Data Exploration and Visualization

Agenda

- High Level Process
- Graphing in R: Core and Lattice
- Extended Titanic Exploration
- ggplot2 introduction
- Visualization in Azure

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Learning Guidance

- Don’t get bogged down in details of the syntax
- I will share output samples on the slides often
- Sample code + slides: Data Exploration and Visualization folder

Data > Algorithm

- More data == better performance
  - Even with a simple algorithm
- But there are caveats
  - Diminishing returns
  - High quality and high variety needed
  - Algorithm must be appropriate
  - Feature selection/engineering

Understand Your Data!

- Not spending time on data is a common source of all sorts of problems!
- Are any features correlated with each other?
- What is the scale of your numeric features?
- Are there clear groups of data objects?
- Do you have missing values and where?

And More!

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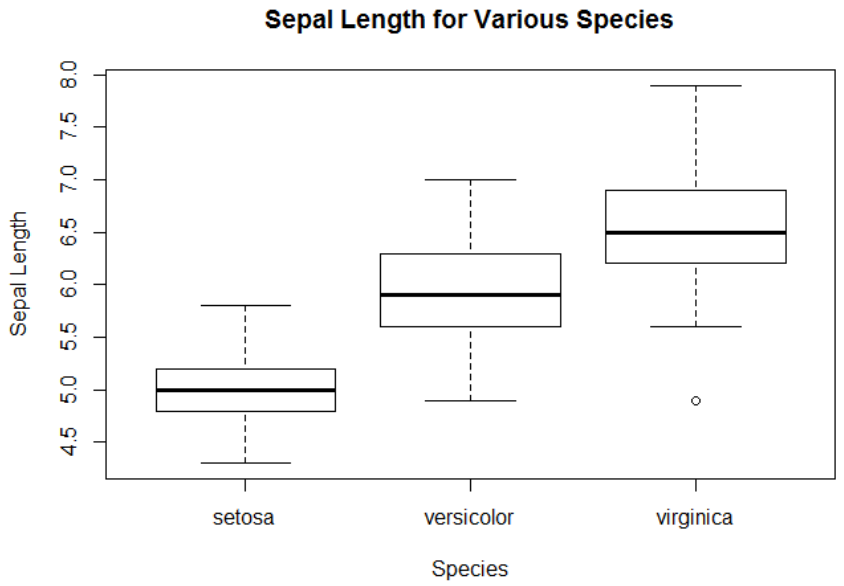
Core Graphics: Box

- Distribution of single feature
- Can partition by target class

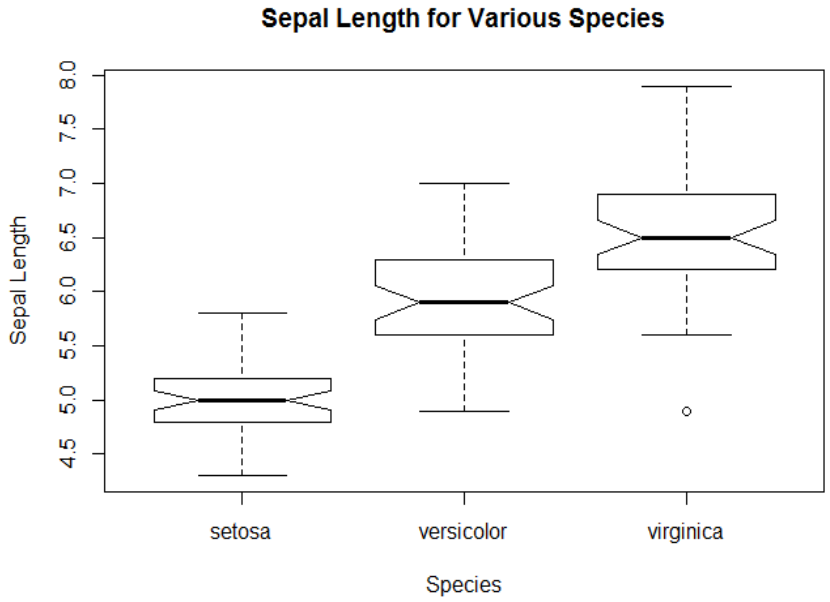
```
data(iris) # reference iris data in R

head(iris) # peak at first 6 rows

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



Core Graphics: Box with Notches

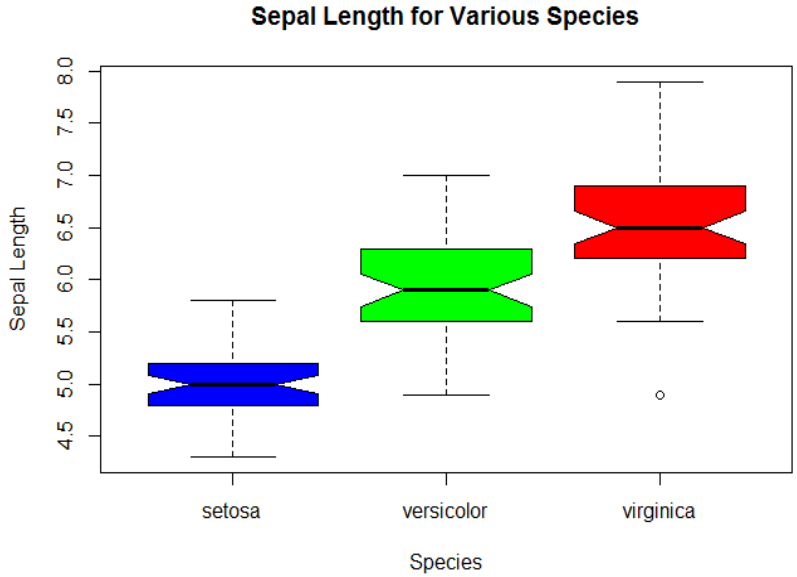
- Estimate of confidence interval of the median
- Notch overlap indicates confidence that median is different

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



Sidebar: Coloring Core 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")
)
```



