

R Tutorial

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Before beginning this tutorial, the packages listed in the README file should be downloaded and installed properly.

In R, comments are indicated in code with a "#" character, and arrays and matrices begin with index 1.

1 Reading in Data and Basic Statistical Functions

1.1 Read in the data.

a) Read the data in as a .csv file.

```
student <- read.csv('/Users/class.csv')
```

[read.csv\(\)](#)

b) Read the data in as a .xls file.

```
# call the gdata package  
library(gdata)
```

```
student_xls <- read.xls('/Users/class.xls', 1)
```

[gdata](#) | [read.xls\(\)](#)

c) Read the data in as a .json file.

There is more code involved in reading a .json file into R so it becomes a proper data frame, however we will not at this time dive into the explanation for all this code, but it should become evident throughout the tutorial.

```
# call the rjson package  
library(rjson)  
  
temp <- fromJSON(file = '/Users/class.json')  
temp <- do.call('rbind', temp)  
temp <- data.frame(temp, stringsAsFactors = TRUE)  
temp <- transform(temp, Name=unlist(Name), Sex=unlist(Sex), Age=unlist(Age),  
                  Height=unlist(Height), Weight=unlist(Weight))  
temp$Name <- as.factor(temp$Name)  
temp$Sex <- as.factor(temp$Sex)  
temp$Age <- as.integer(temp$Age)  
  
student_json <- temp
```

[rjson](#) | [fromJSON\(\)](#)

1.2 Find the dimensions of the data set.

The shape of an R [data frame](#) is available by calling the [dim\(\)](#) function, with the data name as an argument.

```
dim(student)
```

```
## [1] 19 5
```

1.3 Find basic information about the data set.

Information about an R [data frame](#) is available by calling the [str\(\)](#) function, with the data name as an argument.

```
str(student)

## 'data.frame':    19 obs. of  5 variables:
## $ Name   : Factor w/ 19 levels "Alfred","Alice",...: 1 2 3 4 5 6 7 8 9 10
## ...
## $ Sex    : Factor w/ 2 levels "F","M": 2 1 1 1 2 2 1 1 2 2 ...
## $ Age    : int   14 13 13 14 14 12 12 15 13 12 ...
## $ Height: num    69 56.5 65.3 62.8 63.5 57.3 59.8 62.5 62.5 59 ...
## $ Weight: num   112 84 98 102 102 ...
```

1.4 Look at the first 5 observations.

The first 5 observations of a [data frame](#) are available by calling the [head\(\)](#) function, with the data name as an argument. By default, [head\(\)](#) returns 4 observations, but we can alter the function to return 5 observations in the way shown below. The [tail\(\)](#) function is analogous and returns the last observations.

```
head(student, n=5)

##      Name Sex Age Height Weight
## 1  Alfred  M  14   69.0   112.5
## 2  Alice   F  13   56.5    84.0
## 3 Barbara  F  13   65.3    98.0
## 4  Carol   F  14   62.8   102.5
## 5  Henry   M  14   63.5   102.5
```

1.5 Calculate mean of numeric variables.

```
# We must apply the is.numeric function to the data set which returns a
# matrix of booleans that we then use to subset the dataset to return
# only numeric variables
```

```
# Then we can use the colMeans function to return the mean of
# column variables
```

```
colMeans(student[sapply(student, is.numeric)])
```

```
##      Age      Height      Weight
## 13.31579 62.33684 100.02632
```

```
colMeans() | sapply() | is.numeric
```

1.6 Compute summary statistics of the data set.

Summary statistics of a [data frame](#) are available by calling the `summary()` function, with the data name as an argument.

```
summary(student)
```

##	Name	Sex	Age	Height	Weight
##	Alfred : 1	F: 9	Min. :11.00	Min. :51.30	Min. : 50.50
##	Alice : 1	M:10	1st Qu.:12.00	1st Qu.:58.25	1st Qu.: 84.25
##	Barbara: 1		Median :13.00	Median :62.80	Median : 99.50
##	Carol : 1		Mean :13.32	Mean :62.34	Mean :100.03
##	Henry : 1		3rd Qu.:14.50	3rd Qu.:65.90	3rd Qu.:112.25
##	James : 1		Max. :16.00	Max. :72.00	Max. :150.00
##	(Other):13				

1.7 Descriptive statistics functions applied to columns of the data set.

Notice the subsetting of student with the \$ character

```
sd(student$Weight)

## [1] 22.77393

sum(student$Weight)

## [1] 1900.5

length(student$Weight)

## [1] 19

max(student$Weight)

## [1] 150

min(student$Weight)

## [1] 50.5

median(student$Weight)

## [1] 99.5
```

1.8 Produce a one-way table to describe the frequency of a variable.

a) Produce a one-way table of a discrete variable.

```
table(student$Age)

##
## 11 12 13 14 15 16
##  2  5  3  4  4  1
```

b) Produce a one-way table of a categorical variable.

```
table(student$Sex)
```

```
##  
##   F   M  
##  9 10
```

table()

1.9 Produce a two-way table to visualize the frequency of two categorical (or discrete) variables.

```
table(student$Age, student$Sex)
```

```
##  
##           F M  
##    11 1 1  
##    12 2 3  
##    13 2 1  
##    14 2 2  
##    15 2 2  
##    16 0 1
```

table()

1.10 Select a subset of the data that meets a certain criterion.

```
# The "," character tells R to select all columns of the data set  
females <- student[which(student$Sex == 'F'), ]  
head(females, n=5)
```

```
##      Name Sex Age Height Weight  
## 2  Alice  F  13   56.5   84.0  
## 3 Barbara  F  13   65.3   98.0  
## 4  Carol  F  14   62.8  102.5  
## 7   Jane  F  12   59.8   84.5  
## 8  Janet  F  15   62.5  112.5
```

which()

1.11 Determine the correlation between two continuous variables.

```
height_weight <- subset(student, select = c(Height, Weight))  
cor(height_weight, method = "pearson")
```

```
##           Height      Weight  
## Height 1.0000000 0.8777852  
## Weight 0.8777852 1.0000000
```

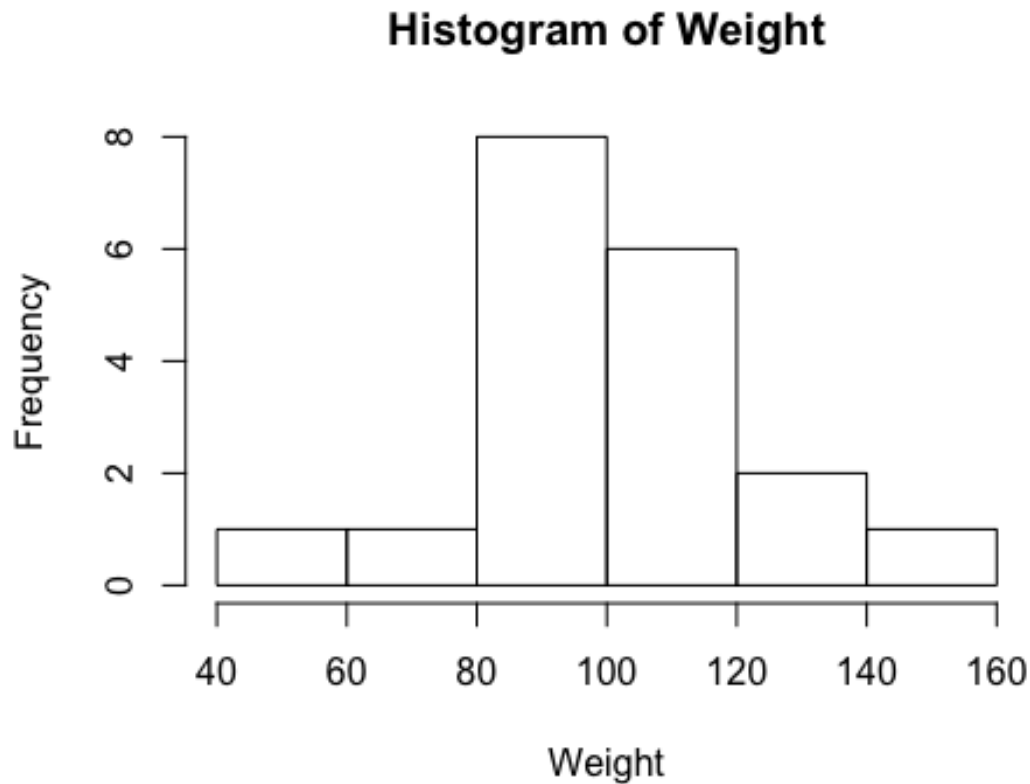
subset() | cor()

2 Basic Graphing and Plotting Functions

2.1 Visualize a single continuous variable by producing a histogram.

Setting student\$Weight to a new variable "Weight" cleans up the labeling of the histogram

```
Weight <- student$Weight  
hist(Weight)
```

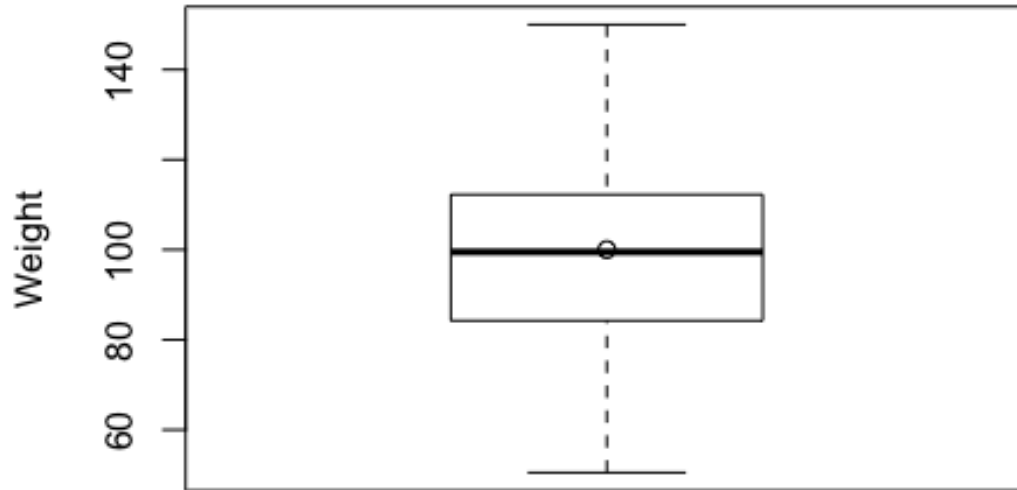


hist()

2.2 Visualize a single continuous variable by producing a boxplot.

points(mean(Weight)) tells R to plot the mean of the variable on the boxplot

```
boxplot(Weight, ylab="Weight")  
points(mean(Weight))
```



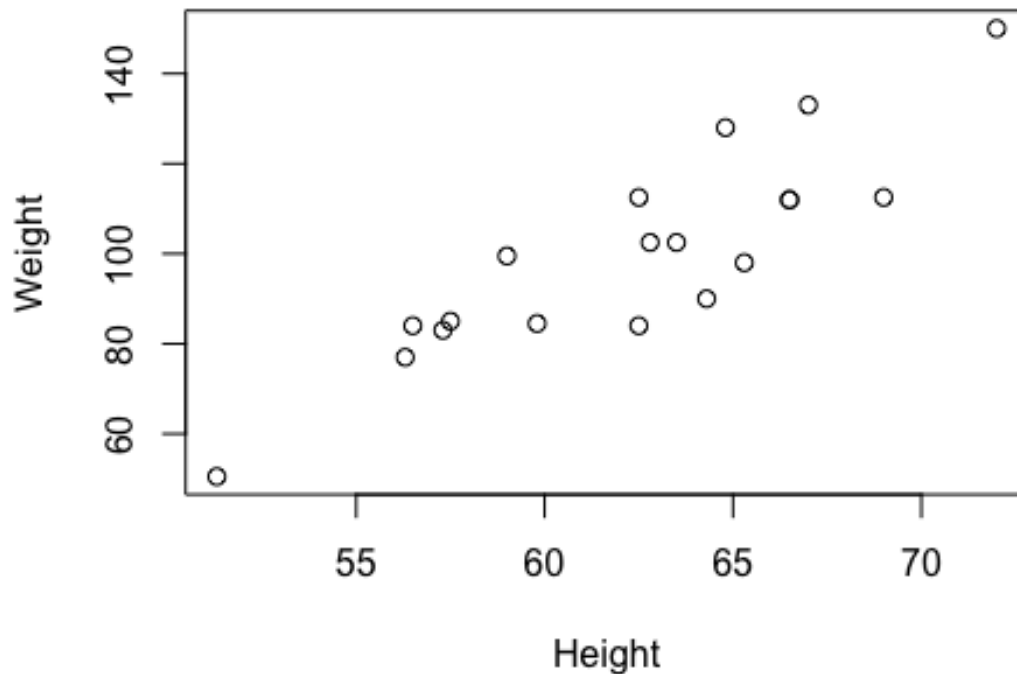
`boxplot()` | `points()`

2.3 Visualize two continuous variables by producing a scatterplot.

```
Height <- student$Height
```

Notice here you specify the x variable, followed by the y variable

```
plot(Height, Weight)
```



