

Linear Models for Data Science

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Preface

Who is this book for?

There are many books on linear models, with various expectations for different levels of familiarity with statistical, mathematical, and coding concepts. These books generally fall into one of two camps:

1. Little to no familiarity with statistical and mathematical concepts, but fairly familiar to coding. These books tend to be written for programmers who want to get into data science. These books tend to explain linear models while trying to avoid statistical and mathematical concepts as much, only covering these concepts if absolutely necessary. These books tend to present linear models in a recipe format giving readers directions on what to do to build their models.

The drawback of such books is that readers do not get much understanding of the underlying concepts of linear models. It is impossible to give directions covering every possible scenario in the real world as real data are messy. Practitioners of data science often have to think outside the box in order to make linear models work for their particular data, and it is difficult to do so without understanding the mathematical framework of linear models.

2. Familiarity with mathematical notation and introductory statistical concepts such as statistical inference, and little to no familiarity with coding. These books tend to be written for mathematicians (or anyone with a strong background in mathematics) who want to get into data science. These books cover the mathematical framework of linear models thoroughly.

The drawback of such books is that readers must be comfortable with mathematical notation. This limits the audience for such books to people with fairly thorough training in mathematics. People without such training will get lost trying to read such books, and do not understand why we need to know the mathematical foundations to use linear models in data science.

This book is meant to be readable by both groups of readers. Some foundational mathematical knowledge will be presented, but will be written so that is

readable by anyone. This book will also explain what these knowledge mean in the context of data science. Practical advice, based on the foundational mathematical knowledge, will also be given.

This book accompanies the course STAT 6021: Linear Models for Data Science, for the Masters of Data Science (MSDS) program at the University of Virginia School of Data Science.

As introductory statistics and introductory programming are pre-requisites for entering the MSDS program, this book assumes basic knowledge of statistical inference and coding. Review materials covering these concepts are provided separately for enrolled students.

Data sets used

I have tried to use as many open source data sets as much as possible so that readers can work on the various examples I have provided on their own. However, some data sets may not be open source and have come from my experience teaching this class since 2019 (and variations of the class since 2013), and have used some data sets that were shared by other statistics and data science educators. It is my goal to eventually use only open source data sets.

Chapters

The chapters for the book is as follows:

Other resources

Some other resources that readers may want to check out:

- *OpenIntro Statistics*, 4th ed. Diez, Cetinkaya-Rundel, Barr, OpenIntro. Get free PDF version at <https://leanpub.com/os>, just set the price that you want to pay to \$0. This is a good book for introductory statistics.
- *Linear Models with R*, 2nd ed. Faraway. This is probably one of the few books that balances between the two camps that I wrote about earlier. It does require familiarity with matrices and linear algebra though.
- *Introduction to Linear Regression Analysis*, 5th or 6th ed. Montgomery, Peck, Vining. You may be able to access an e-version of the book through your university library if you are affiliated with a university. This book is mathematically rigorous so is useful to those who are interested in mathematical proofs that is not covered.
- *Applied Linear Statistical Models* (ALSM), Kutner, Nachtsheim, Neter, Li, 5th ed. This book covers a wide range of topics in linear models and is also mathematically rigorous.

- *Applied Linear Regression Models* (ALRM), Kutner, Nachtsheim, Neter, 4th ed. ALRM is the same as the first 14 chapters of ALSM. The second part of ALSM covers topics in Design of Experiments, which I highly recommend if you are interested in those topics.

Chapter 1

Data Wrangling with R

1.1 Introduction

The data structure that we will be dealing with most often will be data frames. When we read data in to R, they are typically stored as a data frame. A data frame can be viewed like an EXCEL spreadsheet, where data are stored in rows and columns. Before performing any analysis, we want the data frame to have this basic structure:

- Each row of the data frame corresponds to an observation.
- Each column of the data frame corresponds to a variable.

Sometimes, data are not structured in this way, and we will have to transform the data to take on this basic data structure. This process is called data wrangling. The most common and basic operations to transform the data are:

- Selecting a subset of columns of the data frame.
- Selecting a subset of rows of the data frame based on some criteria.
- Change column names.
- Find missing data.
- Create new variables based on existing variables.
- Combine multiple data frames.

We will explore two approaches to data wrangling:

- Using functions that already come pre-loaded with R (sometimes called base R).
- Using functions from the `dplyr` package.

These two approaches are quite different but can achieve the same goals in data wrangling. Each user of R usually ends up with their own preferred way of performing data wrangling operations, but it is important to know both approaches so you are able to work with a broader audience.

1.2 Data Wrangling using Base R Functions

We will use the dataset `ClassDataPrevious.csv` as an example. The data were collected from an introductory statistics class at UVa from a previous semester. Download the dataset from Canvas and read it into R.

```
Data<-read.csv("ClassDataPrevious.csv", header=TRUE)
```

We check the number of rows and columns in this dataframe.

```
dim(Data)
```

```
## [1] 298 8
```

There are 298 rows and 8 columns: so we have 298 students and 8 variables. We can also check the names for each column.

```
colnames(Data)
```

```
## [1] "Year"      "Sleep"     "Sport"     "Courses"   "Major"     "Age"       "Computer"
## [8] "Lunch"
```

The variables are:

1. **Year**: the year the student is in
2. **Sleep**: how much sleep the student averages a night (in hours)
3. **Sport**: the student's favorite sport
4. **Courses**: how many courses the student is taking in the semester
5. **Major**: the student's major
6. **Age**: the student's age (in years)
7. **Computer**: the operating system the student uses (Mac or PC)
8. **Lunch**: how much the student usually spends on lunch (in dollars)

1.2.1 View specific row(s) and/or column(s) of a data frame

We can view specific rows and/or columns of any data frame using the square brackets `[]`, for example:

```
Data[1,2] ##row index first, then column index
```

```
## [1] 8
```

The row index is listed first, then the column index, in the square brackets. This means the first student sleeps 8 hours a night. We can also view multiple rows and columns, for example:

```
Data[c(1,3,4),c(1,5,8)]
```

```
##      Year                Major Lunch
## 1 Second                Commerce    11
## 3 Second Cognitive science and psychology    10
```

```
## 4 First Pre-Comm 4
```

to view the 1st, 5th, and 8th variables for observations 1, 3, and 4.

There are several ways to view a specific column. For example, to view the 1st column (which is the variable called `Year`):

```
Data$Year ##or
Data[,1] ##or
Data[,c(2:8)]
```

Note the comma separates the indices for the row and column. An empty value before the comma means we want all the rows, and then the specific column. To view multiple columns, for example the first four columns:

```
Data[,1:4]
Data[,c(1,2,3,4)]
```

To view the values of certain rows, we can use

```
Data[c(1,3),]
```

to view the values for observations 1 and 3. An empty value after the comma means we want all the columns for those specific rows.

1.2.2 Select observations by condition(s)

We may want to only analyze certain subsets of our data, based on some conditions. For example, we may only want to analyze students whose favorite sport is soccer. The `which()` function in R helps us find the indices associated with a condition being met. For example:

```
which(Data$Sport=="Soccer")
```

```
## [1] 3 20 25 26 31 32 33 38 44 46 48 50 51 64 67 71 87 92 98
## [20] 99 118 122 124 126 128 133 136 137 143 146 153 159 165 174 197 198 207 211
## [39] 214 226 234 241 255 259 260 266 274 278 281 283 294 295
```

informs us which rows belong to observations whose favorite sport is soccer, i.e. the 3rd, 20th, 25th (and so on) students. We can create a new data frame that contains only students whose favorite sport is soccer:

```
SoccerPeeps<-Data[which(Data$Sport=="Soccer"),]
dim(SoccerPeeps)
```

```
## [1] 52 8
```

We are extracting the rows which satisfy the condition, favorite sport being soccer, and storing these rows into a new data frame called `SoccerPeeps`. We can see that this new data frame has 52 observations.

Suppose we want to have a data frame that satisfies two conditions: that the favorite sport is soccer and they are 2nd years at UVa. We can type:

```
SoccerPeeps_2nd<-Data[which(Data$Sport=="Soccer" & Data$Year=="Second"),]
dim(SoccerPeeps_2nd)
```

```
## [1] 25 8
```

This new data frame `SoccerPeeps_2nd` has 25 observations.

We can also set conditions based on numeric variables, for example, we want students who sleep more than eight hours a night

```
Sleepy<-Data[which(Data$Sleep>8),]
```

We can also create a data frame that contains students who satisfy at least one out of two conditions, for example, the favorite sport is soccer or they sleep more than 8 hours a night:

```
Sleepy_or_Soccer<-Data[which(Data$Sport=="Soccer" | Data$Sleep>8),]
```

1.2.3 Change column name(s)

For some datasets, the names of the columns are complicated or do not make sense. We should always give descriptive names to columns that make sense. For this dataset, the names are self-explanatory so we do not really need to change them. As an example, suppose we want to change the name of the 7th column from `Computer` to `Comp`:

```
names(Data)[7]<- "Comp"
```

To change the names of multiples columns (for example, the 1st and 7th columns), type:

```
names(Data)[c(1,7)]<-c("Yr", "Computer")
```

1.2.4 Find and remove missing data

There are a few ways to locate missing data. Using the `is.na()` function directly on a data frame produces a lot of output that can be messy to view:

```
is.na(Data)
```

On the other hand, using the `complete.cases()` function is more pleasing to view:

```
Data[!complete.cases(Data),]
```

##	Yr	Sleep	Sport	Courses	Major
## 103	Second	NA	Basketball	7	psychology and youth and social innovation
## 206	Second	8	None	4	Cognitive Science

```
##      Age Computer Lunch
## 103  19      Mac    10
## 206  19      Mac    NA
```

The code above will extract rows that are not complete cases, in other words, rows that have missing entries. The output informs us observation 103 has a missing value for `Sleep`, and observation 206 has a missing value for `Lunch`.

If you want to remove observations with a missing value, you can use one of the following two lines of code to create new data frames with the rows with missing values removed:

```
Data_nomiss<-na.omit(Data) ##or
Data_nomiss2<-Data[complete.cases(Data),]
```

A word of caution: these lines of code will remove the entire row as long as at least a column has missing entries. As noted earlier, observation 103 has a missing value for only the `Sleep` variable. But this observation still provides information on the other variables, which are now removed.

1.2.5 Summarizing variable(s)

Very often, we want to obtain some characteristics of our data. A common way to summarize a numerical variable is to find its mean. We have four numerical variables in our data frame, which are in columns 2, 4, 6, and 8. To find the mean of all four numerical variables, we can use the `apply()` function:

```
apply(Data[,c(2,4,6,8)],2,mean)
```

```
##      Sleep    Courses      Age      Lunch
##      NA  5.016779 19.573826      NA
```

```
apply(Data[,c(2,4,6,8)],2,mean,na.rm=T)
```

```
##      Sleep    Courses      Age      Lunch
## 155.559259  5.016779 19.573826 156.594175
```

Notice that due to the missing values, the first line has `NA` for some of the variables. The second line includes an optional argument, `na.rm=T`, which will remove the observations with an `NA` value for the variable from the calculation of the mean.

There are at least 3 arguments that are supplied to the `apply()` function:

1. The first argument is a data frame containing all the variables which we want to find the mean of. In this case, we want columns 2, 4, 6, and 8 of the data frame `Data`.
2. The second argument takes on the value 1 or 2. Since we want to find the mean of columns, rather than rows, we type 2. If want to mean of a row, we will type 1.

3. The third argument specifies the name of the function you want to apply to the columns of the supplied data frame. In this case, we want the mean. We can change this to find the median, standard deviation, etc, of these numeric variables if we want to.

We notice the means for some of the variables are suspiciously high, so looking at the medians will be more informative.

```
apply(Data[,c(2,4,6,8)],2,median,na.rm=T)
```

```
##   Sleep Courses      Age   Lunch
##    7.5      5.0    19.0     9.0
```

1.2.6 Summarizing variable by groups

Sometimes we want to summarize a variable by groups. Suppose we want to find the median amount of sleep separately for 1st years, 2nd years, 3rd years, and 4th years get. We can use the `tapply()` function:

```
tapply(Data$Sleep,Data$Yr,median,na.rm=T)
```

```
## First Fourth Second Third
##    8.0     7.0    7.5   7.0
```

This informs us the median amount of sleep first years get is 8 hours a night; for fourth years the median amount is 7 hours a night.

There are at least 3 arguments that are supplied to the `tapply()` function:

1. The first argument contains the vector which we want to summarize.
2. The second argument contains the factor which we use to subset our data. In this example, we want to subset according to `Yr`.
3. The third argument is the function which we want to apply to each subset of our data.
4. The fourth argument is optional, in this case, we want to remove observations with missing values from the calculation of the mean.

Notice the output orders the factor levels in alphabetical order. For our context, it is better to rearrange the levels to First, Second, Third, Fourth using the `factor()` function:

```
Data$Yr<-factor(Data$Yr, levels=c("First","Second","Third","Fourth"))
```

```
levels(Data$Yr)
```

```
## [1] "First" "Second" "Third" "Fourth"
```

```
tapply(Data$Sleep,Data$Yr,median,na.rm=T) ##much nicer
```

```
## First Second Third Fourth
##      8.0    7.5    7.0    7.0
```

This output makes a lot more sense for this context.

If we want to summarize a variable on groups formed by more than one variable, we need to adjust the second argument in the `tapply()` function by creating a list. Suppose we want to find the median sleep hour based on the `Yr` and the preferred operating system of the observations,

```
tapply(Data$Sleep,list(Data$Yr,Data$Computer),median,na.rm=T)
```

```
##           Mac    PC
## First  NA 8.0 7.50
## Second  7 7.5 7.50
## Third  NA 7.5 7.00
## Fourth NA 7.0 7.25
```

Interestingly, it looks like there were observations who did not specify which operating system they use, hence the extra column in the output.

1.2.7 Create a new variable based on existing variable(s)

Depending on the context of our analysis, we may need to create new variables based on existing variables. There are a few variations of this task, based on the type of variable you want to create, and the type of variable it is based on.

1.2.7.1 Create a numeric variable based on another numeric variable

The variable `Sleep` is in number of hours. Suppose we need to convert the values of `Sleep` to number of minutes, we can simply perform the following mathematical operation:

```
Sleep_mins<-Data$Sleep * 60
```

and store the transformed variable into a vector called `Sleep_mins`.

1.2.7.2 Create a binary variable based on a numeric variable

Suppose we want to create a binary variable (categorical variable with two levels), called `deprived`. An observation will obtain a value of “yes” if they sleep for less than 7 hours a night, and “no” otherwise. The `ifelse()` function is useful in creating binary variables:

```
deprived<-ifelse(Data$Sleep<7, "yes", "no")
```

There are 3 arguments associated with the `ifelse()` function:

1. The first argument is the condition that we wish to use.

2. The second argument is the value of the observation if the condition is true.
3. The third argument is the value of the observation if the condition is false.

1.2.7.3 Create a categorical variable based on a numeric variable

Suppose we want to create a categorical variable based on the number of courses a student takes. We will call this new variable `CourseLoad`, which takes on the following values:

- `light` if 3 courses or less,
- `regular` if 4 or 5 courses,
- `heavy` if more than 5 courses .

The `cut()` function is used in this situation

```
CourseLoad<-cut(Data$Courses, breaks = c(-Inf, 3, 5, Inf),
               labels = c("light", "regular", "heavy"))
```

There are three arguments that are applied to the `cut()` function:

1. The first argument is the vector which you are basing the new variable on.
2. The argument `breaks` lists how you want to set the intervals associated with `Data$Courses`. In this case, we are creating three intervals: one from $(-\infty, 3]$, another from $(3, 5]$, and the last interval from $(5, \infty]$.
3. The argument `labels` gives the label for `CourseLoad` associated with each interval.

1.2.7.4 Collapse levels

Sometimes, a categorical variable has more levels than we need for our analysis, and we want to collapse some levels. For example, the variable `Yr` has four levels: First, Second, Third, and Fourth. Perhaps we are more interested in comparing upperclassmen and underclassmen, so we want to collapse First and Second years into underclassmen, and Third and Fourth years into upperclassmen:

```
levels(Data$Yr)

## [1] "First" "Second" "Third" "Fourth"

new.levels<-c("und", "und", "up", "up")
Year2<-factor(new.levels[Data$Yr])
levels(Year2)

## [1] "und" "up"
```

The levels associated with the variable `Yr` are ordered as First, Second, Third, Fourth. The character vector `new.levels` has `und` as the first two characters,

and `upper` as the last two characters to correspond to the original levels in the variable `Yr`. The new variable is called `Year2`.

1.2.8 Combine data frames

We have created four new variables, `Sleep_mins`, `deprived`, `CourseLoad`, and `Year2`, based on previously existing variables. Since these variables are all based on the same observations, we can combine them with an existing data frame using the `data.frame()` function:

```
Data<-data.frame(Data,Sleep_mins,deprived,CourseLoad,Year2)
head(Data)
```

##	Yr	Sleep	Sport	Courses	Major	Age	Computer
## 1	Second	8	Basketball	6	Commerce	19	Mac
## 2	Second	7	Tennis	5	Psychology	19	Mac
## 3	Second	8	Soccer	5	Cognitive science and psychology	21	Mac
## 4	First	9	Basketball	5	Pre-Comm	19	Mac
## 5	Second	4	Basketball	6	Statistics	19	PC
## 6	Third	7	None	4	Psychology	20	PC

##	Lunch	Sleep_mins	deprived	CourseLoad	Year2
## 1	11	480	no	heavy	und
## 2	10	420	no	regular	und
## 3	10	480	no	regular	und
## 4	4	540	no	regular	und
## 5	0	240	yes	heavy	und
## 6	11	420	no	regular	up

Notice that since we listed the four new variables after `Data` in the `data.frame()` function, they appear after the original columns in the data frame.

Alternatively, we can use the `cbind()` function which gives the same data frame:

```
Data2<-cbind(Data,Sleep_mins,deprived,CourseLoad,Year2)
```

If you are combining data frames which have different observations but the same columns, we can merge them using `rbind()`:

```
dat1<-Data[1:3,1:3]
dat3<-Data[6:8,1:3]
res.dat2<-rbind(dat1,dat3)
head(res.dat2)
```

##	Yr	Sleep	Sport
## 1	Second	8	Basketball
## 2	Second	7	Tennis
## 3	Second	8	Soccer
## 6	Third	7	None
## 7	Second	7	Basketball

```
## 8 First      7 Basketball
```

1.2.9 Export data frame in R to a .csv file

To export a data frame to a .csv file, type:

```
write.csv(Data, file="newdata.csv", row.names = FALSE)
```

A file newdata.csv will be created in the working directory. Note that by default, the argument `row.names` is set to be `TRUE`. This will add a column in the dataframe which is an index number. I do not find this step useful in most analyses so I almost always set `row.names` to be `FALSE`.

1.2.10 Sort data frame by column values

To sort your data frame in ascending order by Age:

```
Data_by_age<-Data[order(Data$Age),]
```

To sort in descending order by Age:

```
Data_by_age_des<-Data[order(-Data$Age),]
```

To sort in ascending order by Age first, then by Sleep:

```
Data_by_age_sleep<-Data[order(Data$Age, Data$Sleep),]
```

1.3 Data Wrangling Using dplyr Functions

In the previous section, we were performing data wrangling operations using functions that are built in with base R. In this module, we will be using functions mostly from a package called `dplyr`, which can perform the same operations as well.

Before performing data wrangling operations, let us clear our environment, so that previously declared objects are removed. This allows us to start with a clean slate, which is often desirable when starting on a new analysis. This is done via:

```
rm(list = ls())
```

The `dplyr` package is a subset of the `tidyverse` package, so we can access these functions after installing and loading either package. After installing the `tidyverse` package, load it by typing:

```
##library(dplyr) or  
library(tidyverse)
```

The `dplyr` package was developed to make the syntax more intuitive to a broader range of R users, primarily through the use of pipes. However, the code involved

with functions from `dplyr` tends to be longer than code involved with base R functions, and there are more functions to learn with `dplyr`.

You will find a lot of articles on the internet by various R users about why each of them believes one approach to be superior to the other. I am not fussy about which approach you use as long as you can perform the necessary operations. It is to your benefit to be familiar with both approaches so you can work with a broader range of R users.

We will continue to use the dataset `ClassDataPrevious.csv` as an example. Download the dataset from Canvas and read it into R:

```
Data<-read.csv("ClassDataPrevious.csv", header=TRUE)
```

In the examples below, we are performing the same operations as in the previous section, but using `dplyr` functions instead of base R functions.

1.3.1 Select specific column(s) of a data frame

The `select()` function is used to select specific columns. There are a couple of ways to use this function. First:

```
select(Data, Year)
```

to select the column `Year` from the data frame called `Data`.

1.3.1.1 Pipes

Alternatively, we can use pipes:

```
Data%>%  
  select(Year)
```

Pipes in R are typed using `%>%` or by pressing Ctrl + Shift + M on your keyboard. To think of the operations above, we can read the code as

1. take the data frame called `Data`
2. and then select the column named `Year`.

We can interpret a pipe as “and then”. Commands after a pipe should be placed on a new line (press enter). Pipes are especially useful if we want to execute several commands in sequence, which we will see in later examples.

1.3.2 Select observations by condition(s)

The `filter()` function allows us to subset our data based on some conditions, for example, to select students whose favorite sport is soccer:

```
filter(Data, Sport=="Soccer")
```

We can create a new data frame called `SoccerPeeps` that contains students whose favorite sport is soccer:

```
SoccerPeeps<-Data%>%
  filter(Sport=="Soccer")
```

Suppose we want to have a data frame, called `SoccerPeeps_2nd`, that satisfies two conditions: that the favorite sport is soccer and they are 2nd years at UVa:

```
SoccerPeeps_2nd<-Data%>%
  filter(Sport=="Soccer" & Year=="Second")
```

We can also set conditions based on numeric variables, for example, we want the students who sleep more than eight hours a night:

```
Sleepy<-Data%>%
  filter(Sleep>8)
```

We can also create a data frame that contains observations as long as they satisfy at least one out of two conditions: the favorite sport is soccer or they sleep more than 8 hours a night:

```
Sleepy_or_Soccer<-Data%>%
  filter(Sport=="Soccer" | Sleep>8)
```

1.3.3 Change column name(s)

It is straightforward to change the names of columns using the `rename()` function. For example:

```
Data<-Data%>%
  rename(Yr=Year, Comp=Computer)
```

allows us to change the name of two columns: from `Year` and `Computer` to `Yr` and `Comp`.

1.3.4 Summarizing variable(s)

The `summarize()` function allows us to summarize a column. Suppose we want to find the mean value of the numeric columns: `Sleep`, `Courses`, `Age`, and `Lunch`:

```
Data%>%
  summarize(mean(Sleep, na.rm = T), mean(Courses), mean(Age), mean(Lunch, na.rm = T))
```

```
##   mean(Sleep, na.rm = T) mean(Courses) mean(Age) mean(Lunch, na.rm = T)
## 1           155.5593      5.016779   19.57383           156.5942
```

The output looks a bit cumbersome. We can give names to each summary

```
Data%>%
  summarize(avgSleep=mean(Sleep,na.rm = T),avgCourse=mean(Courses),avgAge=mean(Age),
            avgLun=mean(Lunch,na.rm = T))

##   avgSleep avgCourse  avgAge  avgLun
## 1 155.5593  5.016779 19.57383 156.5942
```

As mentioned previously, the means look suspiciously high for a couple of variables, so looking at the medians may be more informative:

```
Data%>%
  summarize(medSleep=median(Sleep,na.rm = T),medCourse=median(Courses),
            medAge=median(Age),medLun=median(Lunch,na.rm = T))

##   medSleep medCourse medAge medLun
## 1      7.5         5     19      9
```

Note: For a lot of functions in the `dplyr` package, using American spelling or British spelling works. So we can use `summarise()` instead of `summarize()`.

1.3.5 Summarizing variable by groups

Suppose we want to find the median amount of sleep 1st years, 2nd years, 3rd years, and 4th years get. We can use the `group_by()` function:

```
Data%>%
  group_by(Yr)%>%
  summarize(medSleep=median(Sleep,na.rm=T))

## # A tibble: 4 x 2
##   Yr      medSleep
##   <chr>      <dbl>
## 1 First         8
## 2 Fourth        7
## 3 Second       7.5
## 4 Third         7
```

The way to read the code above is

1. Get the data frame called `Data`,
2. and then group the observations by `Yr`,
3. and then find the median amount of sleep by each `Yr` and store the median in a vector called `medSleep`.

As seen previously, the ordering of the factor levels is in alphabetical order. For our context, it is better to rearrange the levels to First, Second, Third, Fourth. We can use the `mutate()` function whenever we want to transform or create a new variable. In this case, we are transforming the variable `Yr` by reordering the factor levels with the `fct_relevel()` function:

```
Data<- Data%>%
  mutate(Yr = Yr%>%
    fct_relevel(c("First","Second","Third","Fourth")))
```

1. Get the data frame called `Data`,
2. and then transform the variable called `Yr`,
3. and then reorder the factor levels.

Then, we use pipes, the `group_by()`, and `summarize()` functions like before:

```
Data%>%
  group_by(Yr)%>%
  summarize(medSleep=median(Sleep,na.rm=T))
```

```
## # A tibble: 4 x 2
##   Yr      medSleep
##   <fct>      <dbl>
## 1 First         8
## 2 Second       7.5
## 3 Third         7
## 4 Fourth         7
```

This output makes a lot more sense for this context.

To summarize a variable on groups formed by more than one variable, we just add the other variables in the `group_by()` function:

```
Data%>%
  group_by(Yr,Comp)%>%
  summarize(medSleep=median(Sleep,na.rm=T))
```

```
## `summarise()` has grouped output by 'Yr'. You can override using the `.groups`
## argument.
```

```
## # A tibble: 9 x 3
## # Groups:   Yr [4]
##   Yr      Comp medSleep
##   <fct> <chr>      <dbl>
## 1 First "Mac"         8
## 2 First "PC"         7.5
## 3 Second ""          7
## 4 Second "Mac"       7.5
## 5 Second "PC"       7.5
## 6 Third "Mac"       7.5
## 7 Third "PC"         7
## 8 Fourth "Mac"         7
## 9 Fourth "PC"       7.25
```

1.3.6 Create a new variable based on existing variable(s)

As mentioned in the previously, the `mutate()` function is used to transform a variable or to create a new variable. There are a few variations of this task, based on the type of variable you want to create, and the type of variable it is based on.

1.3.6.1 Create a numeric variable based on another numeric variable

The variable `Sleep` is in number of hours. Suppose we need to convert the values of `Sleep` to number of minutes, we can simply perform the following mathematical operation:

```
Data<-Data%>%  
  mutate(Sleep_mins = Sleep*60)
```

and store the transformed variable called `Sleep_mins` and add `Sleep_mins` to the data frame called `Data`.

1.3.6.2 Create a binary variable based on a numeric variable

Suppose we want to create a binary variable, called `deprived`. An observation will obtain a value of `yes` if they sleep for less than 7 hours a night, and `no` otherwise. We will then add this variable `deprived` to the data frame called `Data`:

```
Data<-Data%>%  
  mutate(deprived=ifelse(Sleep<7, "yes", "no"))
```

1.3.6.3 Create a categorical variable based on a numeric variable

Suppose we want to create a categorical variable based on the number of courses a student takes. We will call this new variable `CourseLoad`, which takes on the following values:

- `light` if 3 courses or less,
- `regular` if 4 or 5 courses,
- `heavy` if more than 5 courses

and then add `CourseLoad` to the data frame `Data`. We can use the `case_when()` function from the `dplyr` package, instead of the `cut()` function:

```
Data<-Data%>%  
  mutate(CourseLoad=case_when(Courses <= 3 ~ "light",  
                              Courses >3 & Courses <=5 ~ "regular",  
                              Courses > 5 ~ "heavy"))
```

Notice how the names of the categorical variable are supplied after a specific condition is specified.

1.3.6.4 Collapsing levels

Sometimes, a categorical variable has more levels than we need for our analysis, and we want to collapse some levels. For example, the variable `Yr` has four levels: First, Second, Third, and Fourth. Perhaps we are more interested in comparing between upperclassmen and underclassmen, so we want to collapse First and Second Yrs into underclassmen, and Third and Fourth Yrs into upperclassmen. We will use the `fct_collapse()` function:

```
Data<-Data%>%
  mutate(UpUnder=fct_collapse(Yr,under=c("First","Second"),up=c("Third","Fourth")))
```

We are creating a new variable called `UpUnder`, which is done by collapsing `First` and `Second` into a new factor called `under`, and collapsing `Third` and `Fourth` into a new factor called `up`. `UpUnder` is also added to the data frame `Data`.

1.3.7 Combine data frames

To combine data frames which have different observations but the same columns, we can combine them using `bind_rows()`:

```
dat1<-Data[1:3,1:3]
dat3<-Data[6:8,1:3]
res.dat2<-bind_rows(dat1,dat3)
head(res.dat2)
```

```
##      Yr Sleep      Sport
## 1 Second     8 Basketball
## 2 Second     7      Tennis
## 3 Second     8      Soccer
## 4 Third      7        None
## 5 Second     7 Basketball
## 6 First      7 Basketball
```

`bind_rows()` works the same way as `rbind()`. Likewise, we can use `bind_cols()` instead of `cbind()`.

1.3.8 Sort data frame by column values

To sort your data frame in ascending order by `Age`:

```
Data_by_age<-Data%>%
  arrange(Age)
```

To sort in descending order by `Age`:

```
Data_by_age_des<-Data%>%
  arrange(desc(Age))
```


To sort in ascending order by `Age` first, then by `Sleep`:

```
Data_by_age_sleep<-Data%>%  
  arrange(Age,Sleep)
```


Chapter 2

Data Visualization with R Using ggplot2

2.1 Introduction

Data visualizations are tools that summarize data. Consider the visuals from the CDC covid tracker dashboard to an external site. Without actually having access to the actual data, we have a sense of trends associated with hospitalizations and deaths. Good visualizations are easy to interpret for a wide variety of audiences, and are easier to explain than statistical models.

In this module, you will learn how to create common data visualizations. The choice of data visualization is almost always determined by whether the variable(s) involved is categorical or quantitative. Discrete variables are interesting because depending on the circumstance, they can be viewed as either categorical or quantitative in the context of data visualizations.

We will be using functions from the `ggplot2` package to create visualizations. The `ggplot2` package enables users to create various kinds of data visualizations, beyond the visualizations that can be made in base R. The `ggplot2` package is automatically loaded when we load the `tidyverse` package, although we can load `ggplot2` on its own.

```
library(tidyverse)
```

We will use the dataset `ClassDataPrevious.csv` as an example. The data were collected from an introductory statistics class at UVa from a previous semester. Download the dataset from Canvas and read it into R.

```
Data<-read.csv("ClassDataPrevious.csv", header=TRUE)
```

The variables are:

1. **Year:** the year the student is in
2. **Sleep:** how much sleep the student averages a night (in hours)
3. **Sport:** the student's favorite sport
4. **Courses:** how many courses the student is taking in the semester
5. **Major:** the student's major
6. **Age:** the student's age (in years)
7. **Computer:** the operating system the student uses (Mac or PC)
8. **Lunch:** how much the student usually spends on lunch (in dollars)

2.2 Visualizations with a Single Categorical Variable

2.2.1 Frequency tables

Frequency tables are a common tool to summarize categorical variables. These tables give us the number of observations (sometimes called counts) that belong to each class of a categorical variable. These tables are created using the `table()` function. Suppose we want to see the number of students in each year in our data:

```
table(Data$Year)
```

```
##
##  First Fourth Second  Third
##    83     30   139    46
```

Notice the order of the years could be rearranged to make more sense:

```
Data$Year<-factor(Data$Year, levels=c("First","Second","Third","Fourth"))
levels(Data$Year)
```

```
## [1] "First" "Second" "Third" "Fourth"
```

```
mytab<-table(Data$Year)
mytab
```

```
##
##  First Second  Third Fourth
##    83   139    46    30
```

So we have 83 first years, 139 second years, 46 third years, and 30 fourth years in our dataset.

We can report these numbers using proportions instead of counts, using `prop.table()`:

```
prop.table(mytab)
```

```
##
```

```
##      First      Second      Third      Fourth
## 0.2785235 0.4664430 0.1543624 0.1006711
```

or percentages by multiplying by 100:

```
prop.table(mytab) * 100
```

```
##
##      First      Second      Third      Fourth
## 27.85235 46.64430 15.43624 10.06711
```

To round the percentages to two decimal places, use the `round()` function:

```
round(prop.table(mytab) * 100, 2)
```

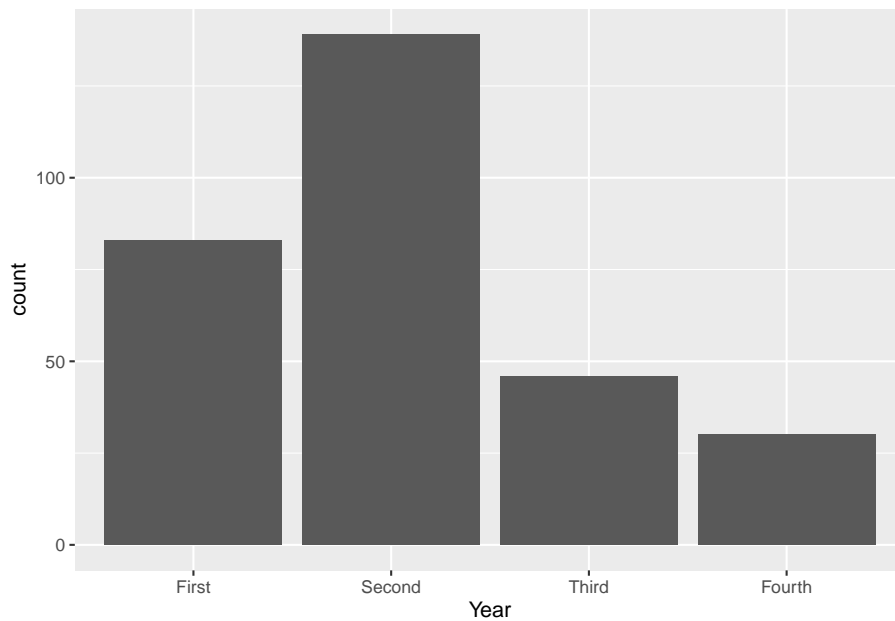
```
##
##      First Second      Third Fourth
##   27.85   46.64   15.44   10.07
```

So about 27.85% of these students are first years, 46.64% are second years, 15.44% are third years, and 10.07% are fourth years.

2.2.2 Bar charts

Bar charts are a simple way to visualize categorical data, and can be viewed as a visual representation of frequency tables. To create a bar chart for the years of these students, we use:

```
ggplot(Data, aes(x=Year)) +
  geom_bar()
```



We can read the number of students who are first, second, third, and fourth years by reading off the corresponding value on the vertical axis.

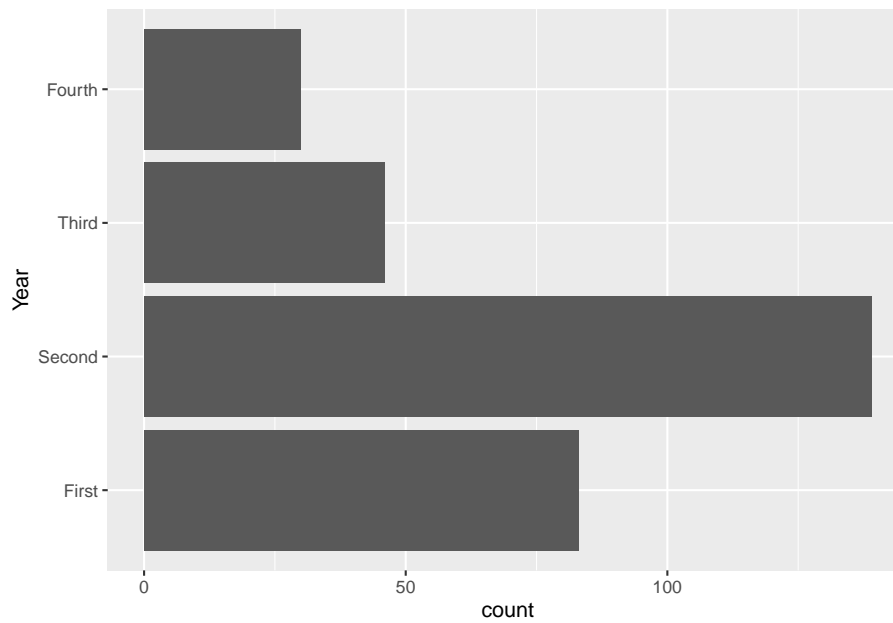
From these two lines we code, we can see the basic structure of creating data visualizations with the `ggplot()` function:

1. Use the `ggplot()` function, and supply the name of the data frame, and the x- and/or y- variables via the `aes()` function. End this line with a `+` operator, and then press enter.
2. In the next line, specify the type of graph we want to create (called `geoms`). For a bar chart, type `geom_bar()`.

Some describe these lines of code as two layers of code. These two layers must be supplied for all data visualizations with `ggplot()`.

Additional optional layers can be added (these usually deal with the details of the visuals). Suppose we want to change the orientation of this bar chart, we can add an optional line, or layer:

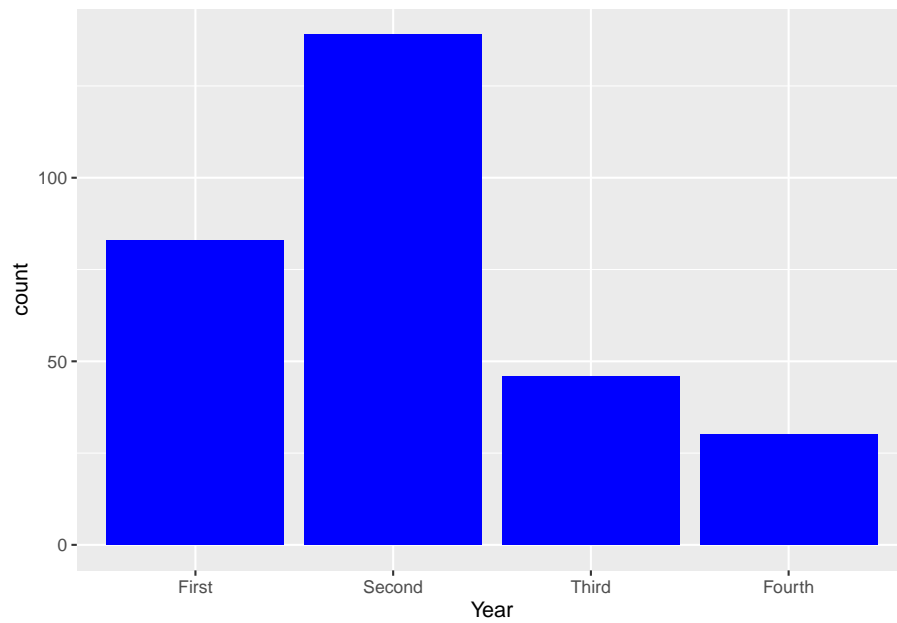
```
ggplot(Data, aes(x=Year))+
  geom_bar()+
  coord_flip()
```



It is recommended that each layer is typed on a line below the previous layer. A + sign is used at the end of each layer to add another layer below.

