R Tutorial

In R, comments are indicated in code with a "#" character.

1 Reading in Data and Basic Statistical Functions

1.1 Read in the data.

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

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

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

First we need to install the gdata package, and then call the package to use.

```r
# The package we need to read in a .xls file (gdata) must first be
# installed and then called to use
library(gdata)

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

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

First we need to install the rjson (install.packages(pkgs='rjson')), and then call the package to use. 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.

```r
# The package we need to read in a .json file (rjson) must first be
# installed and then called to use
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
```

1.2 Find the dimensions of the data set.

Information about 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.

```
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
```

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
```

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
```

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.

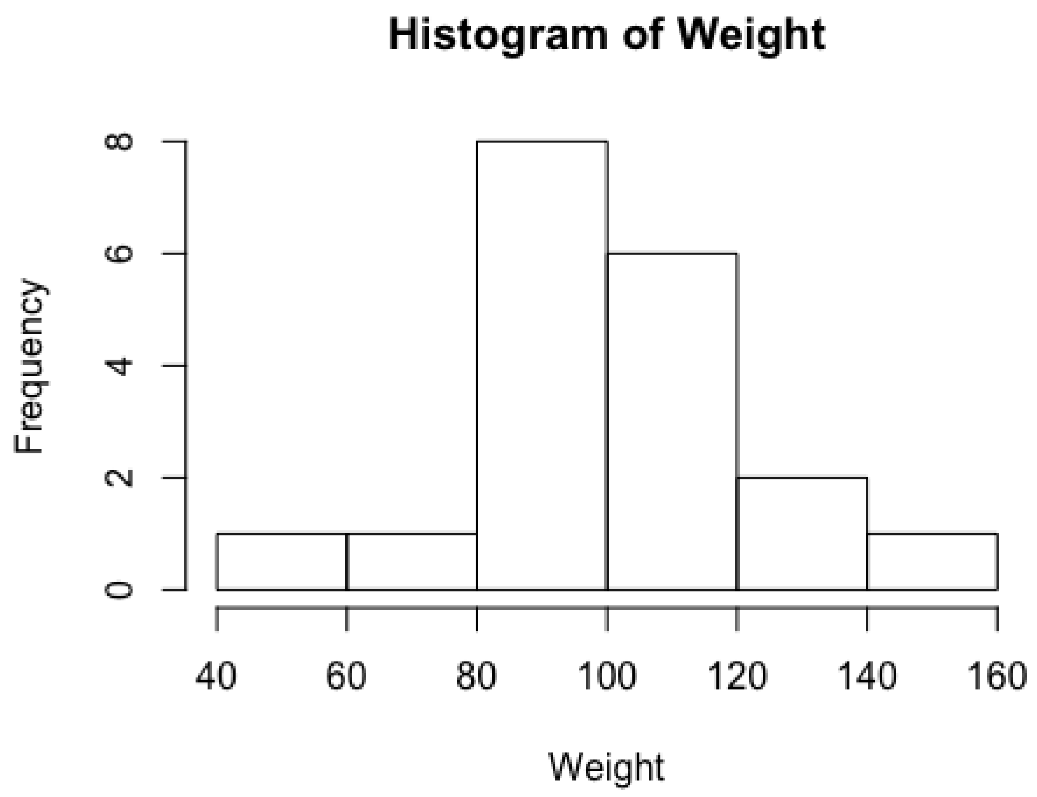
```
height_weight <- subset(student, select = c(Height, Weight))
cor(height_weight, method = "pearson")

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

cor()

2 Basic Graphing and Plotting Functions

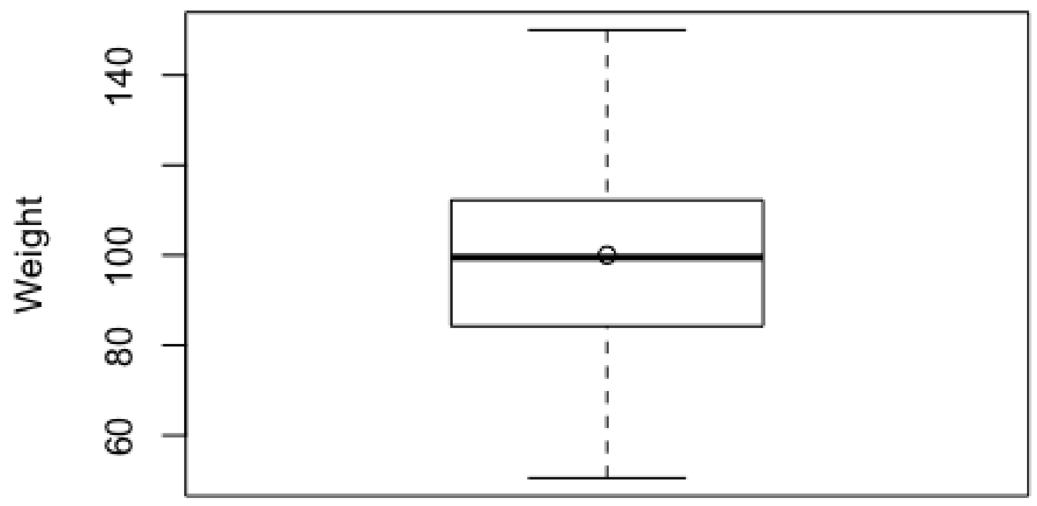
2.1 Visualize a single continuous variable by producing a histogram.

```
# Setting student$Weight to a new variable “Weight” cleans up the labeling of
# the histogram
Weight <- student$Weight
hist(Weight)
```



