# Data Exploration, Visualization, and Feature Engineering

Data Science Dojo

# Agenda

- Why data exploration and visualization
- Exploration and visualization using R
  - Core R functionality – iris dataset
  - Lattice package – mtcars dataset
  - ggplot2 package – diamonds data set
- Story-telling with data
  - Titanic data set

# WHY DATA EXPLORATION AND VISUALIZATION

# 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



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# 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, data exploration, feature engineering, pre-processing etc…
  - 20% : Model building

# EXPLORATION AND VISUALIZATION USING R

# Objectives

- Develop an understanding of the high-level thinking process of data exploration
- Making sense of data using visualization techniques
- Learning to perform feature engineering
- Becoming a good story teller.

# I am new to R

- Focus on ideas/concepts rather than exact syntax. R help is your friend. ☺

  ?mean, ?sd

  help( )
  example( )
- All slides have code samples
- Sample code + slides: ‘Data Exploration and Visualization’ folder

# Common Graphical Parameters

- Title of graph using the **main** function, main = “title”
- Label x- axis by using the **xlab** function, xlab = “label x axis”
- Label x- axis by using the **ylab** function, ylab = “label y axis”
- Colors controlled by **col**
- Get legends of layered plots with **auto.key**=TRUE

# R to start exploring data commands

| Commands | Description |
|---|---|
| **read.csv() , read.table()** | Load data/file into a dataframe |
| **data()** | Loads or resets a dataset |
| **names()** | List names of variables in a dataframe |
| **head()** | First 6 rows of data |
| **tail()** | Last 6 rows of data |
| **str()** | Display internal structure if R object |
| **View()** | View dataset in spreadsheet format in RStudio |
| **dim()** | Dimensions( rows and columns) of dataframe |
| **summary()** | Display 5-number summary and mean |
| **colnames()** | Provide column names |

# CORE R GRAPHICS

# The “iris” data set

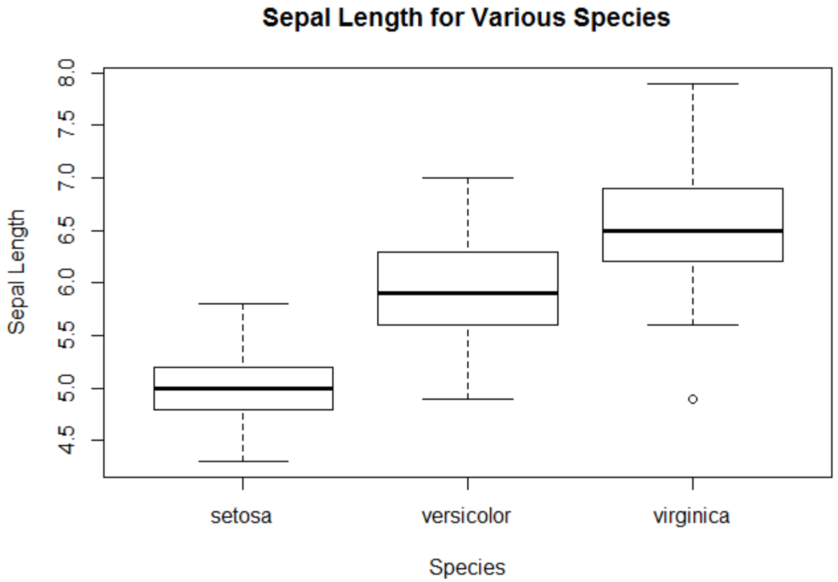
```
data(iris)
head(iris)
```

```
> head(iris)
  Sepal.Length Sepal.Width Petal.Length Petal.Width Species
1          5.1         3.5          1.4         0.2  setosa
2          4.9         3.0          1.4         0.2  setosa
3          4.7         3.2          1.3         0.2  setosa
4          4.6         3.1          1.5         0.2  setosa
5          5.0         3.6          1.4         0.2  setosa
6          5.4         3.9          1.7         0.4  setosa
```

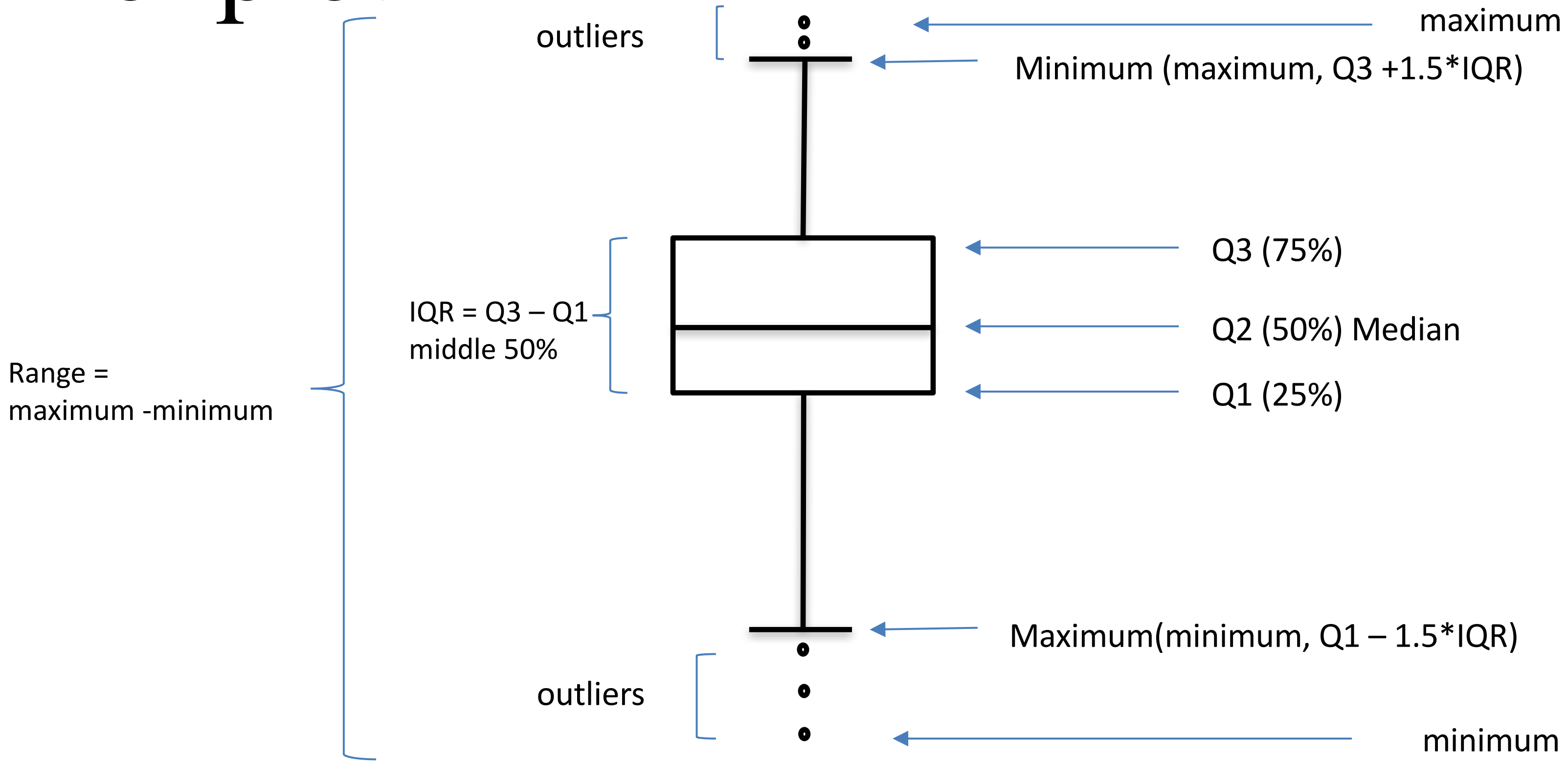
# Boxplots

- Summarizes *quantitative/numeric* data

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



# Boxplot


outliers
maximum
Minimum (maximum, Q3 +1.5*IQR)
IQR = Q3 – Q1
middle 50%
Q3 (75%)
Q2 (50%) Median
Q1 (25%)
Range =
maximum -minimum
Maximum(minimum, Q1 – 1.5*IQR)
outliers
minimum

