HW5_IS457_8

Part I: Plot arguments (4 pts)

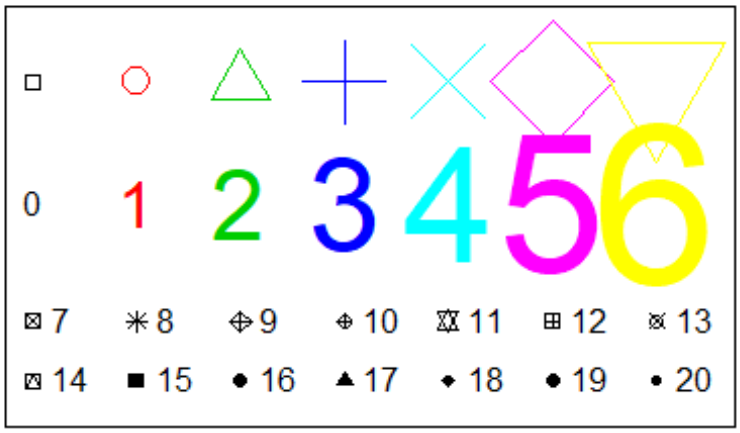
Q1. The parameters control the size, color and shape of plotting symbol for plot funcions.

To understand the parameters like cex, col, pch, pos, etc., run the following code one by one.

Describe the function of these plot arguments. (4 pts.)

e.g., how the symbol/color/size change

```
plot(1, 1, xlim=c(1, 7.5), ylim=c(1.75,5), type="n", axes=F, xlab="",
     ylab="") # Do not plot points
box()
points(1:7, rep(4.5, 7), cex=1:7, col=1:7, pch=0:6)
text(1:7,rep(3.5, 7), labels=paste(0:6), cex=1:7, col=1:7)
points(1:7,rep(2.5,7), pch=(0:6)+7) # Plot symbols 7 to 13
text((1:7), rep(2.5,7), paste((0:6)+7), pos=4) # Label with symbol number
points(1:7,rep(2,7), pch=(0:6)+14) # Plot symbols 14 to 20
text((1:7), rep(2,7), paste((0:6)+14), pos=4) # Labels with symbol number
```


0 1 2 3 4 5 6
7 8 9 10 11 12 13
14 15 16 17 18 19 20

Your answer here

plot(1, 1, xlim=c(1, 7.5), ylim=c(1.75,5), type="n", axes=F, xlab="",

ylab="")

this creates a new plot with an x axis in the range(1,7.5) and y axis in the

range(1.75,5). type is set to "n" meaning the plot will not produce any points or lines

axes is set to F meaning the x and y axis calibrations will not be visible

in the plot. xlab and ylab values are not set so both axes will not have labels

box()

This function draws a box around the plot

points(1:7, rep(4.5, 7), cex=1:7, col=1:7, pch=0:6)

this function creates 7 points on the plot.The col parameter determines the number(range)of colors used

in creating the points and the pch parameter determines the symbols that will be used in creating the points

text(1:7,rep(3.5, 7), labels=paste(0:6), cex=1:7, col=1:7)

this creates 7 figures(text symbols) labelled 0,1,2,3,4,5,6 pasted in 7 different colors

points(1:7,rep(2.5,7), pch=(0:6)+7)

this creates 7 new symbols in the plot ,symbols 7 to 13 to be precise

text((1:7), rep(2.5,7), paste((0:6)+7), pos=4)

This pasted 7 new figures: text 7,8,9,10,11,12,13 on the plot positioned beside the plot symbols 7-13.

points(1:7,rep(2,7), pch=(0:6)+14)

this created 7 new symbols , plot symbols 14- 20

text((1:7), rep(2,7), paste((0:6)+14), pos=4)

this pasted 7 text figures 14,15,16,17,18,19,20 on the plot positioned beside plot symbols 14-20

