME to math. To test the hypothesis, we can fit a model illustrated below.

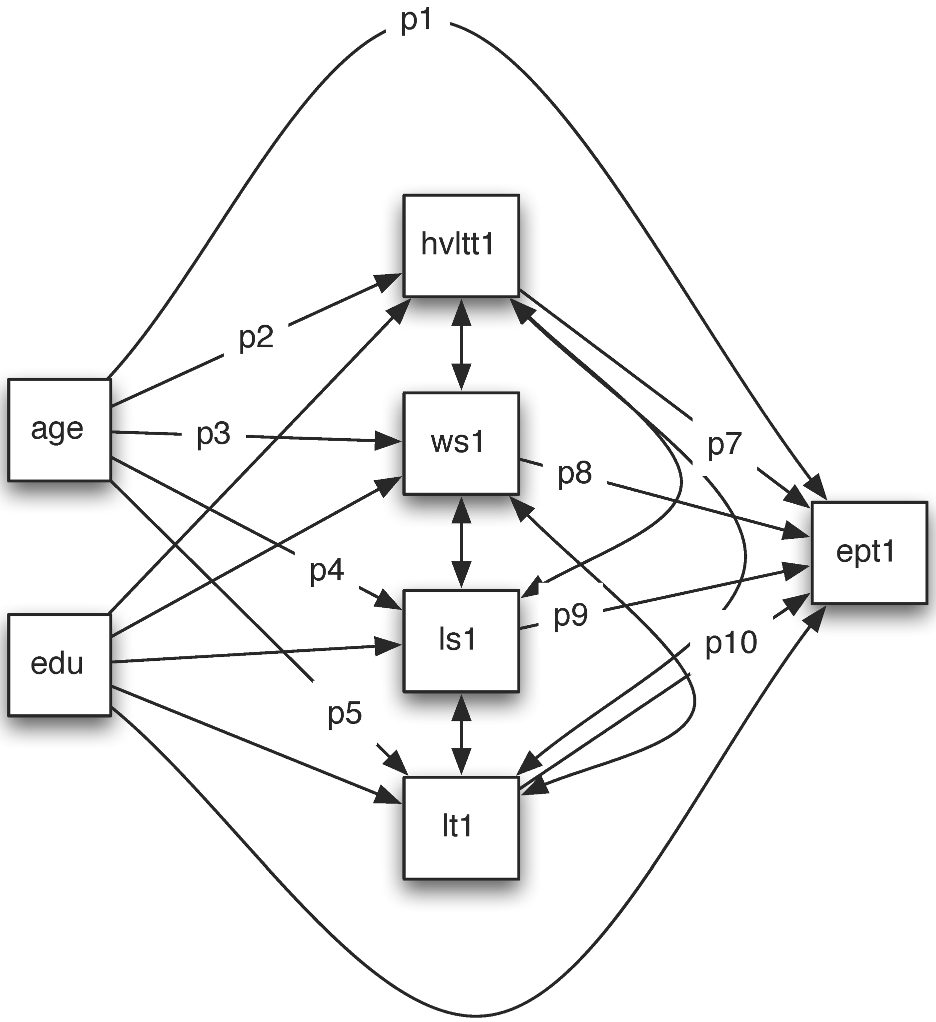


The input and output of the analysis are given below. To evaluate the hypothesis, we can check the model fit. The null hypothesis is €œH_0: The model fits the data well or the model is supported. The alternative hypothesis is €œH_1: The model does not fit the data or the model is rejected. The model with the direct effect fits the data perfectly. Therefore, if the current model also fits the data well, we fail to reject the null hypothesis. Otherwise, we reject it. The test of the model can be conducted based on a chi-squared test. From the output, the Chi-square is 14.676 with 1 degree of freedom. The p-value is about 0. Therefore, the null hypothesis is rejected. This indicates that the model without direct effect is not a good model.

```
model2<-'
math ~ b*HE
HE ~ a*ME
'

model2.res<-sem(model2, data=nlsy)
summary(model2.res)
## lavaan 0.6-3 ended normally after 17 iterations
##
##   Optimization method                           NLMINB
##   Number of free parameters                          4
##
##   Number of observations                           371
##
##   Estimator                                         ML
##   Model Fit Test Statistic                      14.676
##   Degrees of freedom                                 1
##   P-value (Chi-square)                           0.000
##
## Parameter Estimates:
##
##   Information                                 Expected
##   Information saturated (h1) model          Structured
##   Standard Errors                             Standard
##
## Regressions:
##                    Estimate  Std.Err  z-value  P(>|z|)
##   math ~
##     HE         (b)    0.556    0.144    3.873    0.000
##   HE ~
##     ME         (a)    0.139    0.043    3.249    0.001
##
## Variances:
##                    Estimate  Std.Err  z-value  P(>|z|)
##    .math             21.453    1.575   13.620    0.000
##    .HE                2.724    0.200   13.620    0.000
```

13.4 Example 3: A more complex path model

Path analysis can be used to test more complex theories. In this example, we look at how age and education influence EPT using the ACTIVE data. Both age and education may influence EPT directly or through memory and reasoning ability. Therefore, we can fit a model shown below.



Suppose we want to test the total effect of `age` on `EPT` and its indirect effect. The direct effect is the path from `age` to `ept1` directly, denoted by `p1`. One indirect path goes through `hvltt1`, that is `p2*p7`. The second indirect effect through `ws1` is `p3*p8`. The third indirect effect through `ls1` is `p4*p9`. The last indirect effect through `lt1` is `p5*p10`. The total indirect effect is `p2*p7+p3*p8+p4*p9+p5*p10`. The total effect is the sum of them `p1+p2*p7+p3*p8+p4*p9+p5*p10`.

The output from such a model is given below. From it, we can see that the indirect effect `ind1=p2*p7` is significant. The total indirect (`indirect`) from age to EPT is also significant. Finally, the total effect (`total`) from age to EPT is significant.

```
library(lavaan)
active.full<-read.table('data/active.full.r.txt', header=T)

active.model<-'
hvltt1 ~ p1*age + edu
ws1 ~ p2*age + edu
ls1 ~ p3*age + edu
lt1 ~ p4*age + edu
ept1 ~ p5*age + p6*edu + p7*hvltt1 + p8*ws1 + p9*ls1 + p10*lt1
ws1~~ls1
ws1~~lt1
ls1~~lt1
hvltt1~~ls1
hvltt1~~ws1
hvltt1~~lt1
ind1 := p1*p7
total := p5 + p1*p7 + p2*p8 + p3*p9 + p4*p10
indirect := p1*p7 + p2*p8 + p3*p9 + p4*p10
'

active.res<-sem(active.model, data=active.full)
summary(active.res)
## lavaan 0.6-3 ended normally after 79 iterations
##
##   Optimization method                           NLMINB
##   Number of free parameters                         25
##
##   Number of observations                          1114
##
##   Estimator                                         ML
##   Model Fit Test Statistic                       0.000
##   Degrees of freedom                                 0
##
## Parameter Estimates:
##
##   Information                                 Expected
##   Information saturated (h1) model          Structured
##   Standard Errors                             Standard
##
## Regressions:
##                    Estimate  Std.Err  z-value  P(>|z|)
##   hvltt1 ~
##     age       (p1)   -0.161    0.027   -6.074    0.000
##     edu               0.429    0.052    8.177    0.000
##   ws1 ~
##     age        (p2)   -0.226    0.026   -8.737    0.000
##     edu                0.704    0.051   13.772    0.000
##   ls1 ~
##     age        (p3)   -0.276    0.029   -9.658    0.000
##     edu                0.877    0.057   15.486    0.000
##   lt1 ~
##     age        (p4)   -0.085    0.015   -5.894    0.000
##     edu                0.394    0.029   13.723    0.000
##   ept1 ~
##     age        (p5)    0.014    0.021    0.644    0.519
##     edu        (p6)    0.448    0.045    9.913    0.000
##     hvltt1     (p7)    0.202    0.025    8.045    0.000
##     ws1        (p8)    0.196    0.038    5.179    0.000
##     ls1        (p9)    0.246    0.035    7.090    0.000
##     lt1       (p10)    0.151    0.051    2.953    0.003
##
## Covariances:
##                     Estimate  Std.Err  z-value  P(>|z|)
##  .ws1 ~~
##    .ls1               16.606    0.819   20.287    0.000
##    .lt1                5.714    0.371   15.390    0.000
##  .ls1 ~~
##    .lt1                6.573    0.415   15.852    0.000
##  .hvltt1 ~~
##    .ls1                8.444    0.713   11.838    0.000
##    .ws1                7.572    0.643   11.769    0.000
##    .lt1                2.856    0.349    8.191    0.000
##
## Variances:
##                     Estimate  Std.Err  z-value  P(>|z|)
##    .hvltt1            20.618    0.874   23.601    0.000
##    .ws1               19.588    0.830   23.601    0.000
##    .ls1               24.030    1.018   23.601    0.000
##    .lt1                6.174    0.262   23.601    0.000
##    .ept1              12.177    0.516   23.601    0.000
##
## Defined Parameters:
##                     Estimate  Std.Err  z-value  P(>|z|)
##     ind1              -0.033    0.007   -4.847    0.000
##     total             -0.144    0.026   -5.594    0.000
##     indirect          -0.158    0.017   -9.340    0.000
```

Chapter 14

Factor Analysis

14.1 Measurement Error and Factor Analysis

14.1.1 Measurement error

Suppose we want to measure reasoning ability. For participant i, the true reasoning ability score is T_i and the observed score is y_i. If there is no measurement error, we would expect that

$$y_i = T_i.$$

However, often times, we can not perfectly measure something like reasoning ability because of measurement error. With measurement error, the above equation becomes

$$y_i = T_i + e_i.$$

where e_i is the difference between the observed value and its true score in reasoning ability for participant i. Measurement error is almost always present in a measurement. It is caused by unpredictable fluctuations in the the data collection. It can show up as different results for the same repeated measurement.

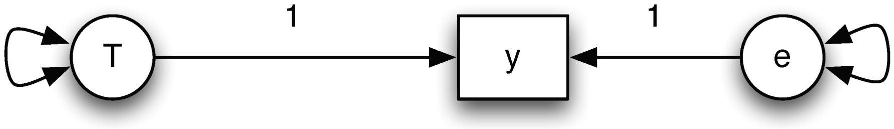
It is often assumed that the mean of e_i is equal to 0. We need to estimate the variance of e_i. Note that we ignore the systematic errors here. The measurement error discussed here is purely random error.

We can express the measurement error using a path diagram shown below. Both the true score and the measurement error are unobserved. The only quantity that is available is the observed score y. From the relationship, we can easily see that

$$Var(y) = Var(T) + Var(e).$$

That is the observed variance is equal to the sum of the true score variance and the measurement error variance. Note that reliability is define as

$$reliability = \frac{Var(T)}{Var(T) + Var(e)}.$$

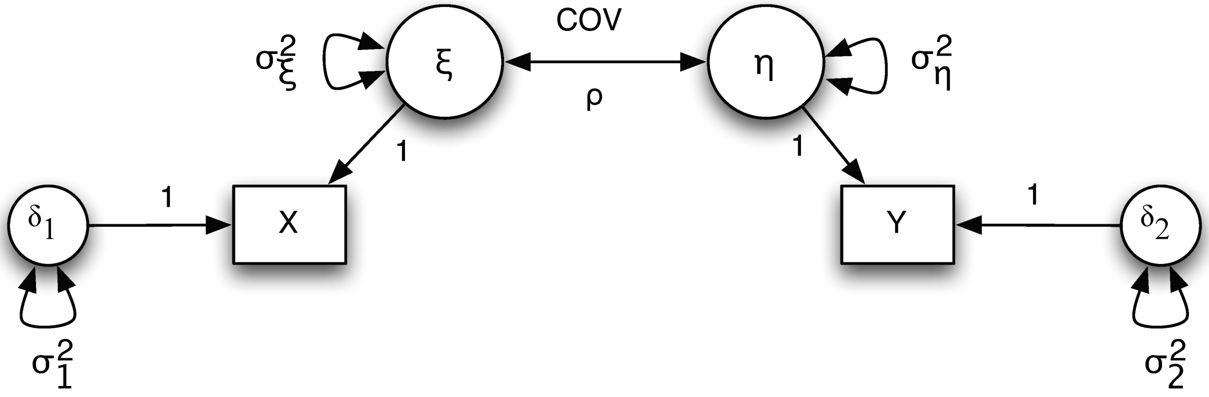


Measurement error can be estimated by comparing multiple measurements, and reduced by averaging multiple measurements.

14.1.2 Influences of measurement error

The most well known influence of measurement error is the attenuation of a relationship. For example, it can lead to reduced correlation between two variables if the two variables are observed with measurement error. In terms of regression analysis, it results in attenuated regression slope estimates, which is also known as regression dilution.

We can illustrate this through an example on correlation. The path diagram for the example is given below.



Note that from the diagram, we have

$$X = \xi + \delta_1 \text{ and } Y = \eta + \delta_2.$$

The variances for the true score ξ and η are σ_ξ^2 and σ_η^2, respectively. The variances for the measurement error δ_1 and δ_2 are σ_1^2 and σ_2^2, respectively. The covariance between ξ and η is $\sigma_{\xi\eta}$

The correlation between the true scores is

$$\rho_{\xi\eta} = \frac{COV(\xi, \eta)}{\sigma_\xi \sigma_\eta} = \frac{\sigma_{\xi\eta}}{\sigma_\xi \sigma_\eta}$$

and the correlation between the observed scores is

$$\rho_{XY} = \frac{COV(X, Y)}{\sqrt{VAR(X)VAR(Y)}} = \frac{\sigma_{\xi\eta}}{\sqrt{(\sigma_\xi^2 + \sigma_1^2)(\sigma_\eta^2 + \sigma_2^2)}}.$$

Clearly, $\rho_{xy} < \rho_{\xi\eta}$.

14.1.3 How to deal with measurement error?

If we know the variance of measurement errors, we can correct the influences by including measurement errors in a model. With only a single indicator for the latent variable T (the true score variable), we cannot estimate the variance of measurement errors. For example, for the measurement error model, we have one pieces of information €“ the variance of y. However, we need to estimate the variance of T and the variance of e. Thus, we are short of information. If we have multiple indicators of T, we can estimate the measurement error variance and the variance of T. This leads to factor models.

14.1.4 Factor analysis

Factor analysis is a statistical method for studying the dimensionality of a set of variables/indicators. Factor analysis examines how underlying constructs influence the responses on a number of measured variables/indicators. It can effectively handle/model measurement errors. There are basically two types of factor analysis: Exploratory Factor Analysis (EFA) and Confirmatory Factor Analysis (CFA).

- Exploratory factor analysis (EFA) attempts to discover the nature of the constructs influencing a set of responses. It can be used to explore the dimensionality of a measurement instrument by finding the smallest number of interpretable factors needed to explain the correlations among a set of variables.
- Confirmatory factor analysis (CFA) tests whether a specified set of constructs is influencing responses in a predicted way. It can be used to study how well a hypothesized factor model fits a new sample from the same population or a sample from a different population.

A typical factor analysis model expresses a set of observed variables $y_j (j = 1, \ldots, p)$ as a function of factors $f_k (k = 1, \ldots, m)$ and residuals/measurement errors/unique factors $e_j (j = 1, \ldots, p)$. Specifically, we have

$$y_{i1} = \lambda_{11} f_{i1} + \lambda_{12} f_{i2} + \ldots + \lambda_{1m} f_{m1} + e_{i1} \tag{14.1}$$

$$\ldots \tag{14.2}$$

$$y_{ij} = \lambda_{j1} f_{i1} + \lambda_{j2} f_{i2} + \ldots + \lambda_{jm} f_{ij} + e_{ij} \tag{14.3}$$

$$\ldots \tag{14.4}$$

$$y_{ip} = \lambda_{p1} f_{i1} + \lambda_{p2} f_{i2} + \ldots + \lambda_{pm} f_{im} + e_{im} \tag{14.5}$$

where λ_{jk} is a factor loading (regression coefficient of f_k on y_j) and f_{ik} is the factor score for Person i on the kth factor.

In a factor model, each observed variable (indicator y_1 through indicator y_p) is influenced by both the underlying common factors f (factor 1 through factor m), and the underlying unique factors e (error 1 through error p). The strength of the link between each factor and each indicator, measured by the factor loading, varies, such that a given factor influences some indicators more than others. Factor analyses can be performed by examining the pattern of correlations (or covariances) among the observed variables. Measures that are highly correlated (either positively or negatively) are likely influenced by the same factors, while those that are relatively uncorrelated are likely influenced by different factors.

14.2 Exploratory Factor Analysis

The primary objectives of an exploratory factor analysis (EFA) are to determine (1) the number of common factors influencing a set of measures, (2) the strength of the relationship between each factor and each observed measure and (3) the factor scores

Some common uses of EFA are to

- To reduce a large number of variables to a smaller number of factors for modeling purposes, where the large number of variables precludes modeling all the measures individually.
- To establish that multiple tests measure the same factor, thereby giving justification for administering fewer tests. Factor analysis originated a century ago with Charles Spearman's attempts to show that a wide variety of mental tests could be explained by a single underlying intelligence factor
- To validate a scale or index by demonstrating that its constituent items load on the same factor, and to drop proposed scale items which cross-load on more than one factor.
- To select a subset of variables from a larger set, based on which original variables have the highest correlations with the principal component factors.
- To create a set of factors to be treated as uncorrelated variables as one approach to handling multicollinearity in such procedures as multiple regression.
- To identify the nature of the constructs underlying responses in a specific content area.
- To determine what sets of items €œhang together in a questionnaire.

- To demonstrate the dimensionality of a measurement scale. Researchers often wish to develop scales that respond to a single characteristic.
- To determine what features are most important when classifying a group of items.
- To generate factor scores representing values of the underlying constructs for use in other analyses.

