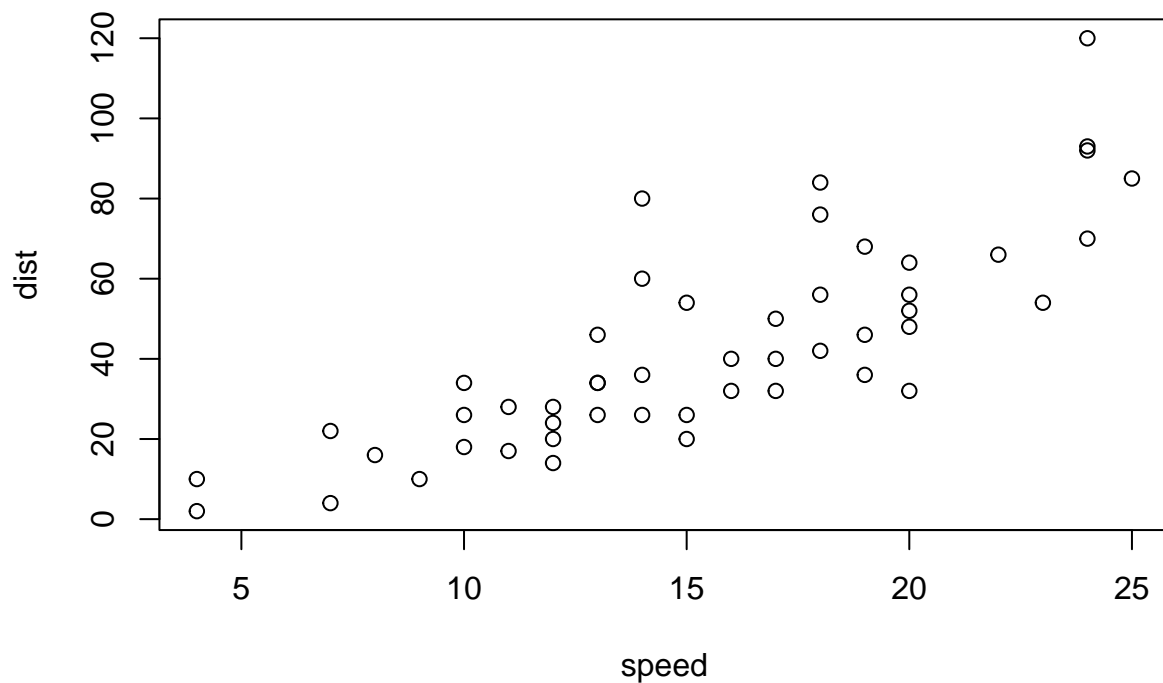


# Week 5: Data Visualization Lab

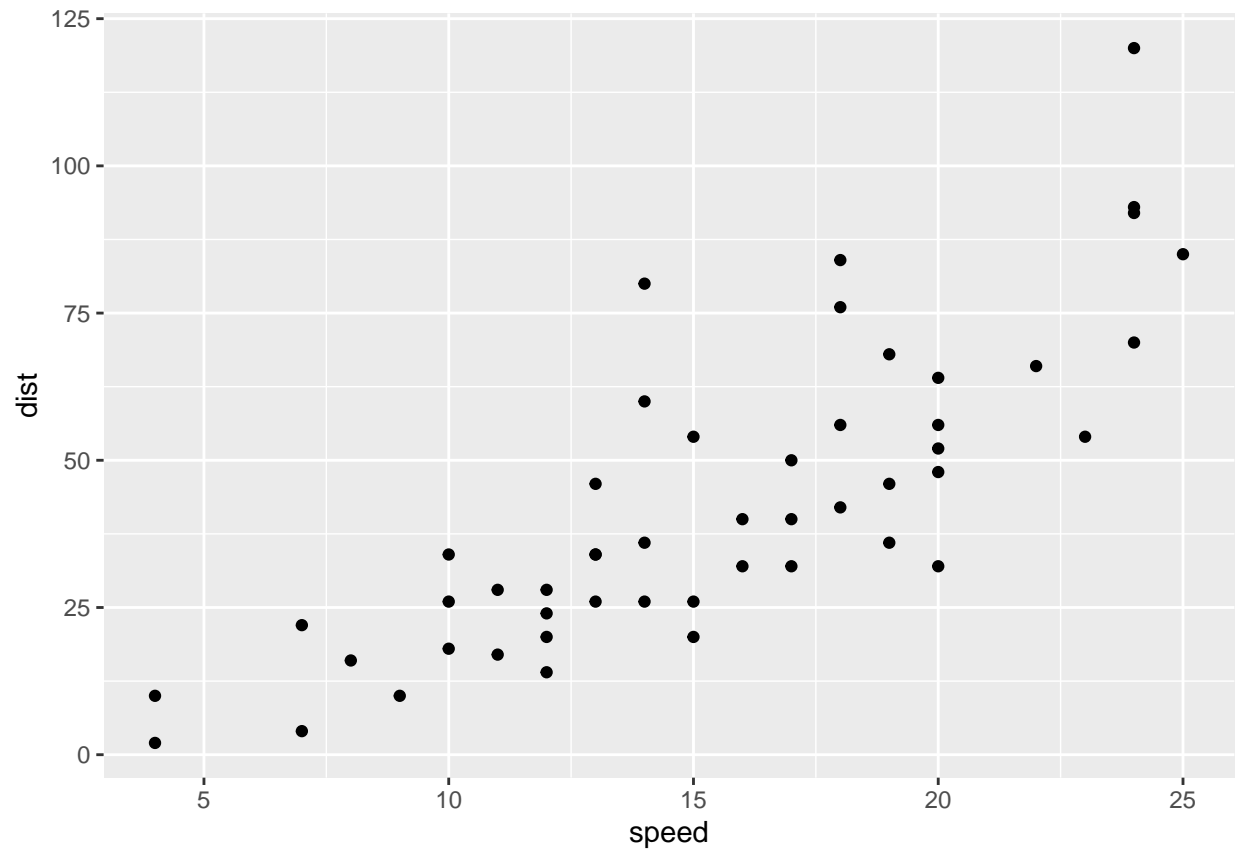
Ralph Goguanco (PID A15937787)

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```
# Week 5 Data visualization Lab  
  
# Install the package ggplot2  
# install.packages("ggplot2")  
  
# Any time I want to use this  
# Package I need to load it  
library(ggplot2)  
  
#View(cars)  
  