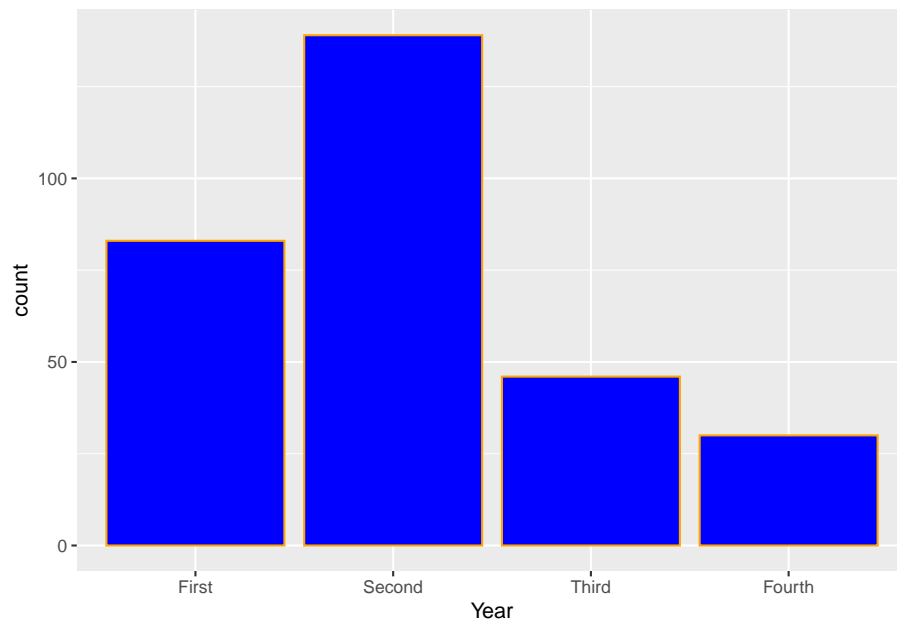
To change the color of the bars:

```
ggplot(Data, aes(x=Year))+  
  geom_bar(fill="blue")
```



To have a different color to outline the bars:

```
ggplot(Data, aes(x=Year))+  
  geom_bar(fill="blue",color="orange")
```

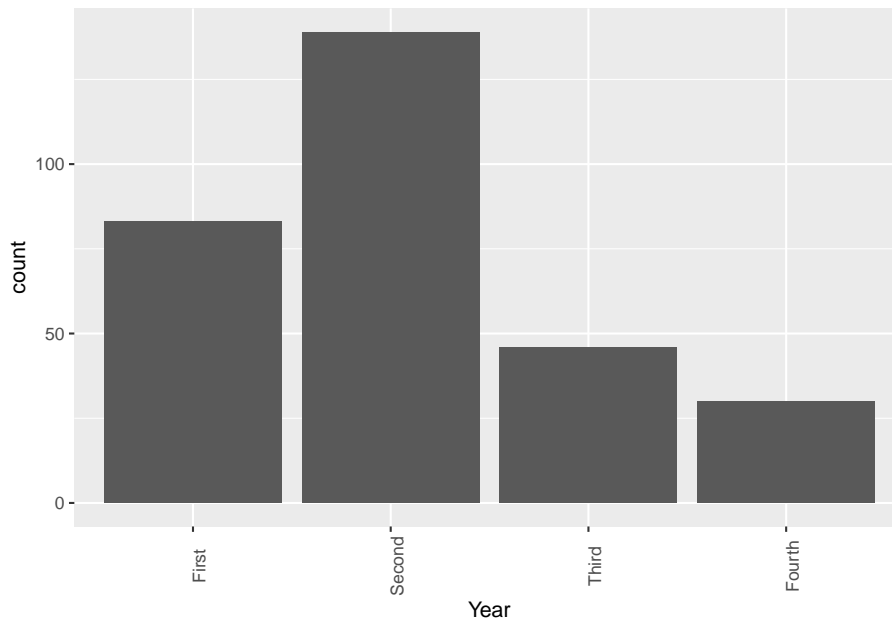


2.2.2.1 Customize title and labels of axes in bar charts

To change the orientation of the labels on the horizontal axis, we add an extra layer called `theme`. This will be useful when we have many classes and/or labels with long names.

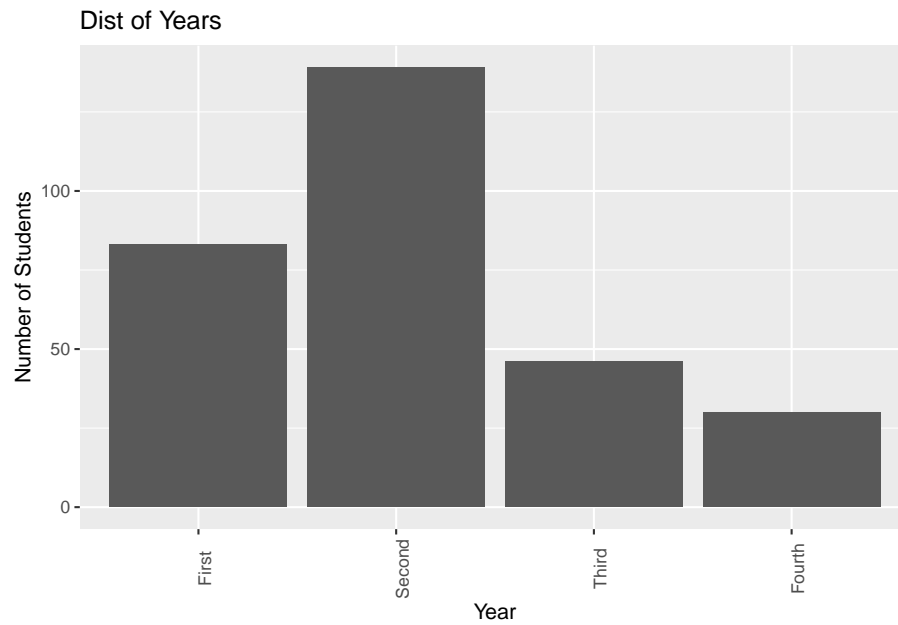
To rotate the labels on the horizontal by 90 degrees:

```
ggplot(Data, aes(x=Year)) +  
  geom_bar() +  
  theme(axis.text.x = element_text(angle = 90))
```



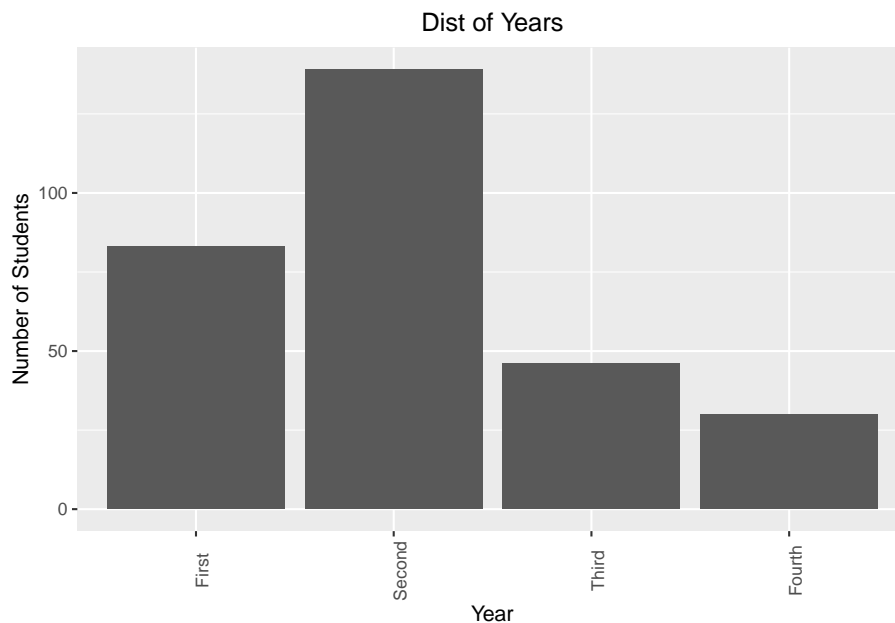
As we create more visualizations, it is good practice to give short but meaningful and descriptive names for each axis and provide a title. We can change the labels of the x- and y- axes, as well as add a title for the bar chart by adding another layer called `labs`:

```
ggplot(Data, aes(x=Year)) +  
  geom_bar() +  
  theme(axis.text.x = element_text(angle = 90)) +  
  labs(x="Year", y="Number of Students", title="Dist of Years")
```



We can also adjust the position of the title, for example, center-justify it via `theme`:

```
ggplot(Data, aes(x=Year))+  
  geom_bar()+  
  theme(axis.text.x = element_text(angle = 90),  
        plot.title = element_text(hjust = 0.5))+  
  labs(x="Year", y="Number of Students", title="Dist of Years")
```



2.2.2.2 Create a bar chart using proportions

Suppose we want to create a bar chart where the y-axis displays the proportions, rather than the counts of each level. There are a few steps to produce such a bar chart. First, we create a new dataframe, where each row represents a year, and we add the proportion of each year into a new column:

```
newData<-Data%>%
  group_by(Year)%>%
  summarize(Counts=n())%>%
  mutate(Percent=Counts/nrow(Data))
```

The code above does the following:

1. Creates a new data frame called **newData** by taking the data frame called **Data**,
2. and then groups the observations by **Year**,
3. and then counts the number of observations in each **Year** and stores these values in a vector called **Counts**,
4. and then creates a new vector called **Percent** by using the mathematical operations as specified in **mutate()**. **Percent** is added to **newData**.

We can take a look at the contents of **newData**:

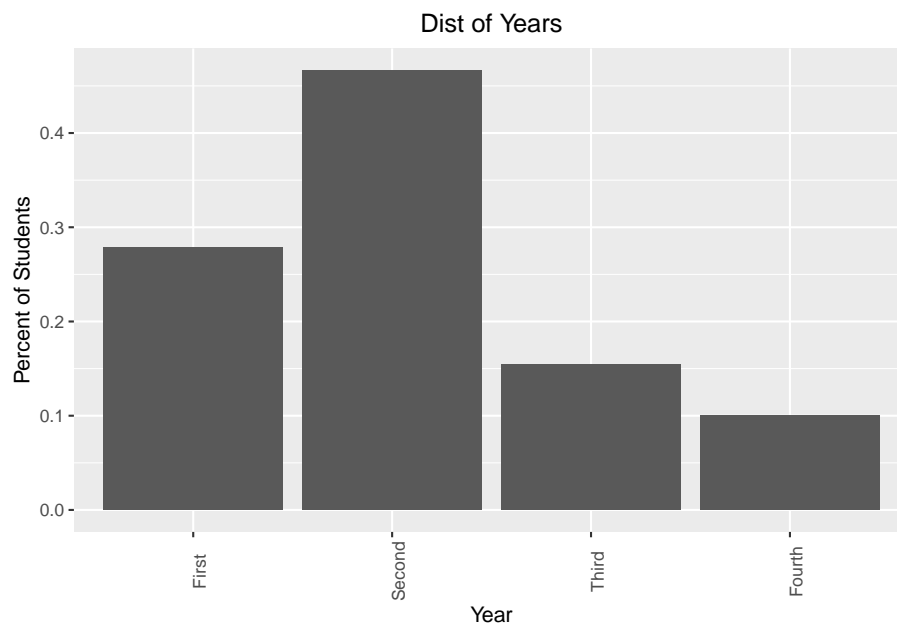
```
newData

## # A tibble: 4 x 3
##   Year    Counts Percent
```

```
##   <fct>    <int>    <dbl>
## 1 First      83    0.279
## 2 Second    139    0.466
## 3 Third     46    0.154
## 4 Fourth    30    0.101
```

To create a bar chart using proportions:

```
ggplot(newData, aes(x=Year, y=Percent))+
  geom_bar(stat="identity")+
  theme(axis.text.x = element_text(angle = 90),
        plot.title = element_text(hjust = 0.5))+
  labs(x="Year", y="Percent of Students", title="Dist of Years")
```



Note the following:

1. In the first layer, we use `newData` instead of the old data frame. In `aes()`, we specified a y-variable, which we want to be `Percent`.
2. In the second layer, we specified `stat="identity"` inside `geom_bar()`.

2.3 Visualizations with a Single Quantitative Variable

2.3.1 5 number summary

The `summary()` function, when applied to a quantitative variable, produces the 5 number summary: the minimum, the first quartile (25th percentile), the median (50th percentile), the third quartile (75th percentile), and the maximum, as well as the mean. For example, to obtain the 5 number summary of the ages of these students:

```
summary(Data$Age)
```

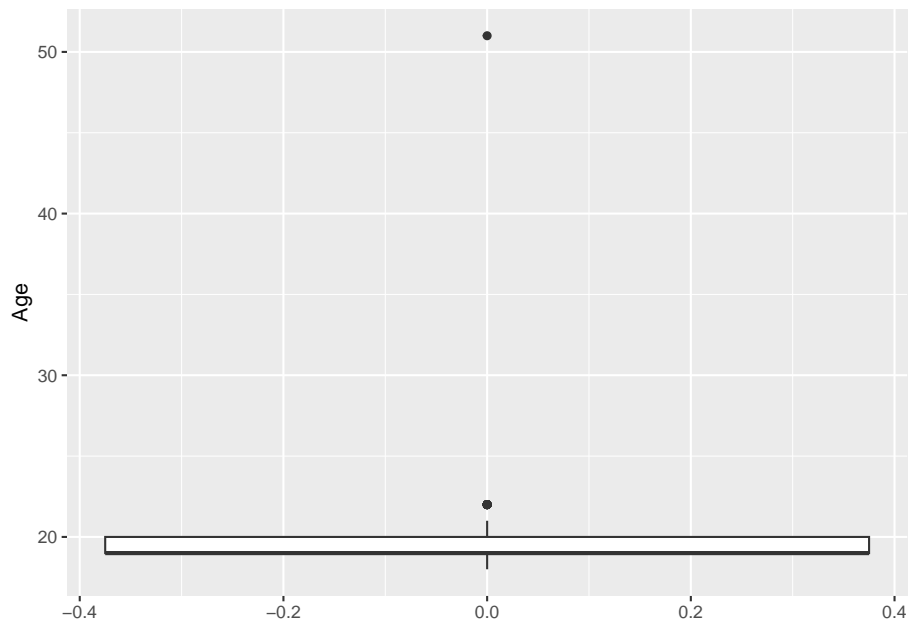
```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##  18.00   19.00   19.00   19.57   20.00   51.00
```

The average age of the observations in this dataset is 19.57 years old. Notice the first quartile and the median are both 19 years old, that means at least a quarter of the observations are 19 years old. Also note the maximum of 51 years old, so we have a student who is quite a lot older than the rest.

2.3.2 Boxplots

A boxplot is a graphical representation of the 5 number summary. To create a generic boxplot, we have the following two lines of code when using the `ggplot()` function:

```
ggplot(Data, aes(y=Age))+
  geom_boxplot()
```



Note we are still using the same structure when creating data visualizations with `ggplot()`:

1. Use the `ggplot()` function, and supply the name of the data frame, and the x- and/or y- variables via the `aes()` function. End this line with a `+` operator, and then press enter.
2. In the next line, specify the type of graph we want to create (called **geoms**). For a boxplot, type `geom_boxplot`.

Notice there are outliers (observations that are a lot older or younger) that are denoted by the dots. One is the 51 year old, and 22 year olds are deemed to be outliers. The rule being used is the $1.5 \times IQR$ rule.

Similar to bar charts, we can change the orientation of boxplots by adding an additional layer as before:

```
ggplot(Data, aes(y=Age))+
  geom_boxplot()+
  coord_flip()
```

We can change the color of the box and the outliers similarly:

```
ggplot(Data, aes(y=Age))+
  geom_boxplot(color="blue", outlier.color = "orange" )
```

2.3.3 Histograms

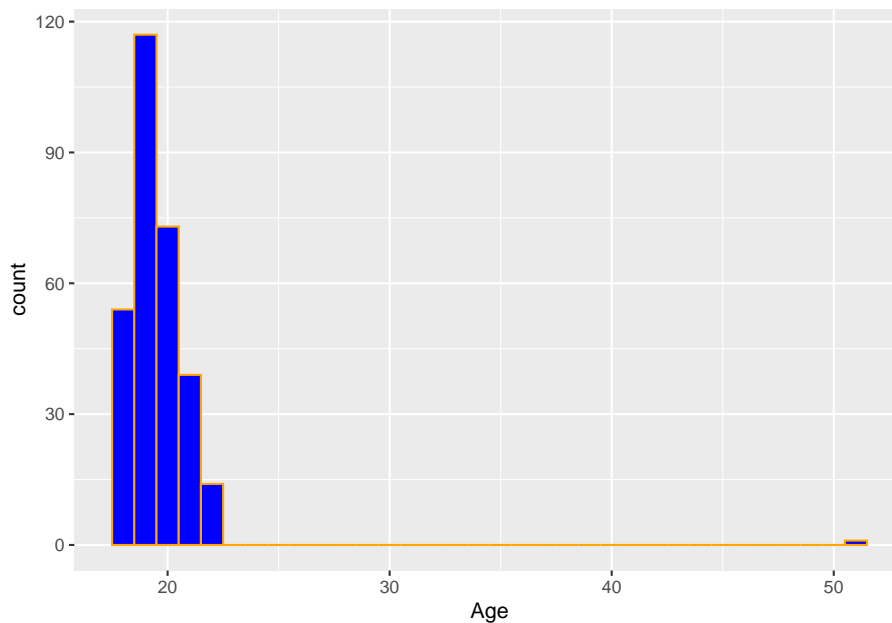
A histogram displays the number of observations within each bin on the x-axis:

```
ggplot(Data,aes(x=Age))+  
  geom_histogram()
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

Notice a warning message is displayed when creating a basic histogram. To fix this, we use the `binwidth` argument within `geom_histogram`. We try `binwidth=1` for now, which means the width of the bin is 1 unit:

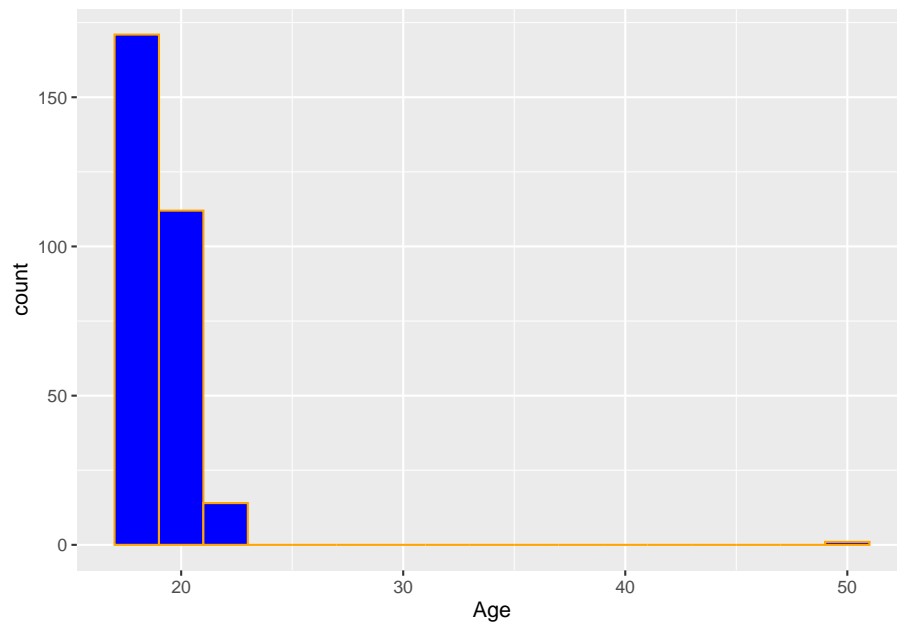
```
ggplot(Data,aes(x=Age))+  
  geom_histogram(binwidth = 1,fill="blue",color="orange")
```



The ages of the students are mostly young, with 19 and 20 years olds being the most commonly occurring.

A well-known drawback of histograms is that the width of the bins can drastically affect the visual. For example, suppose we change the `binwidth` to 2:

```
ggplot(Data,aes(x=Age))+  
  geom_histogram(binwidth = 2,fill="blue",color="orange")
```

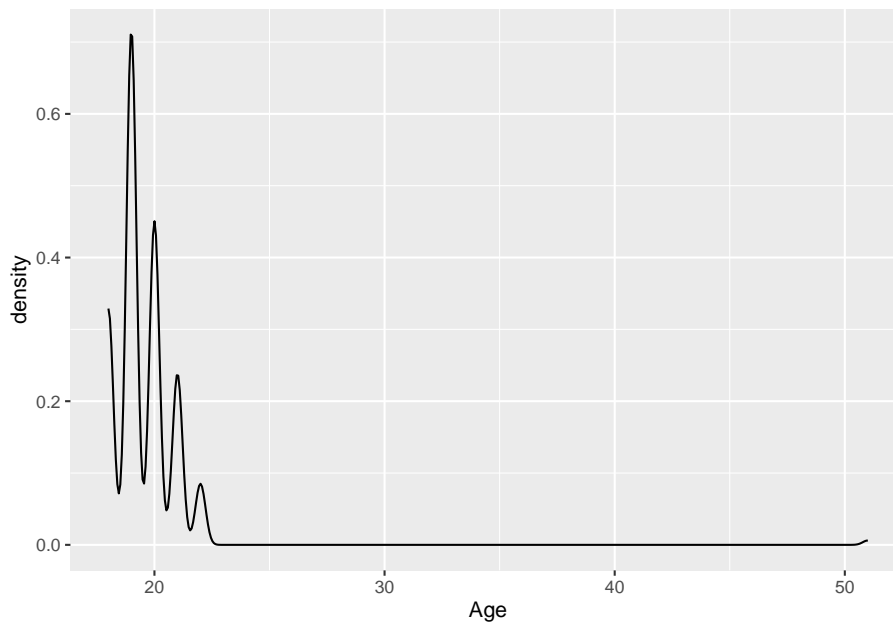


Each bar now contains two ages: the first bar contains the 18 and 19 year olds. Notice how the shape has been changed a little bit from the previous histogram with a different binwidth?

2.3.4 Density plots

Density plots are a variation of histograms, where the plot attempts to use a smooth mathematical function to approximate the shape of the histogram, and is unaffected by binwidth:

```
ggplot(Data, aes(x=Age)) +  
  geom_density()
```

We can see that 19 and 20 year olds are the most common ages in this data. Be careful in interpreting the values on the vertical axis: these do not represent proportions. A characteristic of density plots is that the area under the plot is always one.

2.4 Bivariate Visualizations

We will now look at visualizations we can create to explore the relationship between two variables. The term bivariate means that we are looking at two variables.

We will be using a new dataset as an example, so we clear the environment:

```
rm(list = ls())
```

We will be using the dataset, `gapminder`, from the `gapminder` package. Install and load the `gapminder` package. Also load the `tidyverse` package (which automatically loads the `ggplot2` package):

```
library(tidyverse)
library(gapminder)
```

We can take a look at the `gapminder` dataset:

```
gapminder[1:15,]
```

```
## # A tibble: 15 x 6
```

	country	continent	year	lifeExp	pop	gdpPercap
	<fct>	<fct>	<int>	<dbl>	<int>	<dbl>
##	1 Afghanistan	Asia	1952	28.8	8425333	779.
##	2 Afghanistan	Asia	1957	30.3	9240934	821.
##	3 Afghanistan	Asia	1962	32.0	10267083	853.
##	4 Afghanistan	Asia	1967	34.0	11537966	836.
##	5 Afghanistan	Asia	1972	36.1	13079460	740.
##	6 Afghanistan	Asia	1977	38.4	14880372	786.
##	7 Afghanistan	Asia	1982	39.9	12881816	978.
##	8 Afghanistan	Asia	1987	40.8	13867957	852.
##	9 Afghanistan	Asia	1992	41.7	16317921	649.
##	10 Afghanistan	Asia	1997	41.8	22227415	635.
##	11 Afghanistan	Asia	2002	42.1	25268405	727.
##	12 Afghanistan	Asia	2007	43.8	31889923	975.
##	13 Albania	Europe	1952	55.2	1282697	1601.
##	14 Albania	Europe	1957	59.3	1476505	1942.
##	15 Albania	Europe	1962	64.8	1728137	2313.

Per the documentation, the variables are

1. country
2. continent
3. year: from 1952 to 2007 in increments of 5 years
4. lifeExp: life expectancy at birth, in years
5. pop: population of country
6. gdpPercap: GDP per capita in US dollars, adjusted for inflation

We notice that data are collected from each country across a number of different years: 1952 to 2007 in increments of five years. For this example, we will mainly focus on the data for the most recent year, 2007:

```
Data <- gapminder %>%
  filter(year == 2007)
```

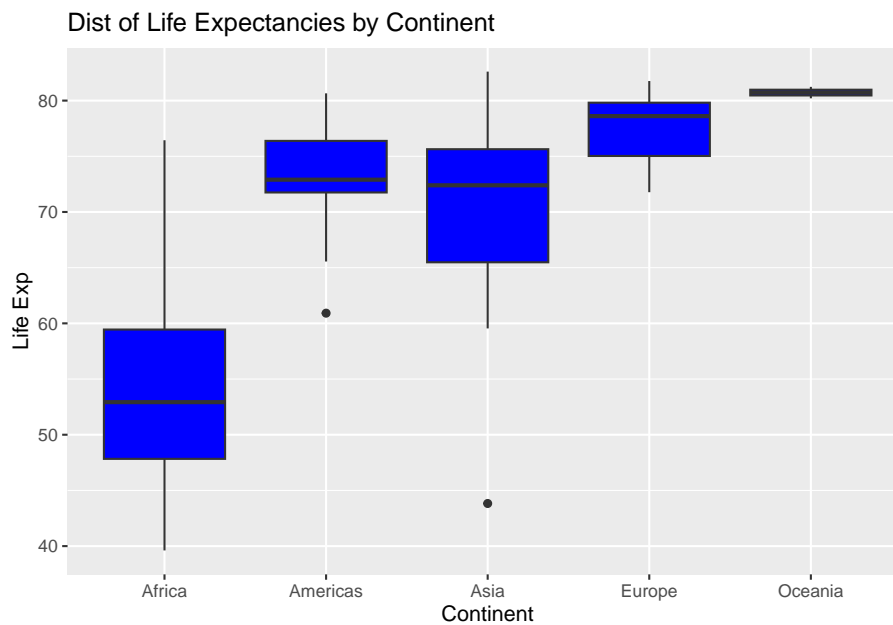
The specific visuals to use will again depend on the type of variables we are using, whether they are categorical or quantitative.

2.4.1 Compare quantitative variable across categories

2.4.1.1 Side by side boxplots

Side by side boxplots are useful to compare a quantitative variable across different classes of a categorical variable. For example, we want to compare life expectancies across the different continents in the year 2007:

```
ggplot(Data, aes(x=continent, y=lifeExp)) +
  geom_boxplot(fill="Blue") +
  labs(x="Continent", y="Life Exp", title="Dist of Life Expectancies by Continent")
```

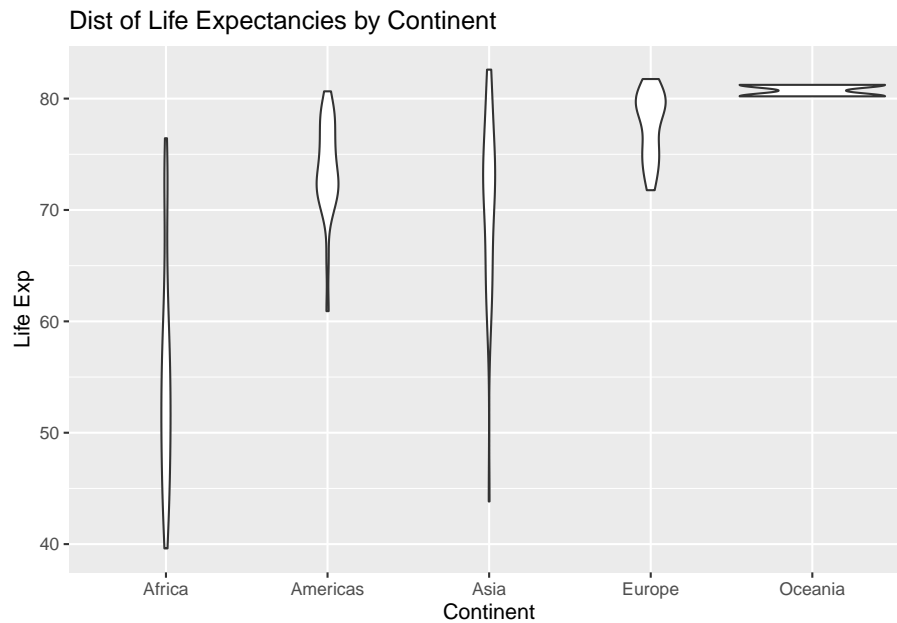


Countries in the Oceania region have long life expectancies with little variation. Comparing the Americas and Asia, the median life expectancies are similar, but the spread is larger for Asia.

2.4.1.2 Violin plots

Violin plots are an alternative to boxplots. To create these plots to compare life expectancies across the different continents in the year 2007:

```
ggplot(Data, aes(x=continent, y=lifeExp))+  
  geom_violin()+  
  labs(x="Continent", y="Life Exp", title="Dist of Life Expectancies by Continent")
```



The width of the violin informs us which values are more commonly occurring. For example, look at the violin for Europe. The violin is wider at higher life expectancies, so longer life expectancies are more common in European countries.

2.4.2 Summarizing two categorical variables

For this example, we create a new binary variable called `expectancy`, which will be denoted as `low` if the life expectancy in the country is less than 70 years, and `high` otherwise:

```
Data<-Data%>%
  mutate(expectancy=ifelse(lifeExp<70,"Low","High"))
```

2.4.2.1 Two-way tables

Suppose we want to see how `expectancy` varies across the continents. A two-way table can be created for produce counts when two categorical variables are involved:

```
mytab2<-table(Data$continent, Data$expectancy)
##continent in rows, expectancy in columns
mytab2
```

```
##
##           High Low
## Africa         7 45
```

```
## Americas 22 3
## Asia      22 11
## Europe    30 0
## Oceania   2 0
```

The first variable in `table()` will be placed in the rows, the second variable will be placed in the columns.

From this table, we can see that 22 countries in the Americas have high life expectancies, while 3 countries in the Americas have low life expectancies.

We may be interested in looking at the proportions, instead of counts, of countries in each continent that have high or low life expectancies. To convert this table to proportions, we can use `prop.table()`:

```
prop.table(mytab2, 1)
```

```
##
##           High      Low
## Africa  0.1346154 0.8653846
## Americas 0.8800000 0.1200000
## Asia     0.6666667 0.3333333
## Europe   1.0000000 0.0000000
## Oceania  1.0000000 0.0000000
```

We want proportions for each continent, so we want proportions in each row to add up to 1. Therefore, the second argument in `prop.table()` is 1. Enter 2 for this argument if we want the proportions in each column to add up to 1.

As before, to convert to percentages and round to 2 decimal places:

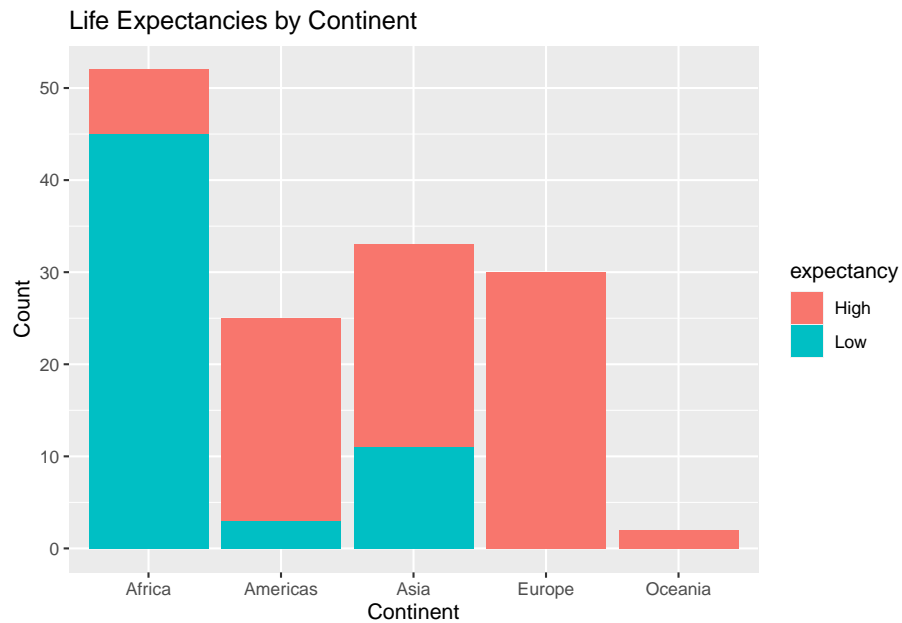
```
round(prop.table(mytab2, 1) * 100, 2)
```

```
##
##           High    Low
## Africa    13.46  86.54
## Americas   88.00  12.00
## Asia       66.67  33.33
## Europe    100.00   0.00
## Oceania    100.00   0.00
```

2.4.2.2 Bar charts

A stacked bar chart can be used to display the relationship between the binary variable `expectancy` across continents:

```
ggplot(Data, aes(x=continent, fill=expectancy))+
  geom_bar(position = "stack")+
  labs(x="Continent", y="Count", title="Life Expectancies by Continent")
```

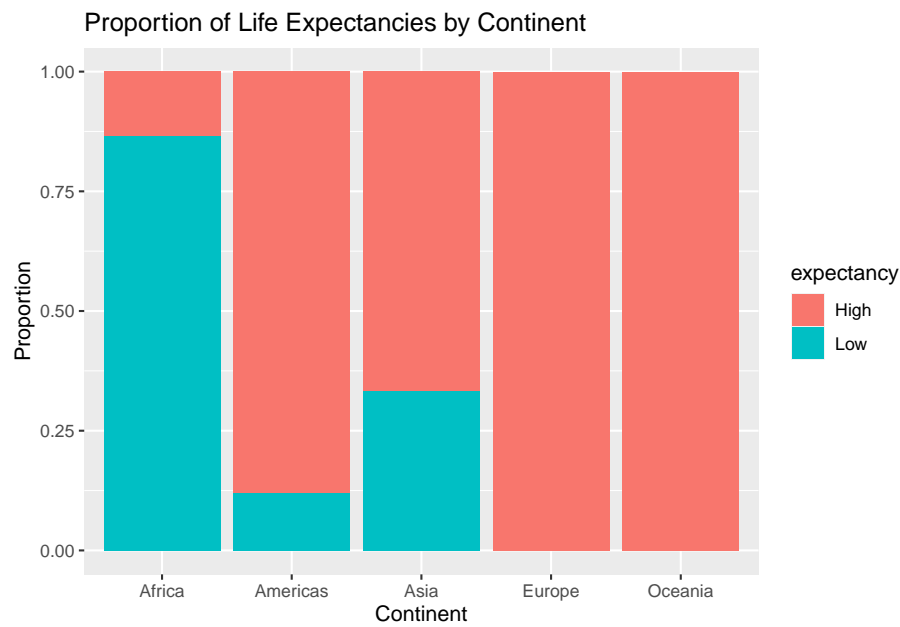


We can see how many countries exist in each continent, and how many of these countries in each continent have high or low life expectancies. For example, there are about 25 countries in the Americas with the majority having high life expectancies.

We can change the way the bar chart is displayed by changing `position` in `geom_bar()` to `position = "dodge"` or `position = "fill"`, the latter being more useful for proportions instead of counts:

```
ggplot(Data, aes(x=continent, fill=expectancy))+
  geom_bar(position = "dodge")
```

```
ggplot(Data, aes(x=continent, fill=expectancy))+
  geom_bar(position = "fill")+
  labs(x="Continent", y="Proportion",
       title="Proportion of Life Expectancies by Continent")
```

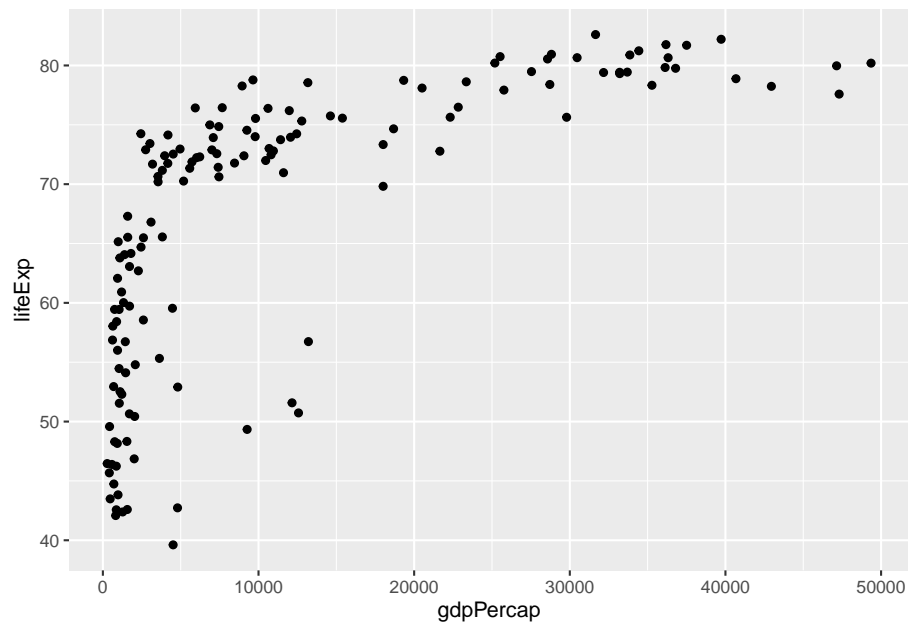


2.4.3 Summarizing two quantitative variables

2.4.3.1 Scatterplots

Scatterplots are the standard visualization when two quantitative variables are involved. To create a scatterplot for life expectancy against GDP per capita:

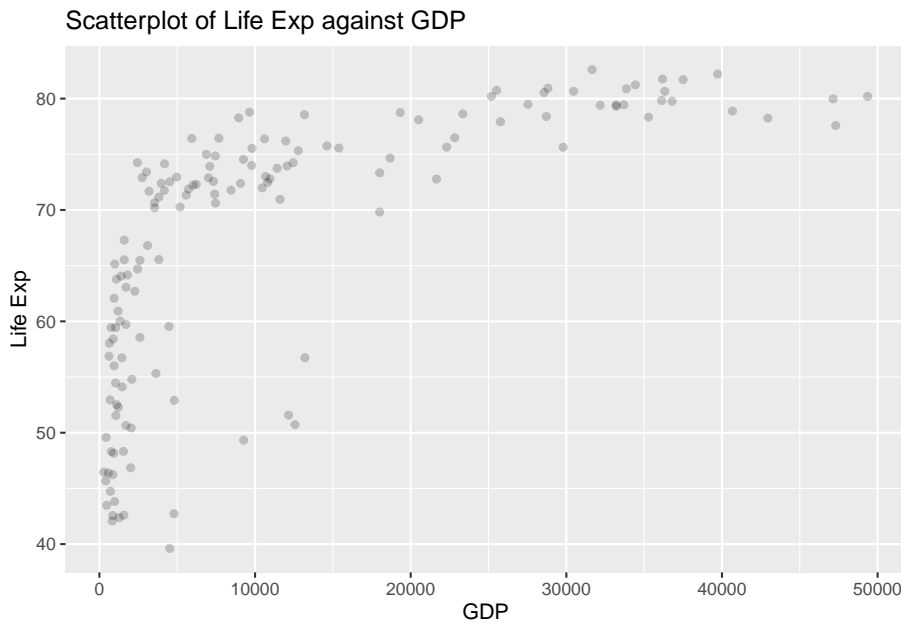
```
ggplot(Data, aes(x=gdpPercap, y=lifeExp)) +  
  geom_point()
```



We see a curved relationship between life expectancies and GDP per capita. Countries with higher GDP per capita tend to have longer life expectancies.

When there are many observations, plots on the scatterplot may actually overlap each other. To have a sense of how many of these exist, we can add a transparency scale called `alpha=0.2` inside `geom_point()`:

```
ggplot(Data, aes(x=gdpPercap,y=lifeExp))+
  geom_point(alpha=0.2)+
  labs(x="GDP", y="Life Exp",
       title="Scatterplot of Life Exp against GDP")
```

The default value for `alpha` is 1, which means the points are not at all transparent. The closer this value is to 0, the more transparent the points are. A darker point indicates more observations with those specific values on both variables.

2.5 Multivariate Visualizations

We will now look at visualizations we can create to explore the relationship between multiple (more than two) variables. The term multivariate means that we are looking at more than two variables.

2.5.1 Bar charts

Previously, we created a bar chart to look at how `expectancy` varies across the continents. Suppose we want to see how these bar graphs vary across the years, so we use the `year` variable as a third variable via a layer `facet_wrap`:

```
##another data frame across all years plus a binary variable
##for expectancy
Data.all<-gapminder%>%
  mutate(expectancy=ifelse(lifeExp<70,"Low","High"))

ggplot(Data.all,aes(x=continent, fill=expectancy))+
  geom_bar(position = "fill")+
  facet_wrap(~year)
```

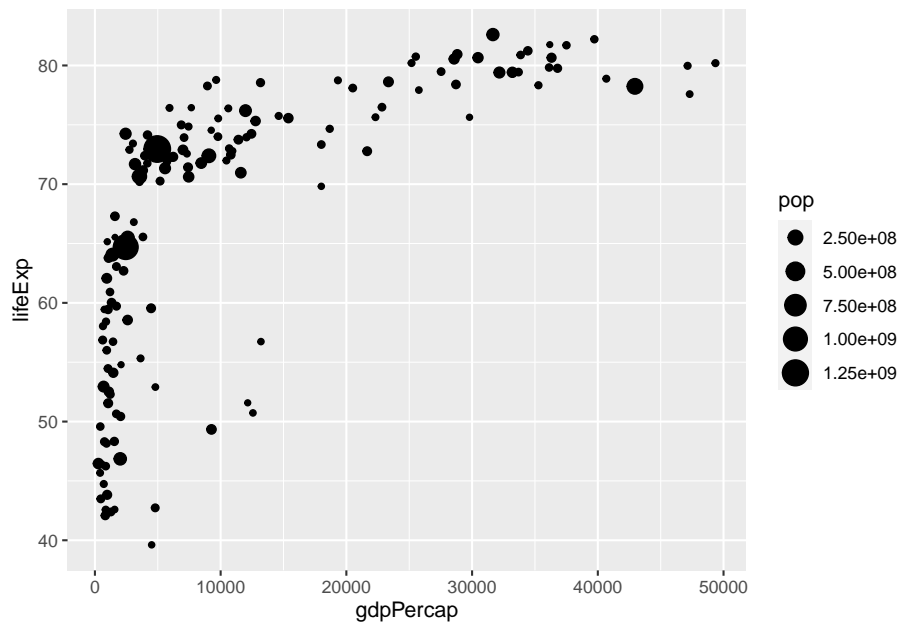


Notice that three categorical variables are summarized in this bar chart. Is there something that can be done to improve this bar chart? How would you make this improvement?

2.5.2 Scatterplots

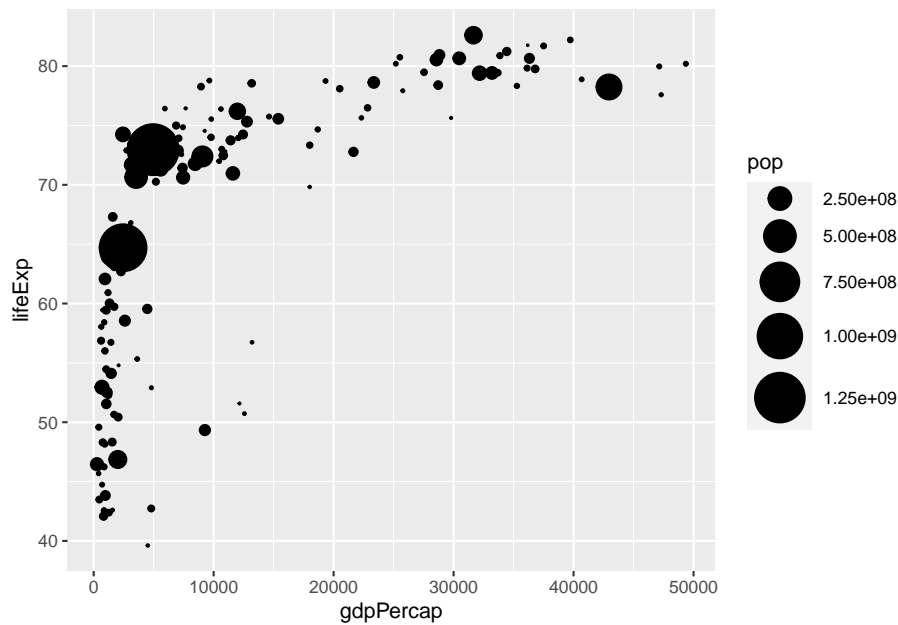
Previously, we created a scatterplot of life expectancy against GDP per capita. We can include another quantitative variable in the scatterplot, by using the size of the plots. We can use the size of the plots to denote the population of the countries. This is supplied via `size` in `aes()`:

```
ggplot(Data, aes(x=gdpPercap, y=lifeExp, size=pop))+  
  geom_point()
```



We can adjust the size of the plots by adding a layer `scale_size()`:

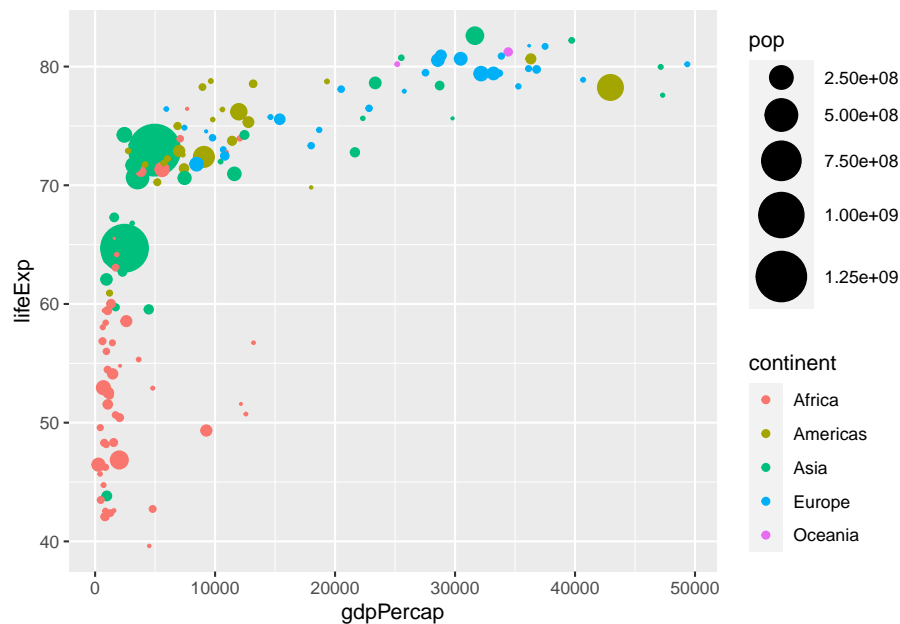
```
ggplot(Data, aes(x=gdpPercap, y=lifeExp, size=pop))+  
  geom_point()+  
  scale_size(range = c(0.1,12))
```



This scatterplot summarizes three quantitative variables.

We can use different-colored plots to denote which continent each point belongs to:

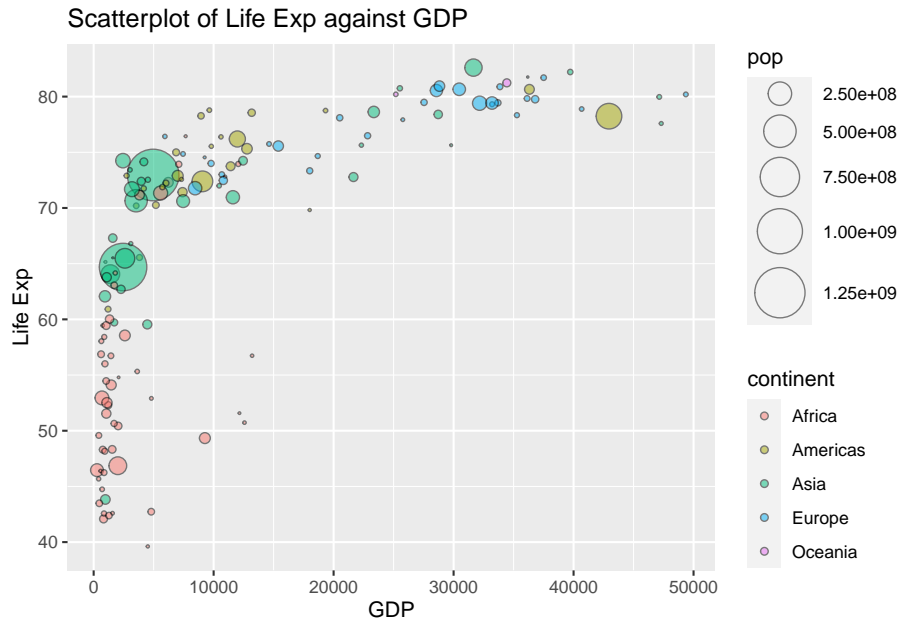
```
ggplot(Data, aes(x=gdpPercap, y=lifeExp, size=pop, color=continent))+
  geom_point()+
  scale_size(range = c(0.1,12))
```



This scatterplot summarizes three quantitative variables and one categorical variable.

We can adjust the plots by changing its shape and making it more translucent via `shape` and `alpha` in `aes()`:

```
ggplot(Data, aes(x=gdpPercap, y=lifeExp, size=pop, fill=continent))+
  geom_point(shape=21, alpha=0.5)+
  scale_size(range = c(0.1,12))+
  labs(x="GDP", y="Life Exp", title="Scatterplot of Life Exp against GDP")
```



Chapter 3

Basics with Simple Linear Regression (SLR)

3.1 Introduction

We will start this module by introducing the simple linear regression model. Simple linear regression uses the term “simple,” because it concerns the study of only one predictor variable with one quantitative response variable. In contrast, multiple linear regression, which we will study in future modules, uses the term “multiple,” because it concerns the study of two or more predictor variables with one quantitative response variable. We start with simple linear regression as it is much easier to visualize concepts in regression models when there is only one predictor variable.

For the time being, we will only consider predictor variables that are quantitative. We will consider predictor variables that are categorical in future modules.

The most common way of visualizing the relationship between one quantitative predictor variable and one quantitative response variable is with a scatter plot. In the simulated example below, we have data from 6000 UVa undergraduate students on the amount of time they spend studying in a week (in minutes), and how many courses they are taking in the semester (3 or 4 credit courses).

```
##create dataframe
df<-data.frame(study,courses)

##fit regression
result<-lm(study~courses, data=df)

##create scatterplot with regression line overlaid
plot(df$courses, df$study, xlab="# of Courses", ylab="Study Time (Mins)")
```

```
abline(result)
```

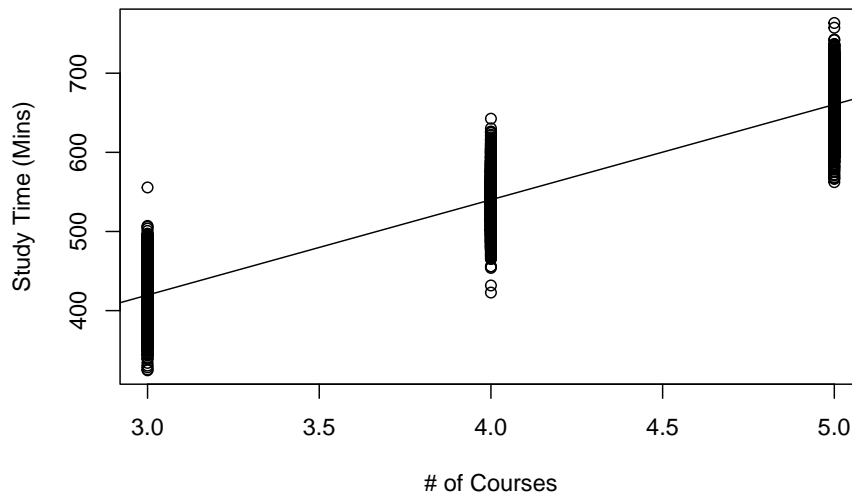


Figure 3.1: Scatterplot of Study Time against Number of Courses Taken

Questions that we may have include:

- Are study time and the number of courses taken related to one another?
- How strong is this relationship?
- Could we use the data to make a prediction for the study time of a student who is not in this scatterplot?
- How confident are we of the prediction?

These questions can be answered using simple linear regression.

Note that we will only be learning about models with just one response variable. We will not cover multivariate regression, which is used when there is more than one response variable. There may be some confusion between “multiple” linear regression and “multivariate” regression due to the closeness in terminology.

3.1.1 Basic Ideas with Statistics

3.1.1.1 Population vs Sample

Statistical methods are usually used to make inferences about the **population** based on information from a **sample**.

- A sample is the collection of units that is actually measured or surveyed in a study.
- The population includes all units of interest.

In the study time example above, the population is all UVa undergraduate students, while the sample is the 6000 students that we have data on and are displayed on the scatterplot.

3.1.1.2 Parameters vs Statistics

- **Parameters** are numerical quantities that describe a population.
- **Statistics** are numerical quantities that describe a sample.

In the study time example, an example of a parameter will be the average study time among all UVa undergraduate students (called the population mean), and an example of a statistic will be the average study time among the 6000 UVa students we have data on (called the sample mean).

Notice that in real life, we will rarely know the actual numerical value of a parameter. So we use the numerical value of the statistic to **estimate** the unknown numerical value of the corresponding parameter.

We also have different notation for parameters and statistics. For example,

- the population mean is denoted as μ .
- the sample mean is denoted as \bar{x} .

We say that \bar{x} is an **estimator** of μ .

It is important to pay attention to whether we are describing a statistic (a known value that can be calculated) or a parameter (an unknown value).

3.1.2 Motivation

Linear regression models generally have two primary uses:

1. **Prediction:** Predict a future value of a response variable, using information from predictor variables.
2. **Association:** Quantify the relationship between variables. How does a change in the predictor variable change the value of the response variable?

We always distinguish between a **response variable, denoted by y** , and a **predictor variable, denoted by x** . In most statistical models, we say that the response variable can be approximated by some **mathematical function, denoted by f** , of the predictor variable, i.e.

$$y \approx f(x).$$

Oftentimes, we write this relationship as

$$y = f(x) + \epsilon,$$

where ϵ **denotes a random error term**, with a mean of 0. The error term cannot be predicted based on the data we have.

There are various statistical methods to estimate f . Once we estimate f , we can use our method for prediction and / or association.

Using the study time example above:

- a prediction example: a student intends to take 4 courses in the semester. What is this student's predicted study time, on average?
- an association example: we want to see how taking more courses increases study time.

3.1.2.1 Practice questions

In the examples below, are we using a regression model for prediction or for association?

1. It is early in the morning and I am heading out for the rest of the day. I want to know the weather forecast for the rest of the day so I know what to wear.
2. An executive for a sports league wants to assess how increasing the length of commercial breaks may impact the enjoyment of sports fans who watch games on TV.
3. The Education Secretary would like to evaluate how certain factors such as use of technology in classrooms and investment in teacher training and teacher pay are associated with reading skills of students.
4. When buying a home, the prospective buyer would like to know if the home is under- or over- priced, given its characteristics.

3.2 Simple Linear Regression (SLR)

In simple linear regression (SLR), the function f that relates the predictor variable with the response variable is typically $\beta_0 + \beta_1 x$. Mathematically, we express this as

$$y \approx \beta_0 + \beta_1 x,$$

or in other words, that the response variable has an approximately linear relationship with the predictor variable.

In SLR, this relationship is more explicitly formulated as the **simple linear regression equation**:

$$E(y|x) = \beta_0 + \beta_1 x. \quad (3.1)$$

- β_0 and β_1 are parameters in the SLR equation, and we want to estimate them.
- These parameters are sometimes called **regression coefficients**.
- β_1 is also called the **slope**. **It denotes the change in y , on average, when x increases by one unit.**
- β_0 is also called the **intercept**. **It denotes the average of y when $x = 0$.**
- The notation on the left hand side of (3.1) denotes the **expected value** of the response variable, for a fixed value of the predictor variable. What (3.1) implies is that, for each value of the predictor variable x , the expected value of the response variable y is $\beta_0 + \beta_1 x$. The expected value is also the population mean. Applying (3.1) to our study time example, it implies that:
 - for students who take 3 courses, their expected study time is equal to $\beta_0 + 3\beta_1$,
 - for students who take 4 courses, their expected study time is equal to $\beta_0 + 4\beta_1$,
 - for students who take 5 courses, their expected study time is equal to $\beta_0 + 5\beta_1$.

So $f(x) = \beta_0 + \beta_1 x$ gives us the value of the expected value of the response variable for a specific value of the predictor variable. But, for each value of the predictor variable, the value of the response variable is not a constant. We say that for each value of x , the response variable y has some variance. The variance of the response variable for each value of x is the same as the variance of the error term, ϵ . Thus we have the **simple linear regression model**

$$y = \beta_0 + \beta_1 x + \epsilon. \quad (3.2)$$

We need to make some assumptions for the error term ϵ . Generally, the assumptions are:

1. The errors have mean 0.
2. The **errors have variance denoted by σ^2** . Notice this variance is constant.
3. The errors are independent.
4. The errors are normally distributed.

From (3.2), notice we have another parameter, σ^2 .

We will go into more detail about what these assumptions mean, and how to assess whether they are met, in module 5.

What these assumptions mean is that for each value of the predictor variable x , the response variable:

1. follows a normal distribution,
2. with mean equal to $\beta_0 + \beta_1 x$,
3. and variance equal to σ^2 .

Using our study time example, it means that:

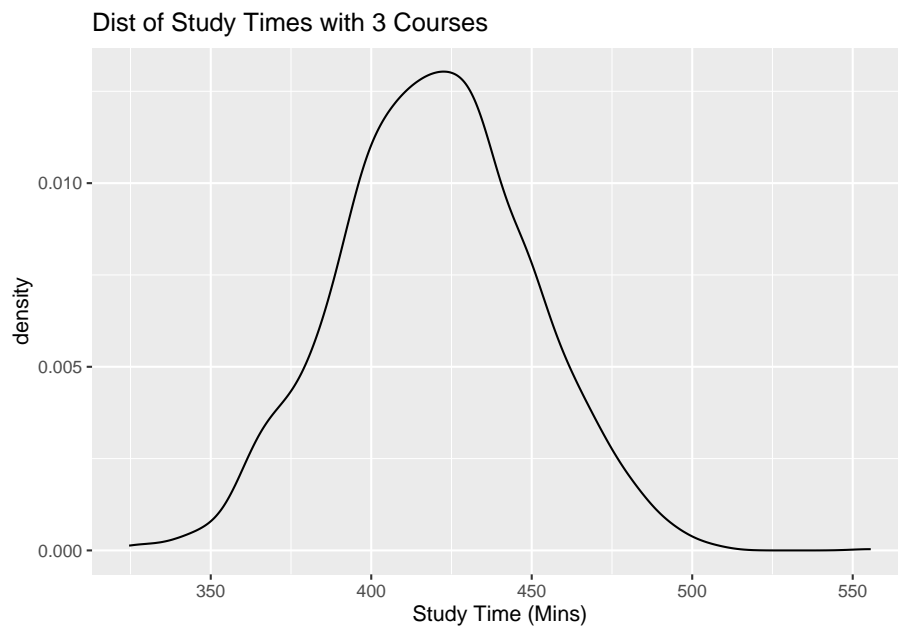
- for students who take 3 courses, the distribution of their study times is $N(\beta_0 + 3\beta_1, \sigma^2)$.
- for students who take 4 courses, the distribution of their study times is $N(\beta_0 + 4\beta_1, \sigma^2)$.
- for students who take 5 courses, the distribution of their study times is $N(\beta_0 + 5\beta_1, \sigma^2)$.

So if we were to subset our dataframe into three subsets, one with students who take 3 courses, another subset for students who take 4 courses, and another subset for students who take 5 courses, and then create a density plot of study times for each subset, each density plot should follow a normal distribution, with different means, and the same spread.

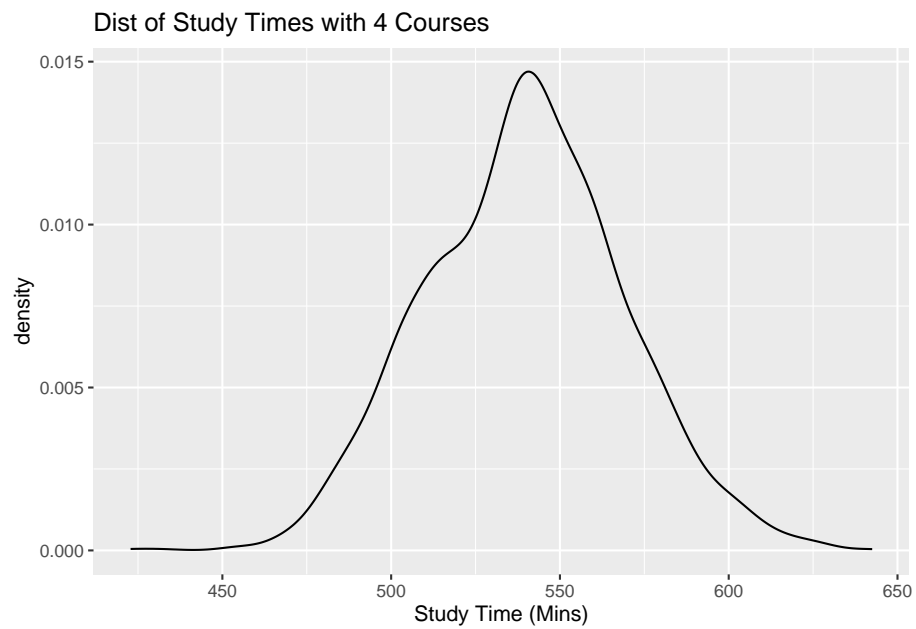
Let us take a look at these density plots next.

```
library(tidyverse)

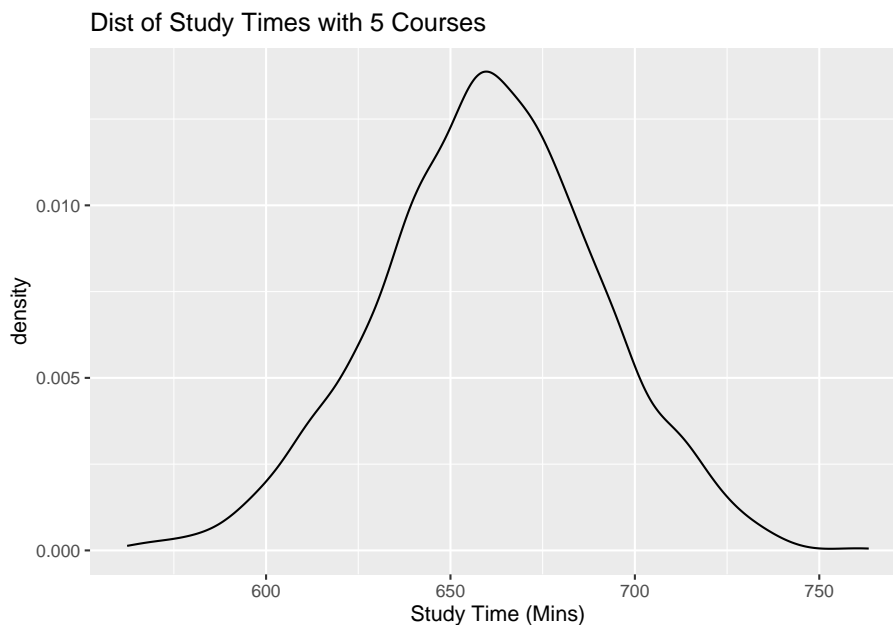
##subset dataframe
x.3<-df[which(df$courses==3),]
##density plot of study time for students taking 3 courses
ggplot(x.3,aes(x=study))+
  geom_density()+
  labs(x="Study Time (Mins)", title="Dist of Study Times with 3 Courses")
```



```
##subset dataframe
x.4<-df[which(df$courses==4),]
##density plot of study time for students taking 4 courses
ggplot(x.4,aes(x=study))+
  geom_density()+
  labs(x="Study Time (Mins)", title="Dist of Study Times with 4 Courses")
```



```
##subset dataframe
x.5<-df[which(df$courses==5),]
##density plot of study time for students taking 5 courses
ggplot(x.5,aes(x=study))+
  geom_density()+
  labs(x="Study Time (Mins)", title="Dist of Study Times with 5 Courses")
```



Notice all of these plots are normal, with different means (centers), and similar spreads.

Please see the associated video for more explanation about the distribution of the response variable, for each value of the predictor variable, in an SLR setting.

3.3 Estimating Regression Coefficients in SLR

From (3.1) and (3.2), we noted that we have to estimate the regression coefficients β_0, β_1 as well as the parameter σ^2 associated with the error term. As mentioned earlier, we are unable to obtain numerical values of these parameters as we do not have data from the entire population. So what we do is use the data from our sample to estimate these parameters.

We estimate β_0, β_1 using $\hat{\beta}_0, \hat{\beta}_1$ based on a sample of observations (x_i, y_i) of size n .

The subscripts associated with the response and predictor variables denote which data point that value belongs to. Let us take a look at the first few rows of the data frame for the study time example:

```
head(df)
```

```
##      study courses
## 1 429.8311      3
## 2 458.4588      3
## 3 391.9406      3
```

```
## 4 378.0196      3
## 5 397.9856      3
## 6 405.7145      3
```

For example, x_1 denotes the number of courses taken by student number 1 in the dataframe, which is 3. y_4 denotes the study time for student number 4 in the dataframe, which is 378.0196456.

Following (3.1) and (3.2), the sample versions are

$$\hat{y} = \hat{\beta}_0 + \hat{\beta}_1 x \quad (3.3)$$

and

$$y = \hat{\beta}_0 + \hat{\beta}_1 x + e \quad (3.4)$$

respectively. (3.3) is called the **estimated SLR equation**, or **fitted SLR equation**. (3.4) is called the **estimated SLR model**.

$\hat{\beta}_1, \hat{\beta}_0$ are the estimators for β_1, β_0 respectively. These estimators can be interpreted in the following manner:

- $\hat{\beta}_1$ denotes the change in the predicted y when x increases by 1 unit. Alternatively, it denotes the change in y , on average, when x increases by 1 unit.
- $\hat{\beta}_0$ denotes the predicted y when $x = 0$. Alternatively, it denotes the average of y when $x = 0$.

From (3.4), notice we use e to denote the residual, or in other words, the “error” in the sample.

From (3.3) and (3.4), we have the following quantities that we can compute:

$$\text{Predicted/Fitted values: } \hat{y}_i = \hat{\beta}_0 + \hat{\beta}_1 x_i. \quad (3.5)$$

$$\text{Residuals: } e_i = y_i - \hat{y}_i. \quad (3.6)$$

$$\text{Sum of Squared Residuals: } SS_{res} = \sum_{i=1}^n (y_i - \hat{y}_i)^2. \quad (3.7)$$

We compute the estimated coefficients $\hat{\beta}_1, \hat{\beta}_0$ using the **method of least squares**, i.e. choose the numerical values of $\hat{\beta}_1, \hat{\beta}_0$ that minimize SS_{res} as given in (3.7).

By minimizing SS_{res} with respect to $\hat{\beta}_0$ and $\hat{\beta}_1$, the estimated coefficients in the simple linear regression equation are

$$\hat{\beta}_1 = \frac{\sum_{i=1}^n (x_i - \bar{x})(y_i - \bar{y})}{\sum_{i=1}^n (x_i - \bar{x})^2} \quad (3.8)$$

and

$$\hat{\beta}_0 = \bar{y} - \hat{\beta}_1 \bar{x} \quad (3.9)$$

$\hat{\beta}_1, \hat{\beta}_0$ are called **least squares estimators**.

The minimization of SS_{res} with respect to $\hat{\beta}_0$ and $\hat{\beta}_1$ is done by taking the partial derivatives of (3.7) with respect to $\hat{\beta}_1$ and $\hat{\beta}_0$, setting these two partial derivatives equal to 0, and solving these two equations for $\hat{\beta}_1$ and $\hat{\beta}_0$.

Let's take a look at the estimated coefficients for our study time example:

```
##fit regression
result<-lm(study~courses, data=df)
##print out the estimated coefficients
result

##
## Call:
## lm(formula = study ~ courses, data = df)
##
## Coefficients:
## (Intercept)      courses
##      58.45      120.39
```

From our sample of 6000 students, we have

- $\hat{\beta}_1 = 120.3930985$. The predicted study time increases by 120.3930985 minutes for each additional course taken.
- $\hat{\beta}_0 = 58.4482853$. The predicted study time is 58.4482853 when no courses are taken. Notice this value does not make sense, as a student cannot be taking 0 courses. If you look at our data, the number of courses taken is 3, 4, or 5. So we should only use our regression when $3 \leq x \leq 5$. We cannot use it for values of x outside the range of our data. Making predictions of the response variable for predictors outside the range of the data is called **extrapolation** and should not be done.

3.4 Estimating Variance of Errors in SLR

The estimator of σ^2 , the variance of the error terms (also the variance of the probability distribution of y given x) is

$$s^2 = MS_{res} = \frac{SS_{res}}{n-2} = \frac{\sum_{i=1}^n e_i^2}{n-2}, \quad (3.10)$$

where MS_{res} is called the **mean squared residuals**.

σ^2 , the variance of the error terms, measures the spread of the response variable, for each value of x . The smaller this is, the closer the data points are to the regression equation.

3.4.1 Practice questions

Take a look at the scatterplot of study time against number of courses taken, Figure 3.1. On this plot, label the following:

- estimated SLR equation
- the fitted value when $x = 3$, $x = 4$, and $x = 5$.
- the residual for any data point on the plot of your choosing.

Try these on your own first, then view the associated video to see if you labeled the plot correctly!

3.5 Assessing Linear Association

As noted earlier, the variance of the error terms inform us how close the data points are to the estimated SLR equation. The smaller the variance of the error terms, the closer the data points are to the estimated SLR equation. This in turn implies the linear relationship between the variables is stronger.

We will learn about some common measures that are used to quantify the strength of the linear relationship between the response and predictor variables. Before we do that, we need to define some other terms.

3.5.1 Sum of squares

$$\text{Total Sum of Squares: } SS_T = \sum_{i=1}^n (y_i - \bar{y})^2. \quad (3.11)$$

Total sum of squares is defined as the **total variance in the response variable**. The larger this value is, the larger the spread is of the response variable.

$$\text{Regression sum of squares: } SS_R = \sum_{i=1}^n (\hat{y}_i - \bar{y})^2. \quad (3.12)$$

Regression sum of squares is defined as the **variance in the response variable that can be explained by our regression**.

We also have residual sum of squares, SS_{res} . Its mathematical formulation is given in (3.7). It is defined as the **variance in the response variable that cannot be explained by our regression**.

It can be shown that

$$SS_T = SS_R + SS_{res}. \quad (3.13)$$

Each of the sums of squares has its associated **degrees of freedom (df)**:

- df for SS_R : $df_R = 1$
- df for SS_{res} : $df_{res} = n - 2$
- df for SS_T : $df_T = n - 1$

Please see the associated video for more explanation about the concept behind degrees of freedom.

3.5.2 ANOVA Table

Information regarding the sums of squares is usually presented in the form of an **ANOVA (analysis of variance) table**:

Source of Variation	SS	df	MS	F
Regression	$SS_R = \sum (\hat{y}_i - \bar{y})^2$	$df_R = 1$	$MS_R = \frac{SS_R}{df_R}$	$\frac{MS_R}{MS_{res}}$
Error	$SS_{res} = \sum (y_i - \hat{y}_i)^2$	$df_{res} = n - 2$	$MS_{res} = \frac{SS_{res}}{df_{res}}$	***
Total	$SS_T = \sum (y_i - \bar{y})^2$	$df_T = n - 1$	***	***

Note:

- Dividing each sum of square with its corresponding degrees of freedom gives the corresponding mean square.
- In the last column, we report an F statistic, which equal to $\frac{MS_R}{MS_{res}}$. This F statistic is associated with an **ANOVA F test**, which we will look at in more detail in the next subsection.

To obtain the ANOVA table for our study time example:

```
anova(result)
```

```
## Analysis of Variance Table
##
## Response: study
##           Df Sum Sq Mean Sq F value    Pr(>F)
## courses      1 57977993 57977993    65404 < 2.2e-16 ***
## Residuals 5998  5317017      886
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Notice that R does not print out the information for the line regarding SS_T .

3.5.3 ANOVA F Test

In SLR, the ANOVA F statistic from the ANOVA table can be used to test if the slope of the SLR equation is 0 or not. In words, this means that whether there is a linear association between the variables or not. If the slope is 0, it means that changes in the value of the predictor variable do not change the value of the response variable, on average; hence the variables are not linearly associated.

The null and alternative hypotheses are:

$$H_0 : \beta_1 = 0, H_a : \beta_1 \neq 0.$$

The test statistic is

$$F = \frac{MS_R}{MS_{res}} \quad (3.14)$$

and is compared with an $F_{1,n-2}$ distribution. Note that $F_{1,n-2}$ is read as an **F distribution with 1 and $n - 2$ degrees of freedom**.

Going back to the study time example, the F statistic is 6.5403586×10^4 . The critical value can be found using

```
qf(1-0.05, 1, 6000-2)
```

```
## [1] 3.84301
```

Since our test statistic is larger than the critical value, we reject the null hypothesis. Our data support the claim that the slope is different from 0, or in other words, that there is a linear association between study time and number of courses taken.

3.5.4 Coefficient of determination

The **coefficient of determination**, R^2 , is

$$R^2 = \frac{SS_R}{SS_T} = 1 - \frac{SS_{res}}{SS_T}. \quad (3.15)$$

R^2 is an indication of how well the data fits our model. In the context of simple linear regression, it denotes **the proportion of variance in the response variable that is explained by the predictor**.

A few notes about R^2 :

- $0 \leq R^2 \leq 1$.
- Values closer to 1 indicate a better fit; values closer to 0 indicate a poorer fit.
- Sometimes reported as a percentage.

To obtain R^2 for our study time example:

```
anova.tab<-anova(result)
##SST not provided, so we add up SSR and SSres
SST<-sum(anova.tab$"Sum Sq")
##R2
anova.tab$"Sum Sq"[1]/SST
```

```
## [1] 0.9159963
```

This implies that the proportion of variance in study time that can be explained by the number of courses taken is 0.9159963.

3.5.5 Correlation

A measure used to quantify the strength of the linear association between two quantitative variables is the **sample correlation**. The sample correlation, $\text{Corr}(x, y)$ or r , is given by

$$r = \frac{\sum_{i=1}^n (x_i - \bar{x})(y_i - \bar{y})}{\sqrt{\sum_{i=1}^n (x_i - \bar{x})^2 (y_i - \bar{y})^2}}. \quad (3.16)$$

A few notes about r :

- $-1 \leq r \leq 1$.
- Sign of correlation indicates direction of association. A positive value indicates a positive linear association: as the predictor variable increases, so does the response variable, on average. A negative value indicates a negative linear association: as the predictor variable increases, the response variable decreases, on average.

- Values closer to 1 or -1 indicate a stronger linear association; values closer to 0 indicate a weaker linear association.
- In SLR, it turns out that $r^2 = R^2$.

Using our study time example, the correlation between study time and number of courses taken is

```
cor(df$study, df$courses)
```

```
## [1] 0.9570769
```

This value indicates a very strong and positive linear association between study time and number of courses taken (remember that this is simulated data and is not real).

3.5.5.1 How strong is strong?

A question that is often raised is how large should the magnitude of the sample correlation be for it to be considered strong? The answer is: it depends on the context. If you are conducting an experiment that is governed by scientific laws (e.g an experiment verifying Newton's 2nd law that $F = ma$), we should expect an extremely high correlation. A correlation of 0.9 in such an instance may be considered weak. The value of the correlation you have should be compared with correlations from similar studies in that domain to determine if it is strong or not.

3.6 A Word of Caution

To be able to use the measures we have learned (such as correlation, R^2) and to interpret the estimated regression coefficients, we must verify via a scatterplot that the association between the two variables is approximately linear. If we see a non linear pattern in the scatterplot, we should not use or interpret these values. We will learn how to remedy the situation if we see a non linear pattern in the scatterplot in module 5.

Please see the associated video for a demonstration on how not looking at the scatterplot can lead to misleading interpretations.

3.7 R Tutorial

For this tutorial, we will work with the dataset `elmhurst` from the `openintro` package in R.

```
library(tidyverse)
library(openintro)
Data<-openintro::elmhurst
```

Type `?openintro::elmhurst` to read the documentation for datasets in R. Always seek to understand the background of your data! The key pieces of information are:

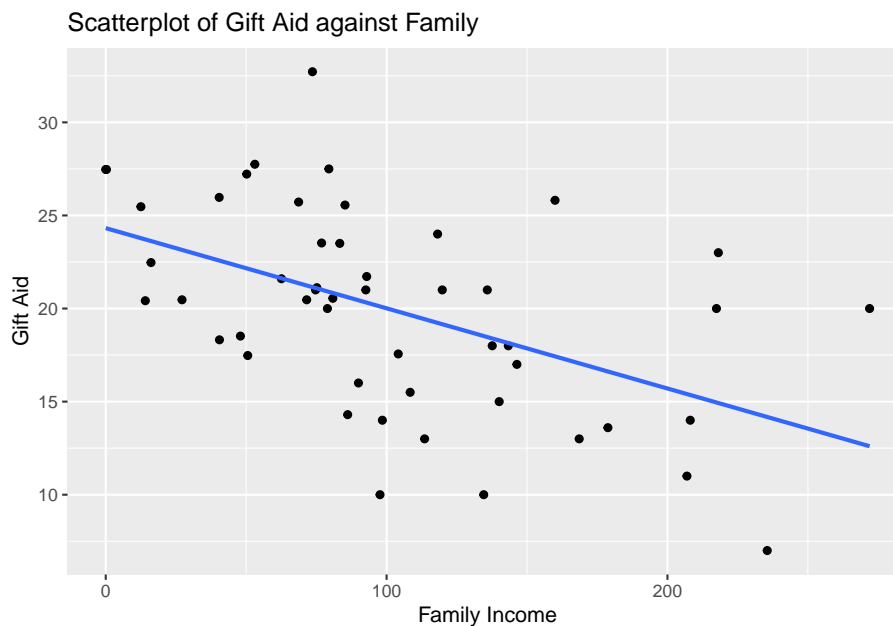
- A random sample of 50 students (all freshman from the 2011 class at Elmhurst College).
- Family income of the student (units are missing).
- Gift aid, in \$1000s.

We want to explore how family income may be related to gift aid, in a simple linear regression framework.

Visualization

We should always verify with scatterplot that the relationship is (approximately) linear before proceeding with correlation and simple linear regression!

```
##scatterplot of gift aid against family income
ggplot2::ggplot(Data, aes(x=family_income,y=gift_aid))+
  geom_point()+
  geom_smooth(method = "lm", se=FALSE)+
  labs(x="Family Income", y="Gift Aid", title="Scatterplot of Gift Aid against Family")
```



We note that the observations are fairly evenly scattered on both sides of the regression line, so a linear association exists. We see a negative linear association. As family income increases, the gift aid, on average, decreases.

We also do not see any observation with weird values that may warrant further investigation.

Regression

We use the `lm()` function to fit a regression model:

```
##regress gift aid against family income
result<-lm(gift_aid~family_income, data=Data)
```

Use the `summary()` function to display relevant information from this regression:

```
##look at information regarding regression
summary(result)
```

```
##
## Call:
## lm(formula = gift_aid ~ family_income, data = Data)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -10.1128  -3.6234  -0.2161   3.1587  11.5707
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   24.31933     1.29145   18.831 < 2e-16 ***
## family_income -0.04307     0.01081   -3.985 0.000229 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 4.783 on 48 degrees of freedom
## Multiple R-squared:  0.2486, Adjusted R-squared:  0.2329
## F-statistic: 15.88 on 1 and 48 DF,  p-value: 0.0002289
```

We see the following values:

- $\hat{\beta}_1 = -0.0430717$. The estimated slope informs us the the predicted gift aid decreases by 0.0430717 thousands of dollars (or \$43.07) per unit increase in family income.
- $\hat{\beta}_0 = 24.319329$. For students with no family income, their predicted gift aid is \$24 319.33. Note: from the scatterplot, we have an observation with 0 family income. We must be careful in not extrapolating when making predictions with our regression. We should only make predictions for family incomes between the minimum and maximum values of family incomes in our data.
- $s = 4.7825989$, is the estimate of the standard deviation of the error terms. This is reported as residual standard error in R. Squaring this gives the estimated variance.

- $F = 15.8772043$. This is the value of the ANOVA F statistic. The corresponding p-value is reported. Since this p-value is very small, we reject the null hypothesis. The data support the claim that there is a linear association between gift aid and family income.
- $R^2 = 0.2485582$. The coefficient of determination informs us that about 24.86% of the variation in gift aid can be explained by family income.

Extract values from R objects

We can actually extract these values that are being reported from `summary(result)`. To see what can be extracted from an R object, use the `names()` function:

```
##see what can be extracted from summary(result)
names(summary(result))

## [1] "call"          "terms"          "residuals"      "coefficients"
## [5] "aliases"        "sigma"          "df"             "r.squared"
## [9] "adj.r.squared" "fstatistic"     "cov.unscaled"
```

To extract the estimated coefficients:

```
##extract coefficients
summary(result)$coefficients

##              Estimate Std. Error   t value    Pr(>|t|)
## (Intercept)  24.31932901 1.29145027 18.831022 8.281020e-24
## family_income -0.04307165 0.01080947 -3.984621 2.288734e-04
```

Notice the information is presented in a table. To extract a specific value, we can specify the row and column indices:

```
##extract slope
summary(result)$coefficients[2,1]
```

```
## [1] -0.04307165
```

```
##extract intercept
summary(result)$coefficients[1,1]
```

```
## [1] 24.31933
```

On your own, extract the values of the residual standard error, the ANOVA F statistic, and R^2 .