14.2.1 An example

We illustrate how to conduct exploratory data analysis using the data from the classic 1939 study by Karl J. Holzinger and Frances Swineford. In the study, twenty-six tests intended to measure a general factor and five specific factors were administered to seventh and eighth grade students in two schools, the Grant-White School ($n = 145$) and Pasteur School ($n = 156$). Data used in this example include nineteen tests intended to measure four domains: spatial ability, verbal ability, speed, and memory. In addition, only data from the 145 students in the Grant-White School are used.

The data are saved in the file `GrantWhite.csv`. The 26 tests are described below with the 19 used in the example are highlighted.

```
GrantWhite <- read.table('data/holzing.txt', header=T)

head(GrantWhite)
##    id female grade agey agem school visual cubes paper lozenge general paragrap
## 1 201      0     7   13    0      0     23    19    13       4      46       10
## 2 202      1     7   11   10      0     33    22    12      17      43        8
## 3 203      0     7   12    6      0     34    24    14      22      36       11
## 4 204      0     7   11   11      0     29    23    12       9      38        9
## 5 205      0     7   12    5      0     16    25    11      10      51        8
## 6 206      1     7   12    6      0     30    25    12      20      42       10
##   sentence wordc wordm add code counting straight wordr numberr figurer object
## 1       17    22    10  69   65       82      156   173      91      96      8
## 2       17    30    10  65   60       98      195   174      81     106      9
## 3       19    27    19  50   49       86      228   168      84     101      1
## 4       19    25    11 114   59      103      144   130      84     101     10
## 5       25    28    24 112   54      122      160   184      98      99      9
## 6       23    28    18  94   84      113      201   188      86     116     10
##   numberf figurew deduct numeric problemr series arithmet paperrev flagssub
## 1       2      10     21      12       17     11       17       13       25
## 2      15      17     33      12       22     31       32       20       37
## 3       7      16     45      10       43     21       18       19       40
## 4      15      14     25      21       26     19       28       11       44
## 5       9      15     28      16       35     21       25       10       28
## 6      10      16     36      14       27     18       30       16       42
```

visual

scores on visual perception test, test 1

cubes

scores on cubes test, test 2

paper

scores on paper form board test, test 3

lozenge

scores on lozenges test, test 4

general

scores on general information test, test 5

paragrap

scores on paragraph comprehension test, test 6

sentence

scores on sentence completion test, test 7

wordc

scores on word classification test, test 8

wordm

scores on word meaning test, test 9

add

scores on add test, test 10

code

scores on code test, test 11

counting

scores on counting groups of dots test, test 12

straight

scores on straight and curved capitals test, test 13

wordr

scores on word recognition test, test 14

numberr

scores on number recognition test, test 15

figurer

scores on figure recognition test, test 16

object

scores on object-number test, test 17

numberf

scores on number-figure test, test 18

figurew

scores on figure-word test, test 19

deduct

scores on deduction test, test 20

numeric

scores on numerical puzzles test, test 21

problemr

scores on problem reasoning test, test 22

series

scores on series completion test, test 23

arithmet

scores on Woody-McCall mixed fundamentals, form I test, test 24

paperrev

scores on additional paper form board test, test 25

flagssub

scores on flags test, test 26

14.2.2 Exploratory factor analysis

The usual exploratory factor analysis involves (1) Preparing data, (2) Determining the number of factors, (3) Estimation of the model, (4) Factor rotation, (5) Factor score estimation and (6) Interpretation of the analysis.

14.2.2.1 Preparing data

In EFA, a correlation matrix is analyzed. The following R code calculates the correlation matrix.

```
fa.var<-c('visual', 'cubes', 'paper', 'lozenge',
'general', 'paragrap', 'sentence', 'wordc',
'wordm', 'add', 'code', 'counting', 'straight',
'wordr', 'numberr', 'figurer', 'object', 'numberf',
'figurew')

fadata<-GrantWhite[,fa.var]
## correlation matrix
fa.cor<-cor(fadata)
## part of the correlation matrix
round(fa.cor[1:5,1:5],3)
##         visual cubes paper lozenge general
## visual   1.000 0.326 0.372   0.449   0.328
## cubes    0.326 1.000 0.190   0.417   0.275
## paper    0.372 0.190 1.000   0.366   0.309
## lozenge  0.449 0.417 0.366   1.000   0.381
## general  0.328 0.275 0.309   0.381   1.000
```

14.2.2.2 Determining the number of factors

With the correlation matrix, we first decide the number of factors. There are several ways to do it. But all the methods are based on the eigenvalues of the correlation matrix. From R, we have the eigenvalues below. First, note the number of eigenvalues is the same as the number of variables. Second, the sum of all the eigenvalues is equal to the number of variables.

```
fa.eigen <- eigen(fa.cor)
fa.eigen$values
##  [1] 6.3041871 1.9473919 1.5265417 1.4877579 0.9398040 0.8747401 0.7639373
##  [8] 0.6559871 0.6508332 0.5719815 0.5481270 0.4640505 0.4371337 0.4070784
## [15] 0.3655828 0.3201049 0.3064701 0.2312029 0.1970878

sum(fa.eigen$values)
## [1] 19
cumsum(fa.eigen$values)
##  [1]  6.304187  8.251579  9.778121 11.265879 12.205683 13.080423 13.844360
##  [8] 14.500347 15.151180 15.723162 16.271289 16.735339 17.172473 17.579552
## [15] 17.945134 18.265239 18.571709 18.802912 19.000000
cumsum(fa.eigen$values)/19
##  [1] 0.3317993 0.4342936 0.5146379 0.5929410 0.6424043 0.6884433 0.7286505
##  [8] 0.7631762 0.7974305 0.8275348 0.8563836 0.8808073 0.9038144 0.9252396
## [15] 0.9444808 0.9613284 0.9774584 0.9896270 1.0000000
```

The basic idea can be related to the variance explained as in regression analysis. With the correlation matrix, we can take the variance of each variable as 1. For a total of p variables, the total variance is therefore p. For factor analysis, we try to find a small number of factors that can explain a large portion of the total variance. The eigenvalues correspond to the variance of each factor. If the eigenvalue corresponding to a factor is large, that means the variance explained by the factor is large. Therefore, the eigenvalues can be used to select the number of factors.

14.2.2.2.1 Rule 1

The first rule to decide the number of factors is to use the number of eigenvalues larger than 1. In this example, we have four eigenvalues larger than 1. Therefore, we can have 4 factors.

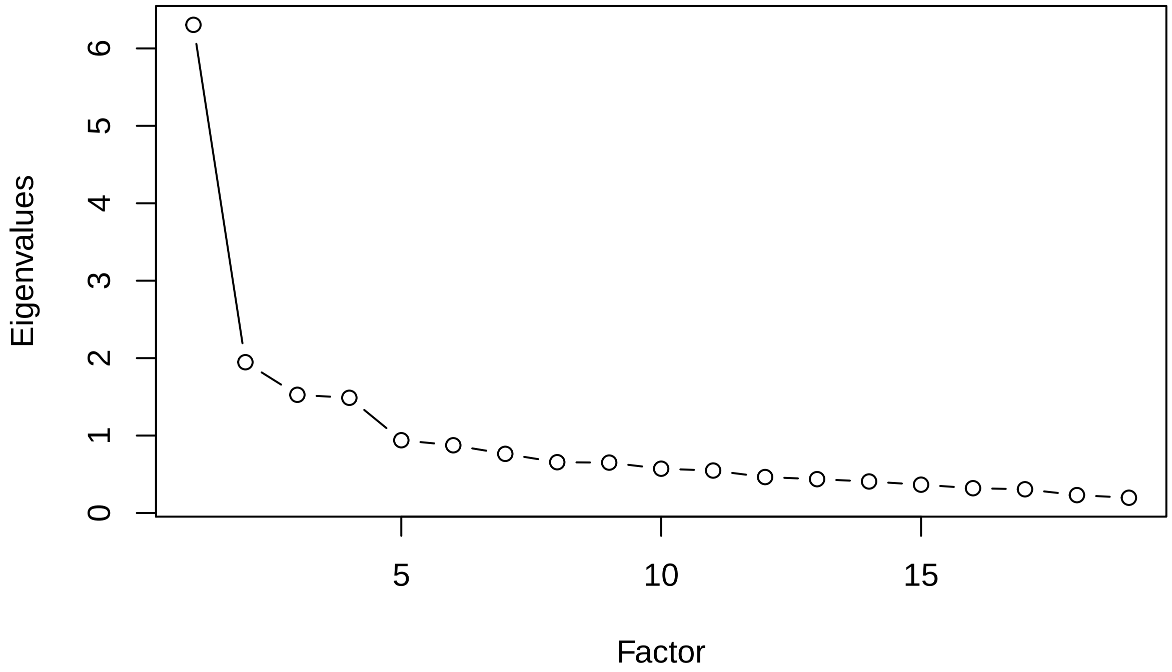
14.2.2.2.2 Rule 2

Another way is to select the number of factors with the cumulative eigenvalues accounting for 80% of the total variance. This is to say if we add the eigenvalues of the selected number of factor, the total values should be larger than 80% of the sum of all eigenvalues.

14.2.2.2.3 Cattell's Scree plot

The Cattell's Scree plot is a plot of eigenvalues on the Y axis along with the number of factors on the X axis. The plot looks like the side of a mountain, and "scree" refers to the debris fallen from a mountain and lying at its base. As one moves to the right, toward later components/factors, the eigenvalues drop. When the drop ceases and the curve makes an elbow toward less steep decline, Cattell's scree test says to drop all further components/factors after the one starting the elbow. For this example, we can identify 4 factors based on the scree plot below.

```r
plot(fa.eigen$values, type='b', ylab='Eigenvalues', xlab='Factor')
```



14.2.2.3 Estimation of model / Factor analysis

Once the number of factors is decided, we can conduct exploratory factor analysis using the R function `factanal()`. The R input and output for this example is given below.

```
fa.res<-factanal(x=fadata, factors=4, rotation='none')
fa.res
##
## Call:
## factanal(x = fadata, factors = 4, rotation = "none")
##
## Uniquenesses:
##   visual    cubes    paper  lozenge  general paragrap sentence    wordc
##    0.465    0.742    0.712    0.549    0.344    0.306    0.287    0.493
##    wordm      add     code counting straight    wordr  numberr  figurer
##    0.270    0.360    0.553    0.377    0.411    0.684    0.710    0.560
##   object  numberf  figurew
##    0.470    0.573    0.777
##
## Loadings:
##          Factor1 Factor2 Factor3 Factor4
## visual    0.536   0.176   0.392  -0.249
## cubes     0.330           0.302  -0.228
## paper     0.440   0.110   0.247  -0.147
## lozenge   0.505           0.358  -0.253
## general   0.762  -0.238  -0.113
## paragrap  0.759  -0.338
## sentence  0.762  -0.322  -0.166
## wordc     0.701
## wordm     0.762  -0.381
## add       0.455   0.475  -0.451
## code      0.545   0.367           0.103
## counting  0.434   0.593  -0.238  -0.162
## straight  0.592   0.393          -0.289
## wordr     0.394           0.149   0.362
## numberr   0.352   0.139   0.219   0.315
## figurer   0.435   0.183   0.425   0.192
## object    0.445   0.241           0.522
## numberf   0.454   0.383   0.221   0.157
## figurew   0.389   0.115   0.133   0.202
##
##                Factor1 Factor2 Factor3 Factor4
## SS loadings      5.722   1.625   1.065   0.945
## Proportion Var   0.301   0.086   0.056   0.050
## Cumulative Var   0.301   0.387   0.443   0.492
##
## Test of the hypothesis that 4 factors are sufficient.
## The chi square statistic is 102.06 on 101 degrees of freedom.
## The p-value is 0.452
```

In EFA, each observed data consists of two part, the common factor part and the uniqueness part. The common factor part is based on the four factors, which are also called the common factors. The uniqueness part is also called uniqueness factor, which is specific to each observed variable.

Using the variable `visual` as an example, we have

$$visual = 0.536 \times Factor1 + 0.176 \times Factor2 + 0.392 \times Factor3 - 0.249 \times Factor4 + u_{visual}$$

Note the factor loadings are from the `Loadings` section of the output. The loadings are the regression coefficients of the latent factors on the manifest indicators or observed variables. The variance of the uniqueness is in the `Uniquenesses` section. For u_{visual}, the variance is 0.465. For the other variables, it's the same.

The other section is related to the variance explained by the factors. `SS loadings` is the sum squared loadings related to each factor. It is the overall variance explained in all the 19 variables by each factor. Therefore, the first factor explains the total of 5.722 variance, that's about `30.1%=5.722/19`. `Proportion Var` is the variances in the observed variables/indicators explained by each factor. `Cumulative Var` is the cumulative proportion of variance explained by all factors.

A test is conducted to test whether the factor model is sufficient to explain the observed data. The null hypothesis that a 4-factor model is sufficient. For this model, the chi-square statistic is 102.06 with
degrees of freedom 101. The p-value for the chi-square test is 0.452 which is larger than .05. Therefore,we fail to reject the null hypothesis that the factor model have a good fit to the data.

14.2.2.4 Factor rotation

Although we have identified 4 factors and found the 4-factor model is a good model. We cannot find a clear pattern in the factor loadings to have a deep understanding of the factors. Through factor rotation, we can make the output more understandable and is usually necessary to facilitate the interpretation of factors. The aim is to find a simple solution that each factor has a small number of large loadings and a large number of zero (or small) loadings. There are many different rotation methods such as the varimax rotation, quadtimax rotation, equimax rotation, oblique rotation, etc. The PROMAX rotation is one kind of oblique rotation and is widely used. After PROMAX rotation, the factor will be correlated.

The output of PROMAX rotation is shown below. In the output, we use `print(fa.res, cut=0.2)` to show factor loadings that are greater than 0.2. Note that after rotation, many loading are actually smaller than 0.2. The pattern of the factor loadings are much clear now. For example, the variable `visual` has a large loading 0.747 on `Factor 2` but small than 0.2 loadings on all the other three factors. In this case, we might say that the variable `visual` is mainly influenced by `Factor 2`.

Different from the variable `visual`, the variable `straight` has large loadings on both `Factor 2` and `Factor 4`. Alternatively, straight measures both factors than just a single factor.

We can also see that the primary indicators for `Factor 1` are `general`, `paragrap`, `sentence`, `wordc`, and `wordm`. And for Factor 4, the indictors include `add`, `code`, `counting`, and `straight`.

The correlation among the factors are given in the section of `Factor Correlation`. For example, the correlation between `Factor 1` and `Factor 2` is 0.368. Note that after rotation, the test of the model is the same as without rotation.

```r
fa.res<-factanal(x=fadata, factors=4, rotation='promax')
print(fa.res, cut=0.2)
##
## Call:
## factanal(x = fadata, factors = 4, rotation = "promax")
##
```

```
## Uniquenesses:
##   visual    cubes    paper  lozenge  general paragrap sentence    wordc
##    0.465    0.742    0.712    0.549    0.344    0.306    0.287    0.493
##    wordm      add     code counting straight    wordr  numberr  figurer
##    0.270    0.360    0.553    0.377    0.411    0.684    0.710    0.560
##   object  numberf  figurew
##    0.470    0.573    0.777
##
## Loadings:
##          Factor1 Factor2 Factor3 Factor4
## visual            0.747
## cubes             0.571
## paper             0.485
## lozenge           0.683
## general   0.760
## paragrap  0.806
## sentence  0.862
## wordc     0.555
## wordm     0.856
## add              -0.245           0.806
## code                      0.290   0.420
## counting                          0.773
## straight          0.489           0.484
## wordr                     0.567
## numberr                   0.544
## figurer           0.376   0.501
## object           -0.244   0.766
## numberf           0.271   0.446
## figurew                   0.381
##
##                Factor1 Factor2 Factor3 Factor4
## SS loadings      3.109   2.231   1.947   1.801
## Proportion Var   0.164   0.117   0.102   0.095
## Cumulative Var   0.164   0.281   0.384   0.478
##
## Factor Correlations:
##         Factor1 Factor2 Factor3 Factor4
## Factor1   1.000   0.368   0.517   0.457
## Factor2   0.368   1.000   0.435   0.432
## Factor3   0.517   0.435   1.000   0.545
## Factor4   0.457   0.432   0.545   1.000
##
## Test of the hypothesis that 4 factors are sufficient.
## The chi square statistic is 102.06 on 101 degrees of freedom.
## The p-value is 0.452
```

14.2.2.5 Interpret the results from EFA

Based on the rotated factor loadings, we can name the factors in the model. This can be done by identifying significant loadings. For example, the `Factor 1` is indicated by `general`, `paragrap`, `sentence`, `wordc`, and `wordm`, all of which are related to verbal perspective of cognitive ability. One way to name the factor is to call it a verbal factor. Similarly, the second is called the spatial factor, the third can be called the memory factor, and the last one can be called the speed factor.