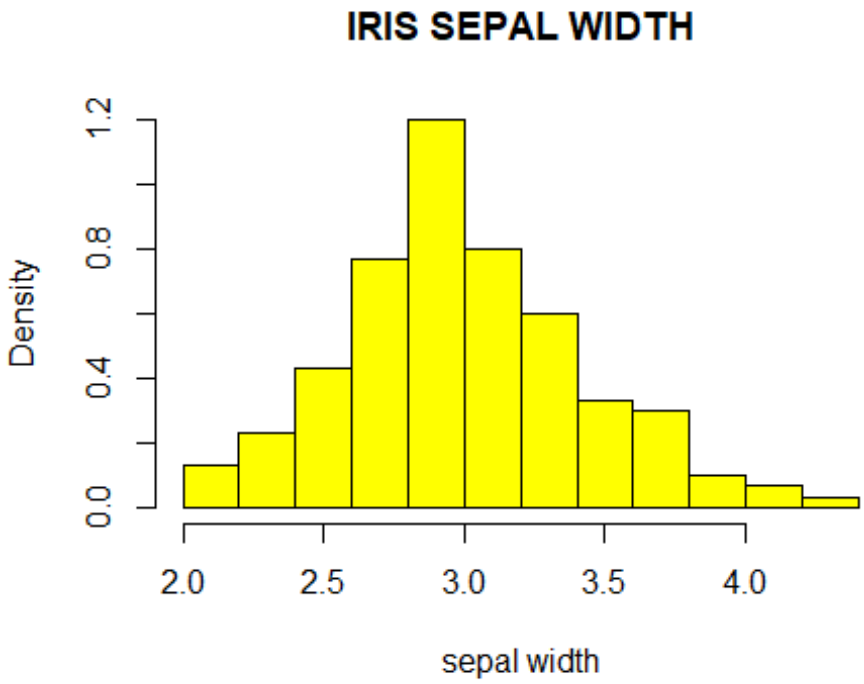
Part II: Plotting Functions (16 pts.)

We will discuss plots with built-in iris dataset which you have already seen before.

Q1. Make a histogram for the variable “Sepal.Width” to show density instead of frequency.(2 pt.)

Your code here

```
data(iris)
hist(iris$Sepal.Width, col = "yellow",prob = TRUE, xlab = "sepal width", main
= "IRIS SEPAL WIDTH")
```

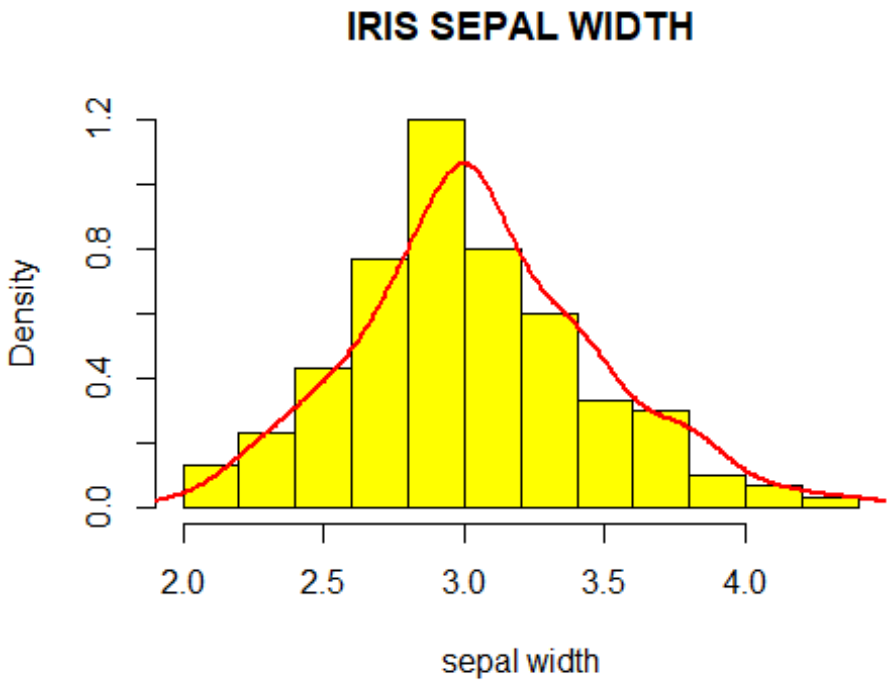


Q2. Add density curve on the histogram from the previous question.(2 pts.)

Hint: Adjust arguments of line() to make the line stand out.

