Data Exploration, Visualization, and Feature Engineering

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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

- Train 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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  - **R core graphics and Lattice**
  - ggplot2
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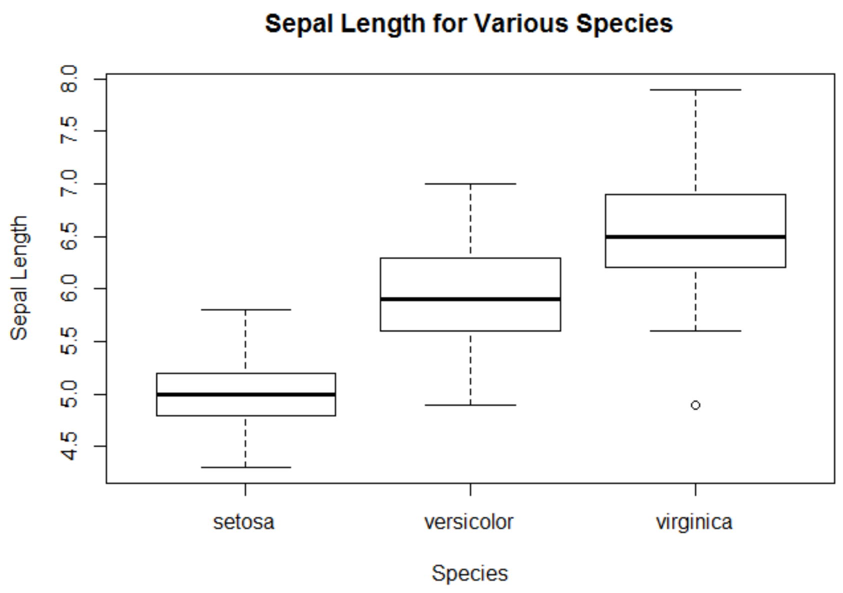
Box plots

- 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"
)
```



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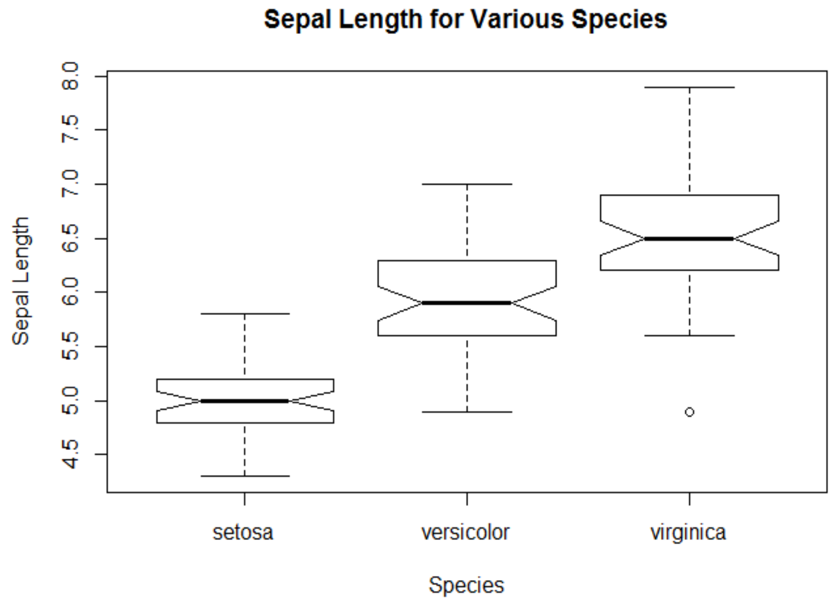
Box plots with notches

- 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

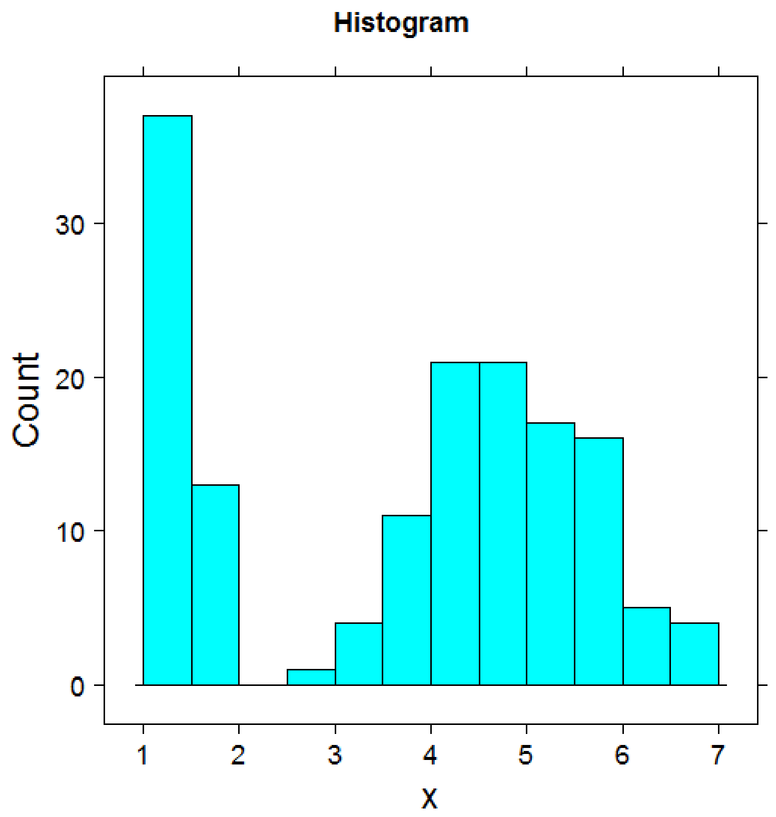
```
pdf("myplot.pdf")

