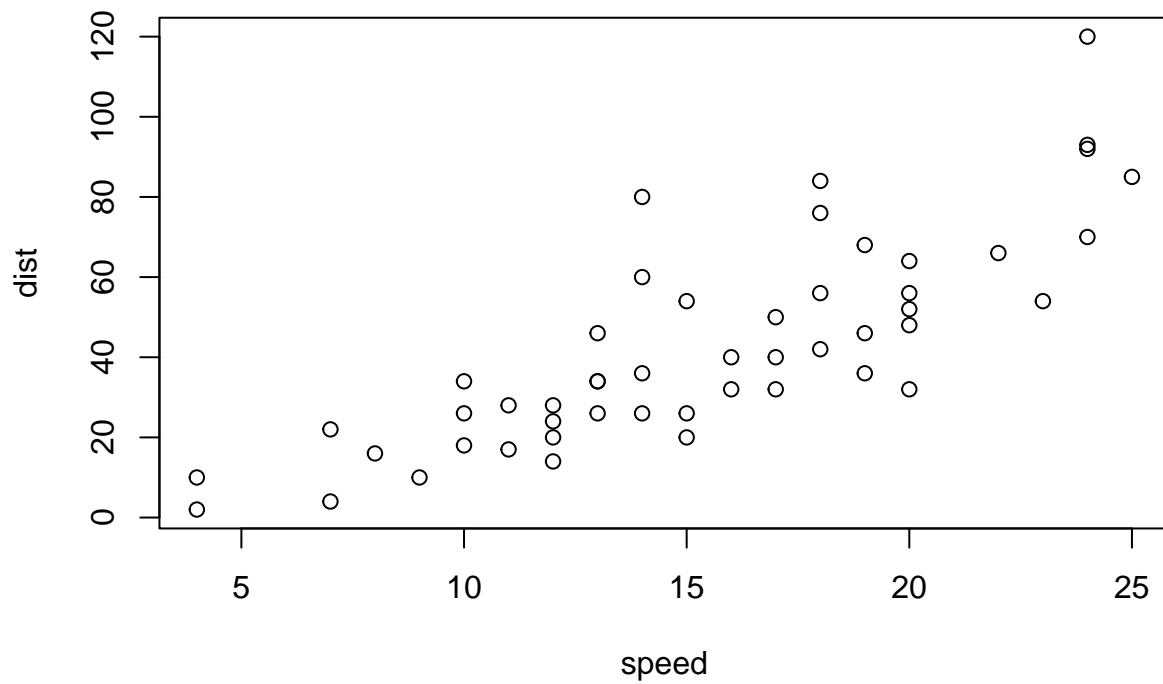


Week 4 Data Visualization Lab

Macy Hoang (PID: A15404564)

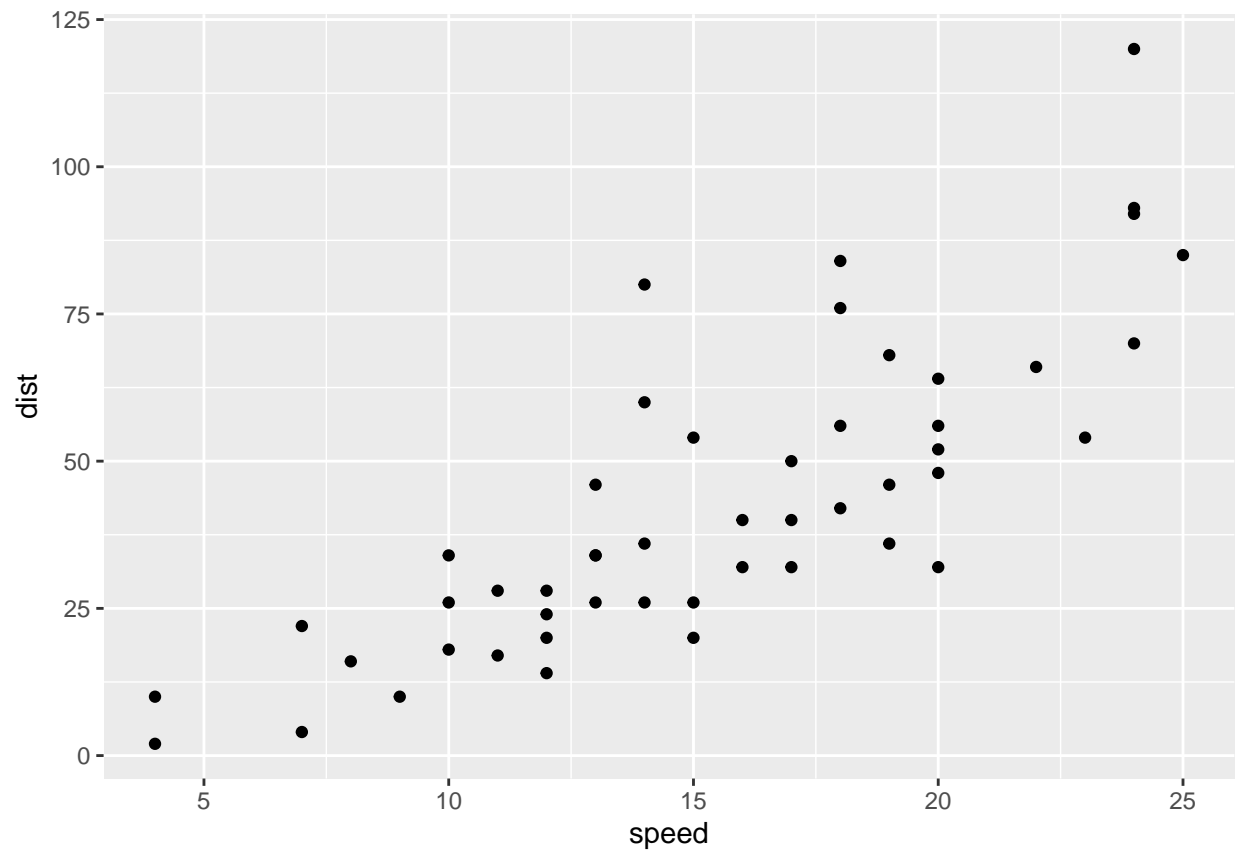
2022-02-06

```
# Week 4 Data Visualization Lab  
  
#install.packages(ggplot2)  
  
#Any time I want to use this package (ggplot2) I need to load it  
library(ggplot2)  
  
View(cars)  
  
# A quick base R plot- this is not a ggplot  
plot(cars)
```



