

Data Exploration, Visualization, and Feature Engineering

Agenda

- Why data exploration and visualization
- Exploration and visualization using R
 - R core graphics and Lattice
 - ggplot2
- Exercises using Titanic data set

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Data beats algorithm but...

- More data usually yields 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 common myths

- There is no single ML algorithm that will take raw data and give you the best model
- 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 source of many problems!
- Remember the 80/20 rule
 - 80% : Data cleaning, exploration, feature engineering etc.
 - 20% : Model building

Session objectives

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

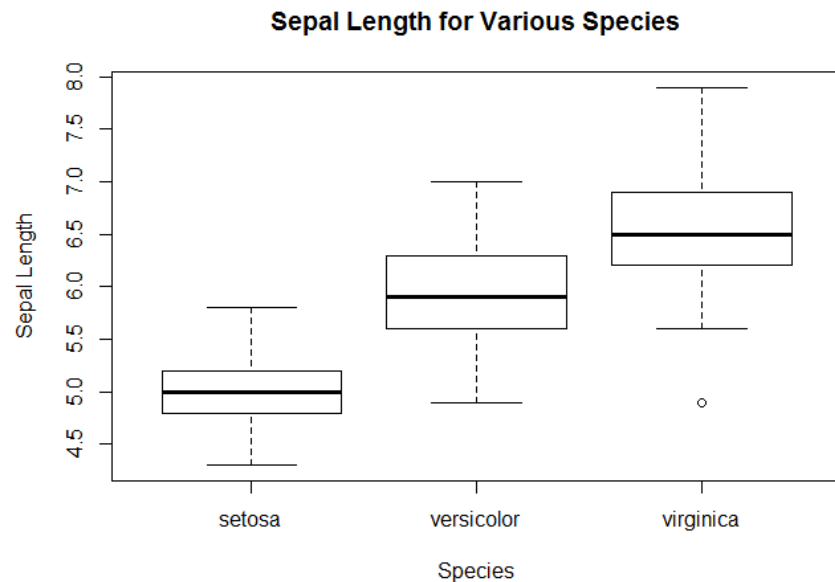
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Box plots

- Distribution of single feature
- Can partition by target class

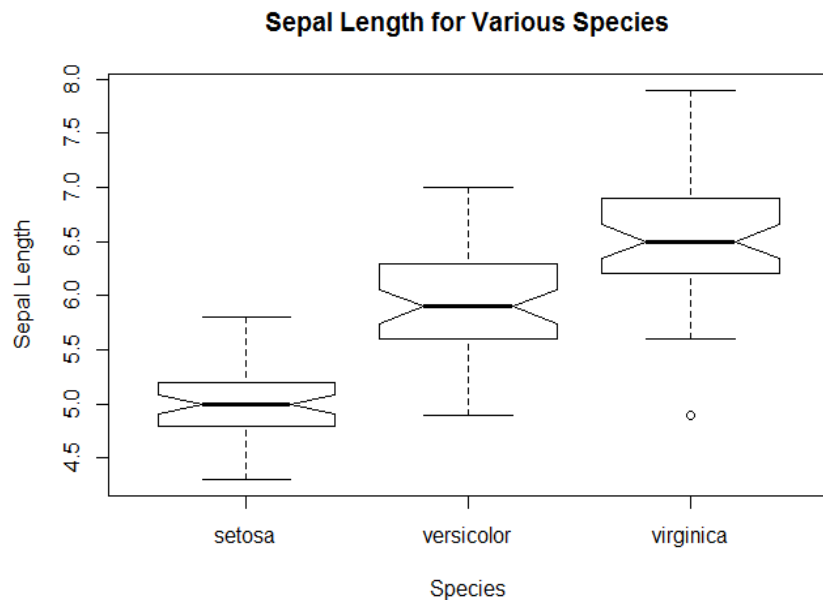
```
data(iris)
boxplot(Sepal.Length ~ Species,
data=iris,
main="Sepal Length for Various
Species",
xlab="Species",
ylab="Sepal Length"
)
```



Box plots with notches

- Estimate of confidence interval of the median

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



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

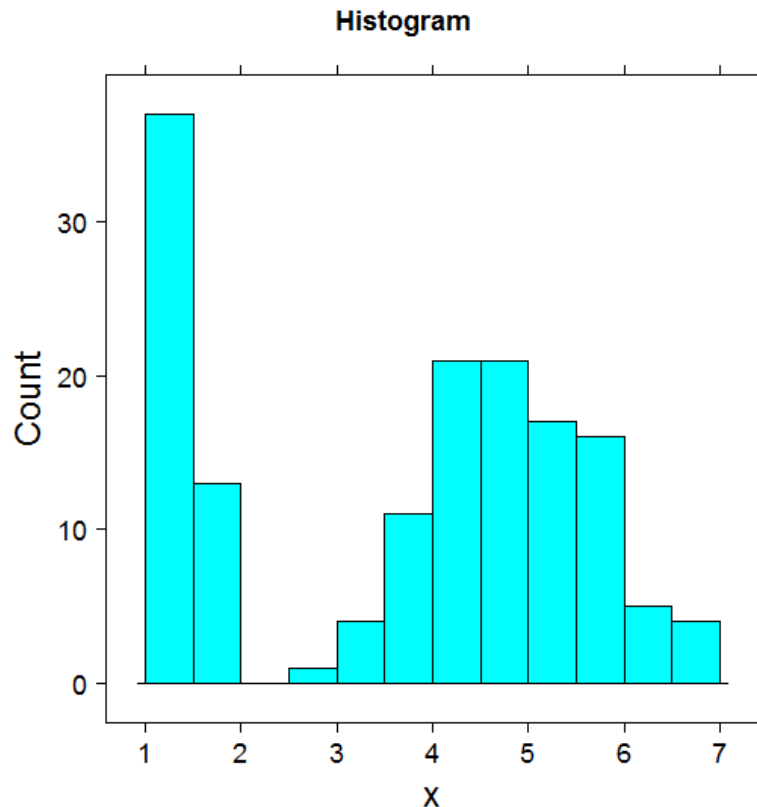
R Studio makes it easier

```
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
```