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
```

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

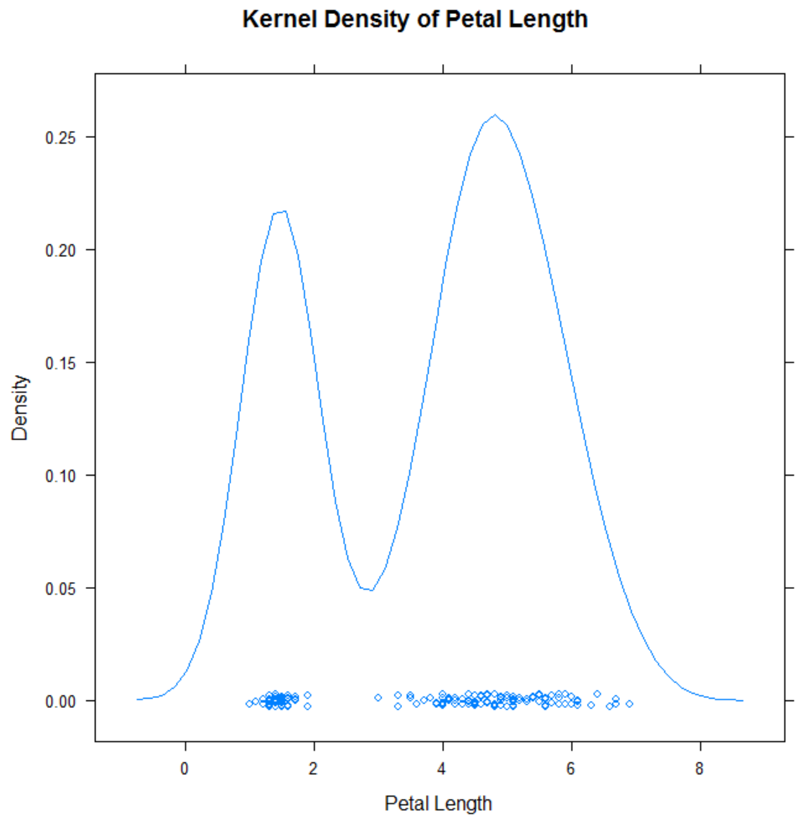
Lattice: Histogram



- 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



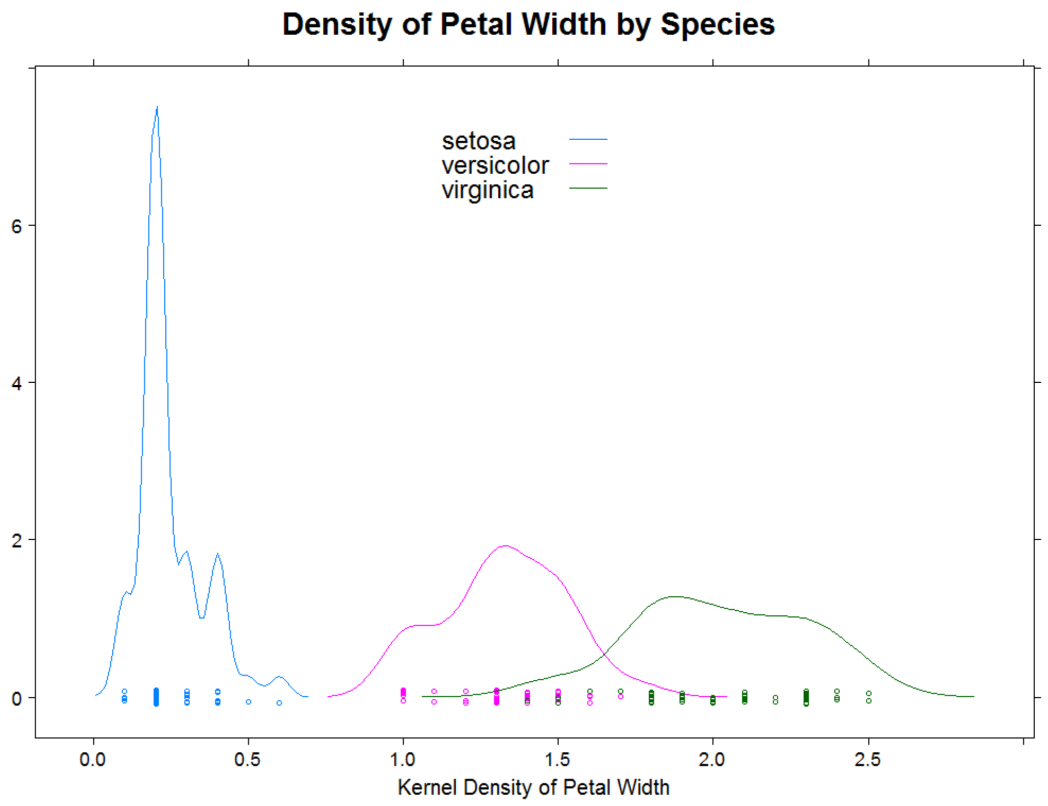
- Variation on histogram
- Estimates density function from counts

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

The devil is in the details

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

Lattice: Multiple density plots



- What does this segmentation show?

```
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)

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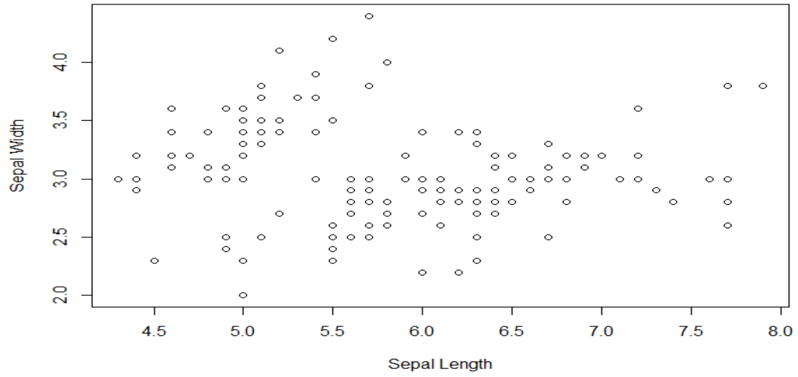
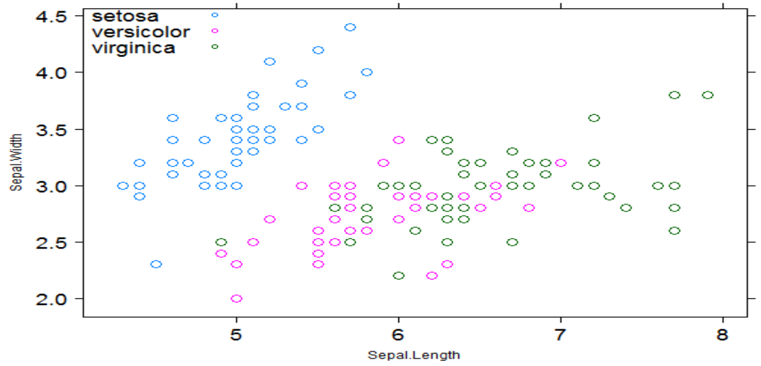
Sample solution

```
# 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))
```



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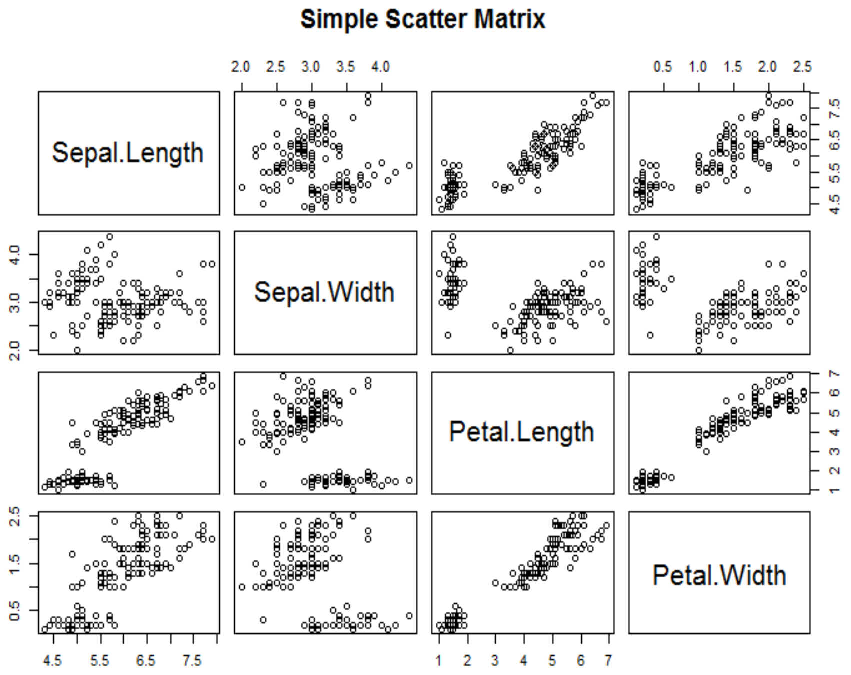
Core: Scatter plot matrix

