

Data Exploration, Visualization, and Feature Engineering

Agenda

- Why Data Exploration and Visualization
- Graphing in R: Core and Lattice
- ggplot2 introduction
- Extended Titanic Exploration
- Visualization in Azure

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Data Beats Algorithm but...

- More data will yield good generalization performance – even with a simple algorithm
- But there are caveats
 - Amount of data may have diminishing returns
 - Data quality and variety matters
 - A decent performing learning algorithm is still needed
 - Most importantly, extracting useful features out of data is important

Dispelling a Common Myth

- There is no algorithm that will take raw data and give you actionable insights
- You do not need to know a lot of machine learning algorithms to build robust predictive models

Janitorial Work is Important

- Not spending time on understanding your data is a common source all sorts of problems!
- Remember the 80/20 rule

Objectives of The Session

- Training you to be a good data science janitor
- High level thinking process of exploring and visualizing a data set before building a model
- How to summarize your findings
- Learn some useful tools along the way

I am new to R...

- Focus on the ideas rather than exact syntax. R help is your friend
- All slides have code samples
- Sample code + slides: Data Exploration and Visualization folder

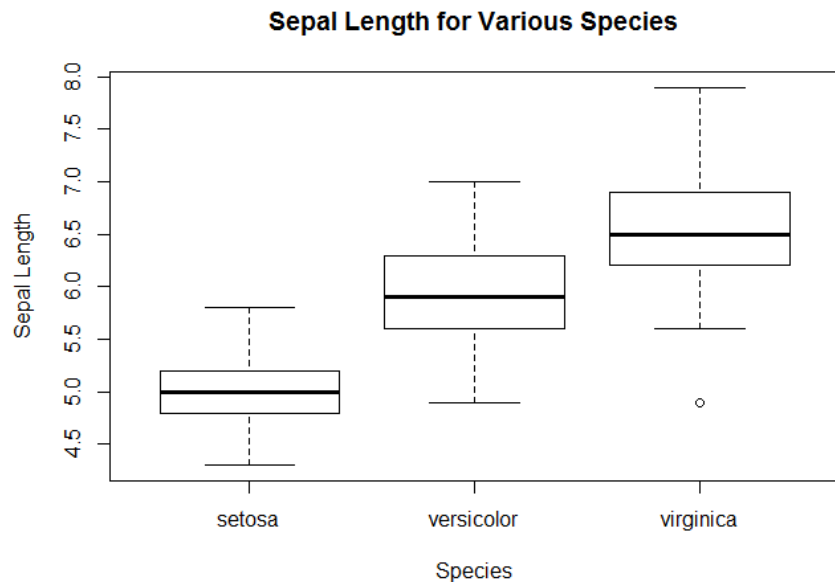
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Box Plots

- Distribution of single feature
- Can partition by target class

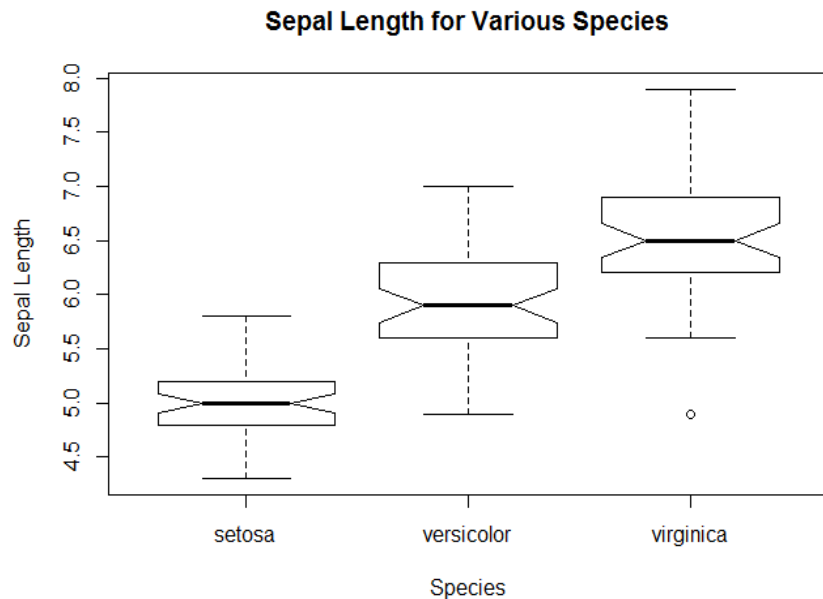
```
data(iris)
boxplot(Sepal.Length ~ Species,
data=iris,
main="Sepal Length for Various
Species",
xlab="Species",
ylab="Sepal Length"
)
```



Box Plots with Notches

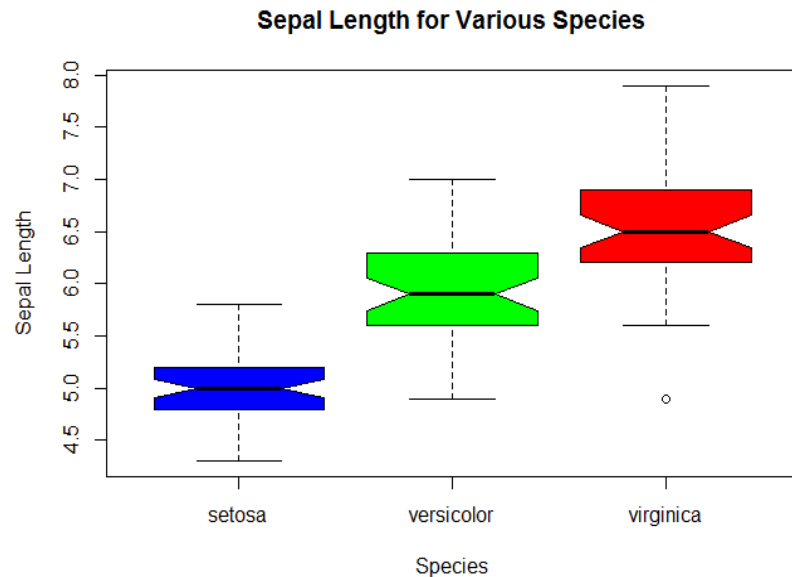
- Estimate of confidence interval of the median
- Notch overlap indicates confidence that median is different

```
boxplot(Sepal.Length ~ Species,  
data=iris,  
main="Sepal Length for Various  
Species",  
xlab="Species",  
ylab="Sepal Length",  
notch=TRUE  
)
```



Coloring Your Plots

```
boxplot(Sepal.Length ~ Species,  
data=iris,  
main="Sepal Length for Various  
Species",  
xlab="Species",  
ylab="Sepal Length",  
notch=TRUE,  
col=c("blue", "green", "red")  
)
```



Saving Plots

Function	Output to
<code>pdf("mygraph.pdf")</code>	pdf file
<code>win.metafile("mygraph.wmf")</code>	windows metafile
<code>png("mygraph.png")</code>	png file
<code>jpeg("mygraph.jpg")</code>	jpeg file
<code>bmp("mygraph.bmp")</code>	bmp file
<code>postscript("mygraph.ps")</code>	postscript file