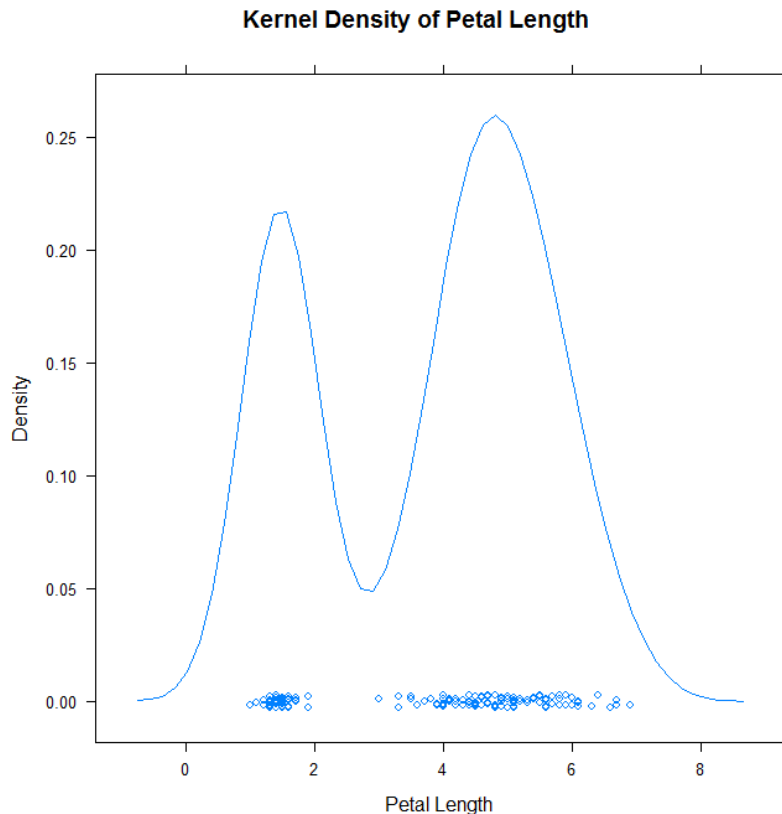
Lattice: Histogram



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

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

Lattice: Density plots

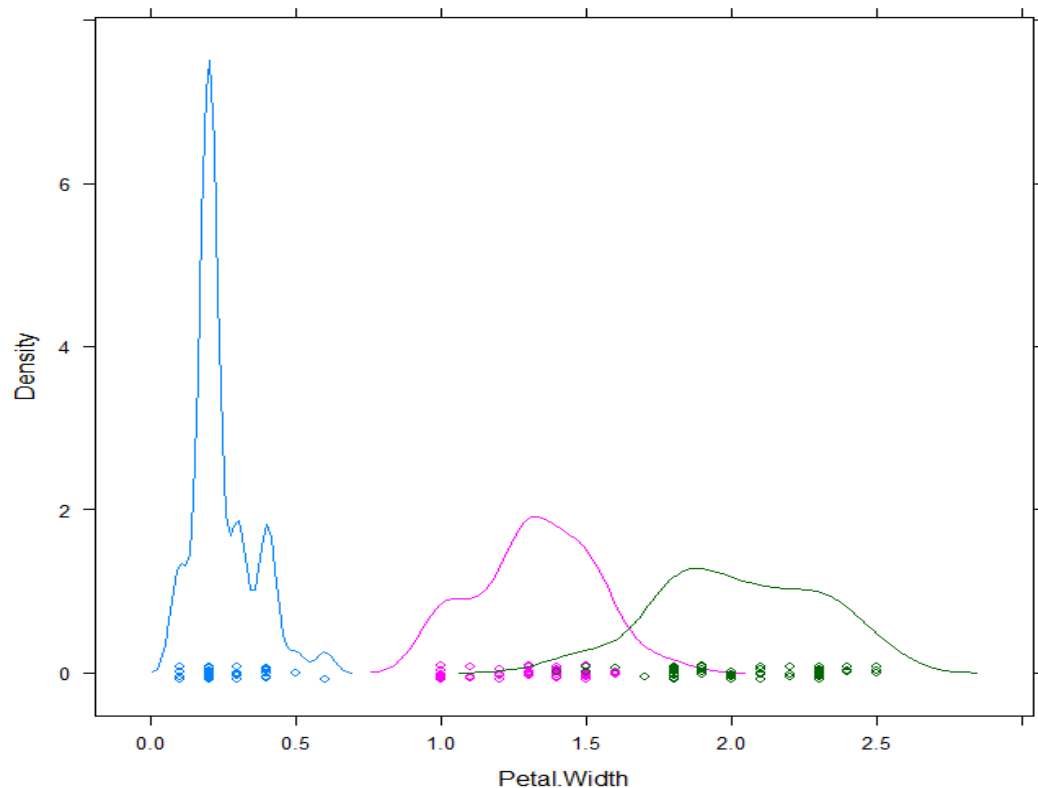


```
densityplot(iris$Petal.Length,main="Kernel Density of Petal Length", xlab="Petal Length")
```

The devil is in the details

- And the details are in segments
- Segmentation reveals pattern that are otherwise hidden
- Create as many segments as possible
 - Your domain understanding will help in creating segments

Lattice: Multiple density plots



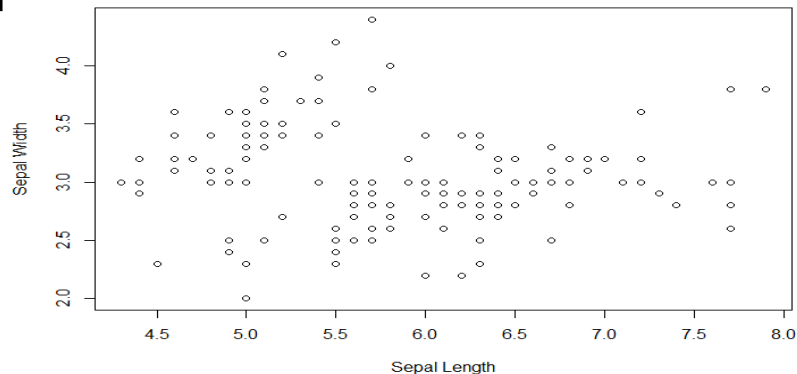
```
densityplot(~Petal.Width,  
data=iris,  
groups=Species)
```


