

lab5_bimm143.R

hope_adams

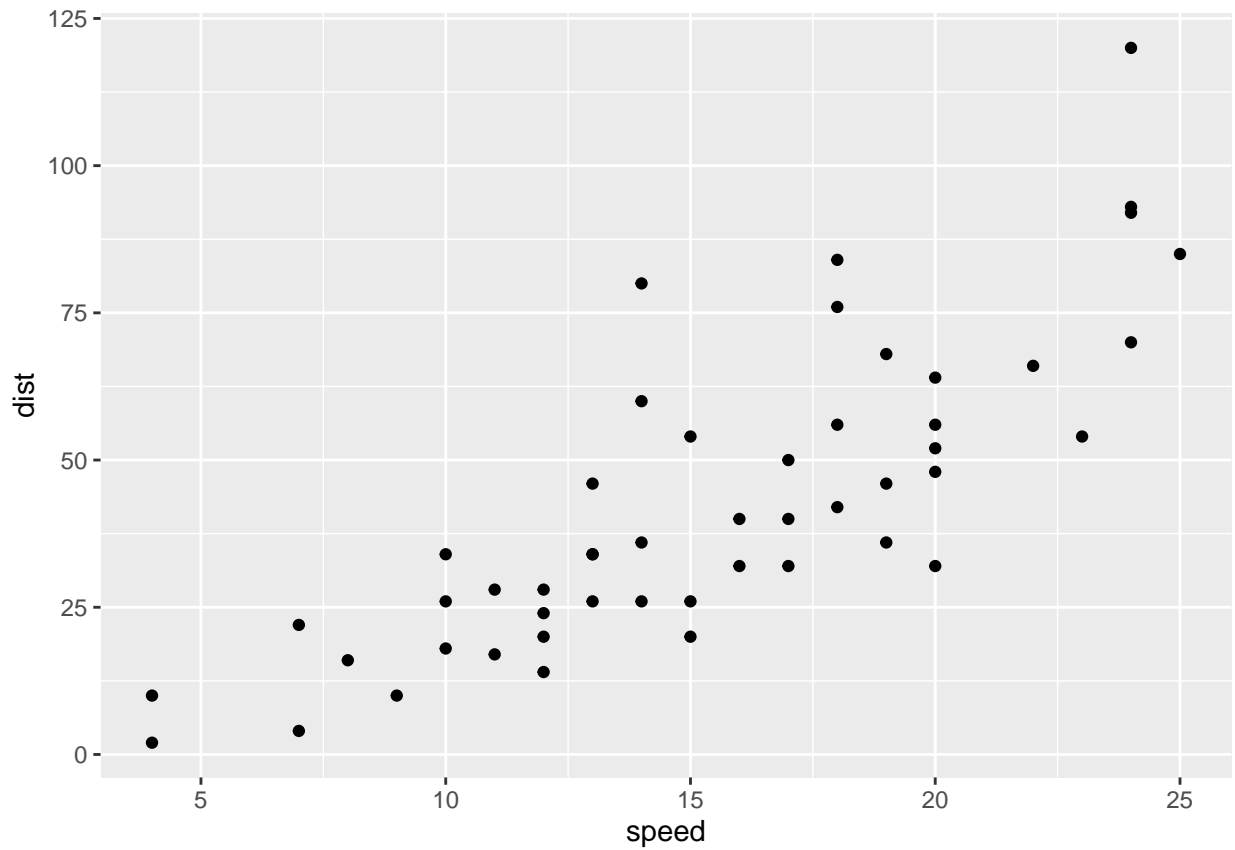
2021-10-12

```
# Class 5 Data Visualization

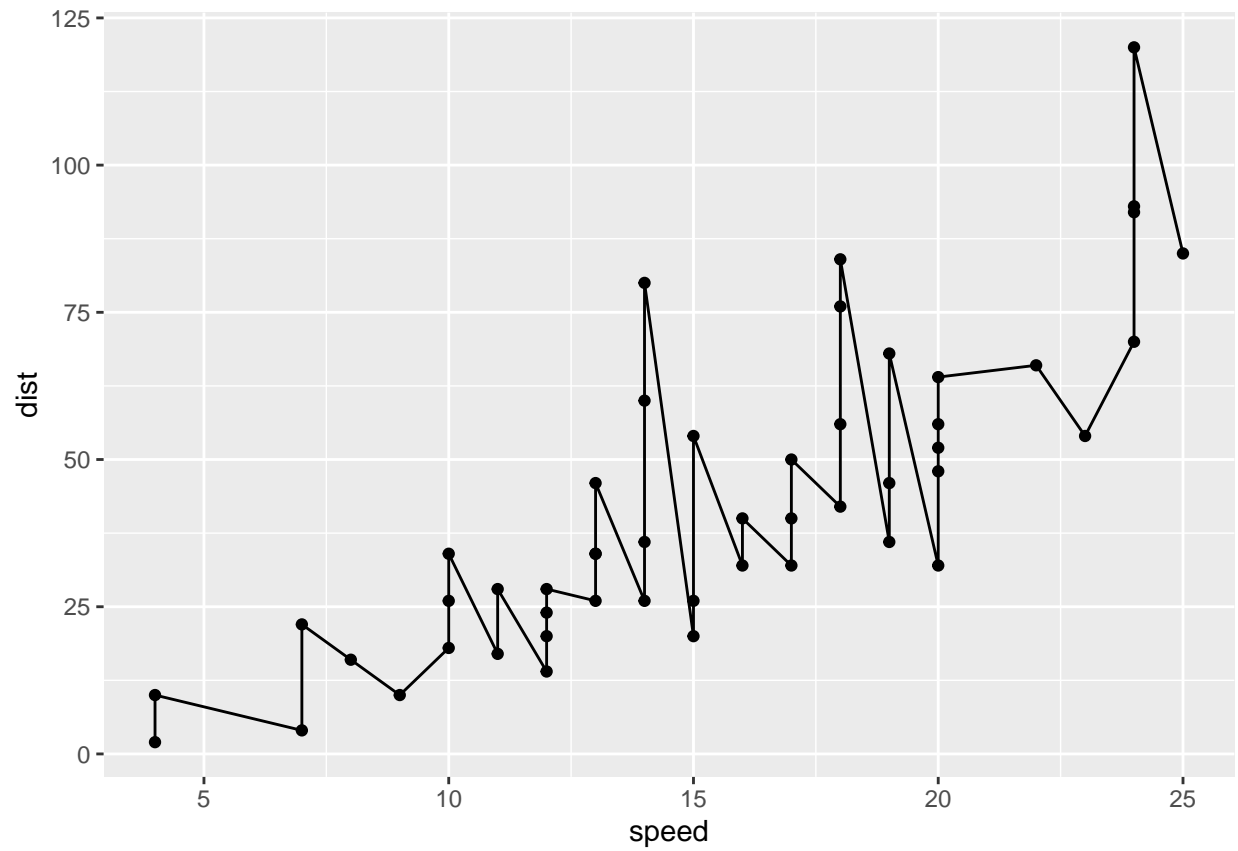
# Lets start with a scatterplot
# Before