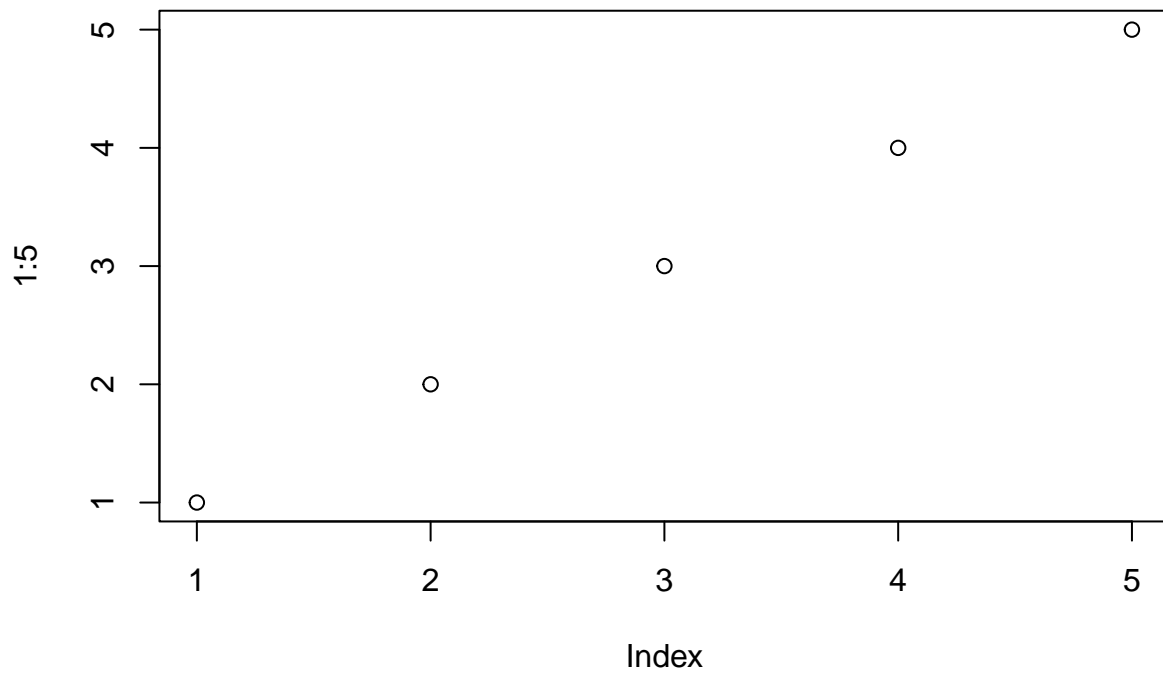


# class05.R

cjade

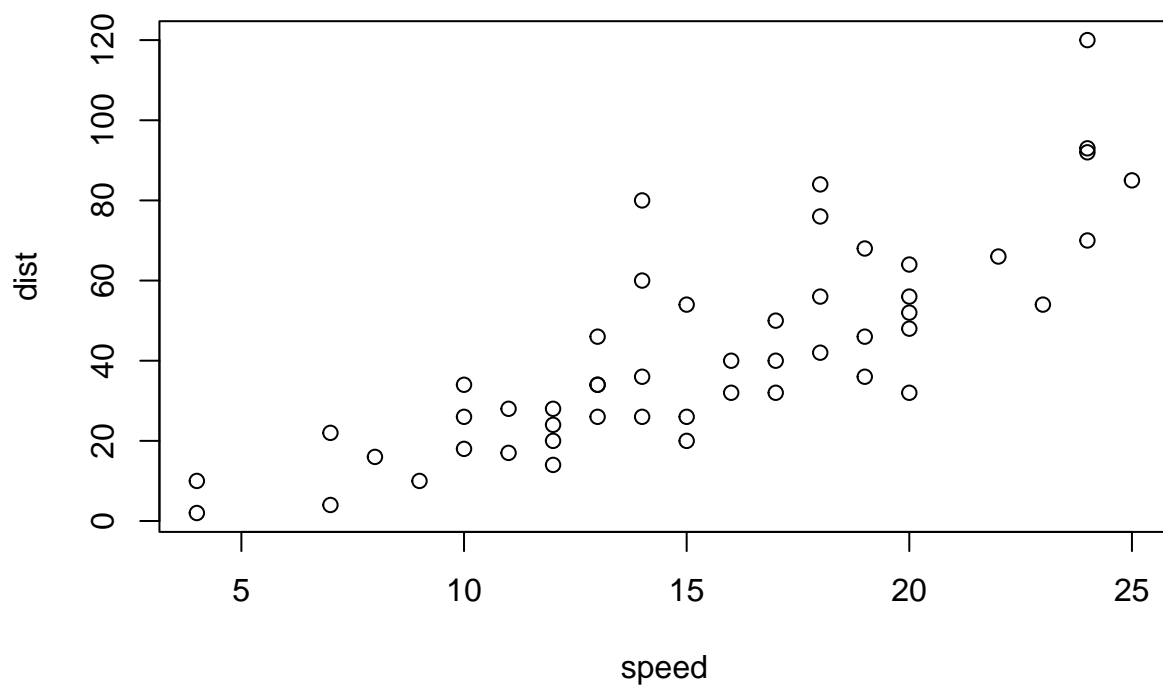
2022-02-04

```
# Class 5 Data Visualization  
  
plot(1:5)  
  
# That was base R plot- quick and not very nice!  
# We will use an add on package called ggplot2  
  
# command to install is install.packages("ggplot2")  
  
library(ggplot2)
```



```
#Before I can use any functions from this package  
# I need to load it with the library() call!
```