Exercise 1

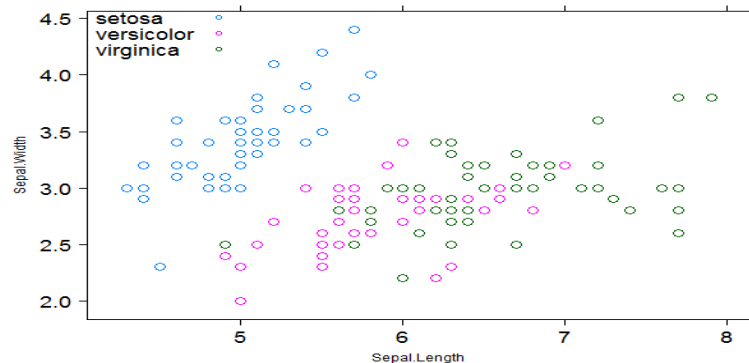
- 2-D scatter plots – plot() and xyplot()
 - Sepal Length vs Sepal Width
 - Petal Length vs Petal Width
 - Segment based on Species (Lattice)

Sample solution

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



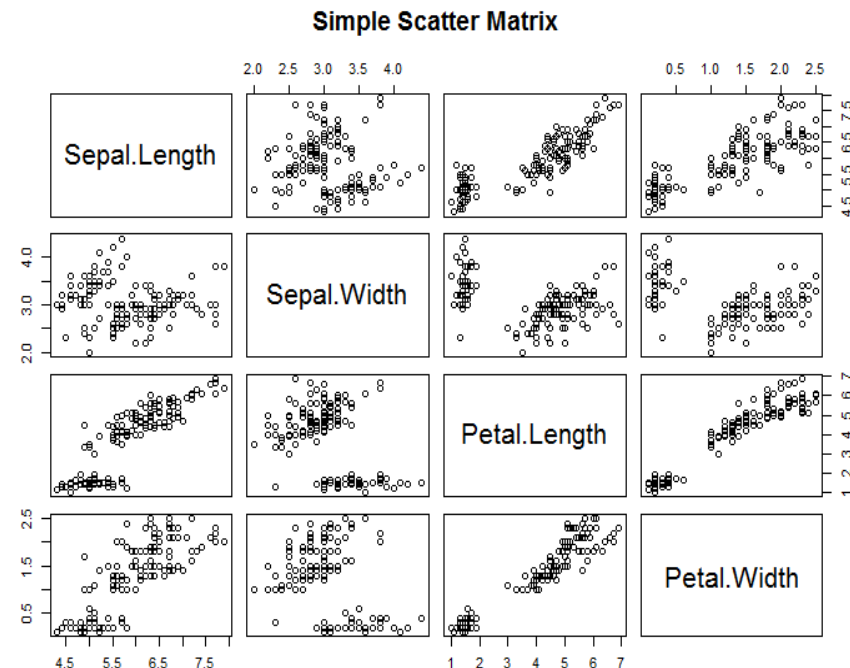
```
# Lattice Graphics
xyplot(Sepal.Width ~ Sepal.Length,
       data=iris, groups=Species,
       auto.key=list(corner=c(0,0), x=0,
                     y=0.85, cex=1.5), cex=1.5,
       scales=list(cex=1.5))
```



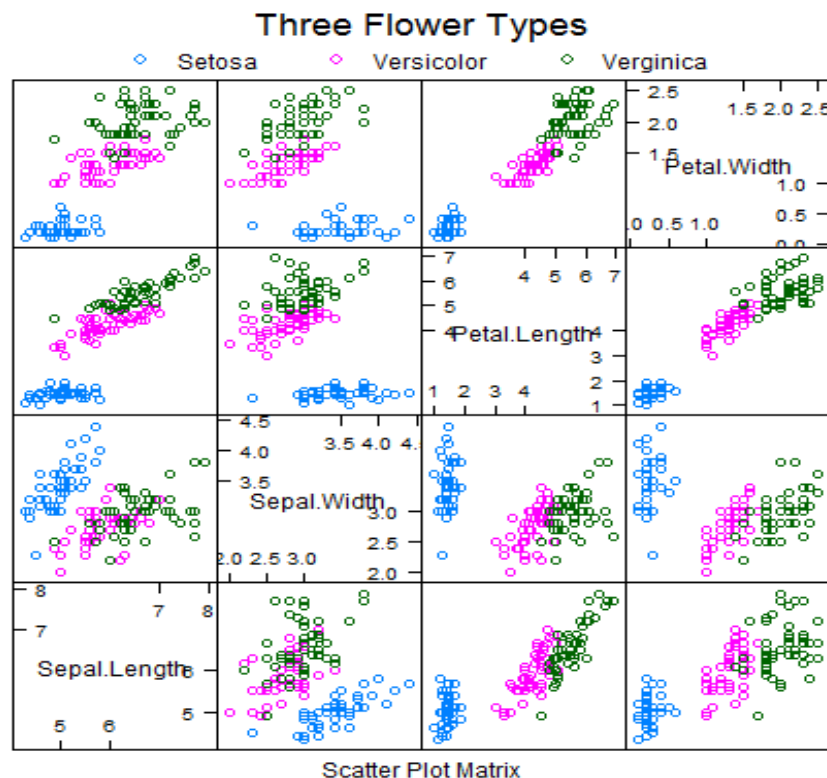
Core: Scatter plot matrix

- 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



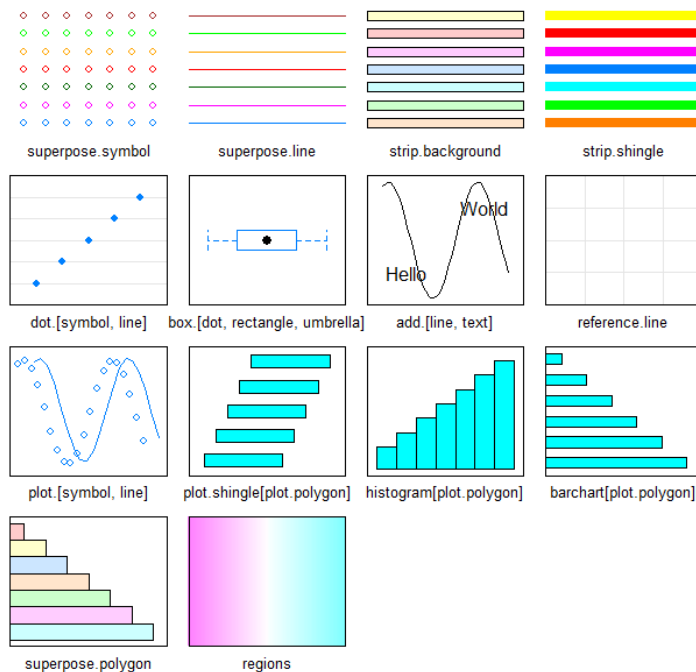
```
# Getting settings for legend
super.sym <-
trellis.par.get("superpose.symbol")

splom(iris[1:4],
groups=iris$Species)
```