14.2.2.6 Factor scores

Sometimes, the purpose of factor analysis is to estimate the score of each latent construct/factor for each participant. Factor scores can be used in further data analysis. In general, there are two methods for estimating factor scores: the regression method and the Bartlett method. The second method generally works better. For example, the following code obtains the Bartlett factor scores. As an example, the linear regression is also fitted.

```
fa.res<-factanal(x=fadata, factors=4,
                 rotation='promax', scores='Bartlett')
head(fa.res$scores)
##          Factor1    Factor2    Factor3    Factor4
## [1,] -0.43901139 -1.7896772 -0.7416310 -1.1652786
## [2,] -0.64032039  0.3301758  0.1765352 -0.6575473
## [3,] -0.05713828  0.8185462 -1.3589951 -1.4069599
## [4,] -0.55427892 -1.0738916 -0.7036627  0.2676821
## [5,]  0.68178108 -1.7044904  0.1877187  0.5317372
## [6,]  0.21943745  0.3296831  1.0497671  0.2068044

summary(lm(Factor2 ~ Factor1,
           data=as.data.frame(fa.res$scores)))
##
## Call:
## lm(formula = Factor2 ~ Factor1, data = as.data.frame(fa.res$scores))
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -2.6901 -0.5732  0.0375  0.6267  2.8976
##
## Coefficients:
##                Estimate Std. Error t value Pr(>|t|)
## (Intercept) -1.759e-16  8.340e-02   0.000        1
## Factor1      4.631e-01  7.975e-02   5.808 3.94e-08 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.004 on 143 degrees of freedom
## Multiple R-squared:  0.1908, Adjusted R-squared:  0.1852
## F-statistic: 33.73 on 1 and 143 DF,  p-value: 3.941e-08
```

14.3 Confirmatory Factor Analysis

Exploratory factor analysis can be used to identify common factors and factor structure among a set of observed variables / indicators. Confirmatory factor analysis (CFA) can be used to study how well a hypothesized factor model fits a new sample from the same population or a sample from a different population. The CFA model is the same as the EFA model with the exception that restrictions can be placed on factor loadings, variances, covariances, and residual variances resulting in a more parsimonious model. Using CFA, one can

- investigate if a factor model fits a new sample from the same population €“ the confirmatory aspect.
- evaluate if a factor model fits a sample from a different population €“ measurement invariance,
- study the behavior of new measurement items embedded in a previously studied measurement instrument, and
- estimate factor scores.

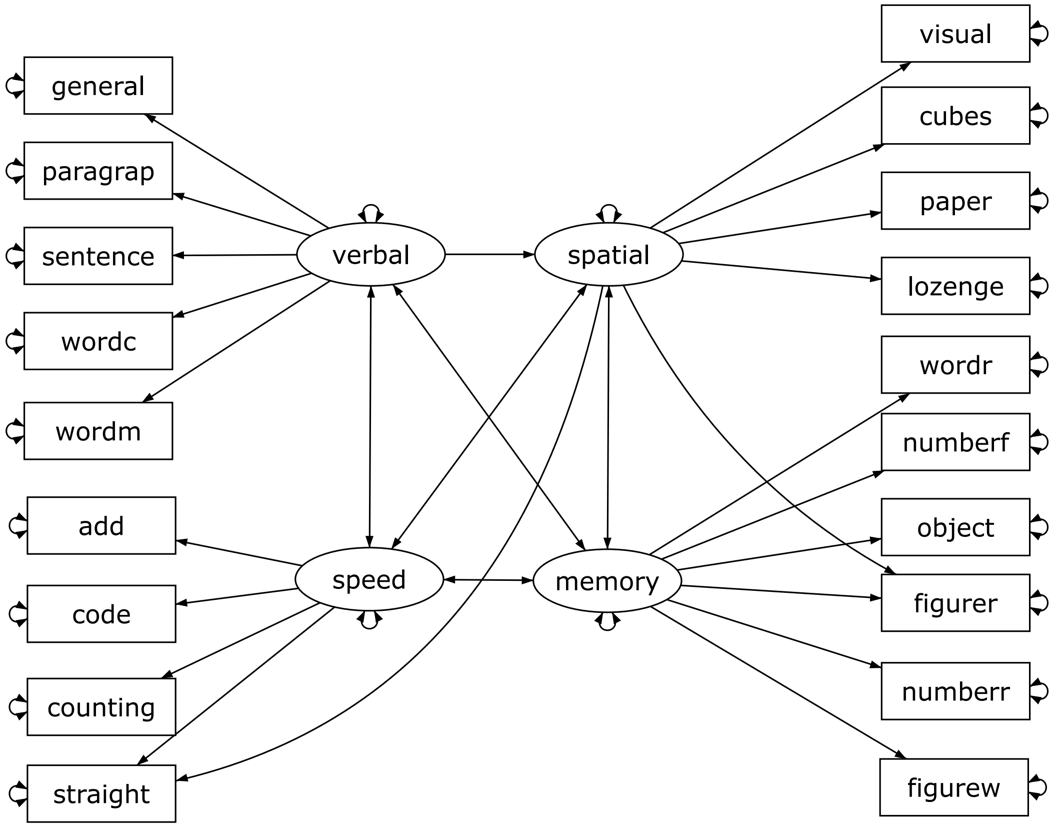
14.3.1 An example

The study by Karl J. Holzinger and Frances Swineford involves data collection from two schools, the Grant-White School ($n = 145$) and Pasteur School ($n = 156$). In the EFA example, we have identified 4 factors with data from the the Grant-White School. We now investigate whether the same factor model would fit the data in the Pasteur School. The data are saved in the file `Pasteur.csv`.

14.3.2 Confirmatory factor analysis

14.3.2.1 The model

The path diagram for the model is given in the figure below. Note that we have assumed there are 4 factors. And the indicators of each factor are also known. This model is based on the EFA of Grant-White school data with the factor loadings greater than 0.3 kept in the model.



14.3.2.2 Model estimation

To estimate a confirmatory factor model, the R package `lavaan` can used. A confirmatory factor model cannot be identified without proper constraints, that's, to fix some parameters to be known values in the model. The reason is that factors are unmeasured and thus have no scales. To identify a model, the factors have to be given specific scales. There are two ways to do this. First, we can fix the variance of a factor to be 1. This is to standardize the factor. Second, we can fix the loading of one observed variable or indicator to be one. This is essentially to make the factor to have the same scale as the observed variables. Fixing a factor loading or a factor variance is the minimum requirement to identify a factor model. However, this does not guarantee a model is identifiable. Practically, if a model cannot be identified, the software used to estimate the model will not run correctly.

The `cfa()` function in `lavaan` can be used to estimate a factor model. To use the function, we need to first specify the factor model. A factor model take the format

```
factor =~ y1 + y2 +y3
```

Note that we use the symbol "`=~`" to define a factor. The factor is on the left of the symbol and the indicators are on the right of it.

The R code for the example is given below.

```
library(lavaan)
Pasteur <- read.csv('data/Pasteur.csv')

cfa.model<-'
spatial =~ visual+cubes+paper+lozenge+straight+figurer
verbal =~ general+paragrap+sentence+wordc+wordm
speed =~ add+code+counting+straight
memory =~ wordr+numberr+figurer+object+numberf+figurew
'

cfa.est<-cfa(cfa.model, data=Pasteur)
summary(cfa.est, fit=TRUE)
## lavaan 0.6-3 ended normally after 251 iterations
##
##   Optimization method                           NLMINB
##   Number of free parameters                         46
##
##   Number of observations                           156
##
##   Estimator                                         ML
##   Model Fit Test Statistic                     238.751
##   Degrees of freedom                               144
##   P-value (Chi-square)                           0.000
##
## Model test baseline model:
##
##   Minimum Function Test Statistic             1149.278
##   Degrees of freedom                               171
##   P-value                                        0.000
##
## User model versus baseline model:
##
##   Comparative Fit Index (CFI)                    0.903
##   Tucker-Lewis Index (TLI)                       0.885
##
## Loglikelihood and Information Criteria:
##
##   Loglikelihood user model (H0)              -9899.892
##   Loglikelihood unrestricted model (H1)      -9780.517
##
##   Number of free parameters                         46
##   Akaike (AIC)                               19891.785
##   Bayesian (BIC)                             20032.078
##   Sample-size adjusted Bayesian (BIC)        19886.474
##
## Root Mean Square Error of Approximation:
##
##   RMSEA                                          0.065
##   90 Percent Confidence Interval          0.050  0.079
##   P-value RMSEA <= 0.05                          0.050
##
## Standardized Root Mean Square Residual:
##
##   SRMR                                           0.079
##
## Parameter Estimates:
##
##   Information                                 Expected
##   Information saturated (h1) model          Structured
##   Standard Errors                             Standard
##
## Latent Variables:
##                    Estimate  Std.Err  z-value  P(>|z|)
##   spatial =~
##     visual            1.000
##     cubes             0.396    0.089    4.465    0.000
##     paper             0.233    0.051    4.547    0.000
##     lozenge           1.087    0.182    5.961    0.000
##     straight          1.599    0.623    2.567    0.010
##     figurer           0.535    0.139    3.836    0.000
##   verbal =~
##     general           1.000
##     paragrap          0.282    0.024   11.846    0.000
##     sentence          0.463    0.035   13.322    0.000
##     wordc             0.388    0.038   10.177    0.000
##     wordm             0.589    0.047   12.585    0.000
##   speed =~
##     add               1.000
##     code              0.835    0.145    5.758    0.000
##     counting          0.708    0.147    4.811    0.000
##     straight          1.091    0.265    4.115    0.000
##   memory =~
##     wordr             1.000
##     numberr           0.537    0.106    5.040    0.000
##     figurer           0.486    0.106    4.570    0.000
##     object            0.379    0.070    5.372    0.000
##     numberf           0.277    0.060    4.638    0.000
##     figurew           0.245    0.055    4.444    0.000
##
## Covariances:
##                    Estimate  Std.Err  z-value  P(>|z|)
##   spatial ~~
##     verbal           21.927    5.770    3.800    0.000
##     speed            24.531    9.382    2.615    0.009
##     memory           10.542    4.998    2.109    0.035
##   verbal ~~
##     speed            66.093   17.349    3.810    0.000
##     memory           10.027    7.727    1.298    0.194
##   speed ~~
##     memory           47.001   14.950    3.144    0.002
##
## Variances:
##                    Estimate  Std.Err  z-value  P(>|z|)
##    .visual           21.376    4.533    4.716    0.000
##    .cubes            19.547    2.401    8.139    0.000
##    .paper             6.472    0.799    8.102    0.000
##    .lozenge          52.062    7.715    6.748    0.000
##    .straight        875.004  110.732    7.902    0.000
##    .figurer          40.094    5.568    7.200    0.000
##    .general          41.308    5.979    6.909    0.000
##    .paragrap          4.185    0.571    7.330    0.000
##    .sentence          6.615    1.058    6.252    0.000
##    .wordc            13.215    1.664    7.943    0.000
##    .wordm            14.218    2.063    6.892    0.000
##    .add             415.730   55.840    7.445    0.000
##    .code             75.538   19.745    3.826    0.000
##    .counting        280.324   35.795    7.831    0.000
##    .wordr            83.348   12.917    6.452    0.000
##    .numberr          43.595    5.790    7.529    0.000
##    .object           16.578    2.329    7.119    0.000
##    .numberf          15.587    1.982    7.865    0.000
##    .figurew          14.000    1.752    7.989    0.000
##     spatial          28.852    6.417    4.496    0.000
##     verbal           96.582   15.354    6.290    0.000
##     speed           200.381   59.608    3.362    0.001
##     memory           60.814   15.974    3.807    0.000
```

14.3.2.2.1 Output

By default, the `cfa()` function fixes a factor loading for each factor to be 1 and estimates the rest factor loadings. Different from EFA, CFA also test the significance of the factor loadings based on a z-test. For example, the factor loading for `cubes` on factor 1 is 0.396 with the standard error 0.089. The corresponding z-value is 4.465 with a p-value almost 0. Therefore, this factor loading is statistically significant from 0. In addition, it also estimates the factor variances and covariances as well as the uniqueness factor variances.

14.3.2.3 Model fit evaluation

CFA provides a lot more information to evaluate whether a model fits a sample. First, a chi-square test can be used. For this test, the null hypothesis is that the model fits the data well. Therefore, one would hope to get a small chi-square statistic and a corresponding large p-value. Typically, when p-value is larger than 0.5, one fails to reject the model.

There are many other fit statistics and indices that can be used to evaluate model fit. The most widely used ones include CFI, RMSEA, and SRMR.

- Comparative fit index (CFI) compares the model under evaluation with a baseline model. One form of the baseline model is the independent model where it assumes the independence among the observed variables. In general, such a baseline model would not fit the data well. Therefore, CFI measures the relative improvement of the current model. It is generally accepted that a CFI greater than 0.96 (or 0.95) indicates a good fit model.
- Root mean square error of approximation (RMSEA) is a measure of chi-square attributed to each participate after controlling the model complexity. Therefore, a smaller value indicates better fit. In the literature,
  - a RMSEA ≤ 0.05 indicates a model fits the data closely.
  - a $0.05 <$ RMSEA ≤ 0.08 indicates a model fits the data reasonably well.
  - a RMSEA > 0.1 indicates a model is a bad model.
- Standardized root mean square residual (SRMR) measures the difference between the observed covariance matrix from the data and the predicted covariance matrix based on the model. A value SRMR=0 indicates a perfect of the model. In general, a value less than 0.08 is considered a good fit of the model under evaluation.

Using these criteria, we can evaluate whether the confirmatory factor model identified using the data from Grant-White school fits the data from the Pasteur school well.

- The chi-square statistic (`Minimum Function Test Statistic` in the output) is 238.75 with the degrees of freedom 144 and a p-value close to 0. Therefore, one would reject the hypothesis that the model fits the data simply based on it.
- Comparative Fit Index (CFI) is 0.903, which is smaller than the cut-off value 0.95. It also suggests a bad fit.
- The RMSEA = 0.065, which lies the range of a reasonable fit model.
- The SRMR = 0.079, which is smaller than but close to the cut-off value 0.08.

Overall, the chi-square test and the other criteria suggest the model barely fits the data. Therefore, we cannot replicate the factor structure identified in EFA for the Grant-White school data in the Pasteur school.

14.3.2.4 Estimate the model with standardized factors

Instead of fitting a factor loading to be 1, we can also fix the factor variances to be 1. The R code below does the analysis. Note that the model fit is exactly the same as before. However, we can now directly estimate the factor correlation matrix.

```
cfa.est<-cfa(cfa.model, data=Pasteur, std.lv=TRUE)
summary(cfa.est, fit=TRUE)
## lavaan 0.6-3 ended normally after 30 iterations
##
##   Optimization method                           NLMINB
##   Number of free parameters                         46
##
##   Number of observations                           156
##
##   Estimator                                         ML
##   Model Fit Test Statistic                     238.751
##   Degrees of freedom                               144
##   P-value (Chi-square)                           0.000
##
## Model test baseline model:
##
##   Minimum Function Test Statistic             1149.278
##   Degrees of freedom                               171
##   P-value                                        0.000
##
## User model versus baseline model:
##
##   Comparative Fit Index (CFI)                    0.903
##   Tucker-Lewis Index (TLI)                       0.885
##
## Loglikelihood and Information Criteria:
##
##   Loglikelihood user model (H0)              -9899.892
##   Loglikelihood unrestricted model (H1)      -9780.517
##
##   Number of free parameters                         46
##   Akaike (AIC)                               19891.785
##   Bayesian (BIC)                             20032.078
##   Sample-size adjusted Bayesian (BIC)        19886.474
##
## Root Mean Square Error of Approximation:
##
##   RMSEA                                          0.065
##   90 Percent Confidence Interval          0.050  0.079
##   P-value RMSEA <= 0.05                          0.050
##
## Standardized Root Mean Square Residual:
##
##   SRMR                                           0.079
##
## Parameter Estimates:
##
##   Information                                 Expected
##   Information saturated (h1) model          Structured
##   Standard Errors                             Standard
##
## Latent Variables:
##                    Estimate  Std.Err  z-value  P(>|z|)
##   spatial =~
##     visual            5.371    0.597    8.993    0.000
##     cubes             2.124    0.433    4.901    0.000
##     paper             1.254    0.250    5.012    0.000
##     lozenge           5.837    0.790    7.385    0.000
##     straight          8.589    3.240    2.651    0.008
##     figurer           2.872    0.697    4.121    0.000
##   verbal =~
##     general           9.828    0.781   12.580    0.000
##     paragrap          2.773    0.234   11.850    0.000
##     sentence          4.551    0.340   13.389    0.000
##     wordc             3.811    0.375   10.172    0.000
##     wordm             5.791    0.459   12.605    0.000
##   speed =~
##     add              14.156    2.105    6.723    0.000
##     code             11.823    1.224    9.658    0.000
##     counting         10.024    1.673    5.990    0.000
##     straight         15.440    3.235    4.773    0.000
##   memory =~
##     wordr             7.798    1.024    7.614    0.000
##     numberr           4.185    0.683    6.129    0.000
##     figurer           3.790    0.707    5.363    0.000
##     object            2.953    0.434    6.798    0.000
##     numberf           2.160    0.398    5.428    0.000
##     figurew           1.913    0.374    5.121    0.000
##
## Covariances:
##                    Estimate  Std.Err  z-value  P(>|z|)
##   spatial ~~
##     verbal            0.415    0.085    4.895    0.000
##     speed             0.323    0.103    3.129    0.002
##     memory            0.252    0.109    2.303    0.021
##   verbal ~~
##     speed             0.475    0.081    5.902    0.000
##     memory            0.131    0.098    1.336    0.181
##   speed ~~
##     memory            0.426    0.097    4.410    0.000
##
## Variances:
##                    Estimate  Std.Err  z-value  P(>|z|)
##    .visual           21.376    4.533    4.716    0.000
##    .cubes            19.547    2.401    8.139    0.000
##    .paper             6.472    0.799    8.102    0.000
##    .lozenge          52.062    7.715    6.748    0.000
##    .straight        875.005  110.732    7.902    0.000
##    .figurer          40.094    5.568    7.200    0.000
##    .general          41.308    5.979    6.909    0.000
##    .paragrap          4.185    0.571    7.330    0.000
##    .sentence          6.615    1.058    6.252    0.000
##    .wordc            13.215    1.664    7.943    0.000
##    .wordm            14.218    2.063    6.892    0.000
##    .add             415.731   55.841    7.445    0.000
##    .code             75.538   19.745    3.826    0.000
##    .counting        280.324   35.795    7.831    0.000
##    .wordr            83.348   12.917    6.452    0.000
##    .numberr          43.595    5.790    7.529    0.000
##    .object           16.578    2.329    7.119    0.000
##    .numberf          15.587    1.982    7.865    0.000
##    .figurew          14.000    1.752    7.989    0.000
##     spatial           1.000
##     verbal            1.000
##     speed             1.000
##     memory            1.000
```

Chapter 15

Structural Equation Models

Simply speaking, a structural equation model (SEM) is a combination of confirmatory factor analysis and path analysis. Structural equation modeling includes two sets of models €“ the measurement model and the structural model. The measurement model can be expressed as a factor model. Figure 1 is a model to measure cognitive ability using three variables €“ verbal ability, math ability, and speed ability (note each of them can be viewed as factors measured by lower level observed variables).