# Saving plots

- Save various formats

```
pdf("myplot.pdf")
boxplot(Sepal.Length ~ Species,
data=iris)
dev.off() # Returns plot to the
IDE
```

| 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 |

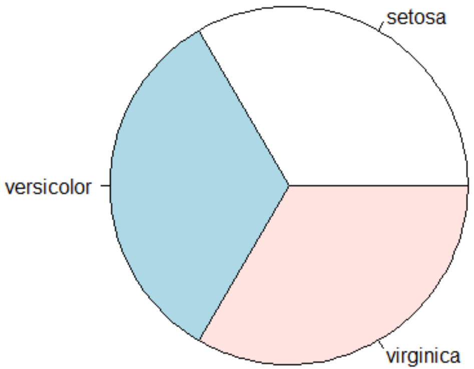
Windows Saves to default: Libraries\Documents

R Studio makes it easier

# Pie Chart

- Summarizes *qualitative/categorical* variables

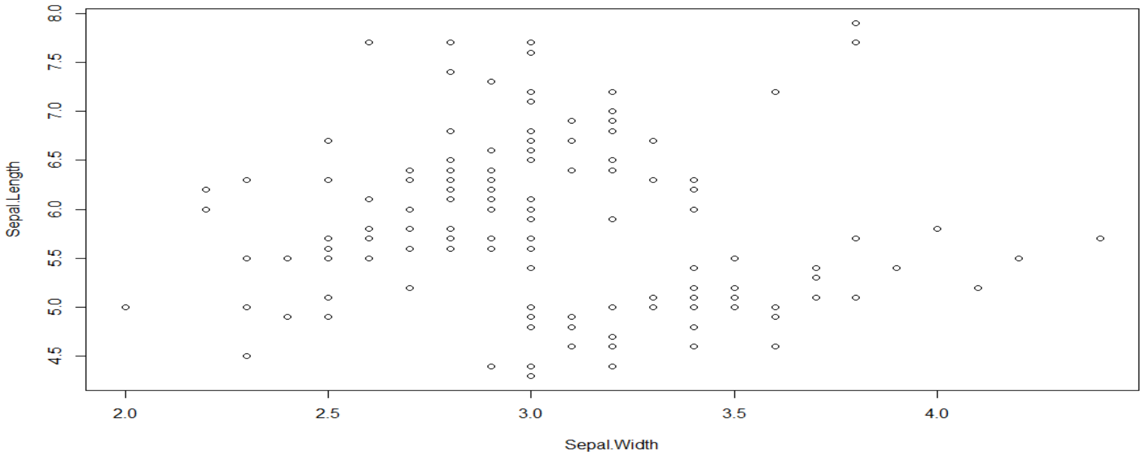
```
# Core Graphics
pie(table(iris$Species))
```



# Plot

- Visual depiction of correlation between numeric quantities

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



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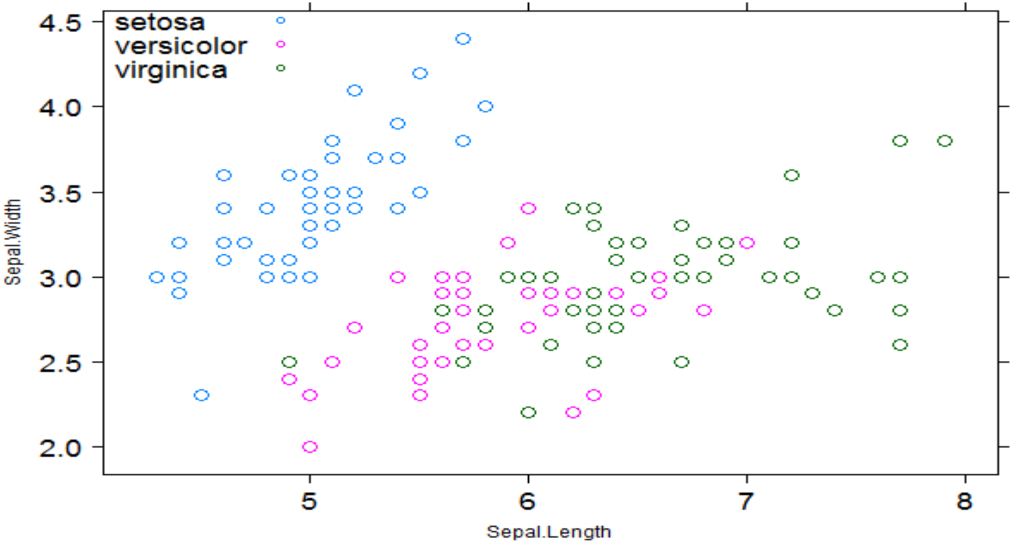
# LATTICE GRAPHICS

# xyplot

- Plot counterpart in Lattice package.

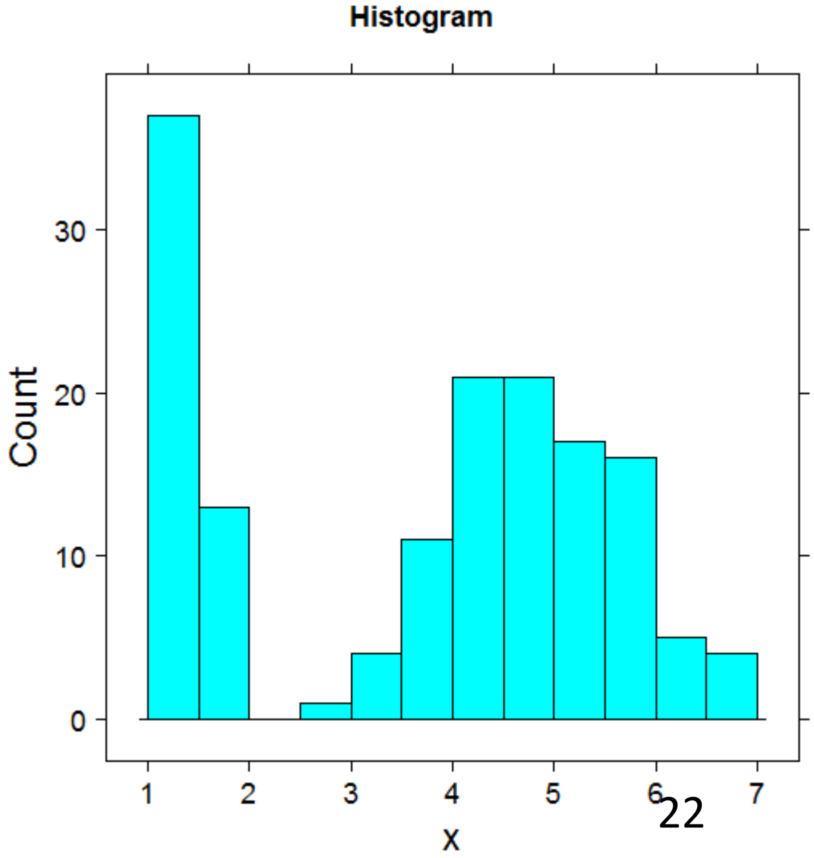
```
# Lattice Graphics
library(lattice)
xyplot(Sepal.Width ~
Sepal.Length, data=iris,
groups=Species,
auto.key=TRUE
)
```



# In-class Exercise 1

Contrast 2-D scatterplots for iris dataset(Petal.Length and Petal.Width) Summarize your findings.