Sidebar: 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

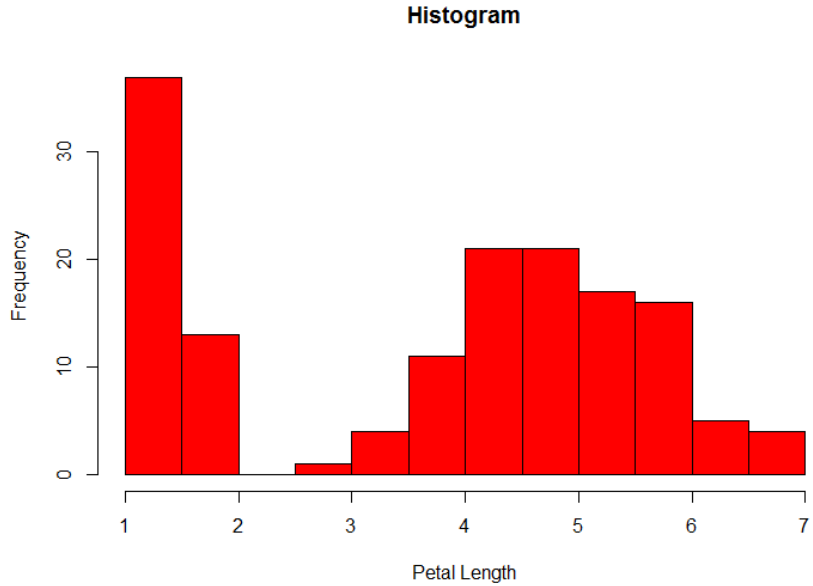
Windows Saves to default: Libraries\Documents

```
pdf("myplot.pdf")

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

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

Core Graphics: Histogram

- Spread of single feature
- Places values in “bins”
- Bin size parameter

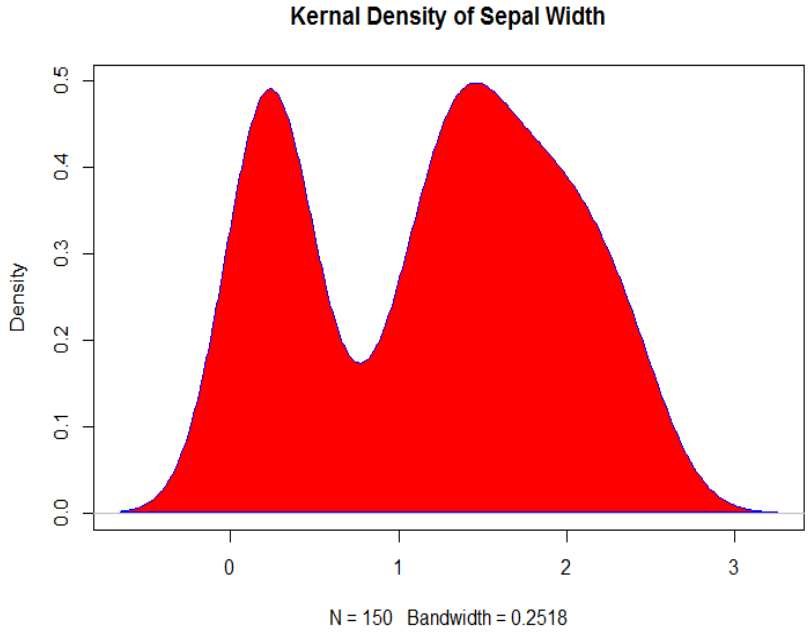
```
h<-hist(
Iris$Petal.Length,
breaks=10,
col="red",
xlab=“Petal Length",
main="Histogram"
)
```



Core Graphics: Density plots

- Variant of Histogram
- Scaled for easy comparisons

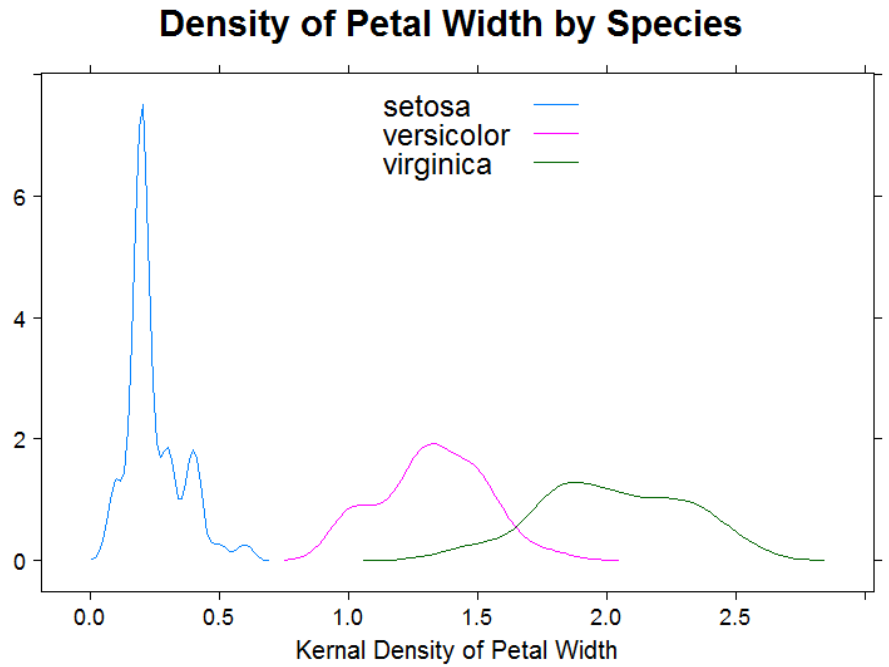
```
p.w <- iris$Petal.Width
p.w.density <- density(p.w)

plot(p.w.density, main =
"Kernal Density of Sepal
Width")

polygon(p.w.density,
col="red", border="blue")
```



Lattice: Multiple Density Plots

- Grouping simple
- Styling is not

```
library(lattice)