I can use it i need to load it up
library(ggplot2)

# Every ggplot has a data + aes + geoms

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

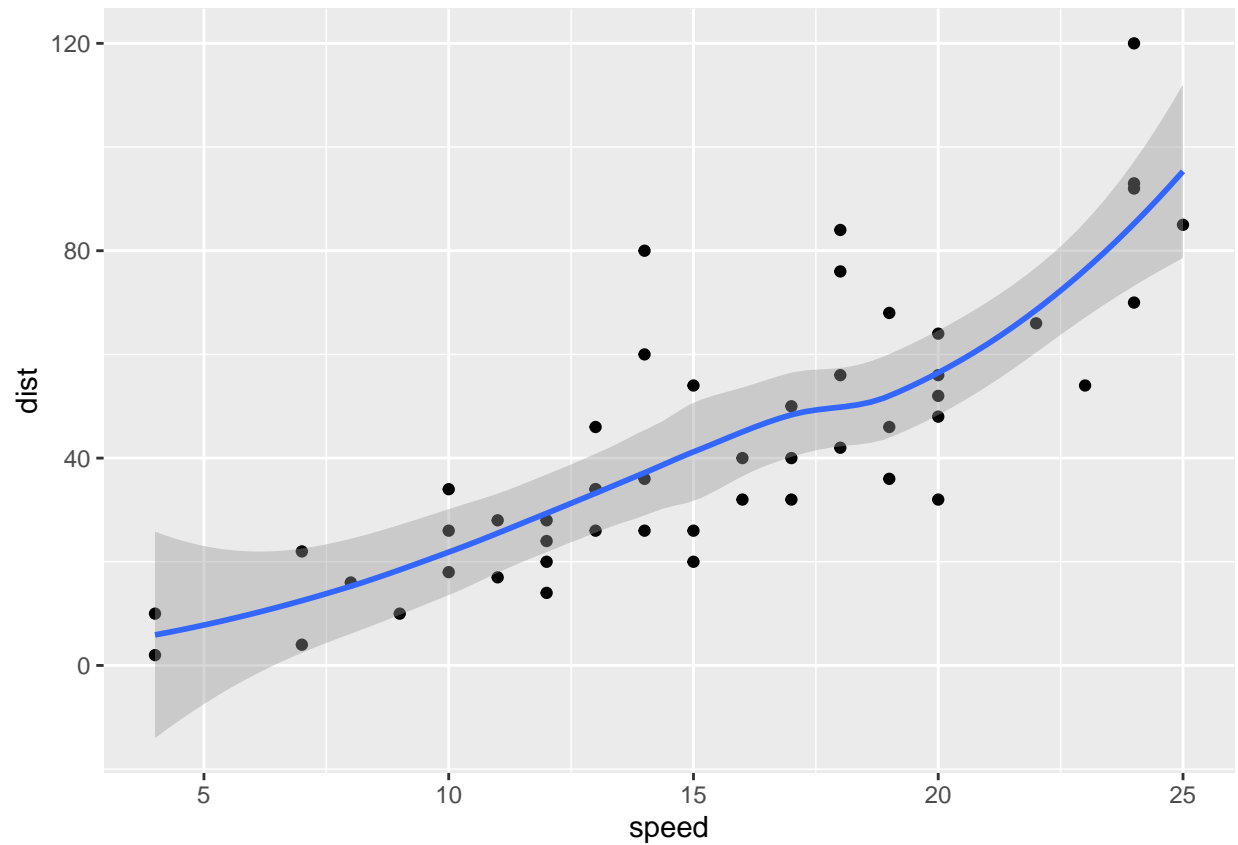