Prediction

A use of regression models is prediction. Suppose I want to predict the gift aid of a student with family income of 50 thousand dollars (assuming the unit is in thousands of dollars). We use the `predict()` function:

```
##create data point for prediction
newdata<-data.frame(family_income=50)
##predicted gift aid when x=50
predict(result,newdata)
```

```
##          1
## 22.16575
```

This student's predicted gift aid is \$22 165.75. Alternatively, you could have calculated this by plugging $x = 50$ into the estimated SLR equation:

```
summary(result)$coefficients[1,1] + summary(result)$coefficients[2,1]*50
```

```
## [1] 22.16575
```

ANOVA table

We use the `anova()` function to display the ANOVA table

```
anova.tab<-anova(result)
anova.tab
```

```
## Analysis of Variance Table
##
## Response: gift_aid
##           Df  Sum Sq Mean Sq F value    Pr(>F)
## family_income  1   363.16   363.16  15.877 0.0002289 ***
## Residuals    48  1097.92    22.87
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The report F statistic is the same as the value reported earlier from `summary(result)`.

The first line of the output gives SS_R , the second line gives SS_{res} . The function doesn't provide SS_T , but we know that $SS_T = SS_R + SS_{res}$.

Again, to see what can be extracted from `anova.tab`:

```
names(anova.tab)
```

```
## [1] "Df"      "Sum Sq"  "Mean Sq" "F value" "Pr(>F)"
```

So SS_T can be easily calculated:

```
SST<-sum(anova.tab$"Sum Sq")
SST
```

```
## [1] 1461.079
```

The R^2 was reported to be 0.2485582. To verify using the ANOVA table:

```
anova.tab$"Sum Sq"[1]/SST
```

```
## [1] 0.2485582
```

Correlation

We use the `cor()` function to find the correlation between two quantitative variables:

```
##correlation  
cor(Data$family_income,Data$gift_aid)
```

```
## [1] -0.4985561
```

The correlation is -0.4985561. We have a moderate, negative linear association between family income and gift aid.

Chapter 4

Inference with Simple Linear Regression (SLR)

4.1 Introduction

Oftentimes, the data we collect come from a random sample that is representative of the population of interest. A common example is an election poll before a presidential election. Random sampling allows the sample to be representative of the population. However, if we obtain another random sample, the characteristics of the new sample are unlikely to be exactly the same as the first sample. For example, the sample proportion who will vote for a certain party is unlikely to be the same for both random samples. What this tells us is that even with representative samples, sample proportions are unlikely to be equal to the population proportion, and sample proportions vary from sample to sample.

Dr. W. Edwards Deming's Red Bead experiment illustrates this concept. A video of this experiment can be found [here](#).

In this video, the number of red beads, which represent bad products, varies each time the worker obtains a random sample of 50 beads. The fact that the number of red beads increases in his second sample does not indicate that he performed his task any worse, as this increase is due to the random variation associated with samples.

Note: Deming's Red Bead experiment was developed to illustrate concepts associated with management. He is best known for his work in developing the Japanese economy after World War II. You will be able to find many blogs/articles discussing the experiment on the World Wide Web. Although many of the articles discuss how this experiment applies in management, it can be used to illustrate concepts of variation.

The same idea extends to the slope and intercept of a regression line. The estimated slope and intercept will vary from sample to sample and are unlikely to be equal to the population slope and intercept. In inferential statistics, we use hypothesis tests and confidence intervals to aid us in accounting for this random variation. In this module, you will learn how to account for and quantify the random variation associated with the estimated regression model, and how to interpret the estimated regression model while accounting for random variation.

4.1.1 Review from previous module

The **simple linear regression model** is written as

$$y = \beta_0 + \beta_1 x + \epsilon. \quad (4.1)$$

We make some assumptions for the error term ϵ . They are:

1. The errors have mean 0.
2. The **errors have variance denoted by σ^2** . Notice this variance is constant.
3. The errors are independent.
4. The errors are normally distributed.

These assumptions allow us to derive the distributional properties associated with our least squares estimators $\hat{\beta}_0, \hat{\beta}_1$, which then enables us to compute reliable confidence intervals and perform hypothesis tests on our SLR reliably.

$\hat{\beta}_1, \hat{\beta}_0$ are the estimators for β_1, β_0 respectively. These estimators can be interpreted in the following manner:

- $\hat{\beta}_1$ **denotes the change in the predicted y when x increases by 1 unit. Alternatively, it denotes the change in y , on average, when x increases by 1 unit.**
- $\hat{\beta}_0$ **denotes the predicted y when $x = 0$. Alternatively, it denotes the average of y when $x = 0$.**

How do the values of these estimators vary from sample to sample?

4.2 Hypothesis Testing in SLR

4.2.1 Distribution of least squares estimators

Gauss Markov Theorem: Under assumptions for a regression model, the least squares estimators $\hat{\beta}_1$ and $\hat{\beta}_0$ are unbiased and have minimum variance among all unbiased linear estimators.

Thus, the least squares estimators have the following properties:

1. $E(\hat{\beta}_1) = \beta_1, E(\hat{\beta}_0) = \beta_0$

Note: An estimator is **unbiased** if its expected value is exactly equal to the parameter it is estimating.

2. The variance of $\hat{\beta}_1$ is

$$\text{Var}(\hat{\beta}_1) = \frac{\sigma^2}{\sum (x_i - \bar{x})^2} \quad (4.2)$$

3. The variance of $\hat{\beta}_0$ is

$$\text{Var}(\hat{\beta}_0) = \sigma^2 \left[\frac{1}{n} + \frac{\bar{x}^2}{\sum (x_i - \bar{x})^2} \right] \quad (4.3)$$

4. $\hat{\beta}_1$ and $\hat{\beta}_0$ both follow a normal distribution.

Note that in (4.2) and (4.3), we use $s^2 = MS_{res}$ to estimate σ^2 since σ^2 is a unknown value.

What these imply is that if we standardize $\hat{\beta}_1$ and $\hat{\beta}_0$, these standardized quantities will follow a t_{n-2} distribution, i.e.

$$\frac{\hat{\beta}_1 - \beta_1}{se(\hat{\beta}_1)} \sim t_{n-2} \quad (4.4)$$

and

$$\frac{\hat{\beta}_0 - \beta_0}{se(\hat{\beta}_0)} \sim t_{n-2}, \quad (4.5)$$

where

$$se(\hat{\beta}_1) = \sqrt{\frac{MS_{res}}{\sum (x_i - \bar{x})^2}} = \frac{s}{\sqrt{\sum (x_i - \bar{x})^2}} \quad (4.6)$$

and

$$se(\hat{\beta}_0) = \sqrt{MS_{res} \left[\frac{1}{n} + \frac{\bar{x}^2}{\sum (x_i - \bar{x})^2} \right]} = s \sqrt{\frac{1}{n} + \frac{\bar{x}^2}{\sum (x_i - \bar{x})^2}} \quad (4.7)$$

Note:

- $se(\hat{\beta}_1)$ is read as the **standard error of $\hat{\beta}_1$** . The standard error of any estimator is essentially the sample standard deviation of that estimator, and measures the spread of that estimator.
- A t_{n-2} distribution is read as a **t distribution with $n - 2$ degrees of freedom**.

4.2.2 Testing regression coefficients

Hypothesis testing is used to investigate if a population parameter is **different from a specific value**. In the context of SLR, we usually want to test if β_1 is 0 or not. If $\beta_1 = 0$, there is no linear relationship between the variables.

The general steps in hypothesis testing are:

- Step 1: State the null and alternative hypotheses.
- Step 2: A test statistic is calculated using the sample, assuming the null is true. The value of the test statistic measures how the **sample deviates from the null**.
- Step 3: Make conclusion, using either critical values or p-values.

In the previous module, we introduced the ANOVA F test. In SLR, this tests if the slope of the SLR equation is 0 or not. It turns out that we can also perform a t test for the slope. In the t test for the slope, the null and alternative hypotheses are:

$$H_0 : \beta_1 = 0, H_a : \beta_1 \neq 0.$$

The test statistic is

$$t = \frac{\hat{\beta}_1 - \text{value in null}}{se(\hat{\beta}_1)} \quad (4.8)$$

which is compared with a t_{n-2} distribution. Notice that (4.8) comes from (4.4).

Let us go back to our simulated example that we saw in the last module. We have data from 6000 UVa undergraduate students on the amount of time they spend studying in a week (in minutes), and how many courses they are taking in the semester (3 or 4 credit courses).

```
##create dataframe
df<-data.frame(study,courses)

##fit regression
result<-lm(study~courses, data=df)
##look at regression coefficients
summary(result)$coefficients
```

```
##              Estimate Std. Error   t value    Pr(>|t|)
## (Intercept)  58.44829   1.9218752  30.41211 4.652442e-189
## courses      120.39310   0.4707614 255.74125 0.000000e+00
```

The t statistic for testing $H_0 : \beta_1 = 0, H_a : \beta_1 \neq 0$ is reported to be 255.7412482, which can be calculated using (4.8): $t = \frac{120.39310 - 0}{0.4707614}$. The reported p-value is virtually 0, so we reject the null hypothesis. The data support the claim that there is a linear association between study time and the number of courses taken.

4.3 Confidence Intervals for Regression Coefficients

Confidence intervals (CIs) are similar to hypothesis testing in the sense that they are also based on the distributional properties of an estimator. CIs may differ in their use in the following ways:

1. We are not assessing if the parameter is different from a specific value.
2. We are more interested in exploring a plausible **range of values for an unknown parameter**.

Because CIs and hypothesis tests are based on the distributional properties of an estimator, their conclusions will be consistent (as long as the significance level is the same).

Recall the general form for CIs:

$$\text{estimator} \pm (\text{multiplier} \times \text{s.e of estimator}). \quad (4.9)$$

We have the following components of a CI

- **estimator (or statistic)**: numerical quantity that describes a sample
- **multiplier**: determined by confidence level and relevant probability distribution
- **standard error of estimator**: measure of variance of estimator (basically the square root of the variance of estimator)

Following (4.9) and (4.4), the $100(1 - \alpha)\%$ CI for β_1 is

$$\hat{\beta}_1 \pm t_{1-\alpha/2; n-2} se(\hat{\beta}_1) = \hat{\beta}_1 \pm t_{1-\alpha/2; n-2} \frac{s}{\sqrt{\sum (x_i - \bar{x})^2}}. \quad (4.10)$$

Going back to our study time example, the 95% CI for β_1 is (119.470237, 121.3159601).

```
##CI for coefficients
confint(result, level = 0.95) [2,]
```

```
##      2.5 %    97.5 %
## 119.4702 121.3160
```

An interpretation of this CI is that we have 95% confidence that the true slope β_1 lies between (119.470237, 121.3159601). In other words, for each additional course taken, the predicted study time increases between 119.470237 and 121.3159601 minutes.

4.3.1 Thought questions

- Is the conclusion from this 95% CI consistent with the hypothesis test for $H_0 : \beta_1 = 0$ in the previous section at 0.05 significance level?
- I have presented hypothesis tests and CIs for the slope, β_1 .
 - How would you calculate the t statistic if you wanted to test $H_0 : \beta_0 = 0, H_0 : \beta_0 \neq 0$?
 - How would you calculate the 95% CI for the intercept β_0 ?

Generally, we are usually more interested in the slope than the intercept.

4.4 CI of the Mean Response

We have established that the least squares estimators $\hat{\beta}_1, \hat{\beta}_0$ have their associated variances. Since the estimated SLR equation is

$$\hat{y} = \hat{\beta}_0 + \hat{\beta}_1 x, \quad (4.11)$$

it stands to reason that \hat{y} has an associated variance as well, since it is a function of $\hat{\beta}_1, \hat{\beta}_0$.

There are two interpretations of \hat{y} :

1. it **estimates the mean of y when $x = x_0$** ;
2. it **predicts the value of y for a new observation when $x = x_0$** .

Note: x_0 denotes a specific numerical value for the predictor variable.

Depending on which interpretation we want, there are two different intervals based on \hat{y} . The first interpretation is associated with the **confidence interval for the mean response, $\hat{\mu}_{y|x_0}$, given the predictor**. This is used when we are interested in the average value of the response variable, when the predictor is equal to a specific value. This CI is

$$\hat{\mu}_{y|x_0} \pm t_{1-\alpha/2, n-2} s \sqrt{\frac{1}{n} + \frac{(x_0 - \bar{x})^2}{\sum (x_i - \bar{x})^2}}. \quad (4.12)$$

Going back to our study time example, suppose we want the average study time for students who take 5 courses, the 95% CI is

```
##CI for mean y when x=5
newdata<-data.frame(courses=5)
predict(result, newdata, level=0.95, interval="confidence")
```

```
##          fit          lwr          upr
## 1 660.4138 659.2224 661.6052
```

We have 95% confidence that the average study time for students who take 5 courses is between 659.2223688 and 661.605187 minutes.

4.5 PI of a New Response

Previously, we found a CI for the mean of y given a specific value of x , (4.12). This CI gives us an idea about the location of the regression line at a specific of x .

Instead, we may have interest in finding an interval for a new value of \hat{y}_0 , when we have a new observation $x = x_0$. This is called a **prediction interval (PI) for a future observation y_0 when the predictor is a specific value**. This interval follows from the second interpretation of \hat{y} .

The PI for \hat{y}_0 takes into account:

1. Variation in location for the distribution of y (i.e. where is the center of the distribution of y ?).
2. Variation **within the probability distribution of y** .

By comparison, the confidence interval for the mean response (4.12) only takes into account the first element. The PI is

$$\hat{y}_0 \pm t_{1-\alpha/2, n-2} s \sqrt{1 + \frac{1}{n} + \frac{(x_0 - \bar{x})^2}{\sum (x_i - \bar{x})^2}}. \quad (4.13)$$

Going back to our study time example, suppose we have a newly enrolled student who wishes to take 5 courses, and the student wants to predict his study time

```
##PI for y when x=5
predict(result, newdata, level=0.95, interval="prediction")
```

```
##          fit          lwr          upr
## 1 660.4138 602.0347 718.7928
```

We have 95% confidence that the study time for this student is between 602.0347305 and 718.7928253 minutes.

4.5.1 Thought questions

- In the following two scenarios, decide if we are more interested in the CI for the mean response given the predictor (4.12), or the PI for a future response given the predictor (4.13).
 - We wish to estimate the waiting time, on average, of DMV customers if there are 10 people in line at the DMV.
 - I enter the DMV and notice 10 people in line. I want to estimate my waiting time.

- Look at the standard errors associated with the intervals given in (4.12) and (4.13). How are they related to each other?

4.6 Supplemental Notes on Statistical Inference

4.6.1 Hypothesis statements

Let's consider a t test for the regression parameter, β_1 . Depending on context, the following could be null and alternative hypotheses

- $H_0 : \beta_1 = 0, H_a : \beta_1 \neq 0$.
- $H_0 : \beta_1 = 0, H_a : \beta_1 > 0$.
- $H_0 : \beta_1 = 0, H_a : \beta_1 < 0$.

The null hypothesis should be stated as a statement of **equality**. This concept holds true for hypothesis tests in general. Some other books / resources might state them as

- $H_0 : \beta_1 = 0, H_a : \beta_1 \neq 0$.
- $H_0 : \beta_1 \leq 0, H_a : \beta_1 > 0$.
- $H_0 : \beta_1 \geq 0, H_a : \beta_1 < 0$.

I prefer using the equality statement for the null hypothesis for the following reasons (theoretical, pedagogical, practical):

1. The null hypothesis being an equality aligns with the definition of the p-value.
- The p-value is the probability of observing our sample estimate (or a value more extreme), if the null hypothesis is true (i.e. β_1 is truly 0). This is what we are assuming in the calculation for the test statistic.
2. People tend to get confused between the null and alternative hypotheses if both involve inequalities (the alternative is the hypothesis you are trying to support).
3. Conclusions are made in terms of supporting (or not supporting) the alternative hypothesis.

4.6.2 Sample size and statistical inference

Generally speaking, there is a relationship between sample size and statistical inference (assuming other characteristics remain the same and our sample was randomly obtained or representative of the population of interest):

- Larger sample sizes (typically) lead to narrower confidence intervals (more precise intervals).
- Sample estimates based on larger samples are more likely to be closer to the true parameters.

- Larger sample (typically) lead to more evidence against the null hypothesis.
 - This means a larger sample size leads to a more powerful test. The power of a test is the probability a hypothesis test is able to correctly reject the null hypothesis.

4.6.2.1 Small sample sizes

Small sample sizes tend to result in:

- Confidence intervals that are wide.
- Sample estimates that are more likely to be further away from the true parameters.
- Hypothesis tests that are more likely to incorrectly fail to reject the null hypothesis when the alternative hypothesis is true.

While larger sample sizes have their advantages, there are also some disadvantages with sample sizes that are extremely large.

4.6.2.2 Large sample sizes

A “statistically significant” result does not necessarily mean that the result has practical consequences. Suppose a 95% confidence interval for β_1 is (0.001, 0.002). The interval excludes 0, so it is “statistically significantly” different from 0 (because it is!), but does this result have practical consequences? A narrow CI that barely excludes the null value can happen when we have a large sample size.

If one was to conduct the corresponding hypothesis test, we would reject the null hypothesis that $\beta_1 = 0$. With large sample sizes, hypothesis tests are sensitive to small departures from the null hypothesis.

In such instances, it may be worth considering hypothesis tests involving a different value in the null hypothesis, one that makes sense for your question. For example, a practically significant slope may need to be greater than a specific numerical value for a certain context.

- Statistical inference to assess statistical significance.
- Subject area knowledge to assess practical significance.

4.6.2.3 Questions

Are the following results statistically significant? If so, are the results also practically significant? Assume a two-sided test with a null value of 0 (These are made up examples):

1. In assessing if studying more is associated with better test scores, a SLR is carried out with test scores (out of 100 points) against study time (in hours). The 95% confidence interval for the slope β_1 is (5.632, 7.829).

2. A SLR is carried out to explore the linear relationship between number of years in school with income (in thousands of dollars). The 95% confidence interval for the slope β_1 is (0.051, 0.243).

4.6.3 Cautions using SLR and Correlation

Simple linear regression and correlation are meant for assessing **linear** relationships. If the relationship is not linear, we will need to transform the variable(s) (so the transformed variables have a linear relationship. Will explore this in Module 5).

- Always verify via a scatterplot that the relationship is at least approximately linear.
- A high correlation or a significant estimated slope by themselves do not prove that we have a strong linear relationship between the variables. Conversely, a correlation close to 0 or an insignificant estimated slope is also not proof that we do not have a relationship between the variables.

4.6.3.1 Outliers

SLR and correlation are sensitive to outliers / influential observations. Generally speaking, these are data that are “far away” or very different from the rest of the observations. These data points can be visually inspected from a scatterplot. Some potential considerations when dealing with such data points:

- Investigate these observations. There is usually something that is making them “stand out” from the rest of the data.
- Data entry errors that can be corrected. Be sure to mention in the report.
- Revisit how the data were sampled. Perhaps the data point is not part of the population of interest. If so, data point can be removed (this is legitimate), but be sure to mention in the report.

With regards to regression analysis:

- Exclusion of data points must be clearly documented.
- Fit the regression with and without the data points in question, and see how similar or different the conclusions become.
- If the data points have large value(s) on the predictor and/or response, a log transformation on the variable can pull in the large values.
- Consider subsetting your data and create separate models for each subset; or focus on a subset and make it clear your analysis is for a subset.
- Knowing your data and context can help a lot in these decisions.

4.6.3.2 Association and causation

Two correlated variables do not mean that one variable causes the other variable to change. For example, consider a plot of ice cream consumption and deaths by drowning during various months. There may be some positive correlation, and

clearly, eating more ice cream does not cause more drownings. The correlation can be explained by a third (lurking) variable: the weather.

A **lurking variable** is a variable that has an impact on the relationship between the variables being studied, but is itself not studied.

A carefully designed **randomized experiment** can control for lurking variables, and causal relationships can be established. Typically, such experiments include:

- A control group and a treatment group.
- Random assignment of large number of observations into the treatment and control groups. Due to the random assignment, the general characteristics of subjects in each group are similar.

Lurking variables are always an issue with **observational studies**. Researchers in observational studies do not intervene with the observations and simply observe the data that the observations generate. Causal relationships are much more difficult to establish with observational studies.

4.6.3.3 Questions

1. Consider the **palmerpenguins** dataset that we have been working on. The data contain size measurements for three different species of penguins on three islands in the Palmer Archipelago, Antarctica over three years. Is this an observational study or randomized experiment?
2. A fertilizer company wishes to evaluate how effective a new fertilizer is in terms of improving the yield of crops. A large field is divided into many smaller plots, and each smaller plot is randomly assigned to receive either the new fertilizer or the standard fertilizer. Is this an observational study or randomized experiment?
3. A professor wishes to evaluate the effectiveness of various teaching methods (traditional vs flipped classroom). The professor uses the traditional approach for a section that meets on Mondays, Wednesdays, and Fridays from 9 to 10am and uses the flipped classroom approach for a section that meets on Mondays, Wednesdays, and Fridays from 2 to 3pm. Students were free to choose whichever section that wanted to register for, with no knowledge of the teaching method being used. What are some potential lurking variables in this study?

4.7 R Tutorial

For this tutorial, we will continue to work with the dataset **elmhurst** from the **openintro** package in R.

```
library(tidyverse)
library(openintro)
Data<-openintro::elmhurst
```

The key pieces of information are:

- A random sample of 50 students (all freshman from the 2011 class at Elmhurst College).
- Family income of the student (units are missing).
- Gift aid, in \$1000s.

We want to explore how family income may be related to gift aid, in a simple linear regression framework.

Hypothesis test for β_1 (and β_0)

Applying the `summary()` function to `lm()` gives the results of hypothesis tests for β_1 and β_0 :

```
##Fit a regression model
result<-lm(gift_aid~family_income, data=Data)

##look at t stats and F stat
summary(result)

##
## Call:
## lm(formula = gift_aid ~ family_income, data = Data)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -10.1128  -3.6234  -0.2161   3.1587  11.5707
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  24.31933     1.29145   18.831 < 2e-16 ***
## family_income -0.04307     0.01081   -3.985 0.000229 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 4.783 on 48 degrees of freedom
## Multiple R-squared:  0.2486, Adjusted R-squared:  0.2329
## F-statistic: 15.88 on 1 and 48 DF,  p-value: 0.0002289
```

Under coefficients, we can see the results of the hypothesis tests for β_1 and β_0 . Specifically, for β_1 :

- $\hat{\beta}_1 = -0.0430717$
- $se(\hat{\beta}_1) = 0.0108095$
- the test statistic is $t = -3.984621$
- the corresponding p-value is 2.2887345×10^{-4}

You can work out the p-value using R (slight difference due to rounding):


```
##pvalue
2*pt(-abs(-3.985), df = 50-2)
```

```
## [1] 0.0002285996
```

Or find the critical value using R:

```
##critical value
qt(1-0.05/2, df = 50-2)
```

```
## [1] 2.010635
```

Either way, we end up rejecting the null hypothesis. The data support the claim that there is a linear association between gift aid and family income.

Note:

- the t tests for regression coefficients are based on $H_0 : \beta_j = 0, H_a : \beta_j \neq 0$. The reported p-value is based on this set of null and alternative hypotheses. If your null and alternative hypotheses are different, you will need to compute your own test statistic and p-value.
- For SLR, the two-sided t test for β_1 gives the exact same result as the ANOVA F test. Notice the p-values are the same. The F statistic of 15.88 is the squared of the t statistic, $(-3.985)^2$.

Confidence interval for β_1 (and β_0)

To find the 95% confidence intervals for the coefficients, we use the `confint()` function:

```
##to produce 95% CIs for all regression coefficients
confint(result, level = 0.95)
```

```
##                2.5 %      97.5 %
## (Intercept)  21.72269421 26.91596380
## family_income -0.06480555 -0.02133775
```

The 95% CI for β_1 is $(-0.0648056, -0.0213378)$. We have 95% confidence that for each additional thousand dollars in family income, the predicted gift aid decreases between \$21.3378 and \$64.8056.

Confidence interval for mean response for given x

Suppose we want a confidence interval for the average gift aid for Elmhurst College students with family income of 80 thousand dollars. We can use the `predict()` function:

```
##to produce 95% CI for the mean response when x=80,
newdata<-data.frame(family_income=80)
predict(result, newdata, level=0.95, interval="confidence")
```

```
##          fit          lwr          upr
## 1 20.8736 19.43366 22.31353
```

The 95% CI for the mean gift aid for students with family income of 80 thousand dollars is (19.4336609, 22.3135327). We have 95% confidence the mean gift aid for students with family income of 80 thousand dollars is between \$19 433.66 and \$22 313.53.

Prediction interval for a response for a given x

For a prediction interval for the gift aid of an Elmhurst College student with family income of 80 thousand dollars:

```
##and the 95% PI for the response of an observation when x=80
predict(result,newdata,level=0.95, interval="prediction")
```

```
##          fit          lwr          upr
## 1 20.8736 11.15032 30.59687
```

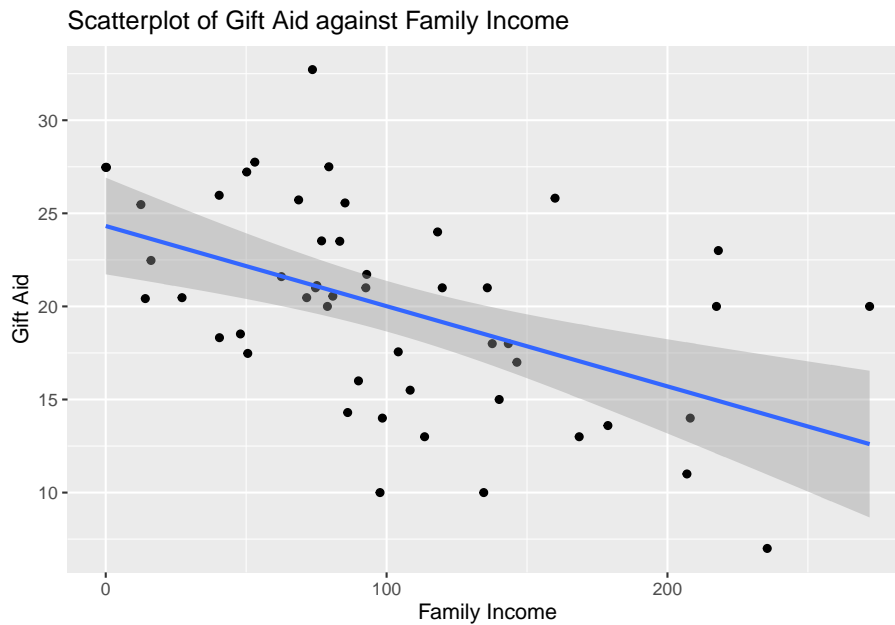
We have 95% confidence that for an Elmhurst College student with family income of 80, this student's gift aid is between \$11 150.32 and \$30 596.87.

Visualization of CI for mean response given x and PI of response given x

When using the `ggplot()` function to create a scatterplot, we can overlay the SLR equation by adding a layer via `geom_smooth(method = lm)`. By default, the CI for the mean response for each value of the predictor gets overlaid as well. In the previous tutorial, we removed this by adding `se=FALSE` inside `geom_smooth()`:

```
##regular scatterplot
##with regression line overlaid, and bounds of CI for mean y
ggplot2::ggplot(Data, aes(x=family_income, y=gift_aid))+
  geom_point() +
  geom_smooth(method=lm)+
  labs(x="Family Income",
       y="Gift Aid",
       title="Scatterplot of Gift Aid against Family Income")
```

```
## `geom_smooth()` using formula = 'y ~ x'
```



Overlaying prediction intervals require a bit more work. We need to compute the lower and upper bounds of the PI for each value of the predictor:

```
##find PIs for each observation
preds <- predict(result, interval="prediction")
```

```
## Warning in predict.lm(result, interval = "prediction"): predictions on current data refer to _
```

Previously, when we used the `predict()` function, we provided the numerical value of x to make a prediction on. If this is not supplied, the function will use all the current values of x to make predictions, and will actually print out a warning message. For our purpose, this is not an issue since this is exactly what we want.

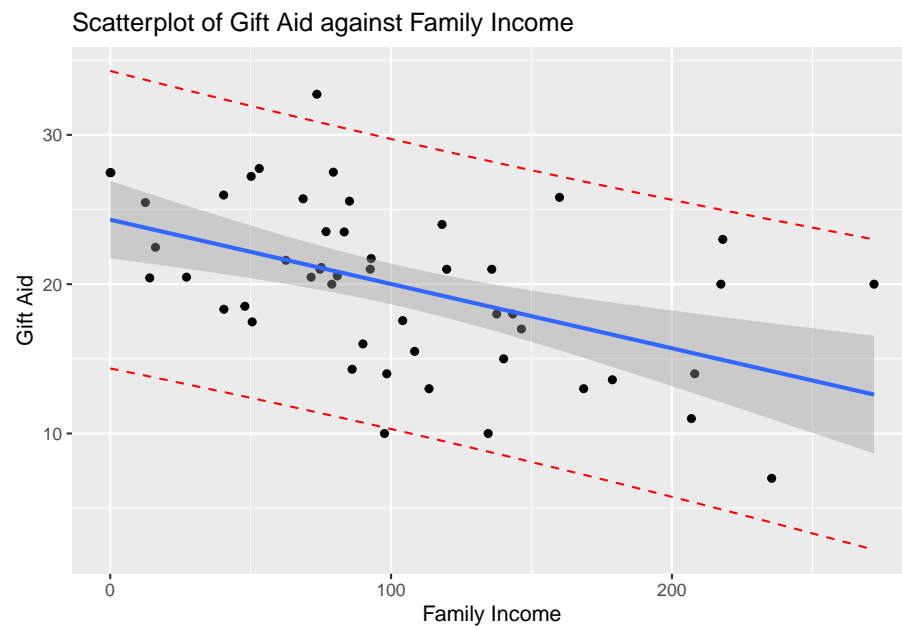
We then add `preds` to the data frame in order to overlay the lower and upper bounds on the scatterplot, by adding extra layers via `geom_line()` in the `ggplot()` function:

```
##add preds to data frame
Data<-data.frame(Data,preds)

##overlay PIs via geom_line()
ggplot2::ggplot(Data, aes(x=family_income, y=gift_aid))+
  geom_point() +
  geom_line(aes(y=lwr), color = "red", linetype = "dashed")+
  geom_line(aes(y=upr), color = "red", linetype = "dashed")+
  geom_smooth(method=lm)+
```

```
labs(x="Family Income",
     y="Gift Aid",
     title="Scatterplot of Gift Aid against Family Income")
```