# Histogram

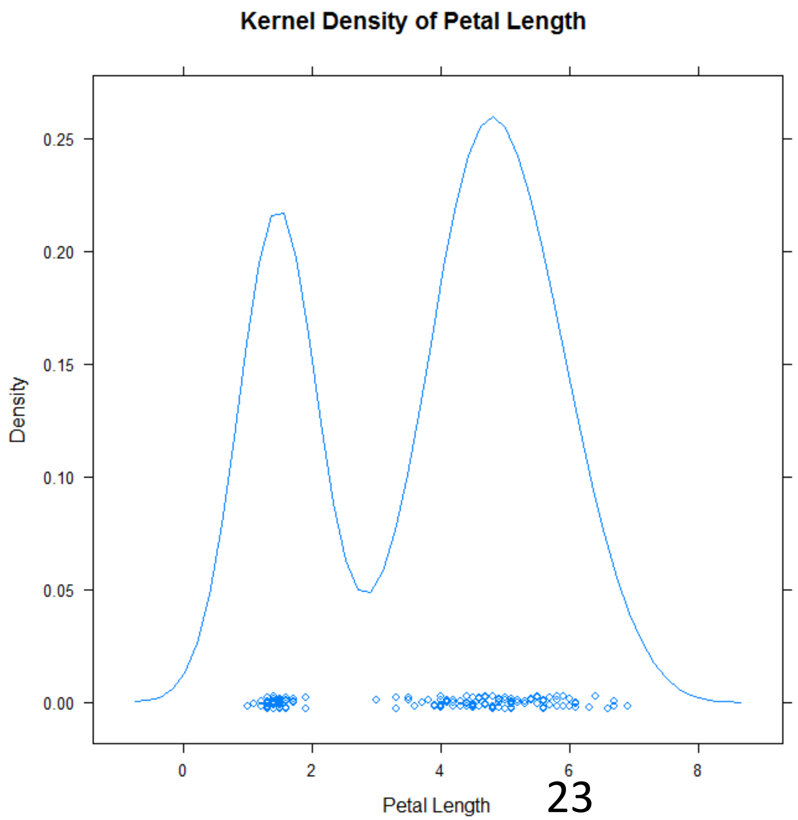



- Spread of a numeric feature
- Places values in "bins“

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

Vary ‘breaks’ parameter

# Density plots




- Variation on histogram
- Estimates density function from counts
- Does not work with missing values

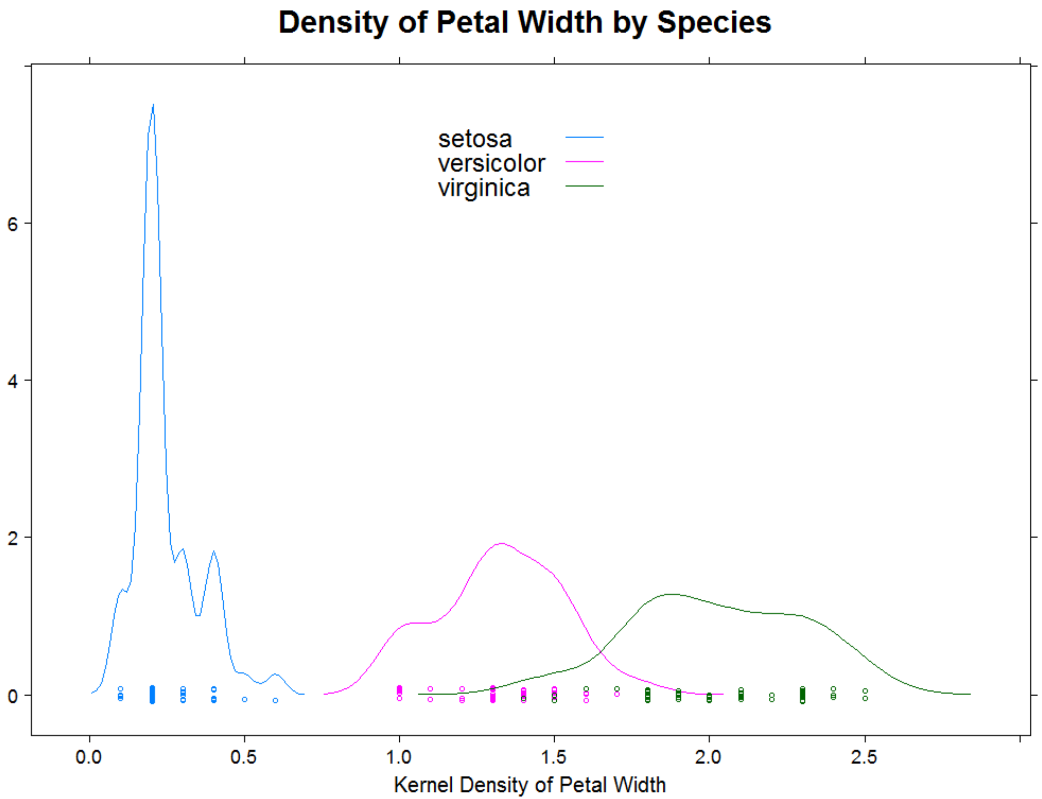
```
densityplot(iris$Petal.Length,
main="Kernel Density of Petal
Length", xlab="Petal Length")
```

Try adding plot.points=F

# The devil is in the details

- The details are in segments
- Segmentation reveals hidden patterns
- Create as many segments as possible
    - Your domain understanding will help in creating segments

# Multiple density plots



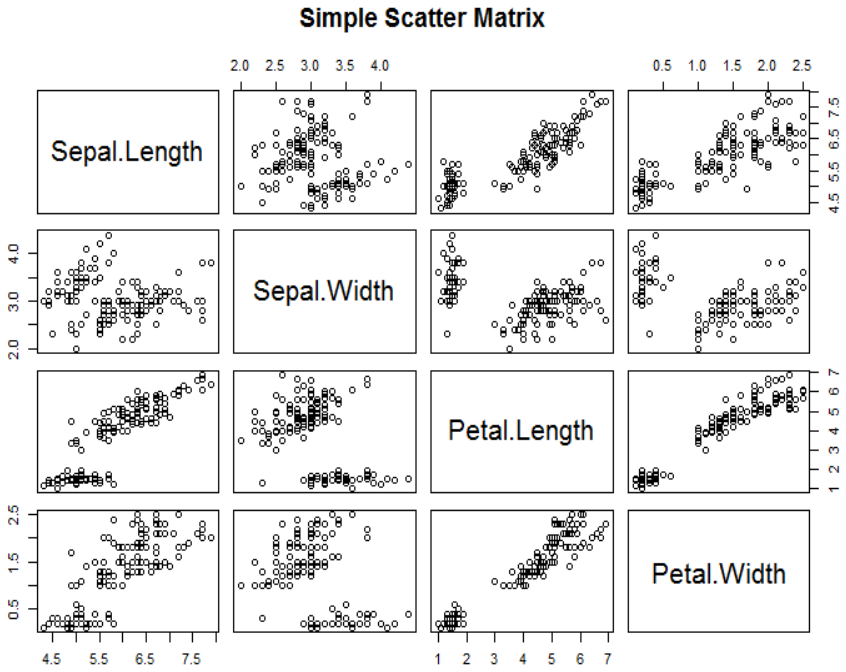

```
densityplot(~Petal.Width,
data=iris,
groups=Species,
auto.key=TRUE,
xlab="Kernel Density of
Petal Width",
ylab="Frequency",
main=list(label="Density
of Petal Width by
Species"))
```

