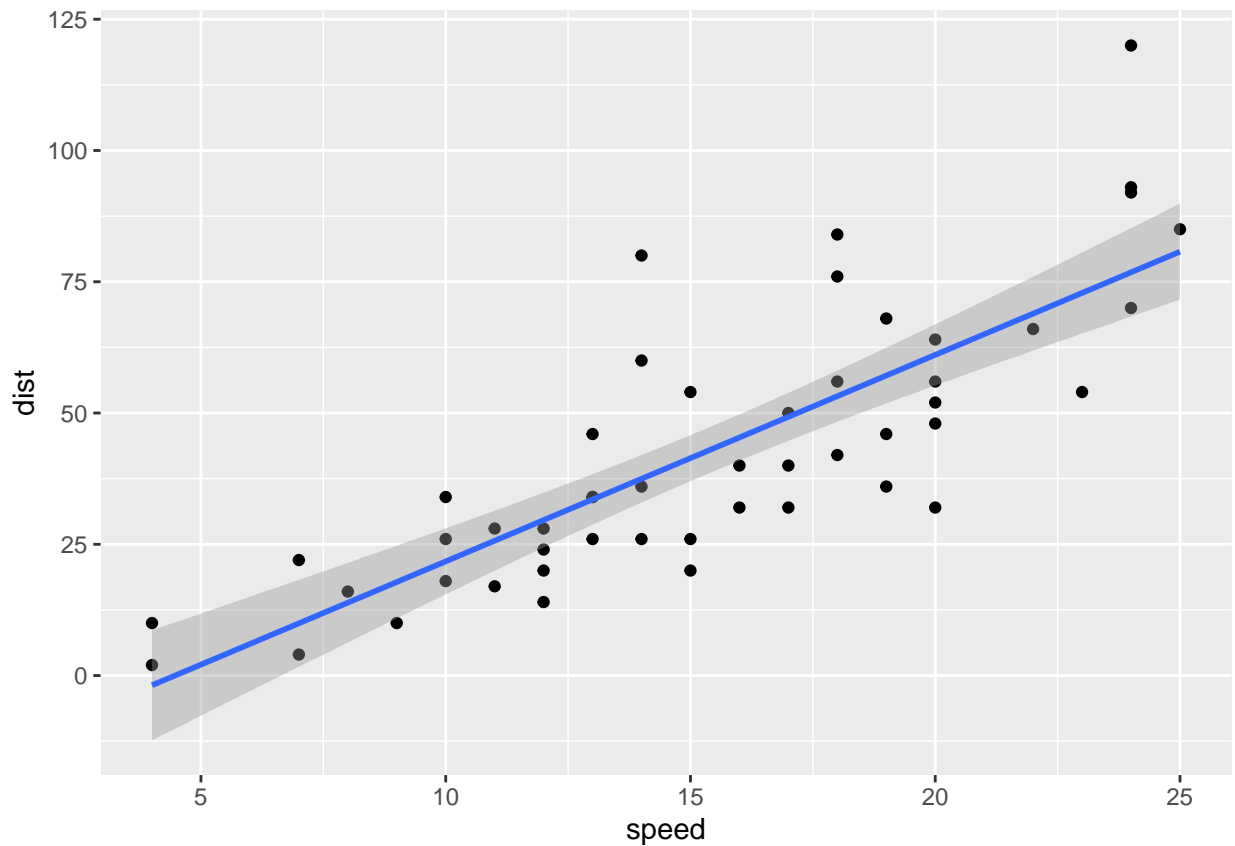# class05rscript.R

Nicole

2021-10-12

```r
# Class 05 Data Visualization
# Nicole Manuguid, A15454343

# Lets start with a scatter plot
# Before we can use it we need to load it up!

library(ggplot2)
# every ggplot has a data + aes + geoms
ggplot(data=cars)+aes(x=speed, y=dist)+geom_point()+geom_smooth(method="lm")
```

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

```
# change to a linear model
p <- ggplot(data=cars) + aes(x=speed, y=dist) + geom_smooth(method="lm") + geom_point()

p + labs(title = "My nice plot", x ="speed (MPH)", y="Stopping distance (ft)")
```