```
## `geom_smooth()` using formula = 'y ~ x'
```



As mentioned in the notes, the CI captures the location of the regression line, whereas the PI captures the data points.

Chapter 5

Model Diagnostics and Remedial Measures in SLR

5.1 Introduction

The regression model is based on a number of assumptions. Those assumptions are made so that we can apply commonly used probability distributions to we quantify the variability associated with our estimated regression model. This means that if the assumptions are not met for our regression model, then how we quantify the variability associated with our model is no longer reliable. All our analysis with statistical inference becomes questionable.

In this module, you will learn how to assess whether the regression assumptions are met. We will explore ways in which we can transform our variables after diagnosing which assumptions are not met so that we can still proceed to build our regression model.

5.2 Assumptions in Linear Regression

In module 3, we stated the SLR model as

$$y = \beta_0 + \beta_1 x + \epsilon. \quad (5.1)$$

where $f(x) = \beta_0 + \beta_1 x$. We need to make some assumptions for the error term ϵ . Mathematically, the assumptions are expressed as

$$\epsilon_1, \dots, \epsilon_n \text{ i.i.d. } \sim N(0, \sigma^2) \quad (5.2)$$

Breaking down (5.2) the assumptions can be expressed as the following:

1. The errors have **mean 0**.
2. The errors have **constant variance denoted by σ^2** .
3. The errors are **independent**.
4. The errors are **normally distributed**.

Let's dig a little deeper into the meaning and implications of these 4 assumptions.

5.2.1 Assumption 1: Errors have mean 0.

For each value of the predictor, the errors have **mean 0**. A by-product of this statement is that the relationship between y and x , as expressed via $y \approx f(x)$, is correct. So, if $f(x) = \beta_0 + \beta_1 x$, then the relationship is approximately linear.

The plots in Figure 5.1 are based on simulated data. The scatterplot shown in Figure 5.1(a) is an example of when this assumption is met. As we move from left to right on the plot, the data points are generally evenly scattered on both sides of the regression line that is overlaid.

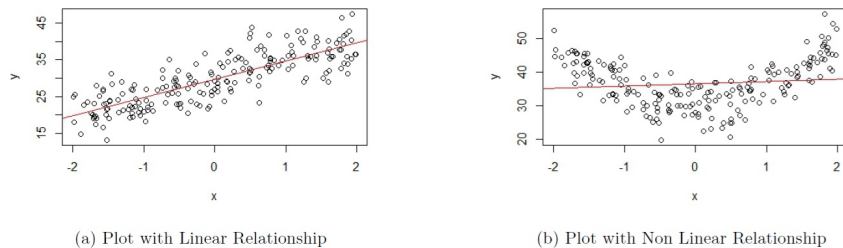


Figure 5.1: Assumption 1

The scatterplot shown in Figure 5.1(b) is an example of when this assumption is **not** met. As we move from left to right on the plot in Figure 5.1(b), the data points are generally not evenly scattered on both sides of the regression line that is overlaid.

- When $-2 \leq x \leq -1.2$, the data points are generally above the regression line;
- then when $-1.2 < x < 1$, the data points are generally below the regression line;
- and then when $x \geq 1$, the data points are generally above the regression line.

Please see the associated video for more explanation on how to use Figure 5.1 to assess assumption 1.

5.2.1.1 Consequences of violating this assumption

Predictions will be biased. This means that predicted values will systematically over- or under- estimate the true values of the response variable. Of the 4 assumptions listed, this is **most crucial assumption**.

Using Figure 5.1(b) as an example, this implies that

- when $-2 \leq x \leq -1.2$, the regression line will systematically under-predict the response variable;
- then when $-1.2 < x < 1$, the regression line will systematically over-predict the response variable;
- and then when $x \geq 1$, the regression line will systematically under-predict the response variable.

5.2.2 Assumption 2: Errors have constant variance

For each value of the predictor, the error terms have **constant variance**, denoted by σ^2 . This implies that when looking at a scatterplot, the vertical variation of data points around the regression equation has the same magnitude everywhere.

The plots in Figure 5.2 are based on simulated data. The scatterplot shown in Figure 5.2(a) is an example of when this assumption is met (this figure is actually the same as Figure 5.1(a), so the data that produced these plots satisfy both assumptions). As we move from left to right on the plot, the vertical variation of the data points about the regression line is approximately constant.

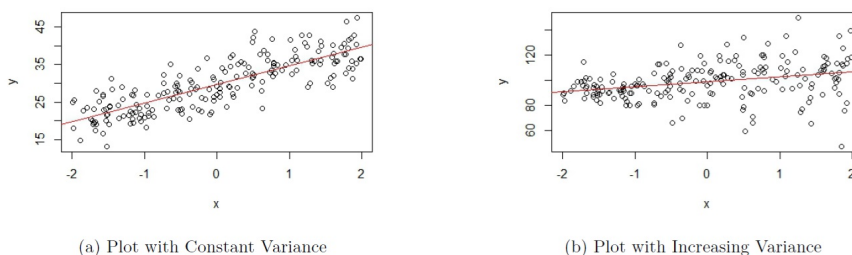


Figure 5.2: Assumption 2

The scatterplot shown in Figure 5.2(b) is an example of when this assumption is **not** met. As we move from left to right on the plot in Figure 5.2(b), the vertical variation of the data points about the regression line becomes larger as the value of the response variable gets larger, so the variance is not constant.

Please see the associated video for more explanation on how to use Figure 5.2 to assess assumption 2.

5.2.2.1 Consequences of violating this assumption

Statistical inference will no longer be reliable. This means that the results from any hypothesis test, confidence interval, or prediction interval are no longer reliable.

Interestingly, for the scatterplot in Figure 5.2(b), we can say that assumption 1 is met, since the data points are generally evenly scattered on both sides of the regression line. Predictions will still be unbiased; the predicted response, \hat{y} , do not systematically over- or under-predict the response variable. So if our goal is to assess if the relationship is approximately linear, this scatterplot is fine. We do lose the utility from hypothesis tests, CIs, and PIs.

5.2.3 Assumption 3: Errors are independent

A by-product of this assumption is that the values of the response variable, y_i , are independent from each other. Any y_i does not depend on other values of the response variable.

5.2.3.1 Consequences of violating this assumption

Statistical inference will no longer be reliable. This means that the results from any hypothesis test, confidence interval, or prediction interval are no longer reliable.

5.2.4 Assumption 4: Errors are normally distributed

If we were to create a density plot of the errors, the errors should follow a normal distribution.

5.2.4.1 Consequences of violating this assumption

The regression model is fairly robust to the assumption that the errors are normally distributed. In other words, violation of this particular assumption is not very consequential. **Of the 4 assumptions, this is the least crucial to satisfy.**

5.3 Assessing Regression Assumptions

There are a few visualizations that help in detecting violations of the regression assumptions. These visualizations are:

- Scatterplot of y against x (assumptions 1 and 2).
- Residual plot (assumptions 1 and 2).
- Autocorrelation function (ACF) plot of residuals (assumption 3).
- Normal probability plot of residuals (often called QQ plot) (assumption 4).

5.3.1 Scatterplot

We can examine the scatterplot of y against x to check for assumptions 1 and 2. We want to see the following in the scatterplot:

- **No nonlinear pattern** (assumption 1).
- Data points **evenly scattered** (for each value on the x-axis) around fitted line (assumption 1).
- Vertical variation of data points constant (assumption 2).

We have used Figure 5.2(a) as an example of a scatterplot that meets these assumptions. Let us take a look at another example that we have worked with. This scatterplot is from the `elmhurst` dataset from the `openintro` package that we have been seeing in tutorials. We are regressing the amount of gift aid a student receives based on the student's family income. The corresponding scatterplot is shown in in Figure 5.3.

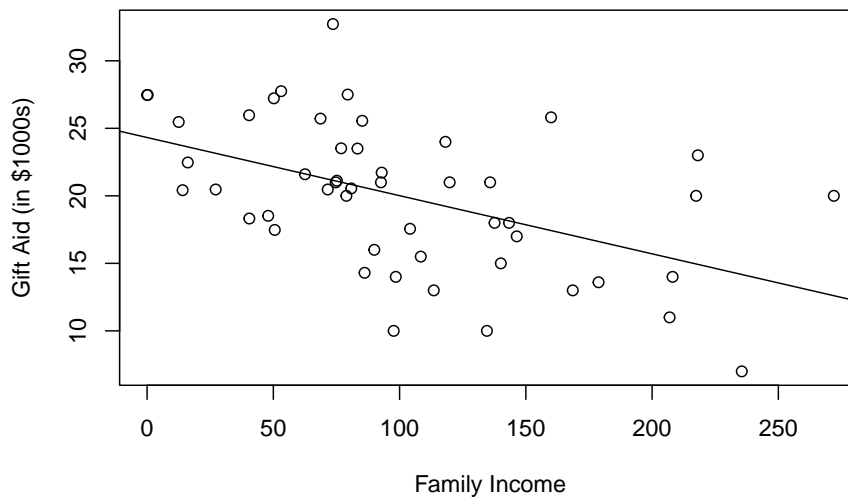


Figure 5.3: Scatterplot of Gift Aid Against Family Income

In Figure 5.3, we see that the data points are evenly scattered around the fitted line. We also see the vertical variation of the data points is fairly constant. So assumptions that the errors have 0 mean and constant variance appear to be met.

5.3.1.1 Practice question

The data are about the prices of used cars. We are regressing the sale price of the car against the age of the car. The corresponding scatterplot is shown in Figure 5.4. Based on Figure 5.4, which of assumptions 1 or 2 (or both, or neither), is met? We will go over this in the tutorial.

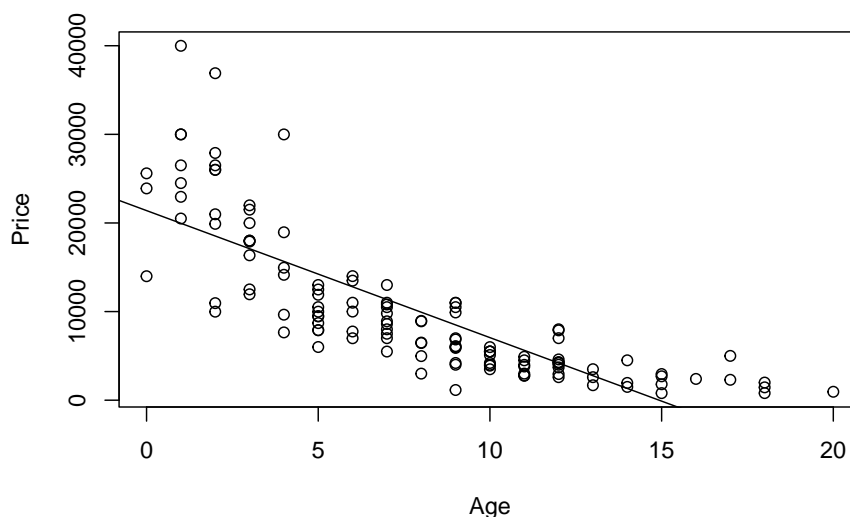


Figure 5.4: Scatterplot of Sale Price Against Age

5.3.2 Residual plot

While using the scatterplot is an intuitive way of assessing regression assumptions, it has a limitation. It cannot be used if we have multiple predictors in our regression, which we will encounter (and happens more often than just having one predictor). Another visualization that we can use to assess assumptions 1 and 2 is a **residual plot**. This is a scatterplot of residuals, e , against fitted values, \hat{y} . We want to observe the following in a residual plot.

- Residuals should be **evenly scattered** across the horizontal axis (assumption 1).
- The residuals should have **similar vertical variation** across the plot (assumption 2).
- Some writers combine these two points into the following statement: the residuals should fall in a **horizontal band around 0** with no apparent pattern (assumption 1, 2).

The residual plots in Figure 5.5 are based on simulated data from Figures 5.1(a), 5.1(b), and 5.2(b).

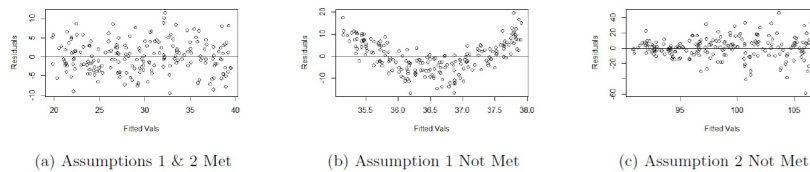


Figure 5.5: Residual Plots from Fig 1(a), 1(b), 2(b) Respectively

We make the following observations:

- From Figure 5.5(a), we see that the residuals are evenly scattered across the horizontal axis, and their vertical variation is fairly constant across the plot. So both assumptions are met.
- From Figure 5.5(b), we see that the residuals are **not** evenly scattered across the horizontal axis, although their vertical variation is fairly constant across the plot. So only assumption 1 is not met.
- From Figure 5.5(c), we see that the residuals are evenly scattered across the horizontal axis, but their vertical variation is **not constant** across the plot. In fact, the vertical variation is increasing as we move from left to right. So only assumption 2 is not met.

If you compare the conclusions from the residuals plots and scatterplots, they are the same. In SLR, the takeaways should be consistent.

Please see the associated video for more explanation on how to use Figure 5.5 to assess assumptions 1 and 2.

5.3.2.1 Practice questions

1. The residual plot in Figure 5.6(a) comes from regressing gift aid against family income for the `elmhurst` dataset. Based on this residual plot, which assumptions are met?
2. The residual plot in Figure 5.6(b) comes from regressing price of cars against age for the used cars dataset. Based on this residual plot, which assumptions are met?

Please see the associated video as I go over these practice questions.

5.3.3 ACF plot

Assumption 3 states that the errors are **independent**. This assumption implies that the values of the response variable are independent from each other. This assumption is typically assessed via knowing the nature of the data.

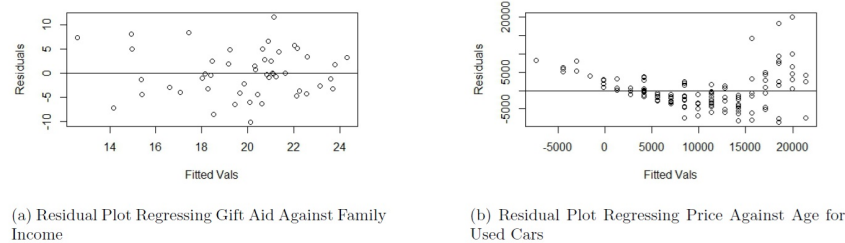


Figure 5.6: Residual Plots for Practice Questions

- If the observations were obtained from a random sample, it is likely that the observations will be independent from each other. This is the very nature of a random sample and why random samples are preferred over convenience samples.
- If the data has some inherent sequence, it is likely the observations will not be independent, and are dependent. For example, if I record the value of a stock at the end of each day, the value at day 2 is likely to be related to its value at day 1. So the values of stock prices at the end of each day are not independent.

An autocorrelation function (ACF) plot of the residuals may be used to help assess if the assumption that the errors are independent is met. However, the plot is not a substitute for using your understanding about the nature of the data and should only be used as a confirmation.

The ACF plot measures the correlation between a vector of observations and the lagged versions of the observations. If the observations are uncorrelated, the correlations between the vector of observations and lagged versions of these observations are theoretically 0. We may create an ACF plot for the residuals from our regression.

The ACF plot in Figure 5.7(a) and is based on simulated data that were independently generated.

A few notes about the ACF plot:

- The ACF at lag 0 is always 1. The correlation of any vector with itself is always 1.
- The dashed horizontal lines represent critical values. An ACF at any lag beyond the critical value indicates an ACF that is significant. We have evidence of correlation (and hence dependence) in our residuals.
- If the observed values for the response variable are independent, then we would expect the ACFs at lags greater than 0 to be insignificant. Do note that because we are conducting multiple hypothesis tests, do not be too

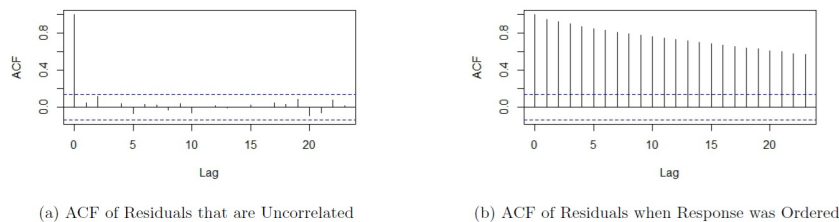


Figure 5.7: Assumption 3

alarmed if the ACFs are slightly beyond the critical values at an isolated lag or 2.

Based on Figure 5.7(a), we see that the ACFs at all lags greater than 0 are insignificant. We do not have evidence the residuals are correlated with each other, so we do not have evidence that assumption 3 is not met.

Sometimes, the dataframe can be sorted in some manner (e.g. increasing order for response variable), and if so, we would actually expect to see significant correlations in the ACF plot. The ACF plot in Figure 5.7(b) is such an example. The residuals are from the same simulated dataset, only with the data sorted by the response variable. If we had just looked at the ACF plot in Figure 5.7(b) without understanding the data were simulated independently and then sorted, we would have erroneously concluded that the residuals are not independent and the regression assumption is not met.

5.3.4 QQ plot

A normal probability plot (also called a QQ plot) is used to assess if the distribution of a variable is normal. It typically plots the residuals against their theoretical residual if they followed a normal distribution. A QQ line is typically overlaid. If the plots fall closely to the QQ line, we have evidence that the observations follow a normal distribution. Figure 5.8 shows a QQ plot that comes from a normally distributed variable.

5.3.5 Remedial measures

We now know how to assess if specific regression assumptions are not met. The remedial measures involve transforming either the predictor variable and / or the response variable. These transformations are chosen to handle violations to assumptions 1 and / or 2 respectively. The general strategy on selecting which variable to transform:

- Transforming the response variable, y , affects both assumptions 1 and 2.

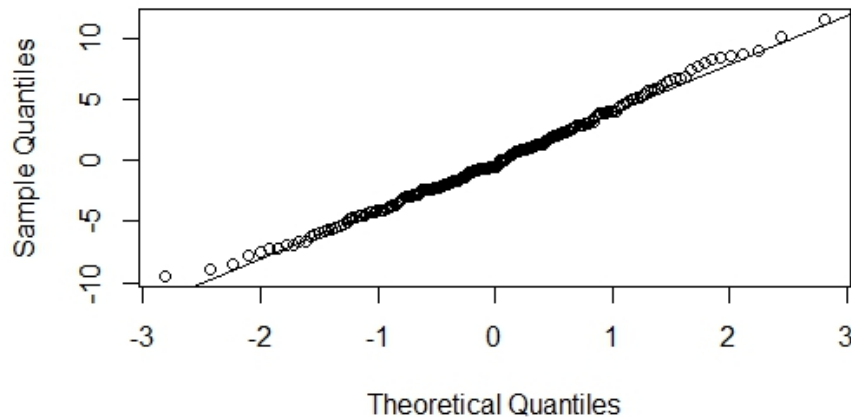


Figure 5.8: QQ Plot

- Visually, we can think of transforming y in terms of stretching or squeezing the scatterplot of y against x vertically. Thus, transforming y affects the shape of the relationship and the vertical spread of the data points.
- However, the **choice on how we transform y is based on handling assumption 2.**
- Transforming the predictor variable, x affects assumption 1 and does not theoretically affect assumption 2.
 - Visually, we can think of transforming x in terms of stretching or squeezing the scatterplot of y against x horizontally. Thus, transforming x affects the shape of the relationship but not the vertical spread of the data points.
 - Therefore, **transforming x is based on handling assumption 1.**
- If assumption 2 is not met, we transform y to stabilize the variance and make it constant.
- If assumption 1 is not met, we transform x to find the appropriate shape to relate the variables.
- If both assumptions are not met, we transform y first to stabilize the variance. Once assumption 2 is solved, check if assumption 1 is not met. If not met, transform x .

Assumption 1 deals with whether the way we have expressed how y and x are related, through $f(x)$, is appropriate. Assumption 2 deals with the vertical variation of the data points in the scatterplot.

5.4 Remedial Measures: Variance Stabilizing Transformations

We transform the response variable to stabilize the variance (assumption 2). There are a couple of ways to decide the appropriate transformation:

1. Pattern seen in residual plot can guide choice in how to transform the response variable.
2. Box-Cox plot.

5.4.1 Use Pattern in Residual Plot

We can stabilize the variance of the errors based on the residual plot, if we see either of the following scenarios:

- vertical variation of residuals **increasing** as fitted response increases, or as we move from left to right, as in Figure 5.9(a), or
- vertical variation of residuals **decreasing** as fitted response increases, or as we move from left to right, as in Figure 5.9(b).

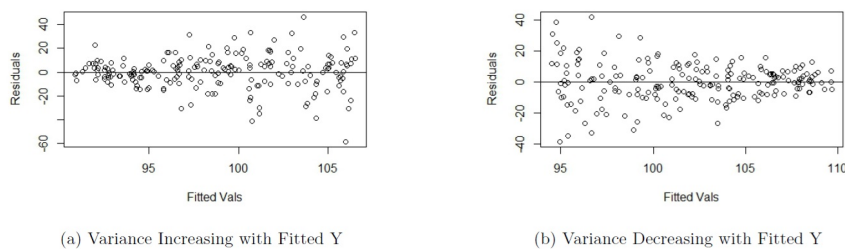


Figure 5.9: Non Constant Variance in Residual Plot

Note that increasing variance as fitted response increases is much more common with real data. Generally, larger values of a variable are associated with larger spread.

We transform y using $y^* = y^\lambda$, with λ chosen based on whether the variance of the residuals is increasing or decreasing with fitted response:

- For Figure 5.9(a), choose $\lambda < 1$.
 - If $\lambda = 0$, it means we use a logarithmic transformation with base e , i.e. $y^* = \log(y)$.
 - Note that a logarithm with no base means a natural log, or \ln .
- For Figure 5.9(b), choose $\lambda > 1$.

So based on the residual plot, we have a range of values for λ .

5.4.2 Box-Cox Plot

We can use a Box-Cox plot to help us narrow the range of λ to use. It is a plot of the log-likelihood function against λ , and we choose λ that maximizes this log-likelihood function. For example, Figure 5.10 shows the Box Cox plot generated for the regression associated with the residual plot in Figure 5.9(b).

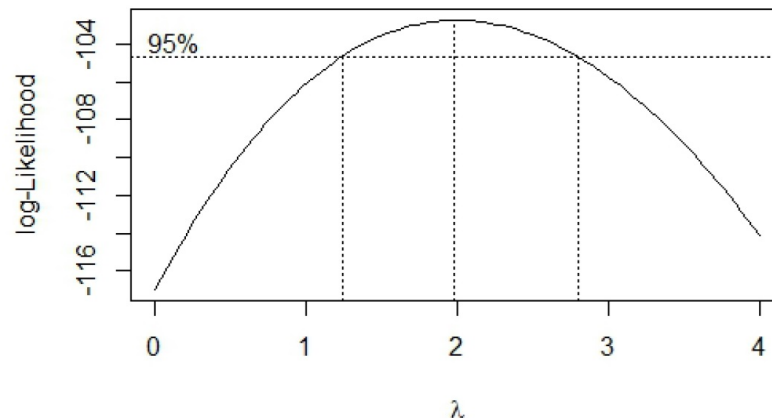


Figure 5.10: Box-Cox Plot based on Figure 9(b)

Notice an approximate 95% CI is provided for λ . A few comments on how to use the Box-Cox plot:

- Three vertical dashed lines are displayed: the middle line corresponds to the optimal value of λ ; the other two lines are the lower and upper bounds of a 95% CI for λ .
- We choose λ within the CI (or even close to it) that is easy to understand. We do not have to choose the optimal value, especially if its value is difficult to interpret. In this example, I will choose $\lambda = 2$, so a square transformation for y . Transform response with $y^* = y^2$. Regress y^* against x .
- If 1 lies in the CI, **no transformation** on y may be needed.
- If a transformation is needed, a **log transformation** is preferred, since we can still interpret the estimated coefficients. It is difficult to interpret with any other type of transformation.
- View the Box-Cox procedure as a guide for selecting a transformation, rather than being definitive.
- Need to recheck the residuals after every transformation to assess if the transformation worked.

5.4.3 Interpretation with Log Transformed Response

A log transformation on the response is preferred over any other transformation, as we can still interpret regression coefficients. A couple of ways to interpret the estimated slope $\hat{\beta}_1$:

- The predicted response variable is **multiplied by a factor** of $\exp(\hat{\beta}_1)$ for a one-unit increase in the predictor.
- We can also subtract 1 from $\exp(\hat{\beta}_1)$ to express the change as a percentage.
 - If $\hat{\beta}_1$ is positive, we have a percent **increase**. The predicted response variable increases by $(\exp(\hat{\beta}_1) - 1) \times 100$ percent for a one-unit increase in the predictor.
 - If $\hat{\beta}_1$ is negative, we have a percent **decrease**. The predicted response variable decreases by $(1 - \exp(\hat{\beta}_1)) \times 100$ percent for a one-unit increase in the predictor.

Please see the associated video as I go over the math explaining how we interpret regression coefficients when the response variable is log transformed.

5.5 Remedial Measures: Linearization Transformations

We first ensure the variance has been stabilized and assumption 2 is met. If $f(x)$ does not accurately capture the relationship between the variables, we transform the predictor variable to meet assumption 1. Some writers call this a linearization transformation, as we seek to make the transformed version of the predictor variable, x^* , to be approximately linear with the response variable (or transformed y), i.e. $y = \beta_0 + \beta_1 x^* + \epsilon$. We do not consider transforming the response variable to deal with assumption 1, as transforming the response variable is likely to reintroduce violation of assumption 2.

The general strategy on how to transform the predictor is via a scatterplot of y (or y^*) against x . We use the pattern seen in the plot to decide how to transform the predictor. Some examples are shown in Figure 5.11 below.

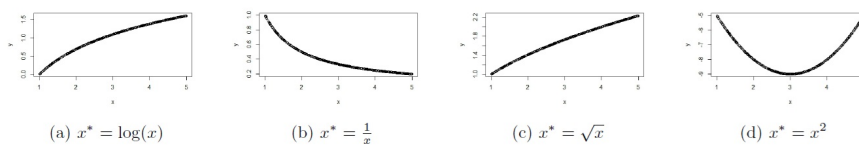


Figure 5.11: Transformations for x

5.5.1 Hierarchical Principle

One thing to be aware of is the **hierarchical principle**: if the relationship between the response and predictor is of a higher order polynomial (e.g. quadratic, cubic), the hierarchical principle states that the lower order terms should remain in the model. For example, if the relationship is of order h , fit $y = \beta_0 + \beta_1 x + \beta_2 x^2 + \dots + \beta_h x^h + \epsilon$ via a multiple linear regression framework. We will see how to do this in the next module.

5.5.2 Interpretation with Log Transformed Predictor

A log transformation on the predictor is preferred over any other transformation, as we can still interpret the regression coefficient, $\hat{\beta}_1$, in a couple of ways:

- For an $a\%$ increase in the predictor, the predicted response **increases by** $\hat{\beta}_1 \log(1 + \frac{a}{100})$.
- $\log(1 + \frac{1}{100}) \approx \frac{1}{100}$ (Taylor series). So an alternative interpretation is: for a 1% increase in the predictor, the predicted response increases by approximately $\frac{\hat{\beta}_1}{100}$.

Please see the associated video as I go over the math explaining how we interpret regression coefficients when the predictor variable is log transformed.

5.5.3 Interpretation with Log Transformed Response and Predictor

If both response and predictor variables are log transformed, the regression coefficient, $\hat{\beta}_1$, can be interpreted in a couple of ways:

- For an $a\%$ increase in the predictor, the predicted response is **multiplied by** $(1 + \frac{a}{100})^{\hat{\beta}_1}$.
- $(1 + \frac{1}{100})^{\hat{\beta}_1} \approx 1 + \frac{\hat{\beta}_1}{100}$ (Taylor series). So an alternative interpretation is: for a 1% increase in the predictor, the predicted response **increases by approximately $\hat{\beta}_1$ percent**. Note that this approximation works better when $\hat{\beta}_1$ is small in magnitude.

Please see the associated video as I go over the math explaining how we interpret regression coefficients when the both response and predictor variables are log transformed.

5.5.4 Some General Comments about Assessing Assumptions and Transformations

- When assessing the assumptions with a residual plot, we are assessing if the assumptions are reasonably / approximately met.
- With real data, assumptions are rarely met 100%.

- If unsure, proceed with model building, and test how model performs on new data. If poor performance, go back to residual plot to assess what transformation will be appropriate.
- Assess the plots to decide which variables need to be transformed, and how. The choice of transformation should be guided by what you see in the plots, and not by trial and error.
- A residual plot should always be produced after each transformation. A Box Cox plot could also be produced. The plots should be assessed if the transformation helped in the way you intended.
- Solve assumption 2 first, then assumption 1.

5.6 R Tutorial

5.6.1 Example 1

The linear regression model involves several assumptions. Among them are:

1. The errors, for each fixed value of x , have mean 0. This implies that the relationship as specified in the regression equation is appropriate.
2. The errors, for each fixed value of x , have constant variance. That is, the variation in the errors is theoretically the same regardless of the value of x (or \hat{y}).
3. The errors are independent.
4. The errors, for each fixed value of x , follow a normal distribution.

To assess assumptions 1 and 2, we can examine scatterplots of:

- y versus x .
- residuals versus fitted values, \hat{y} .

Assumption 3 is assessed based on knowledge of the data. An autocorrelation (ACF) plot of the residuals may also be used.

Assumption 4 is assessed with a normal probability plot, and is considered the least crucial of the assumptions.

We will see how to generate the relevant graphical displays to help us assess whether the assumptions are met, and if needed, carry out transformations on the variable(s) so the assumptions are met.

For this tutorial, we will go over a dataset involving prices of used cars (Mazdas). The two variables are the sales price of the used car, and the age of the car in years. Download the data file, `mazda.txt` and read the data:

```
Data<-read.table("mazda.txt", header=TRUE, sep="")
```

Model Diagnostics with Scatterplots

We can use a scatterplot of the response variable against the predictor to assess assumptions 1 and 2:

```
library(tidyverse)

##scatterplot, and overlay regression line
ggplot2::ggplot(Data, aes(x=Age,y=Price))+
  geom_point()+
  geom_smooth(method = "lm", se=FALSE)+
  labs(x="Age", y="Sales Price", title="Scatterplot of Sales Price against Age")
```



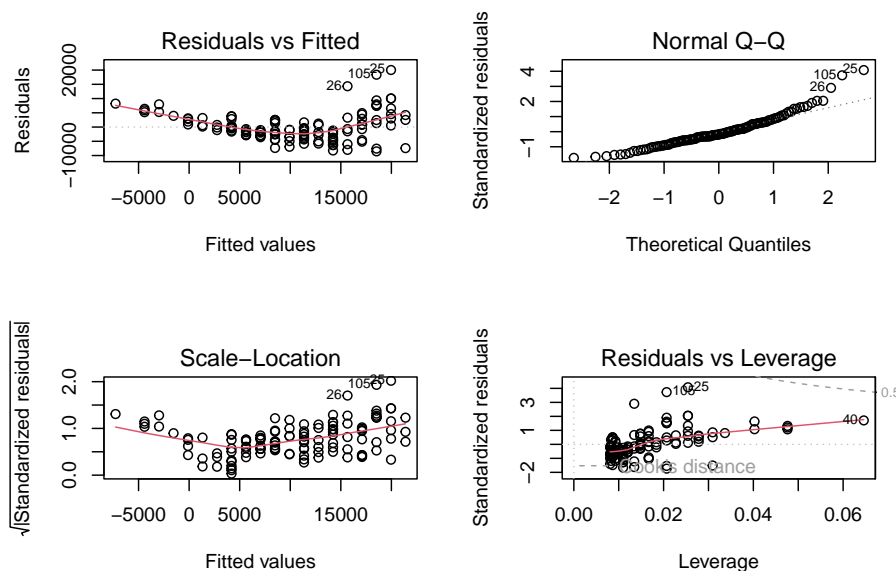
To assess assumption 1, the data points should be evenly scattered on both sides of the regression line, as we move from left to right. We do not see this in the scatterplot, so assumption 1 is not met. When age is between 0 and 2, the data points are mostly above the line. When age is between 5 and 11, the data points are mostly below the line, and when age is greater than 13, the data points are above the line.

To assess assumption 2, the vertical spread of the data points should be constant as we move from left to right. The spread seems to be decreasing as we move from left to right (or in other words, the spread is increasing as the response increases), so assumption 2 is not met.

Model Diagnostics with Residual Plots

Sometimes, a residual plot is easier to visualize than a scatterplot. We fit our SLR model using `lm()` as usual. Applying the `plot()` function to an object created with `lm()` actually produces a four diagnostic plots. To display the four diagnostic plots in a 2 by 2 array, we specify `par(mfrow = c(2, 2))` so the plotting window is split into a 2 by 2 array:

```
result<-lm(Price~Age, data=Data)
par(mfrow = c(2, 2))
plot(result)
```



- The first plot (top left) is the residual plot, with residuals on the y-axis and fitted values on the x-axis. The residual plot can be used to address assumptions 1 and 2. A red line is overlaid to represent the average value of the residuals for differing values along the x-axis. This line should be along the x-axis without any apparent curvature to indicate the form of our model is reasonable. This is not what we see, as we see a clear curved pattern. So assumption 1 is not met. For assumption 2, we want to see the vertical spread of the residuals to be fairly constant as we move from left to right. We do not see this in the residual plot; the vertical spread increases as we move from left to right, so assumption 2 is not met.
- The second plot (top right) is the normal probability plot (also called a QQ plot), and addresses assumption 4. If the residuals are normal, the residuals should fall along the 45 degree line. The regression model is fairly robust to this assumption though; the normality assumption is the

least crucial of the four.

- The third plot (bottom left) is a plot of the square root of the absolute value of the standardized residuals against the fitted values (scale-location). This plot should be used to assess assumption 2, the constant variance assumption. A red line is overlayed to represent the average value on the vertical axis for differing values along the x-axis. If the variance is constant, the red line should be horizontal and the vertical spread of the plot should be constant. This plot should be used to assess assumption 2, if we have a small sample size. Otherwise, this plot should tell a similar story to the first plot (top left) when assessing assumption 2.
- The last plot (bottom right) is a plot to identify influential outliers. Data points that lie in the contour lines with large Cook's distance are influential. None of our data points have Cook's distance greater than 0.5. As a general rule of thumb, observations with Cook's distance greater than 1 are flagged as influential. We will talk more about influential observations in a future module.

Now that we know that both assumptions 1 and 2 are not met. We need to transform the response variable first, to stabilize the variance.

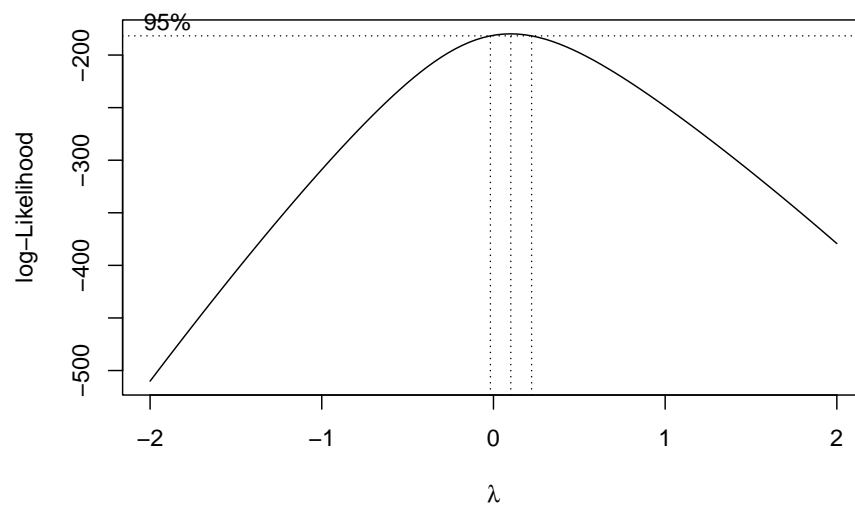
Based on the residual plot, we see that the variance of the residuals increases as we move from left to right. So we know we need to transform the response variable using $y^* = y^\lambda$ with $\lambda < 1$. A log transform should be considered since we can still interpret regression coefficients.

Box Cox Transformation on y

The Box Cox plot can be used to decide how to transform the response variable. The transformation takes the form $y^* = y^\lambda$, with the value of λ to be chosen. If $\lambda = 0$, we perform a log transformation.

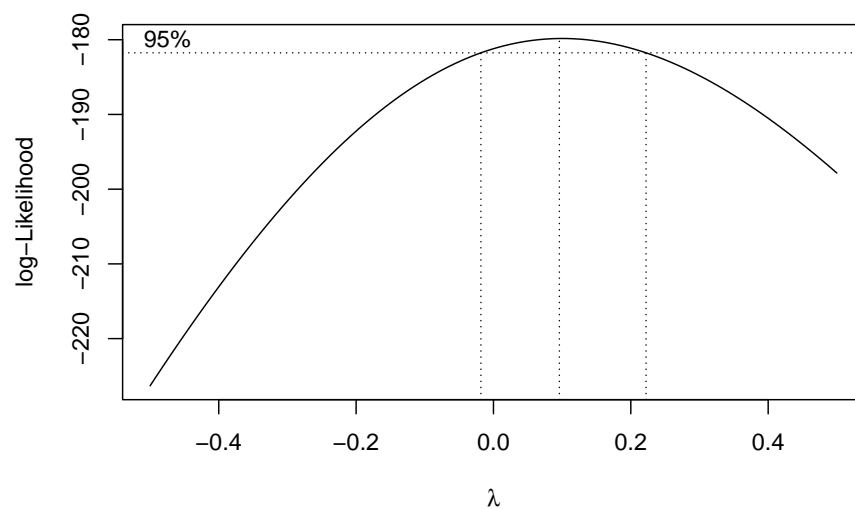
We will use the `boxcox()` function from the MASS package:

```
library(MASS) ##to use boxcox function
MASS::boxcox(result)
```



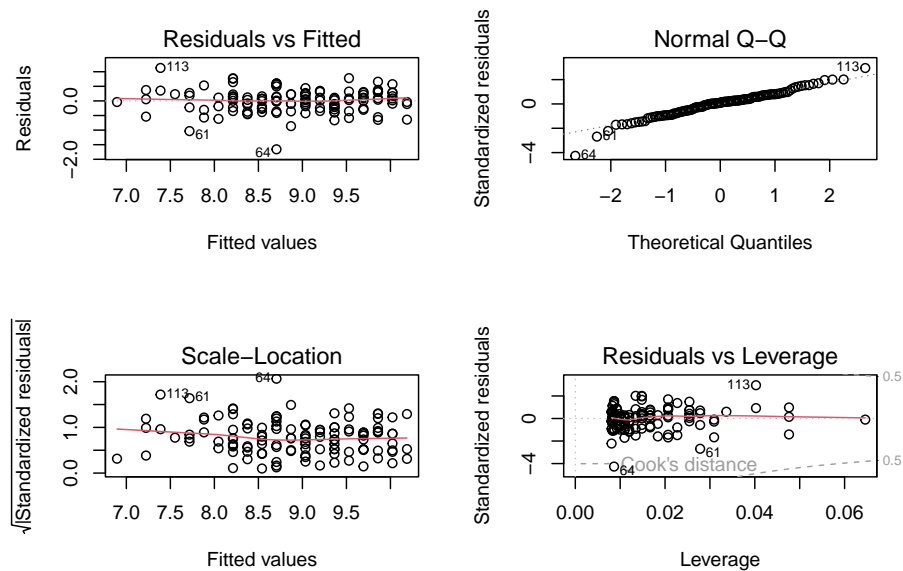
We can “zoom in” on the plot to have a better idea about the value of λ we can use, by specifying the range of `lambda` inside the function:

```
##adjust lambda for better visualization. Choose lambda between -0.5 and 0.5  
MASS::boxcox(result, lambda = seq(-0.5, 0.5, 1/10))
```



We can choose any value of λ within the CI. A log transformation is preferred if possible, since we can still interpret coefficients. Since 0 lies in the CI, we choose $\lambda = 0$, to log transform the response variable to get $y^* = \log(y)$. We regress y^* against x , and check the resulting residual plot:

```
##transform y and then regress ystar on x
ystar<-log(Data$Price)
Data<-data.frame(Data,ystar)
result.ystar<-lm(ystar~Age, data=Data)
par(mfrow = c(2, 2))
plot(result.ystar)
```



We need to reassess assumptions 1 and 2 after the transformation.

- For assumption 2, we see that the vertical spread of the residuals in the residual plot (top left) is fairly constant, as we move from left to right. So assumption 2 is met. The log transformation worked.
- We also notice that the residuals are now evenly scattered across the horizontal axis in the residual plot (top left). So assumption 1 is now met.

We do not need to perform any other transformations.

Interpreting Coefficients with Log Transformed Response

So our regression equation is


```
result.ystar
```

```
##
## Call:
## lm(formula = ystar ~ Age, data = Data)
##
## Coefficients:
## (Intercept)      Age
##    10.1878    -0.1647
```

$\hat{y}^* = 10.1878 - 0.1647x$, where $y^* = \log(y)$. To interpret the slope:

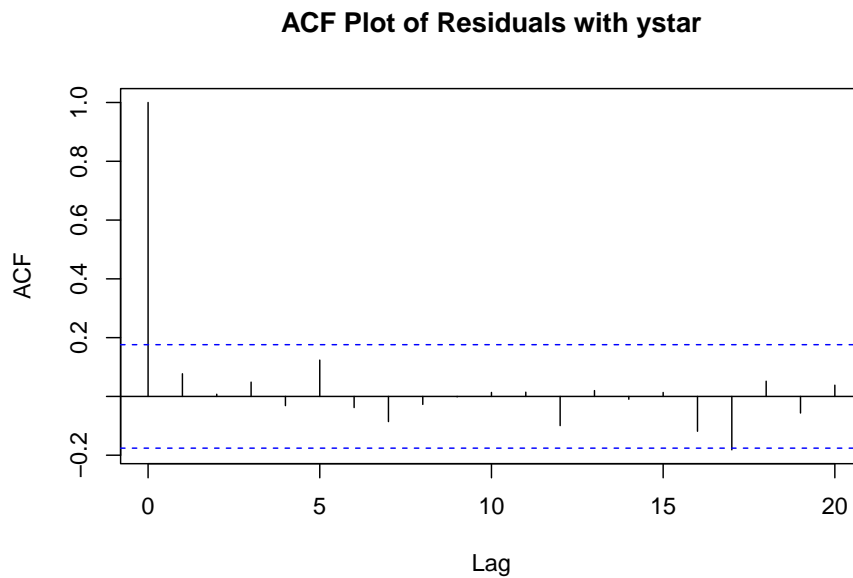
- The price of used Mazdas is multiplied by $\exp(-0.1647) = 0.8481481$ for each year older the car is.
- The price of used Mazdas decreases by $(1 - 0.8481481) \times 100$ percent, or 15.18519 percent, for each year older the car is.

ACF Plot of Residuals

We have yet to assess the assumption that the observed prices are independent from each other. Assuming that these prices are from different cars and not the same car measured repeatedly over time, there is no reason to think the prices are dependent on each other.

We can also produce an ACF plot to confirm our thought:

```
acf(result.ystar$residuals, main="ACF Plot of Residuals with ystar")
```



None of the ACFs beyond lag 0 are significant, so we don't have evidence that the observations are dependent on each other.

5.6.2 Example 2

For this second example, we will go over an example for the `faraway` package. The dataframe is called `gala`. The data are about species diversity on the Galapagos Islands. There are 30 islands, and for each island, we have data on 7 variables. We will focus on the variable `Species`, which denotes the number of plant species found on the island, and `Area`, the area of the island in squared kilometers. We wish to see how the number of plant species of an island is related to the area of the island.

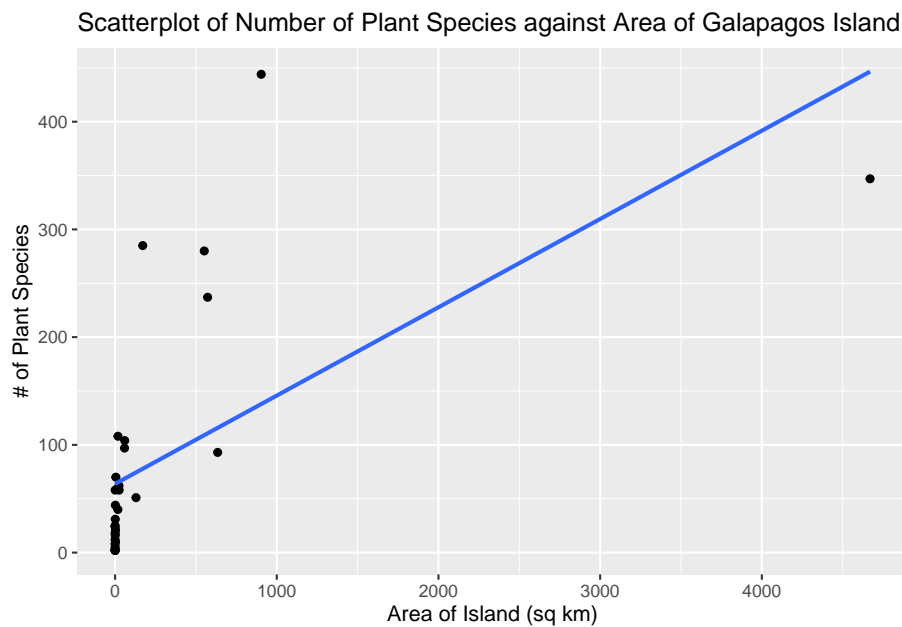
```
library(faraway)
Data<-faraway::gala
```

Model Diagnostics with Scatterplots

We can use a scatterplot of the response variable against the predictor to assess assumptions 1 and 2.

```
library(tidyverse)

##scatterplot, and overlay regression line
ggplot2::ggplot(Data, aes(x=Area,y=Species))+
  geom_point()+
  geom_smooth(method = "lm", se=FALSE)+
  labs(x="Area of Island (sq km)", y="# of Plant Species",
       title="Scatterplot of Number of Plant Species against Area of Galapagos Island")
```



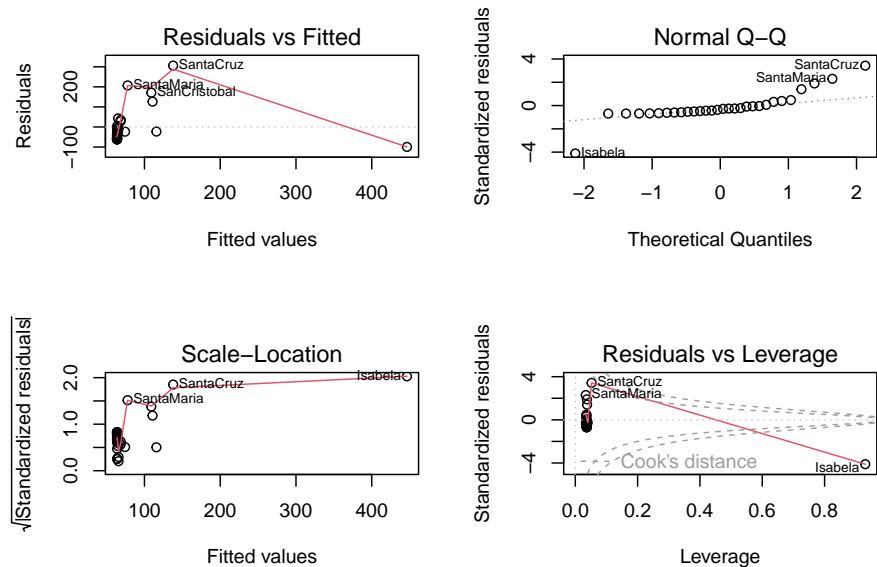
To assess assumption 1, the data points should be evenly scattered on both sides of the regression line, as we move from left to right. This plot looks nonlinear.

To assess assumption 2, the vertical spread of the data points should be constant as we move from left to right. This can be a bit difficult to assess with this scatterplot, although observations with small areas are closer to the line, which suggests the assumption is not met.

Model Diagnostics with Residual Plots

Fairly often, when assessing regression assumptions, a residual plot is easier to visualize than a scatterplot.

