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

Learning Guidance

- Focus on the ideas rather than exact syntax. R help is your friend
- I will share output samples on the slides often
- Sample code + slides: Data Exploration and Visualization folder

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Formula data type

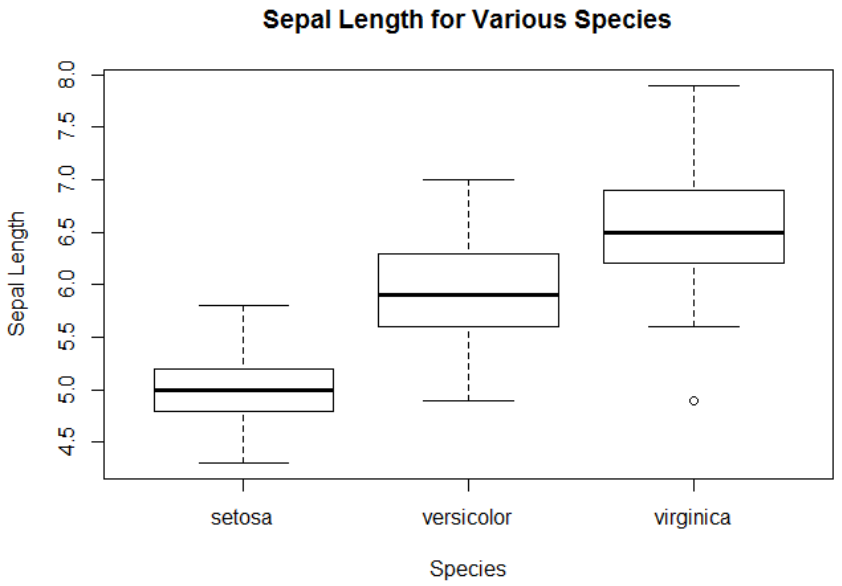
- Built in R type
- Defines relationships between named columns

```
data(iris)
head(iris)

f.1 <- Species ~ .
f.2 <- ~ Species + Petal.Width
f.3 <- ~ Petal.Length | Species

class(f.1)
```

Box Plots

- Distribution of single feature
- Can partition by target class

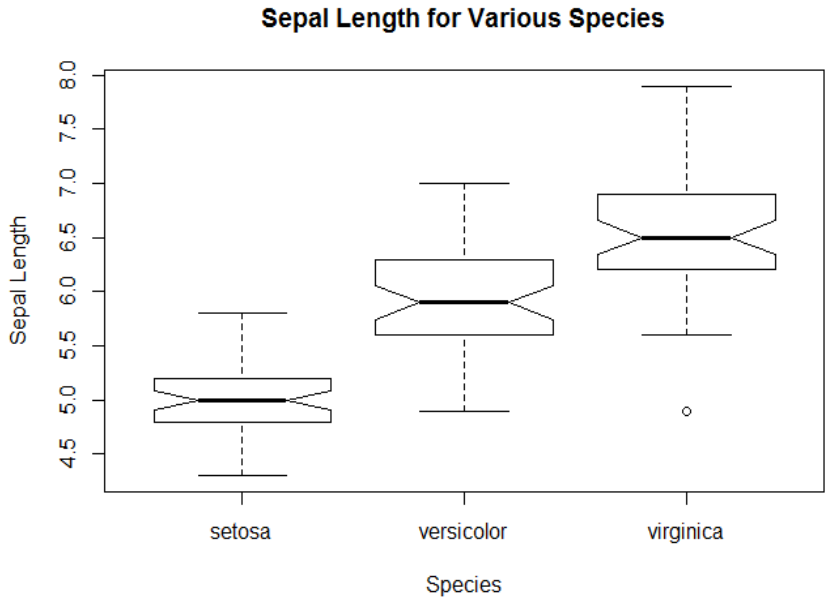
```
data(iris)
boxplot(Sepal.Length ~ Species,
data=iris,
main="Sepal Length for Various
Species",
xlab="Species",
ylab="Sepal Length"
)
```



Box Plots with Notches

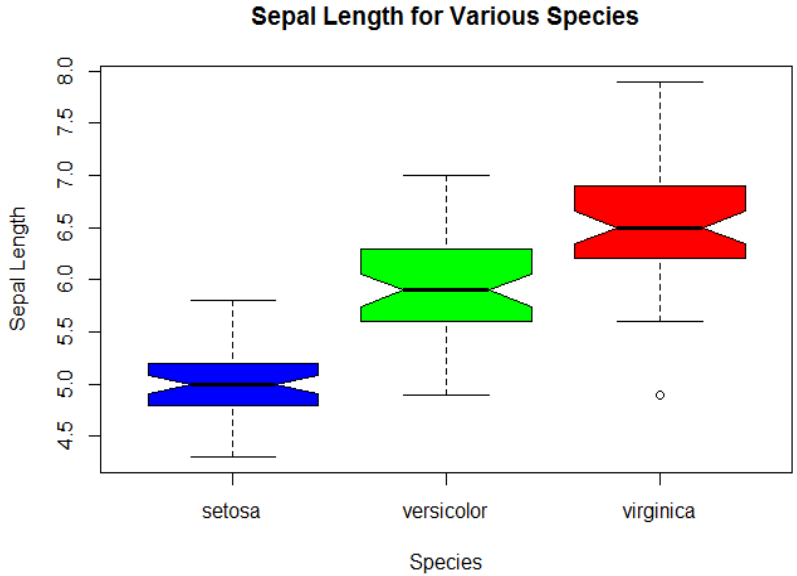
- Estimate of confidence interval of the median
- Notch overlap indicates confidence that median is different

```
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
pdf("mygraph.pdf")	pdf file
win.metafile("mygraph.wmf")	windows metafile
png("mygraph.png")	png file
jpeg("mygraph.jpg")	jpeg file
bmp("mygraph.bmp")	bmp file
postscript("mygraph.ps")	postscript file