`plot()`

2.4 Visualize a relationship between two continuous variables by producing a scatterplot and a plotted line of best fit.

```
plot(Height, Weight)
```

```
# lm() models Weight as a function of Height and returns the parameters  
# of the line of best fit
```

```
model <- lm(Weight~Height)
```

```
coeff <- coef(model)
```

```
intercept <- as.matrix(coeff[1])[1]
```

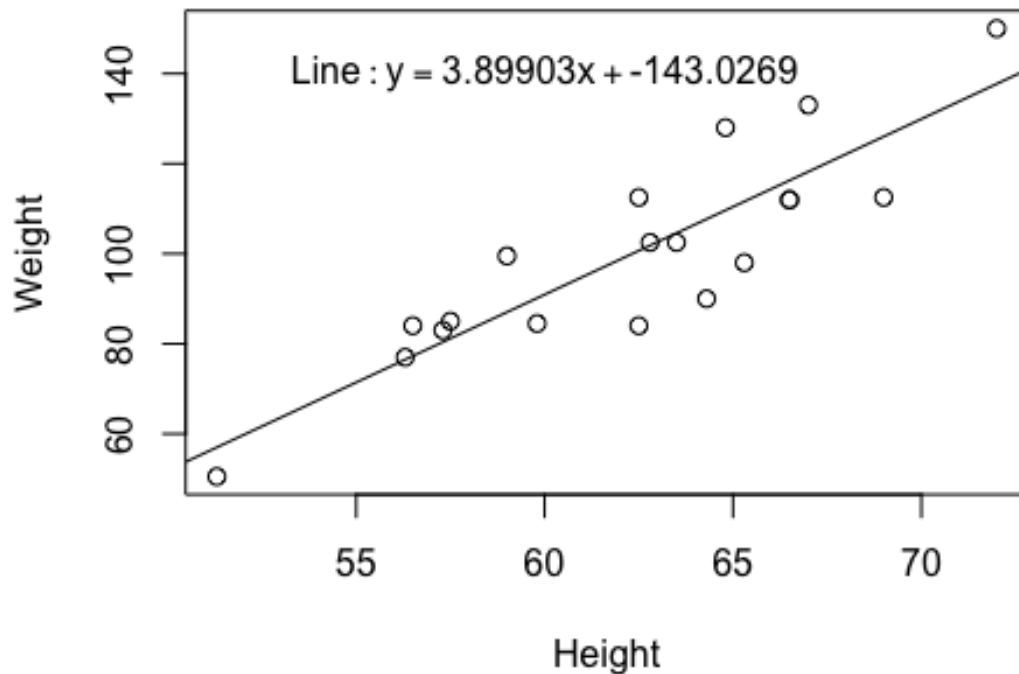
```
slope <- as.matrix(coeff[2])[1]
```

```
# abline() prints the line of best fit
```

```
abline(lm(Weight~Height))
```

```
# text() prints the equation of the line of best fit, with the first  
# two arguments specifying the x and y location, respectively, of where  
# the text should be printed on the graph
```

```
text(60, 140, bquote(Line: y == .(slope) * x + .(intercept)))
```



`lm()` | `coef()` | `as.matrix()` | `abline()` | `text()` | `bquote()`

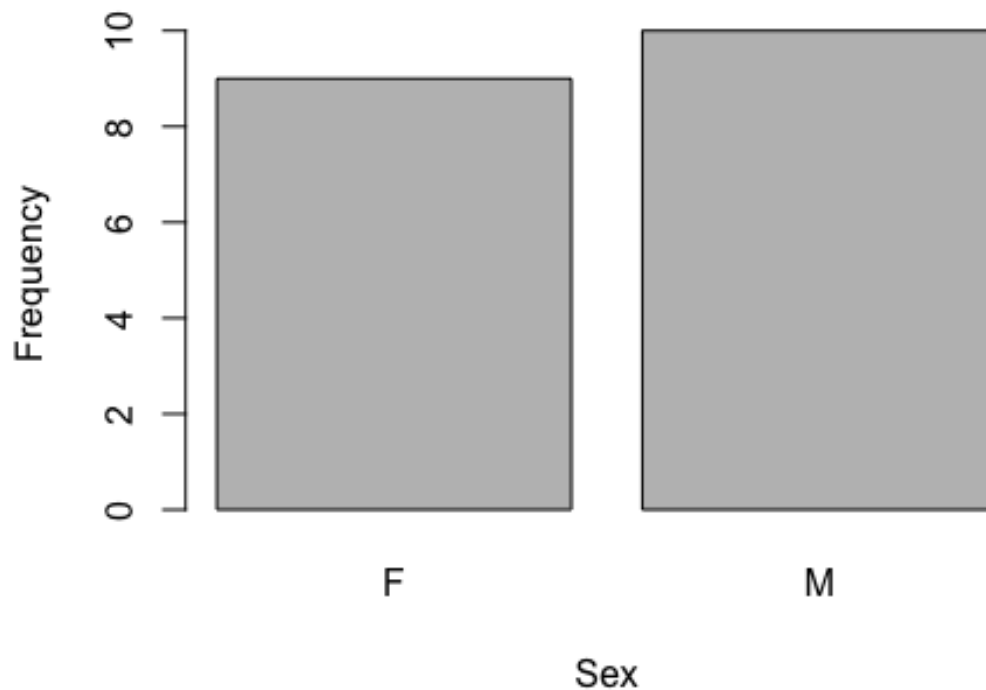
2.5 Visualize a categorical variable by producing a bar chart.

```
counts <- table(student$Sex)
```

```
# beside = TRUE indicates to print the bars side by side instead of on top of
# each other
```

```
# names.arg indicates which names to use to label the bars
```

```
barplot(counts, beside=TRUE, ylab= "Frequency", xlab= "Sex",
        names.arg=names(counts))
```



`barplot() | names()`

2.6 Visualize a continuous variable, grouped by a categorical variable, using side-by-side boxplots.

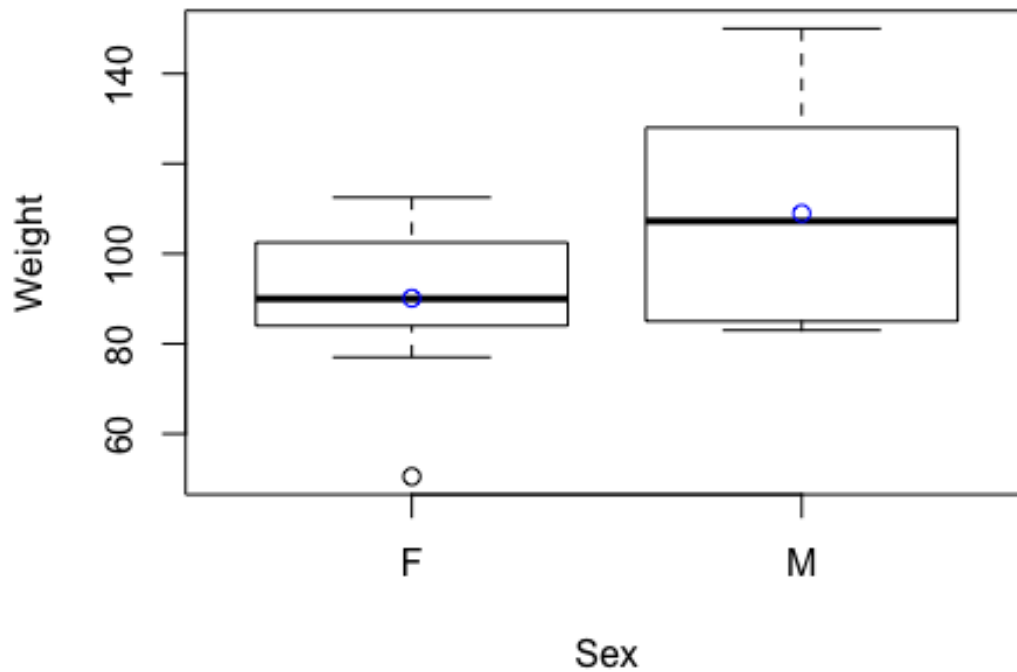
a) Simple side-by-side boxplot without color.

```
# Subset data set to return only female weights, and then only male weights
Female_Weight <- student[which(student$Sex == 'F'), "Weight"]
Male_Weight <- student[which(student$Sex == 'M'), "Weight"]

# Find the mean of both arrays
means <- c(mean(Female_Weight), mean(Male_Weight))

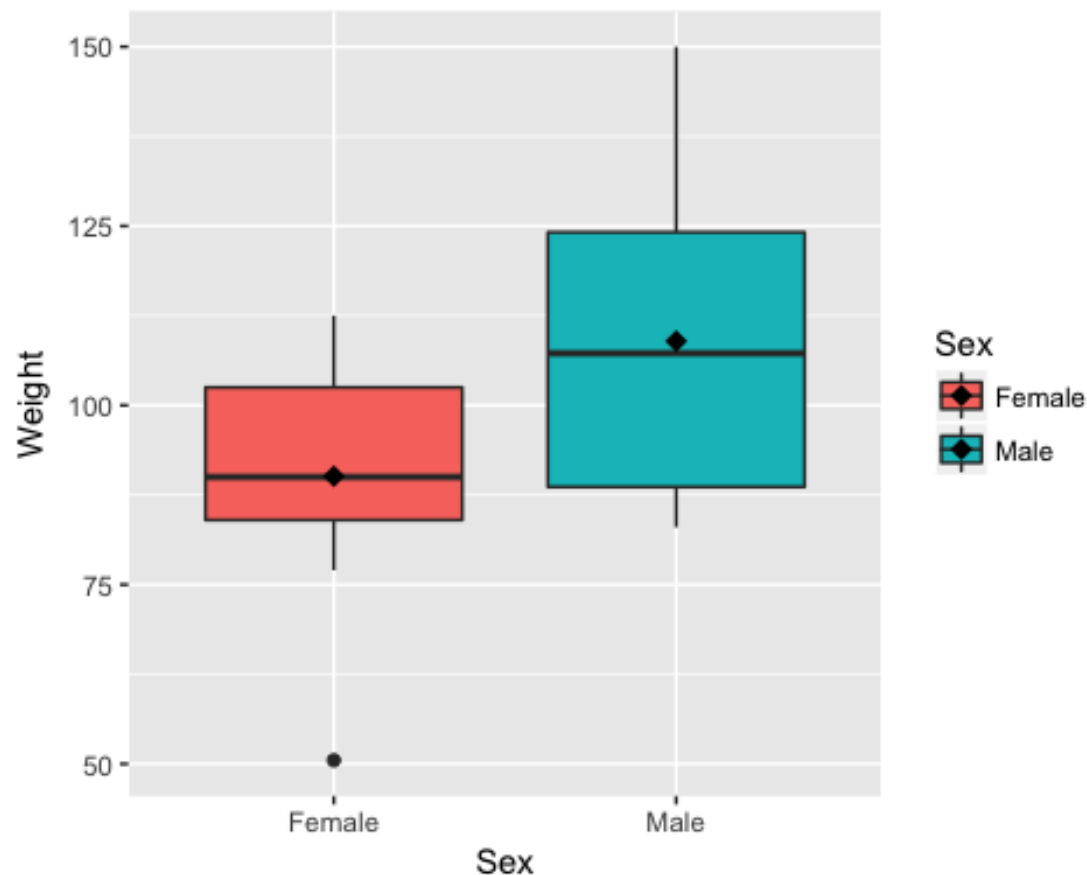
# Syntax indicates Weight as a function of Sex
boxplot(student$Weight ~ student$Sex, ylab= "Weight", xlab= "Sex")

# Plot means on boxplots in blue
points(means, col= "blue")
```



b) More advanced side-by-side boxplot with color.

```
library(ggplot2)
student$Sex <- factor(student$Sex, levels = c("F", "M"),
                      labels = c("Female", "Male"))
ggplot(data = student, aes(x = Sex, y = Weight, fill = Sex)) +
  geom_boxplot() + stat_summary(fun.y = mean,
                              color = "black", geom = "point",
                              shape = 18, size = 3)
```



