

Week_5-1_script.R

HP

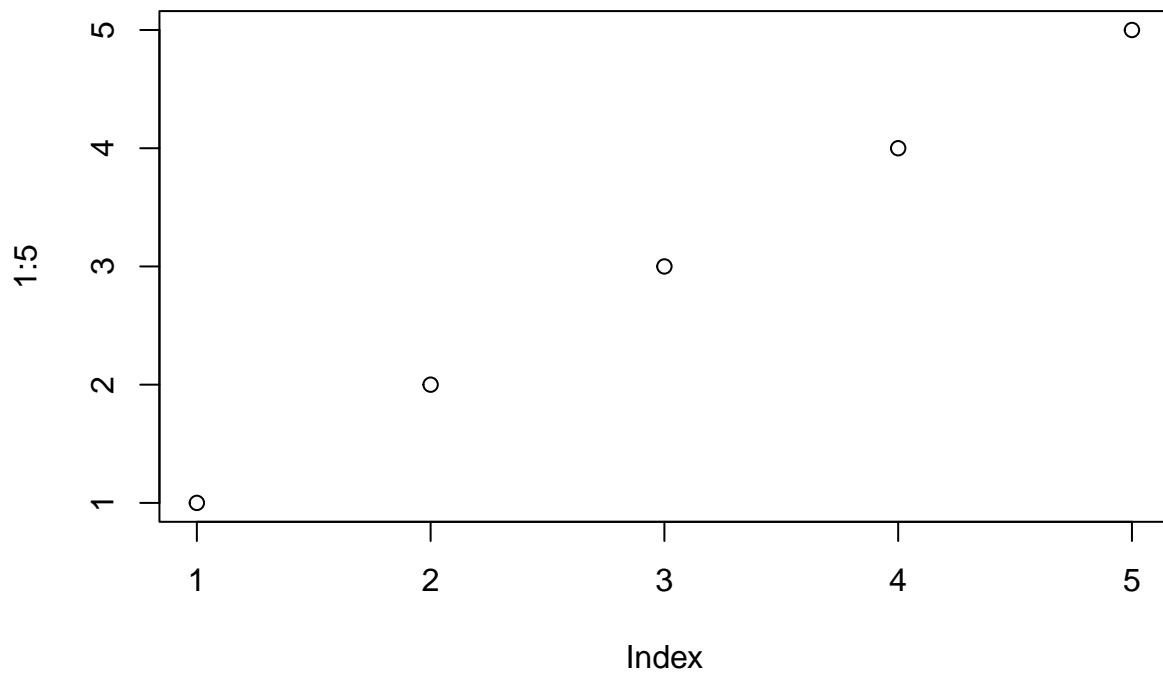
2022-02-02

```
#Class 5 Data Visualization
```