```
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
```

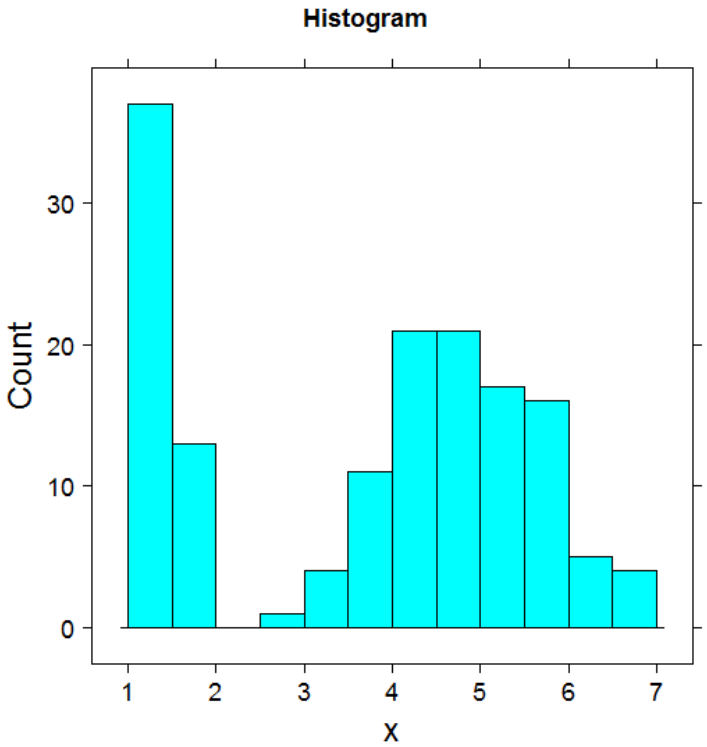
Windows Saves to default: Libraries\Documents

R Studio makes it easier

Lattice: Histogram

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

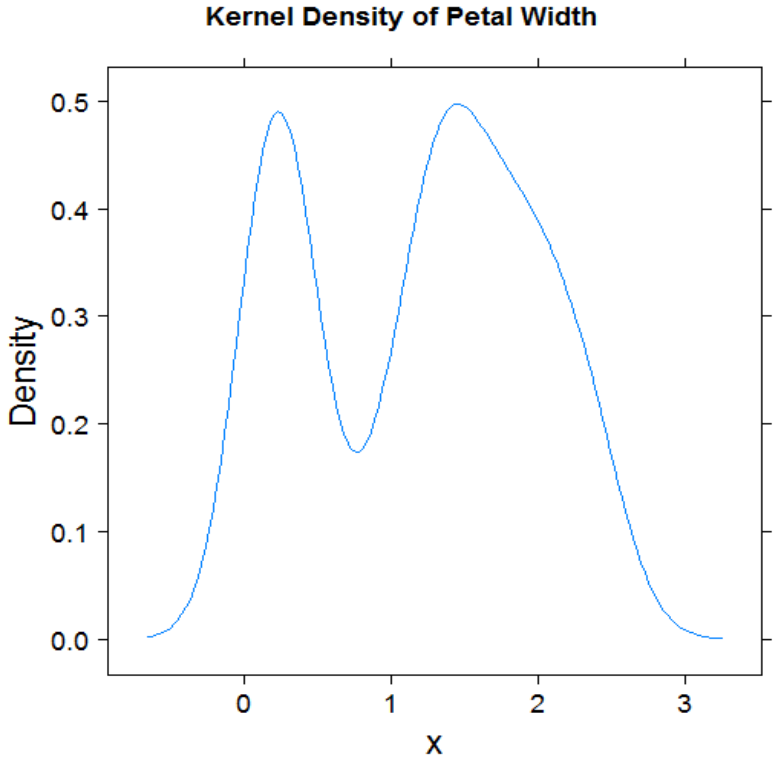
```
histogram(iris$Petal.Length,
breaks=10, type="count",
main="Histogram")
```



Lattice: Density plots

- Variant of Histogram
- Scaled for easy comparisons

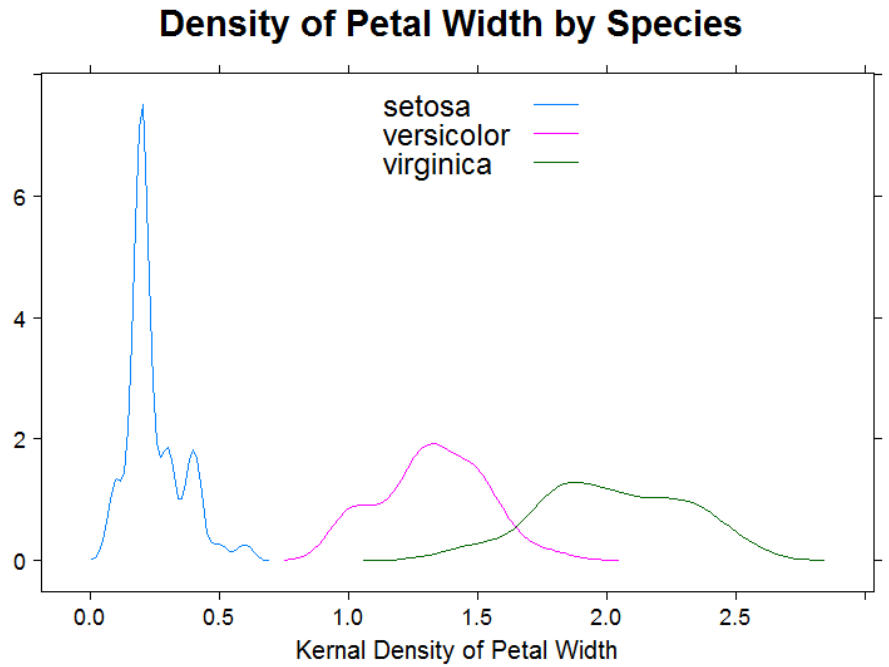
```
densityplot(iris$Petal.Length
,main="Kernel Density of
Petal Length",
type="percent", n=150)
```



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))
```