Windows Saves to default: Libraries\Documents

R Studio makes it easier

```
pdf("myplot.pdf")
```

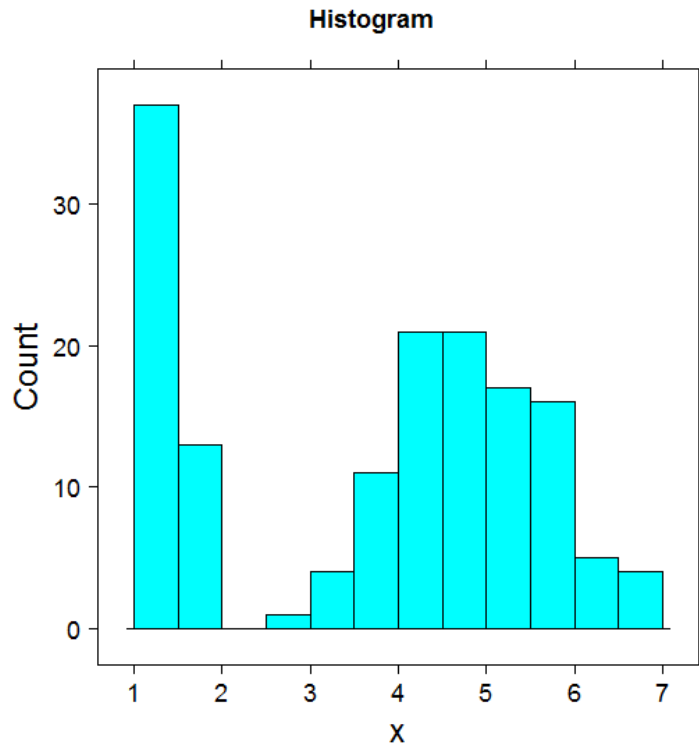
```
boxplot(Sepal.Length ~ Species,  
data=iris,  
main="Sepal Length for Various Species",  
xlab= "Species", ylab="Sepal Length",  
notch=TRUE, col=c("blue", "green", "red")  
)
```

```
dev.off() # Returns plot to the IDE
```

Lattice: Histogram

- Spread of single feature
- Places values in "bins"
- "breaks" - # of bins

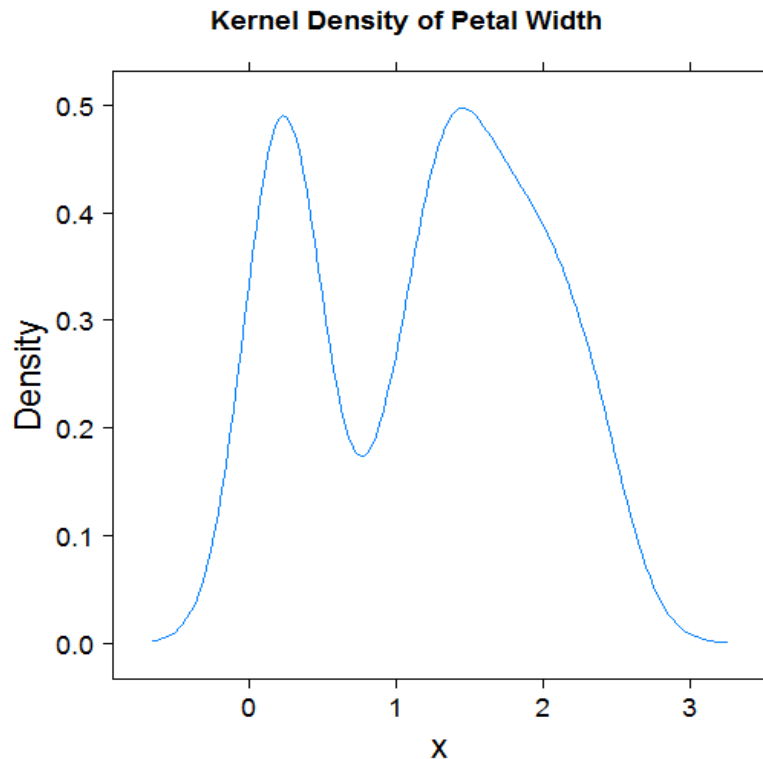
```
histogram(iris$Petal.Length,  
breaks=10, type="count",  
main="Histogram")
```



Lattice: Density plots

- Variant of Histogram
- Scaled for easy comparisons

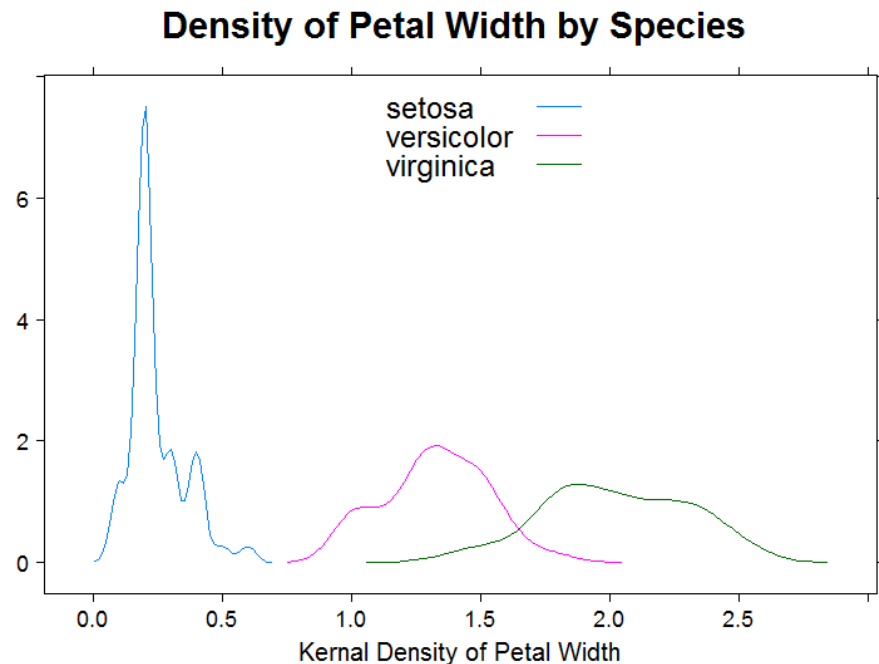
```
densityplot(iris$Petal.Length  
,main="Kernel Density of  
Petal Length",  
type="percent", n=150)
```



Lattice: Multiple Density Plots

- Grouping simple
- Styling is not!

```
densityplot(~ Petal.Width,  
data=iris, groups=Species,  
plot.points=F,  
xlab=list(label="Kernel Density  
of Petal Width", fontsize=20),  
ylab="",  
main=list(label="Density of  
Petal Width by Species",  
fontsize=24),  
auto.key=list(corner=c(0,0),  
x=0.4, y=0.8, cex=2),  
scales=list(cex=1.5))
```