`ggplot2` | `factor()` | `c()` | `aes()` | `geom_boxplot()` | `stat_summary()`

3 Basic Data Wrangling and Manipulation

3.1 Create a new variable in a data set as a function of existing variables in the data set.

Notice here how you can create the BMI column in the data set just by # naming it

```
student$BMI <- student$Weight / (student$Height)**2 * 703
head(student, n=5)
```

```
##      Name    Sex Age Height Weight    BMI
## 1  Alfred   Male  14   69.0  112.5 16.61153
## 2   Alice Female  13   56.5   84.0 18.49855
## 3 Barbara Female  13   65.3   98.0 16.15679
## 4   Carol Female  14   62.8  102.5 18.27090
## 5   Henry   Male  14   63.5  102.5 17.87030
```

3.2 Create a new variable in a data set using if/else logic of existing variables in the data set.

```
# Notice the use of the ifelse() function for a single condition
student$BMI_Class <- ifelse(student$BMI<19.0, "Underweight", "Healthy")
head(student, n=5)
```

##	Name	Sex	Age	Height	Weight	BMI	BMI_Class
## 1	Alfred	Male	14	69.0	112.5	16.61153	Underweight
## 2	Alice	Female	13	56.5	84.0	18.49855	Underweight
## 3	Barbara	Female	13	65.3	98.0	16.15679	Underweight
## 4	Carol	Female	14	62.8	102.5	18.27090	Underweight
## 5	Henry	Male	14	63.5	102.5	17.87030	Underweight

ifelse()

3.3 Create a new variable in a data set using mathematical functions applied to existing variables in the data set.

Using the `log()`, `exp()`, `sqrt()`, `ifelse()` and `abs()` functions.

```
student$LogWeight <- log(student$Weight)
student$ExpAge <- exp(student$Age)
student$SqrtHeight <- sqrt(student$Height)
student$BMI_Neg <- ifelse(student$BMI < 19.0, -student$BMI, student$BMI)
student$BMI_Pos <- abs(student$BMI_Neg)
```

```
# Create a boolean variable
```

```
student$BMI_Check <- (student$BMI == student$BMI_Pos)
head(student, n=5)
```

##	Name	Sex	Age	Height	Weight	BMI	BMI_Class	LogWeight
## 1	Alfred	Male	14	69.0	112.5	16.61153	Underweight	4.722953
## 2	Alice	Female	13	56.5	84.0	18.49855	Underweight	4.430817
## 3	Barbara	Female	13	65.3	98.0	16.15679	Underweight	4.584967
## 4	Carol	Female	14	62.8	102.5	18.27090	Underweight	4.629863
## 5	Henry	Male	14	63.5	102.5	17.87030	Underweight	4.629863

##	ExpAge	SqrtHeight	BMI_Neg	BMI_Pos	BMI_Check
## 1	1202604.3	8.306624	-16.61153	16.61153	TRUE
## 2	442413.4	7.516648	-18.49855	18.49855	TRUE
## 3	442413.4	8.080842	-16.15679	16.15679	TRUE
## 4	1202604.3	7.924645	-18.27090	18.27090	TRUE
## 5	1202604.3	7.968689	-17.87030	17.87030	TRUE

3.4 Drop variables from a data set.

```
# -c() function tells R not to select the columns listed
```

```
student <- subset(student, select = -c(LogWeight, ExpAge, SqrtHeight,
                                       BMI_Neg, BMI_Pos, BMI_Check))
head(student, n=5)
```



```
##      Name    Sex Age Height Weight      BMI  BMI_Class
## 1  Alfred   Male  14   69.0  112.5 16.61153 Underweight
## 2   Alice Female  13   56.5   84.0 18.49855 Underweight
## 3 Barbara Female  13   65.3   98.0 16.15679 Underweight
## 4   Carol Female  14   62.8  102.5 18.27090 Underweight
## 5   Henry   Male  14   63.5  102.5 17.87030 Underweight
```

3.5 Sort a data set by a variable.

a) Sort data set by a continuous variable.

```
student <- student[order(student$Age), ]
# Notice that R uses a stable sorting algorithm by default
head(student, n=5)
```

```
##      Name    Sex Age Height Weight      BMI  BMI_Class
## 11  Joyce Female  11   51.3   50.5 13.49000 Underweight
## 18 Thomas   Male  11   57.5   85.0 18.07335 Underweight
## 6   James   Male  12   57.3   83.0 17.77150 Underweight
## 7   Jane Female  12   59.8   84.5 16.61153 Underweight
## 10  John    Male  12   59.0   99.5 20.09437 Healthy
```

b) Sort data set by a categorical variable.

```
student <- student[order(student$Sex), ]
# Notice that the data is now sorted first by Sex and then within Sex by Age
head(student, n=5)
```

```
##      Name    Sex Age Height Weight      BMI  BMI_Class
## 11  Joyce Female  11   51.3   50.5 13.49000 Underweight
## 7   Jane Female  12   59.8   84.5 16.61153 Underweight
## 13 Louise Female  12   56.3   77.0 17.07770 Underweight
## 2   Alice Female  13   56.5   84.0 18.49855 Underweight
## 3   Barbara Female  13   65.3   98.0 16.15679 Underweight
```

`order()`

3.6 Compute descriptive statistics of continuous variables, grouped by a categorical variable.

```
# Notice the syntax of Age, Height, Weight, and BMI as a function of Sex
aggregate(cbind(Age, Height, Weight, BMI) ~ Sex, student, mean)
```

```
##      Sex      Age      Height      Weight      BMI
## 1 Female 13.22222 60.58889  90.11111 17.05104
## 2  Male 13.40000 63.91000 108.95000 18.59424
```

`aggregate() | cbind()`

3.7 Add a new row to the bottom of a data set.

```
# Look at the tail of the data currently
tail(student, n=5)
```

```
##      Name Sex Age Height Weight      BMI BMI_Class
## 1  Alfred Male  14   69.0  112.5 16.61153 Underweight
## 5   Henry Male  14   63.5  102.5 17.87030 Underweight
## 17 Ronald Male  15   67.0  133.0 20.82847   Healthy
## 19 William Male  15   66.5  112.0 17.80451 Underweight
## 15 Philip Male  16   72.0  150.0 20.34144   Healthy

# rbind.data.frame() function binds two data frames together by rows
student <- rbind.data.frame(student, data.frame(Name='Jane', Sex = 'F',
                                                Age = 14, Height = 56.3,
                                                Weight = 77.0,
                                                BMI = 17.077695,
                                                BMI_Class = 'Underweight'))

tail(student, n=5)

##      Name Sex Age Height Weight      BMI BMI_Class
## 5   Henry Male  14   63.5  102.5 17.87030 Underweight
## 17 Ronald Male  15   67.0  133.0 20.82847   Healthy
## 19 William Male  15   66.5  112.0 17.80451 Underweight
## 15 Philip Male  16   72.0  150.0 20.34144   Healthy
## 110 Jane    F  14   56.3   77.0 17.07769 Underweight
```

[data.frame\(\)](#) | [rbind.data.frame\(\)](#)

3.8 Create a user-defined function and apply it to a variable in the data set to create a new variable in the data set.

```
toKG <- function(lb) {
  return(0.45359237 * lb)
}

student$Weight_KG <- toKG(student$Weight)
head(student, n=5)

##      Name Sex Age Height Weight      BMI BMI_Class Weight_KG
## 11 Joyce Female  11   51.3   50.5 13.49000 Underweight  22.90641
## 7   Jane Female  12   59.8   84.5 16.61153 Underweight  38.32856
## 13 Louise Female  12   56.3   77.0 17.07770 Underweight  34.92661
## 2   Alice Female  13   56.5   84.0 18.49855 Underweight  38.10176
## 3  Barbara Female  13   65.3   98.0 16.15679 Underweight  44.45205
```

[user-defined functions](#)

4 More Advanced Data Wrangling

4.1 Drop observations with missing information.

Notice the use of the fish data set because it has some missing observations

```
fish <- read.csv('/Users/fish.csv')
```

First sort by Weight, requesting those with NA for Weight first

```
fish <- fish[order(fish$Weight, na.last=FALSE), ]
```

```
head(fish, n=5)
```

```
##      Species Weight Length1 Length2 Length3 Height Width
## 14    Bream     NA    29.5    32.0    37.3 13.9129 5.0728
## 41    Roach     0.0    19.0    20.5    22.8  6.4752 3.3516
## 73    Perch     5.9     7.5     8.4     8.8  2.1120 1.4080
## 146   Smelt     6.7     9.3     9.8    10.8  1.7388 1.0476
## 148   Smelt     7.0    10.1    10.6    11.6  1.7284 1.1484
```

--

```
new_fish <- na.omit(fish)
```

```
head(new_fish, n=5)
```

```
##      Species Weight Length1 Length2 Length3 Height Width
## 41    Roach     0.0    19.0    20.5    22.8  6.4752 3.3516
## 73    Perch     5.9     7.5     8.4     8.8  2.1120 1.4080
## 146   Smelt     6.7     9.3     9.8    10.8  1.7388 1.0476
## 148   Smelt     7.0    10.1    10.6    11.6  1.7284 1.1484
## 147   Smelt     7.5    10.0    10.5    11.6  1.9720 1.1600
```

```
na.omit()
```

4.2 Merge two data sets together on a common variable.

a) First, select specific columns of a data set to create two smaller data sets.