Graphical settings

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

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



Enhanced scatter plot matrix



```
library(GGally)
```

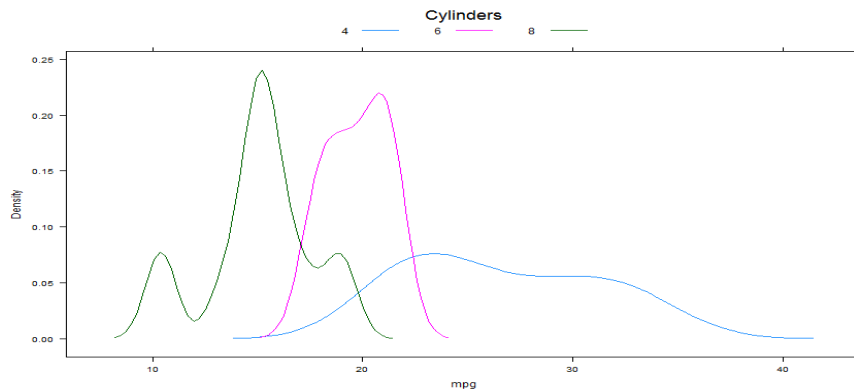
```
ggpairs(iris,  
  ggplot2::aes(color=Species))
```

Exercise 2

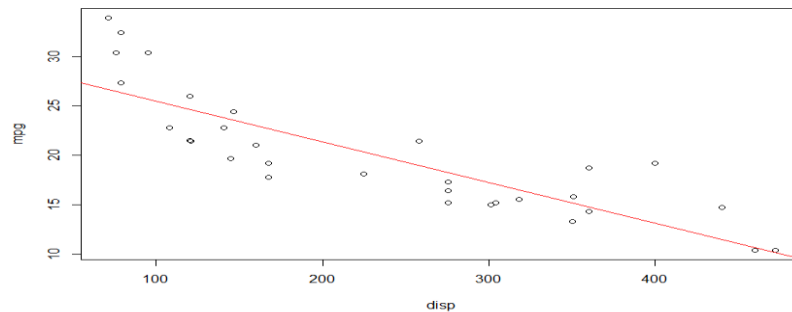
- Load "mtcars" dataset: `data(mtcars)`
 - `?mtcars` for details
 - Eyeball the data
- **Goal:** Predict mpg based on other columns
- Create at least 2 different plots illustrating useful relationships in data

Sample solution

```
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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 - **ggplot2**
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ggplot fundamentals

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

The diamonds data set

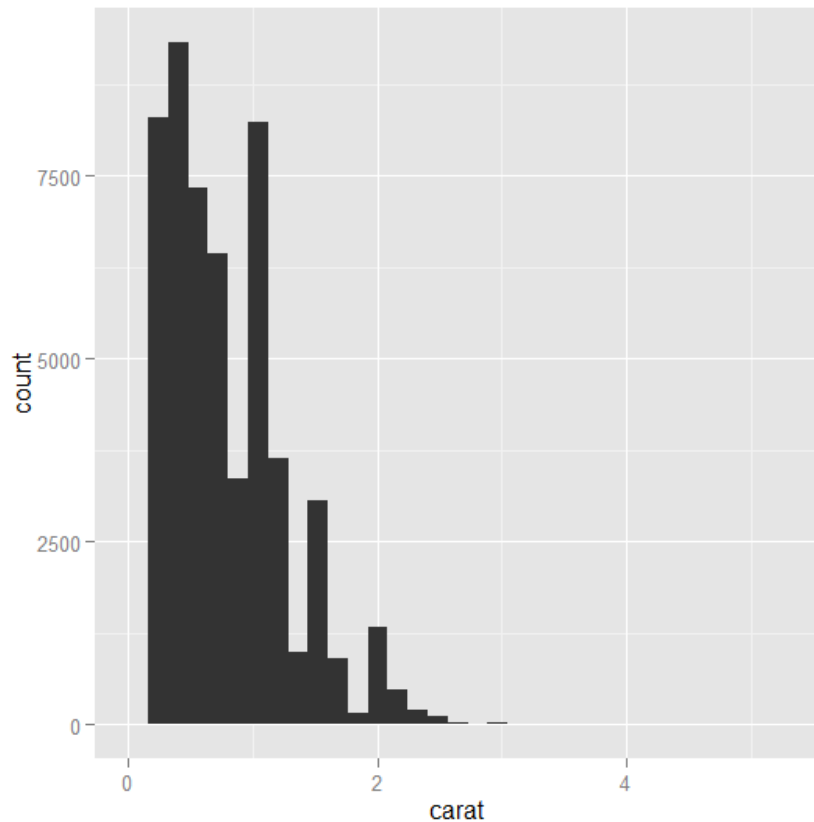
```
library(ggplot2)
data(diamonds)
head(diamonds)
```