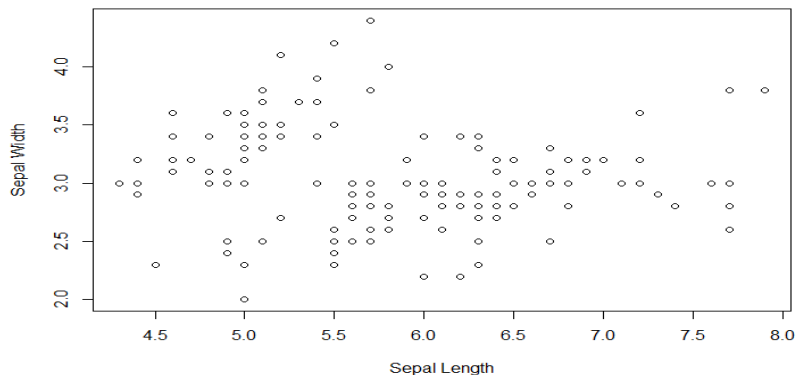


Exercise 1

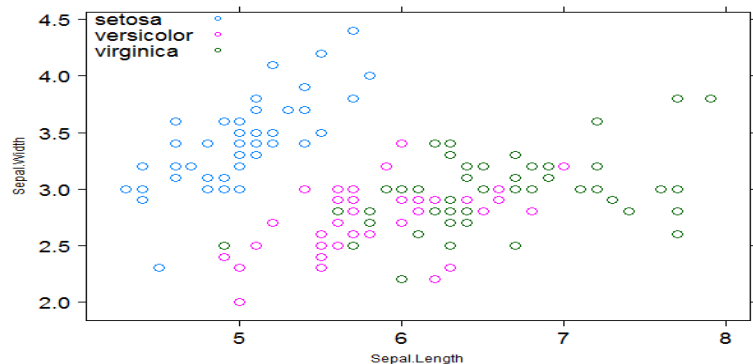
- 2-D Scatter plots – `plot()` and `xyplot()`
 - Sepal Length vs Sepal Width
 - Petal Length vs Petal Width
 - Segment based on Species (lattice)

Sample Solution

```
# Core Graphics
plot(iris$Sepal.Length,
iris$Sepal.Width, xlab="Sepal
Length", ylab="Sepal Width")
```



```
# Lattice Graphics
xyplot(Sepal.Width ~
Sepal.Length, data=iris,
groups=Species,
auto.key=list(corner=c(0,0),
x=0, y=0.85, cex=1.5), cex=1.5,
scales=list(cex=1.5))
```

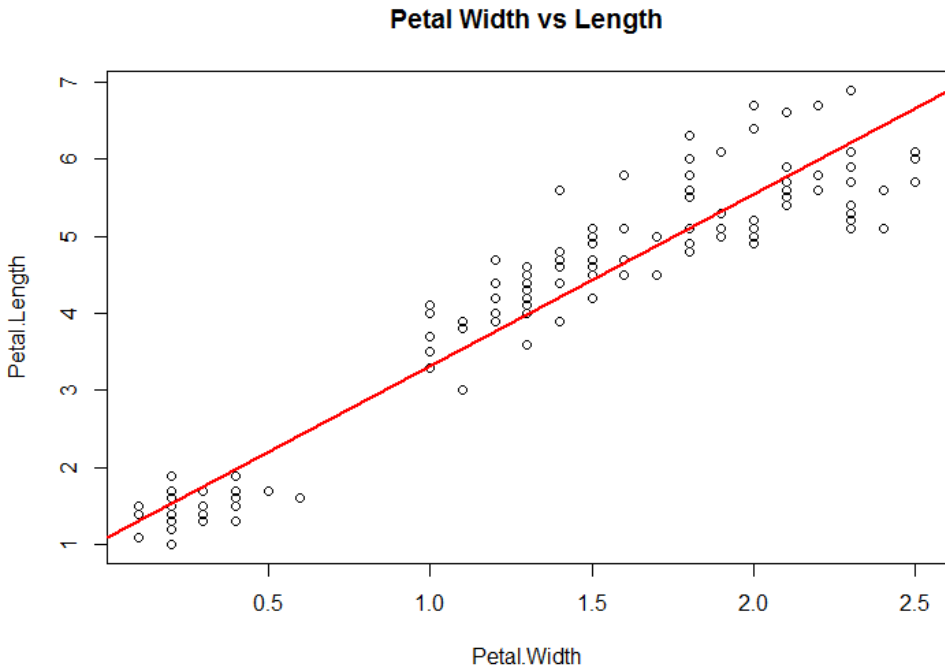


Extended Scatter Plots

- Add a regression line

```
plot(Petal.Length ~  
Petal.Width, data=iris,  
main="Petal Width vs  
Length")
```

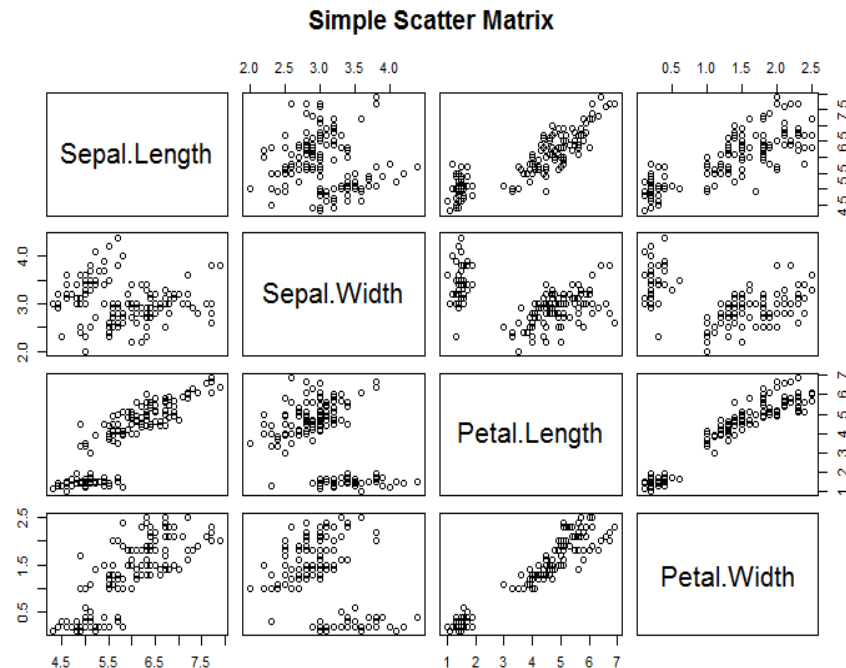
```
abline(lm(Petal.Length ~  
Petal.Width, data=iris),  
col="red", lwd=2)
```



Core: Scatter Plot Matrix

- Multiple relationships on one graph
- Good for initial explorations

```
pairs(~ Sepal.Length +  
      Sepal.Width + Petal.Length +  
      Petal.Width, data=iris,  
      main="Simple Scatter Matrix")
```

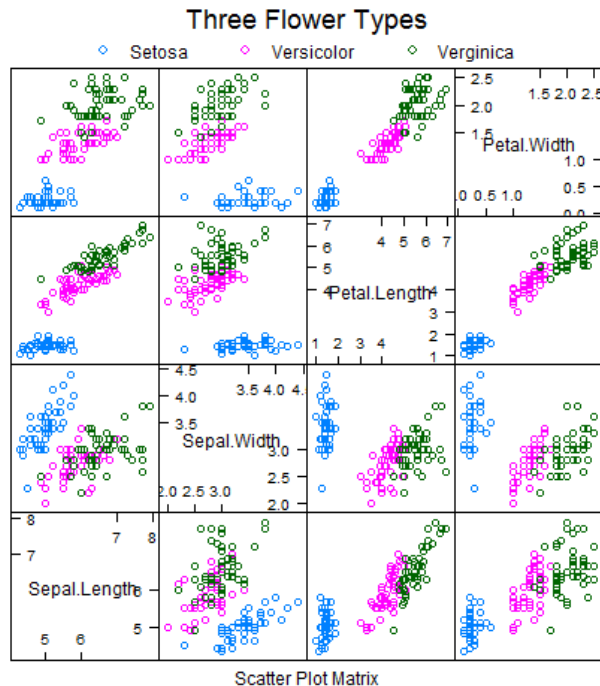


Lattice: Scatter Plot Matrix

- Simple Grouping

```
# Getting settings for legend
super.sym <-
trellis.par.get("superpose.symbol")

splom(iris[1:4],
      groups=iris$Species,
      panel=panel.superpose,
      key=list(title="Three Flower Types",
              columns=3,
              points=list(pch=super.sym$pch[1:3],
                          col=super.sym$col[1:3])),
      text=list(c("Setosa", "Versicolor", "Verginica"))))
```