Your code here

```
hist(iris$Sepal.Width, col="yellow", prob = TRUE, xlab = "sepal width",main =
"IRIS SEPAL WIDTH")
lines(density(iris$Sepal.Width),lwd =2,col = "red")
```



Q3. Add a normal distribution curve on the plot from the previous question

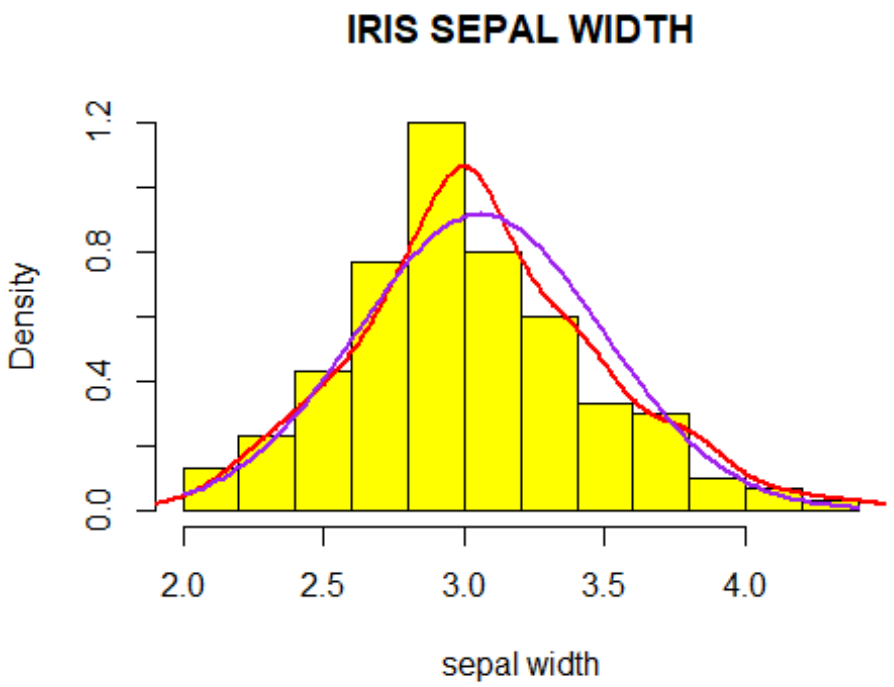
with mean and standard deviation of Sepal.Width. (2 pts.)

Compare two curves and discuss the distribution of Sepal.Width. (2 pts.)

Hint: curve() function may help.

Your code here

```
mean_s.width= mean(iris$Sepal.Width)
sd_s.width = sd(iris$Sepal.Width)
hist(iris$Sepal.Width, col="yellow", prob = TRUE, xlab = "sepal width",main =
"IRIS SEPAL WIDTH")
lines(density(iris$Sepal.Width),lwd =2,col = "red")
curve(dnorm(x, mean=mean(iris$Sepal.Width), sd=sd(iris$Sepal.Width)), add=TRU
E,lwd=2, col = "purple")
```


IRIS SEPAL WIDTH
Density
0.0
0.4
0.8
1.2
2.0
2.5
3.0
3.5
4.0
sepal width

Your answer here

The Sepal.Width distribution seems to follow the usual pattern of a normal distrubution. However, i observe

that it has a longer upper tail or is skewed right slightly which represent the few flowers that have

larger sepal widths.

Q5. Make a horizontal boxplot to show Sepal.Width in different species.

Add a rug to your plot. (2 pts.)

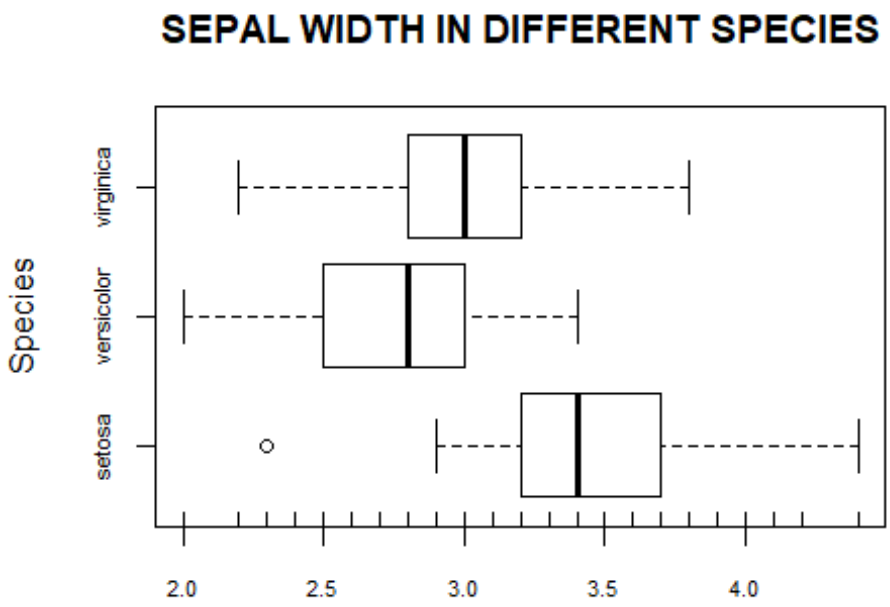
(1) Try to identify the minimum, lower quartile, median, upper quartile and