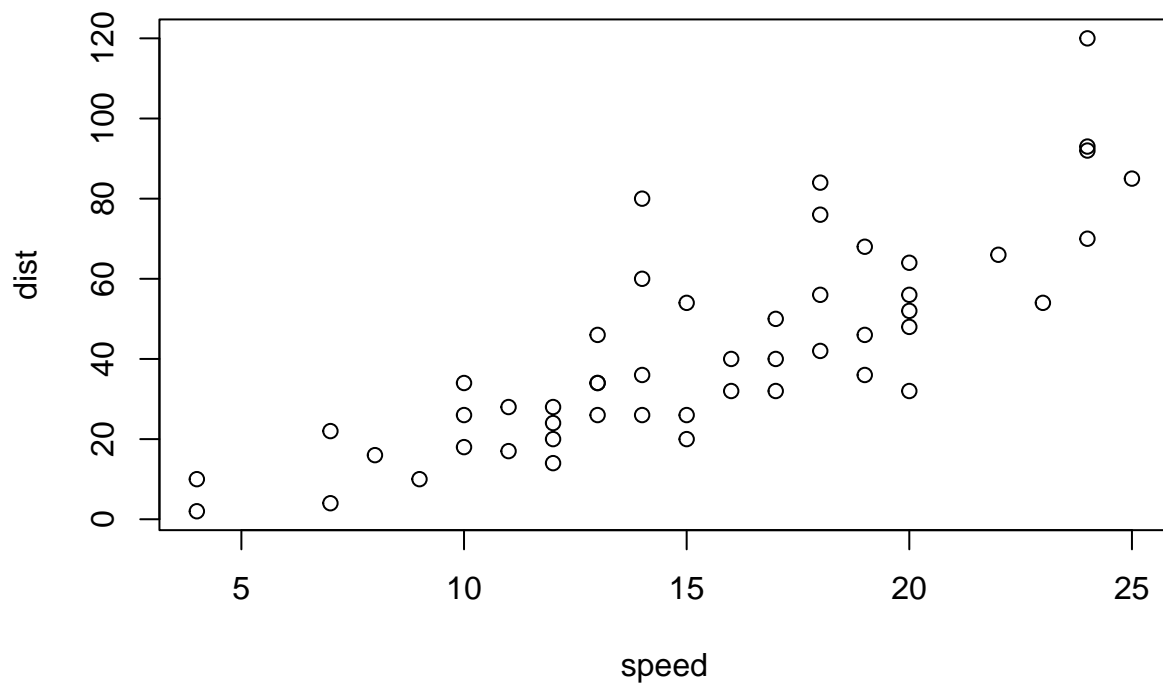
```
plot(1:5)
```

```
#ggplot installed to make plot look nicer. ggplot is loaded below
```

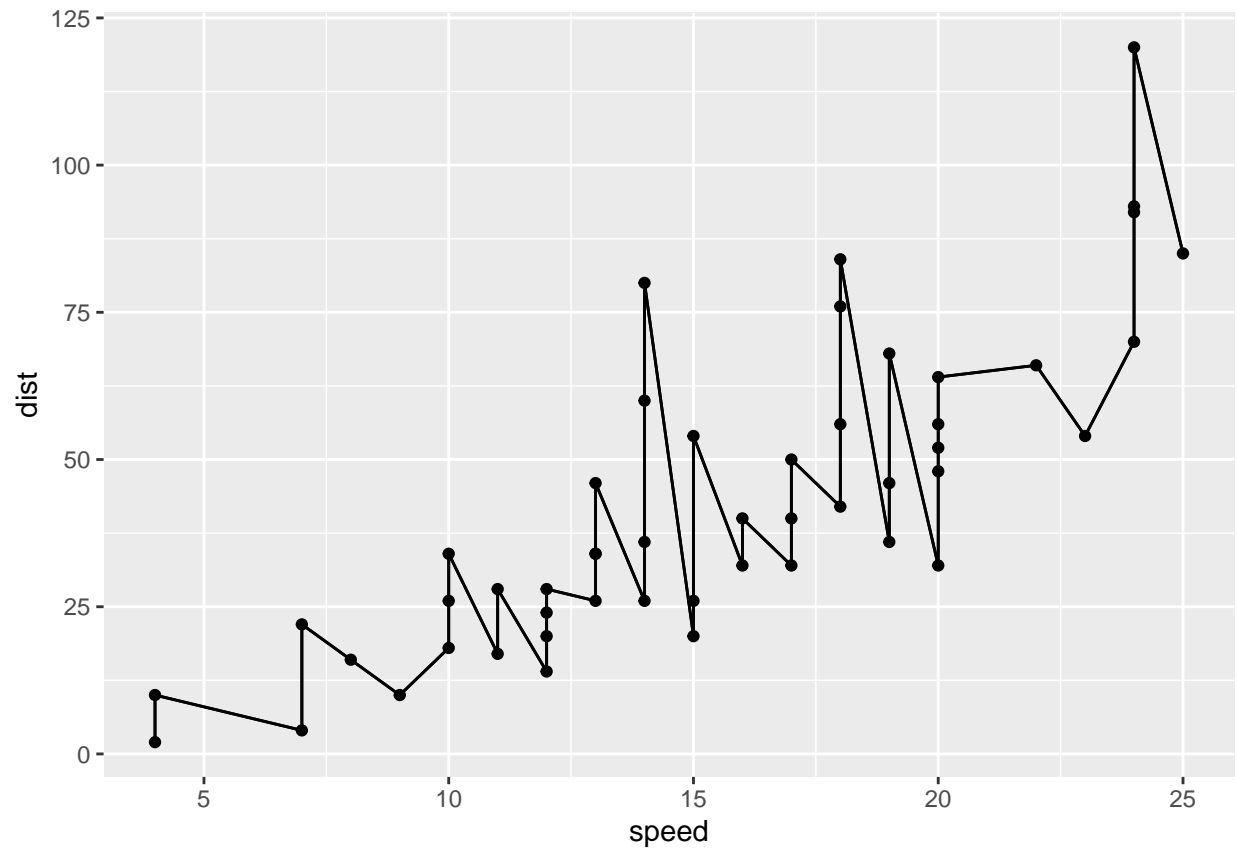
```
library(ggplot2)
```



```
plot(cars)
```