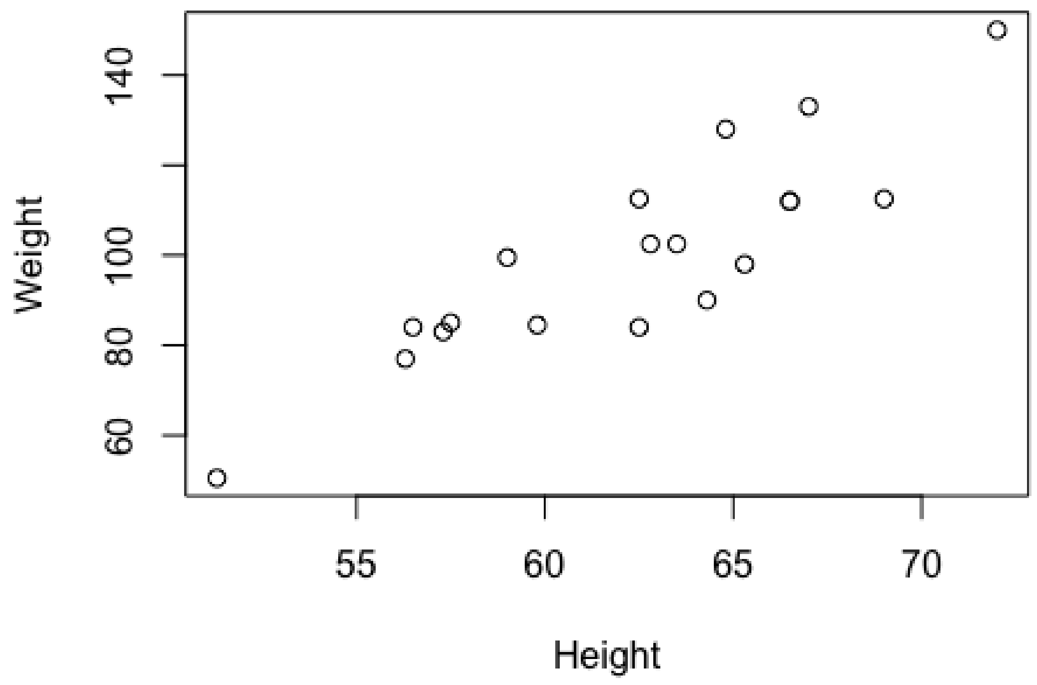
2.2 Visualize a single continuous variable by producing a boxplot.

```
# points(mean(Weight)) tells R to plot the mean of the variable
# on the boxplot
boxplot(Weight, ylab="Weight")
points(mean(Weight))
```



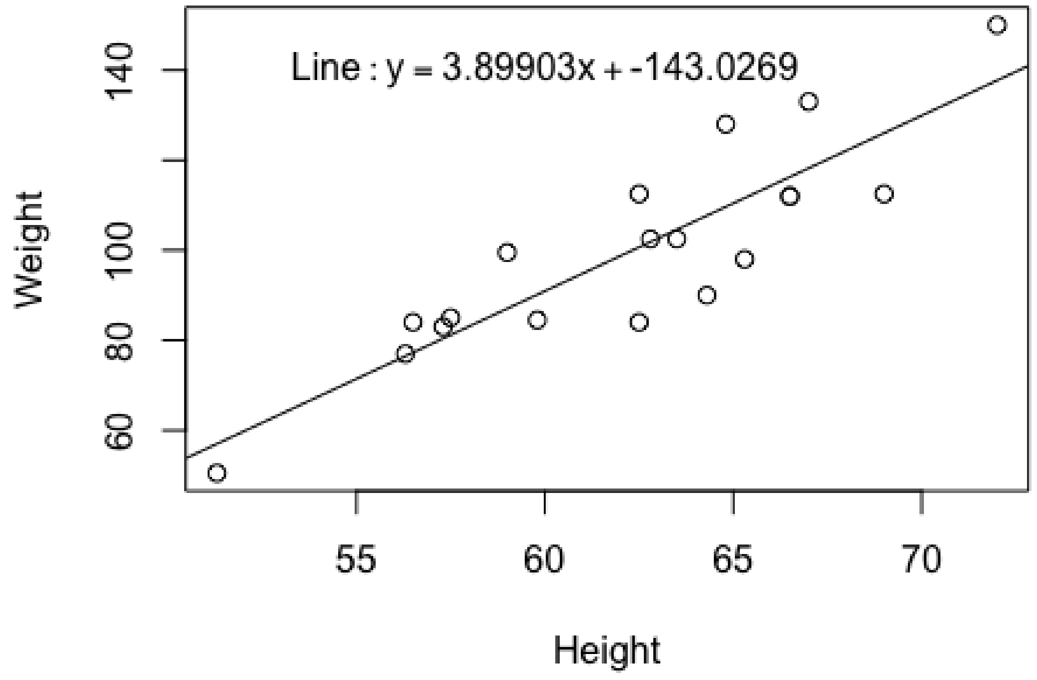
2.3 Visualize two continuous variables by producing a scatterplot.

```
Height <- student$Height
# Notice here you specify the x variable first and then the y variable
plot(Height, Weight)
```



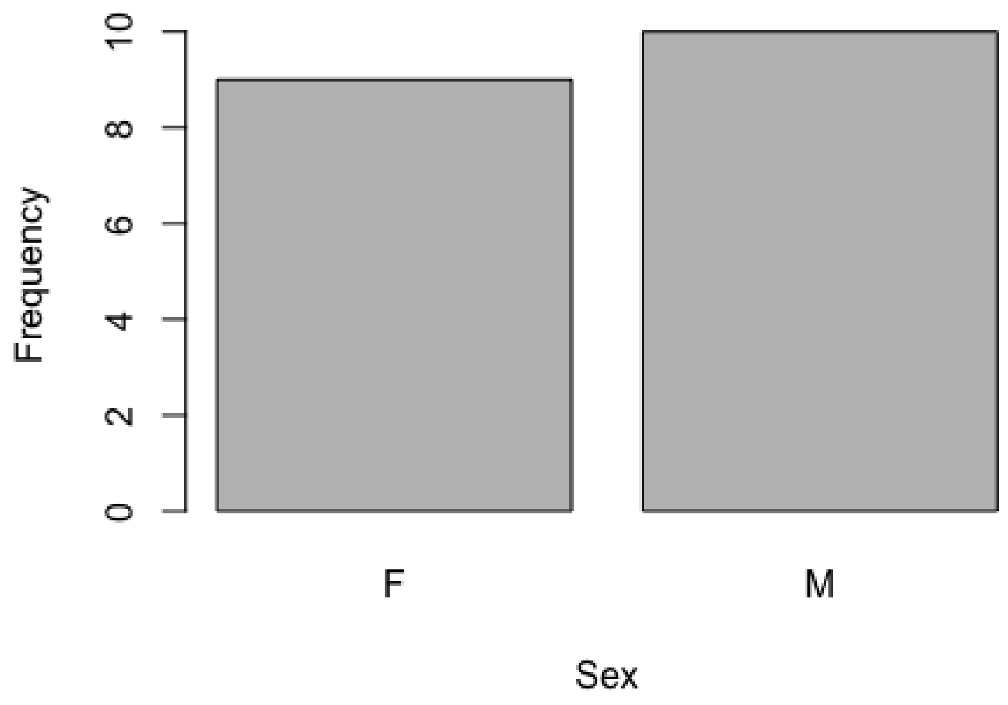
2.4 Visualize a relationship between two continuous variables by producing a scatterplot and a plotted line of best fit.

```
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)))
```