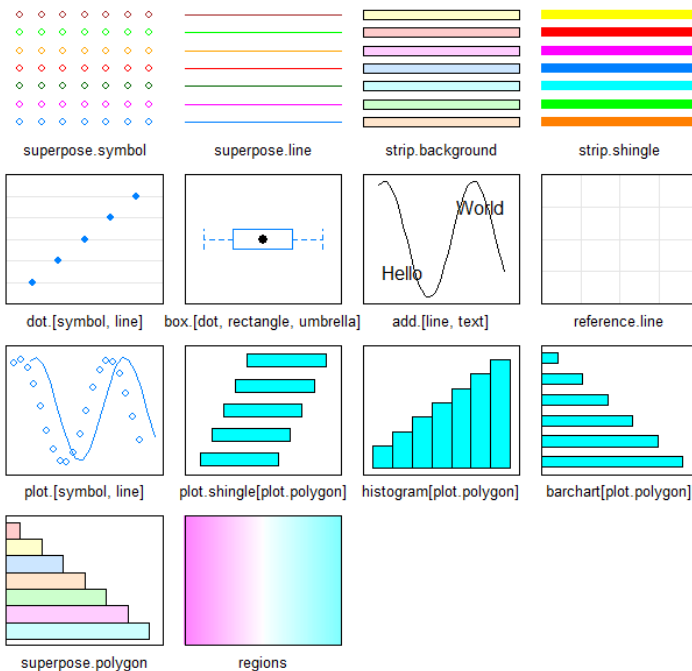


Graphical Settings

■ Simple Grouping

```
my.theme = trellis.par.get()
names(my.theme)
```

```
show.settings()
my.theme$fontsize$text=20
```

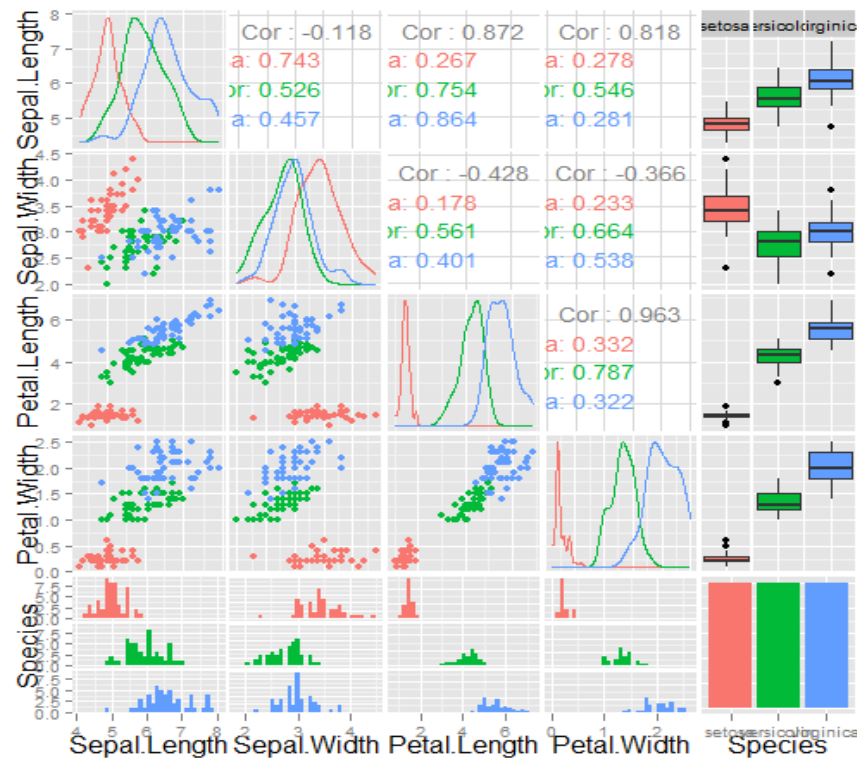


Enhanced Scatter Plot Matrices

```
library(GGally)

ggpairs(iris,
  ggplot2::aes(color=Species))
```

- Many packages have custom pairs implementations

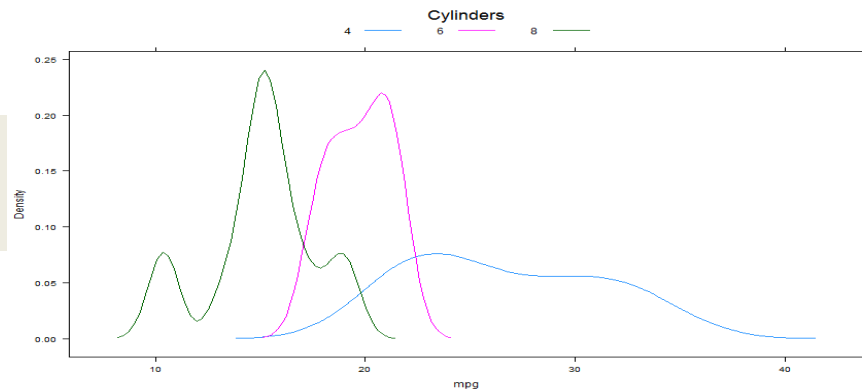


Exercise 2

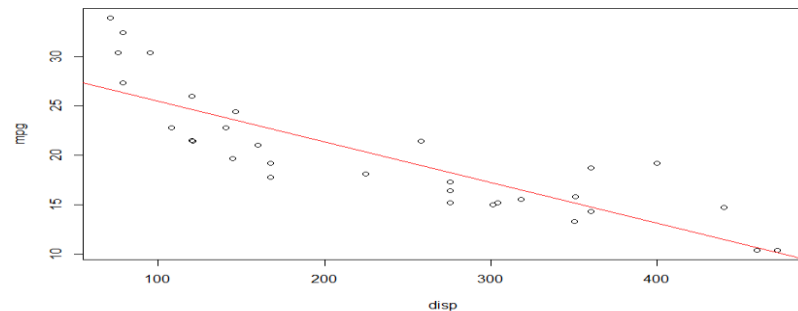
- Load "mtcars" dataset: `data(mtcars)`
 - `?mtcars` for details
- Goal: Predict MPG based on other columns
- Create at least 2 different plots illustrating useful relationships in the data

Sample Solution 2

```
densityplot( ~ mpg, data=mtcars, groups=cyl,  
plot.points=F, auto.key=list(columns=3,  
title="Cylinders"))
```



```
plot(mpg ~ disp, data=mtcars)  
abline(lm(mpg ~ disp, data=mtcars),  
col="red")
```



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Lattice/Core styling is a pain!