Notice the use of the student data set again, however we want to reload it without the changes we've made previously

```
student <- read.csv('/Users/class.csv')
```

```
student1 <- subset(student, select=c(Name, Sex, Age))
```

```
head(student1, n=5)
```

```
##      Name Sex Age
## 1  Alfred  M  14
## 2   Alice  F  13
## 3 Barbara  F  13
## 4   Carol  F  14
## 5   Henry  M  14
```

--

```
student2 <- subset(student, select=c(Name, Height, Weight))
head(student2, n=5)
```

```
##      Name Height Weight
## 1  Alfred   69.0  112.5
## 2   Alice   56.5   84.0
## 3 Barbara   65.3   98.0
## 4   Carol   62.8  102.5
## 5   Henry   63.5  102.5
```

b) Second, we want to merge the two smaller data sets on the common variable.

```
new <- merge(student1, student2)
head(new, n=5)
```

```
##      Name Sex Age Height Weight
## 1  Alfred   M  14   69.0  112.5
## 2   Alice   F  13   56.5   84.0
## 3 Barbara   F  13   65.3   98.0
## 4   Carol   F  14   62.8  102.5
## 5   Henry   M  14   63.5  102.5
```

`merge()`

c) Finally, we want to check to see if the merged data set is the same as the original data set.

```
all.equal(student, new)
```

```
## [1] TRUE
```

`all.equal()`

4.3 Merge two data sets together by index number only.

a) First, select specific columns of a data set to create two smaller data sets.

```
newstudent1 <- subset(student, select=c(Name, Sex, Age))
head(newstudent1, n=5)
```

```
##      Name Sex Age
## 1  Alfred   M  14
## 2   Alice   F  13
## 3 Barbara   F  13
## 4   Carol   F  14
## 5   Henry   M  14
```

--

```
newstudent2 <- subset(student, select=c(Height, Weight))
head(newstudent2, n=5)
```

```
##   Height Weight
## 1   69.0   112.5
## 2   56.5    84.0
## 3   65.3    98.0
## 4   62.8   102.5
## 5   63.5   102.5
```

b) Second, we want to join the two smaller data sets.

```
new2 <- cbind(newstudent1, newstudent2)
head(new2, n=5)
```

```
##      Name Sex Age Height Weight
## 1  Alfred  M  14   69.0   112.5
## 2   Alice  F  13   56.5    84.0
## 3 Barbara  F  13   65.3    98.0
## 4   Carol  F  14   62.8   102.5
## 5   Henry  M  14   63.5   102.5
```

c) Finally, we want to check to see if the joined data set is the same as the original data set.

```
all.equal(student, new2)
```

```
## [1] TRUE
```

4.4 Create a pivot table to summarize information about a data set.

```
# Notice we are using a new data set that needs to be read into the
# environment
```

```
price <- read.csv('/Users/price.csv')
```

```
# call the dplyr package
```

```
library(dplyr)
```

```
# The following code is used to remove the ",", and "$" characters from the
# ACTUAL column so that values can be summed
```

```
price$ACTUAL <- gsub('$', '', price$ACTUAL)
```

```
price$ACTUAL <- as.numeric(gsub(',', '', price$ACTUAL))
```

```
filtered = group_by(price, COUNTRY, STATE, PRODTYPE, PRODUCT)
```

```
basic_sum = summarise(filtered, REVENUE = sum(ACTUAL))
```

```
head(basic_sum, n=5)
```

```
## Source: local data frame [5 x 5]
```

```
## Groups: COUNTRY, STATE, PRODTYPE [3]
```

```
##
```

```
##   COUNTRY      STATE  PRODTYPE  PRODUCT  REVENUE
##   <fctr>      <fctr>    <fctr>   <fctr>    <dbl>
## 1 Canada British Columbia FURNITURE    BED 197706.6
## 2 Canada British Columbia FURNITURE    SOFA 216282.6
## 3 Canada British Columbia   OFFICE    CHAIR 200905.2
```

```
## 4 Canada British Columbia OFFICE DESK 186262.2
## 5 Canada Ontario FURNITURE BED 194493.6
```

`dplyr` | `group_by` | `summarise()`

4.5 Return all unique values from a text variable.

```
print(unique(price$STATE))
```

```
## [1] California Colorado Florida
## [4] Illinois New York North Carolina
## [7] Texas Washington Baja California Norte
## [10] Campeche Michoacan Nuevo Leon
## [13] British Columbia Ontario Quebec
## [16] Saskatchewan
## 16 Levels: Baja California Norte British Columbia California ...
Washington
```

`unique()`

In the following sections several data set will be used more than once for prediction and modeling. Often, they will be re-read into the environment so we are always going back to the original, raw data.

5 Preparation & Basic Regression

5.1 Pre-process a data set using principal component analysis.

Notice we are using a new data set that needs to be read into the environment

```
iris <- read.csv('/Users/iris.csv')
features <- subset(iris, select = -c(Target))
```

```
pca <- prcomp(x = features, scale = TRUE)
print(pca)
```

```
## Standard deviations:
```

```
## [1] 1.7061120 0.9598025 0.3838662 0.1435538
##
```

```
## Rotation:
```

```
##          PC1          PC2          PC3          PC4
## SepalLength 0.5223716 -0.37231836 0.7210168 0.2619956
## SepalWidth -0.2633549 -0.92555649 -0.2420329 -0.1241348
## PetalLength 0.5812540 -0.02109478 -0.1408923 -0.8011543
## PetalWidth 0.5656110 -0.06541577 -0.6338014 0.5235463
```

`prcomp()`

5.2 Split data into training and testing data and export as a .csv file.

```
# Set the sample size of the training data
smp_size <- floor(0.7 * nrow(iris))

# set.seed() is used to specify a seed for a random integer so that the
# results are reproducible
set.seed(29)
train_ind <- sample(seq_len(nrow(iris)), size = smp_size)

train <- iris[train_ind, ]
test <- iris[-train_ind, ]

train2 <- read.csv("/Users/iris_train.csv")
test2 <- read.csv("/Users/iris_test.csv")

write.csv(train, file = "/Users/iris_train.csv")
write.csv(test, file = "/Users/iris_test.csv")
```

`floor()` | `nrow()` | `set.seed()` | `sample()` | `seq_len()` | `write.csv()`

5.3 Fit a logistic regression model.

```
# Notice we are using a new data set that needs to be read into the
# environment
tips <- read.csv('/Users/tips.csv')

# The following code is used to determine if the individual left more
# than a 15% tip
tips$fifteen <- 0.15 * tips$total_bill
tips$greater15 <- ifelse(tips$tip > tips$fifteen, 1, 0)

# Notice the syntax of greater15 as a function of total_bill
logreg <- glm(greater15 ~ total_bill, data = tips, family =
"binomial"(link='logit'))
summary(logreg)

##
## Call:
## glm(formula = greater15 ~ total_bill, family = binomial(link = "logit"),
##      data = tips)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -1.6757  -1.1766   0.8145   1.0145   2.0774
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  1.64772    0.35467   4.646 3.39e-06 ***
## total_bill  -0.07248    0.01678  -4.319 1.57e-05 ***
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##      Null deviance: 335.48  on 243  degrees of freedom
## Residual deviance: 313.74  on 242  degrees of freedom
## AIC: 317.74
##
## Number of Fisher Scoring iterations: 4
```

`glm()`

5.4 Fit a linear regression model.

```
# Notice the syntax of tip as function of total_bill
linreg <- lm(tip ~ total_bill, data = tips)
summary(linreg)

##
## Call:
## lm(formula = tip ~ total_bill, data = tips)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -3.1982 -0.5652 -0.0974  0.4863  3.7434
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.920270   0.159735   5.761 2.53e-08 ***
## total_bill   0.105025   0.007365  14.260 < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.022 on 242 degrees of freedom
## Multiple R-squared:  0.4566, Adjusted R-squared:  0.4544
## F-statistic: 203.4 on 1 and 242 DF,  p-value: < 2.2e-16
```

6 Supervised Machine Learning

Many of the following models will make use of the `predict()` function.

6.1 Fit a logistic regression model on training data and assess against testing data.

a) Fit a logistic regression model on training data.

```
# Notice we are using new data sets that need to be read into the environment
train <- read.csv('/Users/tips_train.csv')
test <- read.csv('/Users/tips_test.csv')
```



```

train$fifteen <- 0.15 * train$total_bill
train$greater15 <- ifelse(train$tip > train$fifteen, 1, 0)
test$fifteen <- 0.15 * test$total_bill
test$greater15 <- ifelse(test$tip > test$fifteen, 1, 0)

logreg <- glm(greater15 ~ total_bill, data = train, family =
"binomial"(link='logit'))
summary(logreg)

##
## Call:
## glm(formula = greater15 ~ total_bill, family = binomial(link = "logit"),
##      data = train)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -1.6409  -1.1929   0.8144   1.0027   2.0381
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  1.64613    0.39459   4.172 3.02e-05 ***
## total_bill  -0.07064    0.01849  -3.820 0.000134 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##      Null deviance: 267.61  on 194  degrees of freedom
## Residual deviance: 250.58  on 193  degrees of freedom
## AIC: 254.58
##
## Number of Fisher Scoring iterations: 4

```

b) Assess the model against the testing data.

```

# Prediction on testing data
predictions <- predict(logreg, test, type = 'response')
predY <- ifelse(predictions < 0.5, 0, 1)

# If the prediction probability is less than 0.5, classify this as a 0
# and otherwise classify as a 1. This isn't the best method -- a better
# method would be randomly assigning a 0 or 1 when a probability of 0.5
# occurs, but this insures that results are consistent

# Determine how many were correctly classified
Results <- ifelse(predY == test$greater15, "Correct", "Wrong")
table(Results)

## Results
## Correct Wrong
##      34    15

```

6.2 Fit a linear regression model on training data and assess against testing data.

a) Fit a linear regression model on training data.

```
# Notice we are using new data sets that need to be read into the environment
train <- read.csv('/Users/boston_train.csv')
test <- read.csv('/Users/boston_test.csv')

# Fit a linear regression model
# The "." character tells the model to use all variables except the response
# variable (Target)
linreg <- lm(Target ~ ., data = train)
summary(linreg)

##
## Call:
## lm(formula = Target ~ ., data = train)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -15.6466  -2.8461  -0.5395   1.7077  26.2160
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  36.108196   6.504968   5.551 5.73e-08 ***
## X0           -0.085634   0.042774  -2.002 0.046077 *
## X1            0.046034   0.017150   2.684 0.007626 **
## X2            0.036413   0.076006   0.479 0.632186
## X3            3.247961   1.074138   3.024 0.002686 **
## X4           -14.872938   4.636090  -3.208 0.001463 **
## X5            3.576869   0.536993   6.661 1.10e-10 ***
## X6           -0.008703   0.016853  -0.516 0.605890
## X7           -1.368905   0.252960  -5.412 1.18e-07 ***
## X8            0.313120   0.082366   3.802 0.000170 ***
## X9           -0.012882   0.004599  -2.801 0.005383 **
## X10          -0.976900   0.170996  -5.713 2.43e-08 ***
## X11           0.011326   0.003359   3.372 0.000832 ***
## X12          -0.526715   0.062563  -8.419 1.08e-15 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 4.988 on 340 degrees of freedom
## Multiple R-squared:  0.7236, Adjusted R-squared:  0.7131
## F-statistic: 68.48 on 13 and 340 DF, p-value: < 2.2e-16
```

b) Assess the model against the testing data.

```
# Predict on testing data
prediction = data.frame(matrix(ncol = 0, nrow = nrow(test)))
prediction$predY = predict(linreg, newdata = test)
```

```

# Compute the squared difference between predicted tip and actual tip
prediction$sq_diff <- (prediction$predY - test$Target)**2

# Compute the mean of the squared differences (mean squared error)
# as an assessment of the model
mean_sq_error <- mean(prediction$sq_diff)
print(mean_sq_error)

## [1] 17.77131

```

6.3 Fit a decision tree model on training data and assess against testing data.

a) Fit a decision tree classification model.

i) Fit a decision tree classification model on training data, plot the tree, and determine variable importance.

```

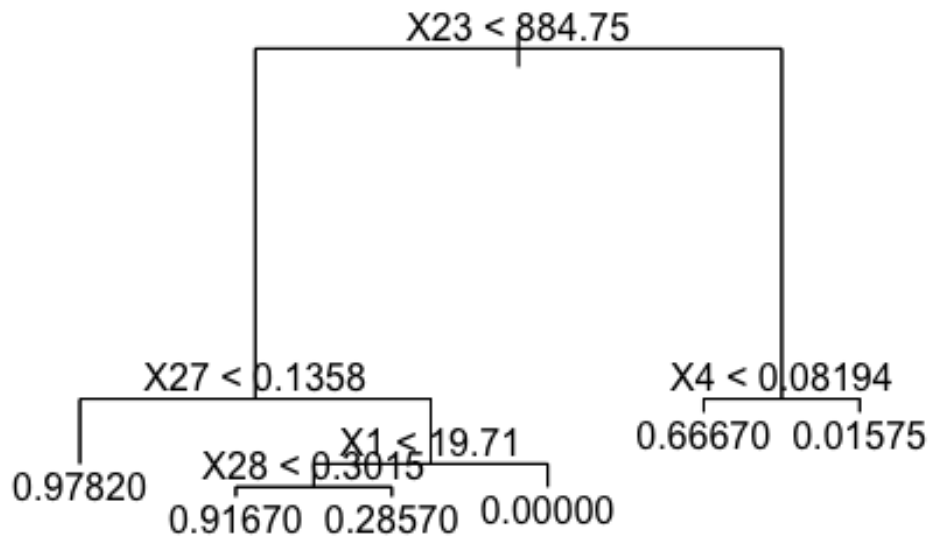
# Notice we are using new data sets that need to be read into the environment
train <- read.csv('/Users/breastcancer_train.csv')
test <- read.csv('/Users/breastcancer_test.csv')

# call the tree package
library(tree)

treeMod <- tree(Target ~ ., data = train, method = "class")

# Plot the decision tree
plot(treeMod)
text(treeMod)

```



```
# Determine variable importance
summary(treeMod)
```

```
##
## Regression tree:
## tree(formula = Target ~ ., data = train, method = "class")
## Variables actually used in tree construction:
## [1] "X23" "X27" "X1" "X28" "X4"
## Number of terminal nodes: 6
## Residual mean deviance: 0.02688 = 10.54 / 392
## Distribution of residuals:
##      Min. 1st Qu.  Median      Mean 3rd Qu.      Max.
## -0.97820 -0.01575  0.02183  0.00000  0.02183  0.98430
```

ii) Assess the model against the testing data.

```
# Prediction on testing data
out <- predict(treeMod, test)
out <- unname(out)
predY <- ifelse(out < 0.5, 0, 1)

# Determine how many were correctly classified
Results <- ifelse(test$Target == predY, "Correct", "Wrong")
table(Results)
```

```
## Results
## Correct   Wrong
##      159      12
```

b) Fit a decision tree regression model.

i) Fit a decision tree regression model on training data, plot the tree, and determine variable importance.