# Scatterplot matrix

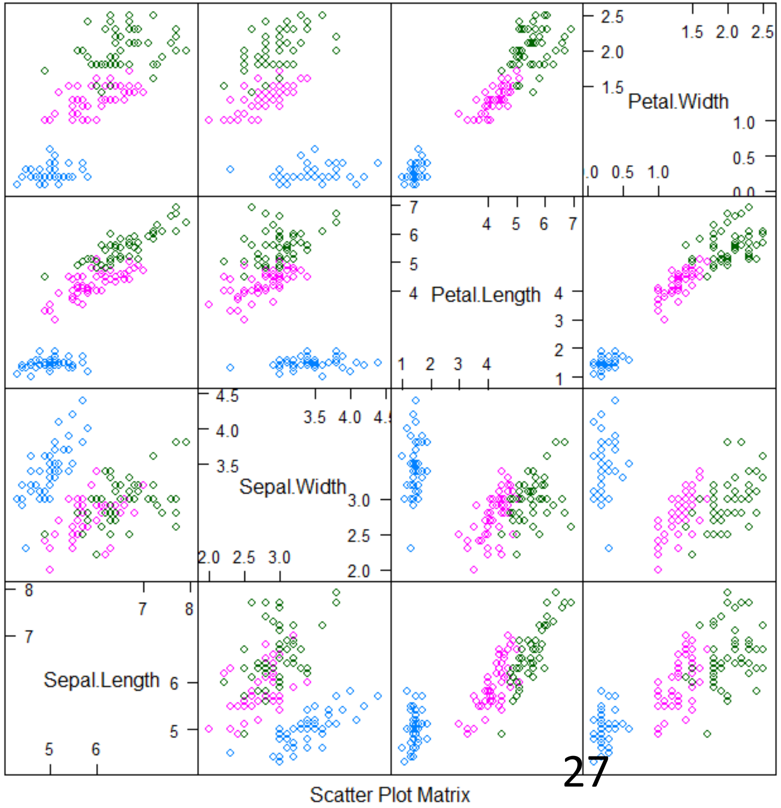
- Multiple relationships on one graph
- Good for initial explorations

```
# Core Graphics

pairs(
iris[,1:4],
main="Scatterplot Matrix"
)
```



# Scatterplot matrix




```
# Lattice Graphics

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

# Enhanced Scatterplot matrix


- Very slow!
- Use carefully

```
library(GGally)

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

# In-class Exercise 2

Using the “mtcars” dataset, predict mpg based on other columns.

Create at least 2 different plots illustrating useful relationships in data and summarize your findings.

# The "mtcars" data set

```
data(mtcars)
head(mtcars)
```

```
> head(mtcars)
                   mpg cyl disp  hp drat    wt  qsec vs am gear carb
Mazda RX4         21.0   6  160 110 3.90 2.620 16.46  0  1    4    4
Mazda RX4 Wag     21.0   6  160 110 3.90 2.875 17.02  0  1    4    4
Datsun 710        22.8   4  108  93 3.85 2.320 18.61  1  1    4    1
Hornet 4 Drive    21.4   6  258 110 3.08 3.215 19.44  1  0    3    1
Hornet Sportabout 18.7   8  360 175 3.15 3.440 17.02  0  0    3    2
Valiant           18.1   6  225 105 2.76 3.460 20.22  1  0    3    1
```

# GGPLOT2 GRAPHICS

# 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
```

# ggplot Fundamentals

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

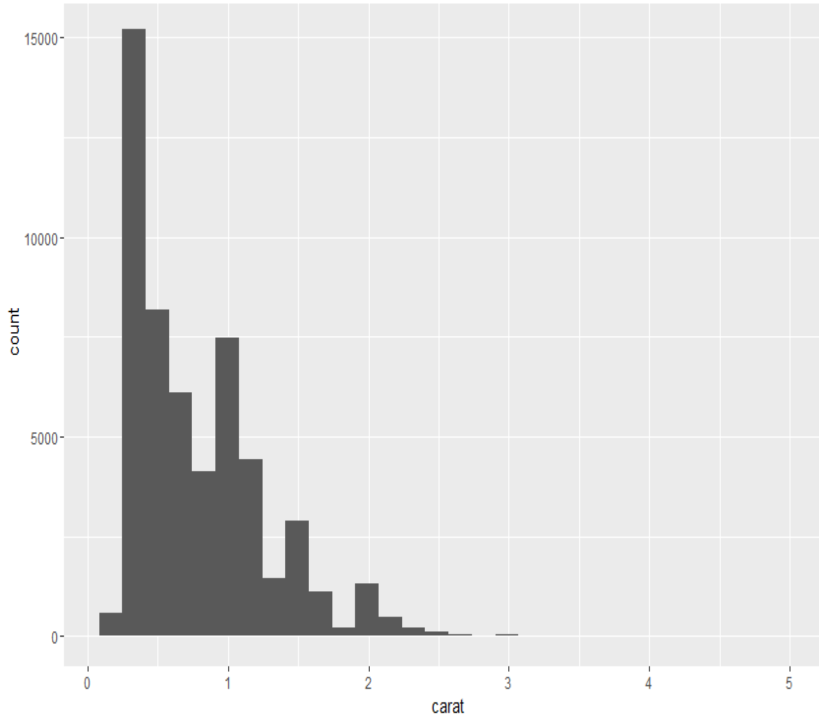
# Layering