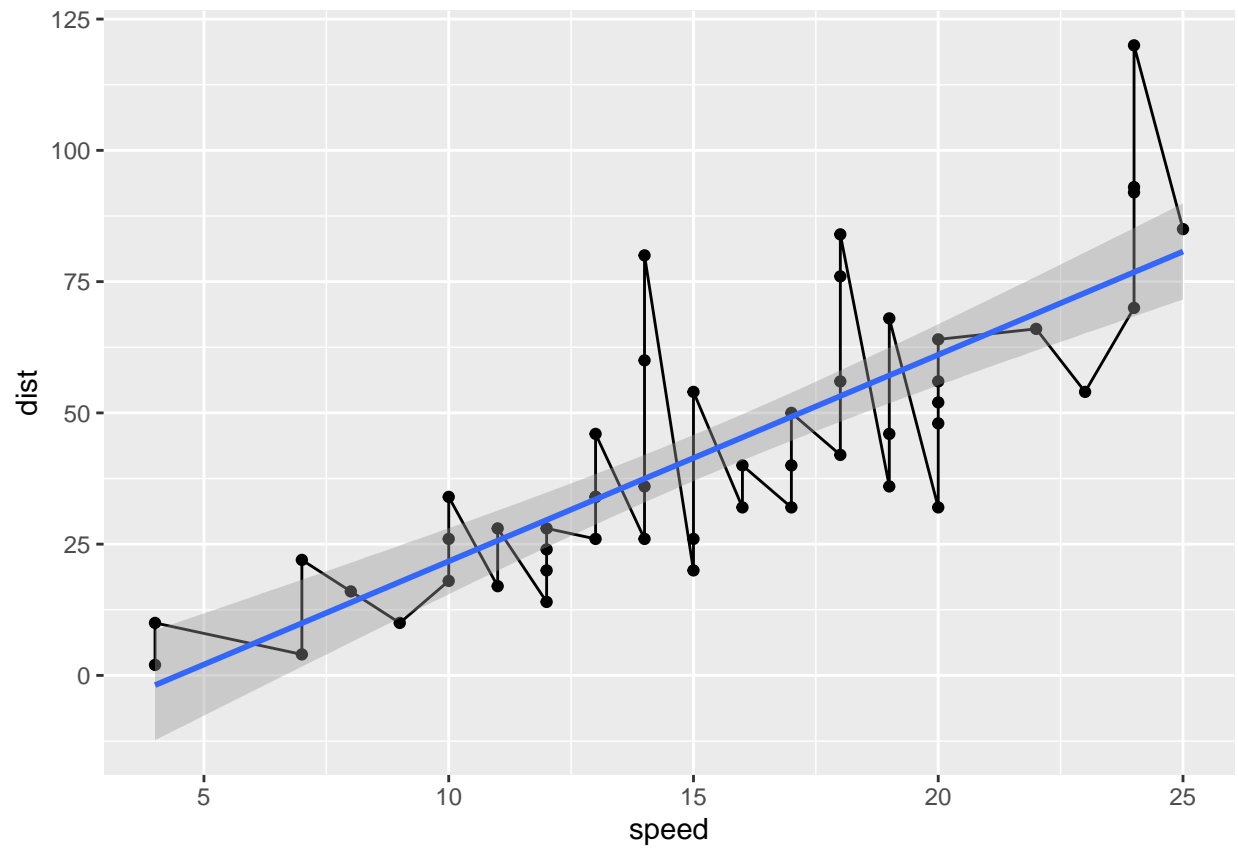


```
#ggplots have multiple layers: data + aesthetics + geometry  
# command is: ggplot(data = ___) + aes(x = , y = ,) + geom_"type"()  
  
p <- ggplot(data= cars) + aes(x= speed, y = dist) + geom_point() + geom_line()  
p + geom_line()
```



```
p + geom_smooth(method = "lm")
```