2.5 Visualize a categorical variable by producing a bar chart.

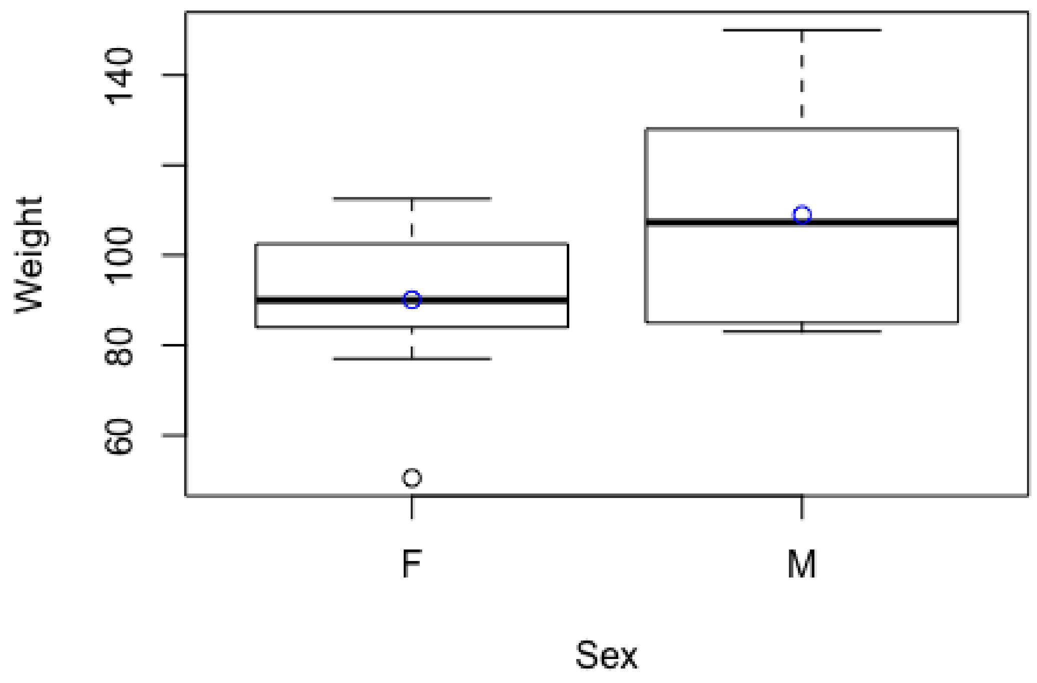
```
counts <- table(student$Sex)
# beside = TRUE indicates to print the bars side by side instead of on top of
# each other
# names.arg indicates which names to use to label the bars
barplot(counts, beside=TRUE, ylab= "Frequency", xlab= "Sex",
names.arg=names(counts))
```



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

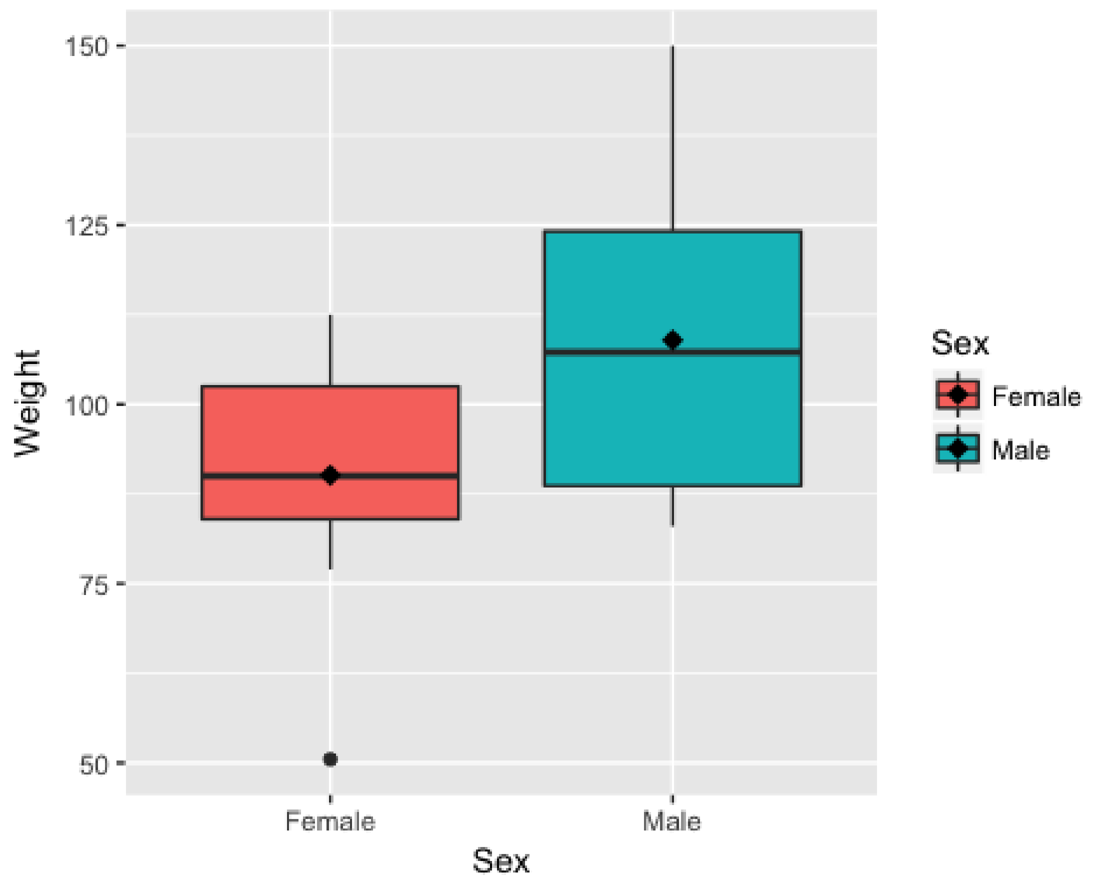
a) Simple side-by-side boxplot without color.

```r
# 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.