```
ggplot(diamonds, aes())   +   geom_point()
```

Layer 1

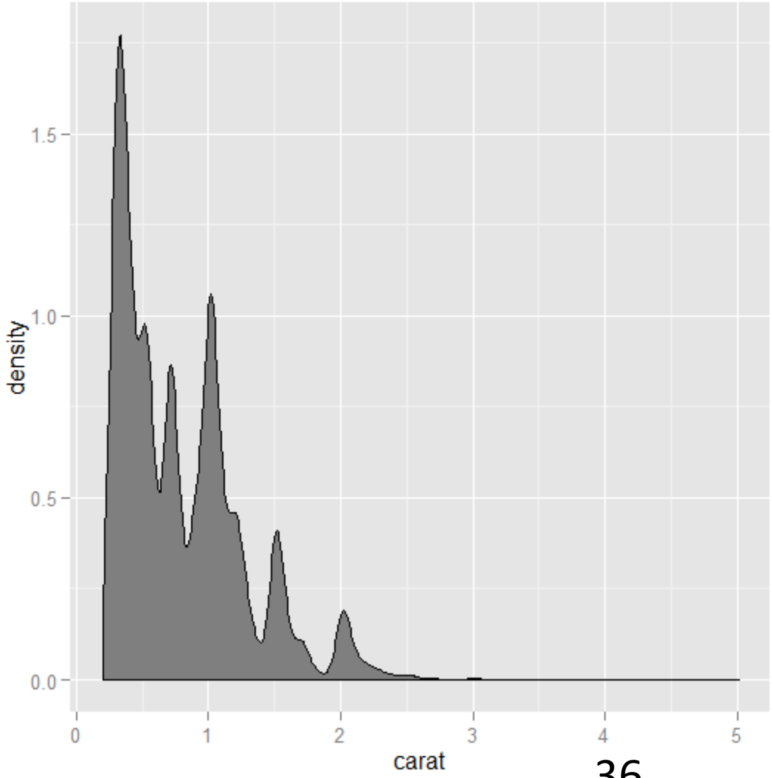
Layer 2

# Histogram




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

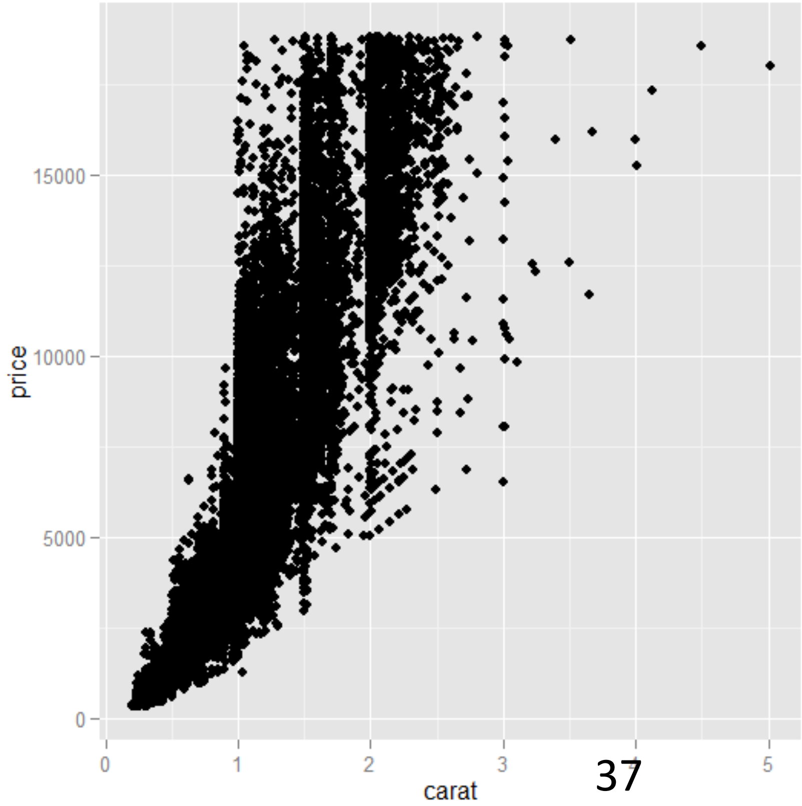
# Density plot




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

- Note the location of aes()

# Scatter plots




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



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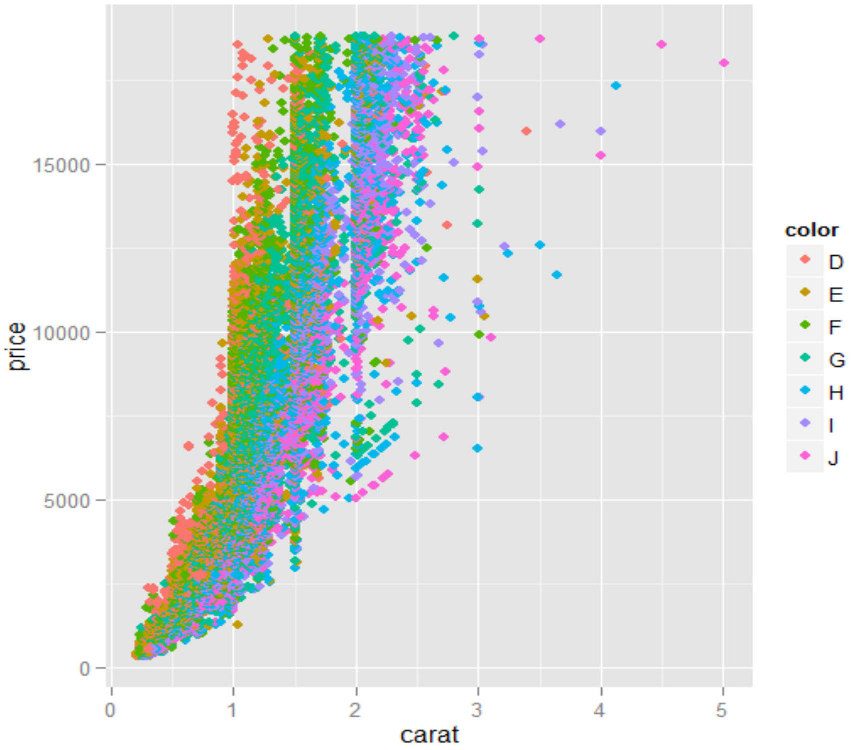
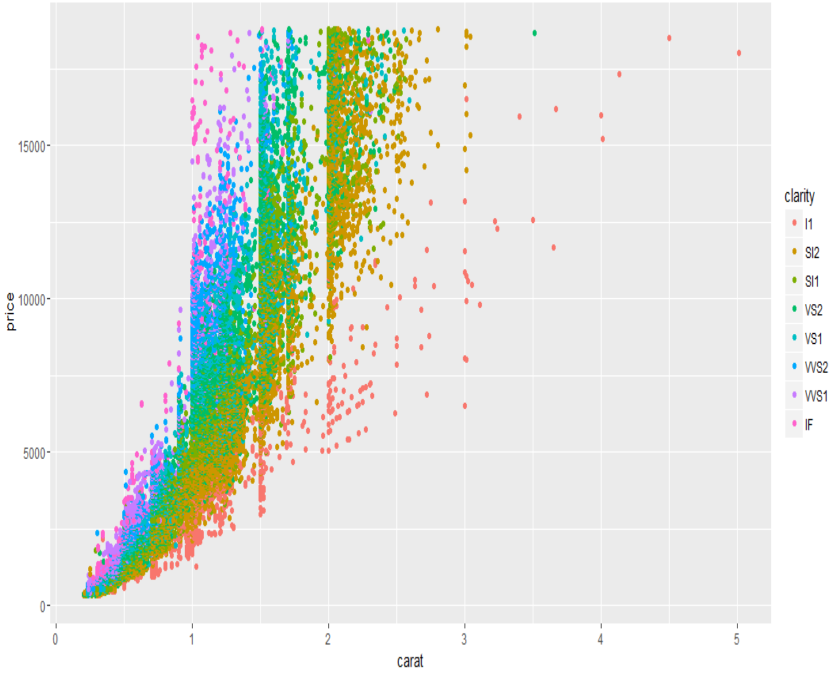
# ggplot object



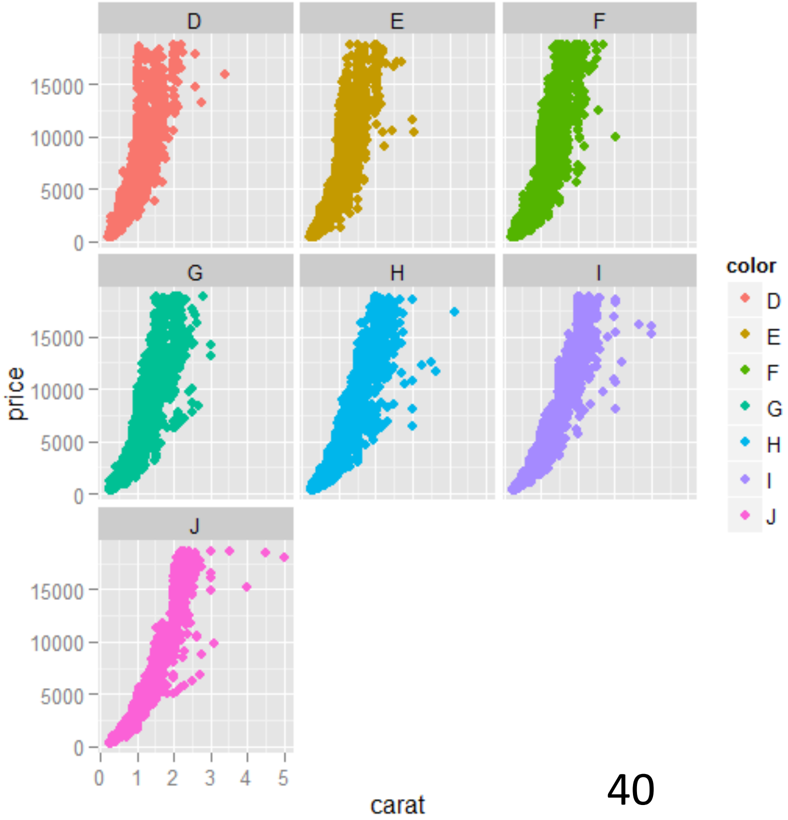