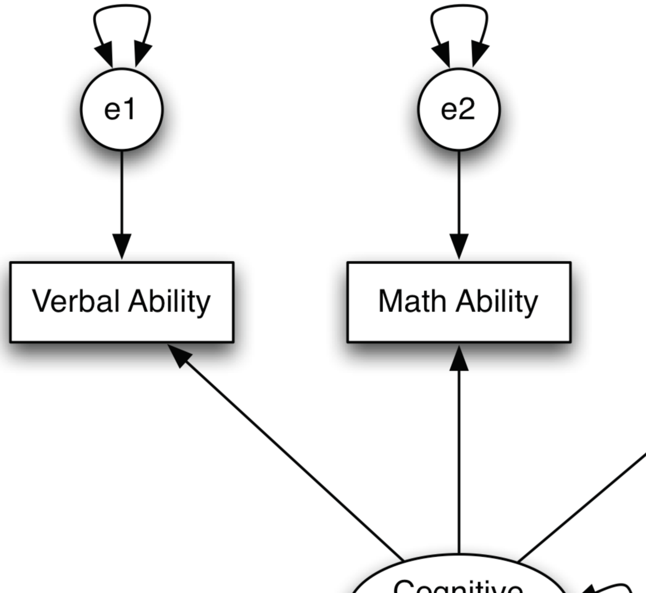
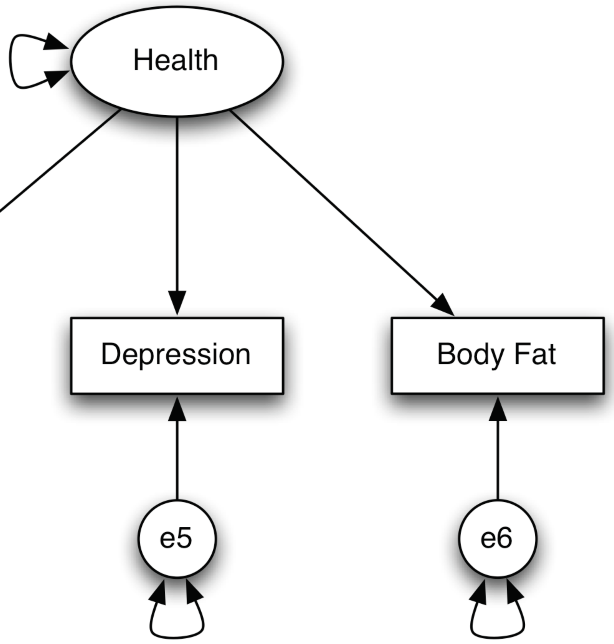
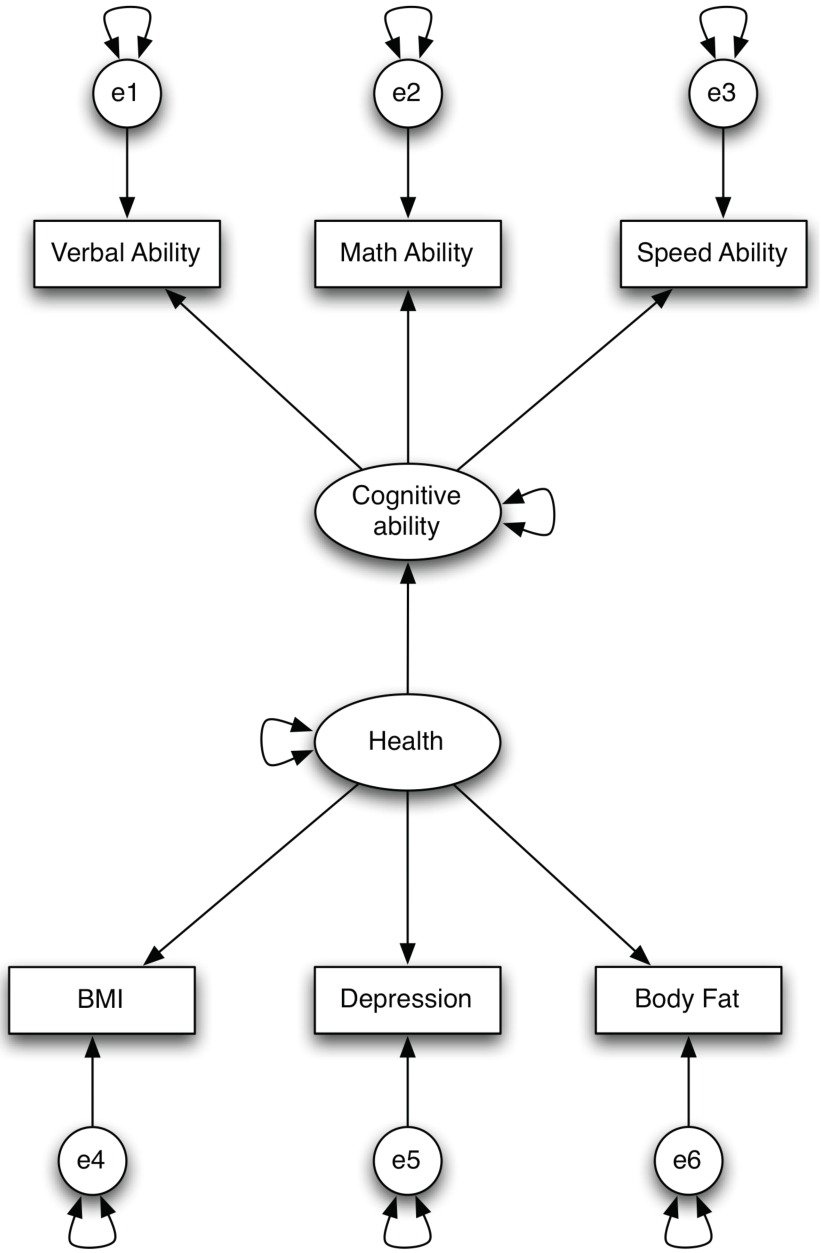


Figure 2 gives another example of measurement model €“ a model to measure health.

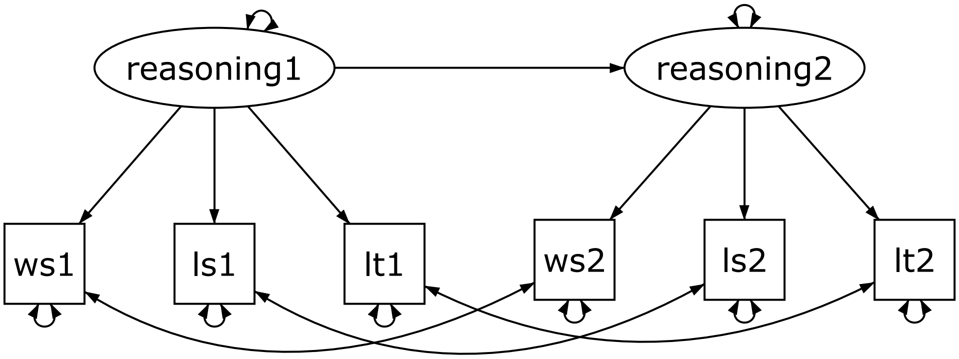


If one believes that health influences cognitive ability, then one can fit a path model using the factors €“ cognitive ability and health. Therefore, a structural model is actually a path model. Putting them together, we have a model in Figure 3. This model is called SEM model.



15.1 Example 1. Autoregressive model

In ACTIVE study, we have three variables €“ word series (ws), letter series (ls), and letter sets (ls) to measure reasoning ability. Also, we have data on all these three variables before and after training. Assume we want to test whether reasoning ability before training can predict reasoning ability after training. Then the SEM model in Figure 4 can be used. Not that we allow the factor in time 1 to predict the factor at time 2. In addition, we allow the uniqueness factors for each observed variable to be correlated. The R code for the analysis is given below.



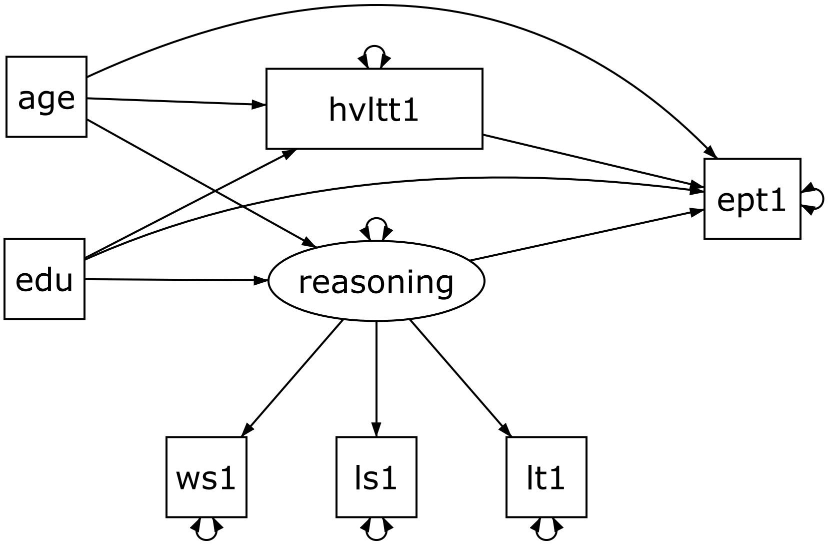
First look at model fit. The chi-square value is 27 with 5 degrees of freedom. The p-value for chi-square test is almost 0. Thus, based on chi-square test, this is not a good model. However, CFI and TFI are both close to 1. The RMSEA is about 0.063 and SRMR is about 0.011. Considering the sample size here is large €“ N=1114, overall, we may accept this model is a fairly good model. Then we can answer our question. Because the regression coefficient from `reasoning1` to `reasoning2` is significant, reasoning ability before training seems to predict reasoning ability after training. In other words, those with higher reasoning ability before training tend to have higher reasoning ability after training.

```
library(lavaan)
active.full <- read.csv('data/active.full.csv')
automodel <- '
reasoning1 =~ ws1 + ls1 + lt1
reasoning2 =~ ws2 + ls2 + lt2
reasoning2 ~ reasoning1
ws1 ~~ ws2
ls1 ~~ ls2
lt1 ~~ lt2
'

auto.res <- sem(automodel, data=active.full)
summary(auto.res, fit=TRUE)
## lavaan 0.6-3 ended normally after 66 iterations
##
##   Optimization method                           NLMINB
##   Number of free parameters                         16
##
##   Number of observations                          1114
##
##   Estimator                                         ML
##   Model Fit Test Statistic                      27.213
##   Degrees of freedom                                 5
##   P-value (Chi-square)                           0.000
##
## Model test baseline model:
```

```
##
##   Minimum Function Test Statistic            5827.630
##   Degrees of freedom                                15
##   P-value                                        0.000
##
## User model versus baseline model:
##
##   Comparative Fit Index (CFI)                    0.996
##   Tucker-Lewis Index (TLI)                       0.989
##
## Loglikelihood and Information Criteria:
##
##   Loglikelihood user model (H0)             -16447.377
##   Loglikelihood unrestricted model (H1)     -16433.771
##
##   Number of free parameters                         16
##   Akaike (AIC)                               32926.755
##   Bayesian (BIC)                             33007.006
##   Sample-size adjusted Bayesian (BIC)        32956.186
##
## Root Mean Square Error of Approximation:
##
##   RMSEA                                          0.063
##   90 Percent Confidence Interval          0.041  0.087
##   P-value RMSEA <= 0.05                          0.151
##
## Standardized Root Mean Square Residual:
##
##   SRMR                                           0.013
##
## Parameter Estimates:
##
##   Information                                 Expected
##   Information saturated (h1) model          Structured
##   Standard Errors                             Standard
##
## Latent Variables:
##                    Estimate  Std.Err  z-value  P(>|z|)
##   reasoning1 =~
##     ws1               1.000
##     ls1               1.192    0.030   40.091    0.000
##     lt1               0.422    0.016   26.301    0.000
##   reasoning2 =~
##     ws2               1.000
##     ls2               1.110    0.026   43.371    0.000
##     lt2               0.411    0.014   29.443    0.000
##
## Regressions:
##                    Estimate  Std.Err  z-value  P(>|z|)
##   reasoning2 ~
##     reasoning1        1.073    0.024   43.919    0.000
##
## Covariances:
##                    Estimate  Std.Err  z-value  P(>|z|)
##  .ws1 ~~
##    .ws2               1.216    0.327    3.718    0.000
##  .ls1 ~~
##    .ls2               0.356    0.401    0.888    0.375
##  .lt1 ~~
##    .lt2               1.596    0.138   11.544    0.000
##
## Variances:
##                    Estimate  Std.Err  z-value  P(>|z|)
##    .ws1               5.511    0.385   14.324    0.000
##    .ls1               4.547    0.475    9.575    0.000
##    .lt1               3.996    0.181   22.065    0.000
##    .ws2               5.021    0.419   11.995    0.000
##    .ls2               5.161    0.507   10.182    0.000
##    .lt2               3.963    0.181   21.875    0.000
##     reasoning1       19.103    1.060   18.014    0.000
##    .reasoning2        2.447    0.289    8.479    0.000
```

15.2 Example 2. Mediation analysis with latent variables

In path analysis, we have fitted a complex mediation model. Since we know that ws1, ls1, and lt1 are measurements of reasoning ability, we can form a latent reasoning ability variable. Thus, our mediation model can be expressed as in Figure 5.



Given CFI = 0.997, RMSEA = 0.034 and SRMR = 0.015, we accept the model as a good model even though the chi-square test is significant. Based on the Sobel test, the total indirect effect from `age` to `ept1` through `hvltt1` and `reasoning` is significant.

```
med.model <- '
reasoning =~ ws1 + ls1 + lt1
reasoning ~ p4*age + p8*edu
hvltt1 ~ p2*age + p7*edu
hvltt1 ~~ reasoning
ept1 ~ p1*age + p6*edu + p3*hvltt1 + p5*reasoning
indirect := p2*p3 + p4*p5
total := p1 + p2*p3 + p7*p3
'

med.res <- sem(med.model, data=active.full)
summary(med.res, fit=TRUE)
## lavaan 0.6-3 ended normally after 51 iterations
##
##   Optimization method                           NLMINB
##   Number of free parameters                         17
##
##   Number of observations                          1114
##
##   Estimator                                         ML
##   Model Fit Test Statistic                      18.363
##   Degrees of freedom                                 8
##   P-value (Chi-square)                           0.019
##
## Model test baseline model:
##
```

```
##   Minimum Function Test Statistic            3344.605
##   Degrees of freedom                                20
##   P-value                                        0.000
##
## User model versus baseline model:
##
##   Comparative Fit Index (CFI)                    0.997
##   Tucker-Lewis Index (TLI)                       0.992
##
## Loglikelihood and Information Criteria:
##
##   Loglikelihood user model (H0)             -14628.420
##   Loglikelihood unrestricted model (H1)     -14619.238
##
##   Number of free parameters                         17
##   Akaike (AIC)                               29290.840
##   Bayesian (BIC)                             29376.107
##   Sample-size adjusted Bayesian (BIC)        29322.110
##
## Root Mean Square Error of Approximation:
##
##   RMSEA                                          0.034
##   90 Percent Confidence Interval          0.013  0.055
##   P-value RMSEA <= 0.05                          0.889
##
## Standardized Root Mean Square Residual:
##
##   SRMR                                           0.015
##
## Parameter Estimates:
##
##   Information                                 Expected
##   Information saturated (h1) model          Structured
##   Standard Errors                             Standard
##
## Latent Variables:
##                    Estimate  Std.Err  z-value  P(>|z|)
##   reasoning =~
##     ws1               1.000
##     ls1               1.181    0.029   41.262    0.000
##     lt1               0.430    0.016   26.758    0.000
##
## Regressions:
##                    Estimate  Std.Err  z-value  P(>|z|)
##   reasoning ~
##     age       (p4)   -0.228    0.023   -9.737    0.000
##     edu       (p8)    0.745    0.047   15.792    0.000
##   hvltt1 ~
##     age       (p2)   -0.161    0.027   -6.074    0.000
##     edu       (p7)    0.429    0.052    8.177    0.000
##   ept1 ~
##     age       (p1)    0.030    0.022    1.389    0.165
##     edu       (p6)    0.396    0.046    8.527    0.000
##     hvltt1    (p3)    0.169    0.026    6.488    0.000
##     reasoning (p5)    0.643    0.035   18.186    0.000
##
## Covariances:
##                    Estimate  Std.Err  z-value  P(>|z|)
##  .reasoning ~~
##    .hvltt1            7.255    0.592   12.263    0.000
##
## Variances:
##                    Estimate  Std.Err  z-value  P(>|z|)
##    .ws1               5.334    0.366   14.594    0.000
##    .ls1               4.850    0.444   10.910    0.000
##    .lt1               3.917    0.181   21.657    0.000
##    .hvltt1           20.618    0.874   23.601    0.000
##    .ept1             11.505    0.522   22.027    0.000
##    .reasoning        13.814    0.777   17.777    0.000
##
## Defined Parameters:
##                    Estimate  Std.Err  z-value  P(>|z|)
##     indirect         -0.174    0.019   -9.368    0.000
##     total             0.075    0.025    3.008    0.003
```

Chapter 16

Multilevel Regression

16.1 Multilevel data

Lee and Bryk (1989) analyzed a set of data in illustrating the use of multilevel modeling. The data set includes mathematics scores for senior-year high school students from 160 schools. For each student, information on her/his social and economic status (SES) is also available. For each school, data are available on the sector (private or public) of the schools. In addition, a school level variable called average SES (MSES) was created from the students' SES to measure the SES of each school.