```
> 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

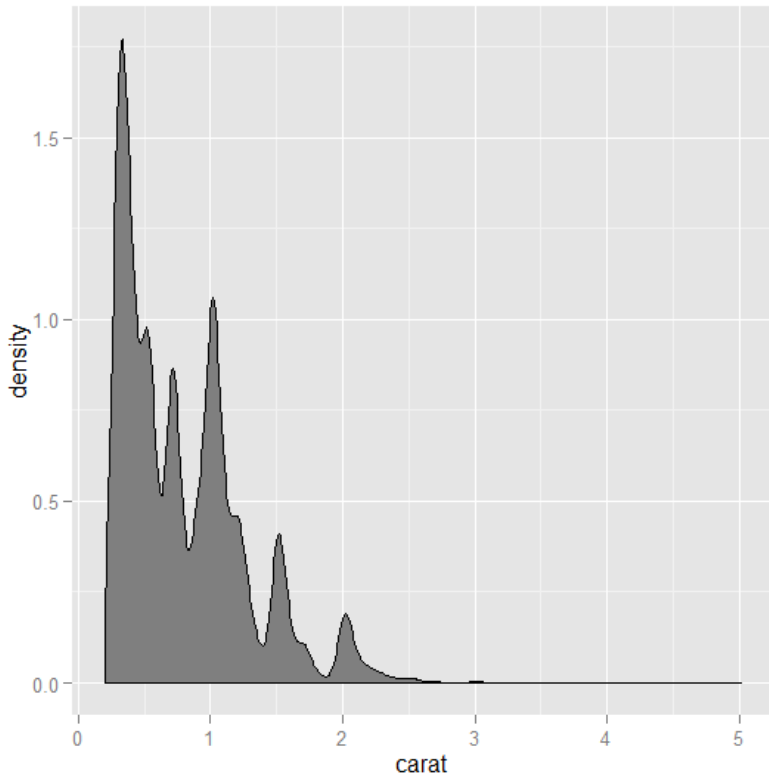
```
> |
```

Histogram



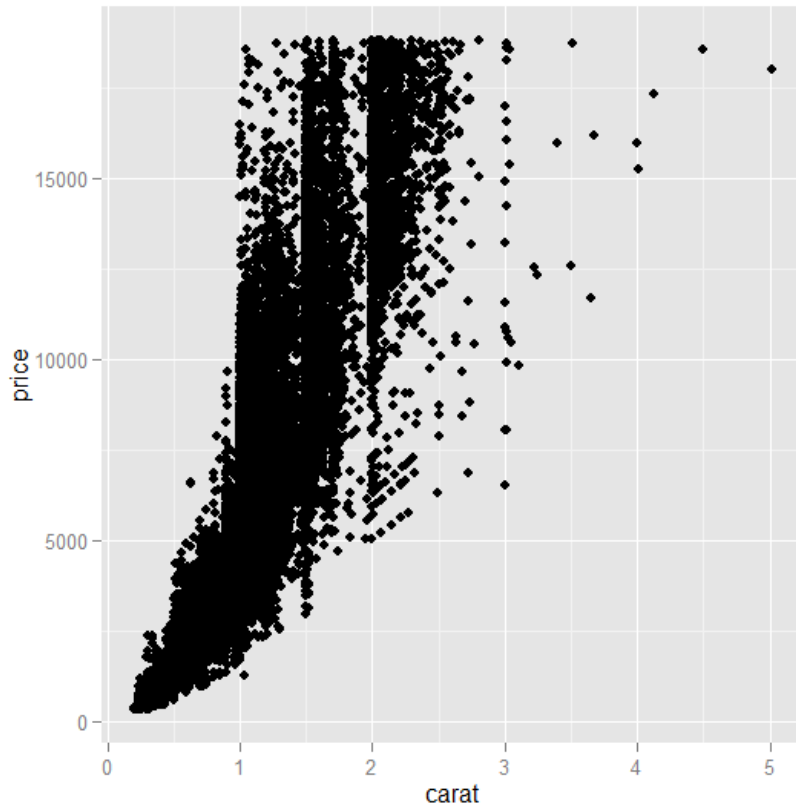
```
ggplot(diamonds, aes(x=carat)) +  
geom_histogram()
```

Density plot



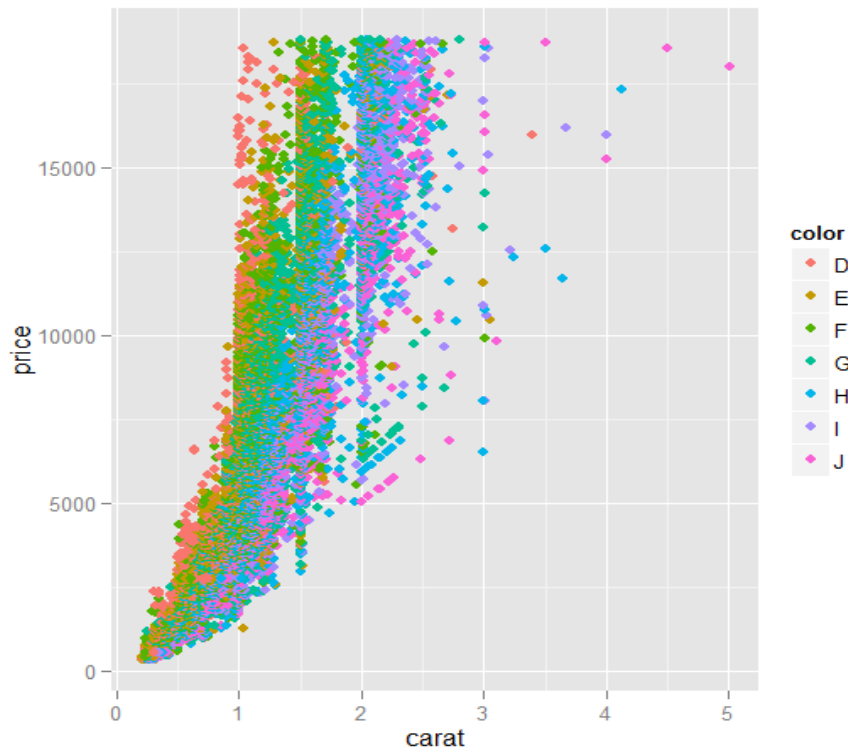
```
ggplot(diamonds) +  
  geom_density(aes(x=carat),  
    fill="gray50")
```