```
# Store the plot for future
modification
g <- ggplot(diamonds,
aes(x=carat, y=price))

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

# ggplot object



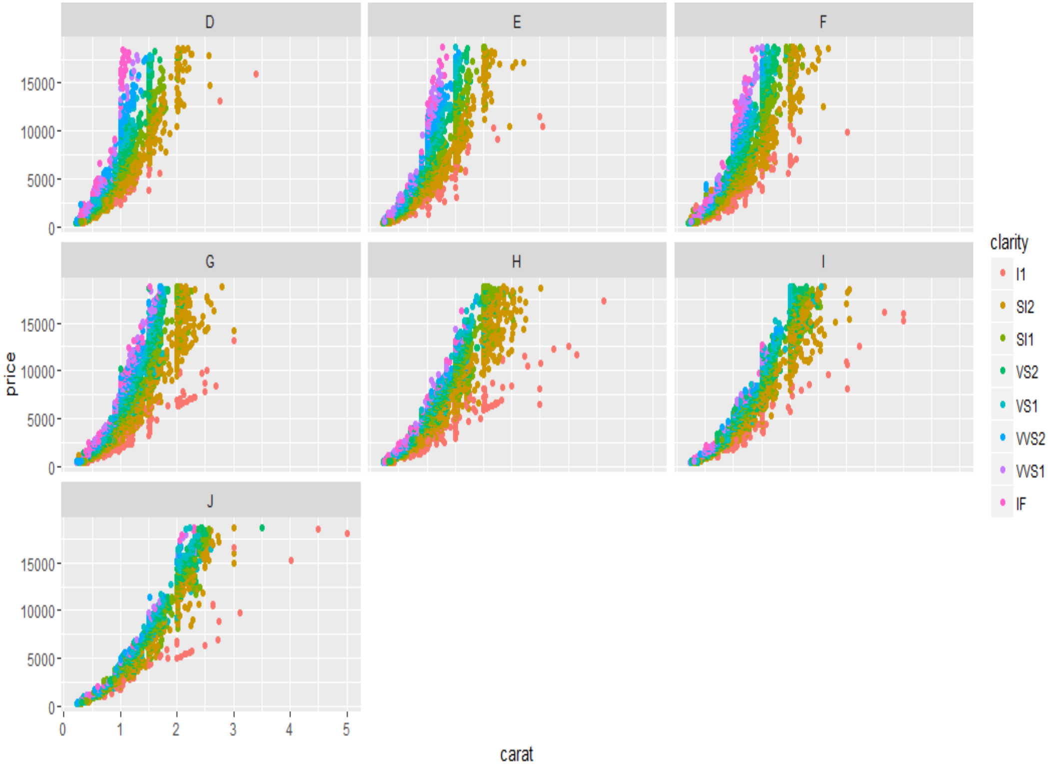

```
# Store the plot for future modification
g <- ggplot(diamonds, aes(x=carat, y=price))

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

# Separating the segments




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

# Separating the segments




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



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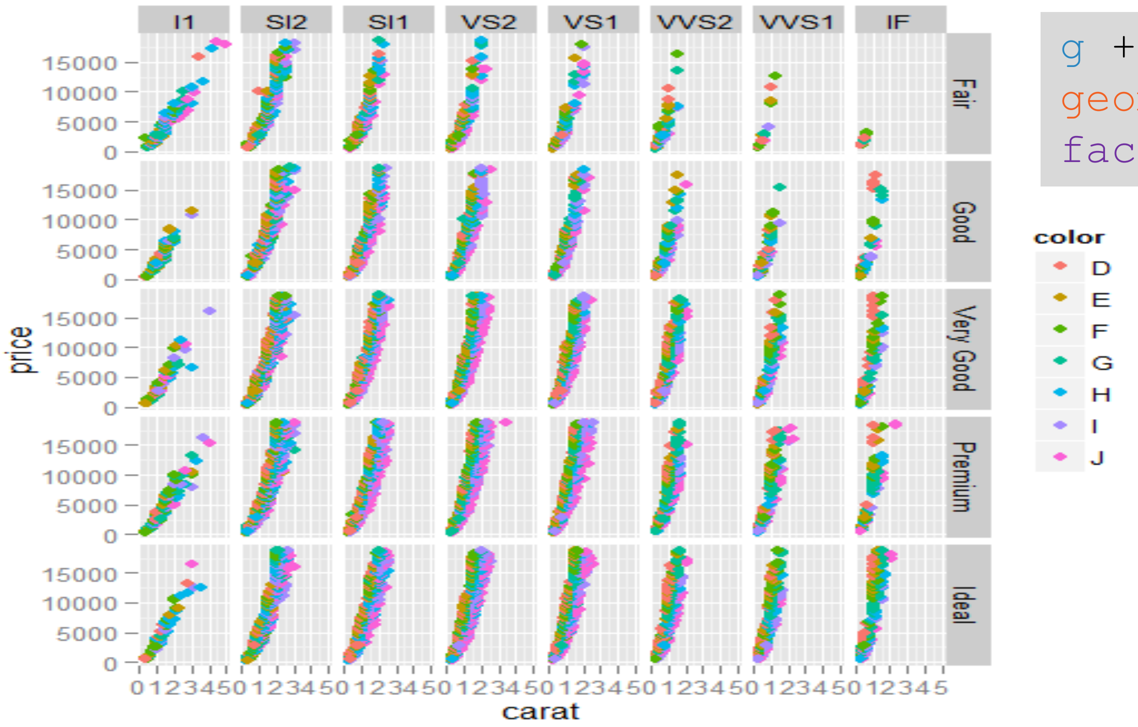
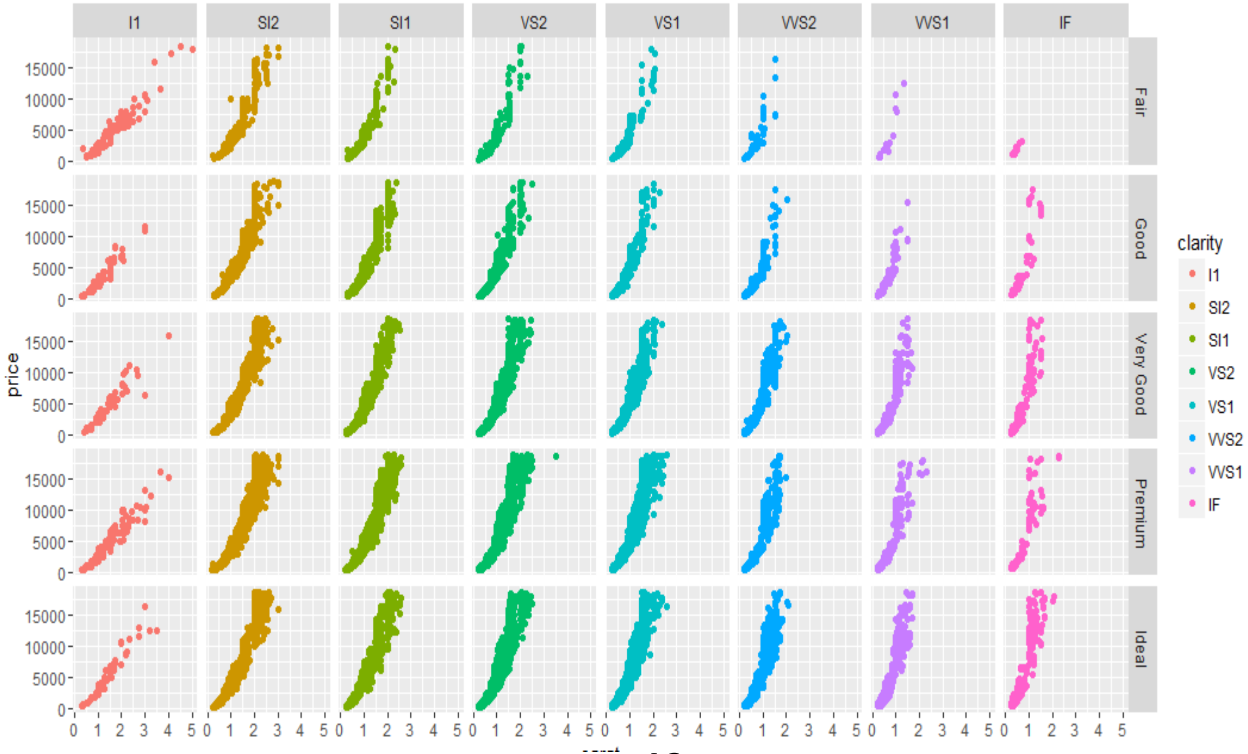
# More segments!




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

# More segments!




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

# Summary

- ✓ Basics of R
- ✓ Graphing in R – core, lattice and ggplot2
  Look at multiple types of graphs.
- ✓ Visualize and segment dataset to gain insights about data.
- ✓ Identify key features
- ✓ Summarizing findings

# STORYTELLING WITH TITANIC

# 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

## Set target column as a factor

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

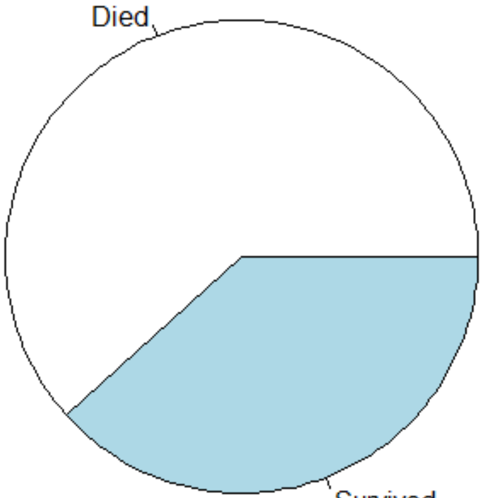
## Rename factors and columns