There is a clear two-level structure in the data. At the first level, the student level, we have information on individual students. At the second level, the school level, we have information on schools. The students are nested within schools. This kind of data are called multilevel data.

16.1.1 Lee and Bryk school achievement data

As an example, we use a subset of data from the Lee and Bryk (1989) study. In total, there are $n = 7,185$ students at the first level. At the second level, there are $J = 160$ schools. The data are saved in the file `LeeBryk.csv`. A subset of data are shown below. `sector=0` indicates a public school and `sector=1` indicates a private Catholic high school.

```
LeeBryk <- read.csv('data/LeeBryk.csv')
head(LeeBryk)
##   schoolid  math   ses  mses sector
## 1        1  5.88 -1.53 -0.43      0
## 2        1 19.71 -0.59 -0.43      0
## 3        1 20.35 -0.53 -0.43      0
## 4        1  8.78 -0.67 -0.43      0
## 5        1 17.90 -0.16 -0.43      0
## 6        1  4.58  0.02 -0.43      0
attach(LeeBryk)
```

16.2 Source of variances

We first look at the mathematical variable alone. The variance of the variable math is 47.31. The variance can be viewed as the residual variance after removing the mean of it or the residual variance by fitting a regression model with intercept only to it. This assumes that every student across all schools has the same mean score or intercept such that

$$math_{ij} = \beta_0 + e_{ij}.$$

Given there are 160 schools, it is more reasonable to believe that the intercept (or average math score) is different for each school. Using a regression model way, we then have

$$math_{ij} = \beta_j + e_{ij},$$

where β_j is the average math score or intercept for each school j.

Because the intercept is different, it can also has its own variation or variance across schools which can also be calculated using a regression model with intercept only

$$\beta_j = \beta_0 + v_j$$

where v_j is the deviation for the average score of school j from the overall average β_0.

With such a specification, the variance of math can be expressed as the sum of the variance of the residuals e_{ij} – within-school variance, and the variance of v_j – between-school variance. Specifically, the variance of math is equal to $8.614 + 39.148 =$ between-school variance + within-school variance.

Combining the two regressions, we have a two-level regression model. Note that the model can be written as

$$math_{ij} = \beta_0 + v_j + e_{ij}.$$

The model is called a mixed-effects model in which β_0 is called the fixed effect. It is the average intercept for all schools and v_j is called the random effect.

16.2.1 Use of R package lme4

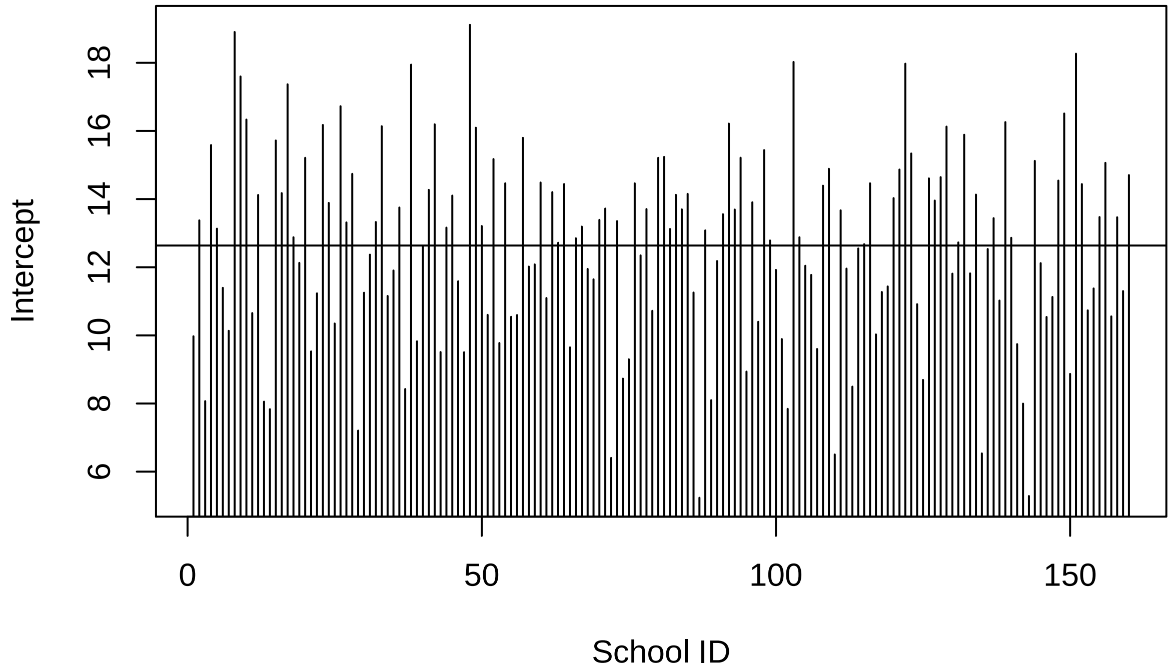
A multilevel model or a mixed-effects model can be estimated using the R package `lme4`. Particularly, the function `lmer()` should be used. The function not only estimates the fixed-effects β_0 but also the random-effects v_j. The function use the format `lmer(math~1 + (1|schoolid), data=school)`. In the function, the first "1" tells to estimate a fixed-effects as the overall intercept. `(1|schoolid)` tells there is a random component in the intercept.

The output includes the `Fixed effects`, for which a t-test is also conducted for its significance. The `Random effects` part includes the variance of the residuals (e_{ij}) and the variance of the random intercept (v_j).

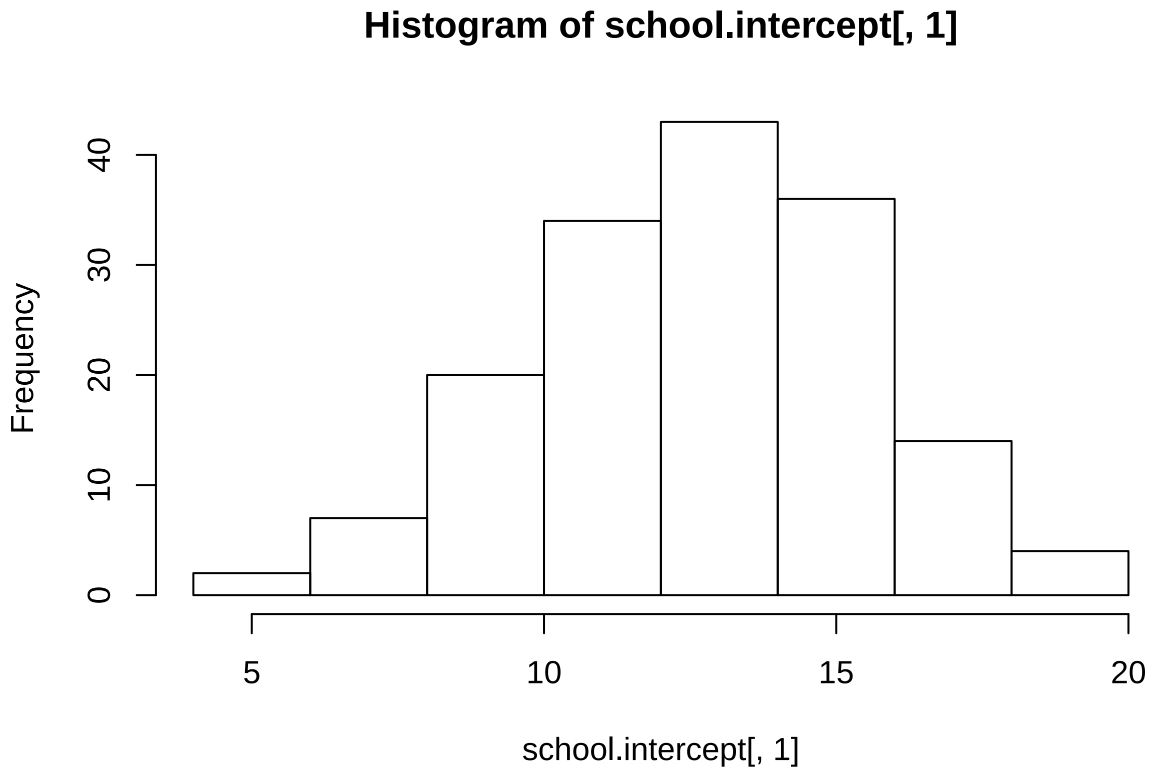
```
library(lme4)

m2<-lmer(math ~ 1 + (1|schoolid), data=LeeBryk)
summary(m2)
## Linear mixed model fit by REML ['lmerMod']
## Formula: math ~ 1 + (1 | schoolid)
##    Data: LeeBryk
##
## REML criterion at convergence: 47116.7
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.06294 -0.75337  0.02658  0.76060  2.74221
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  schoolid (Intercept)  8.614   2.935
##  Residual             39.148   6.257
## Number of obs: 7185, groups:  schoolid, 160
##
## Fixed effects:
##             Estimate Std. Error t value
## (Intercept)  12.6374     0.2444   51.71
```

The random-effects v_j can be obtained using the function `ranef()`. With them, the intercept or average math score for each school can be calculated and also plotted as shown below.

```
m2<-lmer(math ~ 1 + (1|schoolid), data=LeeBryk)
bi<-ranef(m2)

school.intercept <- bi$schoolid + 12.6374
plot(school.intercept[,1],type='h',
     xlab='School ID', ylab='Intercept')
abline(h=12.6374)
```



```
hist(school.intercept[,1])
```



16.2.2 Intraclass correlation coefficient (ICC)

The intraclass correlation coefficient is defined as the ratio of the variance explained by the multilevel structure and the variance of the outcome variable. For the example above, we have intraclass correlation coefficient

$$\tau = \frac{8.614}{8.614 + 39.148} = 0.18.$$

In social science, it often ranges from 0.05 to 0.25. When ICC is large, it means the between-class variance cannot be ignored and therefore a multilevel model is preferred. It has been suggested that if ICC $>$ 0.1, one should consider the use of a multilevel model.

16.2.3 Explain/model the difference

We have shown the differences in the average score or intercept for each school. What causes the differences? School level covariates, such as the average SES or whether the school is private or public, can be used to explore potential factors related to it. In using a two-level model, we can specify a model as

$$math_{ij} = \beta_j + e_{ij} \tag{16.1}$$
$$\beta_j = \beta_0 + \beta_1 mses_j + \beta_2 sector_j + v_j. \tag{16.2}$$

Using a mixed-effect model, it can be written as

$$math_{ij} = \beta_0 + \beta_1 mses_j + \beta_2 sector_j + v_j + e_{ij},$$

where $\beta_k, k = 0, 1, 2$ are fixed-effects parameters. Based on the output of the `lmer()`, both mses and sector are significant given the t-values in the fixed effects table. Note that to get the associated p-value, the R package `lmerTest` can be used.

```r
library(lmerTest)

m3<-lmer(math~1 + mses + sector + (1|schoolid), data=LeeBryk)
summary(m3)
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: math ~ 1 + mses + sector + (1 | schoolid)
##    Data: LeeBryk
##
## REML criterion at convergence: 46946.3
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.08323 -0.75079  0.01932  0.76659  2.78831
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  schoolid (Intercept)  2.312   1.520
##  Residual             39.161   6.258
## Number of obs: 7185, groups:  schoolid, 160
##
## Fixed effects:
##              Estimate Std. Error       df t value Pr(>|t|)
## (Intercept)  12.0994     0.1986 160.5492  60.919  < 2e-16 ***
## mses          5.3336     0.3685 151.0049  14.475  < 2e-16 ***
## sector        1.2196     0.3058 149.5960   3.988 0.000104 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##        (Intr) mses
## mses    0.246
## sector -0.698 -0.357

anova(m3)
## Type III Analysis of Variance Table with Satterthwaite's method
##        Sum Sq Mean Sq NumDF DenDF F value    Pr(>F)
## mses   8205.1  8205.1     1 151.0 209.522 < 2.2e-16 ***
## sector  622.9   622.9     1 149.6  15.907 0.0001038 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

16.3 Multilevel regression

The variable math can be predicted by certain variables such as individual SES. If we ignore the multilevel structure, we can fit a simple regression as

$$math_{ij} = \beta_0 + \beta_1 ses_{ij} + e_{ij}.$$

This is to assume that the relationship, the slope, between math and ses is the same. However, as we showed earlier, the intercepts are different for different schools. So the slopes can also be different. In this case, the model should be written as

$$math_{ij} = \beta_{0j} + \beta_{1j} ses_{ij} + e_{ij},$$

where β_{0j} and β_{1j} are intercept and slope for the jth school. We can also predict the intercept and slope using the school level covariates such as the sector of the school and the SES of the school. Then, we would have a two-level model shown below:

$$math_{ij} = \beta_{0j} + \beta_{1j} ses_{ij} + e_{ij} \tag{16.3}$$

$$\beta_{0j} = \gamma_0 + \gamma_1 mses_j + \gamma_2 sector_j + v_{0j}. \tag{16.4}$$

$$\beta_{1j} = \gamma_3 + \gamma_4 mses_j + \gamma_5 sector_j + v_{1j} \tag{16.5}$$

The above two-level model can again be written as a mixed-effects model

$$\begin{aligned} math_{ij} &= \beta_{0j} + \beta_{1j} ses_{ij} + e_{ij} \\ &= \gamma_0 + \gamma_1 mses_j + \gamma_2 sector_j + v_{0j} \\ &\quad +(\gamma_3 + \gamma_4 mses_j + \gamma_5 sector_j + v_{1j}) * ses_{ij} + e_{ij}. \end{aligned} \tag{16.6}$$

To use the R package for model estimation, we first need to plug in the second level equation to the first level to get a mixed model. In the mixed model, γs are fixed-effects and v_{0j} and

v_{1j} are random effects. The variances of v_{0j} and v_{1j} and their correlation can also be obtained. We can also get the variance of e_{ij}. Those variance parameters are called random-effects parameters while γs are called fixed-effects parameters. In R, each term in the mixed-effects model needs to be specified except for e_{ij}. The random effects are specified using the notation `|` where before it are the random-effects terms and after it is the grouping variable or class variable.

For the math example, the R input and output shown below.

```
m4<-lmer(math~1 + mses + sector
          + ses + ses*mses + ses*sector
          + (1 + ses|schoolid), data=LeeBryk)
summary(m4)
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: math ~ 1 + mses + sector + ses + ses * mses + ses * sector +
##     (1 + ses | schoolid)
##    Data: LeeBryk
##
## REML criterion at convergence: 46505.1
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.14226 -0.72478  0.01375  0.75508  2.98328
##
## Random effects:
##  Groups   Name        Variance Std.Dev. Corr
##  schoolid (Intercept)  2.40635 1.5512
##           ses          0.01441 0.1201   1.00
##  Residual             36.75783 6.0628
## Number of obs: 7185, groups:  schoolid, 160
##
## Fixed effects:
##              Estimate Std. Error        df t value Pr(>|t|)
## (Intercept)   12.1026     0.2028  166.5178  59.684  < 2e-16 ***
## mses           3.3224     0.3884  178.5459   8.554 5.28e-15 ***
## sector         1.1882     0.3080  148.3337   3.857  0.00017 ***
## ses            2.9057     0.1483 4350.7595  19.595  < 2e-16 ***
## mses:ses       0.8475     0.2717 3545.4952   3.119  0.00183 **
## sector:ses    -1.5793     0.2246 4345.3418  -7.033 2.34e-12 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##            (Intr) mses   sector ses    mss:ss
## mses        0.213
## sector     -0.676 -0.345
## ses         0.077 -0.146 -0.065
## mses:ses   -0.143  0.179 -0.082  0.279
## sector:ses -0.062 -0.081  0.094 -0.679 -0.357
## convergence code: 0
## Model failed to converge with max|grad| = 0.00309267 (tol = 0.002, component 1)
anova(m4)
## Type III Analysis of Variance Table with Satterthwaite's method
##              Sum Sq Mean Sq NumDF  DenDF  F value    Pr(>F)
## mses         2689.4  2689.4     1  178.5  73.1664 5.280e-15 ***
## sector        546.9   546.9     1  148.3  14.8792 0.0001704 ***
## ses        14113.5 14113.5     1 4350.8 383.9591 < 2.2e-16 ***
## mses:ses      357.6   357.6     1 3545.5   9.7278 0.0018296 **
## sector:ses  1818.0  1818.0     1 4345.3  49.4592 2.342e-12 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The parameters in the table of `Fixed effects` give the estimates for γs. Hence, we have

$$\beta_{0j} = 12.10 + 3.32 mses_j + 1.19 sector_j + v_{0j} \tag{16.7}$$

$$\beta_{1j} = 2.91 + 0.85 mses_j - 1.58 sector_j + v_{1j} \tag{16.8}$$

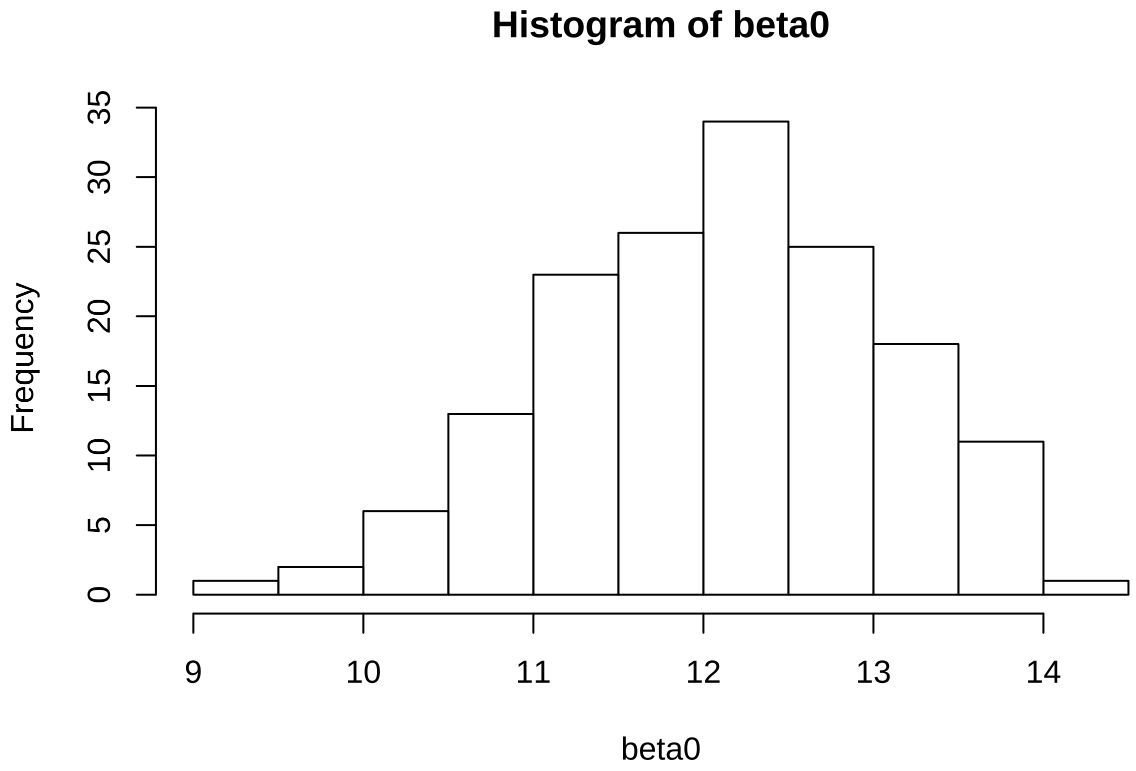
Note that based on the F-test, both ses and the sector of the school are significant predictors of both intercept and slope.