densityplot(~ Petal.Width,
data=iris, groups=Species,
plot.points=F,
xlab=list(label="Kernal 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))
```



Styling is a pain!

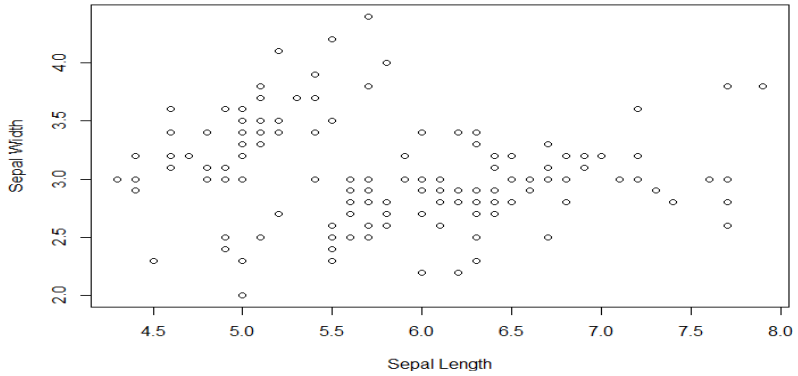
- ggplot2 syntax easier to read/write
  - Less intuitive; harder to get started with
  - More power than often needed
- Learn core/lattice first, then ggplot

Exercise 1

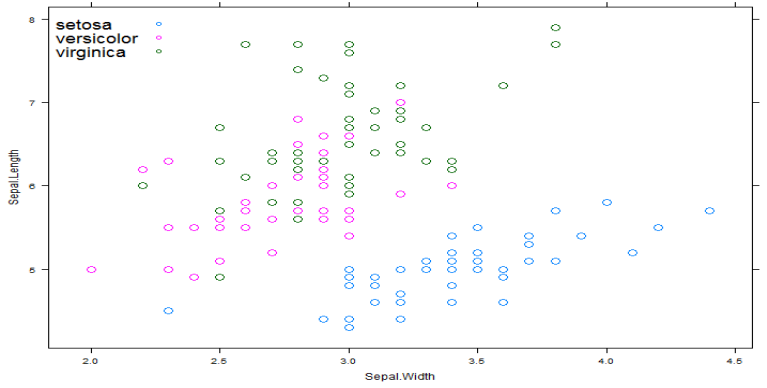
- 2-D Scatter plots – plot() and xyplot()
  - Sepal Length vs Sepal Width
  - Petal Length vs Petal Width
  - Color based on Species (lattice)

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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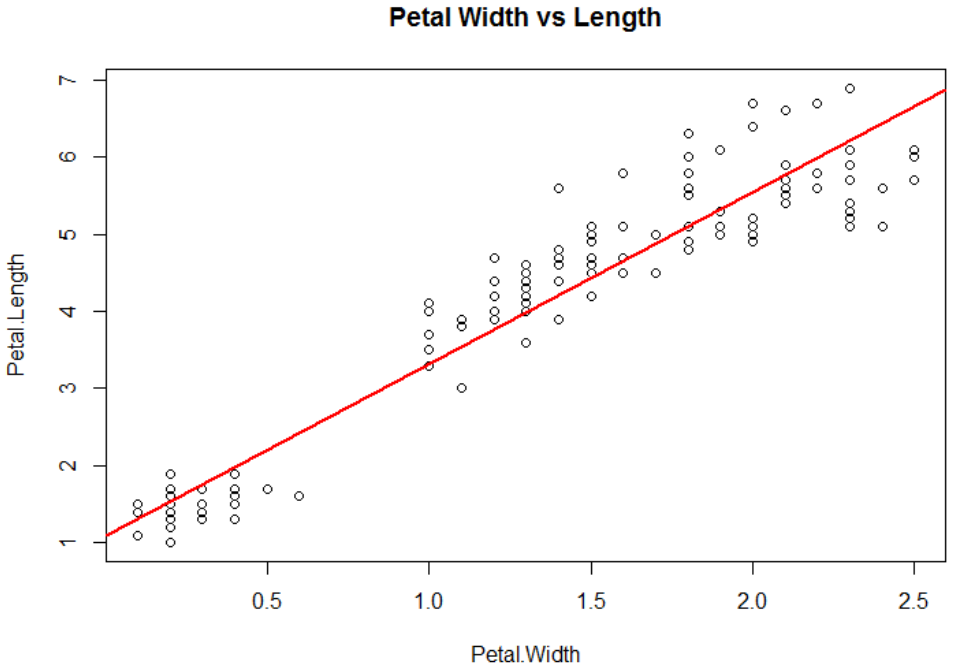
Core: Extended Scatter Plots

- Add a regression line

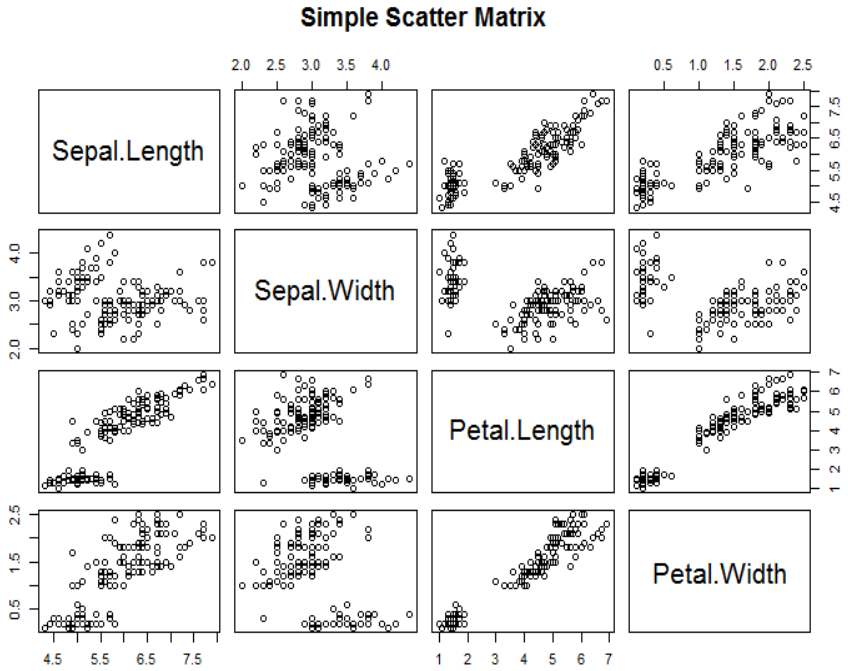
```
plot(Petal.Length ~
Petal.Width, data=iris,
main="Petal Width vs
Length")

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

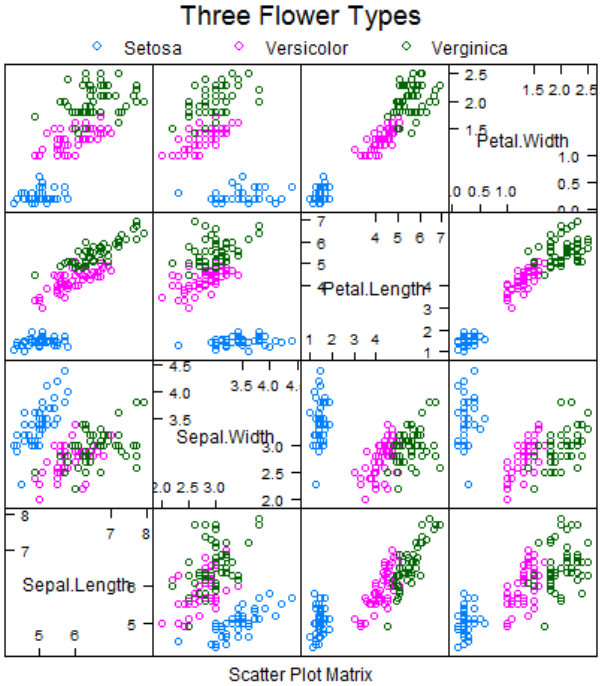
```
pairs(~ Sepal.Length +
Sepal.Width + Petal.Length +
Petal.Width, data=iris,
main="Simple Scatter Matrix")
```