```
ggplot(data = cars) +aes(x = speed, y = dist) + geom_point() + geom_line()
```



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

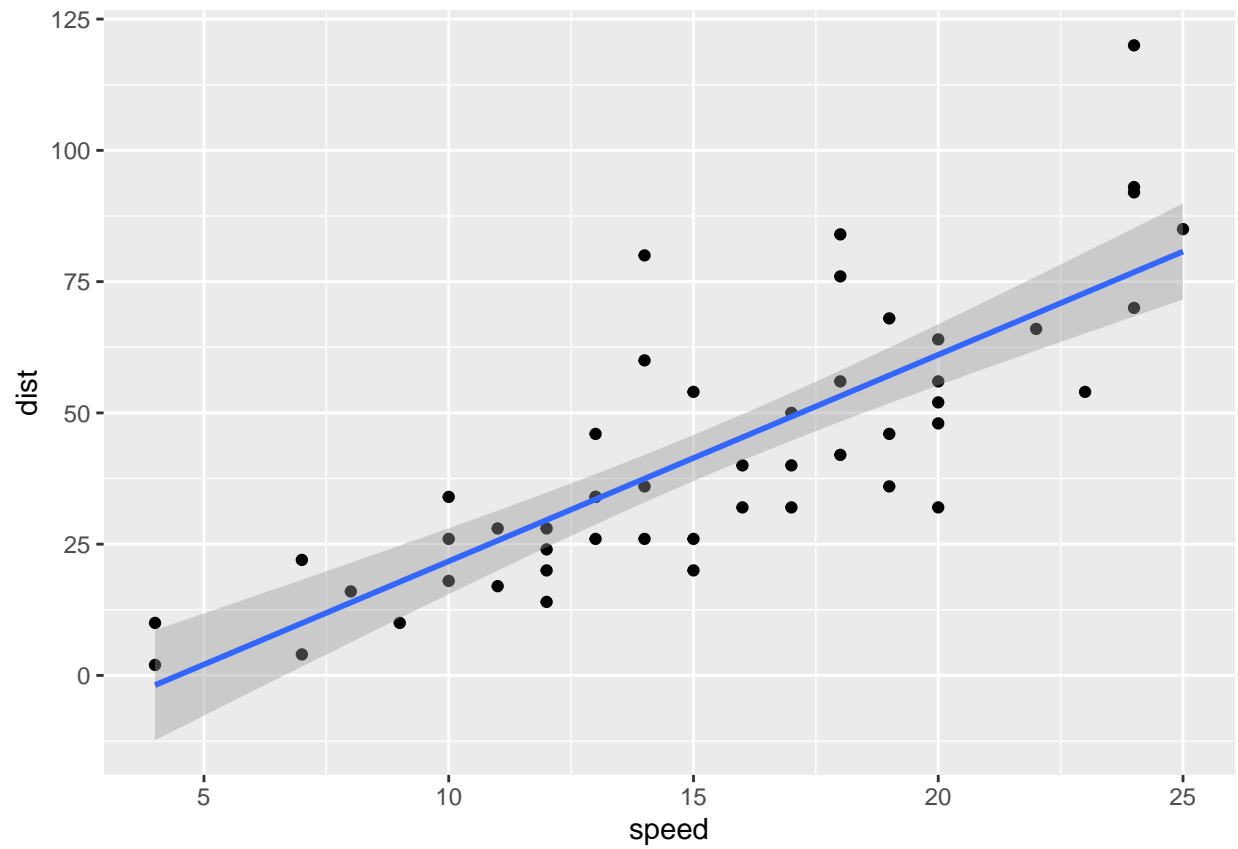
```
## 'geom_smooth()' using method = 'loess' and formula 'y ~ x'
```



