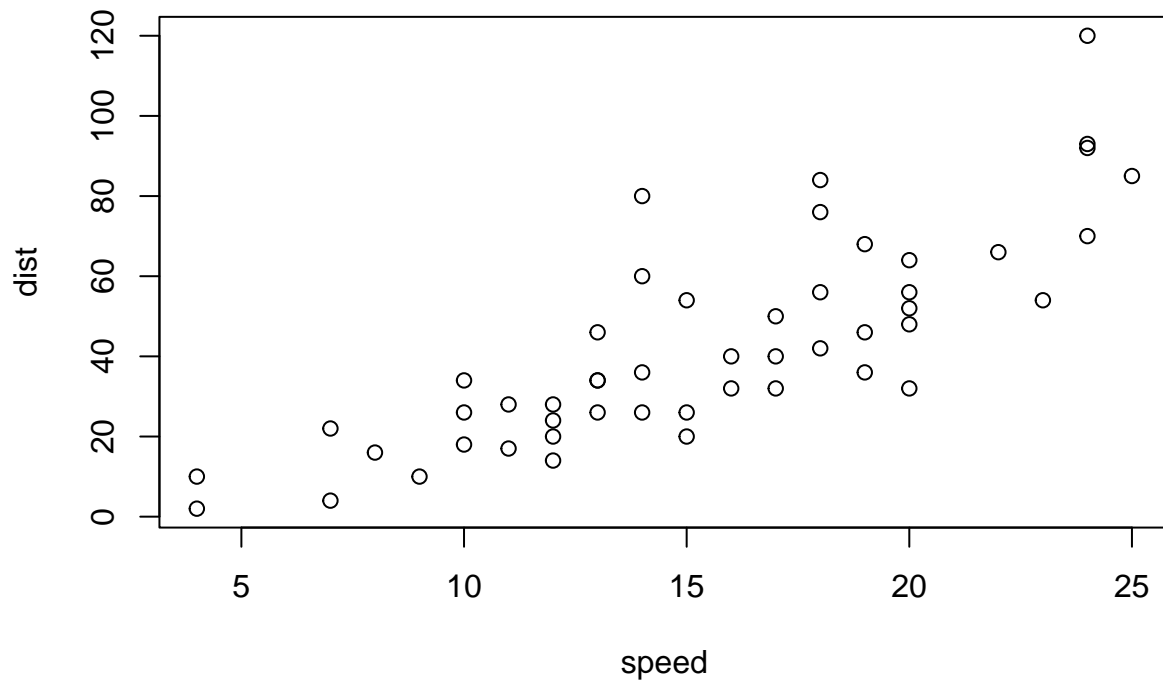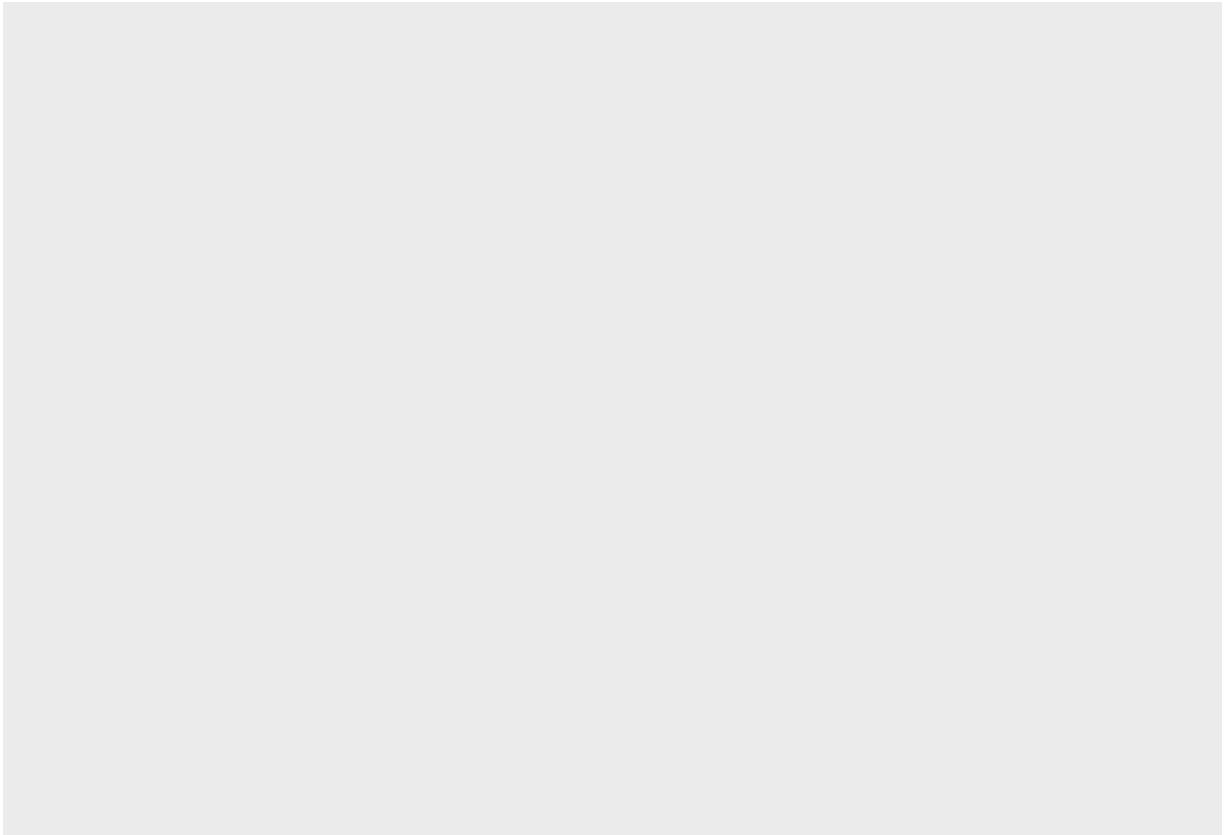# class05.R

rodeo

2022-02-01
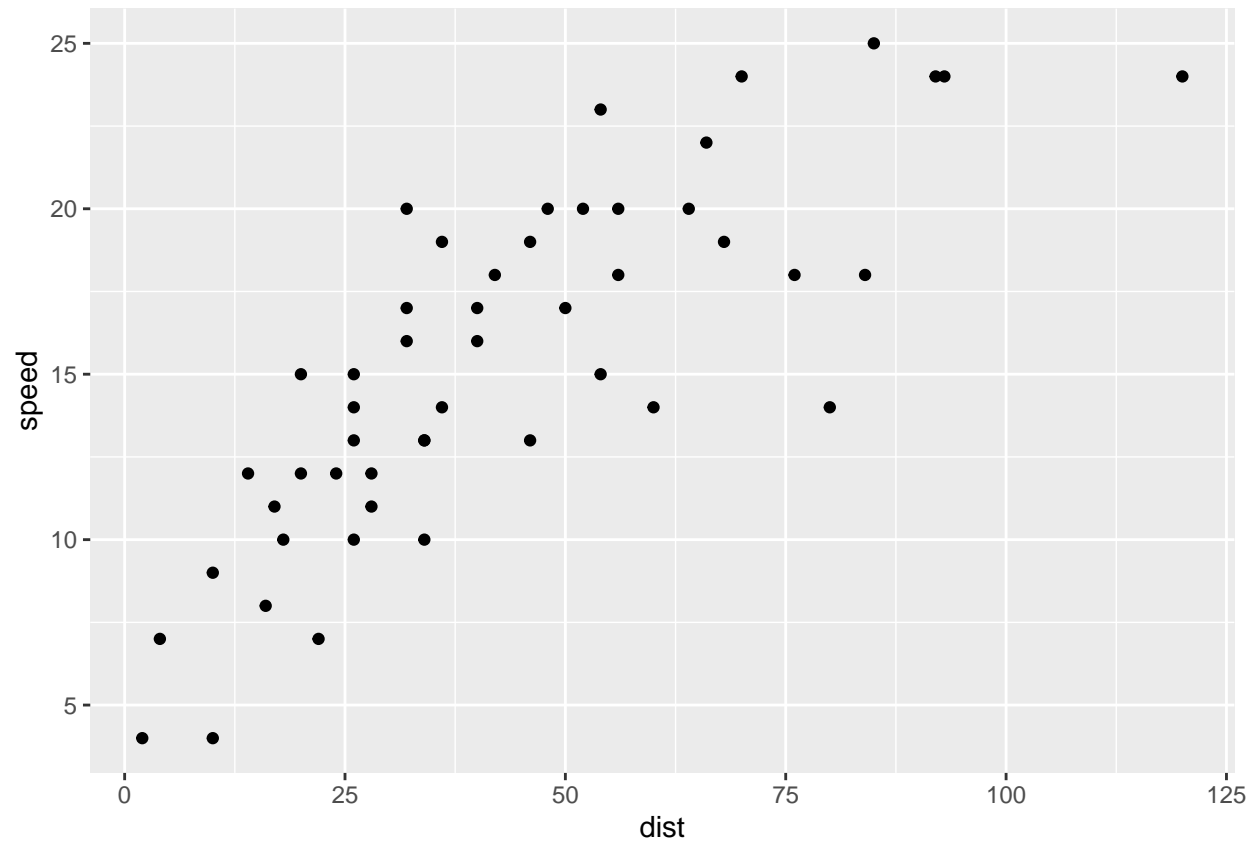
```r
#Class 05 Data Visualization

#This is the "base" R plot
plot(cars)

#Get package ggplot2
#install.packages("ggplot2")

#Load package ggplot2
library("ggplot2")
```



```r
#Plot the data
ggplot(cars)
```
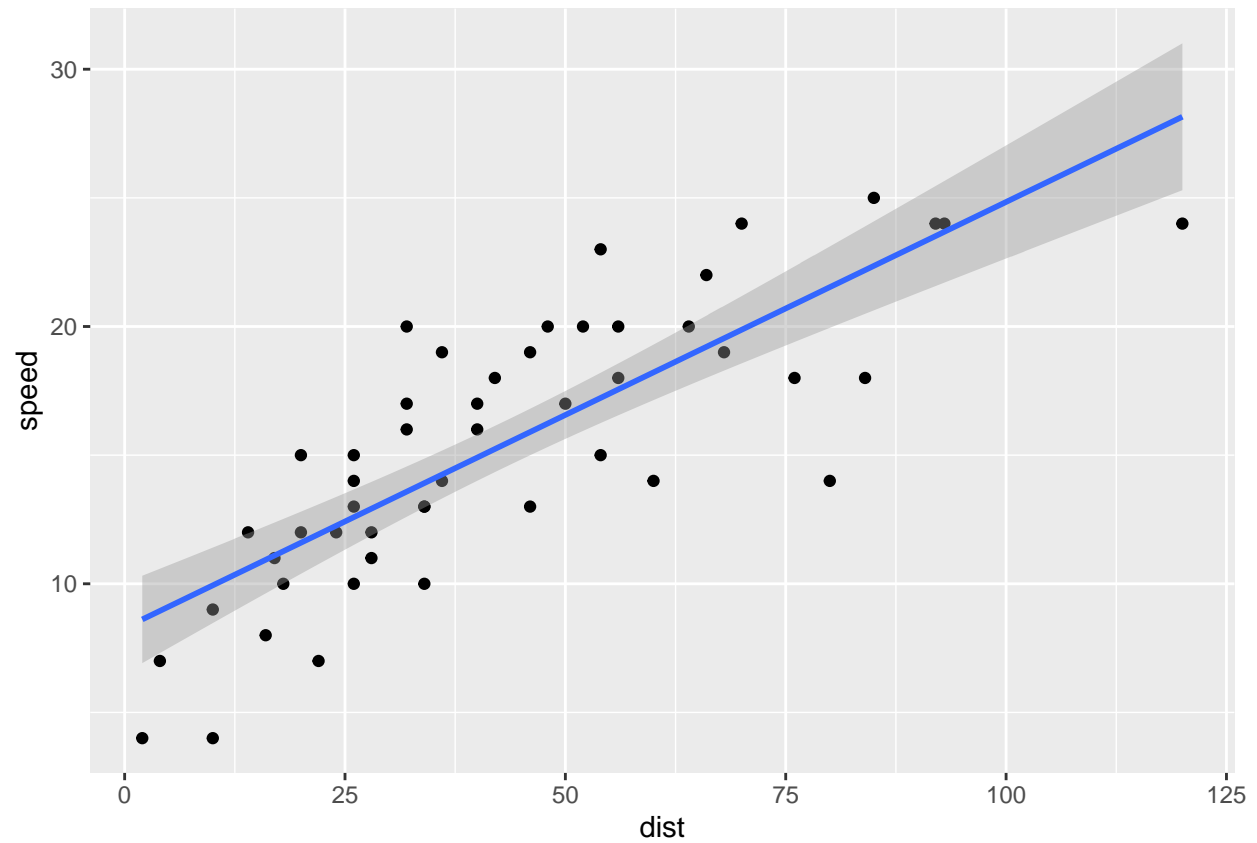