Scatter plots



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

ggplot object

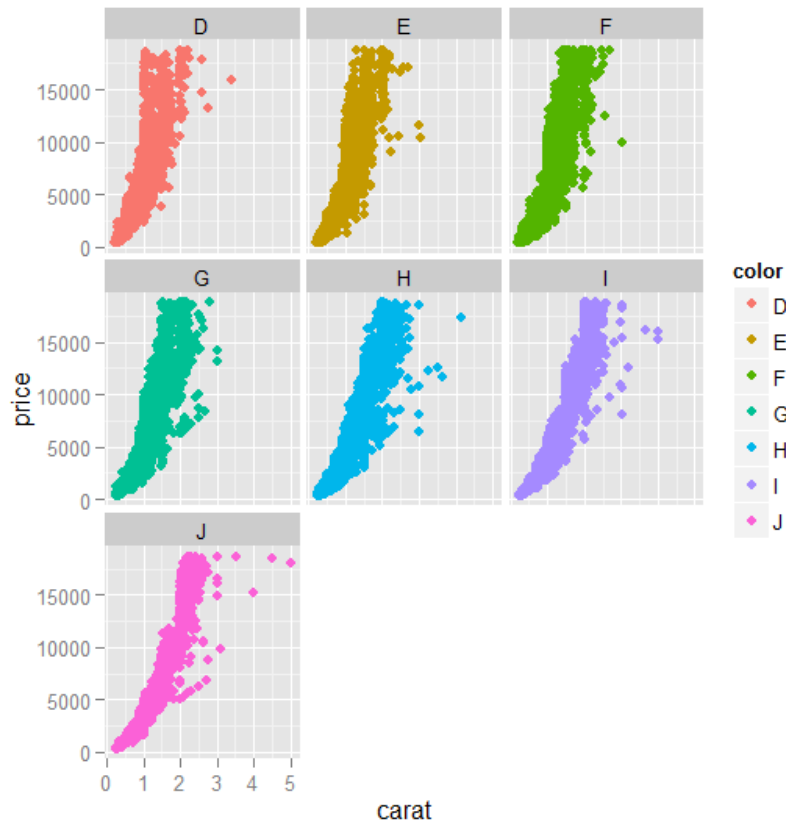


```
# Store the plot for future  
modification  
g <- ggplot(diamonds, aes(x=carat,  
y=price))
```

```
# add settings specific to  
geom_point layer  
g + geom_point(aes(color=color))
```

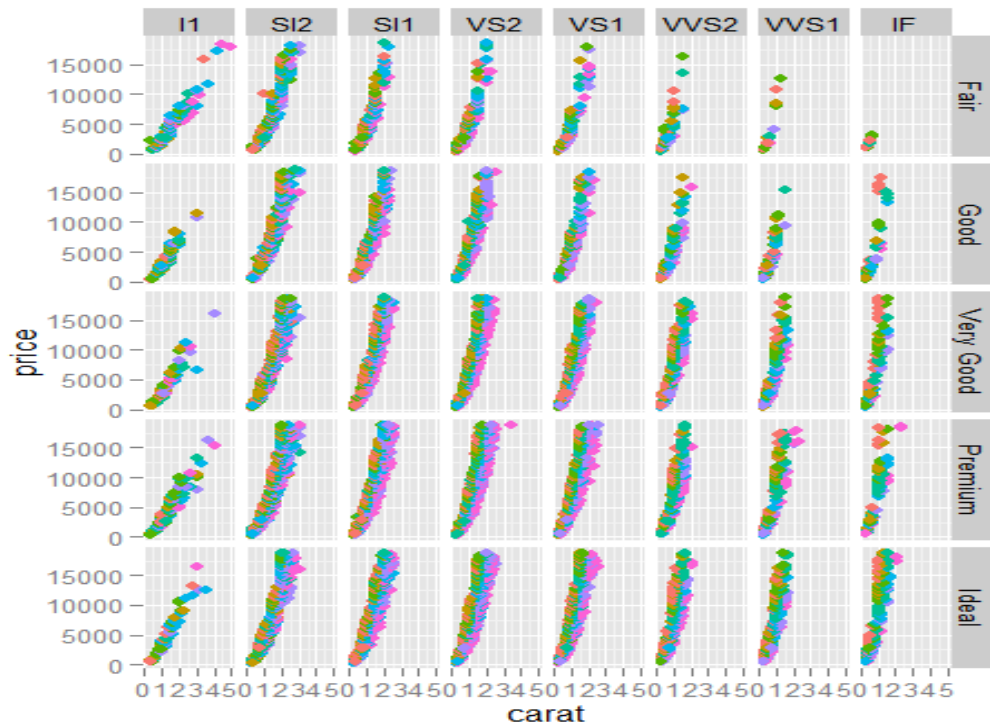


Separating the segments



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

More segments!



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

color

- D
- E
- F
- G
- H
- I
- J

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 data set

- 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          1         0       3    Braund, Mr. Owen Harris male  22     1     0      A/5 21171  7.2500           S  
2          2         1       1 Cumings, Mrs. John Bradley (Florence Briggs Thayer) female  38     1     0      PC 17599 71.2833    C85       C  
3          3         1       3    Heikkinen, Miss. Laina female  26     0     0 STON/O2. 3101282  7.9250           S  
4          4         1       1 Futrelle, Mrs. Jacques Heath (Lily May Peel) female  35     1     0     113803 53.1000   C123       S  
5          5         0       3    Allen, Mr. William Henry male  35     0     0     373450  8.0500           S  
6          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)
```

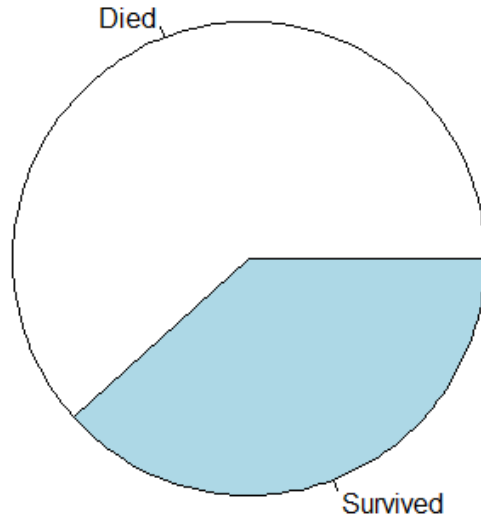
Rename factors and columns