```
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

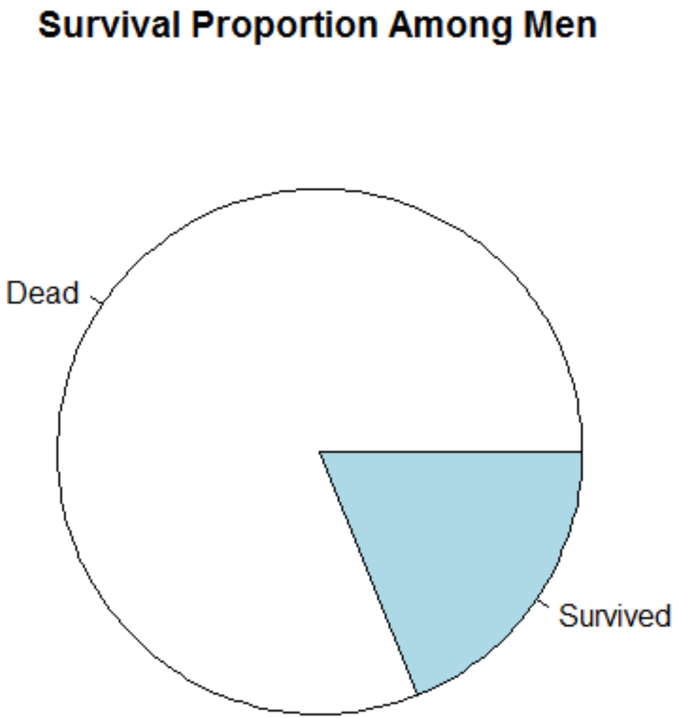
```
survivedTable <- table(titanic$Survived)
par(mar=c(0, 0, 0, 0))
pie(survivedTable, labels=c("Died", "Survived"))
```

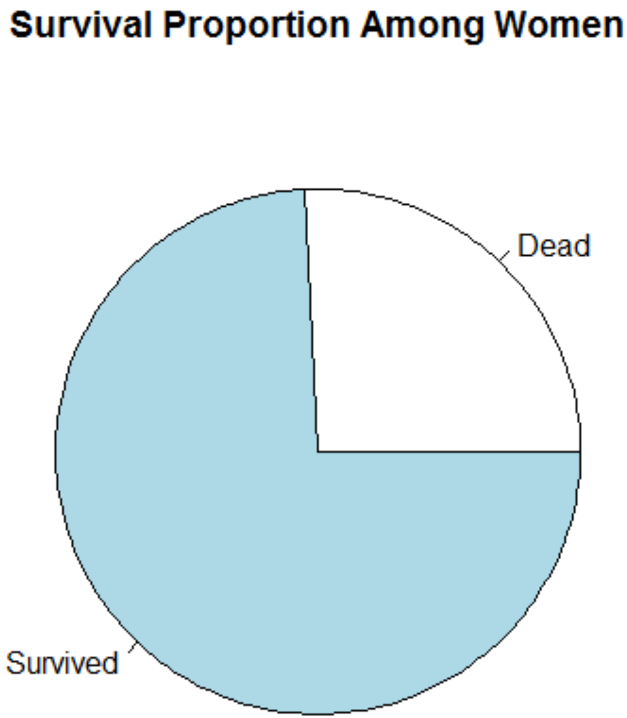


# Is Sex a Good predictor?

```
#Identify where sex = male for all columns
male <- titanic[titanic$Sex == "male",]

#Identify where sex = female for all columns
female <- titanic[titanic$Sex == "female",]

par(mfrow=c(1,2)) #two figures arranged in 1 row and 2 columns
pie(table(male$Survived), labels=c("Dead","Survived"))

pie(table(female$Survive), labels=c("Dead","Survived"))
```