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

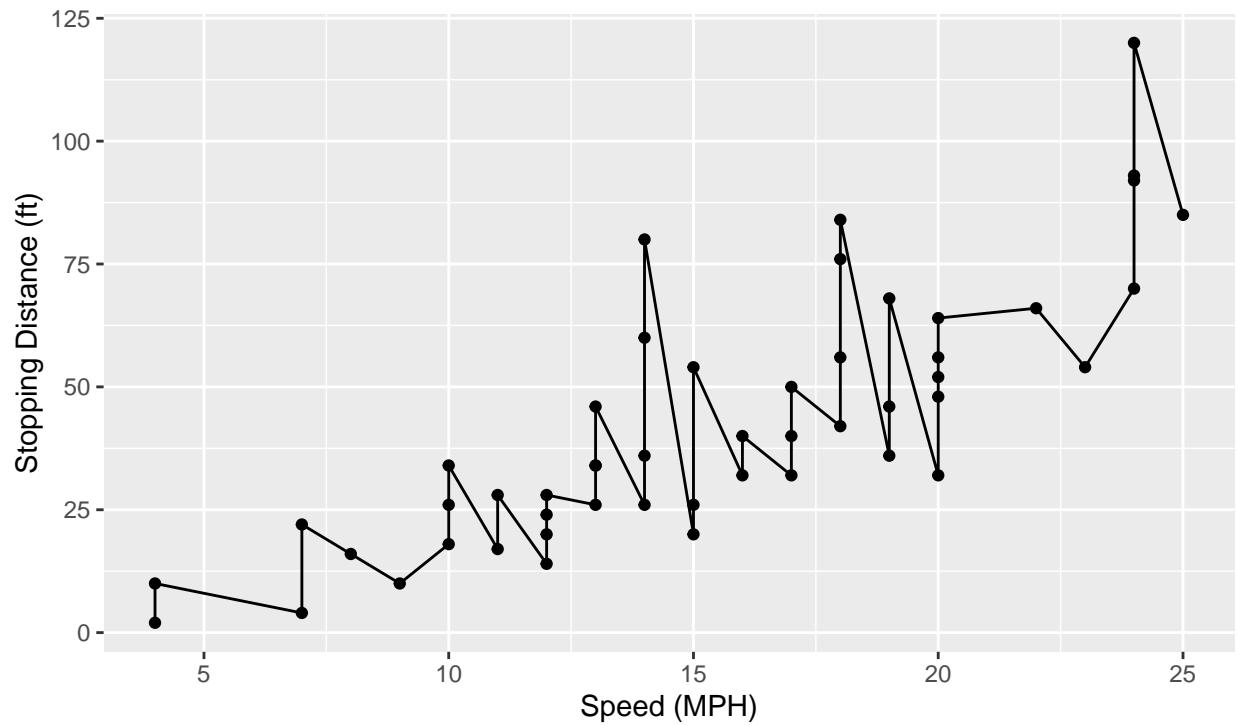


```
#add custom axis labels
```

```
p + labs(title = "Speed and Stopping Distances of Cars", subtitle = "Data Gathered from 1930s", caption
```