- Multiple relationships on one graph
- Good for initial explorations

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



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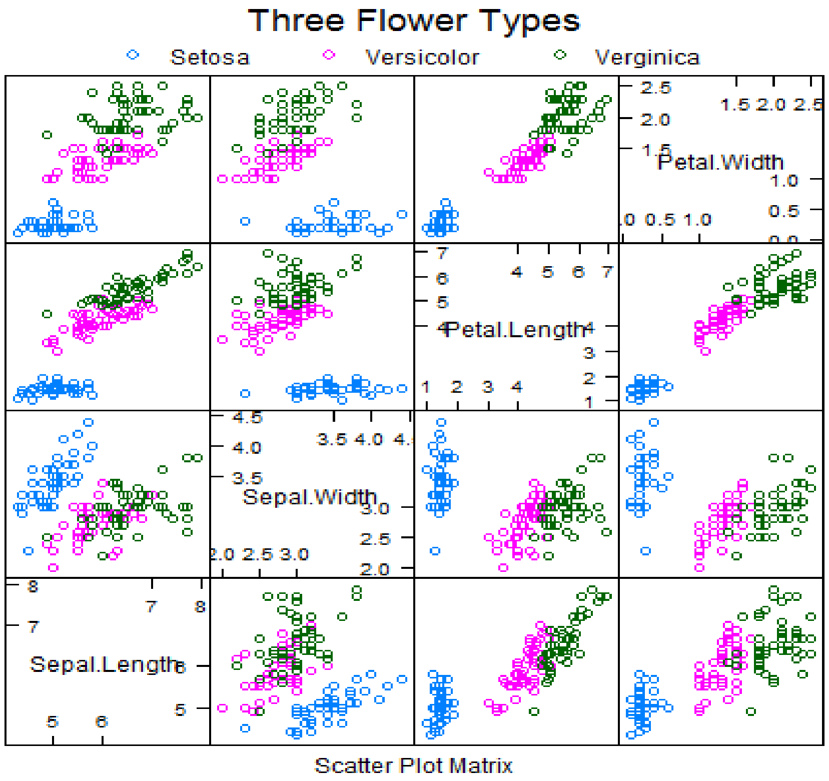
Lattice: Scatter plot matrix



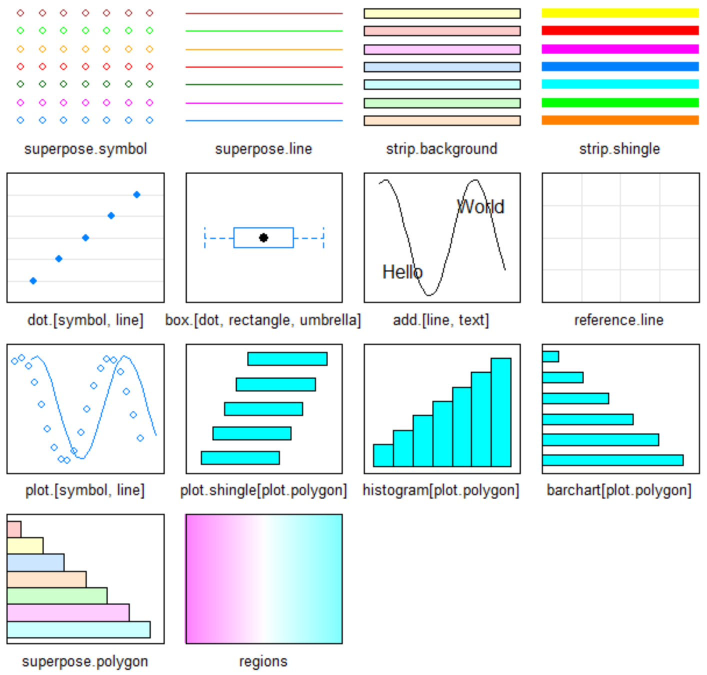
```
# Getting settings for legend
super.sym <-
trellis.par.get("superpose.symbol")

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

Graphical settings

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

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

- Modify global settings
- Useful when generating reports



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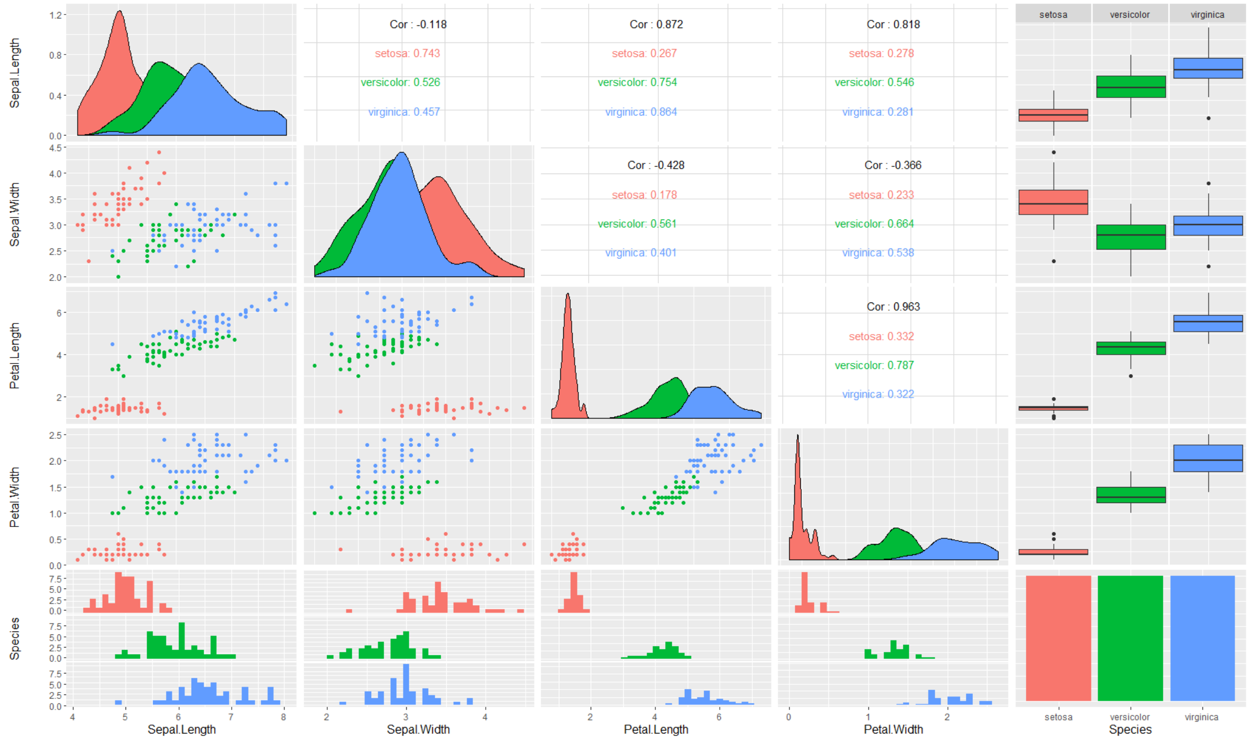
Enhanced scatter plot matrix