# A quick base R plot - this is not ggplot  
plot(cars)
```

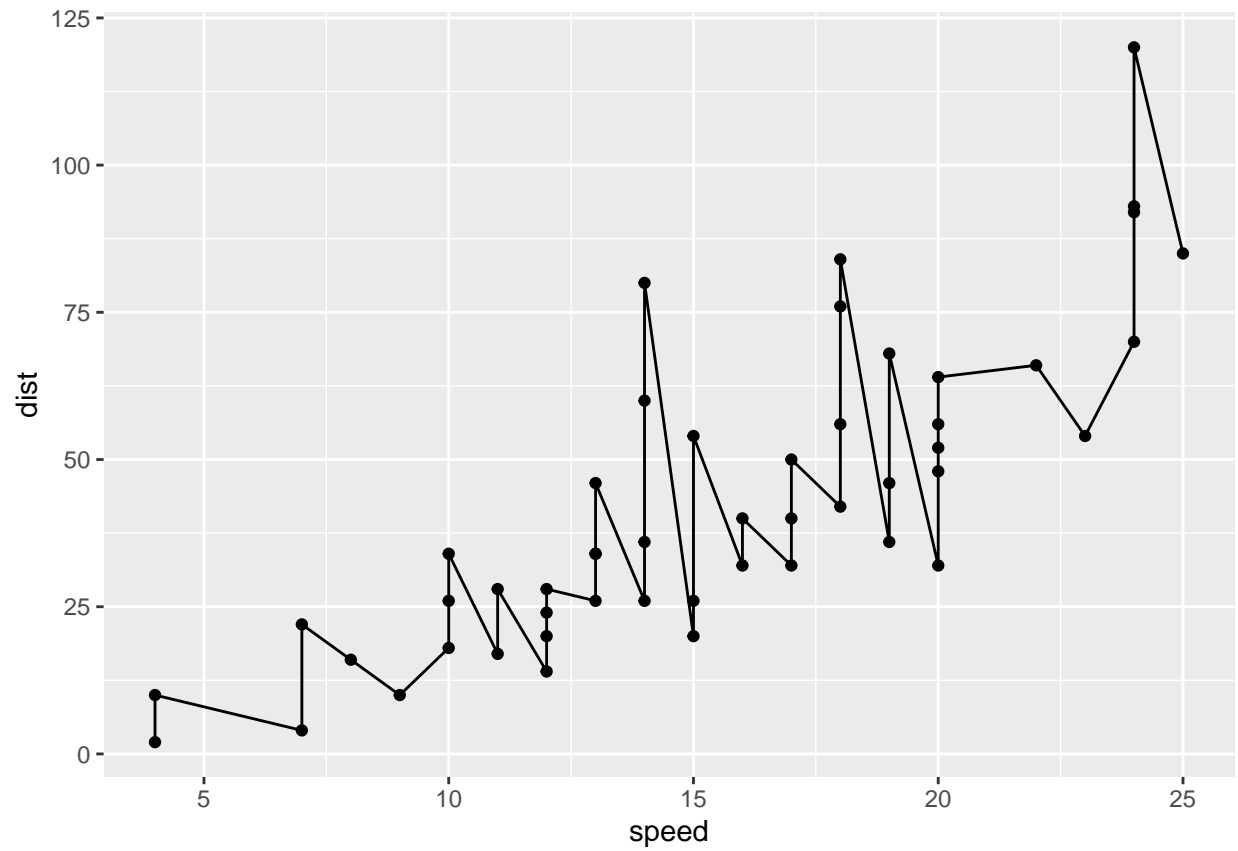


```
# Our first ggplot
# We need data + aes + geoms
ggplot(data=cars) +