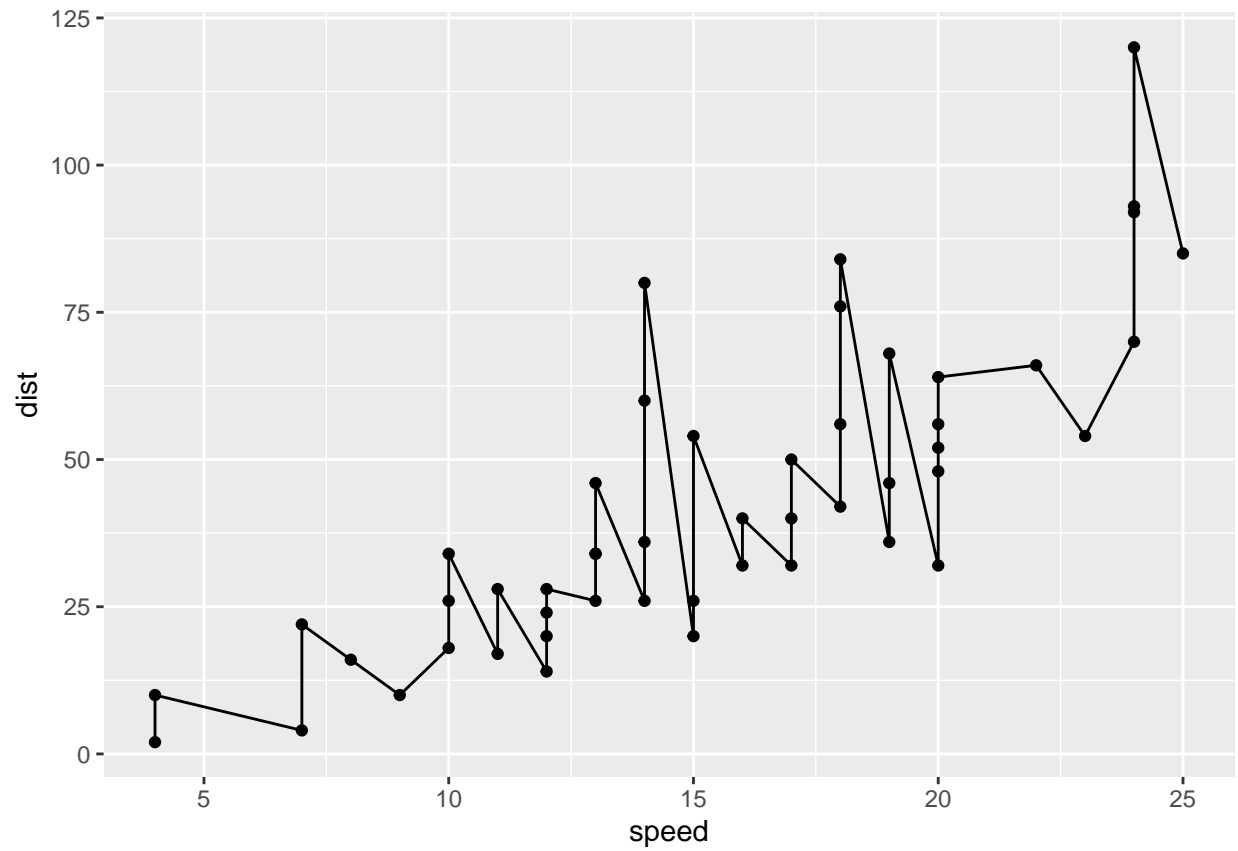
```
# Our first ggplot
# We need data (car) + aes (x,y) + geoms
```

```
ggplot(data = cars) +
  aes(x=speed, y= dist) +
  geom_point()
```