```r
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

---

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 if 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 mathemtical functions applied to existing variables in the data set.

Using the log() function, the exp() function, the sqrt() function, and the abs() function.

```
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 1
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
```

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
```

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
```

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
```

---

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
```

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
```

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
```

merge()

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
```

cbind()

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

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

# The package we need to fix the ACTUAL column (dplyr) must first be
# installed and then called to use
require(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

---

5 Regression & Modeling

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

```r
# 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
## sepal.length..cm.  0.5223716 -0.37231836  0.7210168  0.2619956
## sepal.width..cm.  -0.2633549 -0.92555649 -0.2420329 -0.1241348
## petal.length..cm.  0.5812540 -0.02109478 -0.1408923 -0.8011543
## petal.width..cm.   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, ]

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

sample()

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
reg <- glm(greater15 ~ total_bill, data = tips, family =
"binomial"(link='logit'))
summary(reg)
```

```
##
## 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 on training data and assess against testing data.

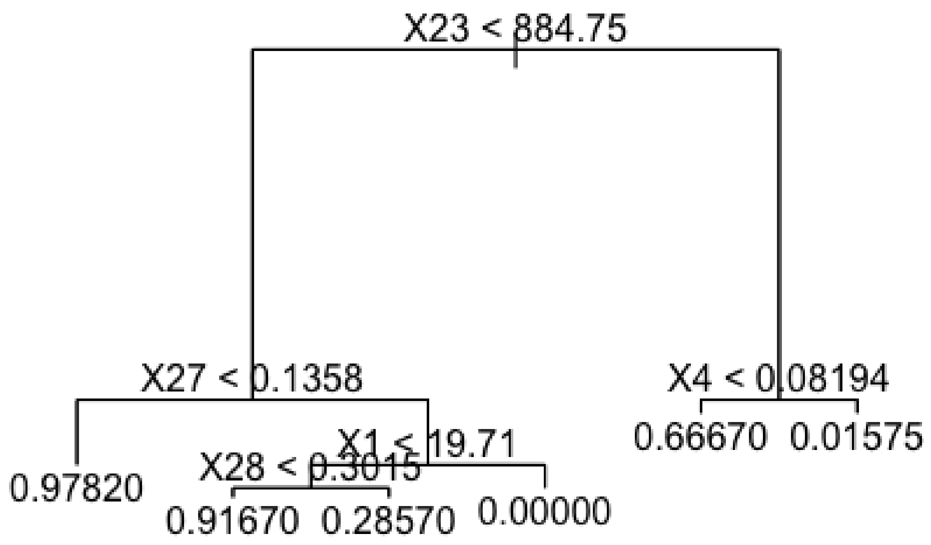
```
# Notice we are using new data sets that need to be read into the environment
train <- read.csv('/Users/tips_train.csv')
test <- read.csv('/Users/tips_test.csv')

# Fit a linear regression model of tip by total_bill on the training data
m <- lm(tip ~ total_bill, data = train)

# Predict the tip based on the total_bill given in the testing data
prediction = data.frame(matrix(ncol = 0, nrow = nrow(test)))
prediction$tip_hat = predict(m, newdata = test)

# Compute the squared difference between predicted tip and actual tip
prediction$diff <- (prediction$tip_hat - test$tip)**2

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

## [1] 1.087594
```

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

a) Fit a decision tree model on training data and do not prune the model before assessing against testing data.

i. Assess the model against the 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')

# The package we need to fit a tree model (tree) must first be
# installed and then called to use
library(tree)

# The "." character tells the model to use all variables except the response
# variabe (Target)
treeMod <- tree(Target ~ ., data = train)

# Prediction on training data
out <- predict(treeMod)
out <- unname(out)

# 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
# occurrs, but this insures that results are consistent.
pred.response <- ifelse(out < 0.5, 0, 1)