```
result<-lm(Species~Area, data=Data)
par(mfrow = c(2, 2))
plot(result)
```



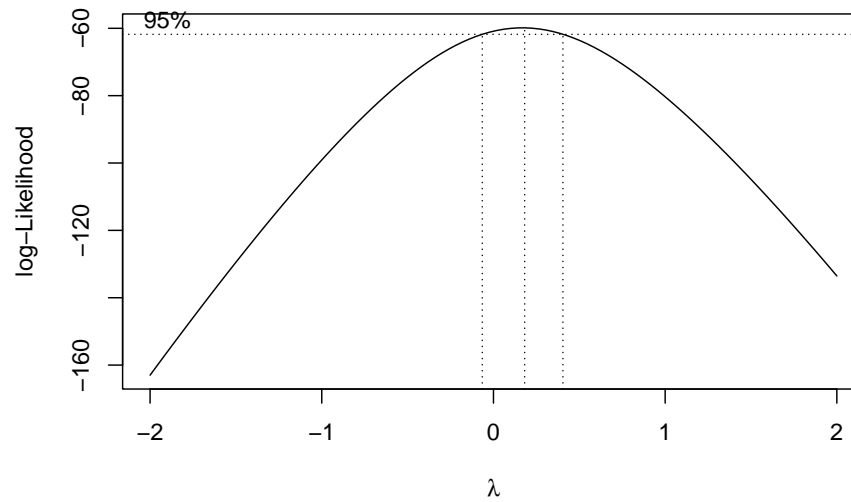
- From the residual plot (top left), we see a curved pattern, so we have a nonlinear relationship. Assumption 1 is not met.
- From the scale-location plot (bottom left), the vertical variance of the plots appear to be higher for islands with larger fitted values, so assumption 2 is not met.

Now that we know that both assumptions 1 and 2 are not met. We need to transform the response variable first, to stabilize the variance.

Box Cox Transformation on y

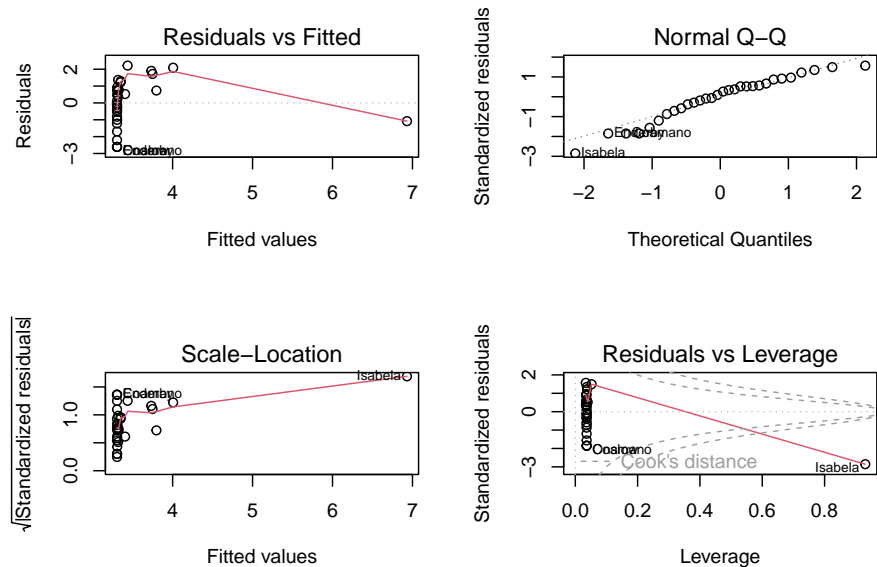
From the scale-location plot, we see the variance of the residuals is increasing, so we expect to transform the response variable with $y^* = y^\lambda$ with $\lambda < 1$. So see which specific value of λ to use, we can use the Box Cox plot:

```
library(MASS)
MASS::boxcox(result)
```



A log transformation is preferred if possible, since we can still interpret coefficients. Since 0 lies in the CI, we choose $\lambda = 0$, to log transform the response variable to get $y^* = \log(y)$. We regress y^* against x , and check the resulting residual plot:

```
##log transform response and add to dataframe
Data$y.star<-log(Data$Species)
##perform new regression
result.ystar<-lm(y.star~Area, data=Data)
par(mfrow = c(2, 2))
plot(result.ystar)
```



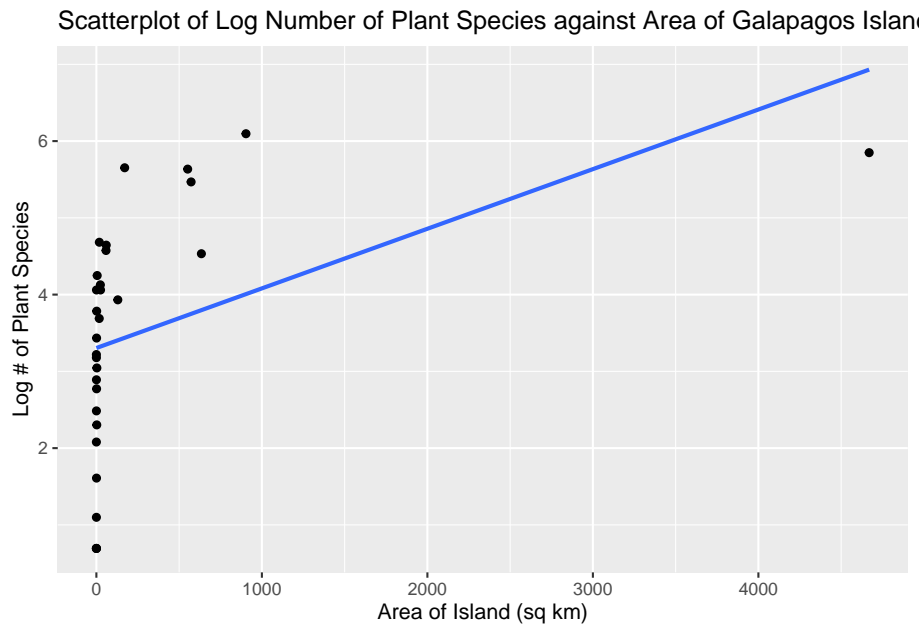
We need to reassess assumptions 1 and 2 after the transformation.

- For assumption 2, we see that the vertical spread of the residuals in the residual plot (top left) is fairly constant, as we move from left to right. So assumption 2 is met. The log transformation worked in stabilizing the variance.
- However, the residual plot still appears to be nonlinear. So assumption 1 is still not met.

Transformation on x

To see which specific transformation on the predictor to use, we create a scatterplot of the transformed response and the predictor.

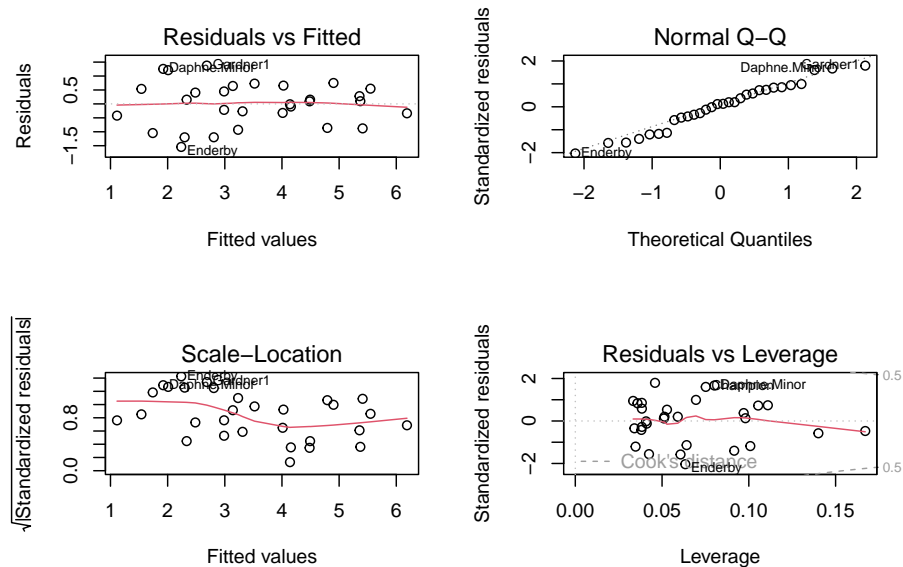
```
ggplot2::ggplot(Data, aes(x=Area,y=y.star))+
  geom_point()+
  geom_smooth(method = "lm", se=FALSE)+
  labs(x="Area of Island (sq km)", y="Log # of Plant Species",
        title="Scatterplot of Log Number of Plant Species against Area of Galapagos Isl.")
```



This plot resembles a logarithmic curve, so we use a log transformation on the predictor, so let $x^* = \log(x)$. As usual, a log transformation is preferred since we can still interpret the regression coefficients. We then perform a regression using both the log transformed response variable and predictor, and assess the diagnostic plots.

```
##log transform predictor and add to dataframe
Data$x.star<-log(Data$Area)

##perform new regression
result.xystar<-lm(y.star~x.star, data=Data)
par(mfrow = c(2, 2))
plot(result.xystar)
```



Based on the residual plot (top left), both assumptions are met. The residuals are evenly scattered across the horizontal axis with no pattern. The vertical spread of the residuals is also constant. So the transformations worked.

Interpreting Coefficients with Log Transformed Response and Predictor

So our regression equation is

```
result.xystar
```

```
##
## Call:
## lm(formula = y.star ~ x.star, data = Data)
##
## Coefficients:
## (Intercept)      x.star
##      2.9037      0.3886
```

$\hat{y}^* = 2.9037 + 0.3886x^*$, where $y^* = \log(y)$ and $x^* = \log(x)$. There are a couple of ways to interpret the slope:

- For a 1% increase in the area of a Galapagos island, the number of plant species found on the island is multiplied by $(1.01)^{0.3886} = 1.003874$, OR
- For a 1% increase in the area of a Galapagos island, the number of plant species increases by about 0.3886%.

Chapter 6

Multiple Linear Regression (MLR)

6.1 Introduction

Linear regression models are used to explore the relationship between variables as well as make predictions. Simple linear regression (SLR) concerns the study of only one predictor variable with one response variable. However, given the context, it may be clear there are multiple predictors that relate to the response variable. In such a context, we want to:

- Improve predictions on the response variable by including more useful predictors.
- Assess how a predictor relates to the response variable when controlling for other predictors.

Multiple linear regression (MLR) models allow us to examine the effect of multiple predictors on the response variable simultaneously.

There are a couple of ways to think about MLR:

- Extension of SLR to MLR.
- SLR as a special case of MLR.

As a motivating example, we look at data regarding black cherry trees. The data, **cherry** come from the **openintro** package. Researchers want to understand the relationship between the volume of these trees and their diameter and height. Data come from 31 trees in the Allegheny National Forest, Pennsylvania.

```
library(openintro)
Data<-openintro::cherry
```

From this context, we know that volume of a tree is influenced by its diameter and height, so we have more than one predictor in this study.

As you read this set of notes, take note of the similarities and differences between SLR and MLR.

6.2 Notation in MLR

We write the **MLR model** as:

$$y_i = \beta_0 + \beta_1 x_{i1} + \beta_2 x_{i2} + \cdots + \beta_k x_{ik} + \epsilon_i. \quad (6.1)$$

In this setup, we have k quantitative predictors. The notation in (6.1) are as follows:

- y_i : value of response variable for observation i ,
- β_0 : **intercept** for MLR model,
- β_j : **coefficient** (or slope) for predictor j , for $j = 1, 2, \dots, k$. We have k predictors, each with its corresponding coefficient.
- x_{ij} : observation i 's value for predictor j . Notice there are two numbers in the subscript. The first number denotes which observation, and the second denotes which predictor.
- ϵ_i : **error** for observation i .

The **assumptions** in MLR are identical to SLR:

$$\epsilon_1, \dots, \epsilon_n \text{ i.i.d. } \sim N(0, \sigma^2). \quad (6.2)$$

Let us use the **cherry** data from **openintro** as an example:

```
head(Data)
```

```
## # A tibble: 6 x 3
##   diam height volume
##   <dbl>   <int>   <dbl>
## 1    8.3     70    10.3
## 2    8.6     65    10.3
## 3    8.8     63    10.2
## 4   10.5     72    16.4
## 5   10.7     81    18.8
## 6   10.8     83    19.7
```

- $y_2 = 10.3$ cubic feet, the volume for observation 2
- $x_{41} = 10.5$ inches, observation 4's diameter (predictor 1)
- $x_{22} = 65$ feet, observation 2's height (predictor 2)

The MLR model in (6.1) is often expressed using matrices, which is a lot neater:

$$\begin{bmatrix} y_1 \\ y_2 \\ \vdots \\ y_n \end{bmatrix} = \begin{bmatrix} 1 & x_{11} & \cdots & x_{1k} \\ 1 & x_{21} & \cdots & x_{2k} \\ \vdots & \vdots & \ddots & \vdots \\ 1 & x_{n1} & \cdots & x_{nk} \end{bmatrix} \begin{bmatrix} \beta_0 \\ \beta_1 \\ \vdots \\ \beta_k \end{bmatrix} + \begin{bmatrix} \epsilon_1 \\ \epsilon_2 \\ \vdots \\ \epsilon_n \end{bmatrix},$$

or

$$y = X\beta + \epsilon. \quad (6.3)$$

The notation in (6.3) are as follows:

- y : **vector of responses** (length n),
- β : **vector of parameters** (length $p = k + 1$, where p denotes the number of regression parameters),
- X : **design matrix** (dimension $n \times p$),
- ϵ : **vector of residuals** (length n).

The formulation in (6.3) is the basis for calling the model a “linear” regression. The model is **linear in the parameters**, not the predictors. A common misconception is that the model is linear in the predictors.

Following (6.1), the **MLR equation** can be written as:

$$E(y|x) = \beta_0 + \beta_1 x_1 + \beta_2 x_2 + \cdots + \beta_k x_k. \quad (6.4)$$

And in turn, the **estimated MLR equation** can be written as:

$$\hat{y} = \hat{\beta}_0 + \hat{\beta}_1 x_1 + \hat{\beta}_2 x_2 + \cdots + \hat{\beta}_k x_k. \quad (6.5)$$

6.2.1 Interpreting coefficients in MLR

The interpretation of estimated coefficients are similar with SLR, with a small caveat: $\hat{\beta}_j$ denotes the change in the predicted response per unit change in x_j , **when the other predictors are held constant**. There are other common ways to state the bold part:

- when controlling for the other predictors.
- when the other predictors are taken into account.
- after adjusting for the effect of the other predictors.

If you are familiar with how a partial derivative is interpreted in multivariate calculus, you will realize that the interpretation of estimated coefficients in MLR sound like how a partial derivative is interpreted.

Let us look at the estimated regression equation for the **cherry** data:

```

result<-lm(volume~., data=Data)
result

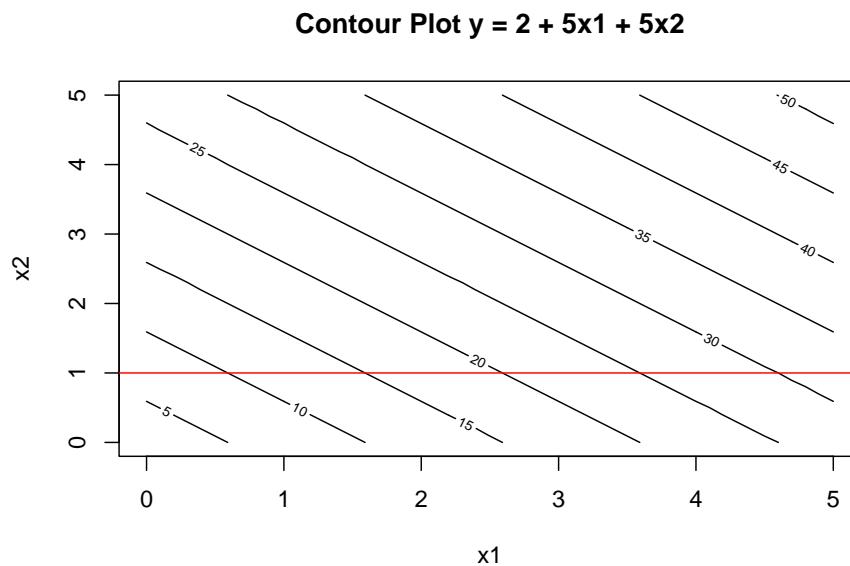
##
## Call:
## lm(formula = volume ~ ., data = Data)
##
## Coefficients:
## (Intercept)      diam      height
##    -57.9877      4.7082      0.3393

```

The estimated MLR equation is $\hat{y} = -57.9877 + 4.7082x_1 + 0.3393x_2$. The estimated coefficient for diameter inform us that for each additional inch in diameter, the predicted volume of a cherry tree increases by 4.7082 cubic feet, while holding height constant.

6.2.2 Visualizing MLR

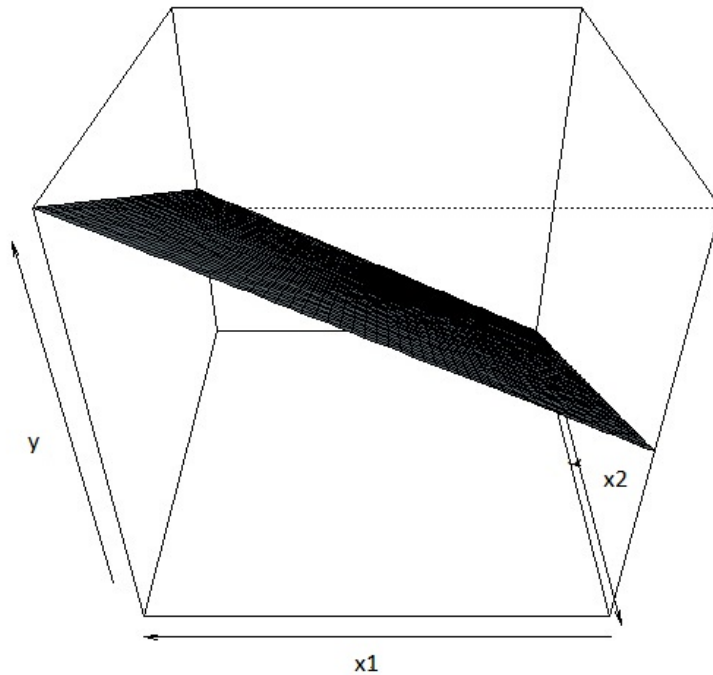
How should we visualize an MLR equation? Suppose we have two predictor variables, x_1 and x_2 , with MLR equation $E(y|x_1, x_2) = 2 + 5x_1 + 5x_2$. A **contour plot** can be used to visualize a response variable with two predictors:



The contour plot creates an axis for each predictor. The value of the response variable is denoted by the contour lines with the actual value displayed on the line. In this toy example, $\beta_1 = 5$. This means that if we hold x_2 constant (e.g. set $x_2 = 1$ per the red horizontal line), increasing x_1 by 1 unit increases

the mean of y by 5 units.

The regression equation $E(y|x_1, x_2) = 2 + 5x_1 + 5x_2$ is sometimes called a **regression plane**, instead of a regression line, since we have more than 1 predictor. We can visualize this regression plane below



Due to limitations in human visualization, going beyond a 3-dimensional plot (1 response and 2 predictors) is difficult.

Please see the associated video for a little more explanation regarding the contour plot and 3-dimensional plot.

6.3 Estimating coefficients in MLR

From (6.5), the predicted response (or fitted values), can be written in matrix form as:

$$\hat{y} = X\hat{\beta}, \quad (6.6)$$

where $\hat{\beta} = (\hat{\beta}_0, \hat{\beta}_1, \dots, \hat{\beta}_k)'$.

We use the **method of least squares** to find the estimated coefficients in MLR. This is the same idea when applied in SLR. The method involves minimizing the **sum of squared residuals**, SS_{res} . In SLR, we minimize

$$\sum_{i=1}^n [y_i - (\hat{\beta}_0 + \hat{\beta}_1 x_i)]^2$$

with respect to $\hat{\beta}_0, \hat{\beta}_1$. In MLR, the SS_{res} can be expressed in matrix form:

$$Q = (y - X\hat{\beta})' (y - X\hat{\beta}) \quad (6.7)$$

To minimize the $Q = SS_{res}$ with respect to $\hat{\beta}_0, \hat{\beta}_1, \dots, \hat{\beta}_k$, We take partial derivatives of Q and set them all to 0, i.e. $\frac{\nabla Q}{\nabla \hat{\beta}} = 0$. Solving for these equations, we get

$$\hat{\beta} = \begin{bmatrix} \hat{\beta}_0 \\ \hat{\beta}_1 \\ \vdots \\ \hat{\beta}_k \end{bmatrix} = (X'X)^{-1} X'y. \quad (6.8)$$

Residuals are found in the same way in SLR:

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

or in matrix form:

$$e = y - \hat{y} = y - X\hat{\beta}. \quad (6.9)$$

6.3.1 Estimating variance of errors

Similar to SLR, MS_{res} is used to estimate σ^2 , the variance of the error terms. MS_{res} is found using

$$MS_{res} = \frac{SS_{res}}{n - p}, \quad (6.10)$$

where p denotes the **number of regression parameters**. In SLR, $p = 2$, since we have an intercept and one slope. Note: I have seen too many people think

p denotes the number of predictors. This is incorrect! As we move forward, we will explore more complicated regression models and we always think in terms of number of regression parameters.

6.3.2 Distribution of least squares estimators

Following the Gauss Markov theorem, the least squares estimators $\hat{\beta}$ are unbiased, i.e.

$$E(\hat{\beta}) = \beta, \quad (6.11)$$

with **variance-covariance matrix** given by

$$Var(\hat{\beta}) = \sigma^2 (X'X)^{-1} \quad (6.12)$$

with σ^2 estimated by MS_{res} . A few notes about the variance-covariance matrix of the least squares estimators:

- it is of dimension $p \times p$,
- the diagonal elements denote the variance of each estimated parameter. For example, the first diagonal element denotes the variance of $\hat{\beta}_0$, the first estimated parameter.
- the off-diagonal elements denote the covariance between respective parameters. For example, the (1,2) entry denotes the covariance between $\hat{\beta}_0$ and $\hat{\beta}_1$.

Please see the associated video for a demonstration on how to read a variance-covariance matrix.

6.4 ANOVA F Test in MLR

6.4.1 Sum of squares

As in simple regression, the **analysis of variance (ANOVA) table** for an MLR model displays quantities that measure how much of the variability in the response variable is explained (and not explained) by the regression model. The underlying conceptual idea for the construction of the analysis of variance table is the same:

$$SS_T = SS_R + SS_{res}. \quad (6.13)$$

What change are the associated degrees of freedom:

- df for SS_R : $df_R = p - 1$
- df for SS_{res} : $df_{res} = n - p$

- df for SS_T : $df_T = n - 1$

Notice the degrees of freedom in SLR has $p = 2$.

6.4.2 ANOVA table

The ANOVA table is thus

Source of Variation	SS	df	MS	F
Regression	$SS_R = \sum (\hat{y}_i - \bar{y})^2$	$df_R = p - 1$	$MS_R = \frac{SS_R}{df_R}$	$\frac{MS_R}{MS_{res}}$
Error	$SS_{res} = \sum (y_i - \hat{y}_i)^2$	$df_{res} = n - p$	$MS_{res} = \frac{SS_{res}}{df_{res}}$	***
Total	$SS_T = \sum (y_i - \bar{y})^2$	$df_T = n - 1$	***	***

6.4.3 ANOVA F test

The null and alternative hypotheses associated with the ANOVA F test are:

$$H_0 : \beta_1 = \beta_2 = \dots = \beta_k = 0, H_a : \text{at least one of the coefficients is not 0.}$$

So the null hypothesis states the regression coefficients for all predictors are 0. Notice how this statement simplifies in SLR.

There are a few different ways to view these hypothesis statements:

- Is our MLR model **useful**?
- Is our MLR model **preferred** over an intercept-only model?
- Can we drop **all** our predictors from the MLR model?

The test statistic is still

$$F = \frac{MS_R}{MS_{res}} \quad (6.14)$$

which is compared with an $F_{p-1, n-p}$ distribution.

6.4.4 Coefficient of determination

The **coefficient of determination**, R^2 , is still

$$R^2 = \frac{SS_R}{SS_T} = 1 - \frac{SS_{res}}{SS_T}, \quad (6.15)$$

where R^2 is interpreted as **the proportion of variance in the response variable that is explained by the predictors**.

6.4.4.1 Caution with R^2

Adding more predictors to a model can only increase R^2 , as SS_{res} never becomes larger with more predictors and SS_T remains the same for a given set of responses.

- So even adding predictors that don't make sense will increase R^2 .
- R^2 should be used to compare models with the same number of parameters.
- R^2 is a popular measure as it has a nice geometric interpretation.

In response to this caution, we have the **adjusted** R^2 , denoted by R_a^2 :

$$R_a^2 = 1 - \frac{\frac{SS_{res}}{n-p}}{\frac{SS_T}{n-1}} = 1 - \left(\frac{n-1}{n-p} \right) \frac{SS_{res}}{SS_T}. \quad (6.16)$$

R_a^2 increases if the added predictors significantly improve the fit of the model, and decreases otherwise.

Let us go back to the **cherry** dataset as an example:

```
summary(result)
```

```
##
## Call:
## lm(formula = volume ~ ., data = Data)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -6.4065 -2.6493 -0.2876  2.2003  8.4847
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) -57.9877      8.6382  -6.713 2.75e-07 ***
## diam         4.7082      0.2643  17.816 < 2e-16 ***
## height       0.3393      0.1302   2.607  0.0145 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.882 on 28 degrees of freedom
## Multiple R-squared:  0.948, Adjusted R-squared:  0.9442
## F-statistic: 255 on 2 and 28 DF, p-value: < 2.2e-16
```

The ANOVA F statistic is 255 with a small p-value. So we reject the null hypothesis and state that our MLR model with diameter and height as predictors

is useful.

The R^2 is 0.948. About 94.8% of the variance in volume of cherry trees can be explained by their diameter and height.

The R_a^2 is 0.9442. This value is used in comparison with another model to decide which should be preferred.

6.5 t Test for Regression Coefficient in MLR

We can assess whether a regression coefficient is significantly different from 0 in an MLR. The null and alternative hypotheses are very much the same as in SLR:

$$H_0 : \beta_j = 0, H_a : \beta_j \neq 0.$$

What these hypotheses mean in words:

- The null hypothesis supports dropping predictor x_j from the MLR model, **in the presence of the other predictors.**
- The alternative hypothesis supports keeping predictor x_j in the MLR model, or that we **cannot drop it in the presence of the other predictors.**

Notice the meaning of the null and alternative hypotheses are a little different than in SLR, where other predictors are not taken into account.

The test statistic is still

$$t = \frac{\hat{\beta}_j}{se(\hat{\beta}_j)} \quad (6.17)$$

which is compared with a t_{n-p} distribution.

Let us take a look at the `cherry` dataset:

```
summary(result)$coefficients
```

##	Estimate	Std. Error	t value	Pr(> t)
## (Intercept)	-57.9876589	8.6382259	-6.712913	2.749507e-07
## diam	4.7081605	0.2642646	17.816084	8.223304e-17
## height	0.3392512	0.1301512	2.606594	1.449097e-02

Notice the t statistics associated with testing for the coefficient for each predictor is highly significant. So we do not have evidence to drop any of the other predictors to simplify the model.

6.5.1 Caution in interpreting t test in MLR

An insignificant t test for a coefficient β_j in MLR indicates that predictor x_j can be removed from the model (and leave the other predictors in). It is **not needed in the presence of the other predictors**.

1. A common misstatement many make is that an insignificant t test for a coefficient β_j in MLR implies that predictor x_j has no linear relation with the response variable. This is not necessarily correct!
 - If x_j is highly correlated with at least one of the other predictors, or is a linear combination of a number of other predictors, x_j will probably be insignificant as the addition of x_j doesn't help in improving the model. This concept is called **multicollinearity** which we will explore in more depth in the next module. x_j does not provide independent information from the other predictors, and so will not be needed when the other predictors are in the model.
 - x_j itself may still be linearly related to the response variable, on its own.
 - If your goal is to assess if x_j is linearly related to the response, need to use SLR.
2. Another common misstatement people make is that if they observe more than one t statistic that is insignificant, it means that all of the associated predictors can be dropped from the model. This again is not necessarily correct.
 - An insignificant t test informs us we can drop that particular predictor, while leaving the other predictors in the model. We can only drop one predictor at a time based on t tests.

Notice the limitation of the t test and ANOVA F test in MLR:

- We can **only drop 1 predictor** based on a t test.
- We can **drop all predictors** based on an ANOVA F test.
- What if we wish to drop more than 1 predictor simultaneously, but not all, from the model? We will explore this via another F test in the next module.

6.6 CIs in MLR

6.6.1 CI for regression coefficient

The general form for CIs is still the same:

$$\text{estimator} \pm (\text{multiplier} \times \text{s.e of estimator}). \quad (6.18)$$

The $100(1 - \alpha)\%$ CI for β_j is

$$\hat{\beta}_j \pm t_{1-\alpha/2; n-p} se(\hat{\beta}_j) = \hat{\beta}_j \pm t_{1-\alpha/2; n-p} s \sqrt{C_{jj}} \quad (6.19)$$

where C_{jj} denotes the j th diagonal entry in variance-covariance matrix of the estimated coefficients, $Var(\hat{\beta})$.

The multiplier is now based on a t_{n-p} distribution, instead of a t_{n-2} distribution for SLR.

6.6.2 CI of the mean response

Since we have multiple predictors, we may be interested in the CI for the mean of the response, when the predictors are each equal to specific values. Let the vector x_0 denote these values on each predictor, specifically

$$x_0 = (1, x_{01}, x_{02}, \dots, x_{0k})',$$

where x_{0j} denotes the value for predictor x_j . The CI for the mean response when $x = x_0$ is

$$\hat{\mu}_{y|x_0} \pm t_{1-\alpha/2; n-p} s \sqrt{x_0' (X'X)^{-1} x_0}. \quad (6.20)$$

6.6.3 PI of a new response

For a new value of the response when $x = x_0$, the PI is

$$\hat{y}_0 \pm t_{1-\alpha/2; n-p} s \sqrt{1 + x_0' (X'X)^{-1} x_0}. \quad (6.21)$$

6.7 R Tutorial

For this tutorial, we will learn how to fit multiple linear regression (MLR) in R. You will realize that fitting MLR is very similar to fitting SLR.

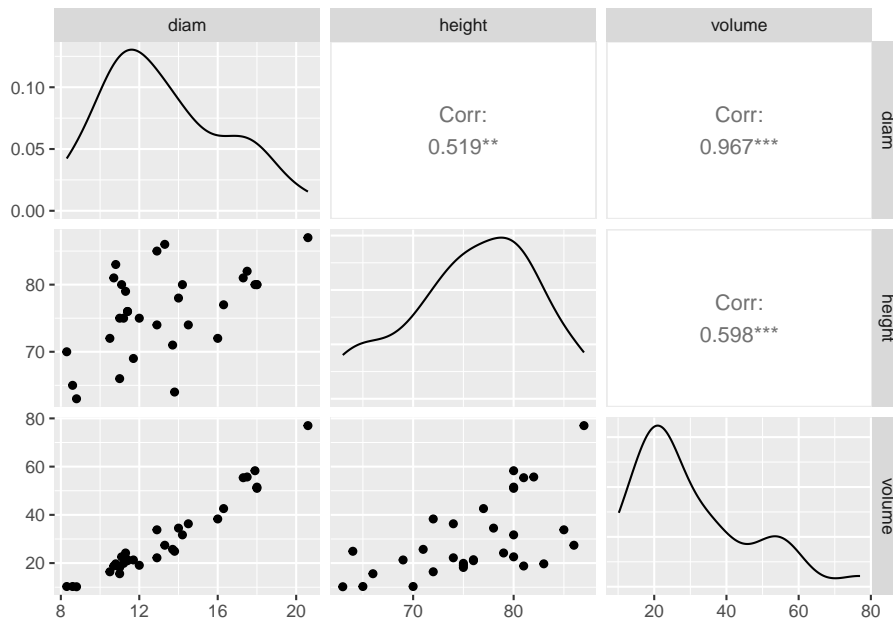
We will look at data regarding black cherry trees. The data, `cherry`, come from the `openintro` package. Researchers want to understand the relationship between the volume (in cubic feet) of these trees and their diameter (in inches, at 54 inches above ground) and height (in feet). Data come from 31 trees in the Allegheny National Forest, Pennsylvania.

```
library(openintro)
Data <- openintro::cherry
```

Scatterplot matrix

A scatterplot matrix is useful to create scatterplots involving more than two quantitative variables. We will use the `ggpairs()` function from the `GGally` package:

```
library(GGally)
##scatterplot matrix
GGally::ggpairs(Data)
```



A few pieces of information are presented in the output. Notice the output is displayed in a matrix format.

- The off-diagonal entries of the output give us the scatterplot and correlation between the corresponding pair of quantitative variables.
 - For example, look at the scatterplot in row 3, column 1 of the output. The corresponding label for the column is `diam` and the label for the row is `volume`. This informs us this is a scatterplot for `volume` on the vertical axis and `diam` on the horizontal axis. We see a strong positive linear association between these two variables.
 - The correlation between `volume` and `diam` is displayed in row 1, column 3. Again, notice the label for the column and row. This correlation is 0.967, which is high.
 - For practice, locate the scatterplot of `volume` and `height` and its corresponding correlation. Also locate the scatterplot of `diam` and `height` and its corresponding correlation.
- The diagonal entries display the density plot of the corresponding variable.

For example, the third diagonal entry displays the density plot for `volume`. We can see that the distribution is somewhat right skewed as most trees have a volume between 10 and 40 cubic feet.

Fit MLR using `lm()`

To fit multiple linear regression (MLR)

```
##Fit MLR model, using + in between predictors
result<-lm(volume~diam+height, data=Data)
```

where we list the predictors after `~` with a `+` operator in between the predictors. Another way would be

```
result<-lm(volume~., data=Data)
```

The `.` after `~` informs the `lm()` function to use every column other than `volume` in the data frame as predictors.

Just like with simple linear regression (SLR) we can get relevant information using `summary()`:

```
summary(result)

##
## Call:
## lm(formula = volume ~ diam + height, data = Data)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -6.4065 -2.6493 -0.2876  2.2003  8.4847
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) -57.9877     8.6382  -6.713 2.75e-07 ***
## diam         4.7082     0.2643  17.816 < 2e-16 ***
## height       0.3393     0.1302   2.607  0.0145 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.882 on 28 degrees of freedom
## Multiple R-squared:  0.948, Adjusted R-squared:  0.9442
## F-statistic: 255 on 2 and 28 DF, p-value: < 2.2e-16
```

- The estimated regression equation is $\hat{y} = -57.988 + 4.708\text{diam} + 0.339\text{height}$.
 - The estimated coefficient for `diam` is interpreted as: the predicted volume of a cherry tree increases by 4.708 cubic feet per inch increase in diameter, while holding height constant.

- The estimated coefficient for `height` is interpreted as: the predicted volume of a cherry tree increases by 0.339 cubic feet per foot increase in height, while holding diameter constant.
- The R^2 is 0.948. About 94.8% of the variance in volume of cherry trees can be explained by their diameter and height.
- The residual standard error is 3.882. This estimates σ , the standard deviation of the error term.

Inference with MLR

Just like SLR, each coefficient is tested against a null hypothesis that $\beta_j = 0$ with a two-sided alternative. The test is significant for both coefficients, so we cannot drop either predictor from the model.

The ANOVA F statistic is 255, with a small p-value. So data supports the claim that our model is useful.

The confidence intervals for the coefficients can be found using `confint()`:

```
confint(result, level = 0.95)

##                2.5 %        97.5 %
## (Intercept) -75.68226247 -40.2930554
## diam         4.16683899   5.2494820
## height       0.07264863   0.6058538
```

The confidence interval for the mean response and the prediction interval for a new observation given a specific value of the predictors can also be found using `predict()`. For example, when the diameter is 10 inches and height is 80 feet:

```
newdata<-data.frame(diam=10, height=80)

predict(result, newdata, level=0.95,
        interval="confidence")

##      fit      lwr      upr
## 1 16.23404 13.36762 19.10047

predict(result, newdata, level=0.95,
        interval="prediction")

##      fit      lwr      upr
## 1 16.23404  7.781596 24.68649
```

You might realize by now we are using the same functions as we did in SLR.

Note: Obviously, all these calculations are performed and interpreted assuming the regression assumptions are met. Regression assumptions are checked in the same way as in SLR. On your own, as practice, assess the regression assumptions.

Chapter 7

General Linear F Test and Multicollinearity

7.1 Introduction

The purpose of multiple linear regression is to use more than one predictor to predict a response variable. This module explores an approach to choosing which variables to include in a multiple regression model. For example, many variables can be used to predict someone's systolic blood pressure, such as their age, weight, height, and pulse rate. While all of those predictors are likely to influence the systolic blood pressure, we want to know if we need all of them, or if a subset of those predictors will perform just as well. We will use the general linear F test to do so.

Another issue with having multiple predictors is that the likelihood that at least one of the predictors are linearly dependent, or correlated, with some other predictors increases. This is called multicollinearity. There are some negative consequences if multicollinearity is present. We will learn about these consequences, how to diagnose the presence of multicollinearity, and some solutions if multicollinearity is present.

7.2 The General Linear F Test

7.2.1 Motivation

In the previous module, we noted the limitation of the t test and ANOVA F test in MLR:

- We can **only drop 1 predictor** based on a t test.
- We can **drop all predictors** based on an ANOVA F test.

What if we wish to drop more than 1 predictor simultaneously, but not all, from the model? We will explore this via the **general linear F test**. In fact, the t test and ANOVA F test are actually special cases of the general linear F test.

Let us look at a motivating example, using the dataset `Peruvian.txt`. The data contains variables relating to blood pressures of Peruvians who have migrated from rural high altitude areas to urban lower altitude areas. The variables are:

- y : Systolic blood pressure
- x_1 : Age
- x_2 : Years in urban area
- x_3 : fraction of life in urban area (x_1/x_2)
- x_4 : Weight in kg
- x_5 : Height in mm
- x_6 : Chin skinfold
- x_7 : Forearm skinfold
- x_8 : Calf skinfold
- x_9 : Resting pulse rate

We want to assess how the systolic blood pressure of these migrants may be predicted and related to these predictors.

```
Data<-read.table("Peruvian.txt", header=TRUE, sep="")
head(Data)
```

```
##   Systol_BP Age Years fraclife Weight Height Chin Forearm Calf Pulse
## 1      170  21    1 0.047619   71.0   1629  8.0    7.0 12.7   88
## 2      120  22    6 0.272727   56.5   1569  3.3    5.0  8.0   64
## 3      125  24    5 0.208333   56.0   1561  3.3    1.3  4.3   68
## 4      148  24    1 0.041667   61.0   1619  3.7    3.0  4.3   52
## 5      140  25    1 0.040000   65.0   1566  9.0   12.7 20.7   72
## 6      106  27   19 0.703704   62.0   1639  3.0    3.3  5.7   72
```

Let us fit an MLR with all the predictors and take a look at the t tests and ANOVA F test:

```
result<-lm(Systol_BP~., data=Data)
summary(result)
```

```
##
## Call:
## lm(formula = Systol_BP ~ ., data = Data)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -12.3443  -6.3972   0.0507   5.7293  14.5257
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
```

```
## (Intercept) 146.81883 48.97099 2.998 0.005526 **
## Age -1.12143 0.32741 -3.425 0.001855 **
## Years 2.45538 0.81458 3.014 0.005306 **
## fraclife -115.29384 30.16903 -3.822 0.000648 ***
## Weight 1.41393 0.43097 3.281 0.002697 **
## Height -0.03464 0.03686 -0.940 0.355196
## Chin -0.94369 0.74097 -1.274 0.212923
## Forearm -1.17085 1.19330 -0.981 0.334613
## Calf -0.15867 0.53716 -0.295 0.769809
## Pulse 0.11455 0.17043 0.672 0.506822
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 8.655 on 29 degrees of freedom
## Multiple R-squared: 0.6674, Adjusted R-squared: 0.5641
## F-statistic: 6.465 on 9 and 29 DF, p-value: 5.241e-05
```

Notice the t tests are insignificant for a lot of the coefficients (the last five). Individually, each t test is informing us that we can drop that specific predictor, while leaving the other predictors in the model.

An erroneous interpretation is to say collectively, these t tests inform us we can drop all of these predictors, x_5 to x_9 , from the model. This is a misconception.

One idea could be to drop the most insignificant predictor, refit the model, and reassess which predictors are insignificant, and continue dropping the most insignificant predictor and refitting the model until all t tests are significant. We will end up conducting multiple hypothesis tests to do so. If possible, we should limit the number of hypothesis tests we conduct: the more tests we do, the likelihood of us wrongly rejecting a null hypothesis increases.

This is where the **general linear F test** (sometimes called a partial F test) is used. We can perform one test to assess if we can simultaneously drop multiple predictors from the model.

Based on this output, we consider dropping x_5, x_6, x_7, x_8, x_9 since their t tests are insignificant.

7.2.2 Setting up the general linear F test

The general linear F test allows us to assess if multiple predictors can be dropped simultaneously from the model. The associated F statistic measures the change in the SS_R (or SS_{res}) with the removal of these predictors from the model. The test is based on the following concepts:

- As long as we have the same response variable, SS_T **is constant**, regardless of the model. This is because $SS_T = \sum(y_i - \bar{y})$. It only involves the response variable.
- $SS_T = SS_R + SS_{Res}$.

- Each time predictors are added to the model, the SS_R increases and the SS_{Res} decreases **by the same amount**, since SS_T stays constant.

The general linear F test answers the question: is the change in SS_R (or change in SS_{res}) significant with the removal or addition of predictor(s)?

This question can be answered in a framework that compares two models:

- a **full model**, denoted by F , that uses all predictors under consideration,
- a **reduced model**, denoted by R , that results if some predictors from the full model are dropped.

7.2.3 Hypothesis statements

Based on this framework, the null and alternative hypotheses for the `Peruvian.txt` dataset is

$$H_0 : \beta_5 = \beta_6 = \beta_7 = \beta_8 = \beta_9 = 0, H_a : \text{at least one coeff in } H_0 \text{ is not zero.}$$

In general, the null hypothesis states that the **parameters of the terms that we wish to drop are all 0**. Therefore, the null hypothesis supports the reduced model, R .

The alternative hypothesis states that we cannot drop all the terms that we wish to drop. Therefore, the alternative hypothesis supports the full model, F .

7.2.4 Test statistic

The associated test statistic for the general linear F test is

$$F_0 = \frac{[SS_R(F) - SS_R(R)]/r}{SS_{res}(F)/(n-p)}, \quad (7.1)$$

or equivalently

$$F_0 = \frac{[SS_{res}(R) - SS_{res}(F)]/r}{SS_{res}(F)/(n-p)}. \quad (7.2)$$

The test statistic F_0 is compared with an $F_{r,n-p}$ distribution. The notation is as follows:

- $SS_R(F)$ denotes the SS_R of full model,
- $SS_R(R)$ denotes the SS_R of reduced model,
- r denotes number of parameters being dropped/tested,
- p denotes the number of parameters in the full model,
- $SS_{res}(F)$ denotes the SS_{res} of full model,

- $SS_{res}(R)$ denotes the SS_{res} of reduced model.

Note that the change in SS_R , $SS_R(F) - SS_R(R)$ is always equal to the change in SS_{res} , $SS_{res}(R) - SS_{res}(F)$. Therefore, (7.1) is always equal to (7.2).

7.2.5 Worked example

Let us look at some output for our `Peruvian.txt` dataset:

```
reduced<-lm(Systol_BP~Age+Years+fraclife+Weight, data=Data)
anova(reduced,result)
```

```
## Analysis of Variance Table
##
## Model 1: Systol_BP ~ Age + Years + fraclife + Weight
## Model 2: Systol_BP ~ Age + Years + fraclife + Weight + Height + Chin +
##           Forearm + Calf + Pulse
##      Res.Df    RSS Df Sum of Sq    F Pr(>F)
## 1         34 2629.7
## 2         29 2172.6   5    457.12 1.2204 0.3247
```

- In the output, model 1 has the predictors are x_1, x_2, x_3, x_4 , while model 2 has the predictors x_1, \dots, x_9 . So model 1 is the reduced model, and model 2 is the full model.
- We see some information presented in a table. The first line corresponds to model 1, the second line corresponds to model 2.
- Under the column **RSS**, we have the values for SS_{res} . Admittedly, this can be a bit confusing, but it is not SS_R . So we can see that $SS_{res}(R) = 2629.7$ and $SS_{res}(F) = 2172.6$. Note that SS_{res} is always smaller for the full model, and SS_R is always larger for the full model.
- Under the column **Res.DF**, we have the degrees of freedom for the SS_{res} of that model. In the calculation of the F statistic, we want the value associated with the full model, 29.
- Under the column **Df**, we have the number of parameters that we are testing to drop, which is 5.
- Under the column **Sum of Sq**, we have the difference in SS_{res} between both models, $SS_{res}(R) - SS_{res}(F) = 2629.7 - 2172.6 = 457.12$.
- Under the column **F**, we have the F statistic, $F_0 = 1.2204$. We can verify this calculation using (7.2), $F_0 = \frac{(2629.7-2172.6)/5}{2172.6/29}$ (with some rounding).
- The p-value of this general linear F test is reported in the last column. This can be found using:

```
1-pf(1.2204, 5, 29)
```

```
## [1] 0.3247085
```

The critical value can be found using:

```
qf(1-0.05, 5, 29)
```

```
## [1] 2.545386
```

So we fail to reject the null hypothesis. The data do not support the alternative hypothesis (i.e. the full model). So we go with the reduced model.

7.2.6 Comparison of general linear F test with other hypothesis tests in MLR

The t test and ANOVA F test in MLR are special cases of the general linear F test, when $r = 1$ and $r = p - 1$ respectively.

- For the t test, the reduced model has 1 less term than the full model. The F_0 statistic is compared with an $F_{1,n-p}$ distribution. It turns out that an $F_{1,n-p}$ distribution is directly related with a t_{n-p} distribution, and so the general linear F test is exactly the same as the t test when dropping 1 term.
- For the ANOVA F test. The reduced model drops all the terms and has only the intercept. Some call this the intercept-only model.

7.2.7 Alternative approach to general linear F test

There is another way in which the information needed to perform a general linear F test. This approach is called the **sequential sums of squares** (sometimes called extra sums of squares). It works on the same principle that every time a predictor is added to the model, the SS_R of the model increases, and the SS_{res} decreases by the same amount, since SS_T is constant. The information is displayed as we add one predictor at a time. Let us define some notation:

- $SS_R(x_1)$ denotes SS_R when x_1 is the only predictor in the model.
- $SS_R(x_1, x_2)$ denotes SS_R when x_1, x_2 are in the model.
- $SS_R(x_2|x_1)$ denotes the increase in SS_R when x_2 is added to the model with x_1 already in it. It is read as SS_R of x_2 given x_1 .

Based on this example, $SS_R(x_2|x_1) = SS_R(x_1, x_2) - SS_R(x_1)$, and so $SS_R(x_1, x_2) = SS_R(x_1) + SS_R(x_2|x_1)$. Note that $SS_R(x_2|x_1)$ is not equal to $SS_R(x_2)$, as the latter denotes SS_R when x_2 is the only predictor in the model.

Let us see how we can use the sequential sums of squares with the `Peruvian.txt` dataset:

```
anova(result)
```

```
## Analysis of Variance Table
##
```

```
## Response: Systol_BP
##           Df Sum Sq Mean Sq F value    Pr(>F)
## Age       1    0.22    0.22  0.0030  0.956852
## Years     1   82.55   82.55  1.1019  0.302514
## fraclife  1 3112.40 3112.40 41.5448 4.728e-07 ***
## Weight    1  706.55  706.55  9.4311  0.004603 **
## Height    1    1.68    1.68  0.0224  0.882113
## Chin      1   297.68  297.68  3.9735  0.055703 .
## Forearm   1   113.91  113.91  1.5205  0.227440
## Calf      1    10.01   10.01  0.1336  0.717419
## Pulse     1    33.84   33.84  0.4518  0.506822
## Residuals 29 2172.59    74.92
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The values under the column “Sum Sq” give the sequential SS_R s. So,

- for the first line, we have $SS_R(x_1) = 0.22$,
- the second line, we have $SS_R(x_2|x_1) = 82.55$,
- then $SS_R(x_3|x_1, x_2) = 3112.40$,
- and so on for each term,
- finally, $SS_R(x_9|x_1, x_2, \dots, x_8) = 33.84$.
- The very last line refers to $SS_{Res}(x_1, x_2, \dots, x_9) = 2172.59$.