The parameters in the table of `Random effects` give the variance estimates. Therefore, the variance of e_{ij} is 36.76. The variance of v_{0j} is 2.41 and the variance of v_{1j} is .014. The correlation between v_{0j} and v_{1j} is almost 1. Individual values for v_{0j} and v_{1j} can be obtained using the function `ranef()`.

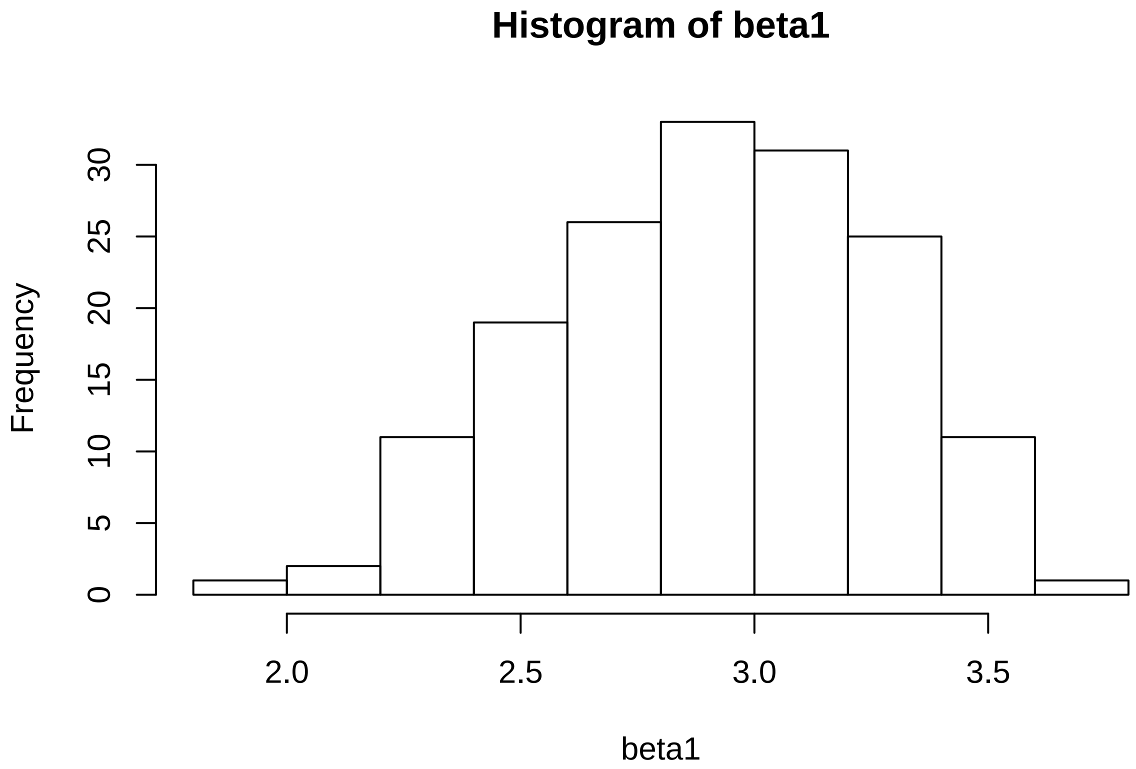
Note that with the fixed effects and random effects, we can calculate the intercept β_{0j} and slope β_{1j} for each school. Then, the individual regression line can be plotted together with the scatterplot of all data.

```
m4<-lmer(math~1 + mses + sector
          + ses + ses*mses + ses*sector
          + (1 + ses|schoolid), data=LeeBryk)

## calculate betas
#random effects
rancof<-ranef(m4)$schoolid
beta0<-beta1<-rep(0, 160)
```

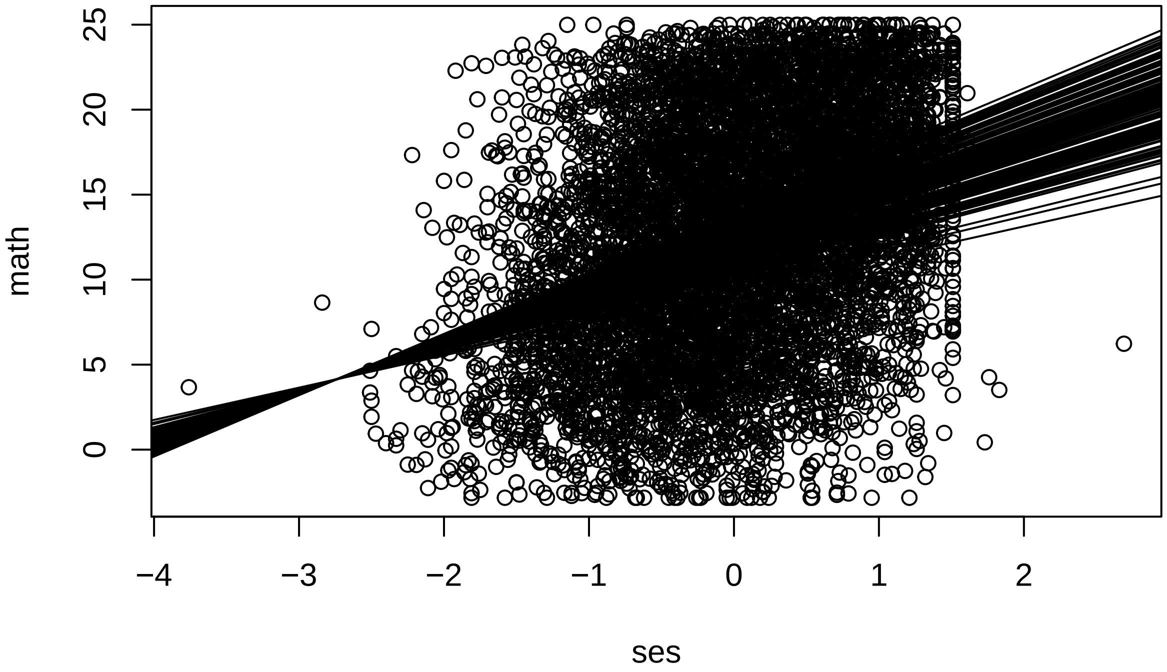
```
for (i in 1:160){
  index<-min(which(schoolid==i))
  beta0[i] <- 12.1026+2.3225*mses[index]
              +1.1882*sector[index]+rancof[i,1]
  beta1[i] <- 2.9057+0.8476*mses[index]
              -1.5793*sector[index]+rancof[i,2]
}

hist(beta0)
```



```
hist(beta1)
```



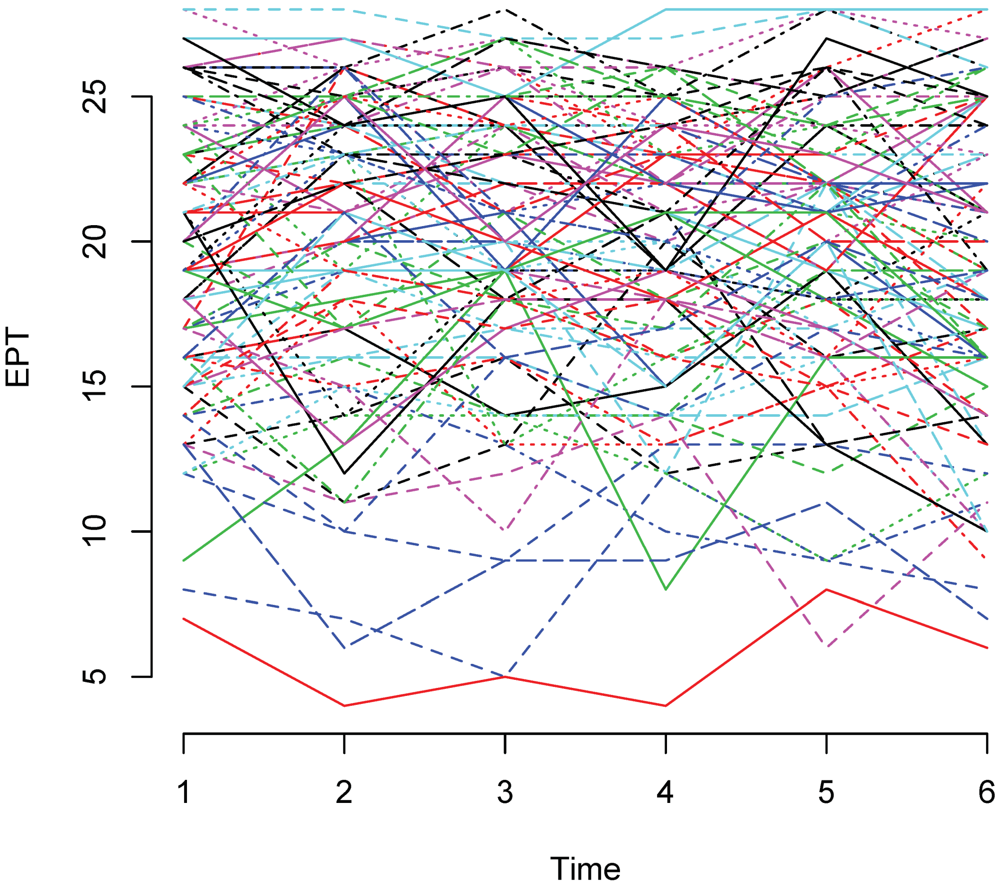
```
## plot the relationship for each school
plot(ses, math)

for (i in 1:160){
  abline(beta0[i], beta1[i])
}
```


math
25
20
15
10
5
0
−4
−3
−2
−1
0
1
2
ses

Chapter 17

Longitudinal Data Analysis

Longitudinal data can be viewed as a special case of the multilevel data where time is nested within individual participants. All longitudinal data share at least three features: (1) the same entities are repeatedly observed over time; (2) the same measurements (including parallel tests) are used; and (3) the timing for each measurement is known (Baltes & Nesselroade, 1979). To study phenomena in their time-related patterns of constancy and change is a primary reason for collecting longitudinal data. Figure 1 show the plot of 50 participants from the ACTIVE study on the variable EPT for 6 times. Clearly, each line represents a participant. From it, we can see how an individual changes over time.



17.1 Growth curve model

Growth curve models (GCM; e.g., McArdle & Nesselroade, 2003; Meredith & Tisak, 1990) exemplify a widely used technique with a direct match to the objectives of longitudinal research described by Baltes and Nesselroade (1979) to analyze explicitly intra-individual change and inter-individual differences in change. In the past decades, growth curve models have evolved from fitting a single curve for only one individual to fitting multilevel or mixed-effects models and from linear to nonlinear models (e.g., McArdle, 2001; McArdle & Nesselroade, 2003; Meredith & Tisak, 1990; Tucker, 1958; Wishart, 1938).

A typical linear growth curve model can be written as

$$y_{it} = \beta_{0i} + \beta_{1i} \times time_{it} + e_{it} \tag{17.1}$$
$$\beta_{0i} = \gamma_0 + v_{0i} \tag{17.2}$$
$$\beta_{1i} = \gamma_1 + v_{1i} \tag{17.3}$$

where y_{it} is data for participant i at time t. For each individual i, a linear regression model can be fitted with its own intercept β_{0i} and slope β_{1i}. On average, there is an intercept γ_0 and slope γ_1 for all individuals. The variation of β_{0i} and β_{1i} represents individual differences.

Individual difference can be further explained by other factors, for example, education level and age. Then the model is

$$y_{it} = \beta_{0i} + \beta_{1i} \times time_{it} + e_{it} \tag{17.4}$$
$$\beta_{0i} = \gamma_0 + \gamma_1 \times edu_i + v_{0i} \tag{17.5}$$
$$\beta_{1i} = \gamma_2 + \gamma_3 \times edu_i + v_{1i} \tag{17.6}$$

17.2 GCM as a mulitlevel/mixed-effect model

A GCM can first be fitted as a multilevel model or mixed-effects model using the R package `lme4`.

To use the package, we would need to rewrite the growth curve model as a mixed-effect model. For the model without second level predictor, we have

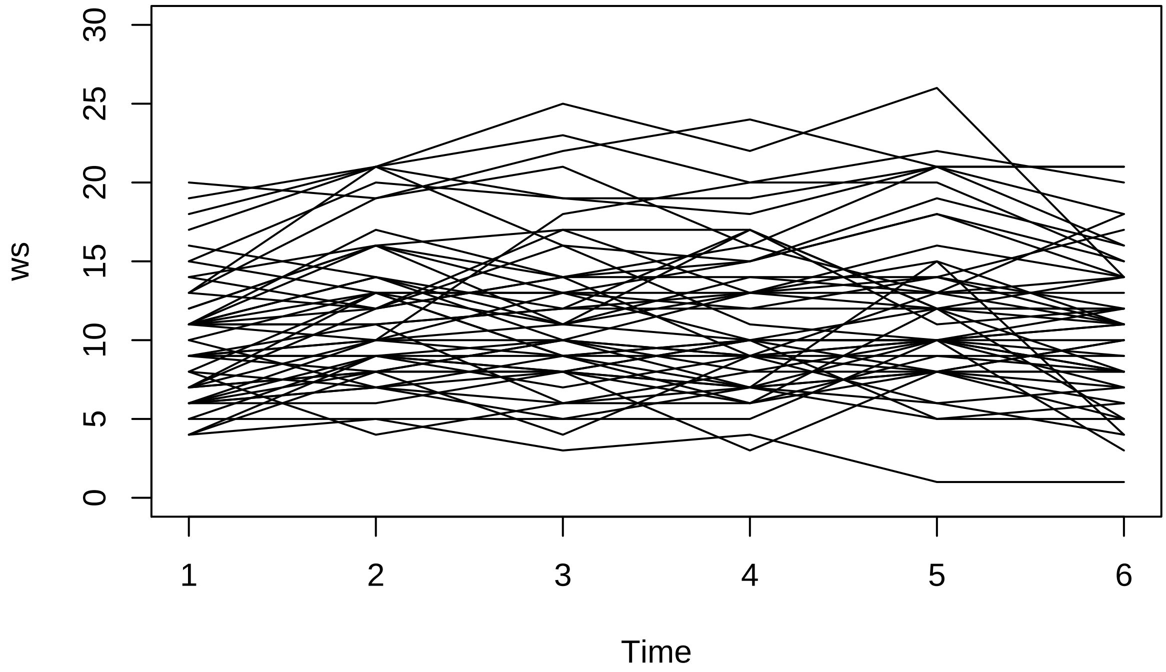
$$y_{it} = \gamma_0 + v_{i0} + \gamma_1 * time_{it} + v_{1i} * time_{it} + e_{it}.$$

For the one with the second level predictor, such as education, we have

$$y_{it} = \gamma_0 + \gamma_1 * edu + v_{0i} + \gamma_2 * time_{it} + \gamma_3 * edu_i * time_{it} + v_{1i} * time_{it} + e_{it}.$$

For demonstration, we investigate the growth of word set test (`ws` in the ACTIVE data set). In the current data set, we have the data in wide format, in which the 6 measures of `ws` are 6 variables. To use the R package, long format data are needed. For the long-format data, we need to stack the data from all waves into a long variable. The R code below reformats the data and plot them.

```
active.full <- read.csv('data/active.full.csv')
attach(active.full)

longdata<-data.frame(ws=c(ws1,ws2,ws3,ws4,ws5,ws6),
                     parti=factor(rep(paste('p', 1:1114, sep=''), 6)),
                     time=rep(1:6, each=1114),
                     edu=rep(edu, 6))

plot(1:6, longdata$ws[longdata$parti=="p1"], type='l',
     xlab='Time', ylab="ws", ylim=c(0, max(longdata$ws)))
for (i in 2:50){
  lines(1:6, longdata$ws[longdata$parti==paste("p", i, sep="")])
}
```



17.2.1 Unconditional model (model without second level predictors)

Fitting the model is actually straightforward using the `lmer()` function. The input and output are given below. Based on the output, the fixed effects for time (.214, t-value=11.59) is significant, therefore, there is a linear growth trend. The average intercept is 11.93 and is also significant.

```
library(lme4)
library(lmerTest)
```

```
longdata<-data.frame(ws=c(ws1,ws2,ws3,ws4,ws5,ws6),
                     parti=factor(rep(paste('p', 1:1114, sep=''), 6)),
                     time=rep(1:6, each=1114),
                     edu=rep(edu, 6))

m1<-lmer(ws~time+(1+time|parti), data=longdata)
summary(m1)
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: ws ~ time + (1 + time | parti)
##    Data: longdata
##
## REML criterion at convergence: 34088.3
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -4.3919 -0.5446 -0.0163  0.5643  4.4923
##
## Random effects:
##  Groups   Name        Variance Std.Dev. Corr
##  parti    (Intercept) 21.11590 4.5952
##           time         0.07362 0.2713   0.15
##  Residual              5.36088 2.3154
## Number of obs: 6684, groups:  parti, 1114
##
## Fixed effects:
##              Estimate Std. Error        df t value Pr(>|t|)
## (Intercept) 1.193e+01  1.521e-01 1.113e+03   78.42   <2e-16 ***
## time        2.140e-01  1.847e-02 1.113e+03   11.59   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##      (Intr)
## time -0.285
anova(m1)
## Type III Analysis of Variance Table with Satterthwaite's method
##      Sum Sq Mean Sq NumDF DenDF F value    Pr(>F)
## time 720.17  720.17     1  1113  134.34 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

It is useful to test whether random-effects parameters such as the variances of intercept and slope are significance or not to evaluate individual differences. This can be done by comparing the current model with a model without random intercept or slope.

For example, to test the individual differences in slope for time. The random effects for time is .07. Based on ANOVA analysis, it is significant with p-value about 0. Therefore, there is significant individual difference in the growth rate (slope). This indicates that everyone has a different change rate. Note that in `m1.alt`, the random effect for time was not used.