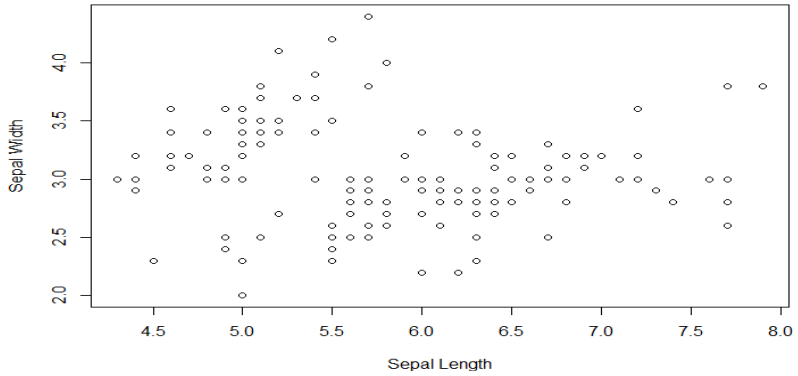


Exercise 1

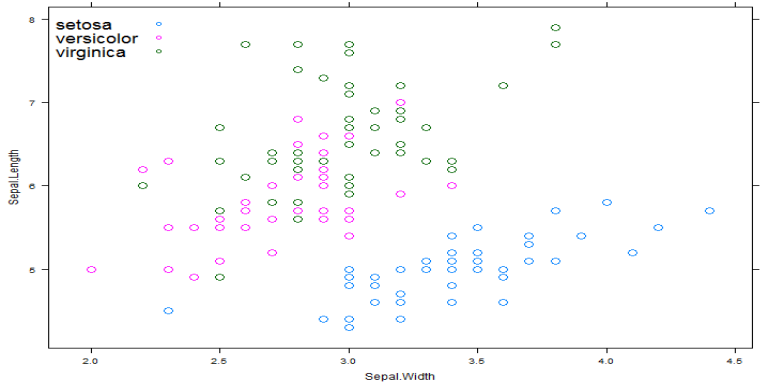
- 2-D Scatter plots – plot() and xyplot()
  - Sepal Length vs Sepal Width
  - Petal Length vs Petal Width
  - Color based on Species (lattice)

Sample Solution

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




```
# Lattice Graphics
xyplot(Sepal.Length ~
Sepal.Width, 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))
```



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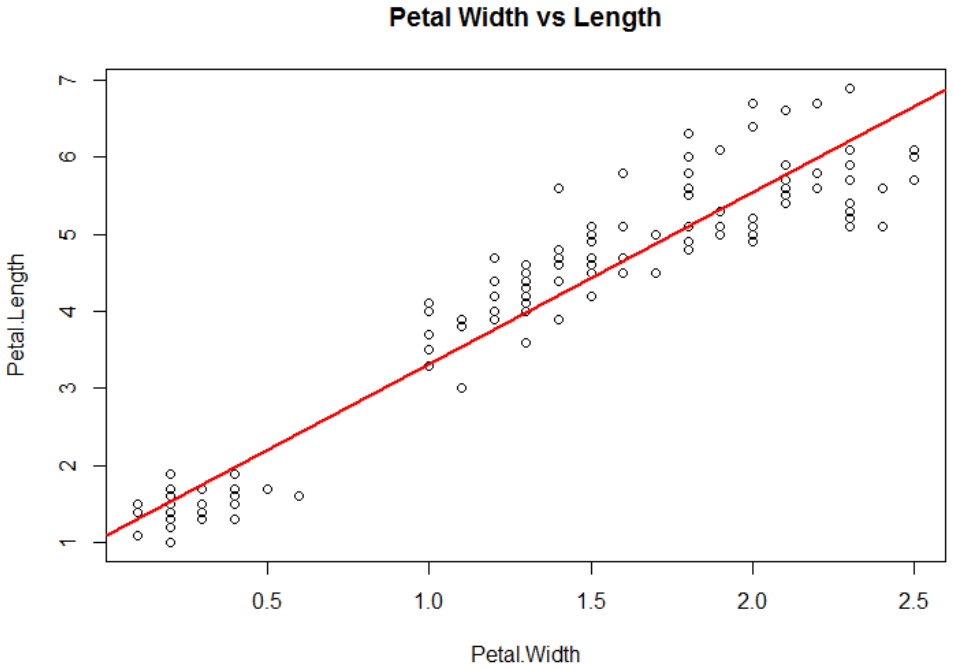
Extended Scatter Plots

- Add a regression line

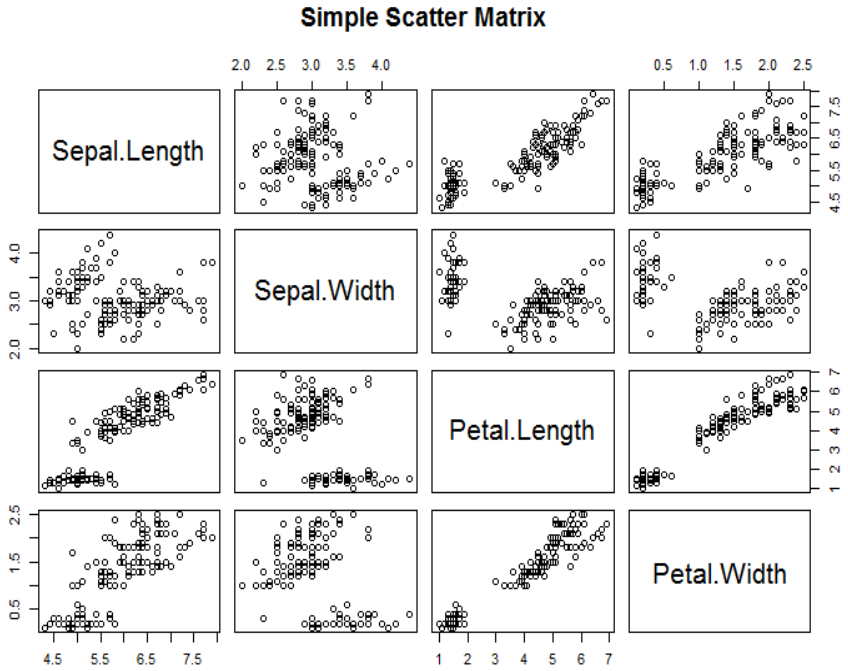
```
plot(Petal.Length ~
Petal.Width, data=iris,
main="Petal Width vs
Length")

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

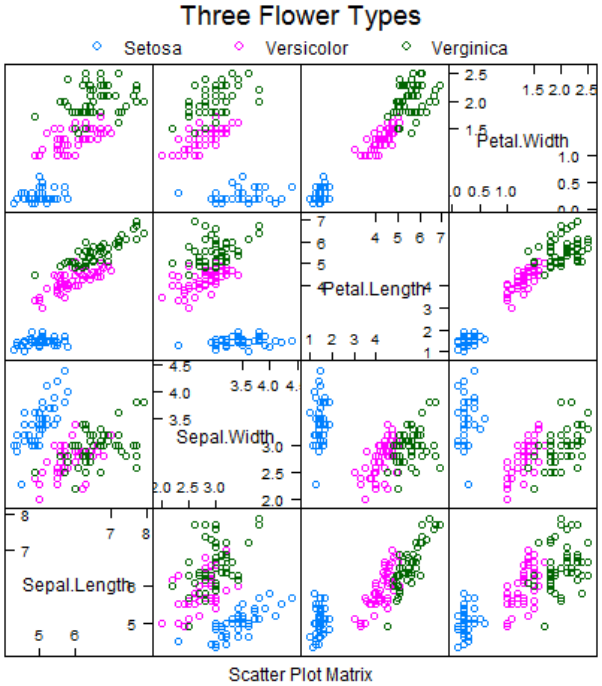
```
pairs(~ Sepal.Length +
Sepal.Width + Petal.Length +
Petal.Width, data=iris,
main="Simple Scatter Matrix")
```



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","Verginic
a"))))
```