```
library(GGally)

ggpairs(iris,
ggplot2::aes(color=Sp
ecies))
```

- Very slow!
- Use carefully

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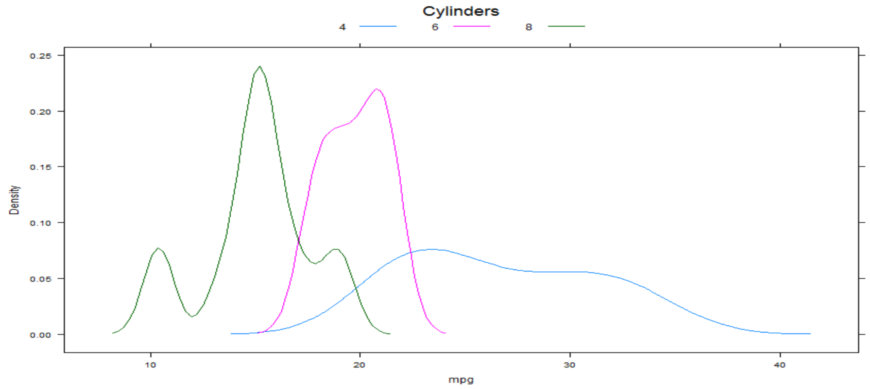
Exercise 2

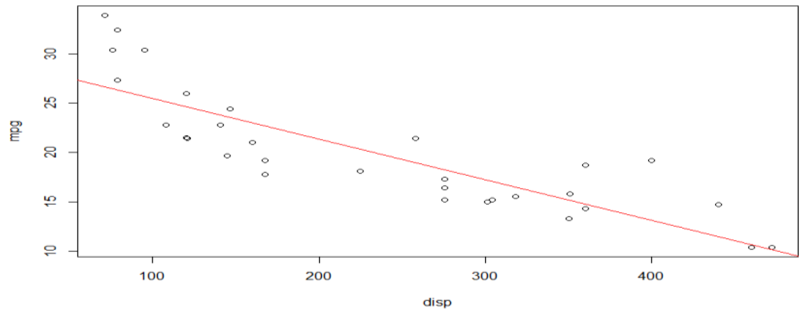
- Load "mtcars" dataset: data(mtcars)
  - ?mtcars for details
  - Eyeball the data
- **Goal:** Predict mpg based on other columns
- Create at least 2 different plots illustrating useful relationships in data

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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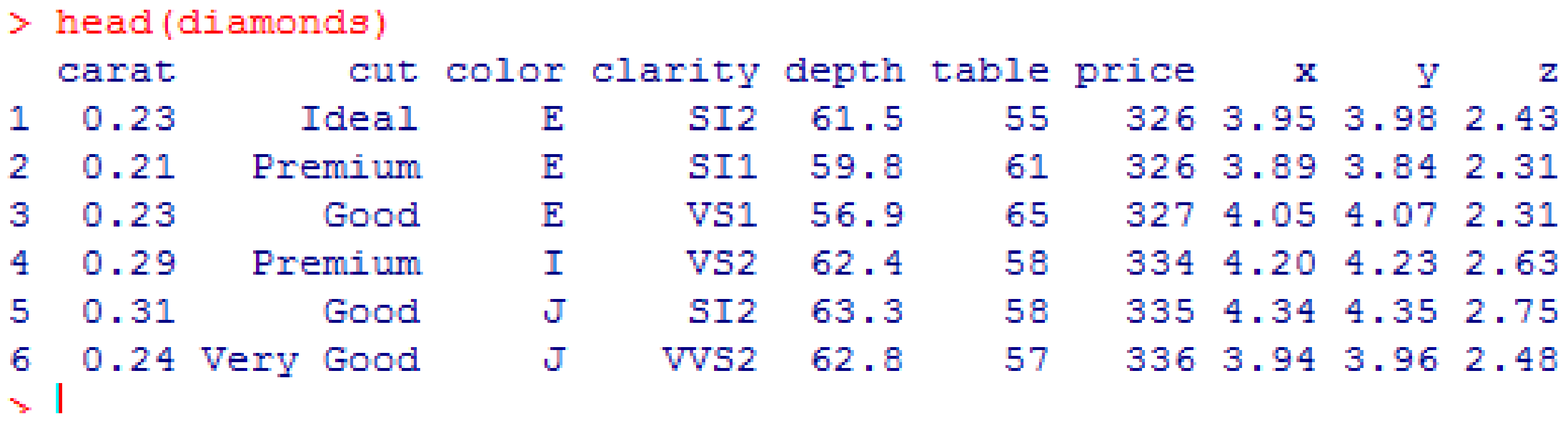
  - **ggplot2**
- Exercises using Titanic data set

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
> 
```

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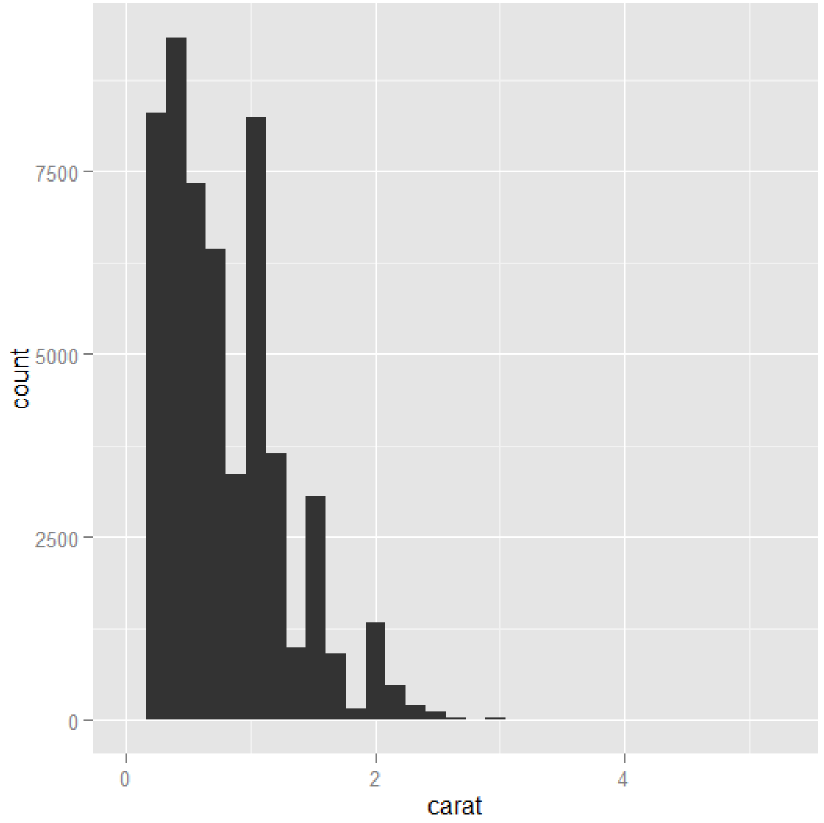
Histogram