Lattice: Scatter Plot Matrix

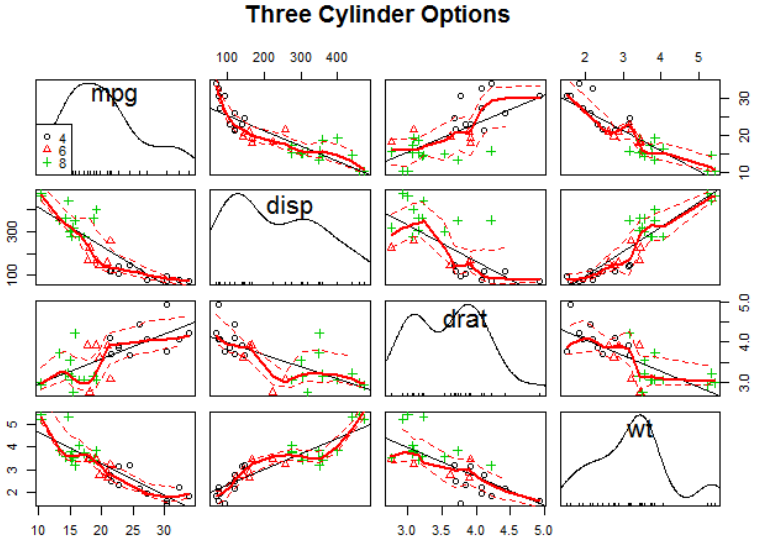
- Simple Grouping

```
# 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"))))
```



Enhanced Scatter Plot Matrices

- install.packages("car")
- library(car)
- scatterplotMatrix(~mpg+disp+drat+wt|cyl, data=mtcars,main="Three Cylinder Options")

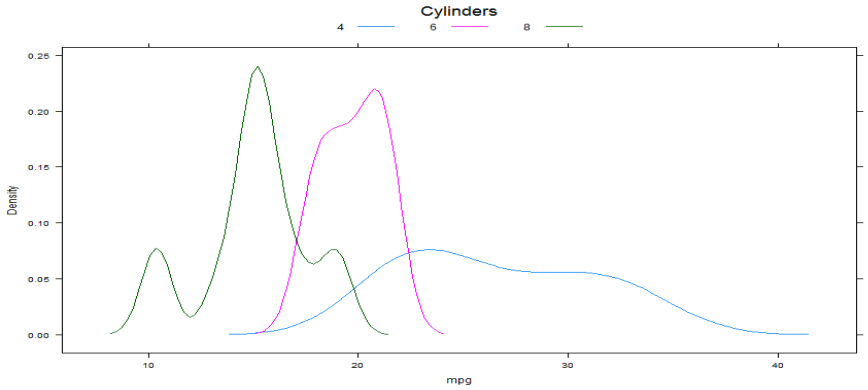


Exercise 2

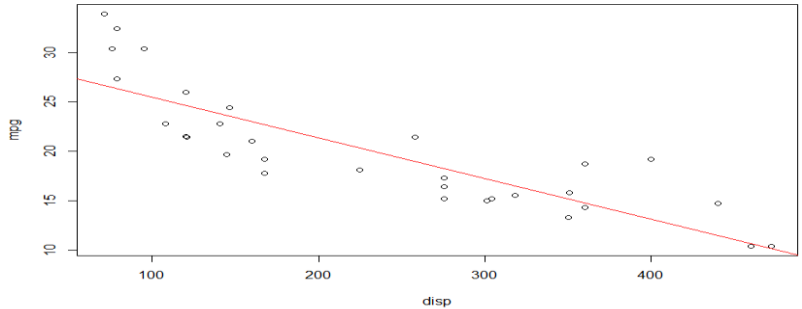
- Load “mtcars” dataset: data(mtcars)
  - ?mtcars for details
- Goal: Predict MPG based on other columns
- Create at least 2 different plots illustrating relationships in the data

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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Finding the Code

- Set your working directory to the bootcamp root
- Open code file in "Data_Exploration_and_Visualization/code/titanic_example.R"
- Follow along line by line

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 would be some good features to consider here?

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 ...
```

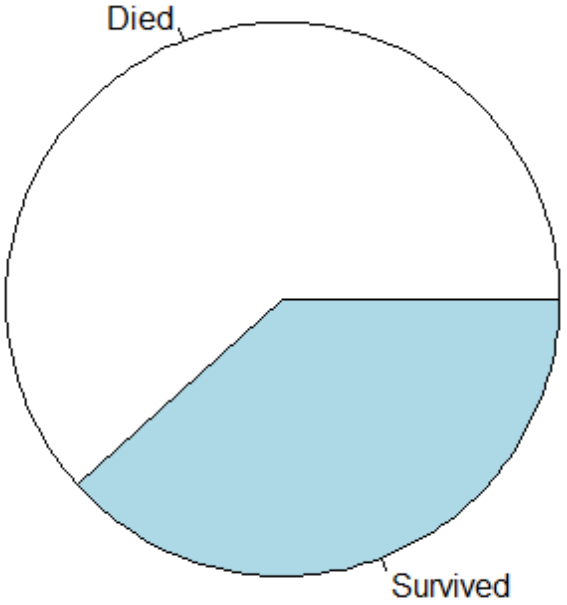
Convert target feature to Factor

```
titanic$Survived <- as.factor(titanic$Survived)
levels(titanic$Survived) <- c("Dead", "Survived")
str(titanic$Survived)
```

```
Factor w/ 2 levels "Dead","Survived": 1 2 2 2 1 1 1 1 2 2 ...
```

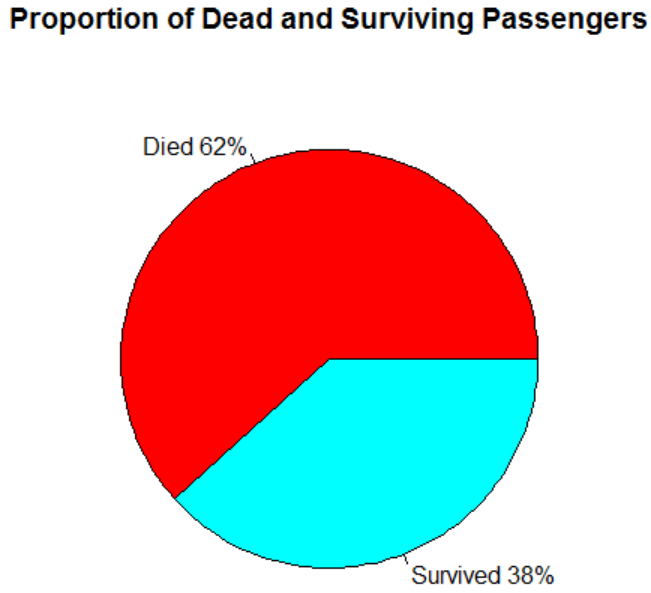
Class distribution: Pie Chart