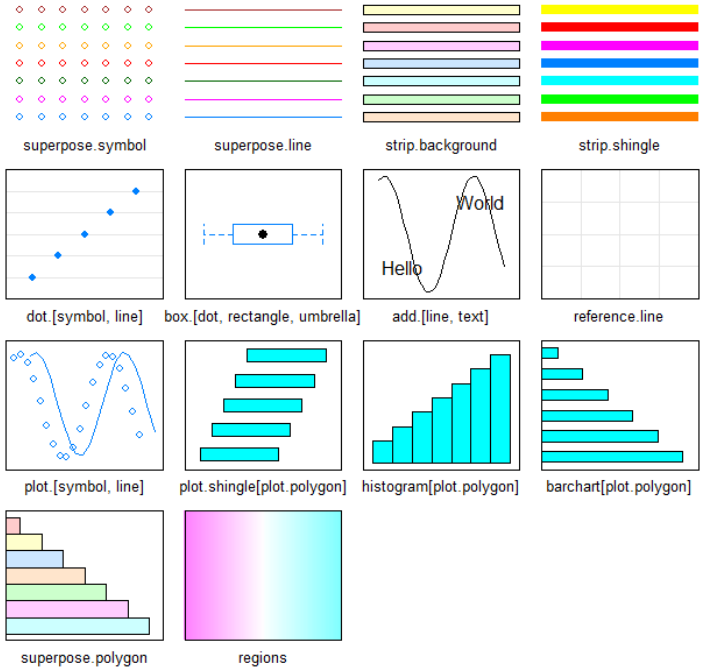


Graphical Settings

- Simple Grouping

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

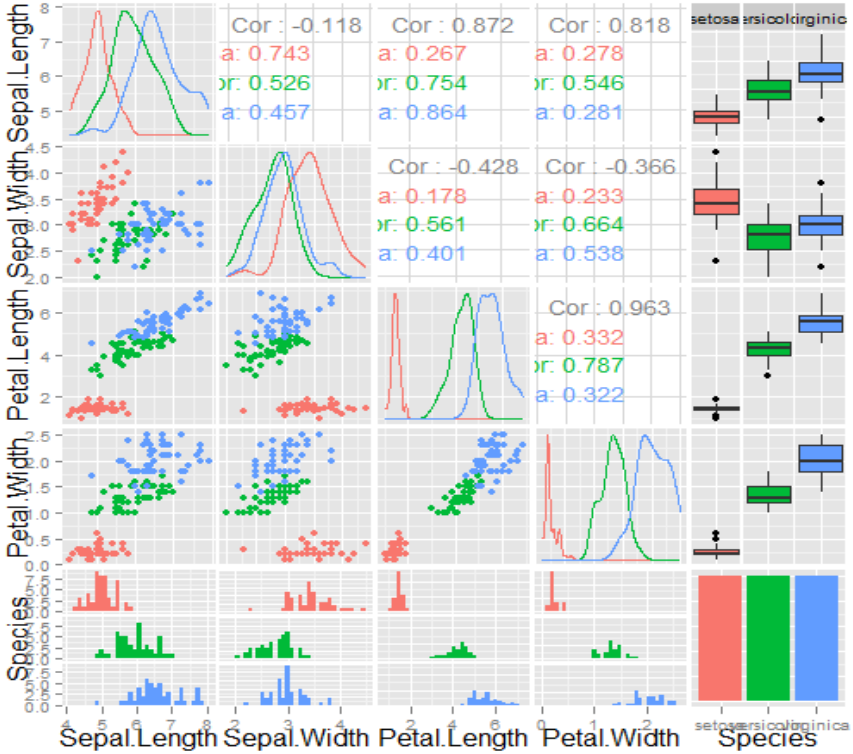
```
show.settings()
my.theme$fontsize$text=20
```



Enhanced Scatter Plot Matrices

```
library(GGally)

ggpairs(iris, color="Species")
```

- Many packages have custom pairs implementations

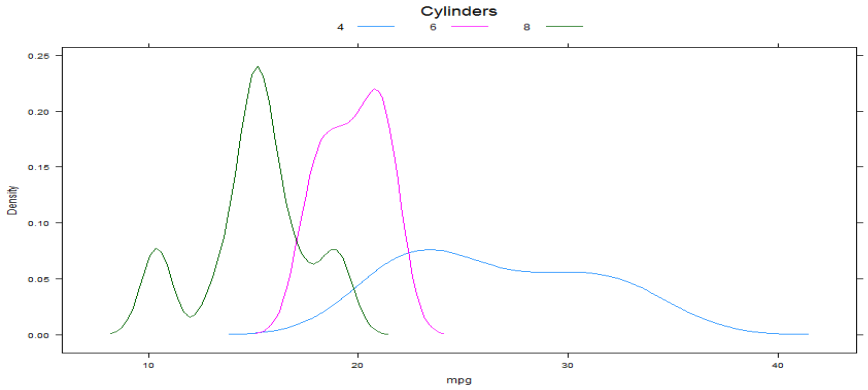


Exercise 2

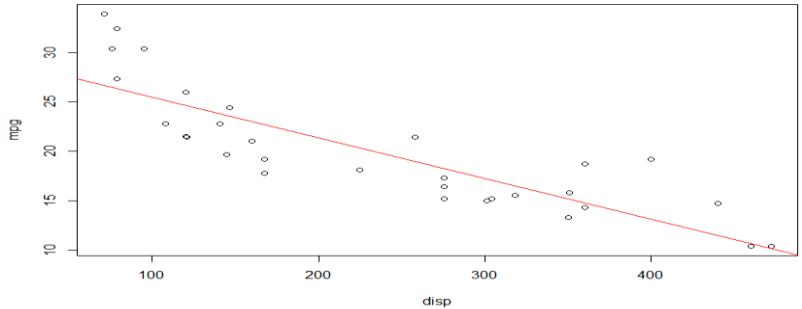
- Load “mtcars” dataset: data(mtcars)
  - ?mtcars for details
- Goal: Predict MPG based on other columns
- Create at least 2 different plots illustrating useful relationships in the data