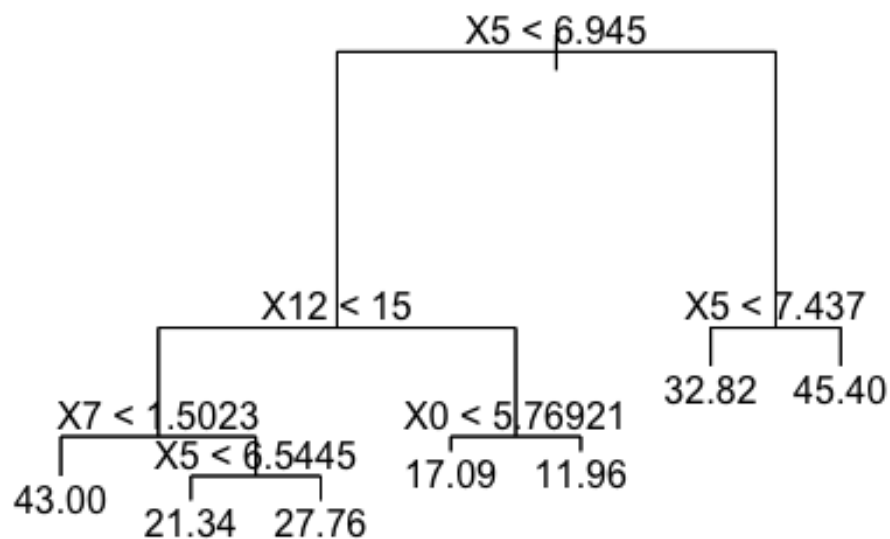
```
train <- read.csv('/Users/boston_train.csv')
test <- read.csv('/Users/boston_test.csv')
```

```
treeMod <- tree(Target ~ ., data = train)
```

Plot the decision tree

```
plot(treeMod)
```

```
text(treeMod)
```



Determine variable importance

```
summary(treeMod)
```

```
##
```

```
## Regression tree:
```

```
## tree(formula = Target ~ ., data = train)
```

```
## Variables actually used in tree construction:
## [1] "X5" "X12" "X7" "X0"
## Number of terminal nodes: 7
## Residual mean deviance: 14.67 = 5091 / 347
## Distribution of residuals:
##      Min. 1st Qu.  Median      Mean 3rd Qu.    Max.
## -28.0000 -1.8070  0.3264   0.0000  2.2320  10.0100
```

ii) Assess the model against the testing data.

```
# Prediction on testing data
prediction = data.frame(matrix(ncol = 0, nrow = nrow(test)))
prediction$predY = predict(treeMod, newdata = test)

# Determine mean squared error
prediction$sq_diff <- (prediction$predY - test$Target)**2
mean_sq_error <- mean(prediction$sq_diff)
print(mean_sq_error)

## [1] 25.12126
```

tree

6.4 Fit a random forest model on training data and assess against testing data.

a) Fit a random forest classification model.

i) Fit a random forest classification model on training data and determine variable importance.

```
train <- read.csv('/Users/breastcancer_train.csv')
test <- read.csv('/Users/breastcancer_test.csv')

# call the randomForest package
library(randomForest)
set.seed(29)

rfMod <- randomForest(as.factor(Target) ~ ., data = train)

# Determine variable importance
var_import <- importance(rfMod)
var_import <- data.frame(sort(var_import, decreasing = TRUE, index.return = TRUE))
var_import$MeanDecreaseGini <- var_import$x
var_import$X <- var_import$ix - 1
var_import <- subset(var_import, select = -c(ix, x))
head(var_import, n=5)

##      MeanDecreaseGini  X
## 1          22.88452 27
```

```
## 2      21.64371  7
## 3      21.56885 22
## 4      20.13103 23
## 5      18.90989 20
```

ii) Assess the model against the testing data.

Prediction on testing data

```
predY <- predict(rfMod, test)
```

Determine how many were correctly classified

```
Results <- ifelse(test$Target == predY, "Correct", "Wrong")
table(Results)
```

```
## Results
## Correct   Wrong
##      166      5
```

b) Fit a random forest regression model.

i) Fit a random forest regression model on training data and determine variable importance.

```
train <- read.csv('/Users/boston_train.csv')
test <- read.csv('/Users/boston_test.csv')
```

call the randomForest package

```
library(randomForest)
set.seed(29)
```

```
rfMod <- randomForest(Target ~ ., data = train)
```

Determine variable importance

```
var_import <- importance(rfMod)
var_import <- data.frame(sort(var_import, decreasing = TRUE, index.return = TRUE))
var_import$MeanDecreaseGini <- var_import$x
var_import$X <- var_import$ix - 1
var_import <- subset(var_import, select = -c(ix, x))
head(var_import, n=5)
```

```
##   MeanDecreaseGini  X
## 1      8662.298 12
## 2      8451.836  5
## 3      2147.288  0
## 4      2105.072  7
## 5      1915.570  2
```

ii) Assess the model against the testing data.

Predict the Target in the testing data

```
prediction = data.frame(matrix(ncol = 0, nrow = nrow(test)))
prediction$predY = predict(rfMod, newdata = test)
```

```
# Determine mean squared error
prediction$sq_diff <- (prediction$predY - test$Target)**2
mean_sq_error <- mean(prediction$sq_diff)
print(mean_sq_error)

## [1] 9.028163
```

randomForest

6.5 Fit a gradient boosting model on training data and assess against testing data.

a) Fit a gradient boosting classification model.

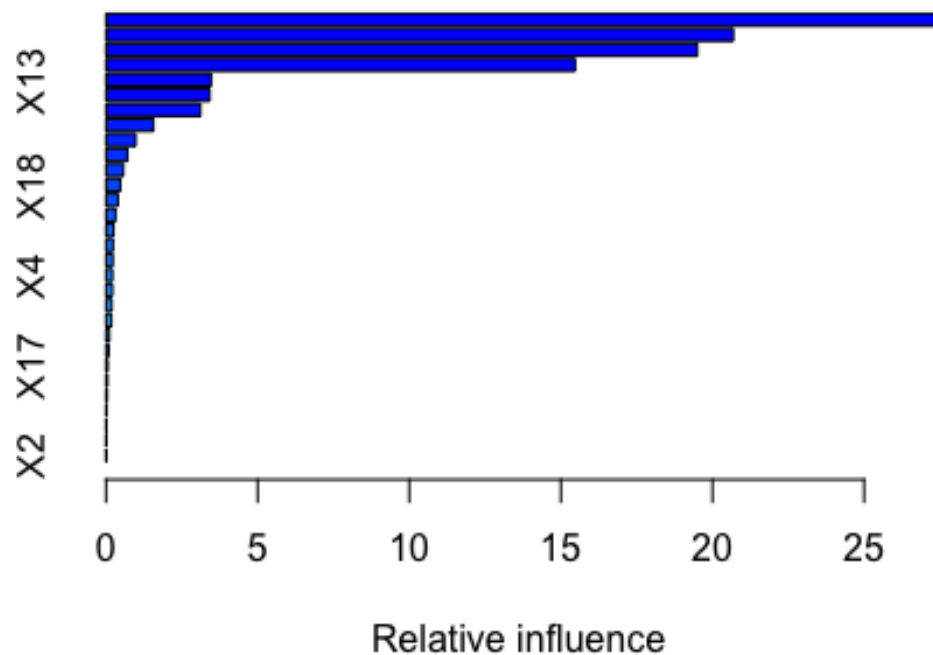
i) Fit a gradient boosting classification model on training data and determine variable importance.

```
train <- read.csv('/Users/breastcancer_train.csv')
test <- read.csv('/Users/breastcancer_test.csv')

# call the gbm package
library(gbm)
set.seed(29)

# distribution = "bernoulli" is appropriate when there are only 2
# unique values
# n.trees = total number of trees to fit which is analogous to the number
# of iterations
# shrinkage = learning rate or step-size reduction, whereas a lower
# learning rate requires more iterations
gbMod <- gbm(Target ~ ., distribution = "bernoulli", data = train,
             n.trees = 2500, shrinkage = .01)

# Determine variable importance
var_import <- summary(gbMod)
```

```
head(var_import, n=5)
```

```
##      var  rel.inf
## X27 X27 27.50103
## X7  X7 20.68575
## X23 X23 19.49976
## X22 X22 15.46766
## X13 X13  3.46162
```

ii) Assess the model against the testing data.

Prediction on testing data

```
out <- predict(object = gbMod, newdata = test,
               type = "response", n.trees = 2500)
predY <- ifelse(out < 0.5, 0, 1)
```

Determine how many were correctly classified

```
Results <- ifelse(test$Target == predY, "Correct", "Wrong")
table(Results)
```

```
## Results
## Correct Wrong
##      167      4
```

b) Fit a gradient boosting regression model.

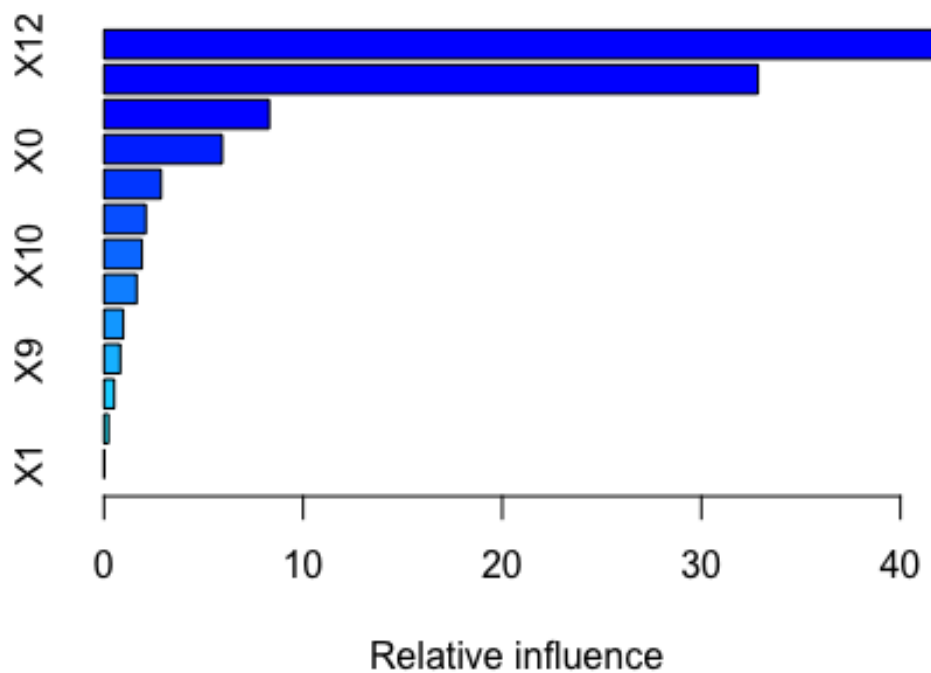
i) Fit a gradient boosting regression model on training data and determine variable importance.

```
train <- read.csv('/Users/boston_train.csv')
test <- read.csv('/Users/boston_test.csv')

# call the gbm package
library(gbm)
set.seed(29)

gbMod <- gbm(Target ~ ., data = train, distribution = "gaussian",
              n.trees = 2500, shrinkage = .01)

# Determine variable importance
var_import <- summary(gbMod)
```



```
head(var_import, n=5)
```

```
##      var  rel.inf
## X12 X12 41.882259
## X5  X5 32.846422
## X7  X7  8.298140
```

```
## X0    X0    5.937391
## X4    X4    2.867877
```

ii) Assess the model against the testing data.