maximum value of virginica's Sepal.Width by your eyes. (2 pts.)

(2) Explain what the overlapping in x axis means (2 pts.)

Your code here

```
boxplot(Sepal.Width~Species,data=iris, main="SEPAL WIDTH IN DIFFERENT SPECIES
", Xlab="Sepal.Width",ylab="Species",horizontal =TRUE, par(cex.axis=0.7))
rug(iris$Sepal.Width)
```


SEPAL WIDTH IN DIFFERENT SPECIES
Species
virginica
versicolor
setosa
2.0
2.5
3.0
3.5
4.0

Your answer here

1)minimum value = 2.2

lower quartile = 2.8

median = 3.0

upper quartile = 3.2

maximum value = 3.8

2) There could be overlapping in the x axis in terms of the axis labels and tick labels but this can be solved by modifying the

graphical parameters, however that is not the case with this plot as there is no overlap in the x axis.

Q6. Make a scatter plot, Petal.Length vs. Petal.Width.

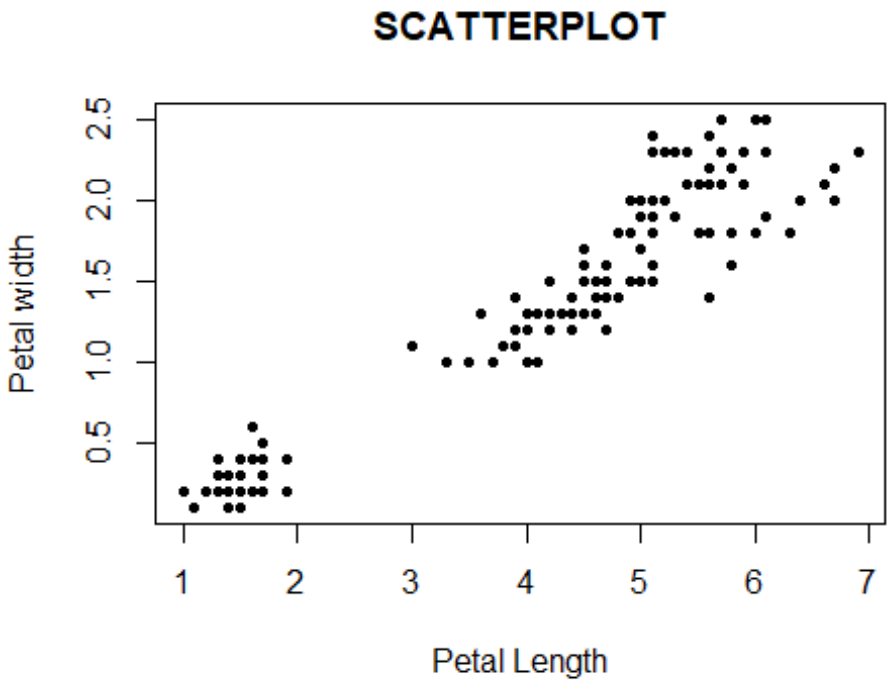
Mark in the points by species. (2 pts)

Hint: You could adjust pch argument.

For example: pch=21 for filled circles, pch=22 for filled squares, pch=23 for filled diamonds.

Your code here

```
plot(iris$Petal.Length,iris$Petal.Width,main="SCATTERPLOT", xlab="Petal Length", ylab="Petal width", pch=20)
```



Part III. ggplot (10 + 4 pts)

This question implements ggplot.

ggplot2 is very powerful, because you can create new graphics

that are precisely tailored to your problem.

Google can be helpful if you find yourself stuck, as well as office hours.