Essentially, the output for each term informs us the increase in SS_R when that term is added to the model, given that the previously listed terms are already in the model.

Notice the order the sequential sums of squares are displayed is the same order used when entering the predictors in `lm()`.

We are still testing

$$H_0 : \beta_5 = \beta_6 = \beta_7 = \beta_8 = \beta_9 = 0, H_a : \text{at least one coeff in } H_0 \text{ is not zero.}$$

Using (7.1), the F statistic for this test is

$$\begin{aligned} F_0 &= \frac{[SS_R(F) - SS_R(R)]/r}{SS_{res}(F)/(n-p)} \\ &= \frac{(1.68 + 297.68 + 113.91 + 10.01 + 33.84)/5}{2172.59/29} \\ &= 1.220339. \end{aligned}$$

Compare this F_0 statistic using this approach with the example shown in Section 2.5. We have the exact same result (other than rounding).

Please view the associated video for more explanation on the extra sums of squares approach.

7.2.7.1 Practice questions

We will use the sequential sums of squares for the `Peruvian.txt` dataset:

```
anova(result)
```

```
## Analysis of Variance Table
##
## Response: Systol_BP
##           Df Sum Sq Mean Sq F value    Pr(>F)
## Age         1    0.22    0.22  0.0030  0.956852
## Years        1   82.55   82.55  1.1019  0.302514
## fraclife     1 3112.40 3112.40 41.5448 4.728e-07 ***
## Weight       1  706.55  706.55  9.4311  0.004603 **
## Height       1    1.68    1.68  0.0224  0.882113
## Chin        1  297.68  297.68  3.9735  0.055703 .
## Forearm      1  113.91  113.91  1.5205  0.227440
## Calf         1   10.01   10.01  0.1336  0.717419
## Pulse        1   33.84   33.84  0.4518  0.506822
## Residuals   29 2172.59   74.92
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

1. Carry out a general linear F test to assess if we can drop x_7, x_8, x_9 from the model with all predictors.
2. What is the value of $SS_R(x_1, x_2, x_3)$?
3. What is the value of $SS_{res}(x_1, x_2, x_3)$?
4. What is the value of $SS_{res}(x_1, x_2, \dots, x_8)$?

Please view the associated video for a review of these practice questions.

7.3 Multicollinearity

What happens if at least one predictor is almost a linear combination of other predictors? This is called multicollinearity, and there are negative consequences on our MLR model. We will learn what these negative consequences are, how to detect multicollinearity, and some solutions. As we consider more and more predictors for our model, multicollinearity is more likely to exist.

7.3.1 Linear dependency & multicollinearity

Before we define multicollinearity, we have to define linear dependency. Recall that we can write the MLR model in matrix form as

$$y = X\beta + \epsilon. \quad (7.3)$$

where X is the design matrix and is

$$\begin{bmatrix} 1 & x_{11} & \cdots & x_{1k} \\ 1 & x_{21} & \cdots & x_{2k} \\ \vdots & \vdots & \ddots & \vdots \\ 1 & x_{n1} & \cdots & x_{nk} \end{bmatrix}$$

Note that each column of the design matrix (other than column 1) represents each predictor variable.

The columns of a matrix are **linearly dependent** if at least one column can be expressed as a linear combination of the other columns (there exist nonzero constants c_i such that $c_1x_1 + c_2x_2 + \dots + c_kx_k = 0$).

As an example, suppose we have three predictors: x_1 denoting SAT verbal score, x_2 denoting SAT math score, and x_3 denoting SAT score. Since SAT score is the sum of the SAT verbal and math scores, $x_3 = x_1 + x_2$. So if we were to create the design matrix for these three predictors, we have linear dependency. With linear dependency, we can predict x_3 from x_1, x_2 with no error. Recall that the least squares estimators are found using

$$\hat{\beta} = (X'X)^{-1} X'y. \quad (7.4)$$

If there is a linear dependence among the columns of X , then $(X'X)^{-1}$ does not exist. This means that unique estimates of β_j 's cannot be determined.

Multicollinearity exists in our model when at least one predictor is **almost linearly dependent**, or can be predicted with a high degree of accuracy, from the other predictors.

An example of multicollinearity would be if we have predictors x_1 denoting right arm length, x_2 denoting right thigh length, and x_3 denoting right calf length. If we know someone's right arm and right thigh lengths, we can probably predict their right calf length with a high degree of accuracy. In this example, we are likely to have multicollinearity.

With multiple predictors, we will always find some degree of **collinearity**. The question is whether this degree is high enough warrant our concern.

When predictors are linearly dependent on each other, they do not provide independent information in their association to the response variable. It becomes difficult to **separate** their effects on the response variable.

7.3.2 Sources of multicollinearity

There are a few reasons for the presence of multicollinearity.

7.3.2.1 Study design

The design of the study might lead to multicollinearity, and so a solution will be to change its design. Let us consider this example:

Suppose the Virginia Department of Motor Vehicles (DMV) wants to study the waiting time customers spend waiting in line, based on the number of people ahead in line and number of counters open.

- The number of people ahead in line and number of counters open could be highly positively correlated; the more people in line, the more counters will be staffed by the DMV. So the nature of the study leads to multicollinearity.
- To break the multicollinearity between the number of people ahead in line and number of counters open, we could collect data on instances where the number of people in line is high, yet the number of counters opened is low, and vice versa. This will allow us to isolate the effect of each predictor on waiting times.

7.3.2.2 Nature of the data

Sometimes, the very nature of the variables lead to multicollinearity and we cannot do much to remedy this.

Suppose we wish to investigate electric consumption in households based on income and size of the home in a city.

- Income and size of the home are likely to be highly correlated, due to high income earners wanting to buy bigger homes, and low income earners being unable to buy bigger homes.
- We cannot force high income earners to live in small homes, or have low income earners buy bigger homes to break the multicollinearity. In this setting, we have to choose one of the predictors.

7.3.2.3 Too many predictors

As we collect data on more and more variables, we are more likely to encounter multicollinearity. We have to ask if some predictors are provide the same, or similar information, as other predictors.

7.3.3 Consequences of multicollinearity

The main consequence with multicollinearity is that we have **high variance with the estimated coefficients**. This means the value of the estimated coefficient may be very different from the true value. The consequences from this are:

- Estimated coefficients can be difficult to interpret, as the estimated value may be different from the true parameter. Also, if 2 predictors are correlated, then holding one constant while increasing the other one may not make much sense.
- Algebraic sign of coefficients can be different from what is known theoretically. If the true coefficient is positive, but because the estimated coefficient is different, it could be negative. So we may think the direction of the association is opposite.
- Predictors that we know should impact the response variable are found to be insignificant, as the standard error of the estimated coefficient is large, and hence the t statistic is small. We may erroneously think that predictor is not related to the response variable.

Interestingly, predictions may still be unbiased if the regression assumptions are met.

So depending on what you are using your regression model for, multicollinearity may or may not be a huge problem. Recall the two main uses of regression models:

1. **Prediction:** Predict a future value of a response variable, using information from predictor variables.
 2. **Association:** Quantify the relationship between variables. How does a change in the predictor variable change the value of the response variable?
- If the goal of your regression analysis is to interpret the coefficients and understand the effects of each the predictors on the response variable, multicollinearity is a big issue.
 - If the goal of your regression analysis is predict future values of the response, then multicollinearity may be less of an issue as long as you do not extrapolate.

7.4 Detecting Multicollinearity

The following are indicators of the presence of multicollinearity:

1. **Insignificant** results in individual tests on the regression coefficients for important predictor variables. A significant ANOVA F test provides more evidence of multicollinearity.
2. The presence of estimated coefficients with **large standard errors**.
3. Estimated regression coefficients with an algebraic sign that is the **opposite** of that expected from theoretical considerations or prior experience.
4. **High correlation** between pairs of predictor variables.
5. **High variance inflation factors** (VIFs).

We have touched upon the first three ways earlier, and using correlation makes intuitive sense. Next, we will look at VIFs in a bit more detail.

7.4.1 Variance inflation factors (VIFs)

Variance inflation factors (VIFs) are associated with the coefficients of the predictor variables in MLR. VIFs measure **how much the variance of the corresponding coefficient is multiplied by due to the presence of collinearity versus the lack of collinearity being present**. Mathematically, VIFs are defined as:

$$(VIF)_j = \frac{1}{1 - R_j^2}, \quad j = 1, 2, \dots, k, \quad (7.5)$$

where R_j^2 is the **coefficient of determination when x_j is regressed on the other $k - 1$ predictors in the model**.

Larger VIFs indicate stronger evidence of multicollinearity. Generally, VIFs greater than 5 indicate some degree of multicollinearity, and VIFs greater than 10 indicate a high level of multicollinearity.

Let us look at the VIFs for the `Peruvian.txt` dataset:

```
library(faraway)
round(faraway::vif(result), 3)
```

```
##      Age      Years fraclife      Weight      Height      Chin      Forearm      Calf
##  3.213  34.289  24.387      4.748      1.914      2.064      3.802      2.415
##      Pulse
##  1.329
```

The VIFs for the coefficients for x_2, x_3 are above 5, indicating some degree of multicollinearity in our data.

7.4.2 Handling multicollinearity

Depends on the source of multicollinearity, as discussed in Section 7.3.2.

- If due to study design, we can collect data on observations to break the collinearity.
- If due to the nature of the data where some predictors are linearly dependent on others, drop predictor(s). Choose a subset of these predictors (maybe even just one) and remove the rest from the model.
- Abandon least squares regression and use other methods. Other methods such as shrinkage methods and principal components regression help improve predictions, but may not aid in helping explore the relationship

between the predictors and response variable. So it depends on what you want to use your regression for.

7.5 R Tutorial

For this tutorial, we will learn how to conduct the general linear F test as well as to detect the presence of multicollinearity in MLR. We will continue to use the `Peruvian.txt` dataset. The data contains variables relating to blood pressures of Peruvians who have migrated from rural high altitude areas to urban lower altitude areas. The variables are:

- y : Systolic blood pressure
- x_1 : Age
- x_2 : Years in urban area
- x_3 : fraction of life in urban area (x_1/x_2)
- x_4 : Weight in kg
- x_5 : Height in mm
- x_6 : Chin skinfold
- x_7 : Forearm skinfold
- x_8 : Calf skinfold
- x_9 : Resting pulse rate

We want to assess how the systolic blood pressure of these migrants may be predicted and related to these predictors.

Download the data file and read the data in.

```
Data<-read.table("Peruvian.txt", header=TRUE, sep="")
```

There are a number of strategies on how to start building a multiple linear regression (MLR) model. One possible strategy is to build an initial model based on what appear to be predictors that are most related to the response variable, the systolic blood pressure. Let us create a correlation matrix of the variables:

```
round(cor(Data),3)
```

##	Systol_BP	Age	Years	fraclife	Weight	Height	Chin	Forearm	Calf
## Systol_BP	1.000	0.006	-0.087	-0.276	0.521	0.219	0.170	0.272	0.251
## Age	0.006	1.000	0.588	0.365	0.432	0.056	0.158	0.055	-0.005
## Years	-0.087	0.588	1.000	0.938	0.481	0.073	0.222	0.143	0.001
## fraclife	-0.276	0.365	0.938	1.000	0.293	0.051	0.120	0.028	-0.113
## Weight	0.521	0.432	0.481	0.293	1.000	0.450	0.562	0.544	0.392
## Height	0.219	0.056	0.073	0.051	0.450	1.000	-0.008	-0.069	-0.003
## Chin	0.170	0.158	0.222	0.120	0.562	-0.008	1.000	0.638	0.516
## Forearm	0.272	0.055	0.143	0.028	0.544	-0.069	0.638	1.000	0.736
## Calf	0.251	-0.005	0.001	-0.113	0.392	-0.003	0.516	0.736	1.000
## Pulse	0.135	0.091	0.237	0.214	0.312	0.008	0.223	0.422	0.209

```
##          Pulse
## Systol_BP 0.135
## Age       0.091
## Years     0.237
## fraclife  0.214
## Weight    0.312
## Height    0.008
## Chin      0.223
## Forearm   0.422
## Calf      0.209
## Pulse     1.000
```

We use the `round()` function so we can limit the number of decimal places the output uses, which in this case is three.

General Linear F Test

It appears from the correlation matrix that x_3, x_4, x_7, x_8 have moderately strong linear associations with systolic blood pressure (they have the highest correlations). So we start with these four predictors for our MLR:

```
##fit MLR
result<-lm(Systol_BP~fraclife+Weight+Forearm+Calf, data=Data)
summary(result)
```

```
##
## Call:
## lm(formula = Systol_BP ~ fraclife + Weight + Forearm + Calf,
##     data = Data)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -17.7706  -7.0950   0.4133   5.8314  24.0159
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  57.11972   15.56936   3.669 0.000827 ***
## fraclife    -27.79798    7.63270  -3.642 0.000892 ***
## Weight       1.33346    0.28858   4.621 5.3e-05 ***
## Forearm     -0.52910    1.14255  -0.463 0.646254
## Calf        -0.06171    0.60134  -0.103 0.918870
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 9.985 on 34 degrees of freedom
## Multiple R-squared:  0.481, Adjusted R-squared:  0.4199
## F-statistic: 7.878 on 4 and 34 DF, p-value: 0.000132
```

Based on the t tests, we consider dropping x_7, x_8 from the model. So we perform a general linear F test with the full model using predictors x_3, x_4, x_7, x_8 and the reduced model only using x_3, x_4 . The null and alternative hypotheses are:

$$H_0 : \beta_7 = \beta_8 = 0,$$

H_a : at least one of the coefficients in H_0 is not 0.

In words, the null hypothesis supports going with the reduced model by dropping x_7, x_8 , whereas the alternative hypothesis supports the full model by not dropping x_7, x_8 .

We explore two approaches to conducting this general linear F test.

Directly comparing the full and reduced models

In this approach, we fit the reduced model, and then use the `anova()` function to compare the reduced model with the full model:

```
reduced<-lm(Systol_BP~fraclife+Weight, data=Data)

##general linear F test to compare reduced model with full model
anova(reduced, result)
```

```
## Analysis of Variance Table
##
## Model 1: Systol_BP ~ fraclife + Weight
## Model 2: Systol_BP ~ fraclife + Weight + Forearm + Calf
##   Res.Df    RSS Df Sum of Sq    F Pr(>F)
## 1      36 3441.4
## 2      34 3389.8  2    51.598 0.2588 0.7735
```

The F statistic from this test is 0.2588, with a p-value of 0.7735. So we fail to reject the null hypothesis, so there is little evidence of supporting the full model. We go with the reduced model over the full model.

Sequential sums of squares

In this other approach, we use the `anova()` function on the full model to obtain the **sequential sums of squares** associated with the full model:

```
anova(result)

## Analysis of Variance Table
##
## Response: Systol_BP
##           Df Sum Sq Mean Sq F value    Pr(>F)
## fraclife   1  498.1   498.06   4.9957  0.03209 *
## Weight     1 2592.0 2592.01 25.9984 1.279e-05 ***
## Forearm    1   50.5   50.55   0.5070  0.48129
```

```
## Calf      1      1.0      1.05  0.0105   0.91887
## Residuals 34 3389.8   99.70
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The values under the column “Sum Sq” give the sequential SS_R s. Notice how the information is provided: in the order in which the predictors were entered into `lm()`.

The general linear F statistic is

$$\begin{aligned}
 F &= \frac{[SS_R(F) - SS_R(R)]/r}{SS_{res}(F)/(n-p)} \\
 &= \frac{[SS_R(x_3, x_4, x_7, x_8) - SS_R(x_3, x_4)]/2}{SS_{res}(x_3, x_4, x_7, x_8)/(39-5)} \\
 &= \frac{SS_R(x_7, x_8|x_3, x_4)/2}{SS_{res}(x_3, x_4, x_7, x_8)/(39-5)} \\
 &= \frac{(50.5 + 1.0)/2}{3389.8/34} \\
 &= 0.2582748
 \end{aligned} \tag{7.6}$$

which is similar to the value found in approach 1 (discrepancy due to rounding off in intermediate steps).

The corresponding p-value is

```
1-pf(0.2582748, 2, 34)
```

```
## [1] 0.7738846
```

and the critical value is

```
qf(0.95, 2, 34)
```

```
## [1] 3.275898
```

So we fail to reject the null hypothesis and go with the reduced model.

Multicollinearity

With the presence of multiple predictors, it is often tempting to start by including all the predictors in the model.

```
##fit MLR with all predictors
all<-lm(Systol_BP~., data=Data)
```

There are a few ways to detect the presence of multicollinearity in our model.

***t* tests and ANOVA *F* test**

The presence of a lot of insignificant *t* tests for the regression coefficients, along a highly significant ANOVA *F* test is an indication that multicollinearity is present:

```
##look at t tests, and F test
summary(all)

##
## Call:
## lm(formula = Systol_BP ~ ., data = Data)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -12.3443  -6.3972   0.0507   5.7293  14.5257
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  146.81883    48.97099   2.998 0.005526 **
## Age          -1.12143     0.32741  -3.425 0.001855 **
## Years         2.45538     0.81458   3.014 0.005306 **
## fraclife     -115.29384    30.16903  -3.822 0.000648 ***
## Weight        1.41393     0.43097   3.281 0.002697 **
## Height       -0.03464     0.03686  -0.940 0.355196
## Chin         -0.94369     0.74097  -1.274 0.212923
## Forearm      -1.17085     1.19330  -0.981 0.334613
## Calf         -0.15867     0.53716  -0.295 0.769809
## Pulse         0.11455     0.17043   0.672 0.506822
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 8.655 on 29 degrees of freedom
## Multiple R-squared:  0.6674, Adjusted R-squared:  0.5641
## F-statistic: 6.465 on 9 and 29 DF,  p-value: 5.241e-05
```

Notice how five of the *t* tests are insignificant, but the ANOVA *F* is highly significant. So we have evidence of multicollinearity.

Standard errors of estimated coefficients

Looking at the output from `summary()`, we do not see any standard errors that are large. If we have strong multicollinearity, standard errors should be large.

Correlation between pairs of predictors

We can also look at the pairwise correlations among predictors:

```
##correlation matrix, round to 3 decimal
round(cor(Data[, -1]), 3)
```

```
##      Age Years fraclife Weight Height Chin Forearm Calf Pulse
## Age      1.000 0.588    0.365  0.432  0.056  0.158  0.055 -0.005 0.091
## Years    0.588 1.000    0.938  0.481  0.073  0.222  0.143  0.001 0.237
## fraclife 0.365 0.938    1.000  0.293  0.051  0.120  0.028 -0.113 0.214
## Weight    0.432 0.481    0.293  1.000  0.450  0.562  0.544  0.392 0.312
## Height    0.056 0.073    0.051  0.450  1.000 -0.008 -0.069 -0.003 0.008
## Chin      0.158 0.222    0.120  0.562 -0.008  1.000  0.638  0.516 0.223
## Forearm   0.055 0.143    0.028  0.544 -0.069  0.638  1.000  0.736 0.422
## Calf     -0.005 0.001   -0.113  0.392 -0.003  0.516  0.736  1.000 0.209
## Pulse     0.091 0.237    0.214  0.312  0.008  0.223  0.422  0.209 1.000
```

Looking at this matrix, we notice that pairs of predictors involving x_1, x_2, x_3 , and x_4, x_6, x_7 have high correlations. For pairs involving other predictors, the correlations are a lot weaker. So there is some degree of multicollinearity.

VIFs

High VIFs are an indication of multicollinearity.

```
##VIFs
library(faraway)
faraway::vif(all)
```

```
##      Age      Years fraclife      Weight      Height      Chin      Forearm      Calf
## 3.213372 34.289220 24.387489  4.747710  1.913992  2.063865  3.802313  2.414603
##      Pulse
## 1.329233
```

The largest VIFs belong to x_2 and x_3 , which are 34.289220 and 24.387489 respectively. VIFs above 10 indicate a strong degree of multicollinearity.

To summarize what we have seen:

- The ANOVA F test is significant, but a lot of the t tests are insignificant.
- We don't see huge standard errors for the estimated coefficients.
- Some of the predictors have high pairwise correlations, e.g. Pairs involving x_1, x_2, x_3 , and x_4, x_6, x_7 .
- The largest VIF is 34.289220.

Collectively, there is some degree of multicollinearity in this model.

Next steps

We have identified that predictors x_1, x_2, x_3 , and x_4, x_6, x_7 are the ones that are most likely to be causing multicollinearity. A solution will be to use a subset of these predictors and not all of them.

Using subject matter knowledge can help with this decision.

Chapter 8

Categorical Predictors in MLR

8.1 Introduction

Thus far, we have only considered predictors that are quantitative in MLR. But what if we need or want to consider predictors that are categorical instead? For example, what if we wish to investigate the earnings of college graduates based on the type of major? The predictor variable, type of major, is clearly categorical and not quantitative. Categorical variables can be incorporated in MLR. In this module, you will learn how to use and interpret the MLR model when categorical predictors are present.

8.1.1 Quantitative vs categorical variable

First, a quick review on variable types. Variables can be divided into two types: quantitative or categorical. A general way to assess the type of a variable is the answer to the following question: Do arithmetic operations on the variable make sense? If yes, the variable is quantitative.

8.1.1.1 Quantitative variable

Quantitative variables are measured in terms of numbers, where the number represents an amount. Quantitative variables can be subdivided into either continuous or discrete.

- **Continuous** quantitative variable: takes on any numerical value within a range. E.g.: height can be measured in terms of centimeters or inches. It is continuous as the value can take on any value between the shortest and tallest person.

- **Discrete** quantitative variable: takes on distinct numerical values. E.g. the number of failures among 10 experiments. It is discrete as it can only take on integers between 0 and 10.

A question to determine if the variable is continuous or discrete: Can you potentially list all the plausible values of the variable? If yes, the variable is discrete. For the example above, we can list the plausible values for the number of failures among 10 experiments as: 0, 1, 2, all the way to 10. For the height variable, the list of numerical values for height will be an infinite list as height can take on an infinite number of decimal places.

8.1.1.2 Categorical variables

Categorical variables express qualitative attributes (often called qualitative variable). The **levels** (or classes) are the various attributes the variable can take on. For example, political affiliation is categorical with three levels: Democrat, Republican, Independent.

A **binary variable** is a categorical variable with two levels. For example, a variable on whether you voted during the 2020 presidential election is binary, as the answer is either yes or no.

The choice of methods used to analyze data are usually driven by whether the variables are quantitative or categorical. You might have noticed this when creating data visualizations: the visualization you use is driven by the type of variable. Discrete variables are interesting since we can use methods meant for quantitative or categorical variables. We will go over how to make this decision in the context of building MLR models later in the module.

We will see how to incorporate categorical predictors in MLR. We will first start with binary predictors before moving on to predictors with more than two levels.

8.2 Indicator Variables and Dummy Coding

Let us start by considering this simple example: In a study of innovation in the insurance industry, an economist wishes to relate the speed with which an insurance innovation is adopted (in months), y , to the size of the firm, x_1 , and the type of firm (mutual or stock firms).

```
Data<-read.table("insurance.txt", header=FALSE,sep="")
colnames(Data)<-c("time","size", "firm")
head(Data)
```

```
##   time size  firm
## 1   17  151 mutual
## 2   26   92 mutual
## 3   21  175 mutual
## 4   30   31 mutual
```

```
## 5    22   104 mutual
## 6     0   277 mutual
```

So we have one categorical variable, the type of firm, that is binary, as it has two levels, mutual or stock. We also have a quantitative predictor, the size of the firm, x_1 , and a quantitative response variable, the time to adopt an innovation.

8.2.1 Indicator variables

Indicator variables that take on the values 0 and 1 are commonly used to represent the levels of categorical predictors. For example, we may have the following two indicator variables to represent the two types of firms:

$$\begin{aligned} x_2 &= \begin{cases} 1 & \text{if mutual firm} \\ 0 & \text{otherwise;} \end{cases} \\ x_3 &= \begin{cases} 1 & \text{if stock firm} \\ 0 & \text{otherwise;} \end{cases} \end{aligned}$$

and the MLR model is written as

$$y_i = \beta_0 + \beta_1 x_{i1} + \beta_2 x_{i2} + \beta_3 x_{i3} + \epsilon_i.$$

However, this will not work in MLR. Recall that the least squares estimators are

$$\hat{\beta} = (X'X)^{-1} X'y. \quad (8.1)$$

The matrix $(X'X)$ is not invertible if we use these indicator variables. Let us consider a toy example where $n = 4$, with the first two observations being mutual firms, and the last two observations being stock firms. The design matrix, X , becomes

$$\begin{bmatrix} 1 & x_{11} & 1 & 0 \\ 1 & x_{21} & 1 & 0 \\ 1 & x_{31} & 0 & 1 \\ 1 & x_{41} & 0 & 1 \end{bmatrix}$$

Notice that in the design matrix, column 1 equals to the sum of column 3 and column 4. This means we have linear dependence among the columns of the design matrix. And when this happens, $(X'X)^{-1}$ cannot be found so unique solutions to the least squares estimators (8.1) do not exist.

To get around this issue, we use what is known as **dummy coding**.

8.2.2 Dummy coding

We drop one of the indicator variables. In general, a categorical variable with a levels will be represented by $a - 1$ indicator variables, each taking on the values of 0 and 1. This method of coding categorical variables is called **dummy coding**. So for our example, since firm type is binary (two levels), we only need one indicator variable.

We can have the following model

$$y = \beta_0 + \beta_1 x_1 + \beta_2 I_1 + \epsilon, \quad (8.2)$$

where x_1 = is the size of the firm and

$$I_1 = \begin{cases} 1 & \text{if stock firm} \\ 0 & \text{otherwise.} \end{cases}$$

So in this formulation, we only use one indicator variable, I_1 . Indicator variables are typically denoted by I . In this formulation, mutual firm is coded 0, and stock firm is coded 1. The level that is coded 0 is called the **reference class** (sometimes called the baseline class). When the variable is binary, the choice for reference class is not important. The interpretation of the model does not change based on the choice for the reference class.

8.2.3 Regression coefficient interpretation

To see how we can interpret the regression coefficients with dummy coding, we can substitute the numerical value of the indicator variable in (8.2) to obtain the regression equation for each firm type:

- Mutual firms: $E(y|x) = \beta_0 + \beta_1 x_1 + \beta_2(0) = \beta_0 + \beta_1 x_1$
- Stock firms: $E(y|x) = \beta_0 + \beta_1 x_1 + \beta_2(1) = (\beta_0 + \beta_2) + \beta_1 x_1$

We make the following observations:

- We have two straight lines, with the **same** slope β_1 , but the intercepts are **different**, β_0 and $\beta_0 + \beta_2$. This formulation assumes the slope in the scatterplot of y against x_1 is the same for both firm types.
- β_2 indicates the **difference in the mean response for stock firms versus mutual firms (stock firms minus mutual firms), when controlling for size of firm.**

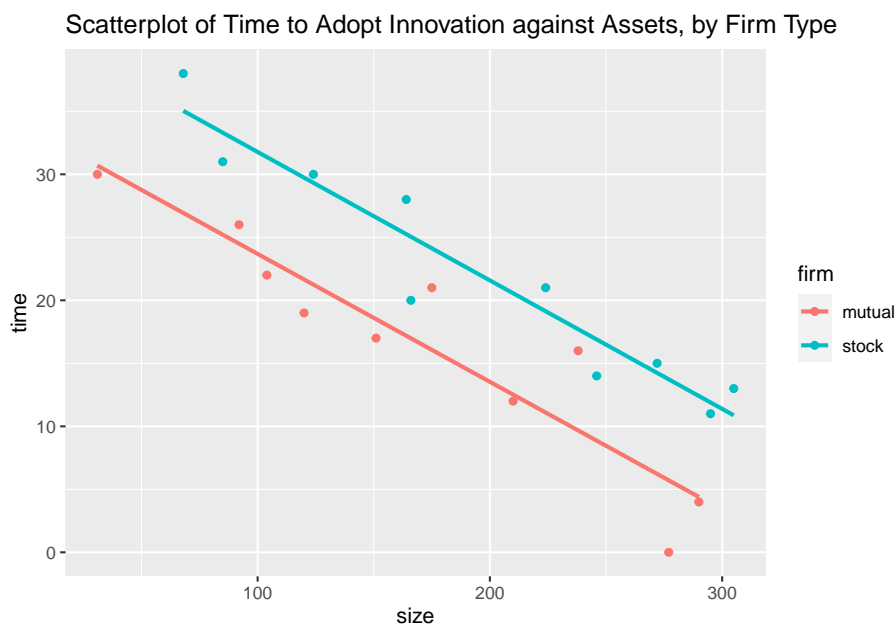
In general, the coefficient of an indicator variable shows how much higher (or lower) the mean response is for the class coded 1 than the reference class, when controlling for x_1 .

Let us look at our example:


```
##convert categorical predictor to factor
Data$firm<-factor(Data$firm)

library(ggplot2)

##scatterplot with separate regression lines
ggplot2::ggplot(Data, aes(x=size, y=time, color=firm))+
  geom_point()+
  geom_smooth(method=lm, se=FALSE)+
  labs(title="Scatterplot of Time to Adopt Innovation against Assets, by Firm Type")
```



We create a scatterplot of the response variable against the quantitative predictor, with separate colors and lines for firm type. Notice that the lines are almost parallel. We noted earlier that the formulation assumes the slopes are parallel.

β_1 denotes the slopes of both of these lines, and β_2 denotes how much higher the line is for stock firms than for mutual firms. Let us take a look at the estimated regression coefficients:

```
result<-lm(time~size+firm, data=Data)
summary(result)

##
## Call:
## lm(formula = time ~ size + firm, data = Data)
##
```

```
## Residuals:
##      Min       1Q   Median       3Q      Max
## -5.6915 -1.7036 -0.4385  1.9210  6.3406
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 33.874069   1.813858  18.675 9.15e-13 ***
## size        -0.101742   0.008891  -11.443 2.07e-09 ***
## firmstock    8.055469   1.459106   5.521 3.74e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.221 on 17 degrees of freedom
## Multiple R-squared:  0.8951, Adjusted R-squared:  0.8827
## F-statistic: 72.5 on 2 and 17 DF,  p-value: 4.765e-09
```

Note the following from the output:

- We know that since the categorical predictor is binary, we should have only 1 indicator variable representing firm type.
- In the output, note that we have one line for the categorical predictor, called `firmstock`. This tells us the name of the predictor, followed by the class that is coded 1. So this tells us that R coded stock firms as 1, and mutual firms as 0.
- The estimated coefficient for `firmstock` is 8.055469. This means that the time to adopt innovation for stock firms is 8.055469 months longer than for mutual firms, when controlling for size of the firm. The associated p-value when testing this coefficient is small, so the data support claim that there is a significant difference in the mean time to adopt innovation based on firm type, when controlling for size of firm. We do not drop firm type as a term in the model. Since the estimated coefficient is positive, the mean time to adopt innovation for stock firms is longer than for mutual firms, when controlling for size of firm.
- The estimated coefficient for `size` is -0.101742. This means the time to adopt innovation decreases by 0.101742 months, per unit increase in firm size, for given firm type. The associated p-value when testing this coefficient is small, so we do not drop `size` as a term in the model.
- The estimated regression equation is $\hat{y} = 33.874069 - 0.101742x_1 + 8.055469I_1$.
- Estimated regression equation for mutual firms: $\hat{y} = 33.874069 - 0.101742x_1 + 8.055469(0) = 33.874 - 0.102x_1$.
- Estimated regression equation for stock firms: $\hat{y} = 33.874069 - 0.101742x_1 + 8.055469(1) = 41.930 - 0.102x_1$.

8.2.4 Thought question

How will the output for this regression change if the dummy coding was changed, i.e. $I_1 = 1$ if mutual firm and 0 if stock firm?

Please view the associated video to review this question, as well as for more commentary on dummy coding.

8.3 Interaction Terms

The regression model as stated in (8.2) is sometimes called a model with **additive effects**. Additive effects assume that each predictor's effect on the response does not depend on the value of the other predictor. As long as we hold the other predictor constant, changing the value of the predictor is associated with the same change in the mean response. Using our example, this implies that when looking at the scatterplot of time to adopt innovation against size of firms, with separate lines for each firm type, the regression lines are parallel.

If the lines are not parallel, it means the effect of changing firm size on the time to adopt innovation depends on the firm type. When the effect of a predictor on the response depends on the value of the other predictor, we have an **interaction effect** between the predictors on the response variable. To add an interaction effect between the predictors into the model, we have

$$y = \beta_0 + \beta_1 x_1 + \beta_2 I_1 + \beta_3 x_1 I_1 + \epsilon \quad (8.3)$$

where $I_1 = 1$ if stock firm and 0 if mutual firm. Substituting the values for I_1 in (8.3), we have the following regression equations for each firm type:

- Mutual firm: $E(y|x) = \beta_0 + \beta_2(0) + \beta_1 x_1 + \beta_3 x_1(0) = \beta_0 + \beta_1 x_1$.
- Stock firm: $E(y|x) = \beta_0 + \beta_2(1) + \beta_1 x_1 + \beta_3 x_1(1) = (\beta_0 + \beta_2) + (\beta_1 + \beta_3) x_1$.

We have different intercepts and different slopes for these regressions, whereas in model (8.2), the slopes are the same.

If there is an interaction, we can see the effect of changing x_1 on the response depends on the other predictor: for mutual firms, increasing x_1 by one unit changes the mean response by β_1 ; while for tool stock firms, increasing x_1 by one unit changes the mean response by $\beta_1 + \beta_3$.

Models with interactions are a bit more difficult to interpret than models with no interactions. Therefore, we typically assess if the interaction term is significant or not. This can be tested in a general linear F test framework, since a model with additive effects (8.2) is the reduced model and a model with interaction effects (8.3) is the full model. If the coefficient of the interaction term is insignificant, we can drop the interaction term and go with the model with just additive effects.

```
##model with interaction
result.int<-lm(time~size*firm, data=Data)
summary(result.int) ##can drop interaction
```

```
##
## Call:
## lm(formula = time ~ size * firm, data = Data)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -5.7144 -1.7064 -0.4557  1.9311  6.3259
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   33.8383695   2.4406498   13.864 2.47e-10 ***
## size          -0.1015306   0.0130525   -7.779 7.97e-07 ***
## firmstock      8.1312501   3.6540517    2.225  0.0408 *
## size:firmstock -0.0004171   0.0183312   -0.023  0.9821
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.32 on 16 degrees of freedom
## Multiple R-squared:  0.8951, Adjusted R-squared:  0.8754
## F-statistic: 45.49 on 3 and 16 DF,  p-value: 4.675e-08
##can also do general linear F test. same as t test since only dropping one term
anova(result,result.int)
```

```
## Analysis of Variance Table
##
## Model 1: time ~ size + firm
## Model 2: time ~ size * firm
##   Res.Df    RSS Df Sum of Sq    F Pr(>F)
## 1      17 176.39
## 2      16 176.38  1 0.0057084 5e-04 0.9821
```

We look at the result of the t test for the line `size:firmstock`, which is the way R denotes the interaction term $x_1 I_1$. This test is insignificant, we do not have evidence that there is an interaction effect between size of firm and firm type. So we can drop the interaction and go with the simpler model with just additive effects. This is expected given that we have seen almost parallel slopes in the scatterplot.

Note that the **hierarchical principle** applies if we have an interaction term: if the interaction term is significant, the lower ordered terms must remain.

8.3.1 Consideration of interaction terms

Typically, people start with an additive order model. Interactions considered at the start if:

- Exploring interactions is part of your research question.
- An interaction makes sense contextually, or is well-established in the literature.
- We have evidence of interaction based on visualizations.

8.3.2 Interaction vs correlation

A question that I often get from students have is “Aren’t variables that interact also correlated?” The short answer is no, as interaction and correlation are two very different concepts.

A short explanation is that if we say that there is an interaction between two variables, x_1, x_2 , it means how each predictor impacts the response variable y depends on the value of the other predictor. Notice that there are three variables, y, x_1, x_2 needed when we talk about an interaction between x_1, x_2 .

Correlation only involves two variables.

For a more detailed explanation, including examples, please read this page.

8.3.3 Dummy coding vs separate regressions

A reasonable question that is often raised is: Why did we not carry out two separate regressions, one for each firm type? When using dummy coding, we are using one regression. The main reason is that it turns out that using one model with dummy coding leads to more precise estimates (smaller standard errors), than creating separate regression for each level. This is true as long as the regression assumptions are met, specifically that the variance of the errors is constant for both levels.

8.4 Beyond Binary Predictors

If we have a categorical predictor with more than two levels, dummy coding is still used in the same manner: a categorical predictor with a levels will be represented by $a - 1$ indicator variables, each taking on the values of 0 and 1.

Let us use another example. In this example, we consider ratings of wines from California. The response variable is average quality rating, y , with predictors average flavor rating, x_1 , and Region indicating which of three regions in California the wine is produced in. The regions are North, Central, and Napa Valley.