Speed and Stopping Distances of Cars

Data Gathered from 1930s



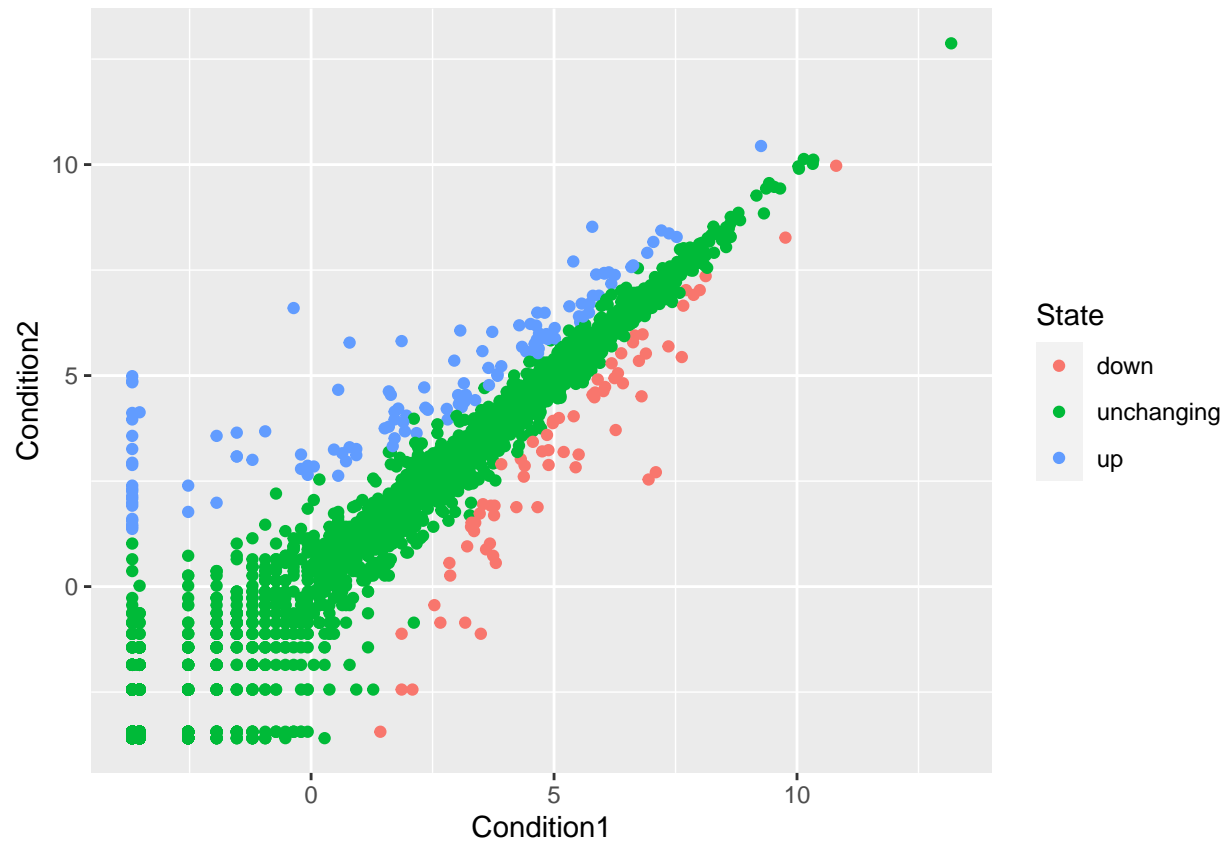
From R Dataset Cars

#RNA-Seq Plot

```
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()
p
```



```
p + scale_colour_manual( values=c("blue","gray","red") ) + labs(title = "Gene Expression Changes Upon D
```

Gene Expression Changes Upon Drug Treatment