# Determine how many were correctly classified
correct <- (train$Target == pred.response)
table(correct)

## correct
## FALSE  TRUE
##    12   386

# 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] "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.

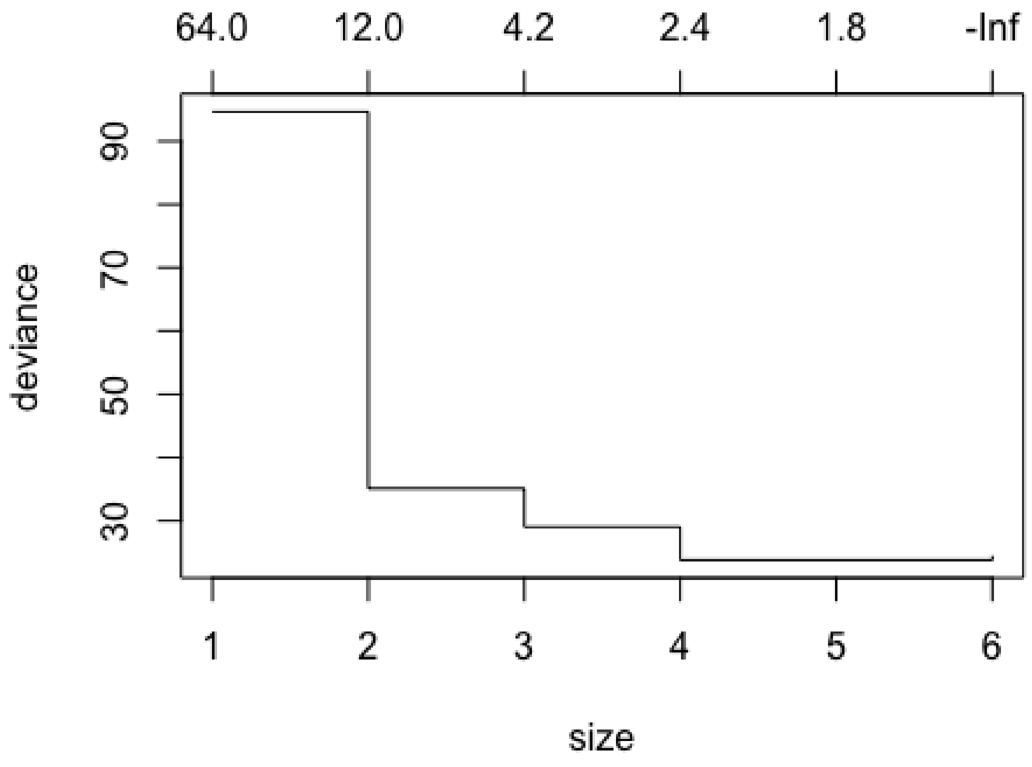
```
# Prediction on testing data
out <- predict(treeMod, test)
out <- unname(out)
pred.response <- ifelse(out < 0.5, 0, 1)

# Determine how many were correctly classified
correct <- (test$Target == pred.response)
table(correct)
```

```
## correct
## FALSE  TRUE
##    12   159
```

b) Fit a decision tree model on training data and prune the model before assessing against testing data.

i. Assess the model against the training data, plot the tree, and determine variable importance.

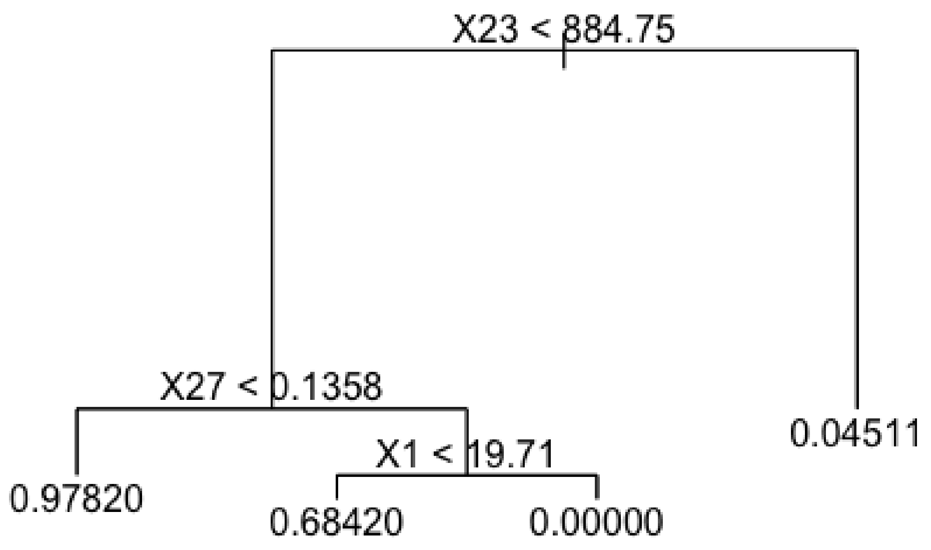
```
treeMod <- tree(Target ~ ., data = train)

# Run the cross validation to determine where to prune
cvTree <- cv.tree(treeMod, rand = c(1,0), FUN = prune.tree)

# Plot to see where to prune
plot(cvTree)
```



```
# Set size corresponding to lowest value in below plot
treePrunedMod <- prune.tree(treeMod, best = 4)

# Prediction on training data
out <- predict(treePrunedMod)
out <- unname(out)

pred.response <- ifelse(out < 0.5, 0, 1)

# Determine how many were correctly classified
correct <- (train$Target == pred.response)
table(correct)
```

```
## correct
## FALSE  TRUE
##    17   381
```

```
# Plot the decision tree
plot(treePrunedMod)
text(treePrunedMod)
```



ii. Assess the model against the testing data.

```
# Prediction on testing data
out <- predict(treePrunedMod, test)
out <- unname(out)
pred.response <- ifelse(out < 0.5, 0, 1)

# Determine how many were correctly classified
```

```
correct <- (test$Target == pred.response)
table(correct)

## correct
## FALSE  TRUE
##     8   163
```

tree

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

a) Build a model, determine variable importance, and assess the model against the training data.

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

# The package we need to fit a random forest model (randomForest) must
# first be installed and then called to use
require(randomForest)
set.seed(29)

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

# Determine variable importance
importance(fit)

##                   MeanDecreaseGini
## sepal.length..cm.         7.063303
## sepal.width..cm.          1.680818
## petal.length..cm.        30.229582
## petal.width..cm.         30.288231

# Prediction on training data
Prediction <- predict(fit, train)
Prediction <- unname(Prediction)

# Determine how many were correctly classified
correct <- (train$Target == Prediction)
table(correct)

## correct
## TRUE
##  105
```

b) Assess the model against the testing data.

```
# Prediction on testing data
Prediction <- predict(fit, test)
Prediction <- unname(Prediction)

# Determine how many were correctly classified
correct <- (test$Target == Prediction)
table(correct)

## correct
## FALSE  TRUE
##     4    41
```

randomForest

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

a) Build a model and assess the model against the training data.