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

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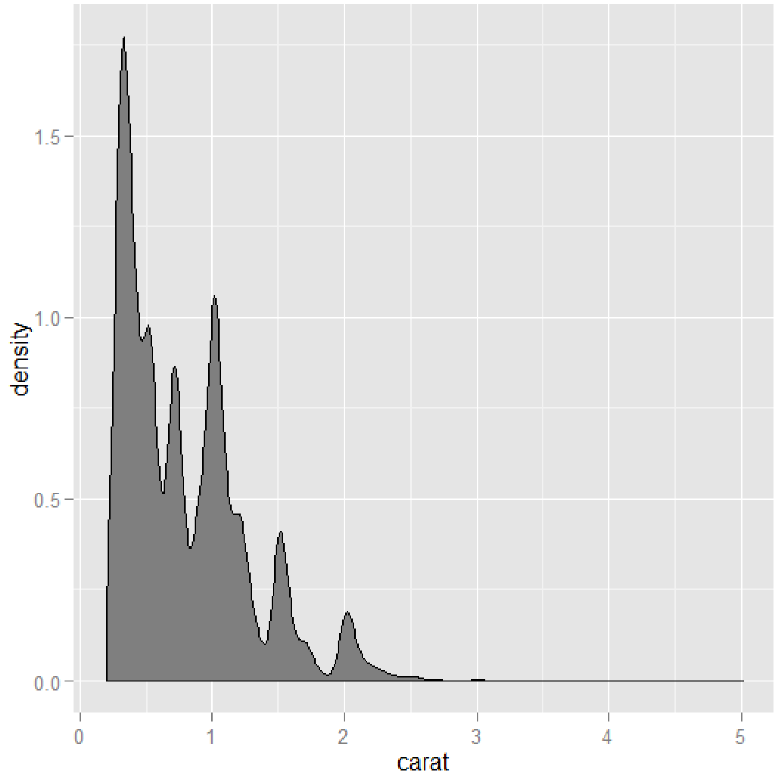
Density plot



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

- Note the location of aes()

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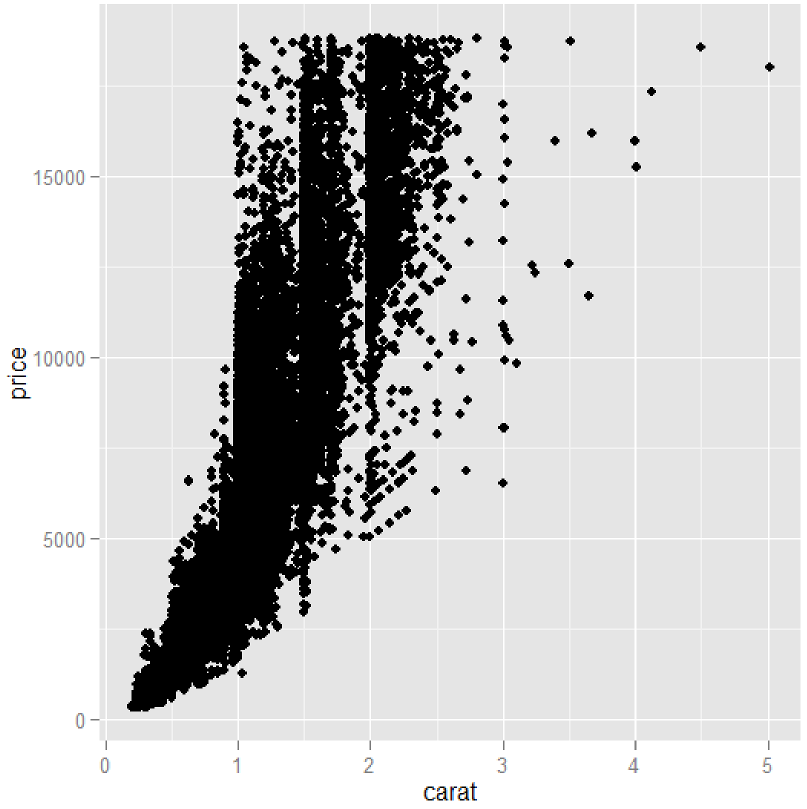
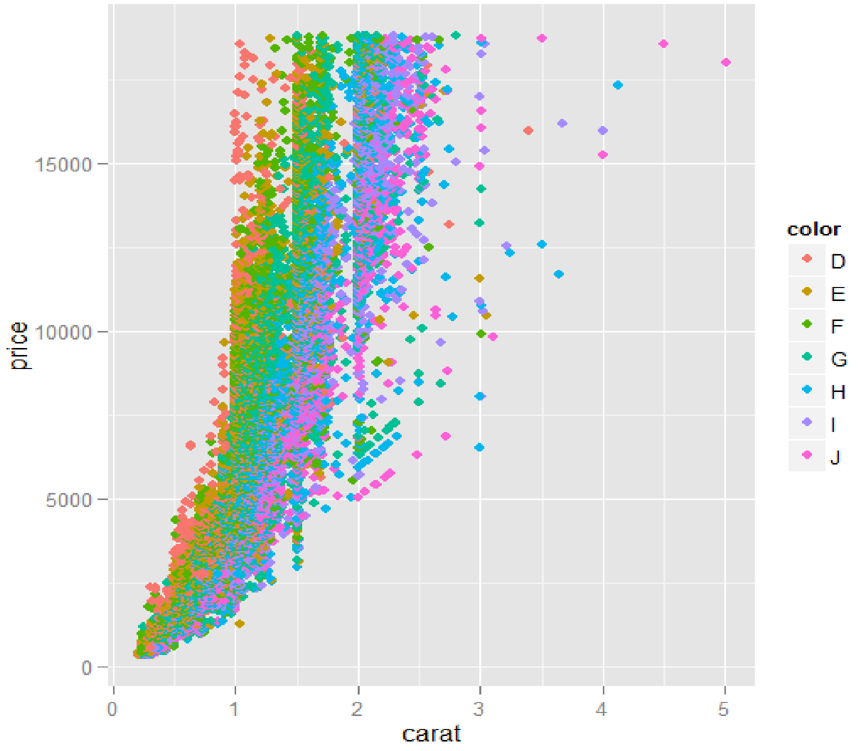
Scatter plots



```
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))
```