- ggplot2 syntax easier to read/write
 - Less intuitive/steeper initial learning curve
 - More power than often needed

ggplot Basics

- `ggplot()` is the basic function
- `geom_*()` creates a graph layer
- `aes()` defines an "aesthetic" either globally or by layer

Loading

```
library(ggplot2)
data(diamonds)
head(diamonds)
```

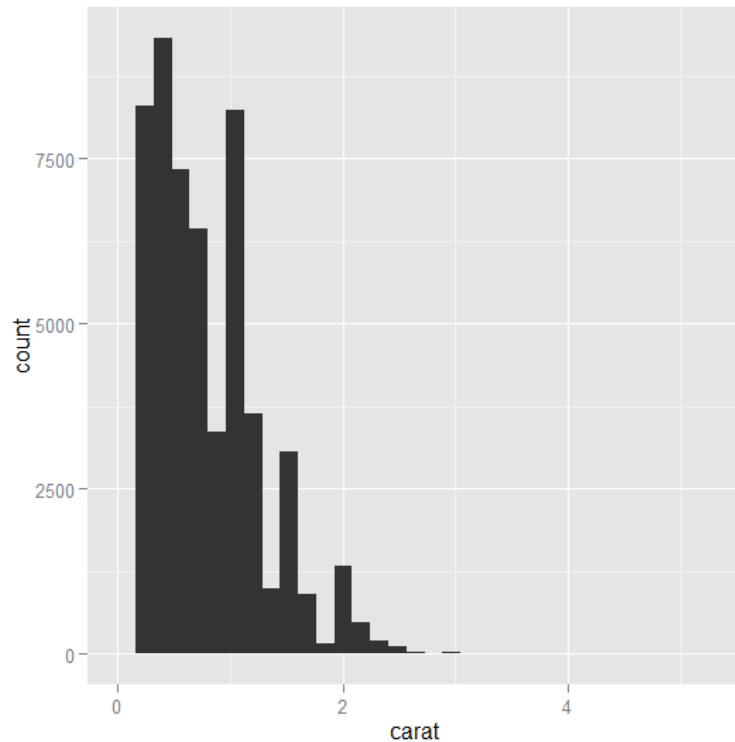
```
> head(diamonds)
```

	carat	cut	color	clarity	depth	table	price	x	y	z
1	0.23	Ideal	E	SI2	61.5	55	326	3.95	3.98	2.43
2	0.21	Premium	E	SI1	59.8	61	326	3.89	3.84	2.31
3	0.23	Good	E	VS1	56.9	65	327	4.05	4.07	2.31
4	0.29	Premium	I	VS2	62.4	58	334	4.20	4.23	2.63
5	0.31	Good	J	SI2	63.3	58	335	4.34	4.35	2.75
6	0.24	Very Good	J	VVS2	62.8	57	336	3.94	3.96	2.48

```
> |
```

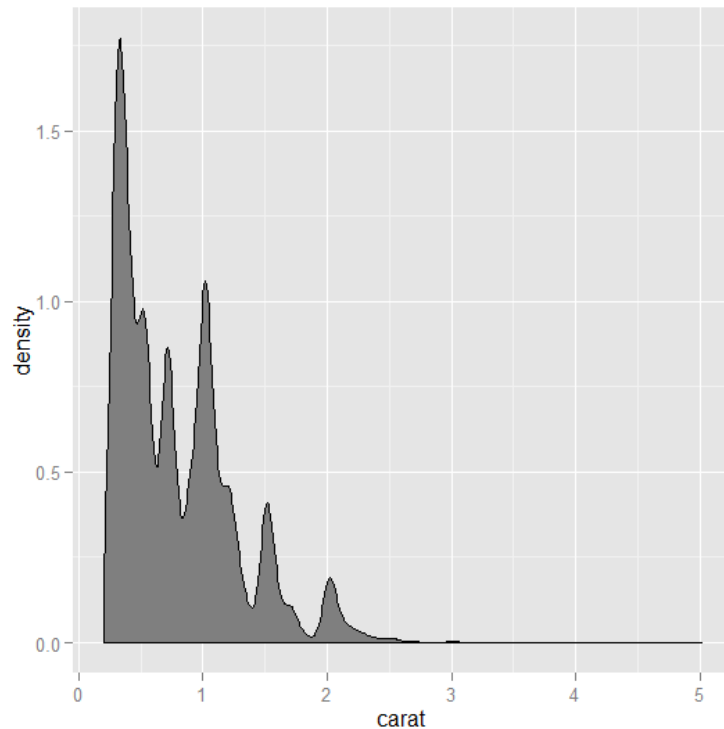
Histogram

```
ggplot(diamonds, aes(x=carat)) +  
  geom_histogram()
```



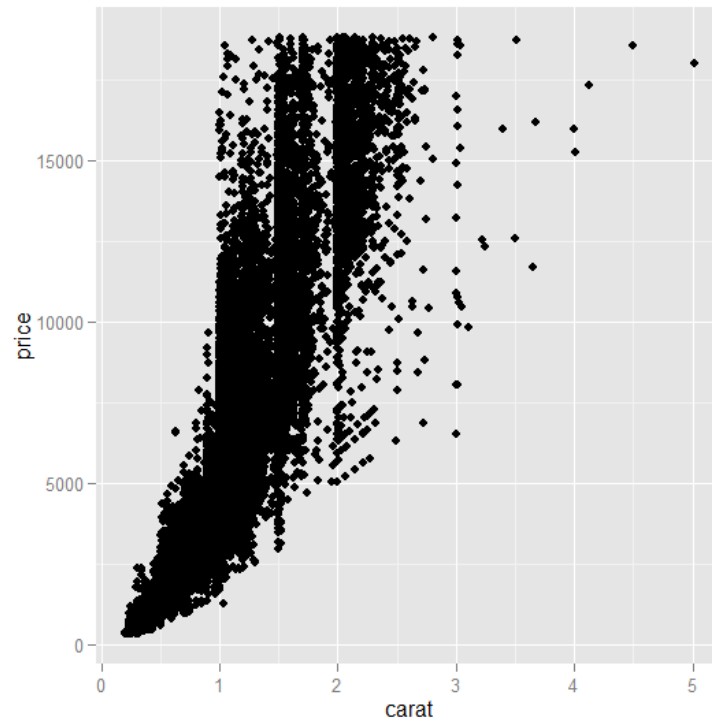
Density plot

```
ggplot(diamonds) +  
  geom_density(aes(x=carat),  
    fill="gray50")
```