First of all, install ggplot2 and access it.

```
#install.packages("ggplot2")
library(ggplot2)

## Warning: package 'ggplot2' was built under R version 3.4.4
```

We will play with plots using diamonds dataset.

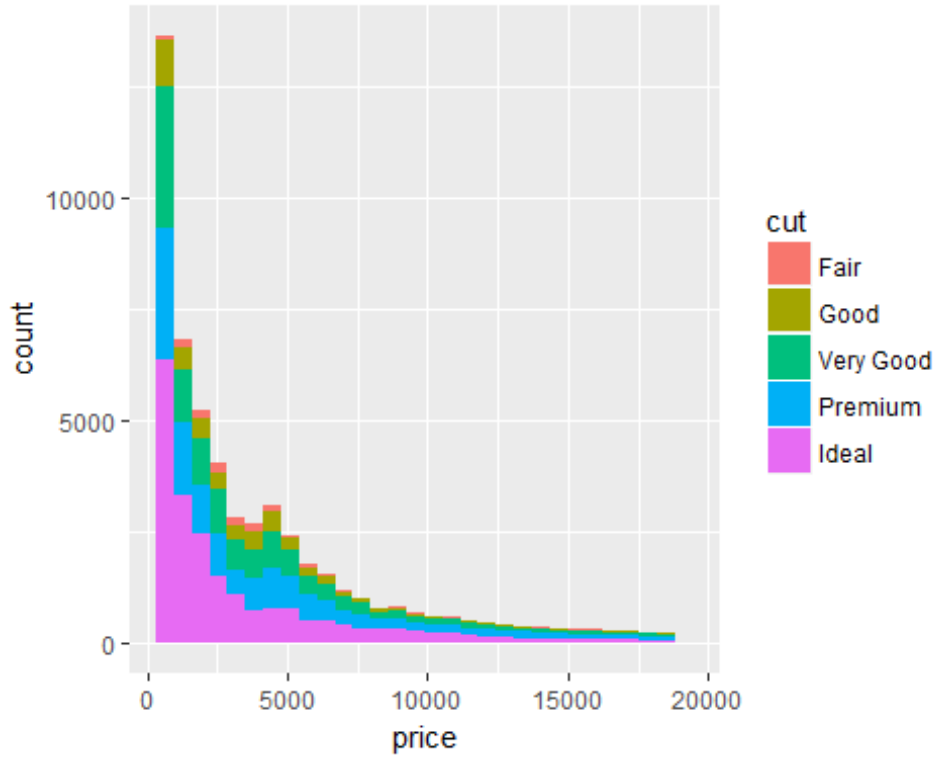
Q1. Use ggplot to make a histogram for the price variable and fill the histogram by the cut Variable.

The plot is similar to

http://ggplot2.tidyverse.org/reference/geom_freqpoly-9.png (2 pts)