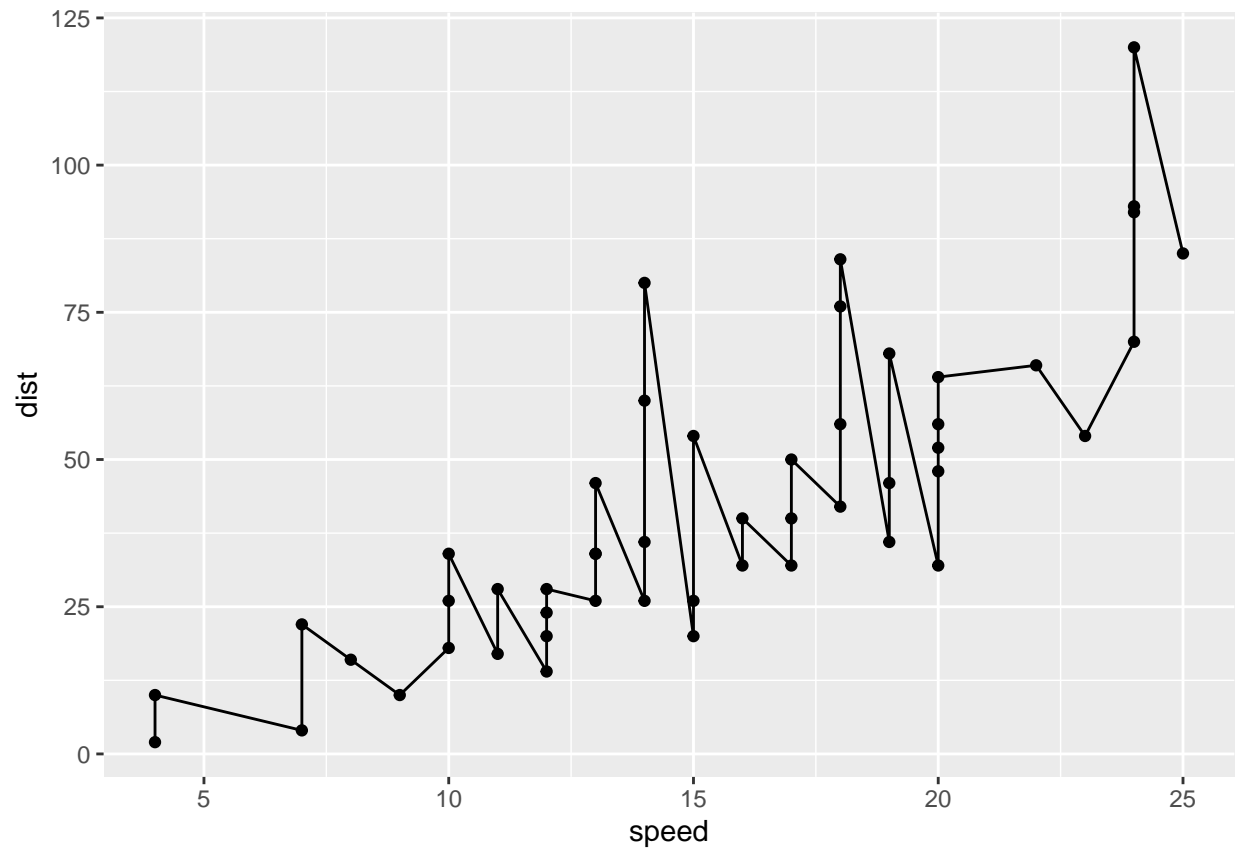
```
plot(cars)
```



```
#Every ggplot has at least 3 layers  
# data + aes + geoms
```