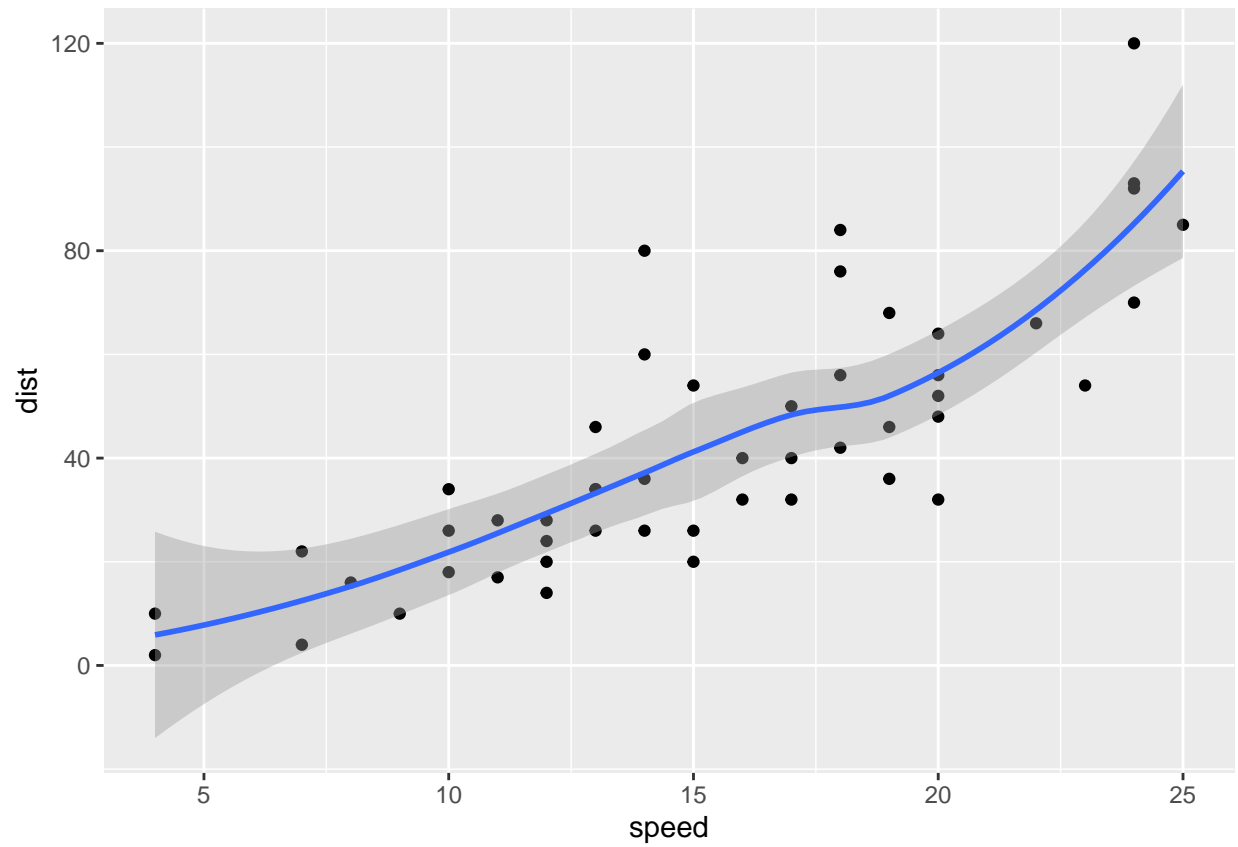
```
p <- ggplot(data = cars) +
  aes(x=speed, y= dist) +
  geom_point()
```

```
# Add a line geom with geom_line
p + geom_line()
```