  aes(x=speed, y=dist) +
  geom_point()
```



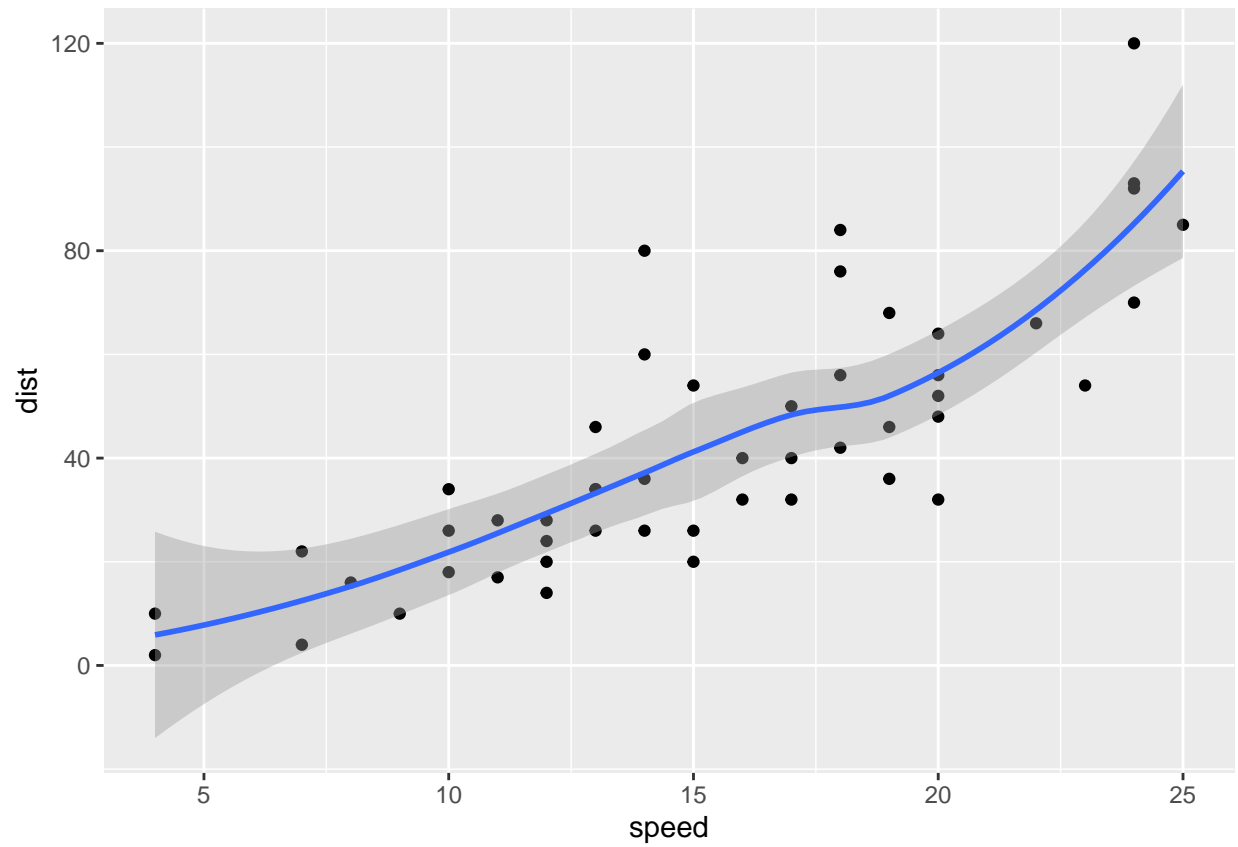
```
p <- ggplot(data=cars) +
  aes(x=speed, y=dist) +
  geom_point()