```
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",]
```

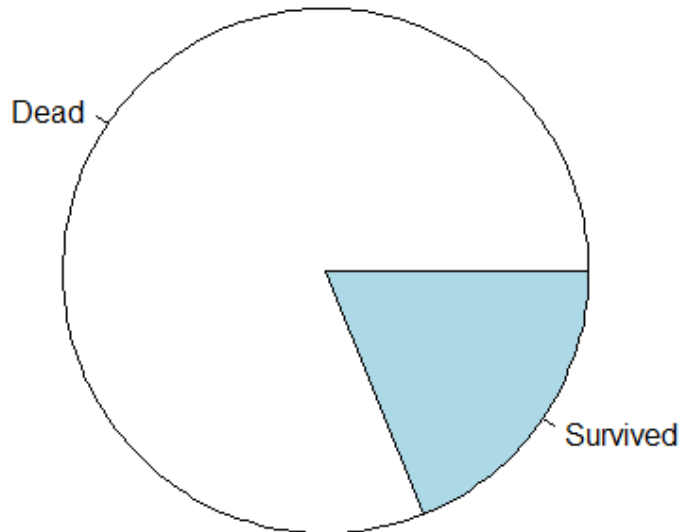
```
par(mfrow=c(1,2))
```

```
pie(table(male$Survived), labels=c("Dead","Survived"),  
main="Survival Portion of Men")
```

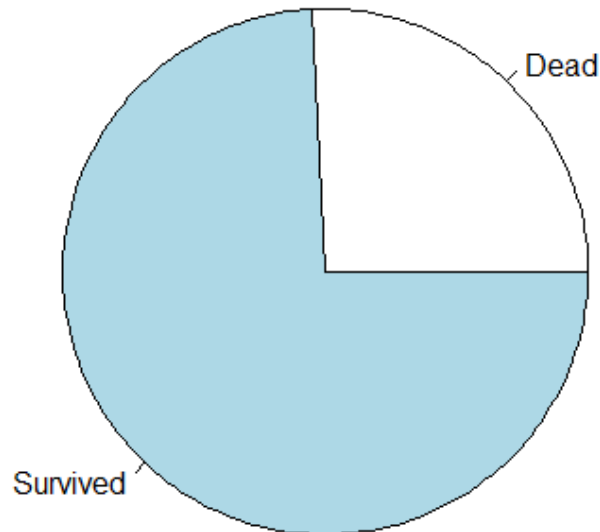
```
pie(table(female$Survive), labels=c("Dead","Survived"),  
main="Survival Portion of Women")
```

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)
```

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

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

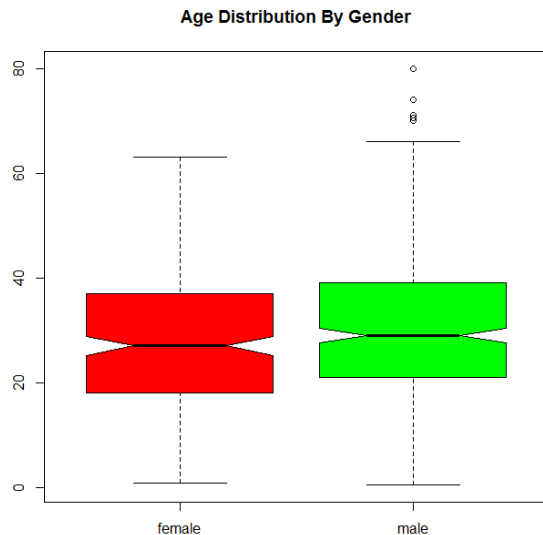
Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
0.42	19.00	28.00	28.34	36.00	80.00	52

Exercise 3

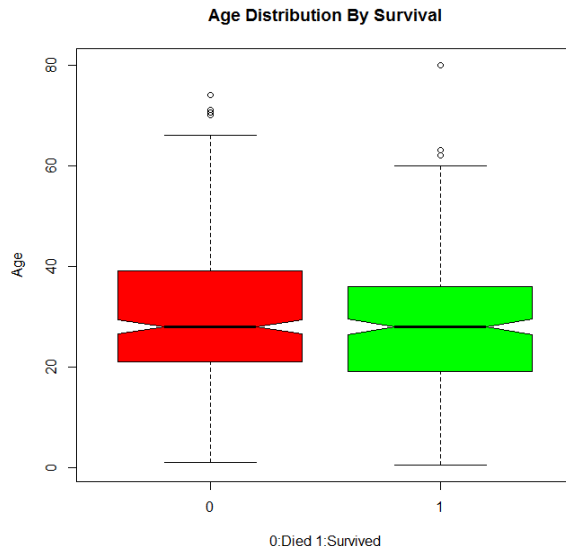
- Create 2 box plots of Age
 - Segmented by Gender
 - Segmented by Survived
- Create a histogram of Age
- Create a density plot of Age
 - `na.omit()` may be useful

Sample solution

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

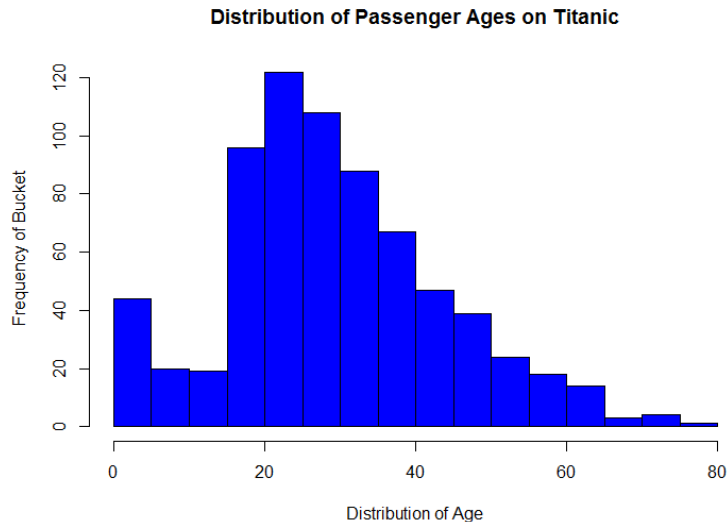


```
boxplot(Age ~ Survived, data=titanic,  
main="Age Distribution By Survival",  
col=c("red","green"), notch=T, ylab="Age")
```