Predict the Target in the testing data, remembering to multiply by 50

```
prediction = data.frame(matrix(ncol = 0, nrow = nrow(test)))
prediction$predY <- predict(object = gbMod, newdata = test,
                           type = "response", n.trees = 2500)
```

Compute mean squared error

```
prediction$sq_diff <- (prediction$predY - test$Target)**2
mean_sq_error <- mean(prediction$sq_diff)
print(mean_sq_error)
```

```
## [1] 11.88728
```

gbm

6.6 Fit an extreme gradient boosting model on training data and assess against testing data.

a) Fit an extreme gradient boosting classification model.

i) Fit an extreme gradient boosting classification model on training data.

```
train <- read.csv('/Users/breastcancer_train.csv')
test <- read.csv('/Users/breastcancer_test.csv')
```

call the xgboost package

```
library(xgboost)
set.seed(29)
```

Fit the model

```
xgbMod <- xgboost(data.matrix(subset(train, select = -c(Target))),
                  data.matrix(train$Target), max_depth = 3, nrounds = 2,
                  objective = "binary:logistic", n_estimators = 2500,
                  shrinkage = .01)
```

```
## [1] train-error:0.037688
```

```
## [2] train-error:0.020101
```

ii) Assess the model against the testing data.

Prediction on testing data

```
predictions <- predict(xgbMod, data.matrix(subset(test, select = -
c(Target))))
predY <- ifelse(predictions < 0.5, 0, 1)
```

Determine how many were correctly classified

```
Results <- ifelse(test$Target == predY, "Correct", "Wrong")
table(Results)
```

```
## Results
## Correct    Wrong
##      165      6
```

b) Fit an extreme gradient boosting regression model.

i) Fit an extreme gradient boosting regression model on training data.

```
train <- read.csv('/Users/boston_train.csv')
test <- read.csv('/Users/boston_test.csv')

# call the xgboost package
library(xgboost)
set.seed(29)

# Fit the model
xgbMod <- xgboost(data.matrix(subset(train, select = -c(Target))),
                  data.matrix(train$Target), max_depth = 3, nrounds = 10,
                  n_estimators = 2500, shrinkage = .01)

## [1] train-rmse:17.131615
## [2] train-rmse:12.419768
## [3] train-rmse:9.116973
## [4] train-rmse:6.777830
## [5] train-rmse:5.182819
## [6] train-rmse:4.113659
## [7] train-rmse:3.403357
## [8] train-rmse:2.955893
## [9] train-rmse:2.677797
## [10] train-rmse:2.485887
```

ii) Assess the model against the testing data.

```
# Predict the target in the testing data, remembering to
# multiply by 50
prediction = data.frame(matrix(ncol = 0, nrow = nrow(test)))
prediction$predY <- predict(xgbMod,
                           data.matrix(subset(test, select = -c(Target))))

# Compute the squared difference between predicted tip and actual tip
prediction$sq_diff <- (prediction$predY - test$Target)**2

# Compute the mean of the squared differences (mean squared error)
# as an assessment of the model
mean_sq_error <- mean(prediction$sq_diff)
print(mean_sq_error)

## [1] 14.27491
```

xgboost

6.7 Fit a support vector model on training data and assess against testing data.

a) Fit a support vector classification model.

i) Fit a support vector classification model on training data.

```
train <- read.csv('/Users/breastcancer_train.csv')
test <- read.csv('/Users/breastcancer_test.csv')

# call the e1071 package
library(e1071)

# Fit a support vector classification model
svMod <- svm(Target ~ ., train, type = 'C-classification', kernel = 'linear')
```

ii) Assess the model against the testing data.

```
# Prediction on testing data
predY <- unname(predict(svMod, subset(test, select = -c(Target))))

# Determine how many were correctly classified
Results <- ifelse(test$Target == predY, "Correct", "Wrong")
table(Results)

## Results
## Correct   Wrong
##      166      5
```

b) Fit a support vector regression model.

i) Fit a support vector regression model on training data.

```
train <- read.csv('/Users/boston_train.csv')
test <- read.csv('/Users/boston_test.csv')
```

```
# call the e1071 package
library(e1071)
```

```
svMod <- svm(Target ~ ., train)
```

ii) Assess the model against the testing data.

```
# Prediction on testing data
prediction = data.frame(matrix(ncol = 0, nrow = nrow(test)))
prediction$predY <- unname(predict(svMod, test))
prediction$sq_diff <- (prediction$predY - test$Target)**2
print(mean(prediction$sq_diff))

## [1] 11.83309
```

e1071 | svm()

6.8 Fit a neural network model on training data and assess against testing data.

a) Fit a neural network classification model.

i) Fit a neural network classification model on training data.

```
train <- read.csv('/Users/digits_train.csv')
test <- read.csv('/Users/digits_test.csv')

trainInputs <- subset(train, select = -c(Target))
testInputs <- subset(test, select = -c(Target))

# call the RSNNS package
library(RSNNS)
set.seed(29)

trainTarget <- decodeClassLabels(train$Target)
testTarget <- decodeClassLabels(test$Target)

nnMod <- mlp(trainInputs, trainTarget, inputsTest=testInputs,
targetsTest=testTarget, size = 100, maxit = 200)
```

ii) Assess the model against the testing data.

```
# Prediction on testing data
predictions <- predict(nnMod, testInputs)

# Determine how many were correctly classified
confusionMatrix(testTarget, predictions)

##           predictions
## targets  1  2  3  4  5  6  7  8  9 10
##      1  55  0  0  0  1  0  1  1  0  0
##      2   0 54  2  0  0  0  1  0  1  0
##      3   0  0 58  0  0  0  0  0  0  0
##      4   0  0  0 56  0  1  0  2  0  0
##      5   0  0  0  0 53  0  0  0  1  0
##      6   0  0  0  0  0 58  1  0  0  0
##      7   0  0  0  0  0  0 41  0  0  0
##      8   0  1  0  0  0  0  0 49  0  1
##      9   1  3  0  3  0  0  0  0 36  2
##     10   0  1  0  0  0  1  0  2  1 52
```

`confusionMatrix()`

a) Fit a neural network regression model.

i) Fit a neural network regression model on training data.

```
train <- read.csv('/Users/boston_train.csv')
test <- read.csv('/Users/boston_test.csv')
```

```

# call the RSNNS package
library(RSNNS)
set.seed(29)

# Scale input data
scaled_train <- data.frame(scale(subset(train, select = -c(Target))))
scaled_test <- data.frame(scale(subset(test, select = -c(Target))))

# Fit neural network regression model, dividing target by 50 for scaling
nnMod <- mlp(scaled_train, train$Target / 50, inputsTest=scaled_test,
targetsTest=test$Target / 50, maxit = 1000)

```

scale()

```

# Assess against testing data, remembering to multiply by 50
preds = data.frame(matrix(ncol = 0, nrow = nrow(test)))
preds$predY <- predict(nnMod, scaled_test)*50
preds$sq_error <- (preds$predY - test$Target)**2
print(mean(preds$sq_error))

## [1] 20.27705

```

RSNNS

7 Unsupervised Machine Learning

7.1 KMeans Clustering

```

iris = read.csv('/Users/iris.csv')

iris$Species = ifelse(iris$Target == 0, "Setosa",
                     ifelse(iris$Target == 1, "Versicolor", "Virginica"))

features <- as.matrix(subset(iris, select = c(PetalLength, PetalWidth,
SepalLength, SepalWidth)))

set.seed(29)

kmeans <- kmeans(features, 3, nstart = 20)

table(iris$Species, kmeans$cluster)

##
##          1  2  3
## Setosa      0  0 50
## Versicolor 48  2  0
## Virginica  14 36  0

```

7.2 Spectral Clustering

```
library(kernlab)
set.seed(29)

spectral <- specc(features, centers = 3, iterations = 10, nystrom.red = TRUE)

labels <- as.data.frame(spectral)

table(iris$Species, labels$spectral)

##
##           1  2  3
## Setosa      50  0  0
## Versicolor  0 47  3
## Virginica   0  3 47
```

[kernlab](#) | `specc()`

7.3 Ward Hierarchical Clustering

```
set.seed(29)

hclust <- hclust(dist(features), method = "ward.D2")

table(iris$Species, cutree(hclust, 3))

##
##           1  2  3
## Setosa      50  0  0
## Versicolor  0 49  1
## Virginica   0 15 35
```

[Hierarchical Clustering in R](#)

7.4 DBSCAN

```
set.seed(29)

library(dbSCAN)

# eps = 0.5 is default in Python
dbscan <- dbSCAN(features, eps = 0.5)

table(iris$Species, dbscan$cluster)

##
##           0  1  2
## Setosa      1 49  0
## Versicolor  6  0 44
## Virginica  10  0 40
```


dbscan

7.5 Self-organized map

Seed chosen to match SAS and R results

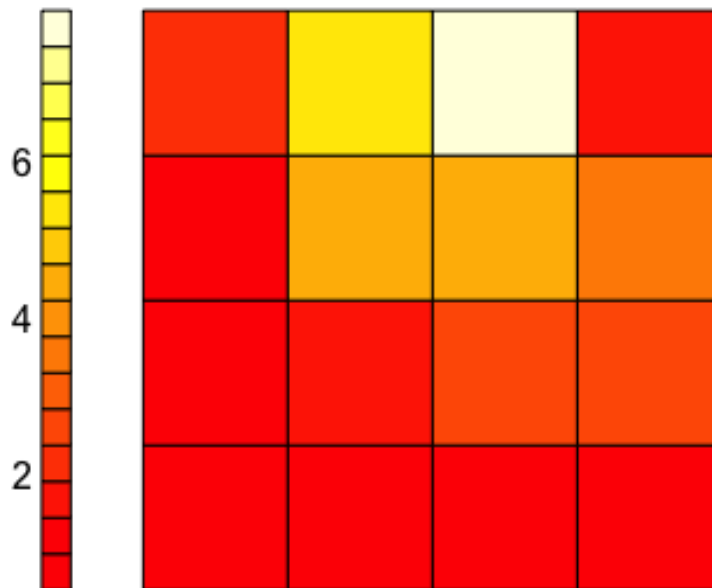
```
set.seed(5)
```

```
library(kohonen)
```

```
fit <- som(features, mode = "online", somgrid(4, 4, "rectangular"))
```

```
plot(fit, type = "dist.neighbour", shape = "straight")
```

Neighbour distance plot



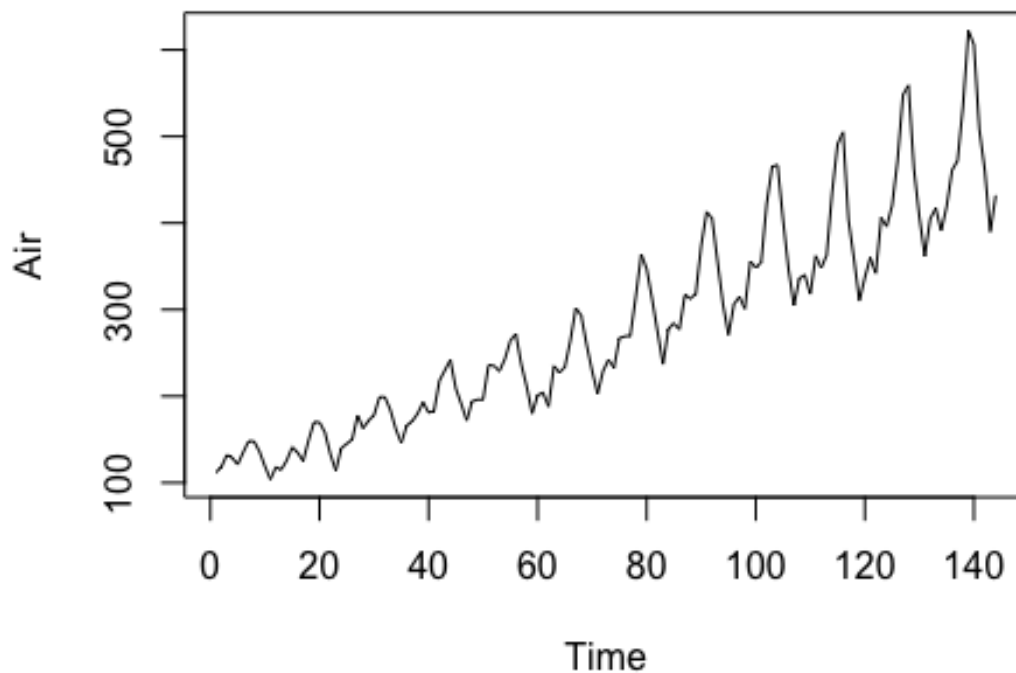
kohonen

8 Forecasting

8.1 Fit an ARIMA model to a timeseries.

a) Plot the timeseries.