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



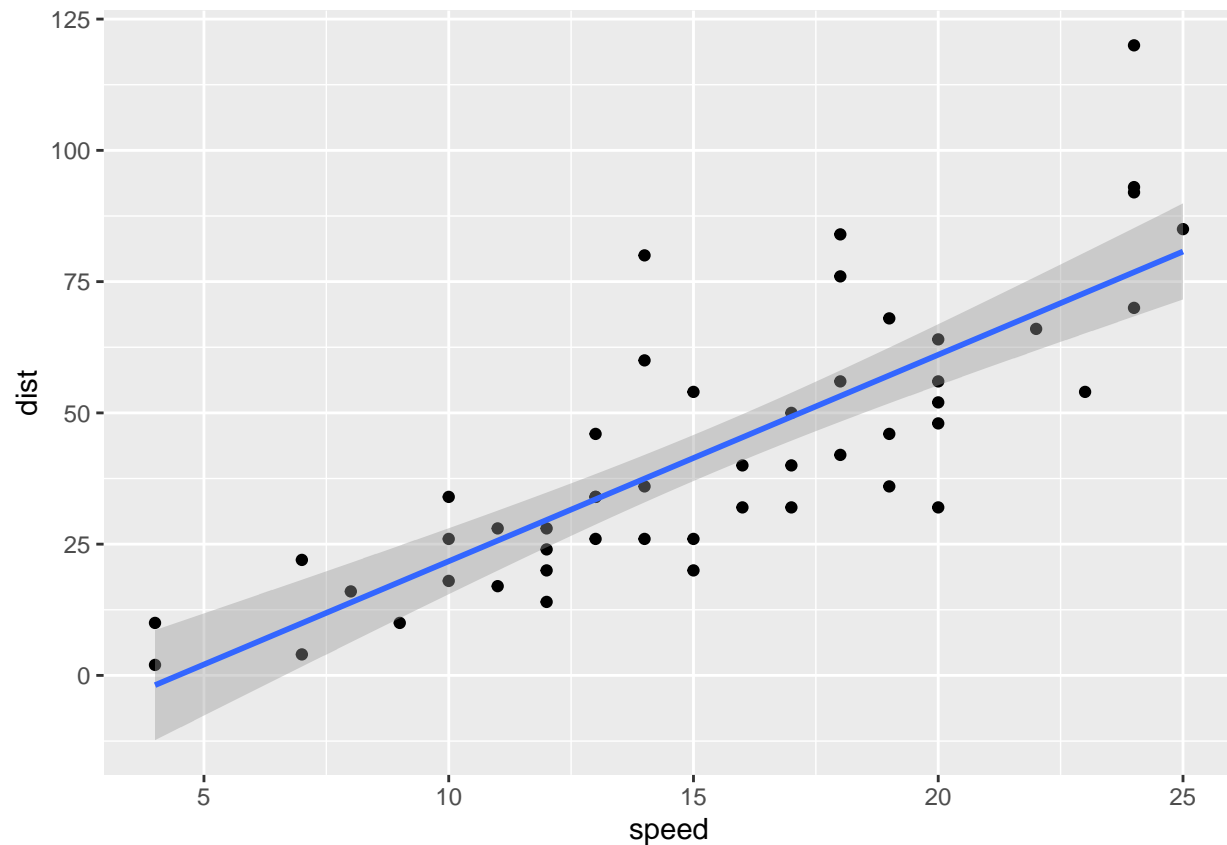
```
# Add a trend line close to the data  
p + geom_smooth()
```

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



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

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

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

```
##  
##      down  unchanging      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()  
  
# Add some color  
#g + scale_color_manual( values=c("blue", "gray", "red")) +  
#   labs(title="Gene expression changes", x="Control (no drug)")  
# theme_bw()
```