A few notes about using dummy coding in this example:

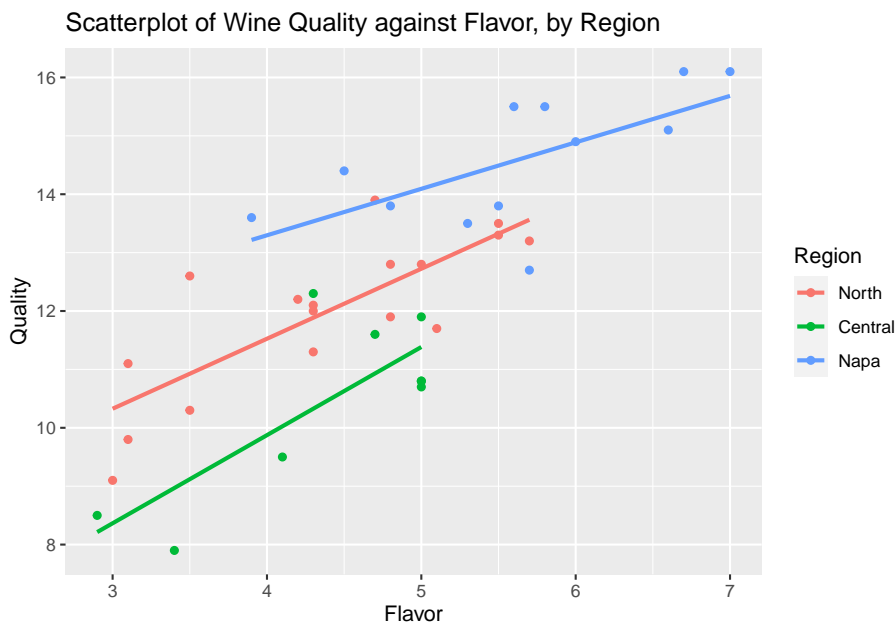
- Since region has three levels, we will have 2 indicator variables, with one class being the reference class.
- The choice of reference class can be arbitrary, or if there is one class that you are most interested in, make that the reference class.
- The interpretations of the regression model will be consistent regardless of choice for reference class.
- If fitting a model with no interactions, the coefficient of each indicator variable denotes **the difference in the mean response between the level that is coded 1 versus the reference class**, while controlling for the other predictor.

Let us create a scatterplot of quality rating against flavor rating, split by region:

```
##clear environment to start new example
rm(list=ls())

Data<-read.table("wine.txt", header=TRUE, sep="")
##convert Region to factor
Data$Region<-factor(Data$Region)
##assign descriptive labels for each region
levels(Data$Region) <- c("North", "Central", "Napa")

library(ggplot2)
##scatterplot of Quality against Flavor,
##separated by Region
ggplot2::ggplot(Data, aes(x=Flavor, y=Quality, color=Region))+
  geom_point()+
  geom_smooth(method=lm, se=FALSE)+
  labs(title="Scatterplot of Wine Quality against Flavor, by Region")
```



The regression equations are almost parallel so we consider a model with no interactions first. We can use the following indicator variables. Note that there are other ways to define them.

Since Napa Valley is California's most famous wine region, we would like to make easy comparisons of other regressions with Napa Valley. So it makes sense to make Napa Valley the reference class.

The corresponding model with just additive effects would be

$$y_i = \beta_0 + \beta_1 x_{i1} + \beta_2 I_{i1} + \beta_3 I_{i2} + \epsilon_i$$

So the regression functions are:

- North: $E\{Y\} = \beta_0 + \beta_1 x_1 + \beta_2(1) + \beta_3(0) = (\beta_0 + \beta_2) + \beta_1 x_1$
- Central: $E\{Y\} = \beta_0 + \beta_1 x_1 + \beta_2(0) + \beta_3(1) = (\beta_0 + \beta_3) + \beta_1 x_1$
- Napa Valley: $E\{Y\} = \beta_0 + \beta_1 x_1 + \beta_2(0) + \beta_3(0) = \beta_0 + \beta_1 x_1$

Recall that this model assumes the slopes are the same for all three regions. β_2 , β_3 indicate how different the mean ratings are for the North and Central regions compared with Napa Valley, respectively, when controlling for the other predictor, the average flavor rating.

Let us fit this model and look at the output:

```
##fit regression with no interaction
reduced<-lm(Quality~Flavor+Region, data=Data)
summary(reduced)

##
## Call:
## lm(formula = Quality ~ Flavor + Region, data = Data)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.97630 -0.58844  0.02184  0.51572  1.94232
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      8.3177      1.0100   8.235 1.31e-09 ***
## Flavor           1.1155      0.1738   6.417 2.49e-07 ***
## RegionNorth     -1.2234      0.4003  -3.056 0.00435 **
## RegionCentral   -2.7569      0.4495  -6.134 5.78e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.8946 on 34 degrees of freedom
## Multiple R-squared:  0.8242, Adjusted R-squared:  0.8087
## F-statistic: 53.13 on 3 and 34 DF,  p-value: 6.358e-13
```

Some observations from the output:

- $\hat{\beta}_2$ is the estimated coefficient for the indicator of the North region. This value is -1.2234. We interpret this as the average quality rating for wines in the North region is 1.2234 lower than wines in the Napa Valley, when controlling for flavor rating.
- $\hat{\beta}_3$ is the estimated coefficient for the indicator of the Central region. The average quality rating for wines in the South region is 2.7569 lower than wines in the Napa Valley, when controlling for flavor rating.
- As mentioned earlier, we can easily make comparisons for any level with the reference class.

8.4.1 Difference in mean response between levels excluding the reference class

Estimating the difference in the mean response between levels excluding the reference class can be done by estimating the difference between the regression coefficients of their respective indicator variables. In this example, $\beta_2 - \beta_3$ measures the difference in mean response between the North and Central regions, for given average flavor rating. The output from our model does not give us

this difference immediately. We can either construct a confidence interval (CI) for $\beta_2 - \beta_3$, or perform a hypothesis test for $\beta_2 - \beta_3$.

8.4.1.1 CI

A $100(1 - \alpha)\%$ confidence interval of estimating the differential effects between these regions will be

$$(\hat{\beta}_2 - \hat{\beta}_3) \pm t_{1-\alpha/2, n-p} se(\hat{\beta}_2 - \hat{\beta}_3), \quad (8.4)$$

where

$$Var(\hat{\beta}_2 - \hat{\beta}_3) = Var(\hat{\beta}_2) + Var(\hat{\beta}_3) - 2Cov(\hat{\beta}_2, \hat{\beta}_3).$$

Note that in general, the variance for the difference in estimated coefficients is

$$Var(\hat{\beta}_j - \hat{\beta}_l) = Var(\hat{\beta}_j) + Var(\hat{\beta}_l) - 2Cov(\hat{\beta}_j, \hat{\beta}_l). \quad (8.5)$$

We need to obtain the variance-covariance matrix of the estimated coefficients:

```
##variance covariance matrix of estimated coefficients
round(vcov(reduced),3) ##display 3 dp
```

```
##              (Intercept) Flavor RegionNorth RegionCentral
## (Intercept)      1.020 -0.170      -0.277      -0.277
## Flavor           -0.170  0.030       0.037       0.037
## RegionNorth      -0.277  0.037       0.160       0.113
## RegionCentral    -0.277  0.037       0.113       0.202
```

Let us compute the CI for $\beta_2 - \beta_3$ using (8.4)

$$\begin{aligned} (\hat{\beta}_2 - \hat{\beta}_3) \pm t_{1-\alpha/2, n-p} \sqrt{Var(\hat{\beta}_2 - \hat{\beta}_3)} \\ (-1.2234 + 2.7569) \pm 2.032245 \sqrt{0.160 + 0.202 - 2 \times 0.113} \\ (0.7840453, 2.2829547) \end{aligned}$$

Note $t_{1-\alpha/2, n-p}$ found using `qt(0.975, 38-4)`.

The CI excludes 0, so there is a significant difference in the mean quality ratings for wines in the North and Central region, when controlling for flavor rating. The CI consists entirely of positive numbers, so the mean quality rating is higher for wines in the North region than the Central region, when controlling for flavor rating.

View the associated video for more in depth explanation for constructing this CI.

8.4.1.2 Hypothesis test

We can also compare between the North and Central regions using hypothesis testing. The hypothesis statements will be:

$$H_0 : \beta_2 - \beta_3 = 0, H_a : \beta_2 - \beta_3 \neq 0.$$

The t statistic is

$$\begin{aligned} t &= \frac{\hat{\beta}_2 - \hat{\beta}_3}{se(\hat{\beta}_2 - \hat{\beta}_3)} \\ &= \frac{-1.2234 + 2.7569}{\sqrt{0.160 + 0.202 - 2 \times 0.113}} \\ &= 4.158286, \end{aligned}$$

which is larger than the critical value $qt(1-0.05/2, 38 - 4) = 2.032245$. So we reject the null hypothesis. Data support the claim that there is a significant difference in the mean quality ratings between wines from the North region and the Central region, when controlling for flavor rating.

8.4.2 Interactions

Suppose we decide to assess if there is an interaction between flavor rating and region. In other words, the effect of flavor rating on quality rating differs by region. From the scatterplot, the slopes are not exactly parallel, so a significant interaction may exist. The model with interaction would be

$$y = \beta_0 + \beta_1 x_1 + \beta_2 I_1 + \beta_3 I_2 + \beta_4 x_1 I_1 + \beta_5 x_1 I_2 + \epsilon_i$$

So regression functions are:

- North: $E\{Y\} = \beta_0 + \beta_1 x_1 + \beta_2(1) + \beta_3(0) + \beta_4 x_1(1) + \beta_5 x_1(0) = (\beta_0 + \beta_2) + (\beta_1 + \beta_4)x_1$
- Central: $E\{Y\} = \beta_0 + \beta_1 x_1 + \beta_2(0) + \beta_3(1) + \beta_4 x_1(0) + \beta_5 x_1(1) = (\beta_0 + \beta_3) + (\beta_1 + \beta_5)x_1$
- Napa Valley: $E\{Y\} = \beta_0 + \beta_1 x_1 + \beta_2(0) + \beta_3(0) + \beta_4 x_1(0) + \beta_5 x_1(0) = \beta_0 + \beta_1 x_1$

Let us perform a general linear F test to see if we should use the model with no interactions or the model with interactions:

```
##consider model with interactions
##(when slopes are not parallel)
result<-lm(Quality~Flavor*Region, data=Data)

##general linear F test for interaction terms
anova(reduced,result)

## Analysis of Variance Table
##
## Model 1: Quality ~ Flavor + Region
## Model 2: Quality ~ Flavor * Region
##   Res.Df    RSS Df Sum of Sq    F Pr(>F)
## 1      34 27.213
## 2      32 25.429  2    1.7845 1.1229 0.3378
```

The general linear F test is insignificant, so we use the reduced model, i.e. the model with no interactions.

8.5 Pairwise Comparisons

When we have a categorical predictor, we may be interested in making comparisons of the mean response between multiple pairs of levels within the categorical predictor. Going back to our wine example, we have a categorical predictor with three levels. This means we can make $\binom{3}{2} = 3$ pairwise comparisons:

- North region vs Napa Valley
- Central region vs Napa Valley
- North region vs Central region

Based on our indicator variables, the regression equations

- North: $E\{Y\} = (\beta_0 + \beta_2) + \beta_1 x_1$
- Central: $E\{Y\} = (\beta_0 + \beta_3) + \beta_1 x_1$
- Napa Valley: $E\{Y\} = \beta_0 + \beta_1 x_1$

So the parameters denoting the **pairwise comparisons** are

- β_2 : North region vs Napa Valley
- β_3 : Central region vs Napa Valley
- $\beta_2 - \beta_3$: North region vs Central region

To assess whether there is a significant difference in the mean response between each pair, we can either:

1. Conduct 3 hypothesis tests:

- $H_0 : \beta_2 = 0, H_a : \beta_2 \neq 0$
- $H_0 : \beta_3 = 0, H_a : \beta_3 \neq 0$

- $H_0 : \beta_3 - \beta_2 = 0, H_a : \beta_3 - \beta_2 \neq 0$

or

2. Construct 3 confidence intervals:

- $\hat{\beta}_2 \pm t_{1-\alpha/2, n-p} se(\hat{\beta}_2)$
- $\hat{\beta}_3 \pm t_{1-\alpha/2, n-p} se(\hat{\beta}_3)$
- $(\hat{\beta}_2 - \hat{\beta}_3) \pm t_{1-\alpha/2, n-p} se(\hat{\beta}_2 - \hat{\beta}_3)$

We have to be careful when conducting multiple tests or constructing multiple CIs.

8.5.1 Significance level

The **significance level**, α , of a hypothesis test is the probability of wrongly rejecting H_0 if it is true. A **Type I** error is defined as wrongly rejecting the null hypothesis if it is true. So an alternate definition of the significance level is the probability of making a Type I error, if the null hypothesis is true.

Suppose we conduct the three hypothesis tests to compare all three pairs of regions, each at significance level α . If the null hypothesis is true for all 3 tests (i.e. there is no significant different in mean response between regions, when controlling for flavor), then the probability of making the right conclusions for all of the tests, assuming the tests are independent, will be $(1-\alpha)^3$. If $\alpha = 0.05$, this probability is $0.95^3 = 0.857375$, not 0.95. A couple of things to consider:

- As we perform more hypothesis tests, the probability of making the right conclusions for all (assuming the null is true for all), decreases.
- Can we do something so that the probability of not making at least one Type I error is still at least $1 - \alpha$?
- For confidence intervals, we want to ensure that the confidence we have that the entire set of intervals capture the true values of the parameters is still at least $1 - \alpha$.

8.5.2 Multiple pairwise comparisons

To account for the fact that we are making multiple pairwise comparisons, we will need to make our confidence intervals wider, and the critical value larger to ensure the chance of making any Type I error is not more than α . There are a few procedures to do this. We will look two common procedures:

- Bonferroni procedure
- Tukey procedure

With the various procedures in multiple comparison:

1. All the confidence intervals take the form

$$\text{estimate} \pm \text{multiplier} \times \text{se}(\text{estimate}) . \quad (8.6)$$

2. For hypothesis tests, we reject the null hypothesis when

$$\text{test statistic} > \text{critical value}. \quad (8.7)$$

Only the multiplier and critical values change.

8.5.3 Bonferroni procedure

Let g denote the number of CIs we wish to construct, or the number of hypothesis tests we need to do to perform our pairwise comparisons.

8.5.3.1 CIs

The Bonferroni procedure to ensure that we have at least $(1-\alpha)100\%$ confidence that all the g CIs capture the true value is

$$\hat{\beta}_j \pm t_{1-\alpha/(2g);n-p} \text{se}(\hat{\beta}_j). \quad (8.8)$$

The multiplier in (8.8) is found using $t_{1-\alpha/(2g);n-p}$ instead of $t_{1-\alpha/2;n-p}$.

Going back to the wine example, suppose we wish to make all three pairwise comparisons. The CI to compare the North region with Napa Valley is

$$\begin{aligned} \hat{\beta}_2 &\pm t_{1-\alpha/(2 \times 3);38-4} \text{se}(\hat{\beta}_2) \\ -1.2234 &\pm 2.518259 \times 0.4003 \\ (-2.2314592 &, -0.2153408). \end{aligned}$$

The CI to compare the Central region with Napa Valley is

$$\begin{aligned} \hat{\beta}_3 &\pm t_{1-\alpha/(2 \times 3);38-4} \text{se}(\hat{\beta}_3) \\ -2.7569 &\pm 2.518259 \times 0.4495 \\ (-3.888858 &, -1.624942). \end{aligned}$$

The CI to compare the North region with the Central region is

$$\begin{aligned} (\hat{\beta}_2 - \hat{\beta}_3) &\pm t_{1-\alpha/(2 \times 3);38-4} \sqrt{\text{Var}(\hat{\beta}_2 - \hat{\beta}_3)} \\ (-1.2234 + 2.7569) &\pm 2.518259 \sqrt{0.160 + 0.202 - 2 \times 0.113} \\ (0.6048119 &, 2.4621881) \end{aligned}$$

All three CIs exclude 0, so there is a significant difference in mean quality rating of wines between all pairs of regions, when controlling for flavor rating.

8.5.3.2 Hypothesis tests

The critical value, based on the Bonferroni procedure, is $t_{1-\alpha/(2g);n-p}$ (instead of $t_{1-\alpha/2;n-p}$). The test statistic still takes the form

$$t = \frac{\text{estimate}}{\text{s.e. of estimate}}.$$

To compare the North region with Napa Valley, we have $H_0 : \beta_2 = 0, H_a : \beta_2 \neq 0$. The test statistic is

$$\begin{aligned} t &= \frac{\hat{\beta}_2}{se(\hat{\beta}_2)} \\ &= \frac{-1.2234}{0.4003} \\ &= -3.056208. \end{aligned}$$

To compare the Central region with Napa Valley, we have $H_0 : \beta_3 = 0, H_a : \beta_3 \neq 0$. The test statistic is

$$\begin{aligned} t &= \frac{\hat{\beta}_3}{se(\hat{\beta}_3)} \\ &= \frac{-2.7569}{0.4495} \\ &= -6.133259. \end{aligned}$$

To compare the North region with the Central region, we have $H_0 : \beta_2 - \beta_3 = 0, H_a : \beta_2 - \beta_3 \neq 0$. The test statistic is

$$\begin{aligned} t &= \frac{\hat{\beta}_2 - \hat{\beta}_3}{se(\hat{\beta}_2 - \hat{\beta}_3)} \\ &= \frac{-1.2234 + 2.7569}{\sqrt{0.160 + 0.202 - 2 \times 0.113}} \\ &= 4.158286. \end{aligned}$$

The critical value is 2.518259, found using `qt(1-0.05/(2*3), 38-4)`. The magnitudes of all of these test statistics are larger than the critical value, so there

is a significant difference in mean quality rating of wines between which pair of regions, when controlling for flavor rating.

View the associated video and the additional set of notes for an explanation of the rationale behind the Bonferroni procedure.

8.5.4 Tukey procedure

The calculations involved in the Tukey procedure are a little bit more involved so we will not cover the details. We can take a look at some output based on the Tukey procedure:

```
library(multcomp)
pairwise<-multcomp::glht(reduced, linfct = mcp(Region= "Tukey"))
summary(pairwise)
```

```
##
## Simultaneous Tests for General Linear Hypotheses
##
## Multiple Comparisons of Means: Tukey Contrasts
##
##
## Fit: lm(formula = Quality ~ Flavor + Region, data = Data)
##
## Linear Hypotheses:
##              Estimate Std. Error t value Pr(>|t|)
## North - Napa == 0    -1.2234    0.4003  -3.056 0.011669 *
## Central - Napa == 0   -2.7569    0.4495  -6.134 < 1e-04 ***
## Central - North == 0  -1.5335    0.3688  -4.158 0.000606 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## (Adjusted p values reported -- single-step method)
```

Each line is showing the result of testing if the mean quality rating differs between the listed pair of regions (when controlling for flavor rating). We note that the results of all three hypothesis tests are significant. So the data support the claim that there is significant difference in the mean quality of wines between all pairs of regions, when controlling for flavor rating.

Given the negative values for the difference in the estimated coefficients, wines from the Napa valley have the highest ratings, followed by wines from the North region, and then wines from the Central region, when flavor rating is controlled.

8.5.5 Comments about Multiple Comparisons

These procedures to handle multiple pairwise comparisons require there to be no interactions involving the categorical predictor, as we assume the difference in the mean response is the same as long as we control the other predictors.

Some comments about the Bonferroni procedure:

- The probability of making at least one Type I error is $\leq \alpha$. As g increases, this probability becomes a lot less than α .
- A by product is that **power** (the ability to correctly reject the null hypothesis) is sacrificed, especially as g increases.
- Confidence intervals have a higher level of confidence and are wider.
- Bonferroni procedure is **considered conservative** (less powerful, wider intervals).
- Fine to use if g is known prior to looking at the data and is small.
- Easy to implement with simple adjustment to multiplier and critical value.

On the other hand, the Tukey procedure is less conservative and more powerful. Typically used when g is larger.

8.6 Practical Considerations

8.6.1 Categorical predictor with many levels

For a categorical predictor with many levels, the output can be daunting to look at, as the number of indicator variables (and hence number of regression coefficients) increases as we have more levels. A few things to consider:

- Are you really interested in exploring the differences in the mean response across all the levels?
- Is there a logical way to **collapse** some levels together that still answers your research question and reduces the number of regression parameters?
- Having more parameters than needed may lead to poorer predictive performance.

8.6.2 Discrete predictors

Do we treat discrete predictors as quantitative or categorical in MLR? A few things to consider:

- Are we fine with assuming they have a “linear” relationship with the response variable? If yes, more likely we should treat the variable as quantitative.
- How many distinct values are there in the discrete variable? The more distinct values, the more likely we should treat the variable as quantitative.
- Are we concerned about needlessly adding parameters to our model especially if we have a small sample size? If yes, more likely we should treat the variable as quantitative.

8.7 R Tutorial

In this tutorial, we will use the data set `wine.txt`. The data set contains ratings of various wines produced in California. We will focus on the response variable y = `Quality` (average quality rating), x_1 = `Flavor` (average flavor rating), and `Region` indicating which of three regions in California the wine is produced in. The regions are coded 1 = North, 2 = Central, and 3 = Napa.

Read the data in and also load the `tidyverse` package

```
library(tidyverse)
Data<-read.table("wine.txt", header=TRUE, sep="")
head(Data)
```

```
##   Clarity Aroma Body Flavor Oakiness Quality Region
## 1      1    3.3  2.8   3.1     4.1     9.8      1
## 2      1    4.4  4.9   3.5     3.9    12.6      1
## 3      1    3.9  5.3   4.8     4.7    11.9      1
## 4      1    3.9  2.6   3.1     3.6    11.1      1
## 5      1    5.6  5.1   5.5     5.1    13.3      1
## 6      1    4.6  4.7   5.0     4.1    12.8      1
```

Data Wrangling

Notice from the description that the variable `Region` is recorded numerically, even though it is a categorical variable. We need to make sure that R is viewing its type correctly by applying the function `class()` to this variable:

```
##is Region a factor?
class(Data$Region)
```

```
## [1] "integer"
```

We need to convert `Region` to be viewed as categorical by using `factor()`, otherwise R will treat it as a quantitative predictor and not use dummy coding:

```
##convert Region to factor
Data$Region<-factor(Data$Region)
##check Region is now the correct type
class(Data$Region)
```

```
## [1] "factor"
```

We can check how the levels are being described:

```
##how are levels described
levels(Data$Region)
```

```
## [1] "1" "2" "3"
```

Notice the names of the levels of the regions are not descriptive. We should also give more descriptive names to the levels of `Region`:

```
##Give names to the levels
levels(Data$Region) <- c("North", "Central", "Napa")
levels(Data$Region)
```

```
## [1] "North" "Central" "Napa"
```

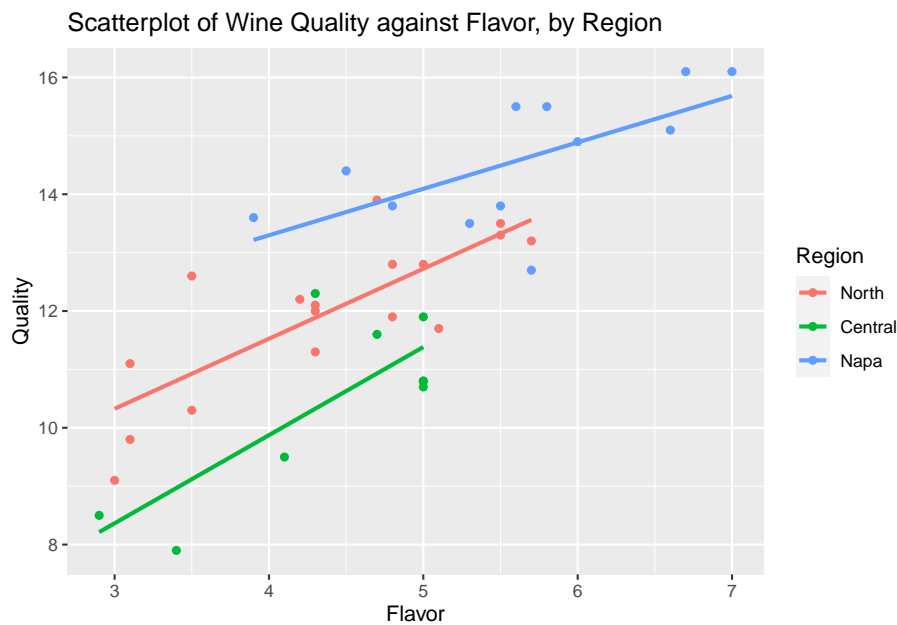
We have done the needed data wrangling: making sure categorical variables are viewed as factors, and giving descriptive names to the levels of the categorical variable.

Note: if categorical variables are already dummy coded, we do not need to convert them to factor when fitting MLR using `lm()`. The `lm()` function converts factors to dummy codes.

Scatterplot with categorical predictor

Since we have a quantitative response variable, `Quality`, a quantitative predictor `Flavor` and a categorical predictor `Region`, we can create a scatterplot, with `Quality` on the y-axis, `Flavor` on the x-axis, and use different colored plots to denote the different regions:

```
ggplot2::ggplot(Data, aes(x=Flavor, y=Quality, color=Region))+
  geom_point()+
  geom_smooth(method=lm, se=FALSE)+
  labs(title="Scatterplot of Wine Quality against Flavor, by Region")
```



We notice a positive linear association between **Quality** and **Flavor** across all three regions, the better the flavor of the wine, the higher the quality rating of the wine.

The slopes are not exactly parallel, indicating that there may exist an interaction between the region of the wine and its flavor; the impact of flavor on quality rating differs among the regions. So a regression model with interaction between region and flavor may be appropriate.

Fitting MLR

Since the categorical variable **Region** has three levels, we know that there will be two indicator variables created to represent the various regions. We check the dummy coding using the `contrasts()` function:

```
##check dummy coding
contrasts(Data$Region)
```

```
##           Central Napa
## North           0    0
## Central         1    0
## Napa            0    1
```

This output informs us the **North** region is the reference class, as it is coded 0 for both indicator variables. We can change the reference class to the **Napa** region via the `relevel()` function:

```
##Set a different reference class
Data$Region<-relevel(Data$Region, ref = "Napa")
contrasts(Data$Region)
```

```
##           North Central
## Napa      0           0
## North     1           0
## Central   0           1
```

Based on the possibility of non-parallel slopes in the scatterplot, we consider fitting a regression model with an interaction term between the predictors:

```
result<-lm(Quality~Flavor*Region, data=Data)
summary(result)
```

```
##
## Call:
## lm(formula = Quality ~ Flavor * Region, data = Data)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.94964 -0.58463  0.04393  0.49607  1.97295
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      10.1144     1.6692   6.060 9.14e-07 ***
## Flavor           0.7957     0.2936   2.710  0.0107 *
## RegionNorth     -3.3833     2.0153  -1.679  0.1029
## RegionCentral    -6.2775     2.4491  -2.563  0.0153 *
## Flavor:RegionNorth  0.4029     0.3878   1.039  0.3066
## Flavor:RegionCentral 0.7137     0.4992   1.430  0.1625
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.8914 on 32 degrees of freedom
## Multiple R-squared:  0.8357, Adjusted R-squared:  0.8101
## F-statistic: 32.56 on 5 and 32 DF,  p-value: 1.179e-11
##notice hierarchical principle is used
```

Given that the t tests for the interaction terms are insignificant, we conduct a partial F test to see if all the interaction terms can be dropped:

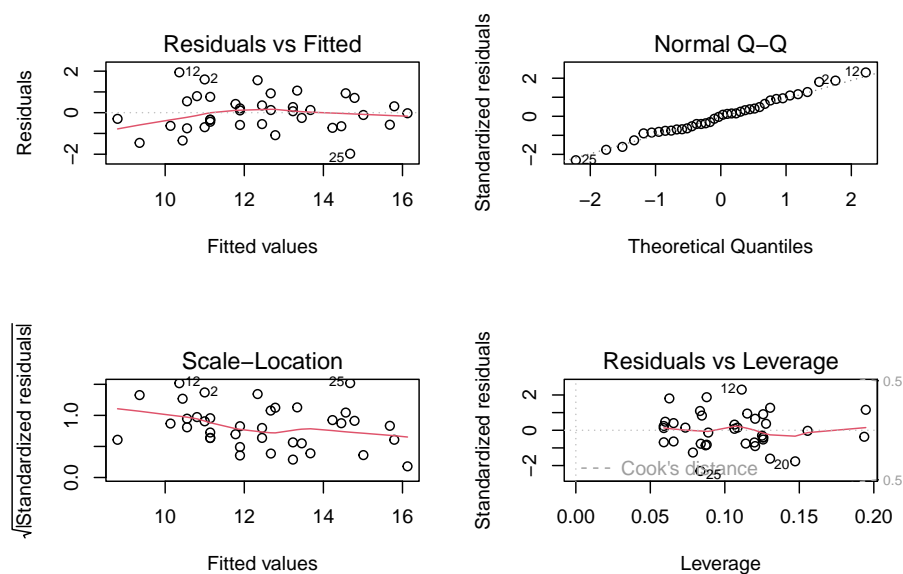
```
##fit regression with no interaction
reduced<-lm(Quality~Flavor+Region, data=Data)
##general linear F test for interaction terms
anova(reduced,result)
```

```
## Analysis of Variance Table
##
## Model 1: Quality ~ Flavor + Region
## Model 2: Quality ~ Flavor * Region
##   Res.Df    RSS Df Sum of Sq    F Pr(>F)
## 1      34 27.213
## 2      32 25.429   2    1.7845 1.1229 0.3378
```

The insignificant result of the partial F test means we can drop the interaction terms. There is little evidence that the slopes are truly different.

The regression assumptions when a categorical predictor is involved are pretty much the same, assessed similarly as before.

```
par(mfrow=c(2,2))
plot(reduced)
```



Multiple comparisons

Since we have a model with no interactions, we can interpret the coefficients of the indicator variables as the difference in the mean quality rating, given the flavor rating, between the class in question and the reference class. Our regression equation is

$$E(y|x) = \beta_0 + \beta_1 x_1 + \beta_2 I_1 + \beta_3 I_2$$

where $I_1 = 1$ if **North** and 0 otherwise, $I_2 = 1$ if **Central** and 0 otherwise.

Plugging in the values of the indicator variables, we can write regression equations for each region

- North: $E(y|x) = \beta_0 + \beta_2 + \beta_1 x_1$.
- Central: $E(y|x) = \beta_0 + \beta_3 + \beta_1 x_1$.
- Napa: $E(y|x) = \beta_0 + \beta_1 x_1$.

Since there are 3 levels, there will be 3 possible pairs of regions to compare (while controlling for flavor rating):

- North and Napa: denoted by β_2
- Central and Napa: denoted by β_3
- North and Central: $\beta_2 - \beta_3$

Let's take a look at the estimated coefficients

```
summary(reduced)

##
## Call:
## lm(formula = Quality ~ Flavor + Region, data = Data)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.97630 -0.58844  0.02184  0.51572  1.94232
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      8.3177     1.0100   8.235 1.31e-09 ***
## Flavor           1.1155     0.1738   6.417 2.49e-07 ***
## RegionNorth     -1.2234     0.4003  -3.056 0.00435 **
## RegionCentral   -2.7569     0.4495  -6.134 5.78e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.8946 on 34 degrees of freedom
## Multiple R-squared:  0.8242, Adjusted R-squared:  0.8087
## F-statistic: 53.13 on 3 and 34 DF,  p-value: 6.358e-13
```

The estimated difference in the mean quality rating between the sampled wines in the North and Napa regions is -1.22, for given flavor ratings.

The first two comparisons are easy as we can just refer to the coefficients for the indicator variables. A little bit of work needs to be done to compare the North and Central regions. Also, note we are performing three hypothesis tests. So we need to use multiple comparison methods to ensure that the probability of making at least one Type I error is at most the significance level of 0.05.

Bonferroni procedure

As noted earlier, there are 3 pairs of regions to compare (while controlling for flavor rating):

- North and Napa: denoted by β_2
- Central and Napa: denoted by β_3
- North and Central: $\beta_2 - \beta_3$

The t multiplier and critical value is now $t_{1-\frac{\alpha}{2g}, n-p}$, which we can find with:

```
n<-dim(Data)[1]
p<-4
g<-3
t.bon<-qt(1-0.05/(2*g), n-p)
t.bon
```

```
## [1] 2.518259
```

Pairwise comparison with reference class For the difference in mean quality rating between wines in the North and Napa regions, when controlling for flavor, we use the confidence interval for β_2 , i.e.,

$$\hat{\beta}_2 \pm t_{1-\frac{\alpha}{2g}, n-p} se(\hat{\beta}_2) = -1.2234 \pm 2.518259 \times 0.4003 = (-2.2315, -0.2153)$$

which excludes 0, so we have a significant difference in the mean quality rating between wines in the North and Napa regions, when controlling for flavor. Since the interval is negative, we can say that the mean quality rating for wines in the Napa region is higher than the North region, when controlling for flavor.

To conduct the hypothesis test $H_0 : \beta_2 = 0, H_a : \beta_2 \neq 0$, we can use the critical value (which is the same as the t multiplier) of 2.518259. The test statistic is

$$\frac{\hat{\beta}_2}{se(\hat{\beta}_2)} = \frac{-1.2234}{0.4003} = -3.056$$

which is larger in magnitude than the critical value, so we reject the null hypothesis.

Notice the result from the confidence interval and hypothesis test are consistent at the same level of significance.

Pairwise comparison excluding reference class Comparisons excluding the reference require a bit more work. For the difference in mean quality rating between wines in the North and Central regions, when controlling for flavor, we use the CI for $\beta_2 - \beta_3$:

$$(\hat{\beta}_2 - \hat{\beta}_3) \pm t_{1-\frac{\alpha}{2g}, n-p} se(\hat{\beta}_2 - \hat{\beta}_3)$$

The output from `summary()` does not provide $se(\hat{\beta}_2 - \hat{\beta}_3)$. To obtain the values to calculate this, we need to produce the variance-covariance matrix for the estimated coefficients

```
vcov(reduced)
```

```
##              (Intercept)      Flavor RegionNorth RegionCentral
## (Intercept)      1.0201363 -0.16975148 -0.27722389  -0.27700199
## Flavor           -0.1697515  0.03022282  0.03748222   0.03744271
## RegionNorth     -0.2772239  0.03748222  0.16026554   0.11313506
## RegionCentral   -0.2770020  0.03744271  0.11313506   0.20201780
```

So we have

$$Var(\hat{\beta}_2 - \hat{\beta}_3) = Var(\hat{\beta}_2) + Var(\hat{\beta}_3) - 2Cov(\hat{\beta}_2, \hat{\beta}_3) = 0.1603 + 0.2020 - 2 \times 0.1131 = 0.1361$$

Therefore, the CI for $\beta_2 - \beta_3$ is

$$(-1.2234 - -2.7569) \pm 2.518259 \times \sqrt{0.1361} = (0.6045, 2.4625)$$

which excludes 0, so we have a significant difference in the mean quality rating between wines in the North and Central regions, when controlling for flavor. Since the interval is positive, we can say that the mean quality rating for wines in the North region is higher than the Central region, when controlling for flavor.

To perform the hypothesis test $H_0 : \beta_2 - \beta_3 = 0$, $H_a : \beta_2 - \beta_3 \neq 0$, we need to calculate the t-statistic

$$t-stat = \frac{\hat{\beta}_2 - \hat{\beta}_3}{se(\hat{\beta}_2 - \hat{\beta}_3)} = \frac{-1.2234 - -2.7569}{\sqrt{0.1361}} = 4.1568$$

which is larger in magnitude than the critical value of 2.518259, so we reject the null hypothesis. Again, the conclusions from the hypothesis test and CI are consistent.

Tukey procedure

Another procedure for multiple pairwise comparisons is the Tukey procedure. We use the `glht()` function from the `multcomp` package

```
library(multcomp)
pairwise<-multcomp::glht(reduced, linfct = mcp(Region= "Tukey"))
summary(pairwise)
```



```
##
## Simultaneous Tests for General Linear Hypotheses
##
## Multiple Comparisons of Means: Tukey Contrasts
##
##
## Fit: lm(formula = Quality ~ Flavor + Region, data = Data)
##
## Linear Hypotheses:
##              Estimate Std. Error t value Pr(>|t|)
## North - Napa == 0    -1.2234     0.4003  -3.056 0.011651 *
## Central - Napa == 0   -2.7569     0.4495  -6.134 < 1e-04 ***
## Central - North == 0  -1.5335     0.3688  -4.158 0.000573 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## (Adjusted p values reported -- single-step method)
```

We can see that there is a significant difference in the mean Quality rating for all pairs of regions, for given flavor rating, since these tests are all significant.

Given the negative values for the difference in the estimated coefficients, wines from the Napa valley have the highest ratings, followed by wines from the North region, and then wines from the Central region, when flavor rating is controlled.

Chapter 9

Introduction

You can label chapter and section titles using `{#label}` after them, e.g., we can reference Chapter 9. If you do not manually label them, there will be automatic labels anyway, e.g., Chapter 10.

Figures and tables with captions will be placed in `figure` and `table` environments, respectively.

```
par(mar = c(4, 4, .1, .1))  
plot(pressure, type = 'b', pch = 19)
```

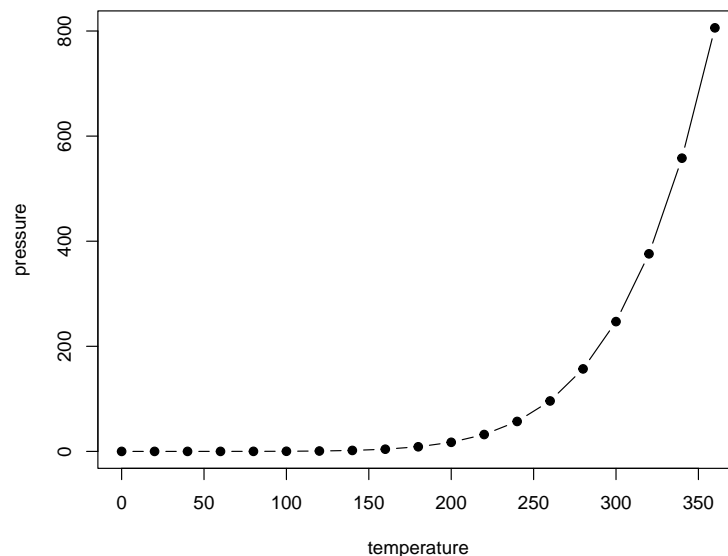


Figure 9.1: Here is a nice figure!

Table 9.1: Here is a nice table!

Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species
5.1	3.5	1.4	0.2	setosa
4.9	3.0	1.4	0.2	setosa
4.7	3.2	1.3	0.2	setosa
4.6	3.1	1.5	0.2	setosa
5.0	3.6	1.4	0.2	setosa
5.4	3.9	1.7	0.4	setosa
4.6	3.4	1.4	0.3	setosa
5.0	3.4	1.5	0.2	setosa
4.4	2.9	1.4	0.2	setosa
4.9	3.1	1.5	0.1	setosa
5.4	3.7	1.5	0.2	setosa
4.8	3.4	1.6	0.2	setosa
4.8	3.0	1.4	0.1	setosa
4.3	3.0	1.1	0.1	setosa
5.8	4.0	1.2	0.2	setosa
5.7	4.4	1.5	0.4	setosa
5.4	3.9	1.3	0.4	setosa
5.1	3.5	1.4	0.3	setosa
5.7	3.8	1.7	0.3	setosa
5.1	3.8	1.5	0.3	setosa

Reference a figure by its code chunk label with the `fig:` prefix, e.g., see Figure 9.1. Similarly, you can reference tables generated from `knitr::kable()`, e.g., see Table 9.1.

```
knitr::kable(
  head(iris, 20), caption = 'Here is a nice table!',
  booktabs = TRUE
)
```

You can write citations, too. For example, we are using the **bookdown** package (Xie, 2023) in this sample book, which was built on top of R Markdown and **knitr** (Xie, 2015).

Chapter 10

Methods

We describe our methods in this chapter.

Math can be added in body using usual syntax like this

10.1 math example

p is unknown but expected to be around $1/3$. Standard error will be approximated

$$SE = \sqrt{\left(\frac{p(1-p)}{n}\right)} \approx \sqrt{\frac{1/3(1-1/3)}{300}} = 0.027$$

You can also use math in footnotes like this¹.

We will approximate standard error to 0.027^2

¹where we mention $p = \frac{a}{b}$

² p is unknown but expected to be around $1/3$. Standard error will be approximated

$$SE = \sqrt{\left(\frac{p(1-p)}{n}\right)} \approx \sqrt{\frac{1/3(1-1/3)}{300}} = 0.027$$

Bibliography

Xie, Y. (2015). *Dynamic Documents with R and knitr*. Chapman and Hall/CRC, Boca Raton, Florida, 2nd edition. ISBN 978-1498716963.

Xie, Y. (2023). *bookdown: Authoring Books and Technical Documents with R Markdown*. R package version 0.34.