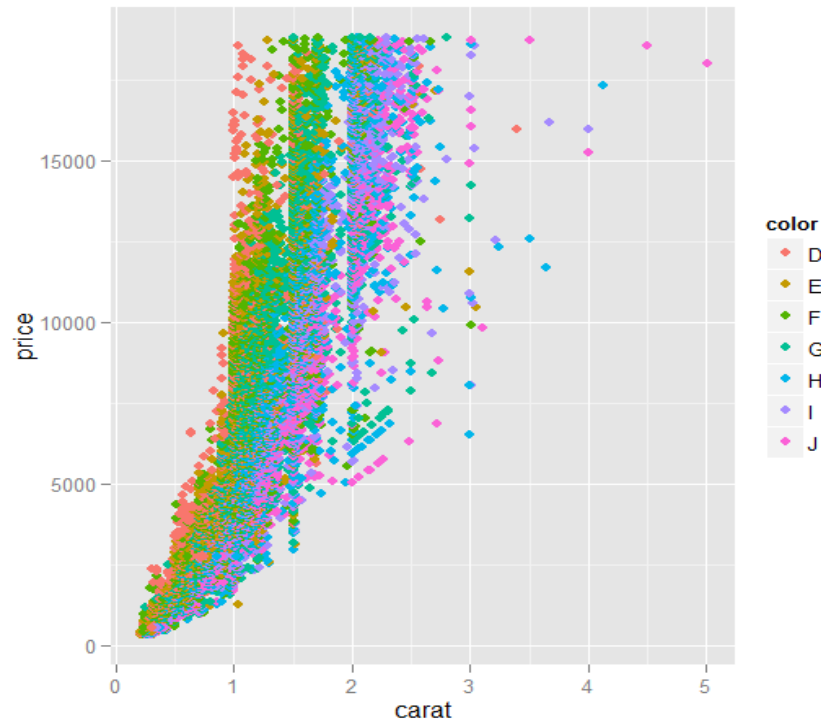
Scatter plots

```
ggplot(diamonds, aes(x=carat, y=price)) +  
geom_point()
```



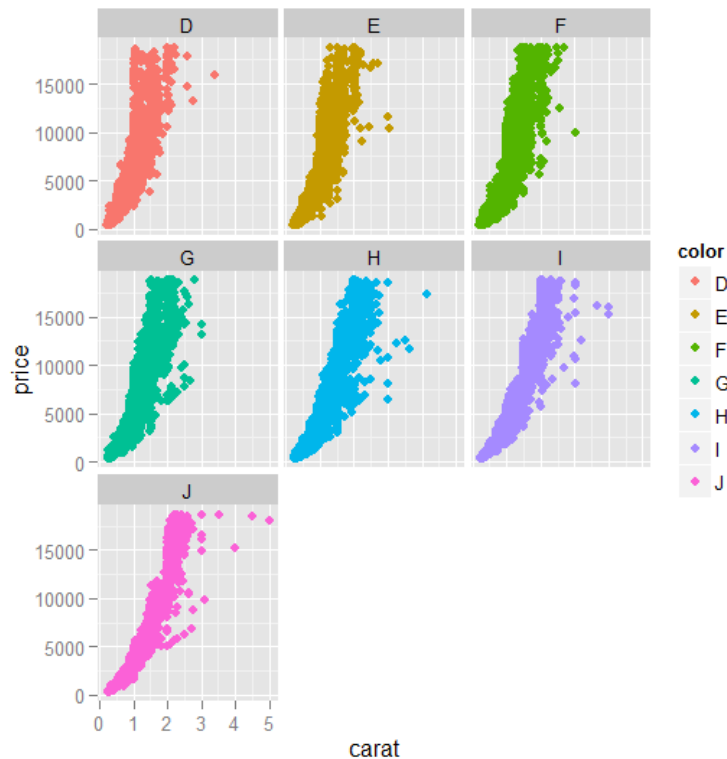
ggplot Object

```
# Store the plot for future modification  
g <- ggplot(diamonds, aes(x=carat, y=price))  
  
# add settings specific to geom_point layer  
g + geom_point(aes(color=color))
```



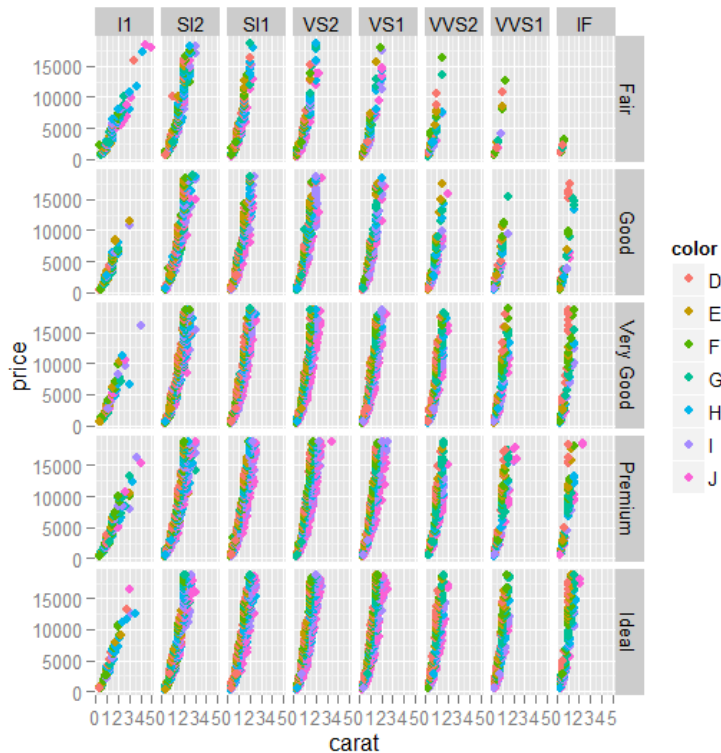
Segment by factor attribute

```
g + geom_point(aes(color=color)) +  
facet_wrap(~ color)
```



More Segments!

```
g + geom_point(aes(color=color)) +  
facet_grid(cut ~ clarity)
```



Practicing ggplot

- Documentation at <http://docs.ggplot2.org/current/>
- Lists all the different geom_* and other functions, with what aes() settings they use

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Finding the Code

- Set your working directory to the bootcamp root
- Load data in from "Datasets/titanic.csv"

Looking at the first few rows

```
titanic <- read.csv("Datasets/titanic.csv")
head(titanic)
```

```
> head(titanic)
```

PassengerId	Survived	Pclass	Name	Sex	Age	SibSp	Parch	Ticket	Fare	Cabin	Embarked
1	0	3	Braund, Mr. Owen Harris	male	22	1	0	A/5 21171	7.2500		S
2	1	1	Cumings, Mrs. John Bradley (Florence Briggs Thayer)	female	38	1	0	PC 17599	71.2833	C85	C
3	1	3	Heikkinen, Miss. Laina	female	26	0	0	STON/O2. 3101282	7.9250		S
4	1	1	Futrelle, Mrs. Jacques Heath (Lily May Peel)	female	35	1	0	113803	53.1000	C123	S
5	0	3	Allen, Mr. William Henry	male	35	0	0	373450	8.0500		S
6	0	3	Moran, Mr. James	male	NA	0	0	330877	8.4583		Q

```
> |
```

What features should we consider?