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

```
p + geom_line()
```

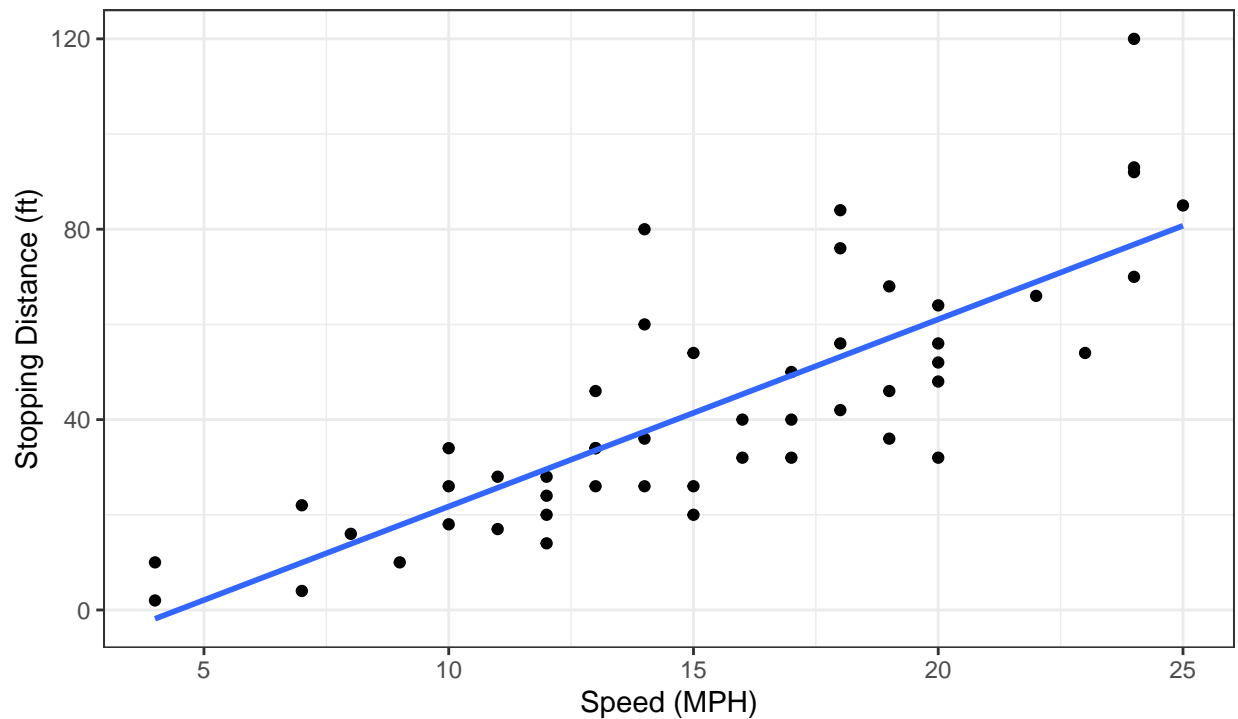


```
p + labs(title="Speed and Stopping Distances of Cars",
  x="Speed (MPH)",
  y="Stopping Distance (ft)",
  subtitle = "STOP! In the Name of Love",
  caption="Dataset: 'cars'") +
  geom_smooth(method="lm", se=FALSE) + theme_bw()
```

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

## Speed and Stopping Distances of Cars

STOP! In the Name of Love



Dataset: 'cars'

```
# RNAseq 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
```

```
p <- ggplot(genes) + aes(x=Condition1, y=Condition2, col=State) +
  geom_point() +
  theme_bw()
```

```
p
```