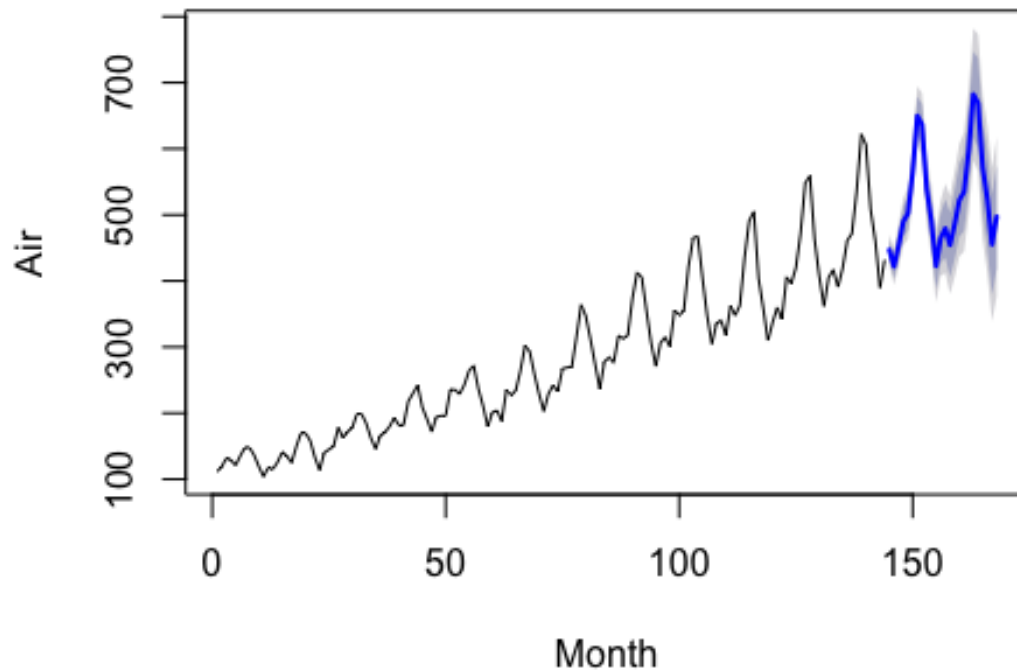
```
air <- read.csv('/Users/air.csv')  
  
air_series <- air$AIR  
  
plot.ts(air_series, ylab="Air")
```



b) Fit an ARIMA model, predict 2 years (24 months) out and plot predictions.

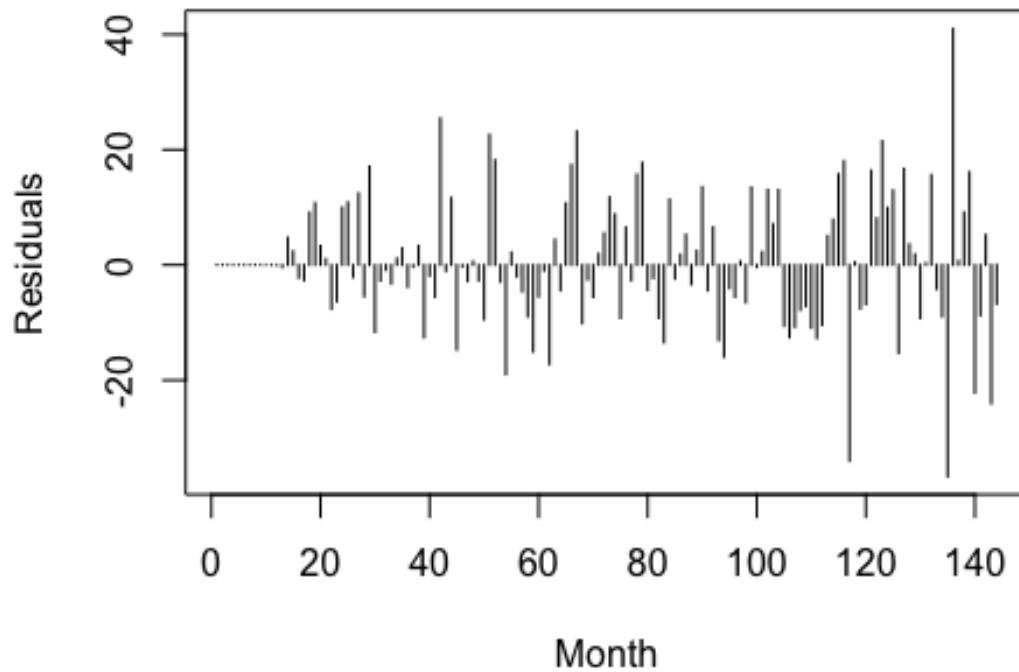
```
a_fit <- arima(air_series, order = c(0,1,1), seasonal = list(order =  
c(0,1,1), period = 12), method = "ML")  
  
library(forecast)  
  
a_forecast <- forecast(a_fit, 24)  
  
plot(a_forecast, xlab = "Month", ylab = "Air")
```

Forecasts from ARIMA(0,1,1)(0,1,1)[12]



c) Plot residuals of predictions and known values.

```
plot(a_fit$residuals, xlab = "Month", ylab = "Residuals", type = 'h')
```

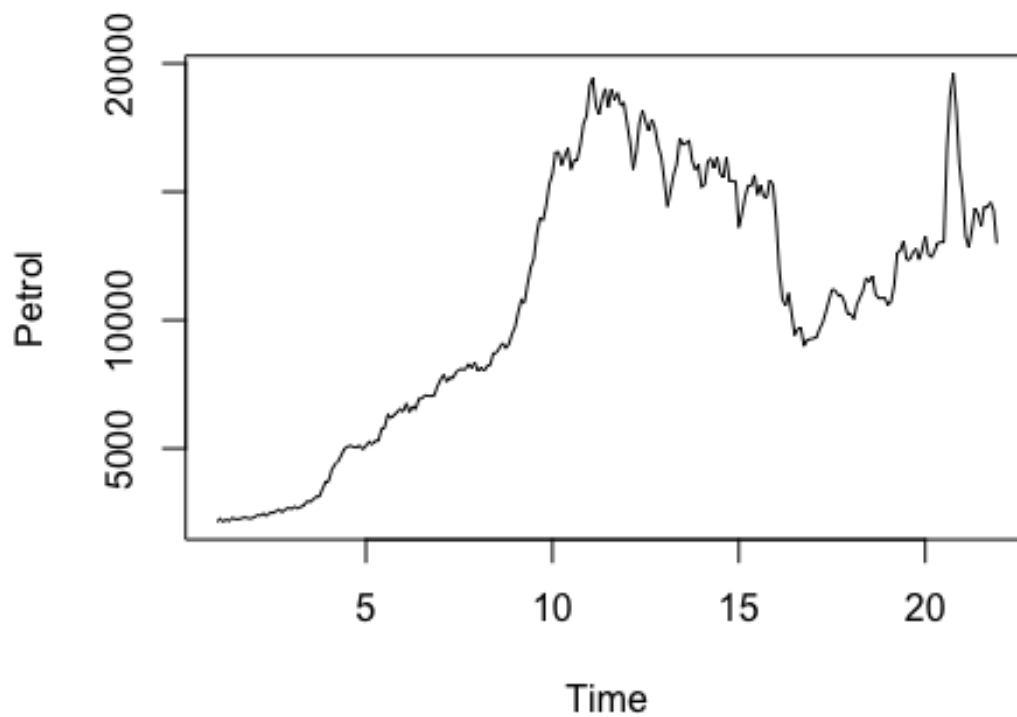


forecast

8.2 Fit a Simple Exponential Smoothing model to a timeseries.

a) Plot the timeseries.

```
usecon <- read.csv('/Users/usecon.csv')  
  
petrol_series <- usecon$PETROL  
  
petrol <- ts(petrol_series, frequency = 12)  
  
plot.ts(petrol, ylab="Petrol")
```



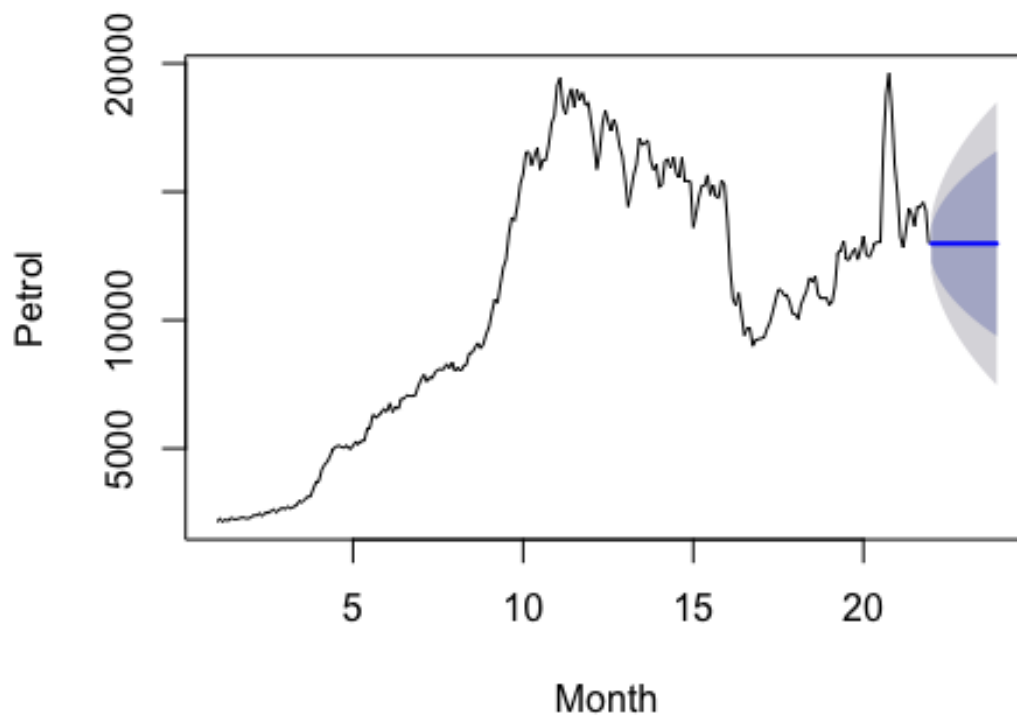
b) Fit a Simple Exponential Smoothing model, predict 2 years (24 months) out and plot predictions.

```
library(forecast)
```

```
ses_fit <- ses(petrol, h=24, alpha = 0.9999)
```

```
plot(ses_fit, xlab = "Month", ylab = "Petrol")
```