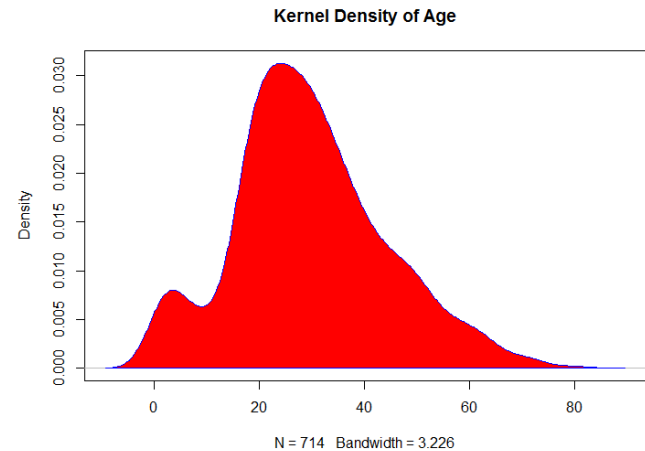


Sample solution

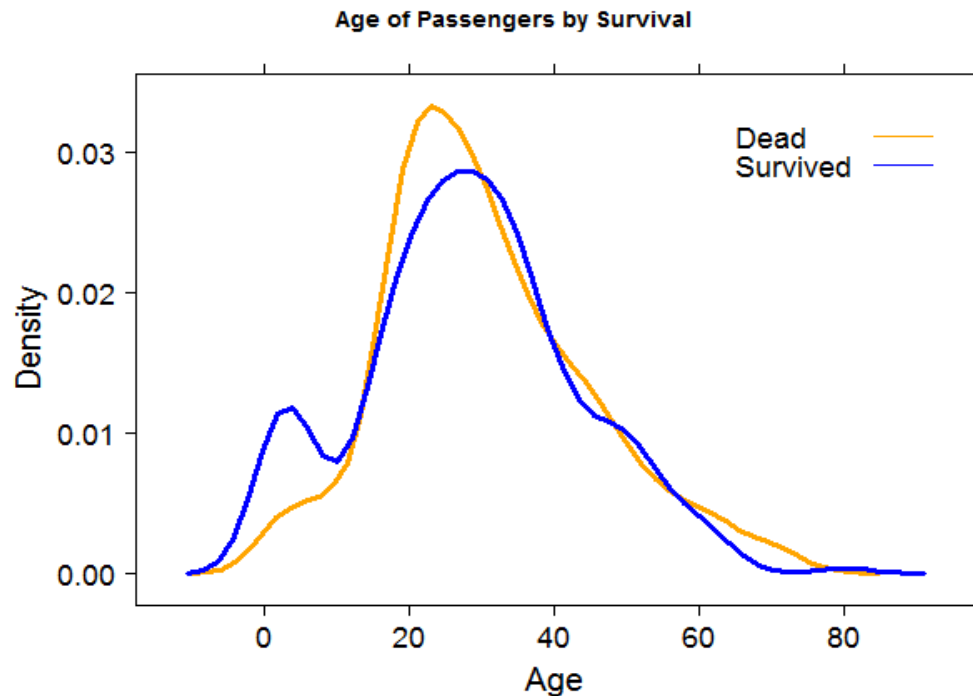
```
hist(titanic$Age, col="blue", breaks=12,  
xlab="Distribution of Age", ylab="Frequency of  
Bucket", main="Distribution of Passenger Ages  
on Titanic")
```



```
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")
```

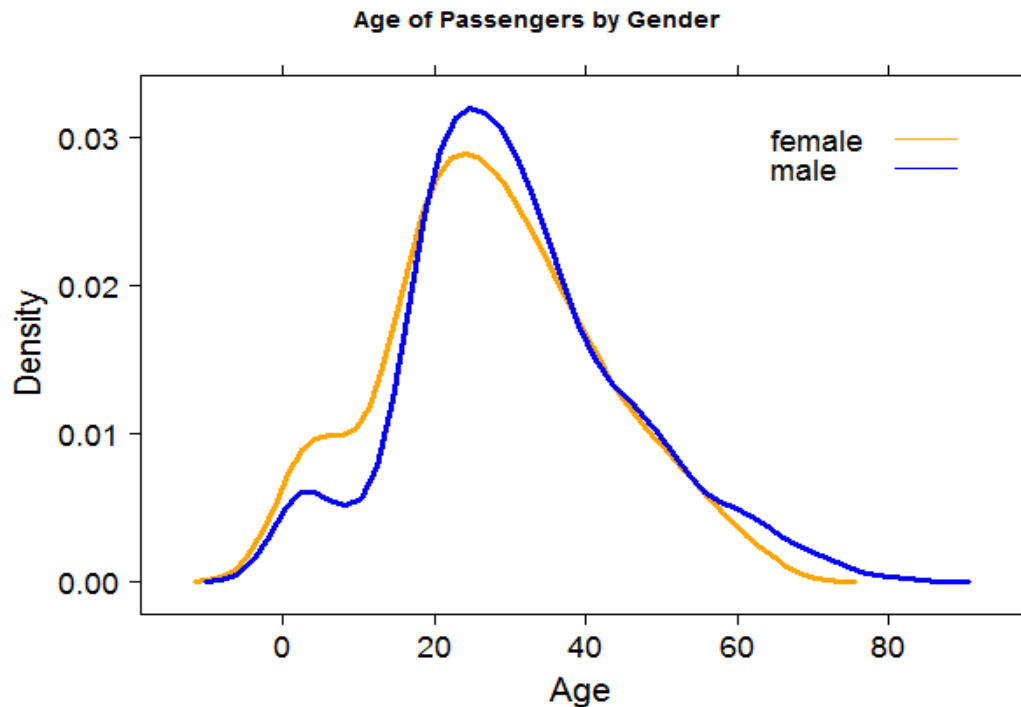


Is Age a good predictor for Survival?



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


Is Age a good predictor for Gender?



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

Homework

- Create a new column called "Child"
 - Assign each row "Adult" or "Child" based on a consistent metric (age < 10 or age ≤ 14 etc.)
- Use ggplot to create a series of box plots relating Fare, Child, Sex, and Survived

Questions?