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

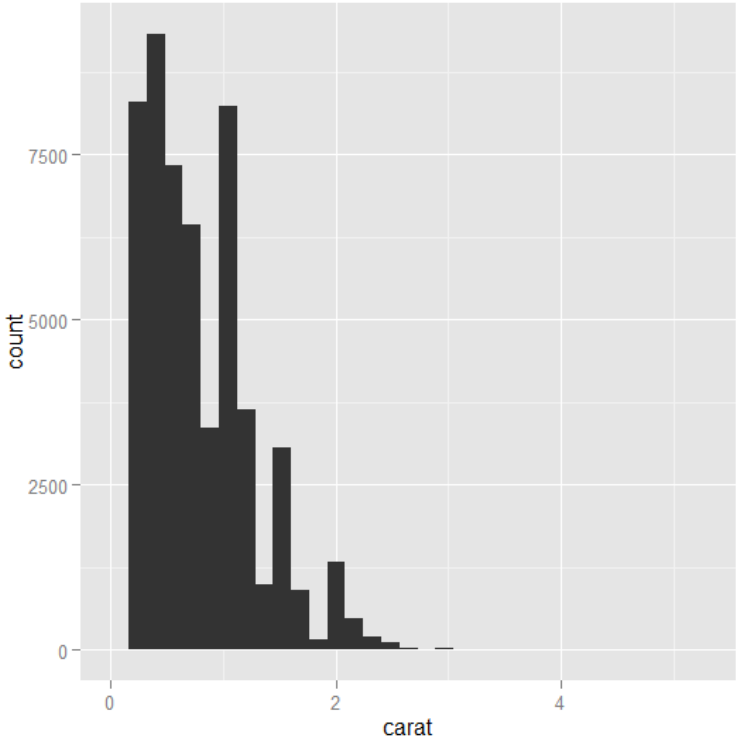
Loading

```
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
>
```