Your code here

```
data(diamonds)
ggplot(diamonds, aes(x = price, fill =cut)) + geom_histogram()

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

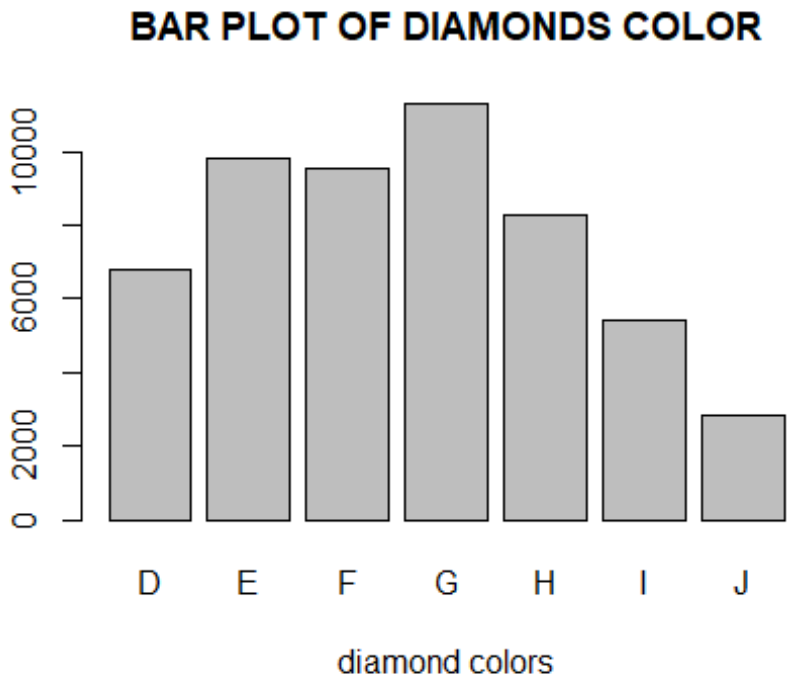


Q2. Make a bar plot for color of diamonds

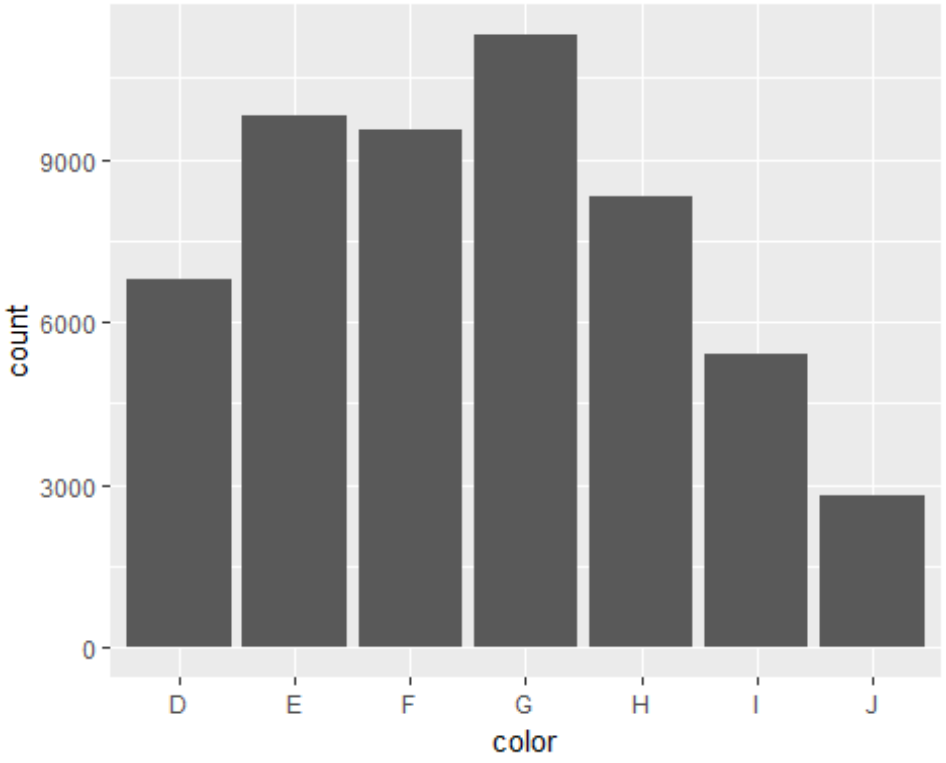
with both basic plotting function (requried) and ggplot2 (bonus) (2+2 pts.).

Your code here

```
diamonds_color = table(diamonds$color)
barplot(diamonds_color, main="BAR PLOT OF DIAMONDS COLOR", xlab="diamond colo
rs")
```