```r
#data + AESthetics + GEOMetries
gg <- ggplot(data=cars) + aes(x=dist, y=speed) + geom_point()
gg
```

```
#Fit a line to the data (lm = linear model)
gg2 <- gg + geom_smooth(method="lm")
gg2
```
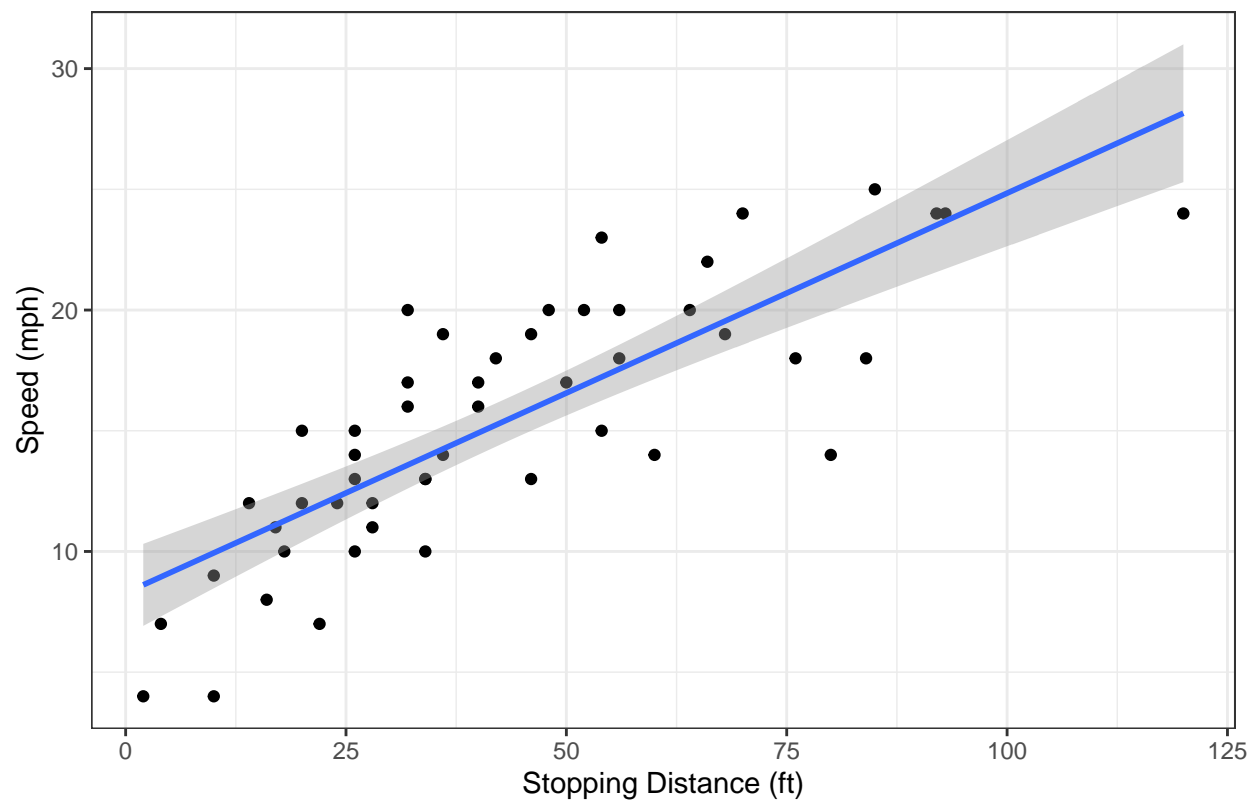
```
## `geom_smooth()` using formula 'y ~ x'
```

```
#Make b/w & Add labels
gg3 <- gg2 + theme_bw() + labs(title = "Stopping Distance of Cars", y = "Speed (mph)", x = "Stopping Di