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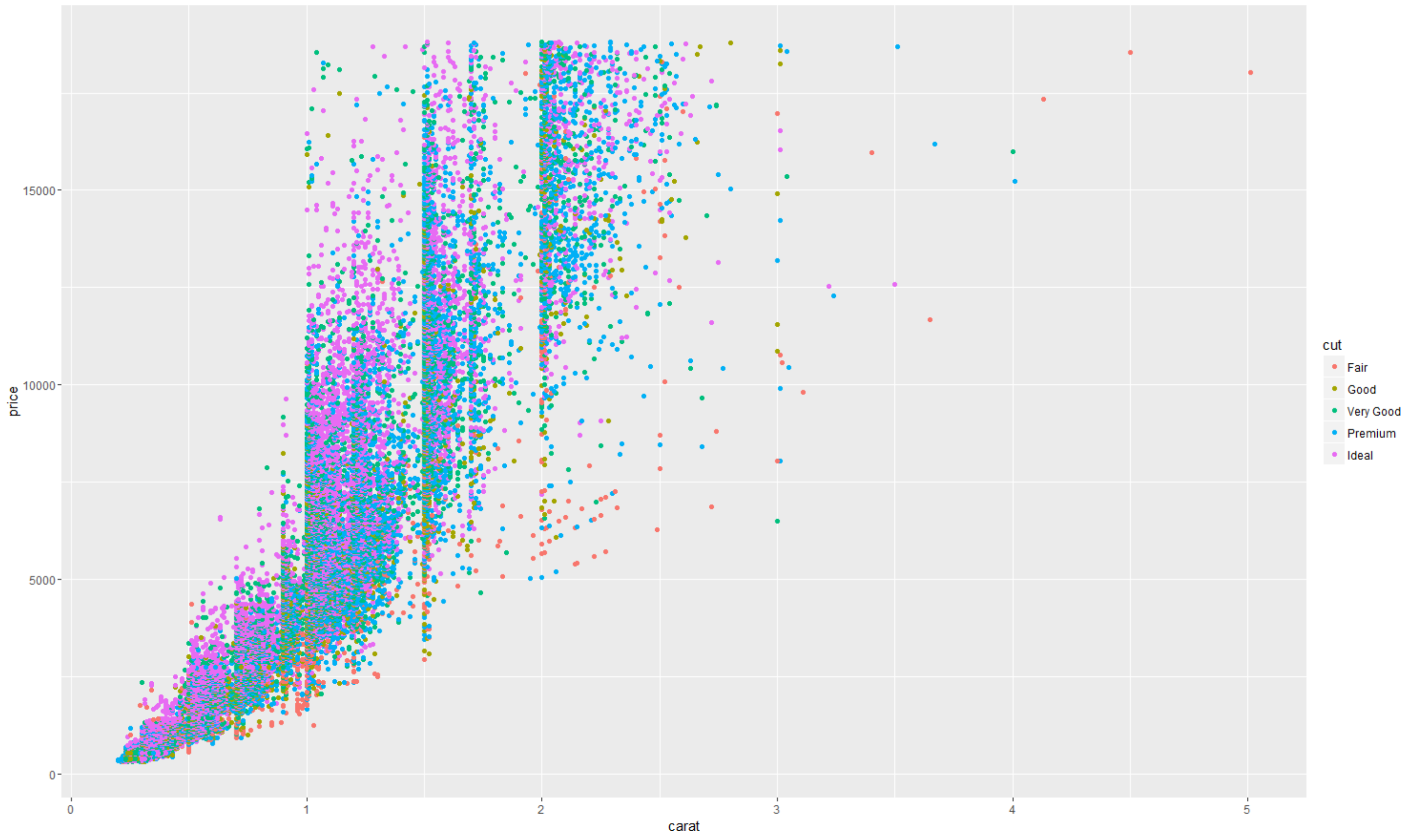

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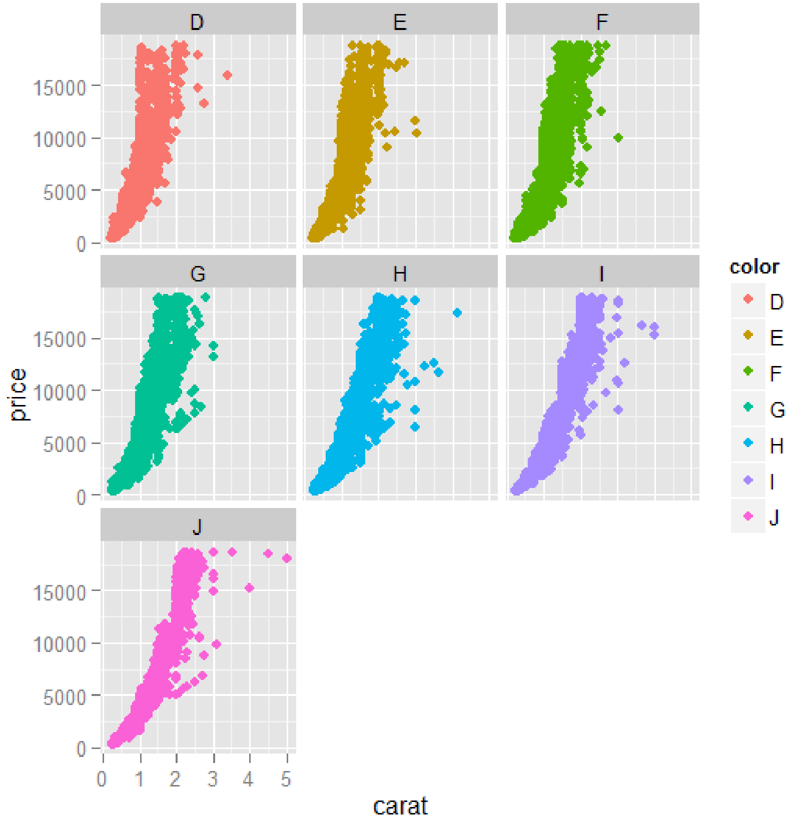
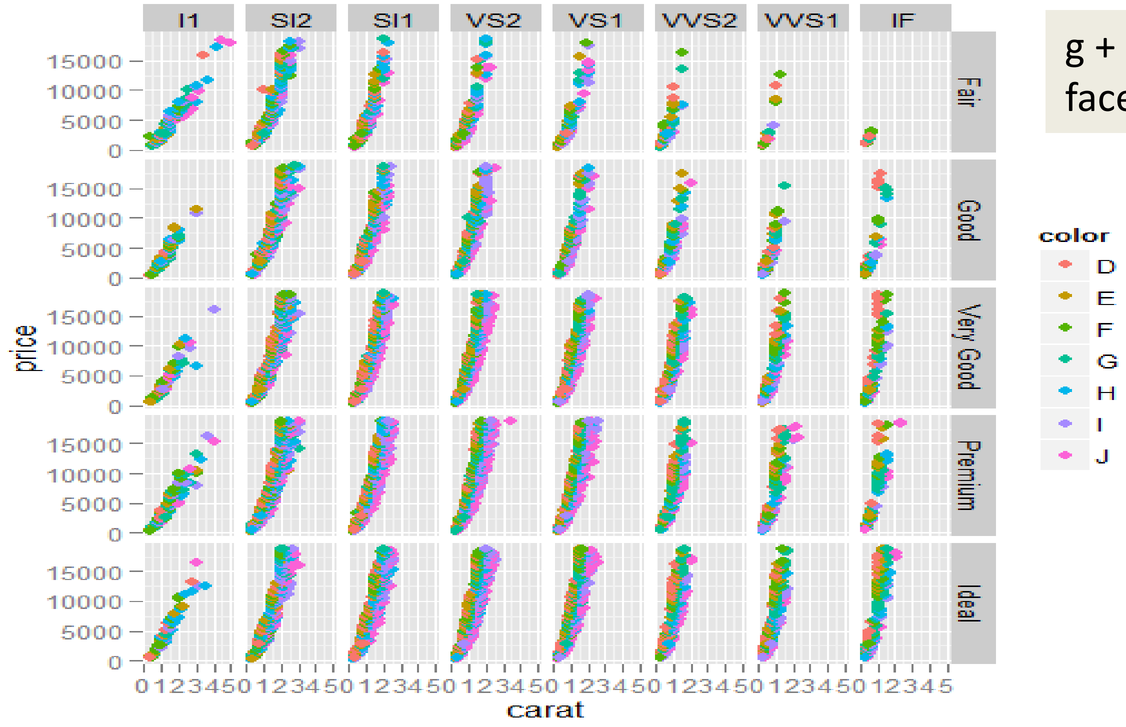
Separating the segments



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

More segments!