Forecasts from Simple exponential smoothing



forecast

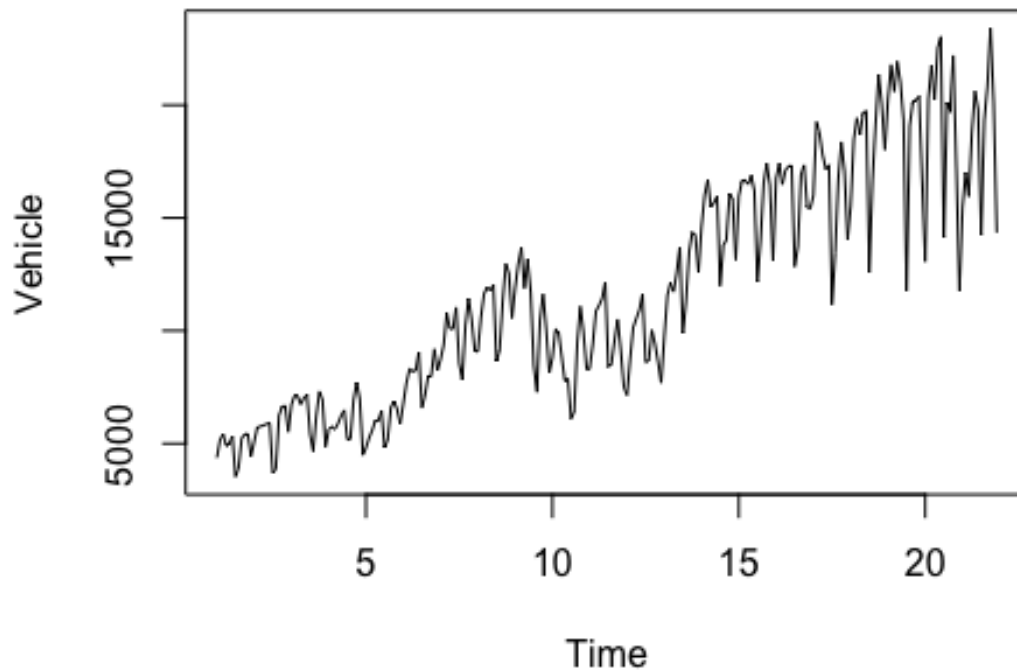
8.3 Fit a Holt-Winters model to a timeseries.

a) Plot the timeseries.

```
vehicle_series <- usecon$VEHICLES
```

```
vehicle <- ts(vehicle_series, frequency = 12)
```

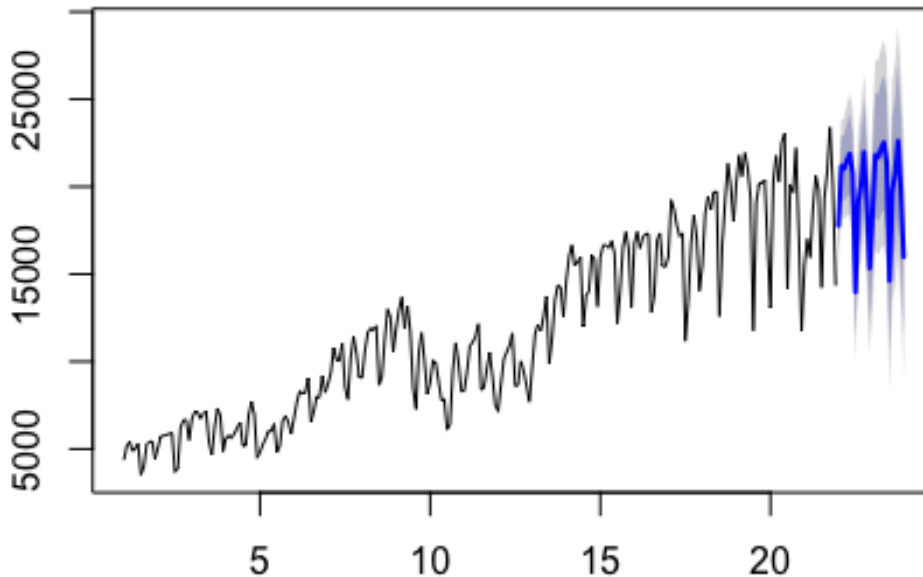
```
plot.ts(vehicle, ylab="Vehicle")
```



b) Fit a Holt-Winters additive model, predict 2 years (24 months) out and plot predictions.

```
add_fit <- HoltWinters(vehicle, seasonal = "additive")  
add_forecast <- forecast(add_fit, 24)  
plot(add_forecast)
```

Forecasts from HoltWinters



9 Model Evaluation & Selection

9.1 Evaluate the accuracy of regression models.

a) Evaluation on training data.

```
train <- read.csv('/Users/boston_train.csv')
test <- read.csv('/Users/boston_test.csv')

# Random Forest Regression Model
set.seed(29)
rfMod <- randomForest(Target ~ ., data = train)

# Evaluation on training data
predY <- predict(rfMod, train)
predY <- unname(predY)

# Determine coefficient of determination score
r2_rf <- 1 - ( (sum((train$Target - predY)**2)) / (sum((train$Target -
mean(train$Target))**2)) )
```



```
print(paste0("Random forest regression model r^2 score (coefficient of
determination): ", r2_rf))
```

```
## [1] "Random forest regression model r^2 score (coefficient of
determination): 0.972080769152132"
```

```
unnname()
```

b) Evaluation on testing data.

```
# Random Forest Regression Model (rfMod)
```

```
# Evaluation on testing data
```

```
predY <- predict(rfMod, test)
predY <- unname(predY)
```

```
# Determine coefficient of determination score
```

```
r2_rf = 1 - ( (sum((test$Target - predY)**2)) / (sum((test$Target -
mean(test$Target)**2)) )
```

```
print(paste0("Random forest regression model r^2 score (coefficient of
determination): ", r2_rf))
```

```
## [1] "Random forest regression model r^2 score (coefficient of
determination): 0.886681832095677"
```

The formula used here for the coefficient score is based off the Python sklearn formula for [r2_score](#). For more information about model assessment in R, please review information about the R package [caret](#).

9.2 Evaluate the accuracy of classification models.

a) Evaluation on training data.

```
train <- read.csv('/Users/digits_train.csv')
test <- read.csv('/Users/digits_test.csv')
```

```
set.seed(29)
```

```
# Random Forest Classification Model
```

```
rfMod <- randomForest(as.factor(Target) ~ ., data = train)
```

```
# Evaluation on training data
```

```
predY <- predict(rfMod, train)
predY <- unname(predY)
```

```
# Determine accuracy score
```

```
accuracy_rf <- (1/nrow(train)) * sum(as.numeric(predY == train$Target))
print(paste0("Random forest model accuracy: ", accuracy_rf))
```

```
## [1] "Random forest model accuracy: 1"
```

b) Evaluation on testing data.

```
# Random Forest Classification Model (rfMod)

# Evaluation on testing data
predY <- predict(rfMod, test)
predY <- unname(predY)

# Determine accuracy score
accuracy_rf <- (1/nrow(test)) * sum(as.numeric(predY == test$Target))
print(paste0("Random forest model accuracy: ", accuracy_rf))

## [1] "Random forest model accuracy: 0.974074074074074"
```

The formula used here for the accuracy score is based off the Python sklearn formula for [accuracy_score](#). For more information about model assessment in R, please review information about the R package [caret](#).

9.3 Evaluation with cross validation.

a) KFold

```
# Notice we are using a new data set that needs to be read into the
# environment
breastcancer = read.csv('/Users/breastcancer.csv')

# call the caret and randomForest packages
library(caret)
library(randomForest)

set.seed(29)

# Create the 5 cross validation folds
train_control <- trainControl(method = "cv", number = 5, savePredictions =
TRUE)

# Convert Target into a factor variable for the random forest model
breastcancer$Target <- factor(breastcancer$Target, levels = c(1,0),
                             labels = c(1, 0))

# Train the model, using the 5 cross validation folds
model <- train(Target~., data = breastcancer, trControl = train_control,
               method = "rf")

# Assess the accuracy of the model
tab <- model$pred
tab$correct <- (tab$pred == tab$obs)
tab$correct_num <- ifelse(tab$correct=="TRUE", 1, 0)
aggdata <- unname(as.matrix(aggregate(correct_num ~ Resample, tab, sum)))
aggdata <- as.numeric(aggdata[,2])
counts <- unname(table(tab$Resample))
```

```

accuracy <- c(0,0,0,0,0)
for (i in 1:5) {
  accuracy[i] <- aggdata[i]/counts[i]
}

print(paste0("Accuracy: ", round(mean(accuracy)*100, digits=2), "% +/- ",
      round(sd(accuracy)*100, digits=2), "%"))

## [1] "Accuracy: 95.77% +/- 1.68%"

```

caret

b) ShuffleSplit

```

# call the caret and randomForest packages
library(caret)
library(randomForest)

set.seed(29)

X = subset(breastcancer, select = -c(Target))
Y = breastcancer$Target

# Create the data partition
trainIndex <- createDataPartition(Y, times = 5, p = 0.7, list = FALSE)
accuracy <- c(0, 0, 0, 0, 0)

for (i in 1:5) {
  nam <- paste("data_train", i, sep = "")
  assign(nam, breastcancer[trainIndex[,i],])
  nam <- paste("data_test", i, sep = "")
  assign(nam, breastcancer[-trainIndex[,i],])
}

data_train <- list(data_train1, data_train2, data_train3, data_train4,
  data_train5)
data_test <- list(data_test1, data_test2, data_test3, data_test4, data_test5)

# Train the model and assess the accuracy
for (i in 1:5) {
  fit <- randomForest(as.factor(Target) ~ ., data = data_train[[i]])
  Prediction <- predict(fit, data_test[[i]])
  Prediction <- unname(Prediction)
  correct <- (data_test[[i]]$Target == Prediction)
  counts <- unname(table(correct))
  accuracy[i] <- counts[2] / sum(counts)
}

print(paste0("Accuracy: ", round(mean(accuracy)*100, digits=2), "% +/- ",
      round(sd(accuracy)*100, digits=2), "%"))

```

```
## [1] "Accuracy: 96.24% +/- 0.53%"
```

`createDataPartition`

10 Text Analytics

11 Deep Learning

Appendix

1 Built-in R Objects

Vectors

- Logical
- Numeric
- Integer
- Complex
- Character
- Raw

Lists

Matrices

Arrays

Factors

Data Frames

2 R packages used in this tutorial

`gdata`

Data manipulation

`rjson`

Converting R objects into JSON objects, and JSON objects into R objects

ggplot2

Visualizations and graphics

dplyr

Working with **data frame** like objects

tree

Decision trees models

randomForest

Random forest models

gbm

Gradient boosting models

xgboost

Extreme gradient boosting models

e1071

Support vector machine models

RSNNS

Neural network models

kernlab

Spectral clustering

dbscan

DBSCAN clustering

kohonen

Supervised and unsupervised self-organizing maps

forecast

Displaying and analyzing time series for forecasting

caret

Training and plotting classification and regression models

Alphabetical Index

Array

A one-dimensional data frame. Please see the following example of array creation and access:

```
my_array <- c(1, 3, 5, 9)
print(my_array)

## [1] 1 3 5 9

print(my_array[1])

## [1] 1
```

Data Frame

An R Data Frame is a two-dimensional tabular structure with labeled axes (rows and columns), where data observations are represented by rows and data variables are represented by columns.

Dictionary

A dictionary is an associative array which is indexed by keys which map to values. Therefore, a dictionary is an unordered set of key:value pairs where each key is unique. In R, a dictionary can be implemented using a [named list](#). Please see the following example of named list creation and access:

```
student <- read.csv('/Users/class.csv')
values <- student$Age
names(values) <- student$Name
print(values["James"])

## James
##      12
```

List

An R list is a sequence of comma-separated objects that need not be of the same type. Please see the following example of list creation and access:

```
list1 <- list('item1', 102)
print(list1)

## [[1]]
## [1] "item1"
##
## [[2]]
## [1] 102
```

```
print(list1[1])  
## [[1]]  
## [1] "item1"
```

Vector

A one-dimensional data structure which is able to hold different classes of elements, but only one class per vector.

For more information on R packages and functions, along with helpful examples, please see [R](#).