```
survivedTable <-
table(titanic$Survived)
pie(survivedTable,
labels=c("Died", "Survived")
```



Pie Chart: Color and Annotate

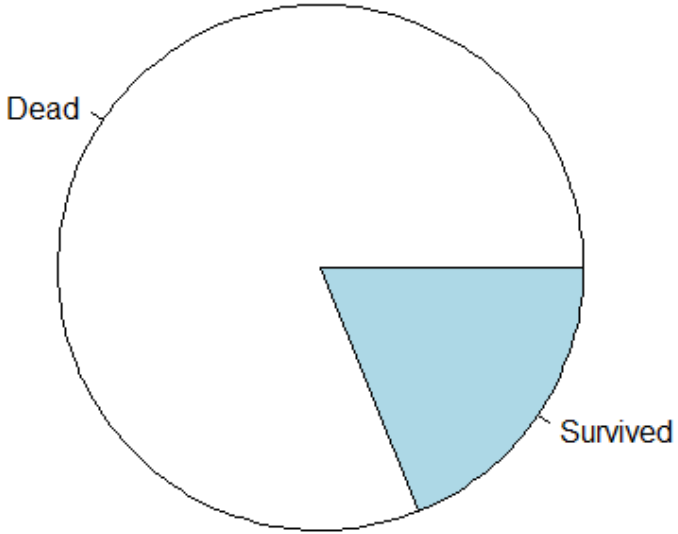
```
pct <- round( (survivedTable /
        sum(survivedTable))*100)
lbls = c("Died","Survived")
lbls = paste(lbls,pct)
lbls = paste(lbls,"%",sep="")
pie(survivedTable, labels=lbls,
col=rainbow(length(lbls)), main="Proportion of
Dead and Surviving Passengers")
```



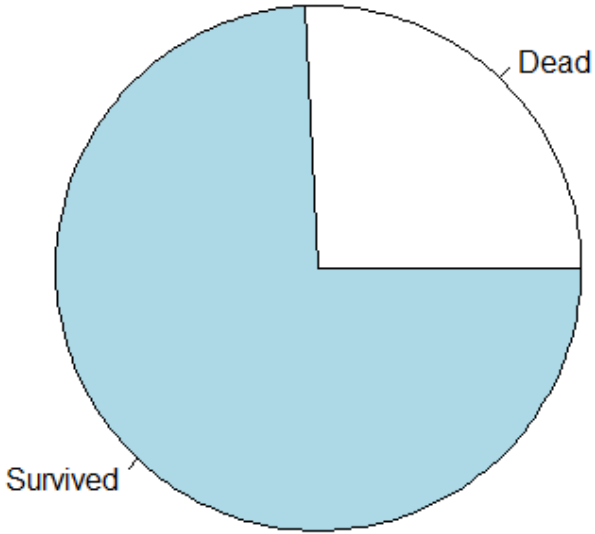
Is Gender a Good predictor?

```
male = titanic[titanic$Sex=="male",]
female = titanic[titanic$Sex=="female",]
par(mfrow=c(1,2))
pie(table(male$Survived),labels=c("Dead","Survived"))
pie(table(female$Survived),labels=c("Dead","Survived"))
```

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)
```

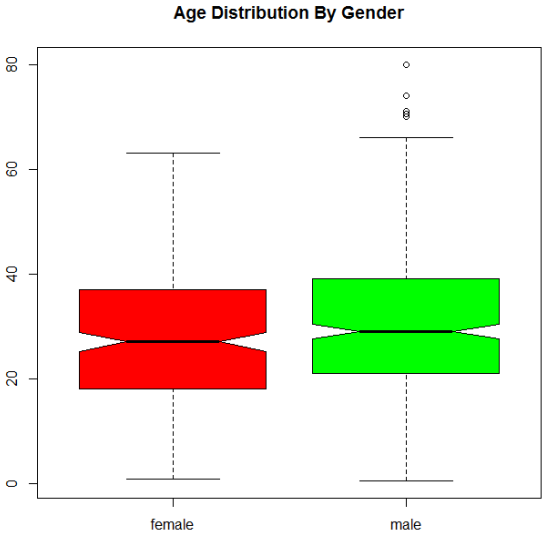
Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
1.00	21.00	28.00	30.63	39.00	74.00	125
Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
0.42	19.00	28.00	28.34	36.00	80.00	52

Exercise 3

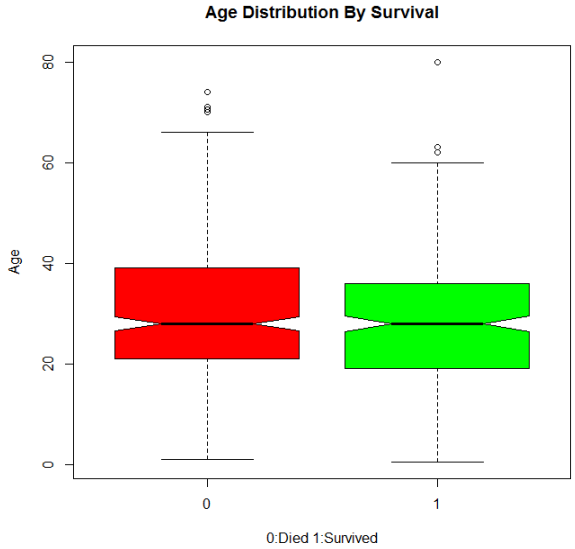
- Create 2 notched box plots of Age
  - Segmented by Gender
  - Segmented by Survived
- Create a histogram of Age
- Create a density plot of Age
  - na.omit() may be useful