```
m1.alt1<-lmer(ws~time+(1|parti), data=longdata)
summary(m1.alt1)
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: ws ~ time + (1 | parti)
##    Data: longdata
## 
## REML criterion at convergence: 34133.4
## 
## Scaled residuals: 
##     Min      1Q  Median      3Q     Max 
## -4.7097 -0.5452  0.0030  0.5784  4.5111 
## 
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  parti    (Intercept) 23.243   4.821   
##  Residual              5.618   2.370   
## Number of obs: 6684, groups:  parti, 1114
## 
## Fixed effects:
##              Estimate Std. Error        df t value Pr(>|t|)    
## (Intercept) 1.193e+01  1.589e-01 1.497e+03   75.07   <2e-16 ***
## time        2.140e-01  1.698e-02 5.569e+03   12.61   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Correlation of Fixed Effects:
##      (Intr)
## time -0.374

anova(m1, m1.alt1)
## Data: longdata
## Models:
## m1.alt1: ws ~ time + (1 | parti)
## m1: ws ~ time + (1 + time | parti)
##         Df   AIC   BIC logLik deviance Chisq Chi Df Pr(>Chisq)    
## m1.alt1  4 34133 34160 -17063    34125                            
## m1       6 34092 34133 -17040    34080    45      2  1.692e-10 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

To test the individual differences in intercept. The random effects for intercept is 21.11. Based on ANOVA analysis below, it is significant. Therefore, there is individual difference or individuals have different intercepts.

```
m1.alt2<-lmer(ws~time+(time-1|parti), data=longdata)
summary(m1.alt2)
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: ws ~ time + (time - 1 | parti)
##    Data: longdata
##
## REML criterion at convergence: 37278
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -3.0574 -0.5435 -0.0079  0.5204  4.5639
##
## Random effects:
##  Groups   Name Variance Std.Dev.
##  parti    time  1.228   1.108
##  Residual      10.230   3.198
## Number of obs: 6684, groups:  parti, 1114
##
## Fixed effects:
##              Estimate Std. Error        df t value Pr(>|t|)
## (Intercept) 1.193e+01  8.921e-02 5.569e+03 133.680  < 2e-16 ***
## time        2.140e-01  4.034e-02 1.986e+03   5.306 1.24e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##      (Intr)
## time -0.510

anova(m1, m1.alt2)
## Data: longdata
## Models:
## m1.alt2: ws ~ time + (time - 1 | parti)
## m1: ws ~ time + (1 + time | parti)
##         Df   AIC   BIC logLik deviance Chisq Chi Df Pr(>Chisq)
## m1.alt2  4 37278 37305 -18635    37270
## m1       6 34092 34133 -17040    34080  3190      2  < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

17.2.2 Conditional model (model with second level predictors)

Using the same set of data, we now investigate whether education is a predictor of random intercept and slope. Given there is individual differences in intercept and slope, we want to explain why. So, we use Edu as a explanatory variable. From the output, we can see that the parameter $\gamma_1 = .78$ is significant. Higher education relates to bigger intercept. In addition, the parameter $\gamma_3 = -.022$ is significant. Higher education relates to lower growth rate of `ws`.

17.3 GCM as a SEM

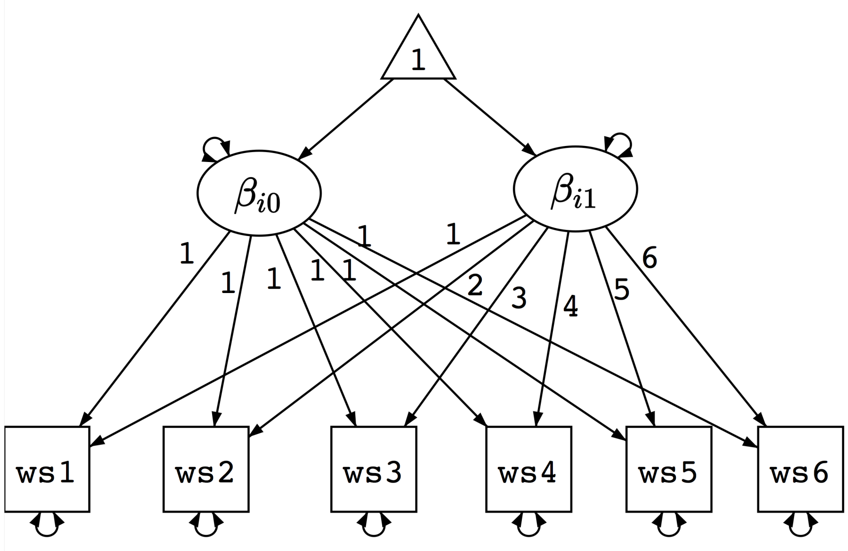
In addition to estimating a GCM as a multilevel or mixed-effects model, we can also estimate it as a SEM. To illustrate this, we consider a linear growth curve model. If a group of participants all have linear change trend, for each individual, we can fit a regression model such as

$$y_{it} = \beta_{i0} + \beta_{i1} t + e_{it}$$

where β_{i0} and β_{i1} are intercept and slope, respectively. Note that here we let $time_{it} = t$. If each individual has different time of data collection, it can still be done in the SEM framework but would be more complex. By writing the time out, we would have

$$\begin{pmatrix} y_{i1} \\ y_{i2} \\ \vdots \\ y_{iT} \end{pmatrix} = \begin{pmatrix} 1 & 1 \\ 1 & 2 \\ 1 & \vdots \\ 1 & T \end{pmatrix} \begin{pmatrix} \beta_{i0} \\ \beta_{i1} \end{pmatrix} + \begin{pmatrix} e_{i1} \\ e_{i2} \\ \vdots \\ e_{iT} \end{pmatrix}$$

Note that the above equation resembles a factor model with two factors - b_0 and b_1 and a factor loading matrix with known factor loading matrix. The individual intercept and slope can be viewed as factor scores to be estimated. Furthermore, we are interested in model with mean structure because the means of β_0 and β_1 have their meaning as average intercept and slope (rate of change). The variances of the factors can be estimated - they indicate the variations of intercept and slope. Using path diagram, the model is shown in the figure below.



With the model, we can estimate it using the `sem()` function in the `lavaan` package. Because of the frequent use of growth curve model, the package also provides a function `growth()` to ease such analysis. Unlike the lme4 package, in using SEM, the wide format of data is directly used. The R input and output for the unconditional model is given below.

Note that the `gcm()` function works similarly as `sem()` function. Using this method, each parameter in the model can be directly tested using a z-test. In addition, we can use the fit statistics for SEM to test the fit of the growth curve model. Particularly for the current analysis, the linear growth curve model does not seem to fit the data well.

```
library(lavaan)

gcm <- '
beta0 =~ 1*ws1 + 1*ws2 + 1*ws3 + 1*ws4 + 1*ws5 + 1*ws6
beta1 =~ 1*ws1 + 2*ws2 + 3*ws3 + 4*ws4 + 5*ws5 + 6*ws6
'

gcm.res <- growth(gcm, data=active.full)
summary(gcm.res, fit=TRUE)
## lavaan 0.6-3 ended normally after 53 iterations
##
##   Optimization method                           NLMINB
##   Number of free parameters                         11
##
##   Number of observations                          1114
##
##   Estimator                                         ML
##   Model Fit Test Statistic                     691.253
##   Degrees of freedom                                16
##   P-value (Chi-square)                           0.000
```

```
##
## Model test baseline model:
##
##   Minimum Function Test Statistic             8065.569
##   Degrees of freedom                                15
##   P-value                                        0.000
##
## User model versus baseline model:
##
##   Comparative Fit Index (CFI)                    0.916
##   Tucker-Lewis Index (TLI)                       0.921
##
## Loglikelihood and Information Criteria:
##
##   Loglikelihood user model (H0)             -16958.575
##   Loglikelihood unrestricted model (H1)     -16612.949
##
##   Number of free parameters                         11
##   Akaike (AIC)                               33939.151
##   Bayesian (BIC)                             33994.324
##   Sample-size adjusted Bayesian (BIC)        33959.385
##
## Root Mean Square Error of Approximation:
##
##   RMSEA                                          0.195
##   90 Percent Confidence Interval          0.182  0.207
##   P-value RMSEA <= 0.05                          0.000
##
## Standardized Root Mean Square Residual:
##
##   SRMR                                           0.095
##
## Parameter Estimates:
##
##   Information                                 Expected
##   Information saturated (h1) model          Structured
##   Standard Errors                             Standard
##
## Latent Variables:
##                    Estimate  Std.Err  z-value  P(>|z|)
##   beta0 =~
##     ws1               1.000
##     ws2               1.000
##     ws3               1.000
##     ws4               1.000
##     ws5               1.000
##     ws6               1.000
##   beta1 =~
##     ws1               1.000
##     ws2               2.000
##     ws3               3.000
##     ws4               4.000
##     ws5               5.000
##     ws6               6.000
##
## Covariances:
##                     Estimate  Std.Err  z-value  P(>|z|)
##   beta0 ~~
##     beta1             0.406    0.106    3.817    0.000
##
## Intercepts:
##                     Estimate  Std.Err  z-value  P(>|z|)
##    .ws1               0.000
##    .ws2               0.000
##    .ws3               0.000
##    .ws4               0.000
##    .ws5               0.000
##    .ws6               0.000
##     beta0            12.263    0.155   79.217    0.000
##     beta1             0.161    0.018    8.770    0.000
##
## Variances:
##                     Estimate  Std.Err  z-value  P(>|z|)
##    .ws1               8.999    0.443   20.293    0.000
##    .ws2               5.614    0.284   19.751    0.000
##    .ws3               3.867    0.209   18.539    0.000
##    .ws4               4.091    0.219   18.639    0.000
##    .ws5               4.712    0.249   18.915    0.000
##    .ws6               6.420    0.343   18.723    0.000
##     beta0            20.854    1.143   18.246    0.000
##     beta1            -0.004    0.019   -0.186    0.853
```

Fitting a conditional model is similar but one would need to use the predictor for the factors.

```
gcm2 <- '
beta0 =~ 1*ws1 + 1*ws2 + 1*ws3 + 1*ws4 + 1*ws5 + 1*ws6
beta1 =~ 1*ws1 + 2*ws2 + 3*ws3 + 4*ws4 + 5*ws5 + 6*ws6
beta0 ~ edu
beta1 ~ edu
```

```
'

gcm2.res <- growth(gcm2, data=active.full)
summary(gcm2.res, fit=TRUE)
## lavaan 0.6-3 ended normally after 54 iterations
##
##   Optimization method                           NLMINB
##   Number of free parameters                         13
##
##   Number of observations                          1114
##
##   Estimator                                         ML
##   Model Fit Test Statistic                     697.223
##   Degrees of freedom                                20
##   P-value (Chi-square)                           0.000
##
## Model test baseline model:
##
##   Minimum Function Test Statistic             8259.498
##   Degrees of freedom                                21
##   P-value                                        0.000
##
## User model versus baseline model:
##
##   Comparative Fit Index (CFI)                    0.918
##   Tucker-Lewis Index (TLI)                       0.914
##
## Loglikelihood and Information Criteria:
##
##   Loglikelihood user model (H0)             -16864.596
##   Loglikelihood unrestricted model (H1)     -16515.985
##
##   Number of free parameters                         13
##   Akaike (AIC)                               33755.192
##   Bayesian (BIC)                             33820.397
##   Sample-size adjusted Bayesian (BIC)        33779.105
##
## Root Mean Square Error of Approximation:
##
##   RMSEA                                          0.174
##   90 Percent Confidence Interval          0.163  0.186
##   P-value RMSEA <= 0.05                          0.000
##
## Standardized Root Mean Square Residual:
```