```
# Notice we are re-using data sets but it is good to re-read the original
# version back into the environment
train <- read.csv('/Users/tips_train.csv')
test <- read.csv('/Users/tips_test.csv')

set.seed(29)

fit <- randomForest(tip ~ total_bill, data = train)

# Prediction on training data
Prediction <- predict(fit, train)
Prediction <- unname(Prediction)

# Determine mean squared error
diff <- (train$tip - Prediction)**2
mean(diff)

## [1] 0.349471
```

b) Assess the model against the testing data.

```
# Prediction on testing data
Prediction <- predict(fit, test)
Prediction <- unname(Prediction)

# Determine mean squared error
diff <- (test$tip - Prediction)**2
mean(diff)

## [1] 1.237201
```

randomForest

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

a) Build a model and assess the model against the training data.

```
# Notice we are re-using data sets but it is good to re-read the original
# version back into the environment
train <- read.csv('/Users/breastcancer_train.csv')
test <- read.csv('/Users/breastcancer_test.csv')

# The package we need to fit a gradient boosting model (gbm) must first
# be installed and then called to use
require(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
# n.minobsinnode = minimum number of observations in the trees terminal nodes
fit <- gbm(Target ~ ., distribution = "bernoulli", data = train,
           n.trees = 2500,
           shrinkage = .01, n.minobsinnode = 20)

# Prediction on training data
gbmTrainPredictions <- predict(object = fit, newdata = train, type =
"response",
                               n.trees = 2500)
pred <- ifelse(gbmTrainPredictions < 0.5, 0, 1)

# Determine how many were correctly classified
correct <- (pred == train$Target)
table(correct)

## correct
## TRUE
##  398
```

b) Assess the model against the testing data.

```
# Prediction on testing data
gbmTestPredictions <- predict(object = fit, newdata = test, type =
"response",
                              n.trees = 2500)
pred <- ifelse(gbmTestPredictions < 0.5, 0, 1)

# Determine how many were correctly classified
```

```
correct <- (pred == test$Target)
table(correct)

## correct
## FALSE  TRUE
##     5   166
```

gbm

5.9 Fit a support vector classification model.

a) Build a model and assess the model against the training data.

```
# Notice we are re-using data sets but it is good to re-read the original
# version back into the environment
train <- read.csv('/Users/breastcancer_train.csv')
test <- read.csv('/Users/breastcancer_test.csv')

# The package we need to fit an svm model (e1071) must first
# be installed and then called to use
library(e1071)

## Warning: package 'e1071' was built under R version 3.3.2

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

# Evaluation on training data
predictedY <- predict(model, train)
prediction <- data.frame(matrix(ncol = 0, nrow = nrow(train)))
prediction$predY <- unname(predictedY)

# Determine how many were correctly classified
prediction$actual <- train$Target
prediction$correct <- (prediction$predY == prediction$actual)
table(prediction$correct)

##
## FALSE  TRUE
##     6   392
```

b) Assess the model against the testing data.

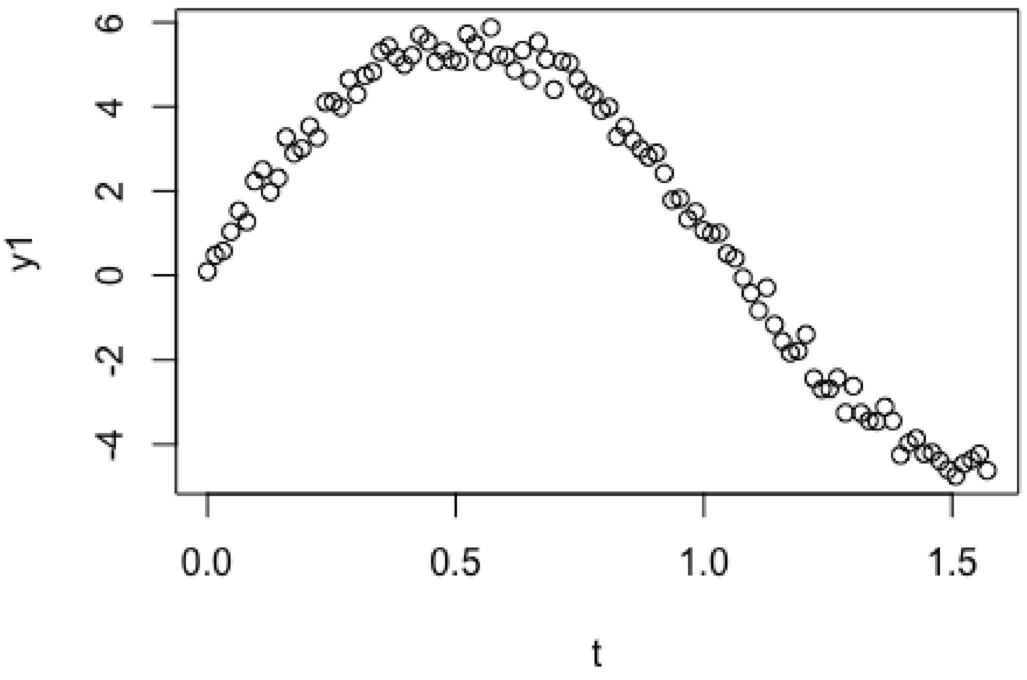
```
# Evaluation on testing data
predictedY <- predict(model, test)
prediction <- data.frame(matrix(ncol = 0, nrow = nrow(test)))
prediction$predY <- unname(predictedY)

# Determine how many were correctly classified
prediction$actual <- test$Target
prediction$correct <- (prediction$predY == prediction$actual)
table(prediction$correct)
```

```
##
## FALSE  TRUE
##     5   166
```

5.10 Fit a support vector regression model.

a) Generate random data based on a sine curve.