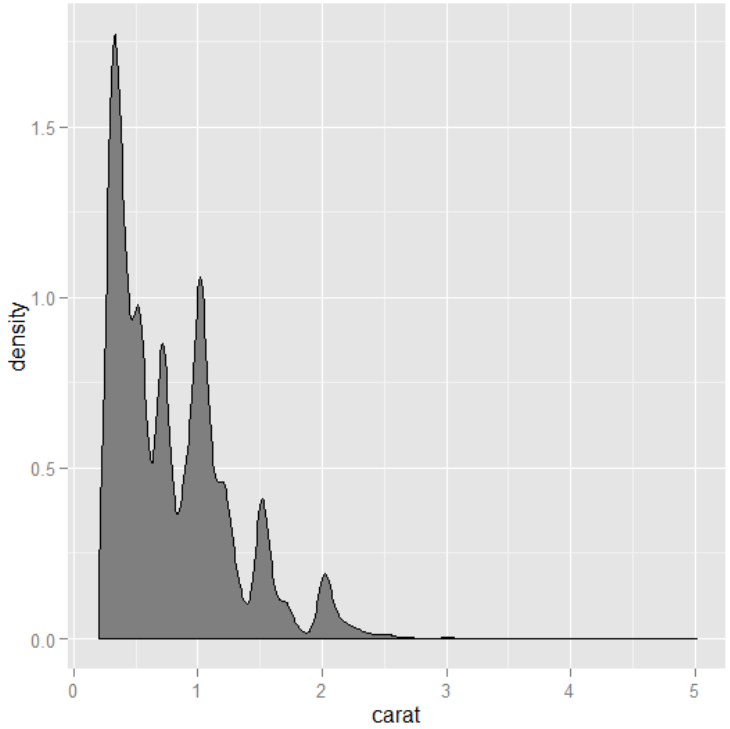
Histogram

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



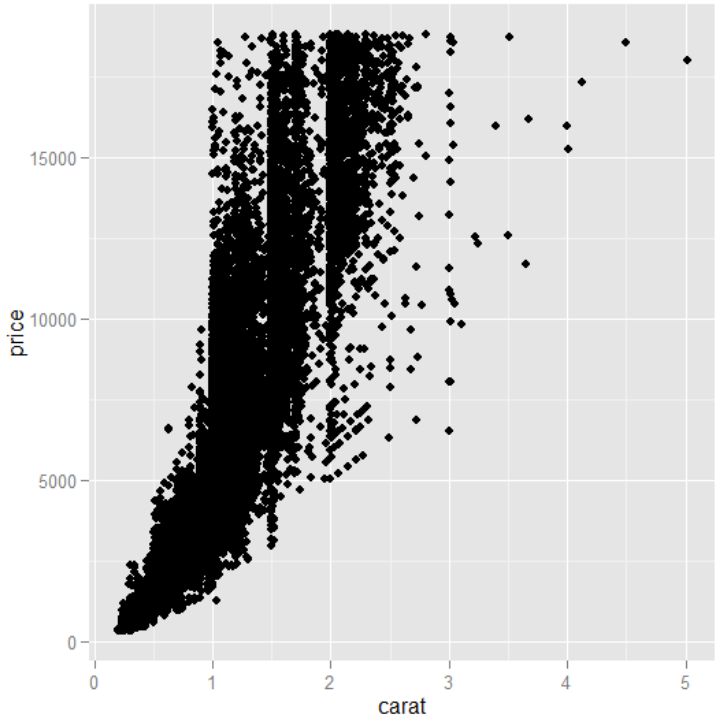
Density plot

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



Scatter plots

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



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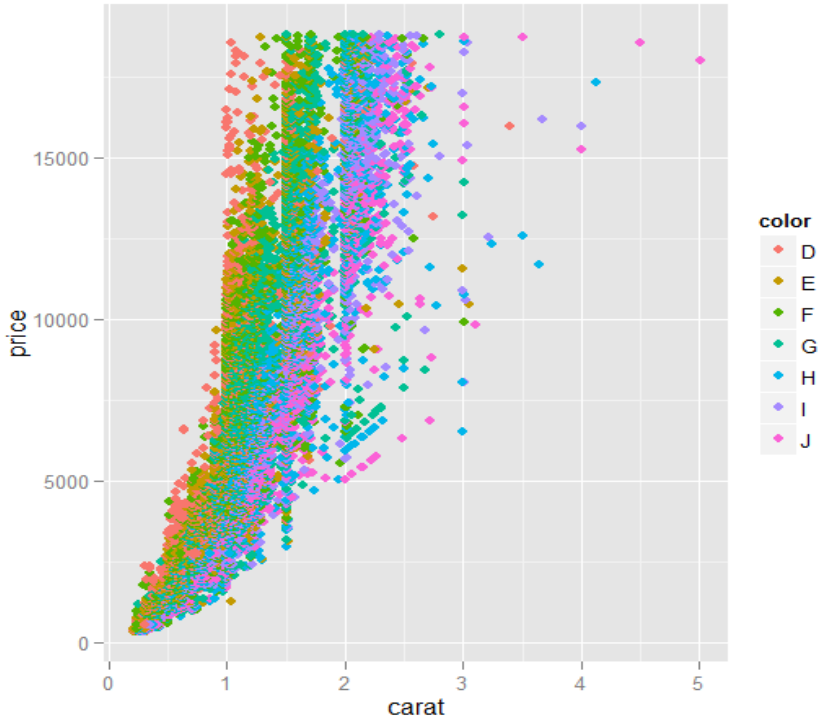
ggplot Object

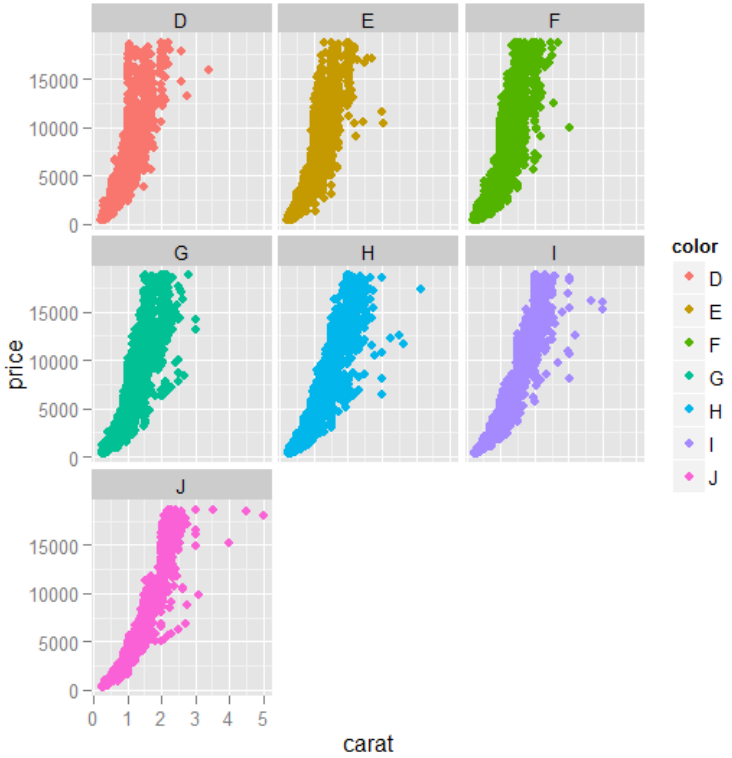
```
# Store the plot for future modification
g <- ggplot(diamonds, aes(x=carat, y=price))

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



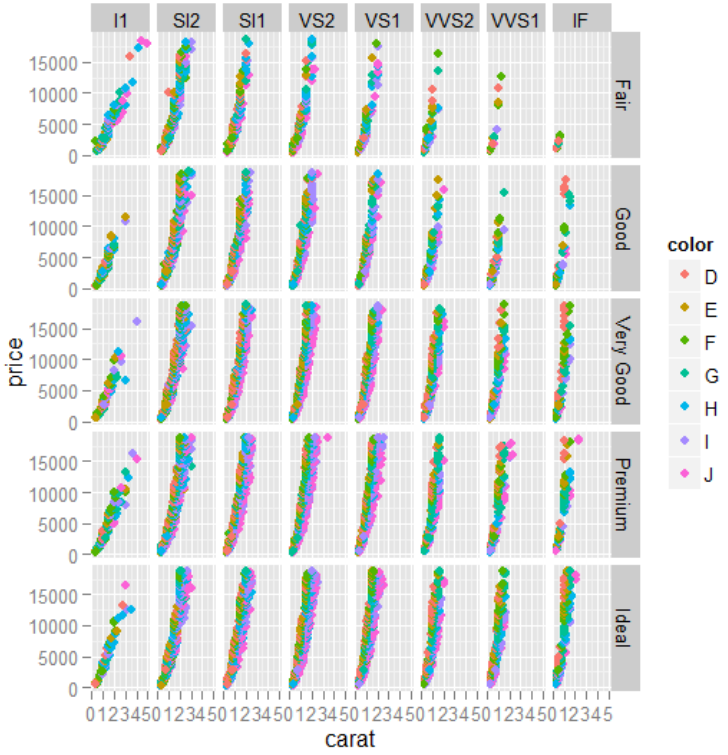
Segment by factor attribute

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



More Segments!

```
g + geom_point(aes(color=color)) +
facet_wrap(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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- Visualization in Azure

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           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)
```

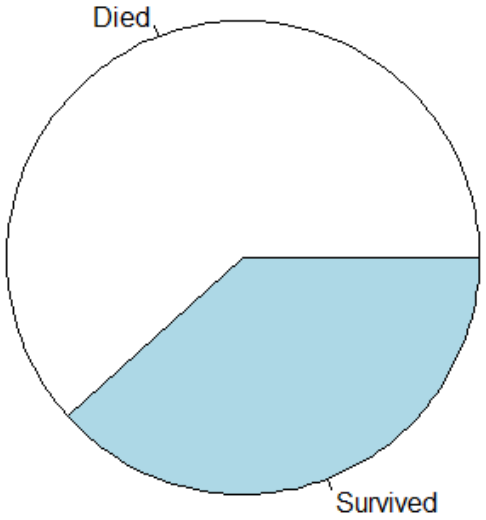
Rename factors and columns