What is the data type of each column?

```
str(titanic)
```

```
'data.frame':      891 obs. of  12 variables:
 $ PassengerId: int  1 2 3 4 5 6 7 8 9 10 ...
 $ Survived   : int  0 1 1 1 0 0 0 0 1 1 ...
 $ Pclass     : int  3 1 3 1 3 3 1 3 3 2 ...
 $ Name       : Factor w/ 891 levels "Abbing, Mr. Anthony",...: 109 191 358 277 16 559 520 629 417 581 ...
 $ Sex        : Factor w/ 2 levels "female","male": 2 1 1 1 2 2 2 2 1 1 ...
 $ Age        : num  22 38 26 35 35 NA 54 2 27 14 ...
 $ SibSp      : int  1 1 0 1 0 0 0 3 0 1 ...
 $ Parch      : int  0 0 0 0 0 0 0 1 2 0 ...
 $ Ticket     : Factor w/ 681 levels "110152","110413",...: 524 597 670 50 473 276 86 396 345 133 ...
 $ Fare       : num  7.25 71.28 7.92 53.1 8.05 ...
 $ Cabin      : Factor w/ 148 levels "", "A10", "A14",...: 1 83 1 57 1 1 131 1 1 1 ...
 $ Embarked   : Factor w/ 4 levels "", "C", "Q", "S": 4 2 4 4 4 3 4 4 4 2 ...
```


Casting & Human Readability

Set target column as a factor

```
titanic$Survived <- as.factor(titanic$Survived)
```

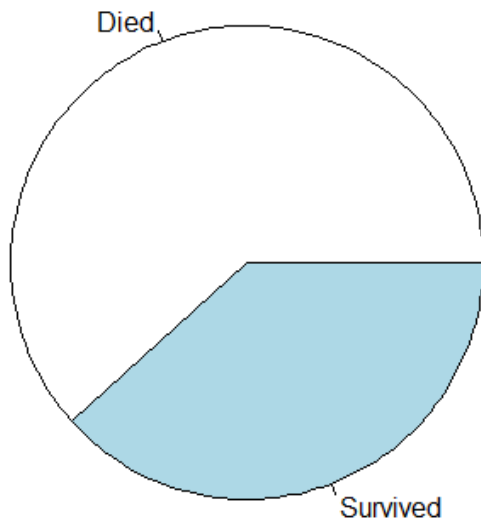
Rename factors and columns

```
levels(titanic$Survived) <- c("Dead", "Survived")  
levels(titanic$Embarked) <- c("Unknown", "Cherbourg",  
                             "Queenstown", "Southampton")  
str(titanic[,c("Embarked", "Survived")])
```

```
'data.frame':      891 obs. of  2 variables:  
 $ Embarked: Factor w/ 4 levels "Unknown","Cherbourg",...: 4 2 4 4 4 3 4 ...  
 $ Survived: Factor w/ 2 levels "0","1": 1 2 2 2 1 1 1 1 2 2 ...
```

Class distribution: Pie Chart

```
survivedTable <- table(titanic$Survived)
par(mar=c(0, 0, 0, 0), oma=c(0, 0, 0, 0),
    cex=1.5)
pie(survivedTable, labels=c("Died", "Survived"))
```

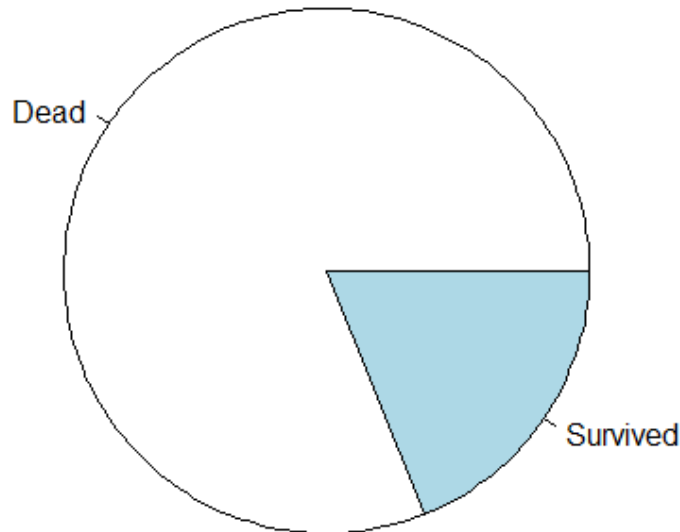


Is Sex a Good predictor?

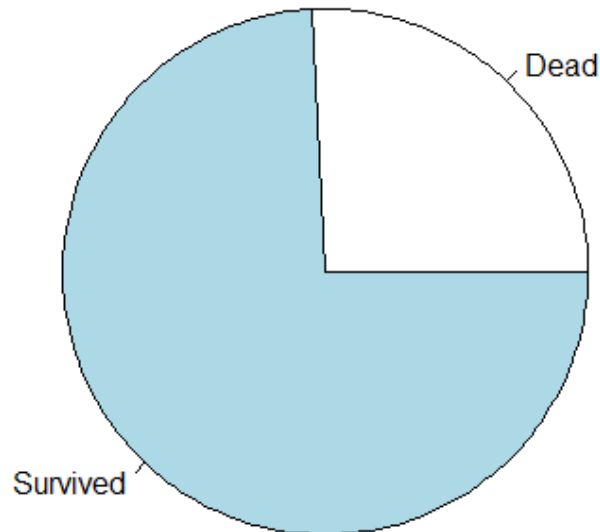
```
male <- titanic[titanic$Sex=="male",]  
female <- titanic[titanic$Sex=="female",]  
par(mfrow=c(1,2))  
pie(table(male$Survived), labels=c("Dead","Survived"),  
main="Survival Portion of Men")  
pie(table(female$Survive), labels=c("Dead","Survived"),  
main="Survival Portion of Women")
```

Is **Sex** a Good predictor?

Survival Proportion Among Men



Survival Proportion Among Women



Is Age a Good Predictor?

```
summary(titanic$Age)
```

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
0.42	20.12	28.00	29.70	38.00	80.00	177

- How about by survival?

```
summary(titanic[titanic$Survived=="Dead",]$Age)  
summary(titanic[titanic$Survived=="Survived",]$Age)
```

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
1.00	21.00	28.00	30.63	39.00	74.00	125

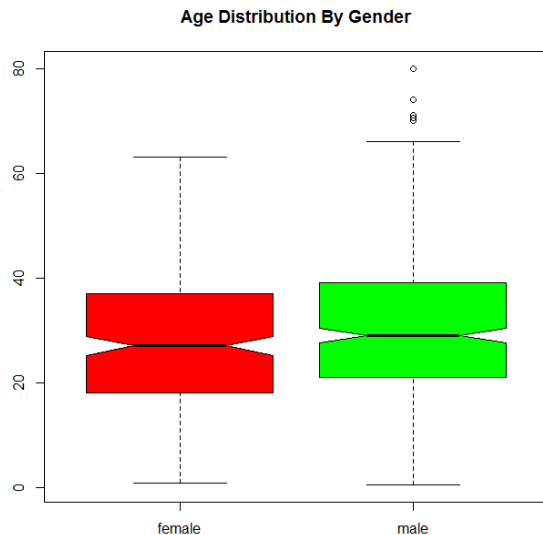
Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
0.42	19.00	28.00	28.34	36.00	80.00	52