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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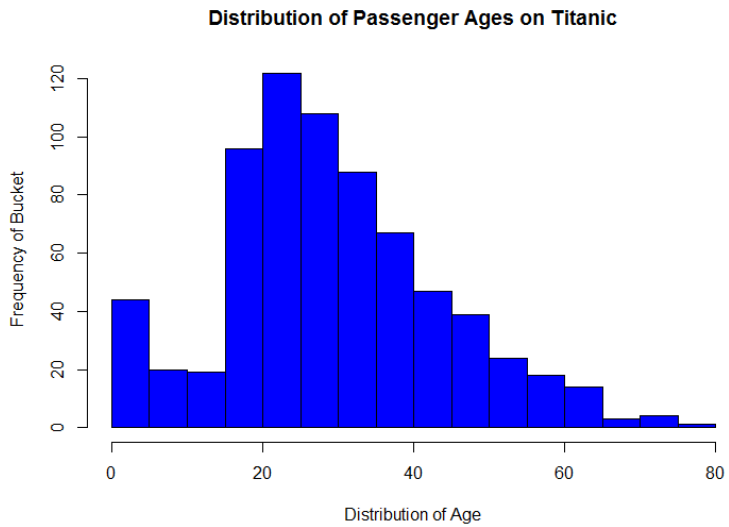
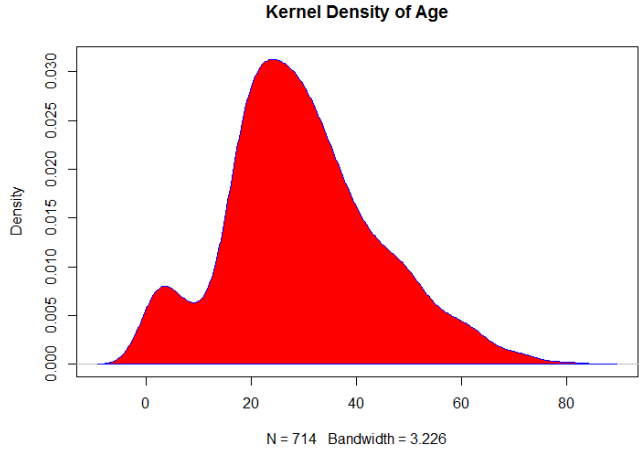
Sample Solution 3

```
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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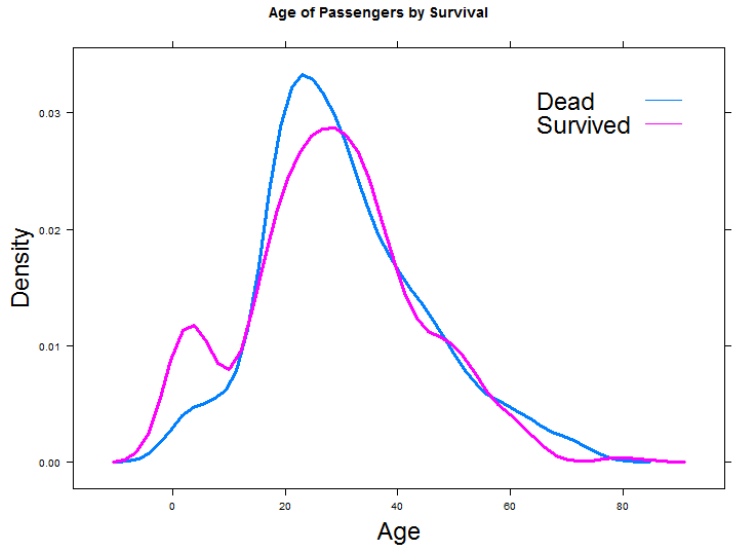
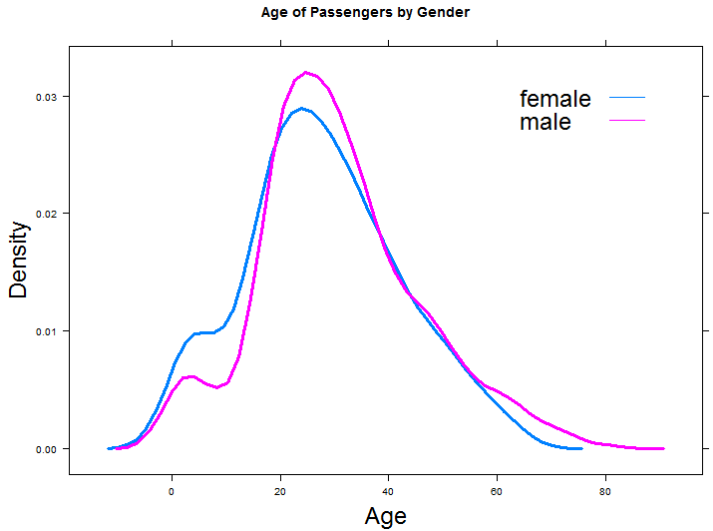
Is Age a Good Predictor?

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



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



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- **ggplot2 introduction**
- Visualization in Azure

ggplot Basics

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

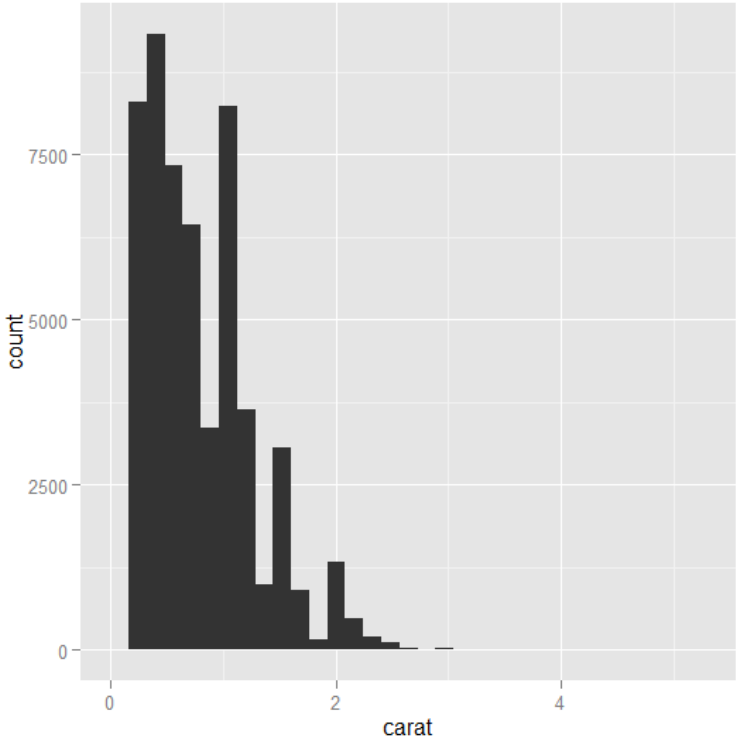
Loading