```
set.seed(29)
# Generate the time variable
t <- seq(from = 0, to = 0.5*pi, ,length.out=100)

# Generate the sine curve with uniform noise
y1 <- 5*sin(3*t) + runif(100)

# Create a data frame for the generated data
random_data <- data.frame(matrix(ncol=0, nrow = 100))
random_data$X <- t
random_data$Y <- y1

# Plot the generated data
plot(t,y1)
```

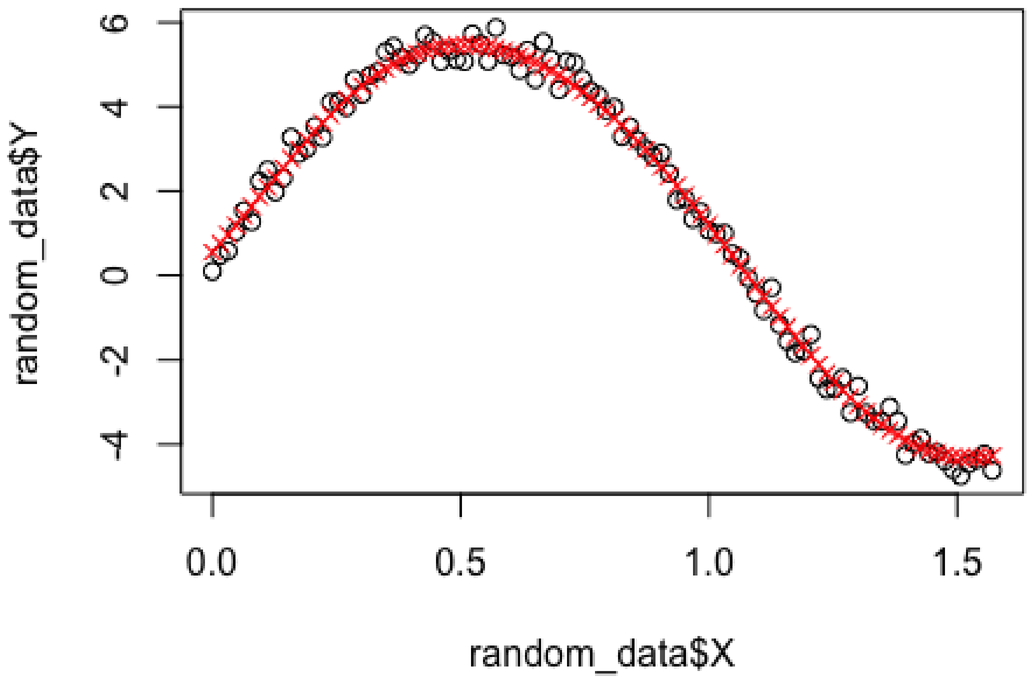


seq()

runif()

b) Fit a support vector regression model to the data.

```
# The package we need to fit an svm model (e1071) must first
# be installed and then called to use
library(e1071)

model <- svm(Y ~ X, random_data)
predictedY <- predict(model, random_data)
plot.new()
plot(random_data$X, random_data$Y)
points(random_data$X, predictedY, col = "red", pch = 4)
```

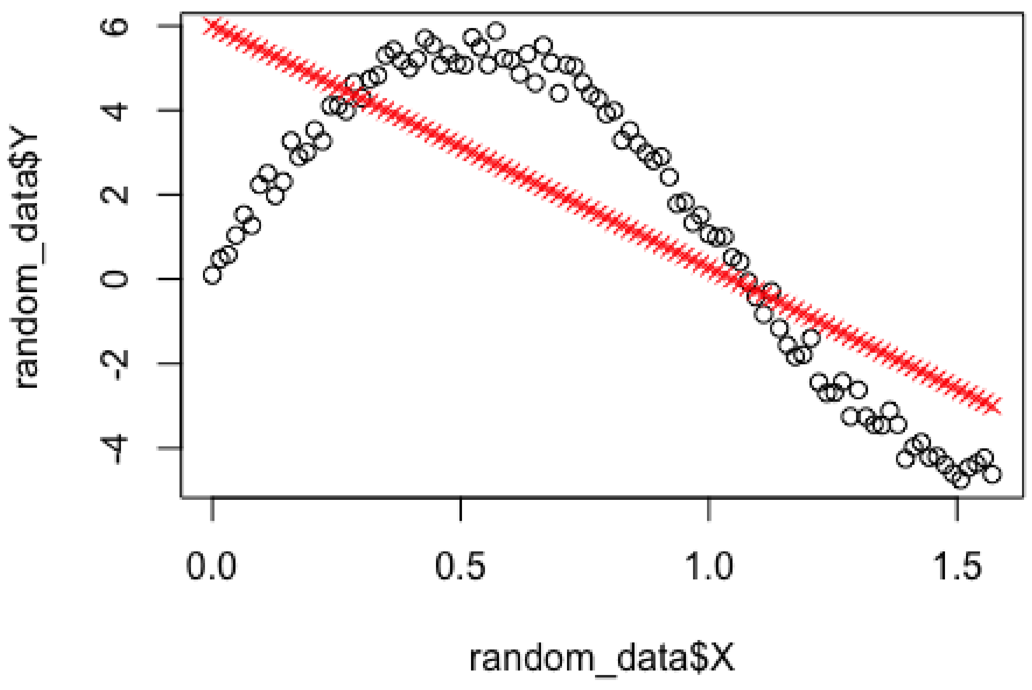


```
prediction = data.frame(matrix(ncol = 0, nrow = nrow(random_data)))
prediction$predY <- predictedY
prediction$actual <- random_data$Y
prediction$sq_diff <- (prediction$predY - prediction$actual)**2
print(mean(prediction$sq_diff))

## [1] 0.08052554
```

svm() points()

c) Fit a linear regression model to the data.

```
linMod <- lm(Y ~ X, data = random_data)

pred_lin <- predict(linMod, newdata = random_data)
plot.new()
plot(random_data$X, random_data$Y)
points(random_data$X, pred_lin, col = "red", pch = 4)
```



```
prediction = data.frame(matrix(ncol = 1, nrow = nrow(random_data)))
prediction$predY <- pred_lin
prediction$actual <- random_data$Y
prediction$sq_diff <- (prediction$predY - prediction$actual)**2
print(mean(prediction$sq_diff))

## [1] 4.904294
```

lm()

6 Model Evaluation & Selection

6.1 Evaluate the accuracy of regression models.

a) Evaluation on training data.