Exercise 3

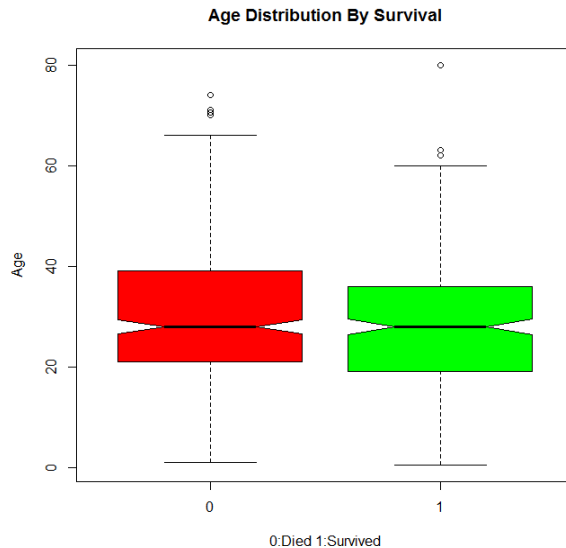
- Create 2 box plots of Age
 - Segmented by Gender
 - Segmented by Survived
- Create a histogram of Age
- Create a density plot of Age
 - `na.omit()` may be useful

Sample Solution 3

```
boxplot(Age ~ Sex, data=titanic,  
main="Age Distribution By Gender",  
col=c("red","green"), notch=T)
```

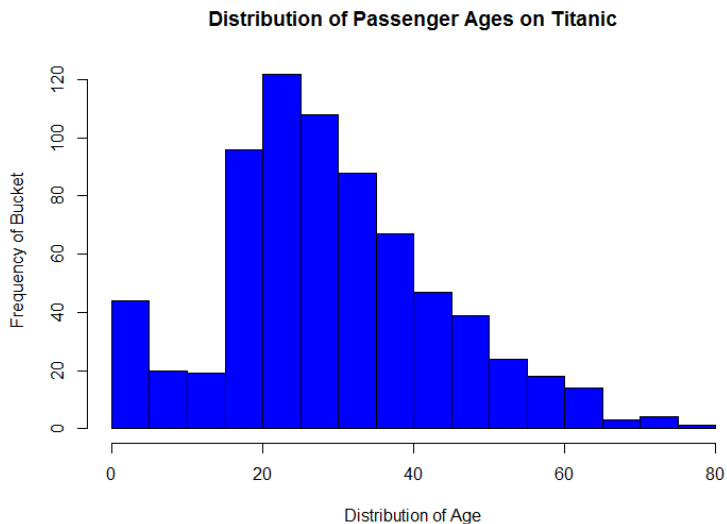


```
boxplot(Age ~ Survived, data=titanic,  
main="Age Distribution By Survival",  
col=c("red","green"), notch=T, ylab="Age")
```

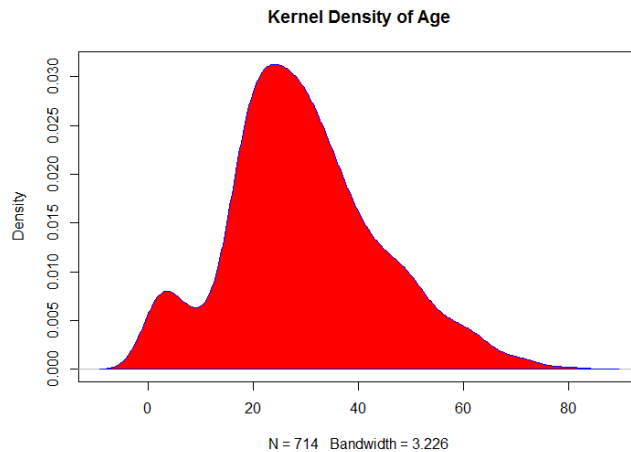


Sample Solution 3

```
hist(titanic$Age, col="blue", breaks=12,  
xlab="Distribution of Age", ylab="Frequency of  
Bucket", main="Distribution of Passenger Ages  
on Titanic")
```

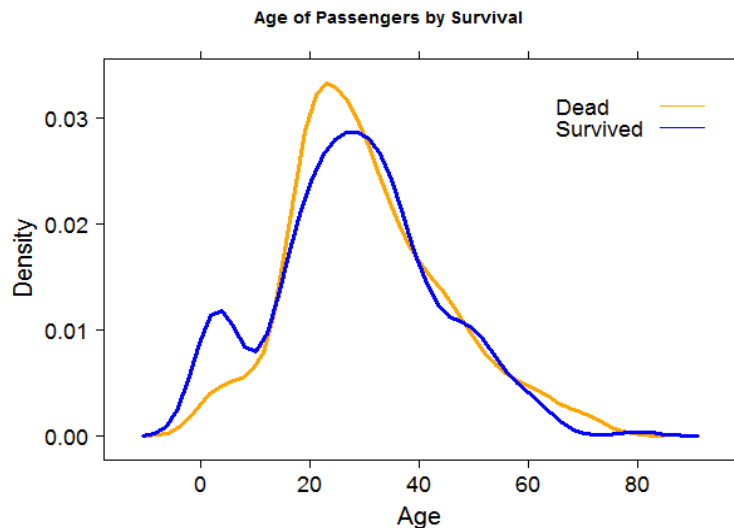


```
density(titanic$Age) #NAs prevent this  
d <- density(na.omit(titanic$Age))  
plot(d, main="Kernel Density of Age")  
polygon(d, col="red", border="blue")
```

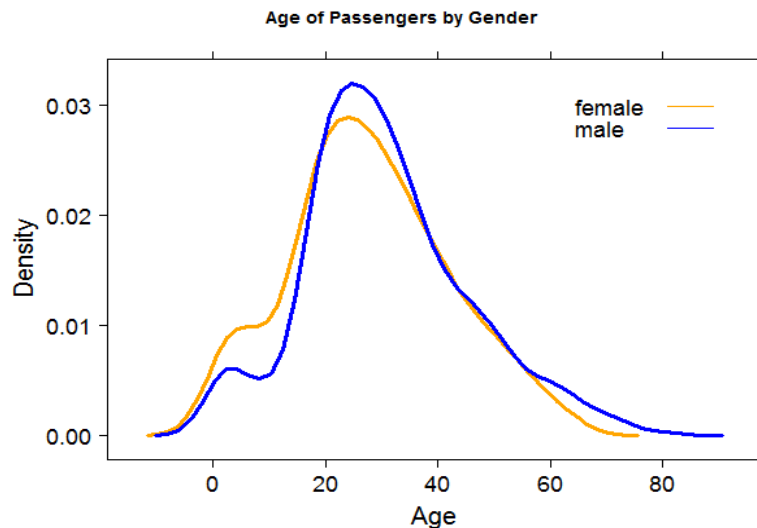


Is Age a Good Predictor?

```
densityplot(~ Age, data=titanic,  
groups=Survived, plot.points=F, lwd=3,  
auto.key=list(corner=c(0,0), x=0.7, y=0.8))
```



```
densityplot(~ Age, data=titanic,  
groups=Sex, plot.points=F, lwd=3,  
auto.key=list(corner=c(0,0), x=0.7, y=0.8))
```



Exercise 4

- Create a new column "Child"
 - Assign each row "Adult" or "Child" based on a consistent metric (age < 10 etc.)
- Use ggplot to create a series of box plots relating Fare, Child, Sex, and Survived

Questions?

Sample Solution 4

```
child <- titanic$Age
child[child < 13] <- 0
child[child >= 13] <- 1
titanic$Child <- as.factor(child)
levels(titanic$Child)
levels(titanic$Child) <- c("Child", "Adult")

g <- ggplot(data=titanic[!is.na(titanic$Child),],
            aes(x=Child, y=Fare))
g.b <- g + geom_boxplot()
g.b + facet_grid(Sex ~ Survived)
```