```
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

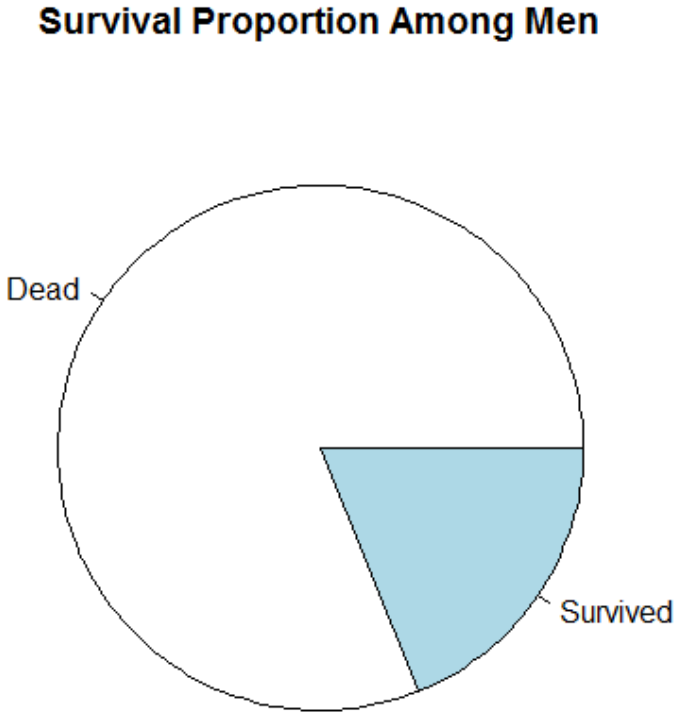
```
survivedTable <- table(titanic$Survived)
par(mar=c(0, 0, 0, 0), oma=c(0, 0, 0, 0),
cex=1.5)
pie
```

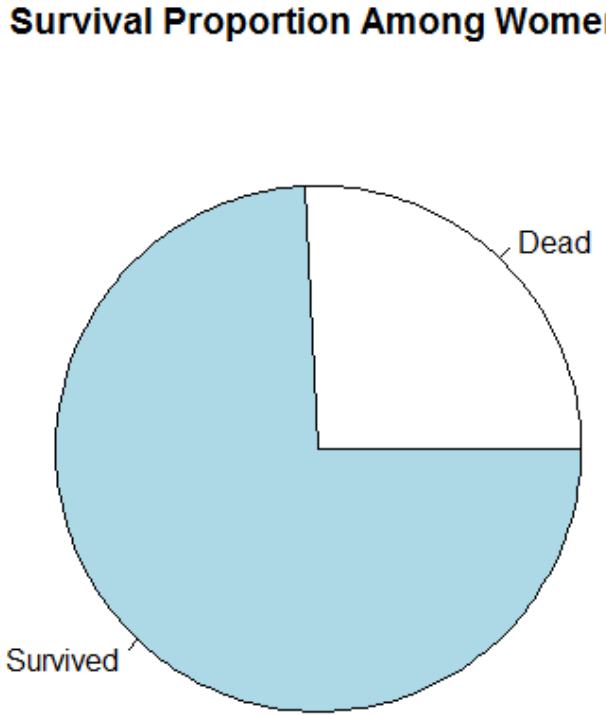


Is Sex a Good predictor?

```
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?





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)
```

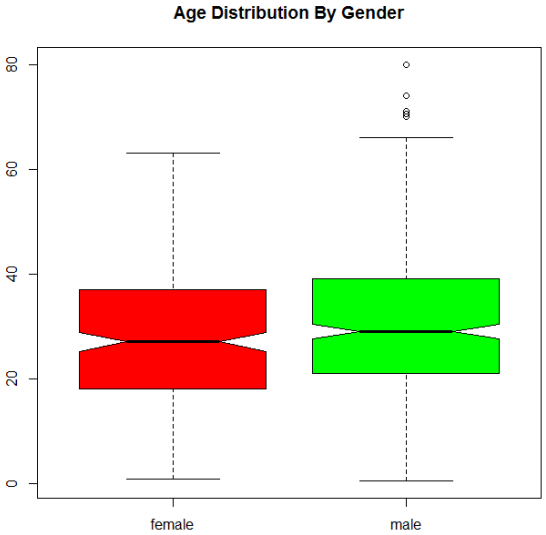
Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
1.00	21.00	28.00	30.63	39.00	74.00	125
Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
0.42	19.00	28.00	28.34	36.00	80.00	52

Exercise 3

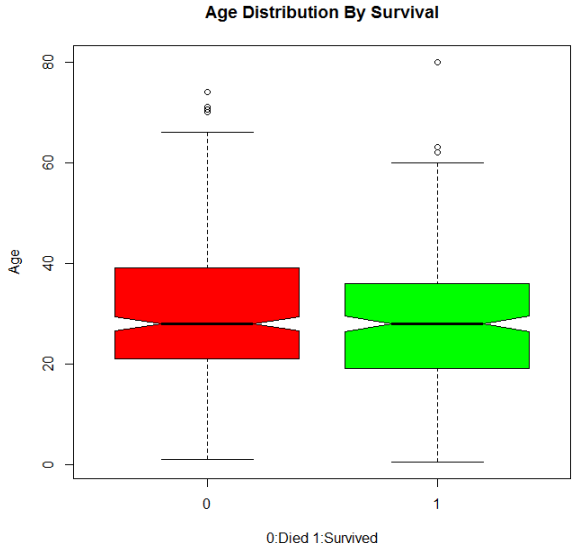
- Create 2 box plots of Age
  - Segmented by Gender
  - Segmented by Survived
- Create a histogram of Age
- Create a density plot of Age
  - na.omit() may be useful