gg3
```

```
## 'geom_smooth()' using formula 'y ~ x'
```
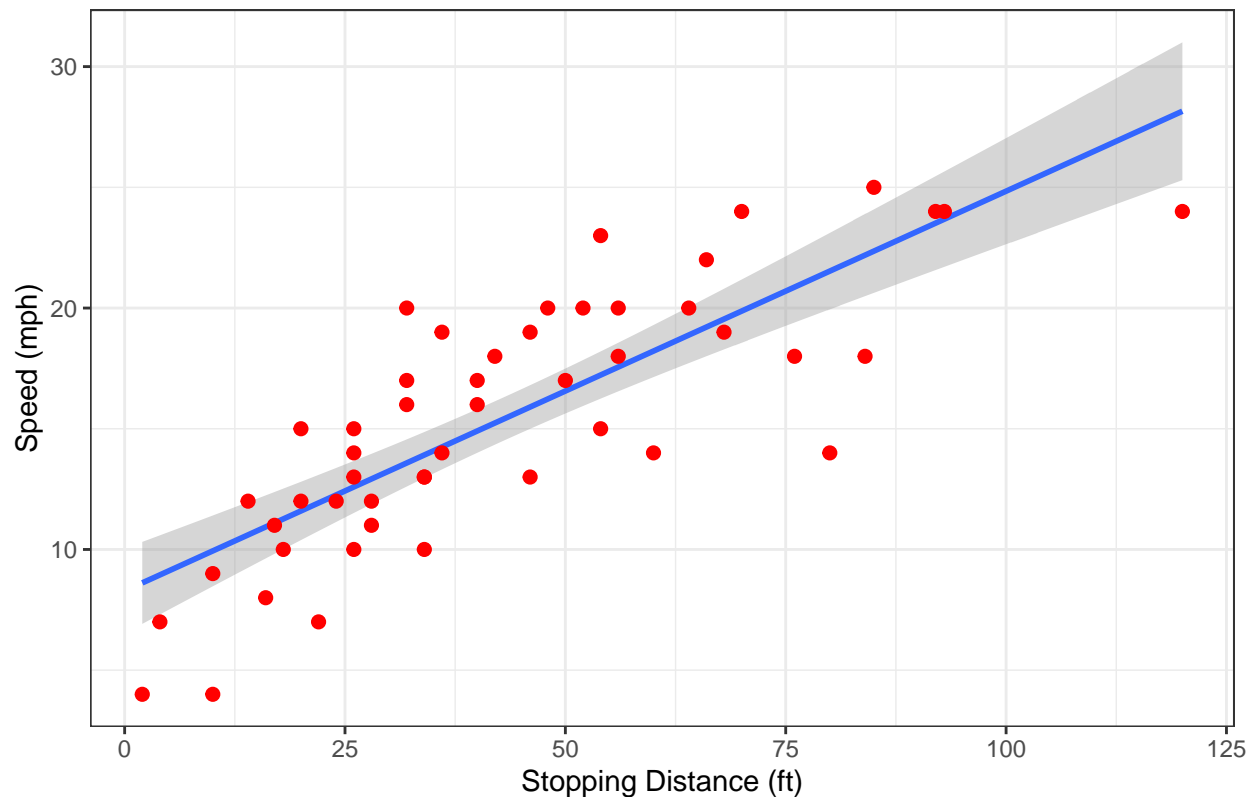
## Stopping Distance of Cars



```
#Change size of point, color of point, point transparency
gg4 <- gg3 + geom_point(size = 2, color = "red", alpha = 10)
gg4
```

```
## `geom_smooth()` using formula 'y ~ x'
```

## Stopping Distance of Cars



```r
#Work with an actual data file
url <- "https://bioboot.github.io/bimm143_S20/class-material/up_down_expression.txt"
genes <- read.delim(url)
head(genes)
```

```
##         Gene Condition1 Condition2       State
## 1      A4GNT -3.6808610 -3.4401355 unchanging
## 2       AAAS  4.5479580  4.3864126 unchanging
## 3      AASDH  3.7190695  3.4787276 unchanging
## 4       AATF  5.0784720  5.0151916 unchanging
## 5       AATK  0.4711421  0.5598642 unchanging
## 6 AB015752.4 -3.6808610 -3.5921390 unchanging
```

```r
#Fit this data to a graph
genes1 <- ggplot(data=genes) + aes(x = Condition1, y = Condition2) + geom_point(color = "red") + geom_sm
genes1
```

```
## `geom_smooth()` using formula 'y ~ x'
```

Competency of a Drug Under Two Different Conditions