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

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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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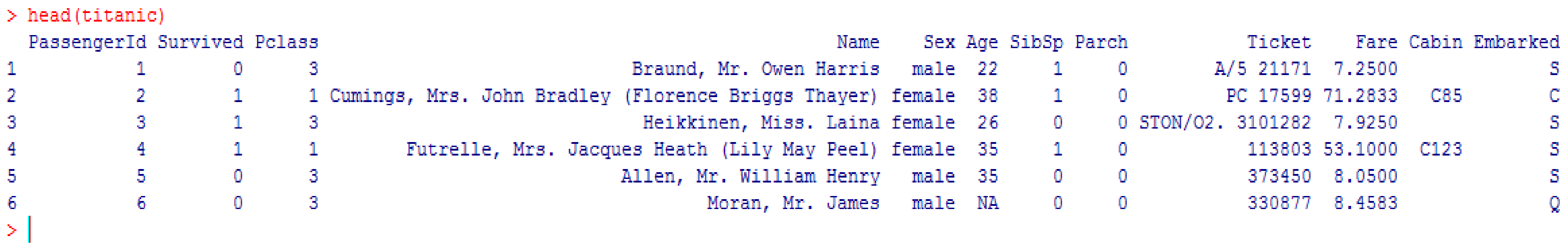
  - ggplot2
- **Exercises using Titanic data set**

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?

```r
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 ...
```

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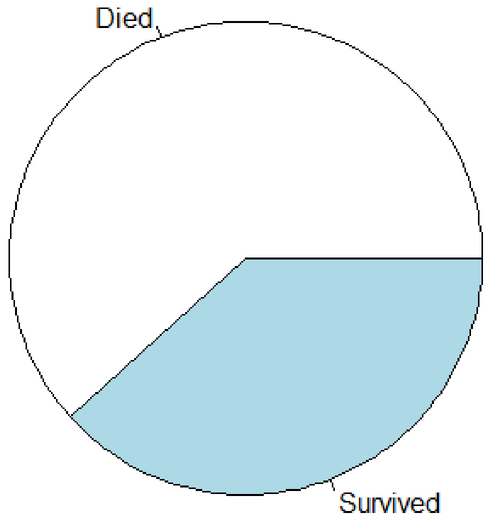
Class distribution: Pie Chart

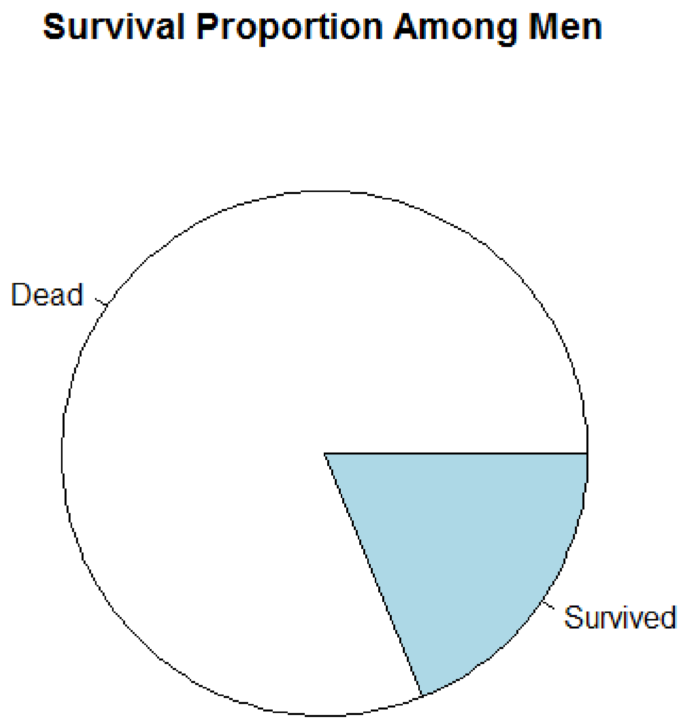
```
survivedTable <- table(titanic$Survived)
par(mar=c(0, 0, 0, 0), oma=c(0, 0, 0, 0),
cex=1.5)
pie(survivedTable, labels=c("Died", "Survived"))
```

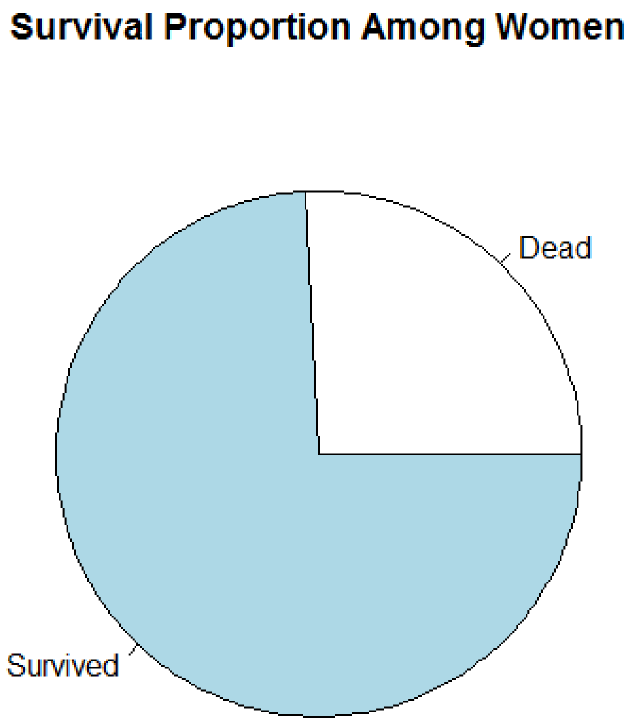


Is Sex a Good predictor?

```
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?





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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
```

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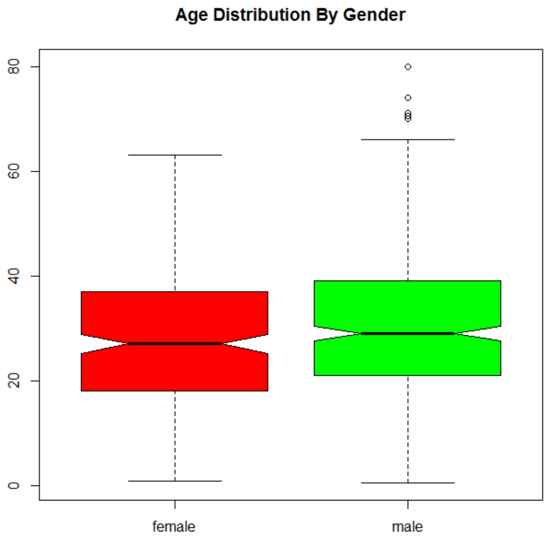
Exercise 3

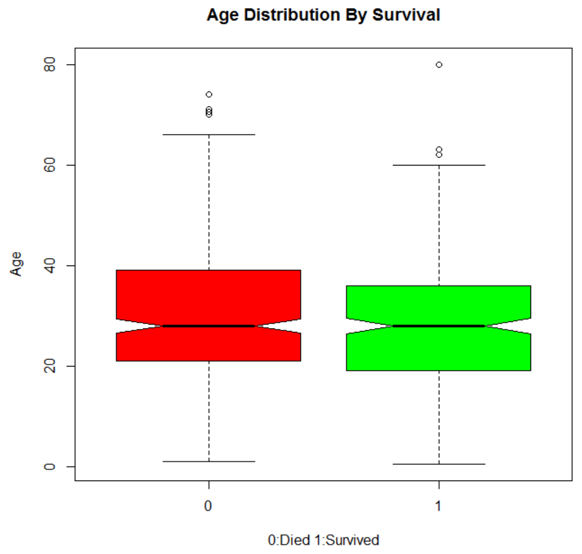
- Create 2 box plots of Age
  - Segmented by Gender
  - Segmented by Survived
- Create a histogram of Age
- Create a density plot of Age
  - na.omit() may be useful