```
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
>
```

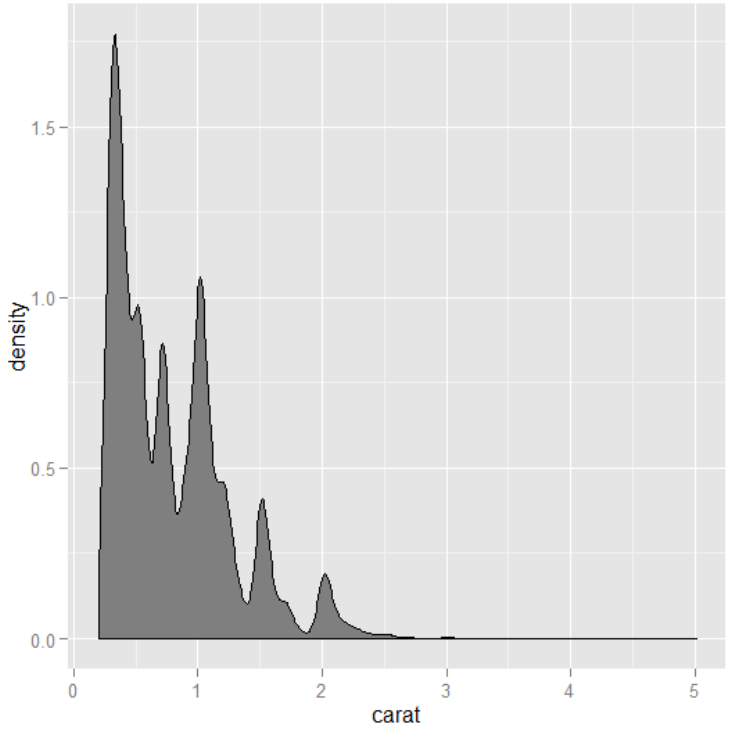
Histogram

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



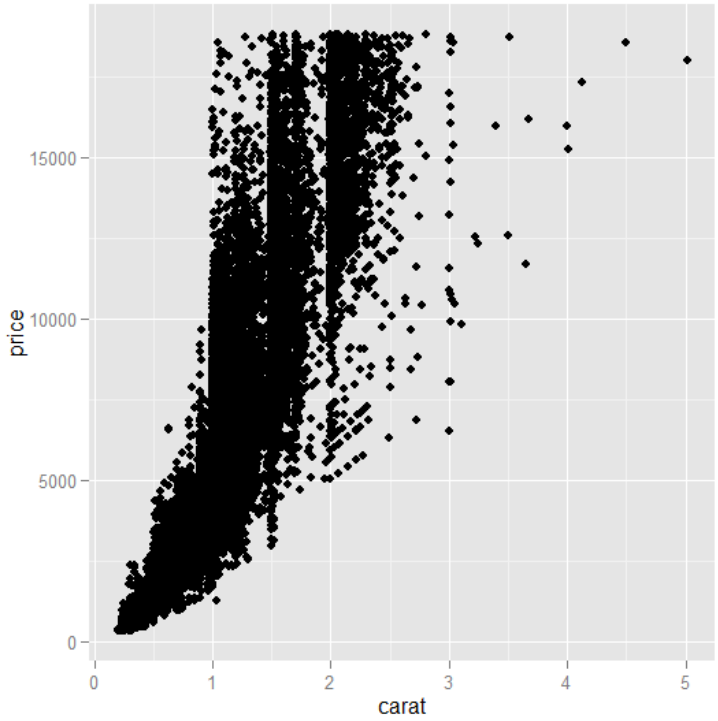
Density plot

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



Scatter plots

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



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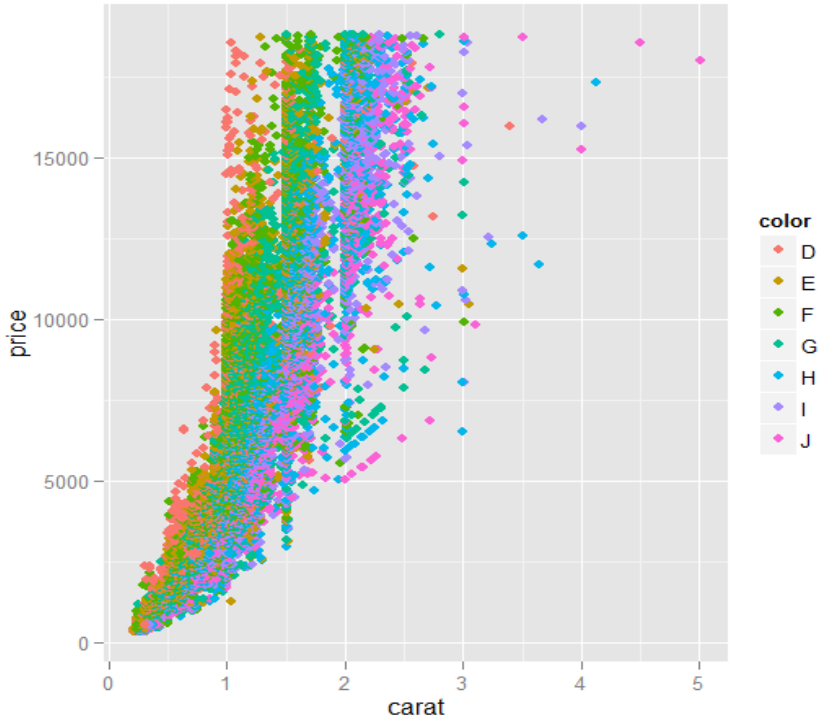
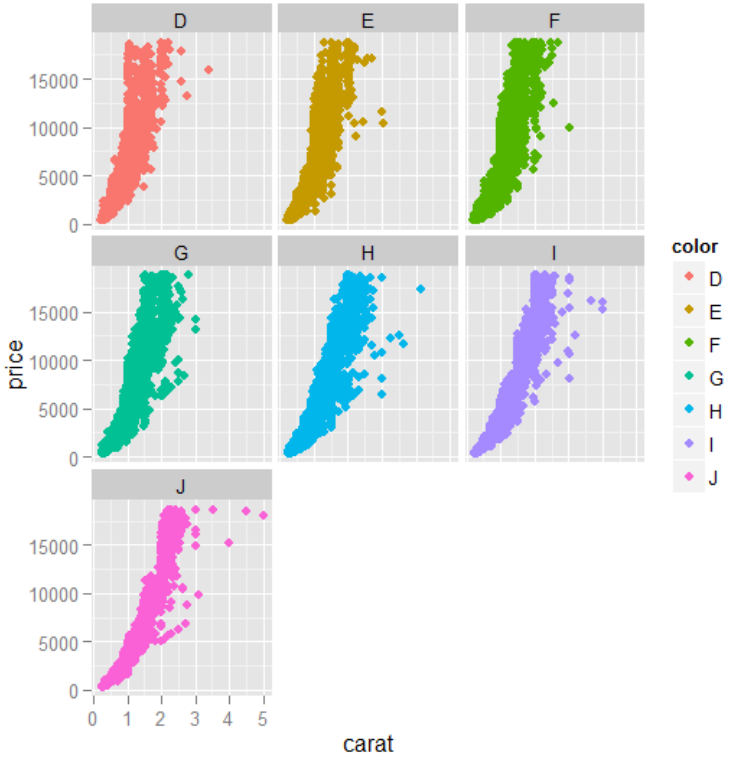
ggplot Object

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

#Add a second aesthetic on top of base
g + geom_point(aes(color=color))
```