```
##
##   SRMR                                           0.083
##
## Parameter Estimates:
##
##   Information                                 Expected
##   Information saturated (h1) model          Structured
##   Standard Errors                             Standard
##
## Latent Variables:
##                    Estimate  Std.Err  z-value  P(>|z|)
##   beta0 =~
##     ws1               1.000
##     ws2               1.000
##     ws3               1.000
##     ws4               1.000
##     ws5               1.000
##     ws6               1.000
##   beta1 =~
##     ws1               1.000
##     ws2               2.000
##     ws3               3.000
##     ws4               4.000
##     ws5               5.000
##     ws6               6.000
##
## Regressions:
##                    Estimate  Std.Err  z-value  P(>|z|)
##   beta0 ~
##     edu               0.782    0.055   14.290    0.000
##   beta1 ~
##     edu              -0.023    0.007   -3.348    0.001
##
## Covariances:
##                    Estimate  Std.Err  z-value  P(>|z|)
##  .beta0 ~~
##    .beta1             0.531    0.098    5.416    0.000
##
## Intercepts:
##                    Estimate  Std.Err  z-value  P(>|z|)
##    .ws1               0.000
##    .ws2               0.000
##    .ws3               0.000
##    .ws4               0.000
##    .ws5              0.000
##    .ws6              0.000
##    .beta0            1.510    0.765    1.974    0.048
##    .beta1            0.486    0.098    4.959    0.000
##
## Variances:
##                    Estimate  Std.Err  z-value  P(>|z|)
##    .ws1              8.860    0.434   20.406    0.000
##    .ws2              5.641    0.283   19.939    0.000
##    .ws3              3.903    0.209   18.686    0.000
##    .ws4              4.090    0.219   18.637    0.000
##    .ws5              4.717    0.249   18.921    0.000
##    .ws6              6.428    0.342   18.772    0.000
##    .beta0           16.695    0.968   17.246    0.000
##    .beta1           -0.006    0.019   -0.340    0.734
```

Chapter 18

Statistical Power Analysis

Performing statistical power analysis and sample size estimation is an important aspect of experimental design. Without power analysis, sample size may be too large or too small. If sample size is too small, the experiment will lack the precision to provide reliable answers to the questions it is investigating. If sample size is too large, time and resources will be wasted, often for minimal gain. Statistical power analysis and sample size estimation allow us to decide how large a sample is needed to enable statistical judgments that are accurate and reliable and how likely your statistical test will be to detect effects of a given size in a particular situation.

18.1 What is statistical power?

The power of a statistical test is the probability that the test will reject a false null hypothesis (i.e. that it will not make a Type II error). Given the null hypothesis H_0 and an alternative hypothesis H_1, we can define power in the following way. The type I error is the probability to incorrect reject the null hypothesis. Therefore

Type I error = Pr(Reject $H_0|H_0$ is true).

The type II error is the probability of failing to reject the null hypothesis while the alternative hypothesis is correct. That is

Type II error = Pr(Fail to reject $H_0|H_1$ is true).

Statistical power is the probability of correctly rejecting the null hypothesis while the alternative hypothesis is correct. That is = 1 - Type II error.

Power = Pr(Fail to reject $H_0|H_1$ is true) = 1 - Type II error.

We can summarize these in the table below.

Fail to reject H_0

Reject H_0

Null Hypothesis H_0 is true

Good

Type I error

Alternative Hypothesis H_1 is true

Type II error

Power

18.1.1 Factors influencing statistical power

Statistical power depends on a number of factors. But in general, power nearly always depends on the following three factors: the statistical significance criterion (alpha level), the effect size and the sample size. In general, power increases with larger sample size, larger effect size, and larger alpha level.

18.1.1.1 alpha level

A significance criterion is a statement of how unlikely a result must be, if the null hypothesis is true, to be considered significant. The most commonly used criteria are probabilities of 0.05 (5%, 1 in 20), 0.01 (1%, 1 in 100), and 0.001 (0.1%, 1 in 1000). If the criterion is 0.05, the probability of obtaining the observed effect when the null hypothesis is true must be less than 0.05, and so on. One easy way to increase the power of a test is to carry out a less conservative test by using a larger significance criterion. This increases the chance of obtaining a statistically significant result (rejecting the null hypothesis) when the null hypothesis is false, that is, reduces the risk of a Type II error. But it also increases the risk of obtaining a statistically significant result when the null hypothesis is true; that is, it increases the risk of a Type I error.

18.1.1.2 Effect size

The magnitude of the effect of interest in the population can be quantified in terms of an effect size, where there is greater power to detect larger effects. An effect size can be a direct estimate of the quantity of interest, or it can be a standardized measure that also accounts for the variability in the population. For example, in an analysis comparing outcomes in a treated and control population, the difference of outcome means $\mu_1 - \mu_2$ would be a direct measure of the effect size, whereas $(\mu_1 - \mu_2)/\sigma$, where σ is the common standard deviation of the outcomes in the treated and control groups, would be a standardized effect size. If constructed appropriately, a standardized effect size, along with the sample size, will completely determine the power. An unstandardized (direct) effect size will rarely be sufficient to determine the power, as it does not contain information about the variability in the measurements.

18.1.1.3 Sample size

The sample size determines the amount of sampling error inherent in a test result. Other things being equal, effects are harder to detect in smaller samples. Increasing sample size is often the easiest way to boost the statistical power of a test. However, a large sample size would require more resources to achieve, which might not be possible in practice.

18.1.1.4 Other factors

Many other factors can influence statistical power. First, increasing the reliability of data can increase power. The precision with which the data are measured influences statistical power. Consequently, power can often be improved by reducing the measurement error in the data. A related concept is to improve the "reliability" of the measure being assessed (as in psychometric reliability).

Second, the design of an experiment or observational study often influences the power. For example, in a two-sample testing situation with a given total sample size n, it is optimal to have equal numbers of observations from the two populations being compared (as long as the variances in the two populations are the same). In regression analysis and Analysis of Variance, there is an extensive theory, and practical strategies, for improving the power based on optimally setting the values of the independent variables in the model.

Third, for longitudinal studies, power increases with the number of measurement occasions. Power may also be related to the measurement intervals.

Fourth, missing data reduce sample size and thus power. Furthermore, different missing data pattern can have difference power.

18.1.2 Calculate power and sample size

To ensure a statistical test will have adequate power, we usually must perform special analyses prior to running the experiment, to calculate how large an n is required. Although there are no formal standards for power, most researchers assess the power using 0.80 as a standard for adequacy. This convention implies a four-to-one trade off between Type II error and Type I error.

We now use a simple example to illustrate how to calculate power and sample size. More complex power analysis can be conducted in the similar way.

Suppose a researcher is interested in whether training can improve mathematical ability. S/he can conduct a study to get the math test scores from a group of students before and after training. The null hypothesis here is the change is 0. S/He believes that change should be 1 unit. Thus, the alternative hypothesis is the change is 1.

$$H_0 : \mu = \mu_0 = 0 \tag{18.1}$$
$$H_1 : \mu = \mu_1 = 1 \tag{18.2}$$

Based on the definition of power, we have

$$\begin{aligned}\text{Power} =& \Pr(\text{reject } H_0|\mu = \mu_1) && (18.3)\\ =& \Pr(\text{change } (d) \text{ is larger than critical value under } H_0|\mu = \mu_1) && (18.4)\\ =& \Pr(d > \mu_0 + c_\alpha s/\sqrt{n}|\mu = \mu_1) && (18.5)\end{aligned}$$

where

- μ_0 is the population value under the null hypothesis
- μ_1 is the population value under the alternative hypothesis
- s is the population standard deviation under the null hypothesis.
- c_α is the critical value for a distribution, such as the standard normal distribution.
- n is the sample size.

Clearly, to calculate the power, we need to know $\mu_0, \mu_1, s, c_\alpha$, the sample size n, and the distributions of d under both null hypothesis and alternative hypothesis. Let's assume that $\alpha = .05$ and the distribution is normal with the same variance s under both null and alternative hypothesis. Then the above power is

$$\begin{aligned}\text{Power} =& \Pr(d > \mu_0 + c_{.95} s/\sqrt{n}|\mu = \mu_1) && (18.6)\\ =& \Pr(d > \mu_0 + 1.645 \times s/\sqrt{n}|\mu = \mu_1) && (18.7)\\ =& \Pr(\frac{d-\mu_1}{s/\sqrt{n}} > -\frac{(\mu_1 - \mu_0)}{s/\sqrt{n}} + 1.645|\mu = \mu_1) && (18.8)\\ =& 1 - \Phi\left(-\frac{(\mu_1 - \mu_0)}{s/\sqrt{n}} + 1.645\right) && (18.9)\\ =& 1 - \Phi\left(-\frac{(\mu_1 - \mu_0)}{s}\sqrt{n} + 1.645\right) && (18.10)\end{aligned}$$

Thus, power is related to sample size n, the significance level α, and the effect size $(\mu_1 - \mu_0)/s$. If we assume $s = 2$, then the effect size is .5. With a sample size 100, the power from the above formulae is .999. In addition, we can solve the sample size n from the equation for a given power. For example, when the power is 0.8, we can get a sample size of 25. That is to say, to achieve a power 0.8, a sample size 25 is needed.

18.2 Practical power analysis using R

The R package webpower has functions to conduct power analysis for a variety of model. We now show how to use it.

18.2.1 Correlation coefficient

Correlation measures whether and how a pair of variables are related. In correlation analysis, we estimate a sample correlation coefficient, such as the Pearson Product Moment correlation coefficient (r). Values of the correlation coefficient are always between -1 and +1 and quantify the direction and strength of an association.

The correlation itself can be viewed as an effect size. The correlation coefficient is a standardized metric, and effects reported in the form of r can be directly compared. According to Cohen (1998), a correlation coefficient of .10 (0.1-0.23) is considered to represent a weak or small association; a correlation coefficient of .30 (0.24-0.36) is considered a moderate correlation; and a correlation coefficient of 0.50 (0.37 or higher) or larger is considered to represent a strong or large correlation.

We can obtain sample size for a significant correlation at a given alpha level or the power for a given sample size using the function `wp.correlation()` from the R package `webpower`. The function has the form of `wp.correlation(n = NULL, r = NULL, power = NULL, p = 0, rho0=0, alpha = 0.05, alternative = c("two.sided", "less", "greater"))`. Intuitively, `n` is the sample size and `r` is the effect size (correlation). If we provide values for `n` and `r` and set `power` to `NULL`, we can calculate a power. On the other hand, if we provide values for `power` and `r` and set `n` to `NULL`, we can calculate a sample size.

18.2.1.1 Example 1. Calculate power

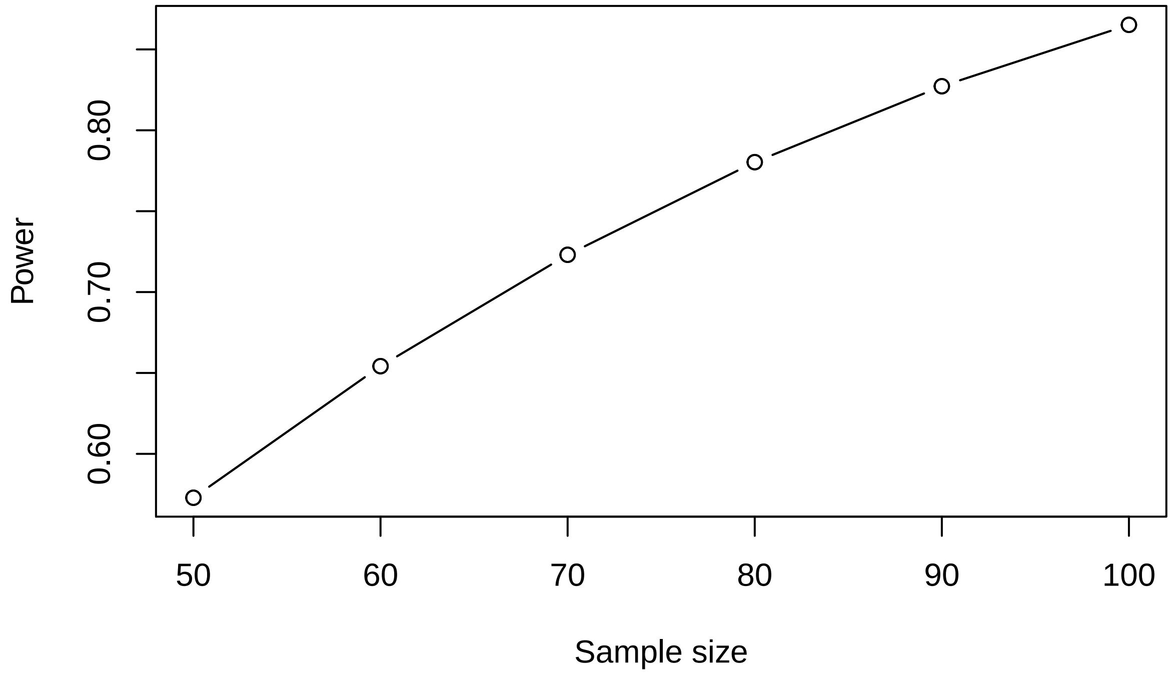
A student wants to study the relationship between stress and health. Based on her prior knowledge, she expects the two variables to be correlated with a correlation coefficient of 0.3. If she plans to collect data from 50 participants and measure their stress and health, what is the power for her to obtain a significant correlation using such a sample? Using R, we can easily see that the power is 0.573.

```
library(WebPower)
wp.correlation(n=50, r=0.3)
## Power for correlation
##
##      n   r alpha     power
##     50 0.3  0.05 0.5728731
##
## URL: http://psychstat.org/correlation
```

18.2.1.2 Example 2. Power curve

A power curve is a line plot of the statistical power along with the given sample sizes. In the example above, the power is 0.573 with the sample size 50. What is the power for a different sample size, say, 100? One can investigate the power of different sample sizes and plot a power curve. To do so, we can specify a set of sample sizes. The power curve can be used for interpolation. For example, to get a power 0.8, we need a sample size about 85.

```
example=wp.correlation(n=seq(50,100,10), r=0.3, alternative = "two.sided")
example
## Power for correlation
##
##       n   r alpha     power
##      50 0.3  0.05 0.5728731
##      60 0.3  0.05 0.6541956
##      70 0.3  0.05 0.7230482
##      80 0.3  0.05 0.7803111
##      90 0.3  0.05 0.8272251
##     100 0.3  0.05 0.8651692
##
## URL: http://psychstat.org/correlation

plot(example,type='b')
```



18.2.1.3 Example 3. Sample size planning

In practice, a power 0.8 is often desired. Given the power, the sample size can also be calculated as shown in the R output below. In the output, we can see a sample size 84, rounded to the near integer, is needed to obtain the power 0.8.

```
wp.correlation(n=NULL,r=0.3, power=0.8)
## Power for correlation
##
##            n   r alpha power
##     83.94932 0.3  0.05   0.8
##
## URL: http://psychstat.org/correlation
```

18.2.2 Two-sample mean (t-test)

A t-test is a statistical hypothesis test in which the test statistic follows a Student's t distribution if the null hypothesis is true, and a non-central t distribution if the alternative hypothesis is true. The t test can assess the statistical significance of the difference between population mean and a specific value, the difference between two independent population means and difference between means of matched pairs (dependent population means).

The effect size for a t-test is defined as

$$d = \frac{|\mu_1 - \mu_2|}{\sigma}$$

where μ_1 is the mean of the first group, μ_2 is the mean of the second group and σ^2 is the common error variance. In practice, there are many ways to estimate the effect size. One is Cohen's d, which is the sample mean difference divided by pooled standard deviation. For Cohen's d an effect size of 0.2 to 0.3 is a small effect, around 0.5 a medium effect and 0.8 to infinity, a large effect. Note the definition of small, medium, and large effect sizes is relative.

The power analysis for t-test can be conducted using the function `wp.t()`.

18.2.2.1 Example 1. Paired two-sample t-test

To test the effectiveness of a training intervention, a researcher plans to recruit a group of students and test them before and after training. Suppose the expected effect size is 0.3. How many participants are needed to maintain a 0.8 power?

```
wp.t(n1=NULL, d=.3, power=0.8, type='paired')
## Paired t-test
##
##            n   d alpha power
##     89.14936 0.3  0.05   0.8
##
## NOTE: n is number of *pairs*
## URL: http://psychstat.org/ttest
```

18.2.2.2 Example 2. Unpaired two-sample t-test

For the above example, suppose the researcher would like to recruit two groups of participants, one group receiving training and the other not. What would be the required sample size based on a balanced design (two groups are of the same size)?

```
wp.t(n1=NULL, d=.3, power=0.8, type='two.sample')
## Two-sample t-test
##
##            n   d alpha power
##     175.3847 0.3  0.05   0.8
##
## NOTE: n is number in *each* group
## URL: http://psychstat.org/ttest
```

18.2.2.3 Example 3. Unpaired two-sample t-test with unbalanced design

For the above example, if one group has a size 100 and the other 250, what would be the power?

```
wp.t(n1=100, n2=250, d=.3, power=NULL, type='two.sample.2n')
## Unbalanced two-sample t-test
##
##      n1  n2   d alpha     power
##     100 250 0.3  0.05 0.7151546
##
## NOTE: n1 and n2 are number in *each* group
## URL: http://psychstat.org/ttest2n
```

18.2.3 One-Way ANOVA

One-way analysis of variance (one-way ANOVA) is a technique used to compare means of two or more groups (e.g., Maxwell et al., 2003). The ANOVA tests the null hypothesis that samples in two or more groups are drawn from populations with the same mean values.

The statistic f can be used as a measure of effect size for one-way ANOVA as in Cohen (1988, p. 275). The f is the ratio between the standard deviation of the effect to be tested σ_b (or the standard deviation of the group means, or between-group standard deviation) and the common standard deviation within the populations (or the standard deviation within each group, or within-group standard deviation) σ_w such that

$$f = \frac{\sigma_b}{\sigma_w}.$$

Given the two quantities σ_m and σ_w, the effect size can be determined. Cohen defined the size of effect as: small 0.1, medium 0.25, and large 0.4.

The power analysis for one-way ANOVA can be conducted using the function `wp.anova()`.

18.2.3.1 Example 1. Power

A student hypothesizes that freshman, sophomore, junior and senior college students have different attitude towards obtaining arts degrees. Based on his prior knowledge, he expects that the effect size is about 0.25. If he plans to interview 25 students on their attitude in each student group, what is the power for him to find the significant difference among the four groups?

```
wp.anova(f=0.25,k=4,n=100,alpha=0.05)
## Power for One-way ANOVA
##
```

```
##     k   n    f alpha     power
##     4 100 0.25  0.05 0.5181755
##
## NOTE: n is the total sample size (overall)
## URL: http://psychstat.org/anova
```

18.2.3.2 Example 2. Minimum detectable effect

One can also calculate the minimum detectable effect to achieve certain power given a sample size. For the above example, we can see that to get a power 0.8 with the sample size 100, the population effect size has to be at least 0.337.

```
wp.anova(f=NULL,k=4,n=100,power=0.8, alpha=0.05)
## Power for One-way ANOVA
##
##     k   n         f alpha power
##     4 100 0.3369881  0.05   0.8
##
## NOTE: n is the total sample size (overall)
## URL: http://psychstat.org/anova
```

18.2.4 Linear regression

Linear regression is a statistical technique for examining the relationship between one or more independent variables and one dependent variable. The independent variables are often called predictors or covariates, while the dependent variable are also called outcome variable or criterion. Although regression is commonly used to test linear relationship between continuous predictors and an outcome, it may also test interaction between predictors and involve categorical predictors by utilizing dummy or contrast coding.

We use the effect size measure f^2 proposed by Cohen (1988, p.410) as the measure of the regression effect size. Cohen discussed the effect size in three different cases, which actually can be generalized using the idea of a full model and a reduced model by Maxwell et al. (2003). The f^2 is defined as

$$f^2 = \frac{R^2_{Full} - R^2_{Reduced}}{1 - R^2_{Full}},$$

where R^2_{Full} and $R^2_{Reduced}$ are R-squared for the full and reduced models respectively. Suppose we are evaluating the impact of one set of predictors (B) above and beyond a second set of predictors (A). Then R^2_{Full} is variance accounted for by variable set A and variable set B together and $R^2_{Reduced}$ is variance accounted for by variable set A only.

Cohen suggests f^2 values of 0.02, 0.15, and 0.35 represent small, medium, and large effect sizes. The power analysis for linear regression can be conducted using the function `wp.regression()`.

18.2.4.1 Example 1. Power

A researcher believes that a student's high school GPA and SAT score can explain 50% of variance of her/his college GPA. If she/he has a sample of 50 students, what is her/his power to find significant relationship between college GPA and high school GPA and SAT?

In this case, the $R^2_{Full} = 0.5$ for the model with both predictors (p1=2). Since the interest is about both predictors, the reduced model would be a model without any predictors (p2=0). Therefore, $R^2_{Reduced} = 0$. Then, the effect size $f^2 = 1$. Given the sample size, we can see the power is 1.

```
wp.regression(n=100, p1=2, f2=1)
## Power for multiple regression
##
##       n p1 p2 f2 alpha power
##     100  2  0  1  0.05     1
##
## URL: http://psychstat.org/regression
```

18.2.4.2 Example 2. Sample size

Another researcher believes in addition to a student's high school GPA and SAT score, the quality of recommendation letter is also important to predict college GPA. Based on some literature review, the quality of recommendation letter can explain an addition of 5% of variance of college GPA. In order to find significant relationship between college GPA and the quality of recommendation letter above and beyond high school GPA and SAT score with a power of 0.8, what is the required sample size?

In this case, the $R^2_{Full} = 0.55$ for the model with all three predictors (p1=3). Since the interest is about recommendation letter, the reduced model would be a model SAT and GPA only (p2=2). Therefore, $R^2_{Reduced} = 0.55$. Then, the effect size $f^2 = 0.111$. Given the required power 0.8, the resulting sample size is 75.

```
wp.regression(n=NULL, p1=3, p2=2, f2=0.111, power=0.8)
## Power for multiple regression
##
##            n p1 p2    f2 alpha power
##     74.68203  3  2 0.111  0.05   0.8
##
## URL: http://psychstat.org/regression
```

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