

# labweek5.R

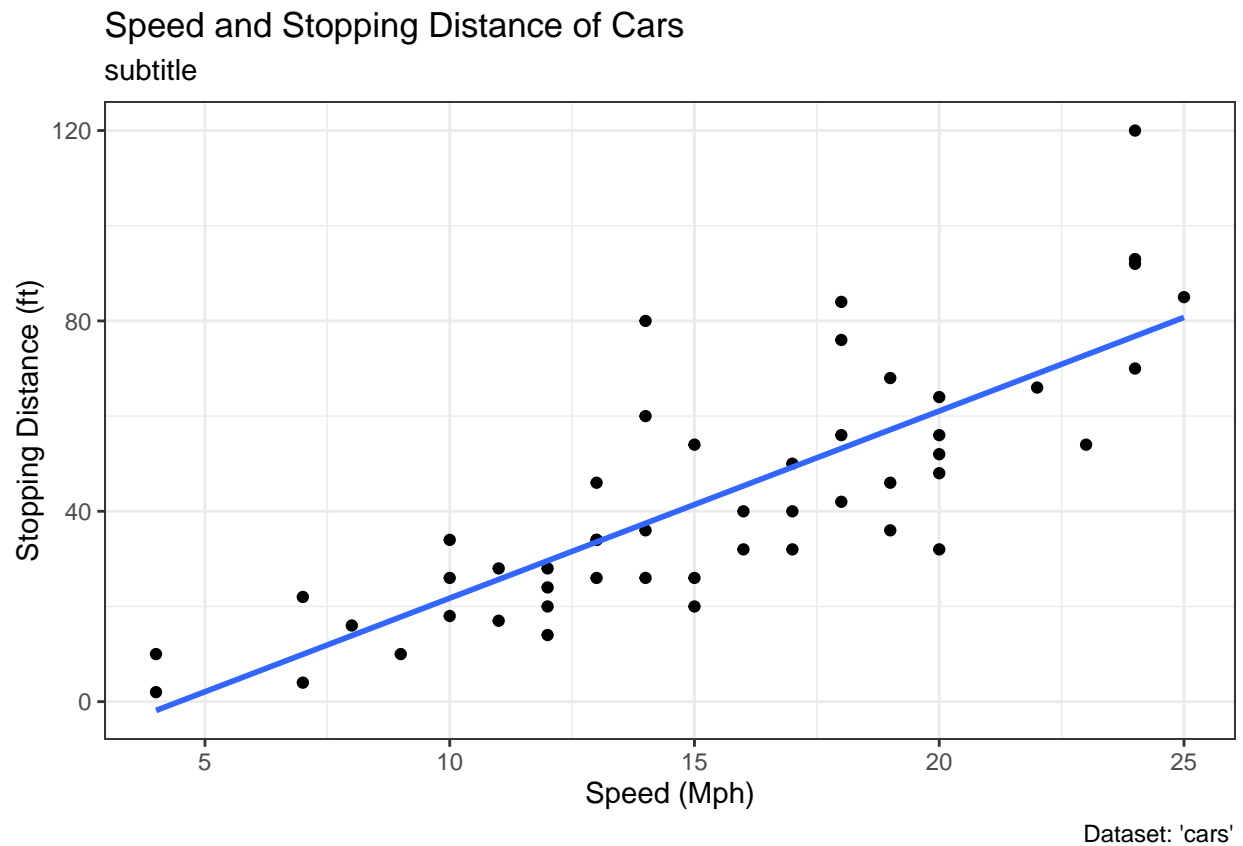
Rachel

2022-02-06

```
#installed ggplot2 package  
library(ggplot2)  
ggplot(cars)
```

```
ggplot(cars) +  
  aes(x=speed, y=dist)+  
  geom_point()+  
  labs(title="Speed and Stopping Distance of Cars",  
        x="Speed (Mph)",  
        y="Stopping Distance (ft)",  
        subtitle="subtitle",  
        caption="Dataset: 'cars'") +  
  geom_smooth(method="lm", se=FALSE)+  
  theme_bw()
```