```
ggplot(diamonds, aes(x = color)) + geom_bar()
```



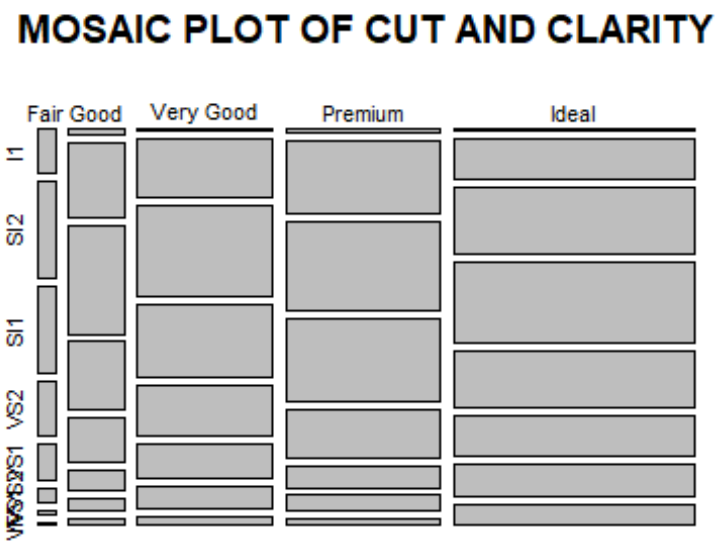
Q3. Make a mosaic plot with cut and clarity variables.

You can use a basic plotting function (required) and ggplot2 (bonus).

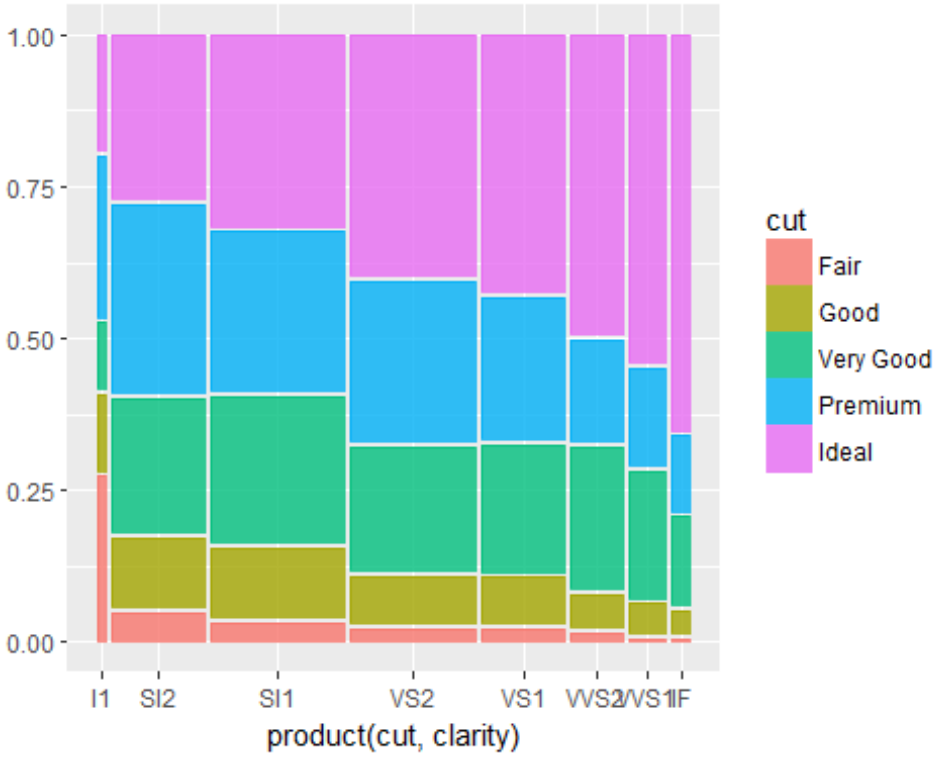
To make a mosaic plot with ggplot, you will need the ggmosaic package. (2+2 pts.)

Your code here

```
mosaicplot(table(diamonds$cut,diamonds$clarity), main = "MOSAIC PLOT OF CUT
AND CLARITY")
```




```
#install.packages("ggmosaic")
library(ggmosaic)

## Warning: package 'ggmosaic' was built under R version 3.4.4

## Loading required package: productplots

## Warning: package 'productplots' was built under R version 3.4.4

##
## Attaching package: 'ggmosaic'

## The following objects are masked from 'package:productplots':
##
##     ddecker, hspine, mosaic, prodcalc, spine, vspine

ggplot(data=diamonds) + geom_mosaic(aes(x=product(cut,clarity), fill=cut))
```


1.00
0.75
0.50
0.25
0.00
I1
SI2
SI1
VS2
VS1
VVS2
VVS1
IF
product(cut, clarity)
cut
Fair
Good
Very Good
Premium
Ideal

Q4. Why is the Data Life Cycle is crucial to understanding

the opportunities and challenges of making the most of digital data?

Give two examples. (4 pts.)

The data life cycle provides a detailed, systematic approach for dealing with data. Every stage of the data life cycle

corresponds to certain tasks that need to be carried out. While there are many variations of the data life cycle that

which can be employed, certain important tasks such as data cleaning, analysis are compulsory to ensure that data is correctly utilized to generate insights

Also the data life cycle needs to be employed in a thorough manner because this ensures that documentation is available for future use , further exploration and discovery.