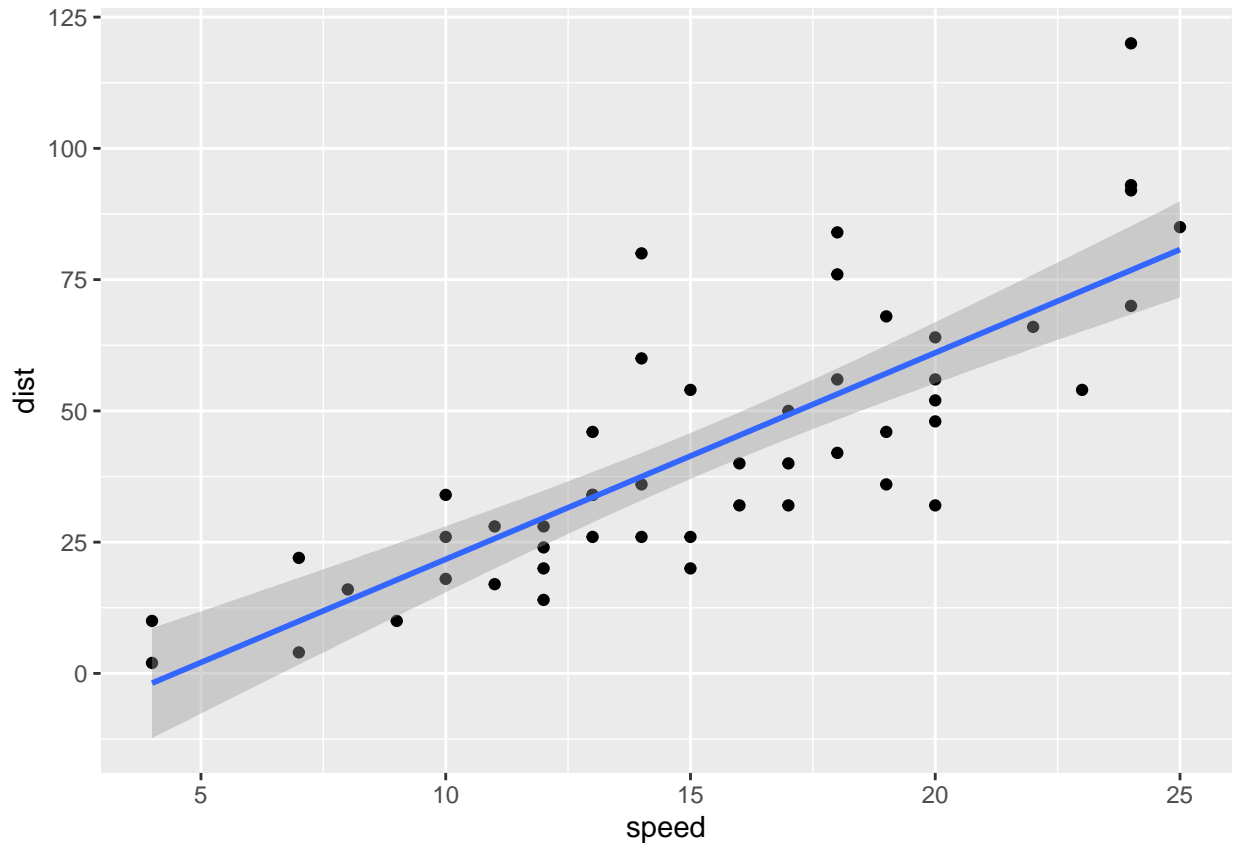
```
# Add a trend line closer to the data  
p+ geom_smooth()
```

```
## 'geom_smooth()' using method = 'loess' and formula 'y ~ x'
```



```
# Add a linear line  
p+ geom_smooth(method = "lm")
```

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



```
# Read in our drug expression data
```

```
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
```

```
# Q. How many genes are in this dataset?
```

```
nrow(genes)
```

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

```
# Q. What are the column names and how many are there?
```

```
colnames(genes)
```

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

```
ncol(genes)
```

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

```
# Q. How many upregulated genes  
table(genes$State)
```

```
##  
##      down  unchanged      up  
##      72      4997      127
```

```
# Q. What fraction of total genes is up-regulated?  
round((table(genes$State)/ nrow(genes)) *100, 2)
```

```
##  
##      down  unchanged      up  
##      1.39      96.17      2.44
```

```
# Let's make a first plot attempt  
g <- ggplot(data = genes) + aes(x=Condition1, y= Condition2, col=State) +  
  geom_point()  
  
#g  
  
# Add some color  
g + scale_color_manual(values = c("blue", "gray", "red")) +  
  # labs(title= "Gene expression", x= "Control (no drug)", y= "Drug treatment" ) +  
  # theme_bw()
```