```
# Notice we are re-using data sets but it is good to re-read the original
# version back into the environment
train <- read.csv('/Users/tips_train.csv')
test <- read.csv('/Users/tips_test.csv')

# 1. Linear Regression Model
linMod <- lm(tip ~ ., data = train)

# Evaluation on training data
pred_lin <- predict(linMod, newdata = train)

# Determine coefficient of determination score
r2_lin <- 1 - ( (sum((train$tip - pred_lin)**2)) / (sum((train$tip -
mean(train$tip))**2)) )
print(paste0("Linear regression model r^2 score (coefficient of
determination): ", r2_lin))

## [1] "Linear regression model r^2 score (coefficient of determination):
0.496730342166266"
```

--

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

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

# Determine coefficient of determination score
r2_rf <- 1 - ( (sum((train$tip - pred_rf)**2)) / (sum((train$tip -
mean(train$tip))**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): 0.534405284634815"
```

b) Evaluation on testing data.

```
# 1. Linear Regression Model (linMod)

# Evaluation on testing data
pred_lin <- predict(linMod, newdata = test)
```

```
# Determine coefficient of determination score
r2_lin = 1 - ( (sum((test$tip - pred_lin)**2)) / (sum((test$tip -
mean(test$tip))**2)) )
print(paste0("Linear regression model r^2 score (coefficient of
determination): ", r2_lin))

## [1] "Linear regression model r^2 score (coefficient of determination):
0.270944937190937"
```

--

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

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

# Determine coefficient of determination score
r2_rf = 1 - ( (sum((test$tip - pred_rf)**2)) / (sum((test$tip -
mean(test$tip))**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): 0.330167582821381"
```

The formula used here for the coefficient score is based off the Python skearn formula for r2_score. For more information about model assessment in R, please review information about the R package caret.

6.2 Evaluate the accuracy of classification models.

a) Evaluation on training data.

```
# Notice we are re-using data sets but it is good to re-read the original
version
# back into the environment
train <- read.csv('/Users/breastcancer_train.csv')
test <- read.csv('/Users/breastcancer_test.csv')
set.seed(29)

# 1. Decision Tree Classification Model
treeMod <- tree(Target ~ ., data = train)

# Evaluation on training data
out <- predict(treeMod)
out <- unname(out)
pred_tree <- ifelse(out < 0.5, 0, 1)

# Determine accuracy score
```

```
accuracy_tree <- (1/nrow(train)) * sum(as.numeric(pred_tree == train$Target))
print(paste0("Decision tree model accuracy: ", accuracy_tree))

## [1] "Decision tree model accuracy: 0.969849246231156"
```

--

```
# 2. Random Forest Classification Model
rfMod <- randomForest(as.factor(Target) ~ ., data = train)

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

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

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

--

```
# 3. Gradient Boosting Classifcation Model
gbmMod <- gbm(Target ~ ., distribution = "bernoulli", data = train,
           n.trees = 2500,
           shrinkage = .01, n.minobsinnode = 20)

# Evaluation on training data
pred_gbm <- predict(object = gbmMod, newdata = train, type = "response",
                               n.trees = 2500)
pred_gbm <- ifelse(pred_gbm < 0.5, 0, 1)

# Determine accuracy score
accuracy_gbm <- (1/nrow(train)) * sum(as.numeric(pred_gbm == train$Target))
print(paste0("Gradient boosting model accuracy: ", accuracy_gbm))

## [1] "Gradient boosting model accuracy: 1"
```

b) Evaluation on testing data.

```
# 1. Decision Tree Classification Model (treeMod)

# Evaluation on testing data
out <- predict(treeMod, test)
out <- unname(out)
pred_tree <- ifelse(out < 0.5, 0, 1)

# Determine accuracy score
accuracy_tree <- (1/nrow(test)) * sum(as.numeric(pred_tree == test$Target))
print(paste0("Decision tree model accuracy: ", accuracy_tree))

## [1] "Decision tree model accuracy: 0.929824561403509"
```

--

```
# 2. Random Forest Classification Model (rfMod)

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

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

## [1] "Random forest model accuracy: 0.970760233918129"
```

--

```
# 3. Gradient Boosting Classifcation Model (gbmMod)

# Evaluation on testing data
pred_gbm <- predict(object = gbmMod, newdata = test, type = "response",
                              n.trees = 2500)
pred_gbm <- ifelse(pred_gbm < 0.5, 0, 1)

# Determine accuracy score
accuracy_gbm <- (1/nrow(test)) * sum(as.numeric(pred_gbm == test$Target))
print(paste0("Gradient boosting model accuracy: ", accuracy_gbm))

## [1] "Gradient boosting model accuracy: 0.970760233918129"
```

The formula used here for the accuracy score is based off the Python skearn formula for accuracy_score. For more information about model assessment in R, please review information about the R package caret.

6.3 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')

# The packages we need (caret & randomForest) must first
# be installed and then called to use
library(caret)
library(randomForest)

# 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
```

```r
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: 95.9% +/- 1.26%"
```

caret

b) ShuffleSplit

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

# The package we need to create a data partition (caret) must first
# be installed and then called to use
require(caret)
require(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: 94.24% +/- 1.05%"
```

createDataPartition

caret

Alphabetical Index

caret

caret is an R programming package of tools for training and plotting classification and regression models.

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
```

---

dplyr

dplyr is an R programming package of tools for workng with data frame like objects.

---

gbm

gbm is an R programming package useful for building and analyzing gradient boosting models.

---

gdata

gdata is an R programming package of tools useful for data manipulation.

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"
```

---

randomForest

randomForest is an R programming package of tools useful for building and analyzing classification and regression random forest models.

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rjson

rjson is an R programming package of tools useful for converting R objects into JSON objects, and JSON objects into R objects.

Series/Array

A series is a one-dimensional data frame, which is also called an array in R. 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
```

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tree

tree is an R programming package of tools useful for building and analyzing classification and regression decision trees.

For more information on R packages and functions, along with helpful examples, please see R.