# 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)
```

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

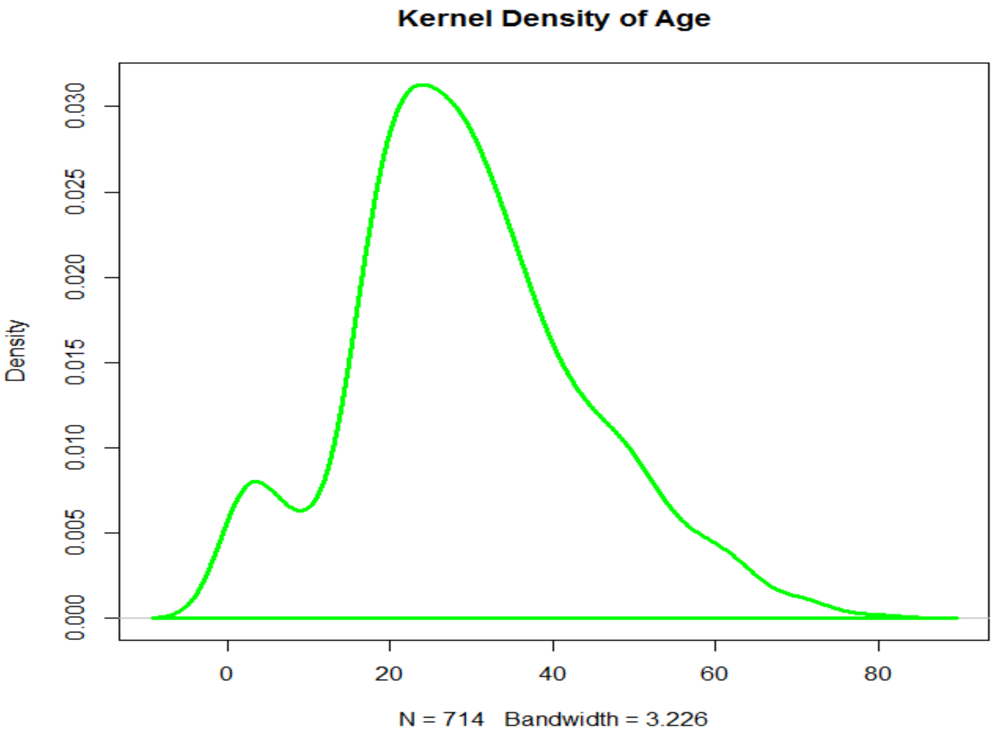
```
summary(titanic[titanic$Survived
=="Survived",]$Age)
```

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

# In-class Exercise 3

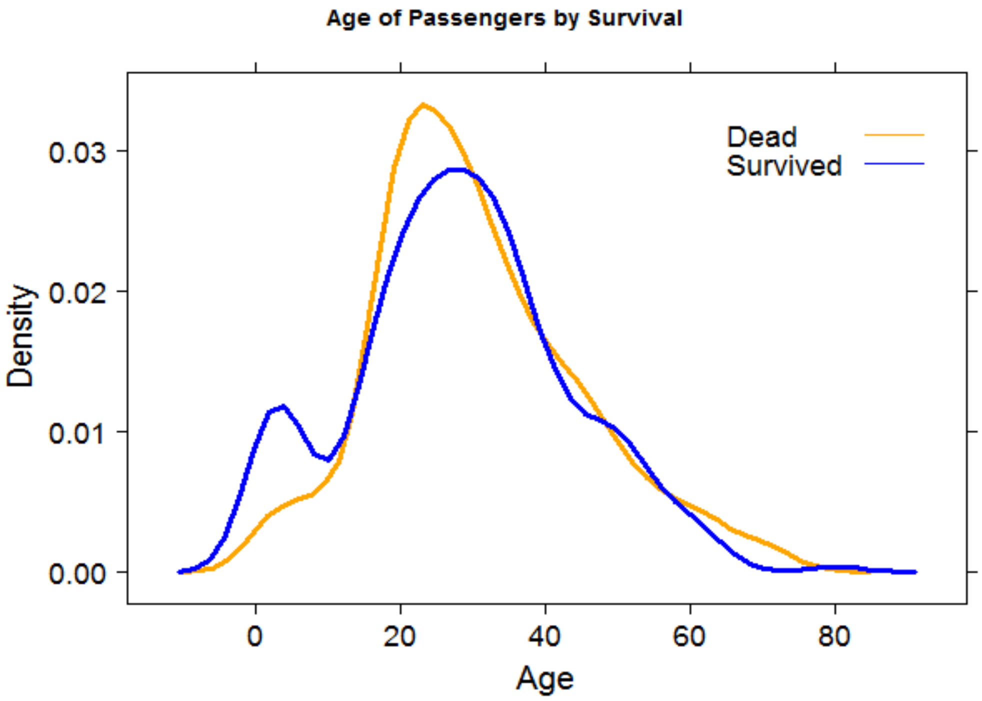
- Create 2 boxplots of Age
  - Segmented by Gender
  - Segmented by Survived
- Create a density plot of Age
  - na.omit() may be useful

# Sample solution




```
density(titanic$Age)
#NAs prevent this
> d <-
density(na.omit(titanic$Ag
e))
> plot(d, main="Kernel
Density of Age")
>
polygon(d,border="green",l
wd=3)
```

# Is Age a good predictor for Survival?




```
densityplot(~ Age,
data=titanic,
groups=Survived,
plot.points=F, lwd=3)
```

Note: will break with missing values



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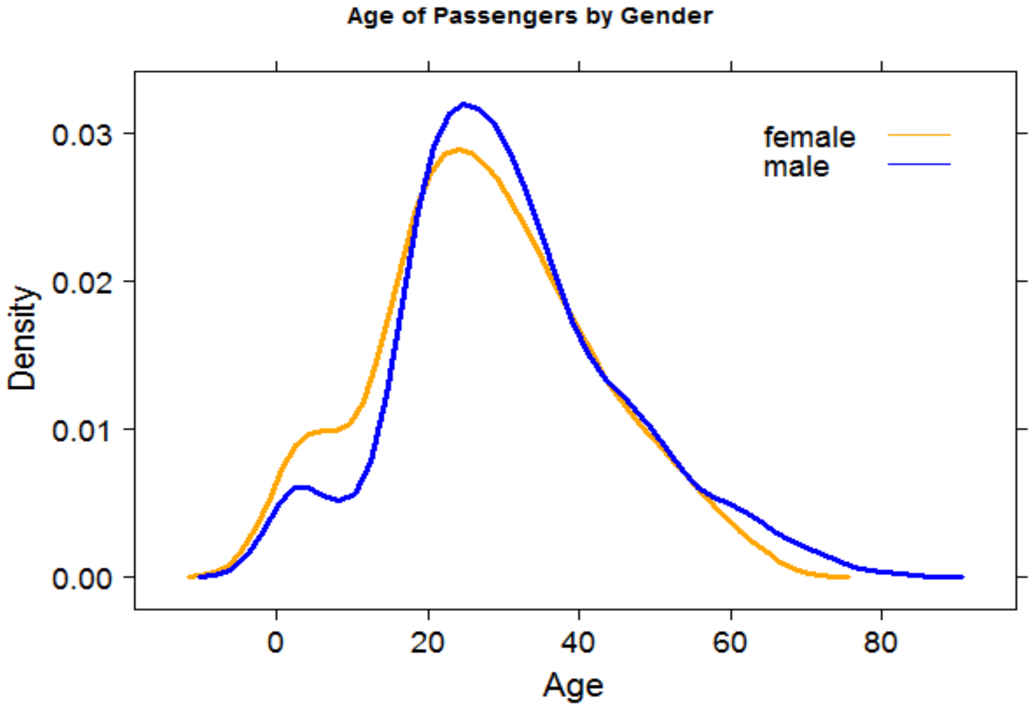
# Is Age a good predictor for Gender?




```
densityplot(~ Age,
data=titanic, groups=Sex,
plot.points=F, lwd=3)
```

# Questions?