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



```
#code for drug testing dataset
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
```

```
nrow(genes)
```

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

```
colnames(genes)
```

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

```
ncol(genes)
```

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

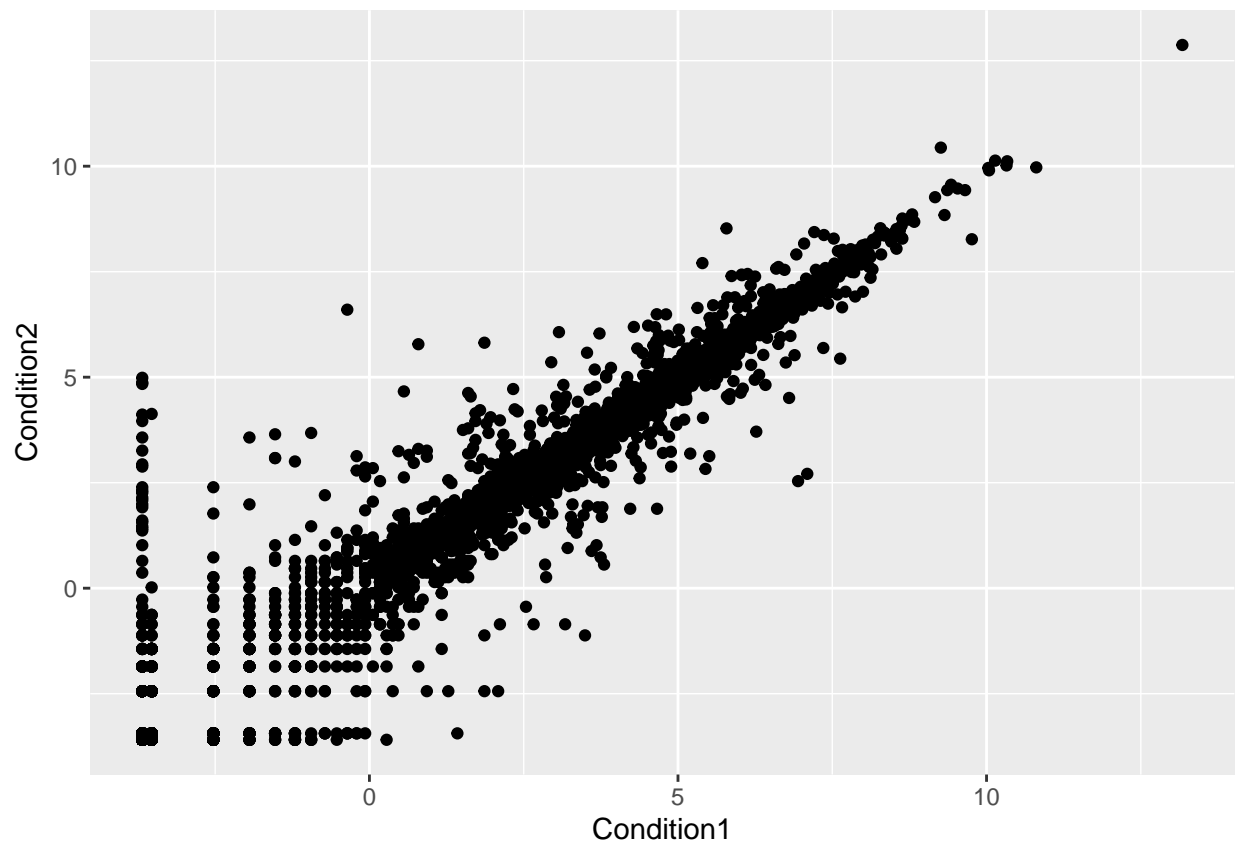
```
table(genes$State)
```

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

```
round(table(genes$State)/nrow(genes)*100,2)
```

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

```
ggplot(genes)+  
  aes(x=Condition1,y=Condition2)+  
  geom_point()
```



```
#installed tinytex for making pdf reports
```