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")
```



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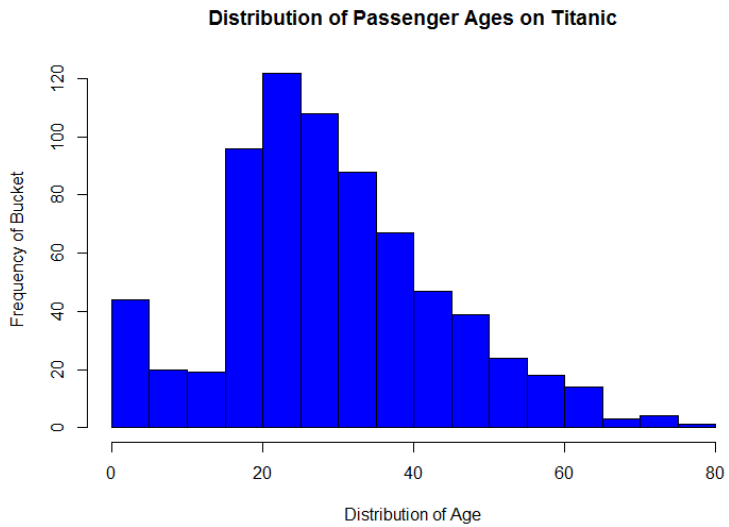
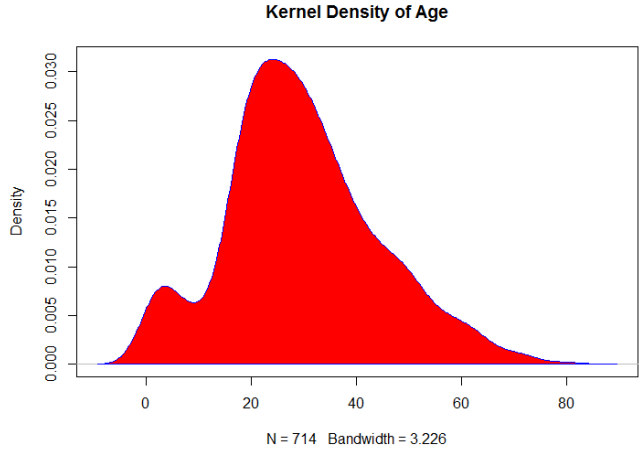
Sample Solution 3

```
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")
```





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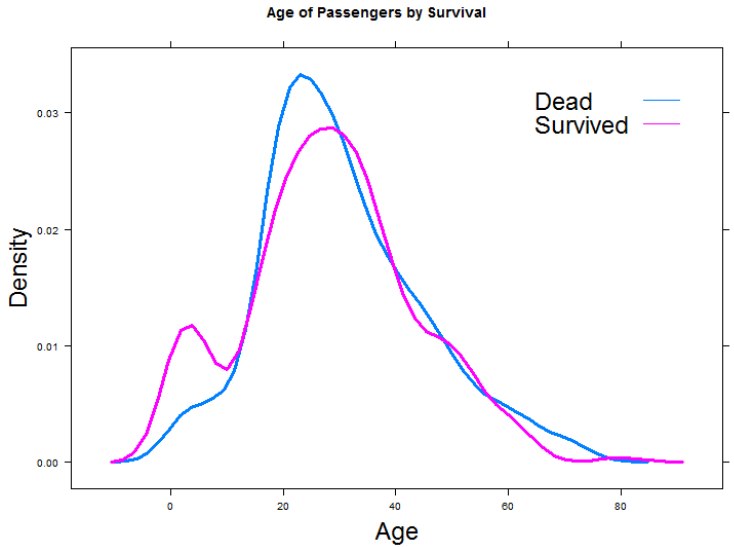
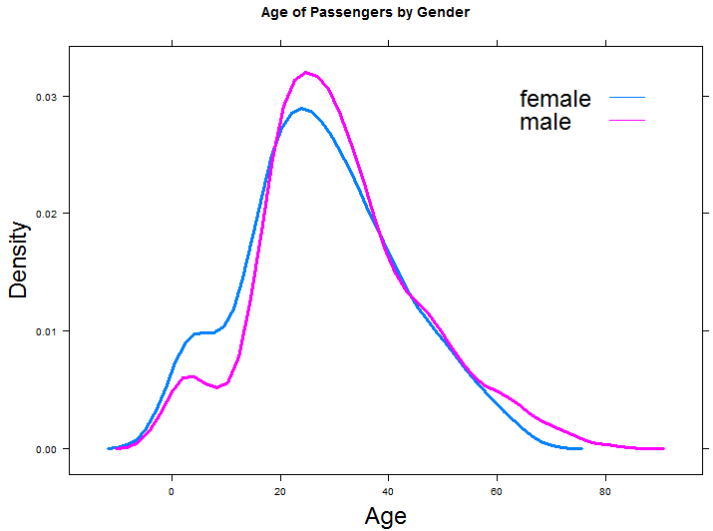
Is Age a Good Predictor?

```
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))
```



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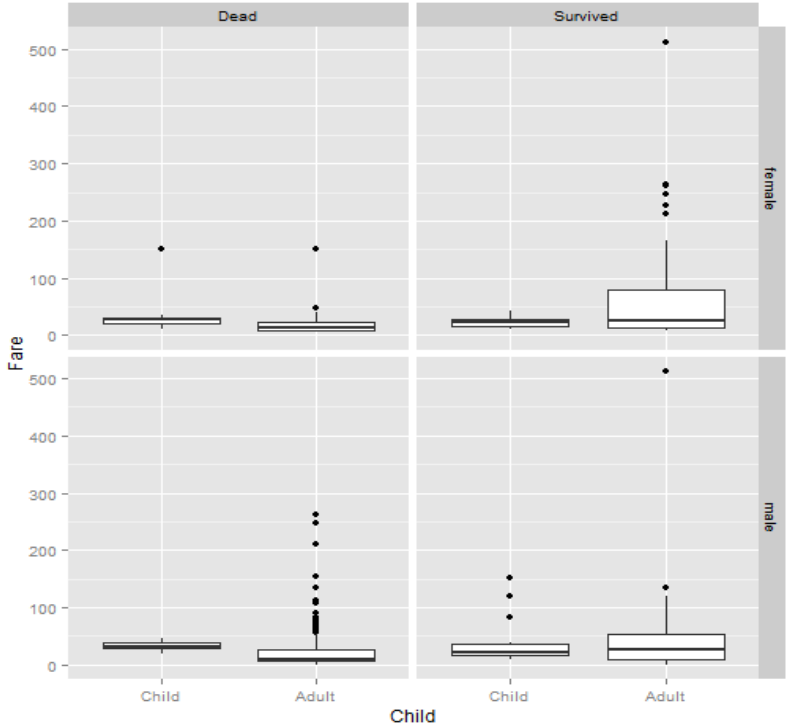
Exercise 4

- Create a new column “Child”
  - Assign each row “Adult” or “Child” based on a consistent metric
- Use ggplot to create a series of box plots relating Fare, Child, Sex, and Survived

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)
```



Agenda

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