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")
```





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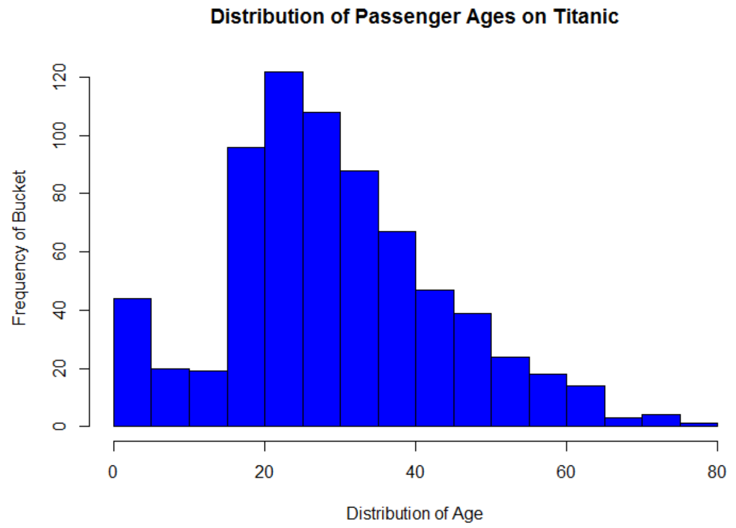
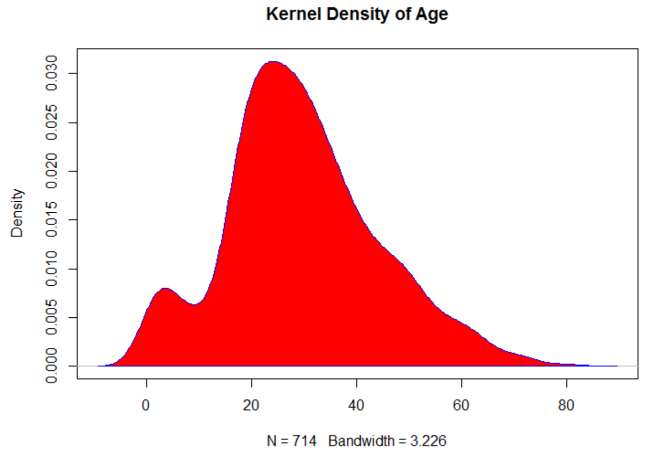
Sample solution

```
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")
```





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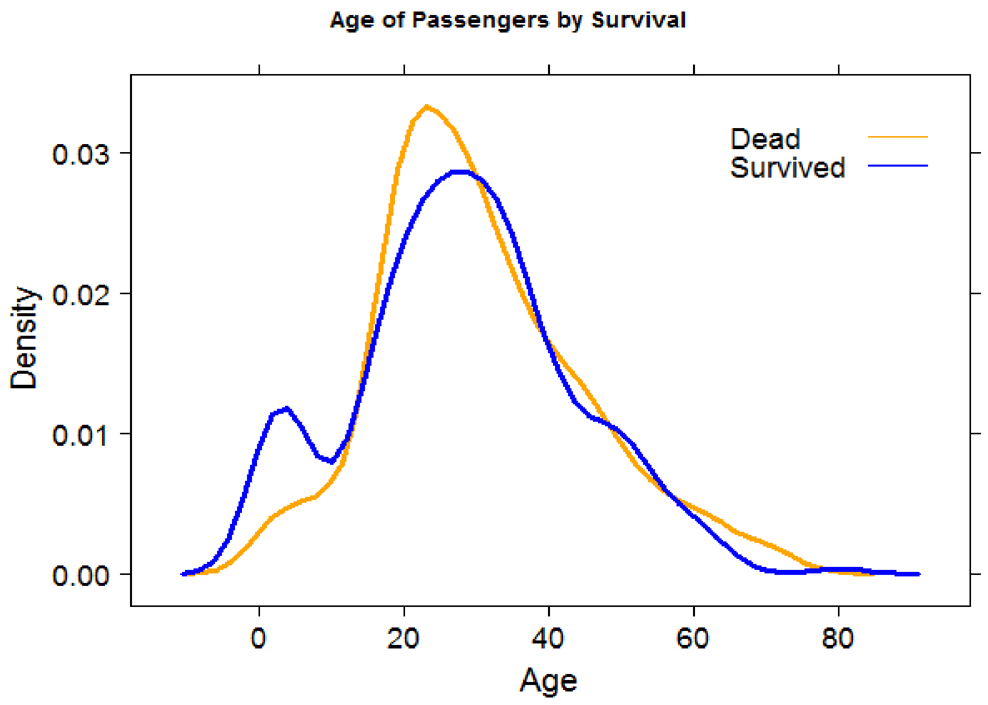
Is Age a good predictor for Survival?



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

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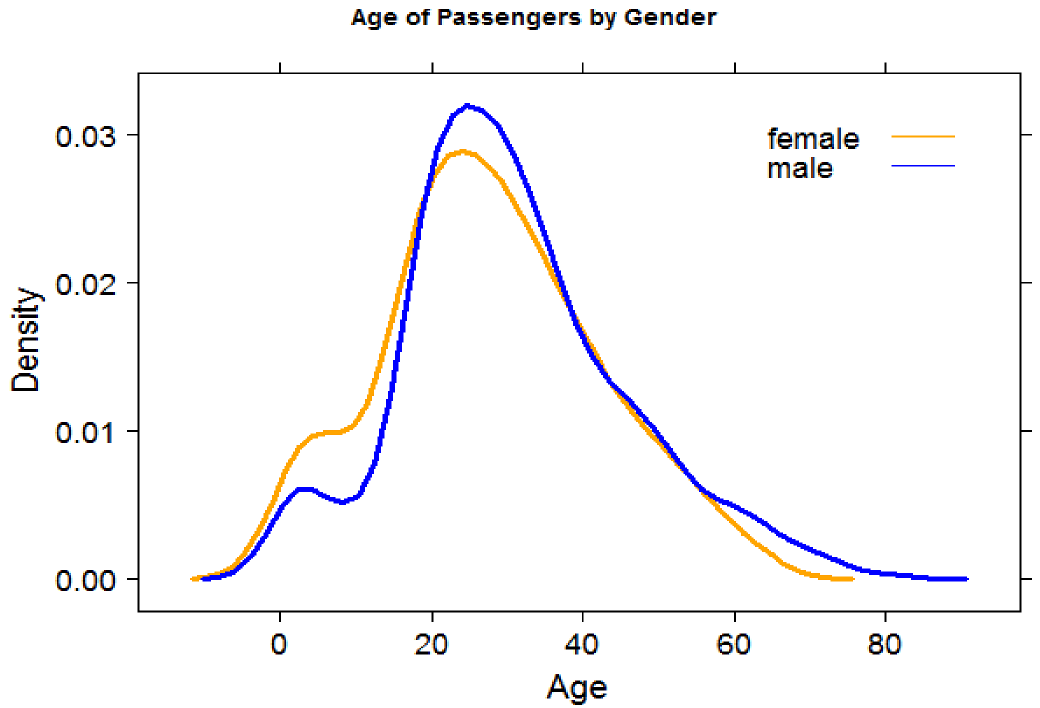
Is Age a good predictor for Gender?



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

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Questions?

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