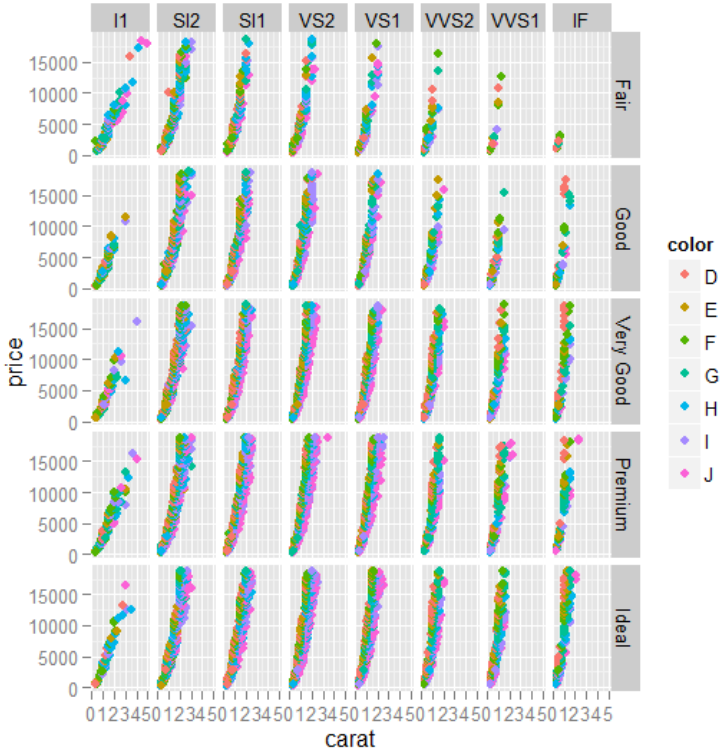
Segment by factor attribute

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



More Segments!

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



Exercise 4

- In Titanic data, create new column “Child”
  - Assign objects value “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

```
# Multi dimensional comparison
> Child <- titanic$Age # Isolating age.

# Now we need to create categories: NA = Unknown, 1 = Child, 2 = Adult

# Every age below 13 (exclusive) is classified into age group 1
> Child[Child<13] <- 1

 # Every child 13 or above is classified into age group 2
> Child[Child>=13] <- 2
```

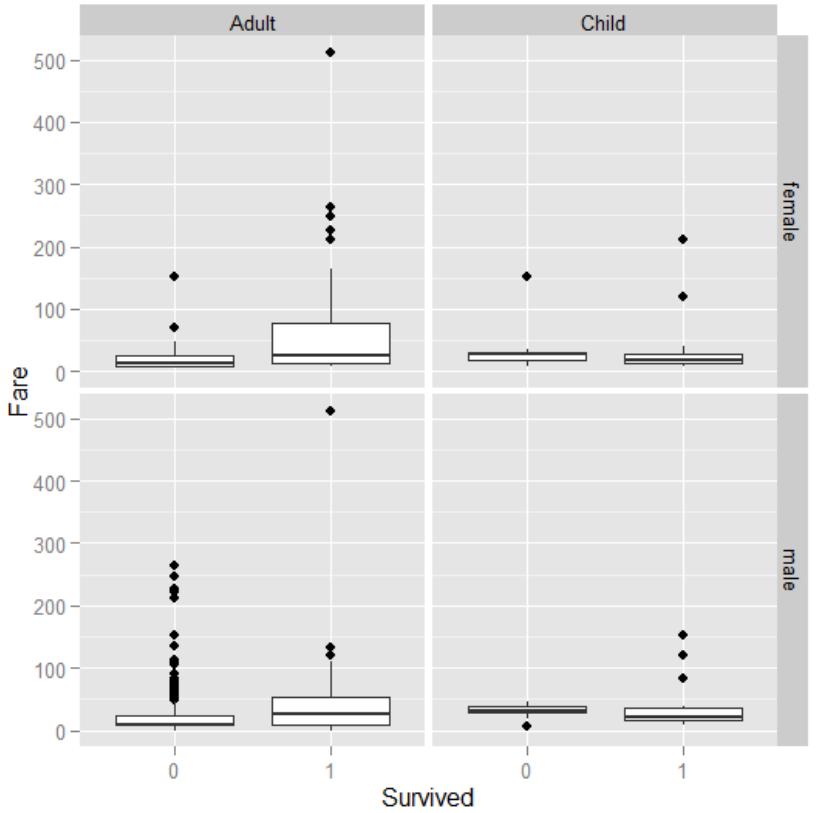
Sample Solution 4

```
# Use labels instead of 0's and 1's
Child[Child==1] <- "Child"
Child[Child==2] <- "Adult"

# Appends the new column to the titanic dataset
titanic_with_child_column <- cbind(titanic, Child)

# Removes rows where age is NA
titanic_with_child_column <-
titanic_with_child_column[!is.na(titanic_with_child_column$Child),]

# Converts $Survived column into a factor
titanic_with_child_column$Survived <- as.factor(titanic_with_child_column$Survived)
```

Sample Solution 4

- > ggplot(titanic_with_child_column, aes(y=Fare, x=Survived)) + geom_boxplot() + facet_grid(Sex~Child)

- # Plot may differ depending # on your definition of a child



Some Variations

- ggplot(titanic_with_child_column, aes(y=Age, x=Survived)) + geom_boxplot() + facet_grid(Sex~SibSp)
- ggplot(titanic_with_child_column, aes(y=Fare, x=Survived)) + geom_boxplot() + facet_grid(Sex~Embarked)

Agenda

- High Level Process
- Graphing in R: Core and Lattice
- Extended Titanic Exploration
- ggplot2 introduction
- **Visualization in Azure**