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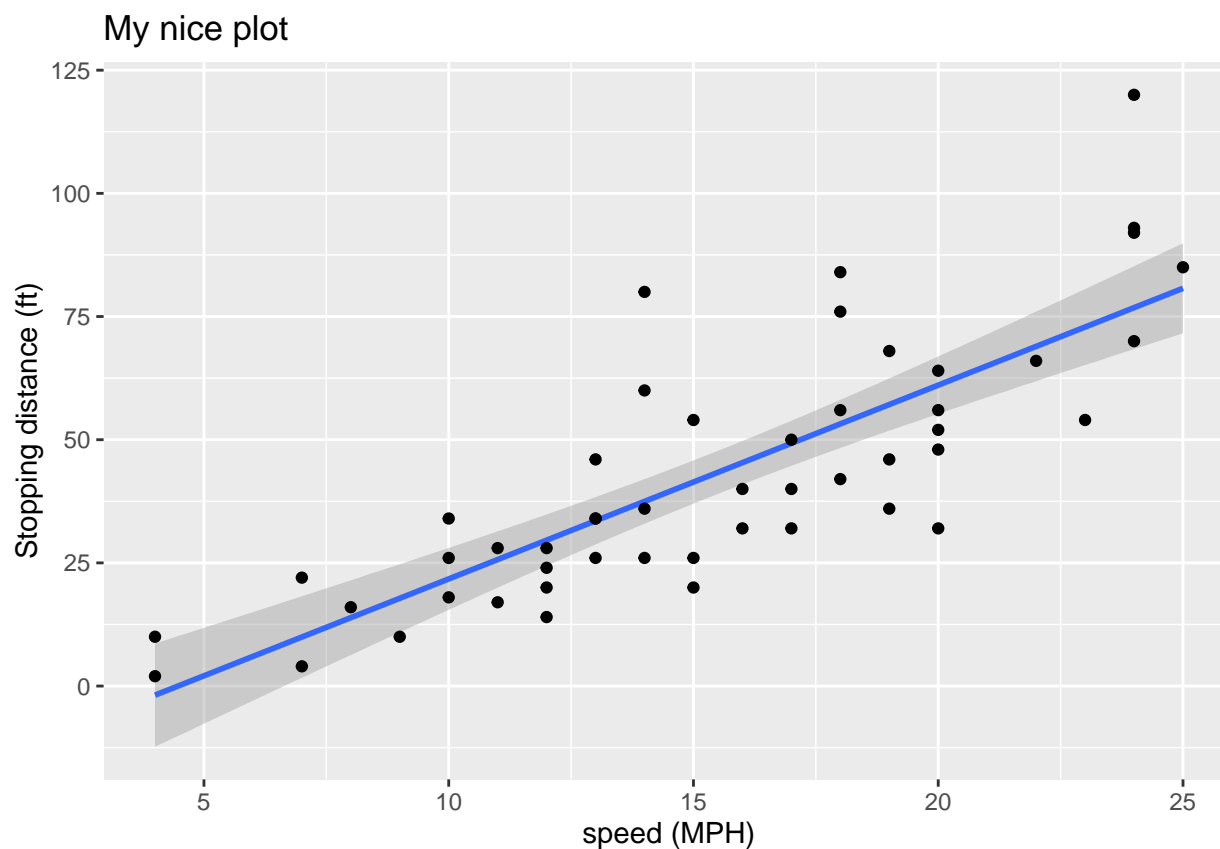

```
# genes

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
```

```
# how many genes
nrow(genes)
```

```
## [1] 5196
```

```
# what are the column names
colnames(genes)
```

```
## [1] "Gene"      "Condition1" "Condition2" "State"
```

```
# how many columns
ncol(genes)
```

```
## [1] 4
```

```
# how many "up" regulated genes?
table(genes$State)
```

```
##
##      down unchanging         up
##        72       4997        127
```

```
# what fraction of ttoal genes is up-regulated?
perc <- table(genes$State)/nrow(genes)*100
round (perc, 2)
```

```
##
##      down unchanging         up
##      1.39      96.17       2.44
```

```
# scatterplot
```

```
p <- ggplot(genes) + aes (x=Condition1, y=Condition2, col=State) + geom_point()
p + scale_colour_manual( values=c( "blue","gray", "red")) + labs (title="Gene Expression Changes Upon D
```

Gene Expression Changes Upon Drug Treatment