```
# Change to a linear model
p <- ggplot(data = cars) + aes(x = speed, y = dist) + geom_point() + geom_smooth(method = lm)

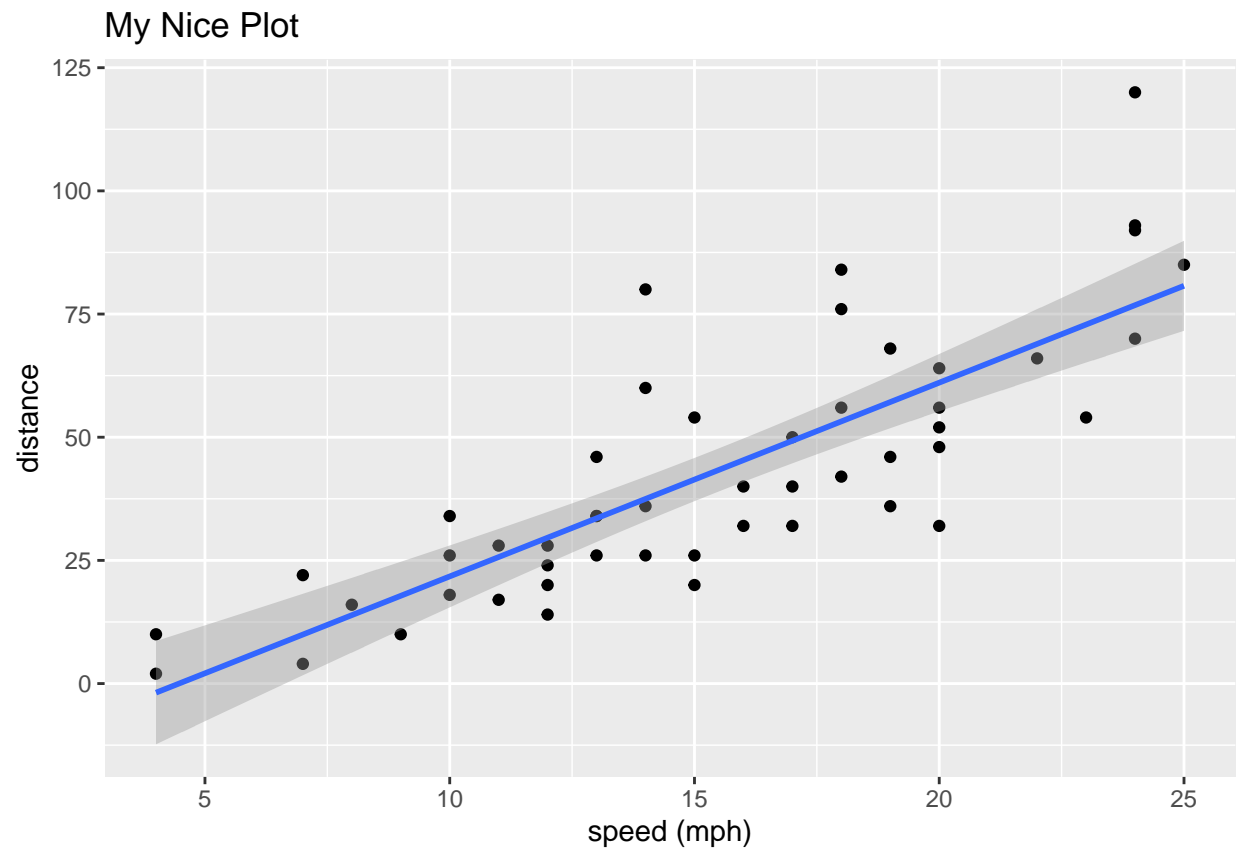
p

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



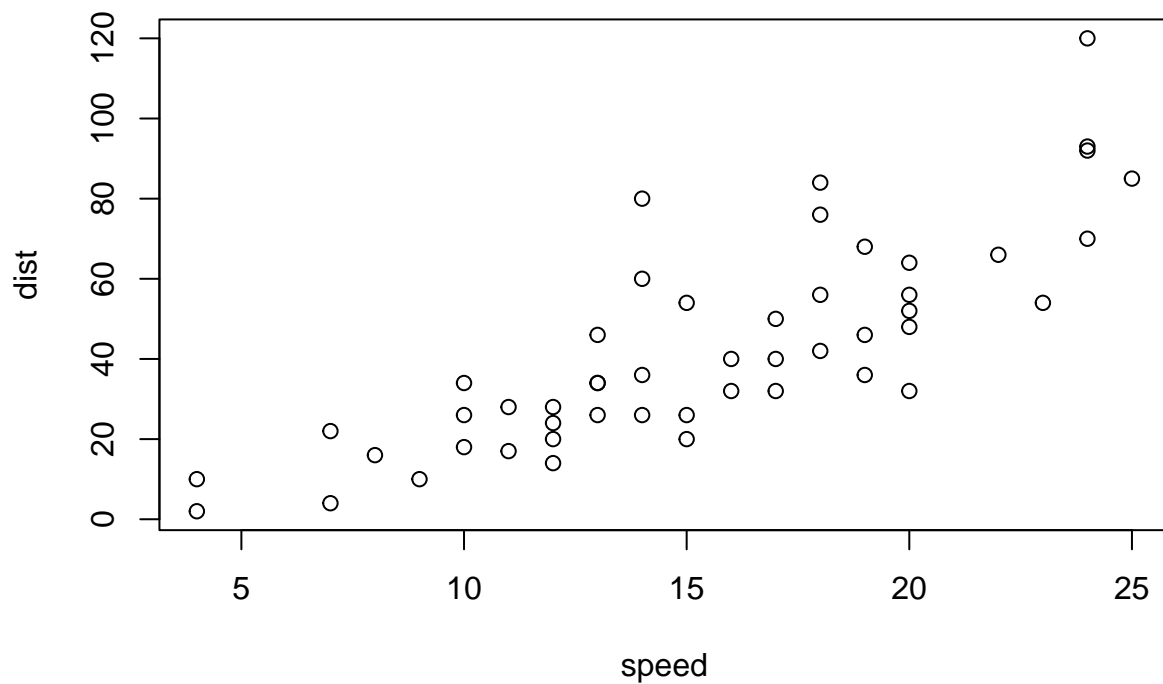
```
# Add a title to the plot and x/y labels  
p + labs(title = "My Nice Plot", x = "speed (mph)", y = "distance")
```

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



Base graphics is shorter

```
plot(cars)
```



```
# New graph showing anti-viral drug being tested
```

```
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
```

```
# Access State of Genes
```

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

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

```
?round  
signif(table(genes$State), digits = 2)
```

```
##  
##      down  unchanging      up  
##      72      5000      130
```

```
table(genes$State)/ nrow(genes)
```

```
##  
##      down  unchanging      up  
## 0.01385681 0.96170131 0.02444188
```

```
table(genes$State)/ nrow(genes) * 100
```

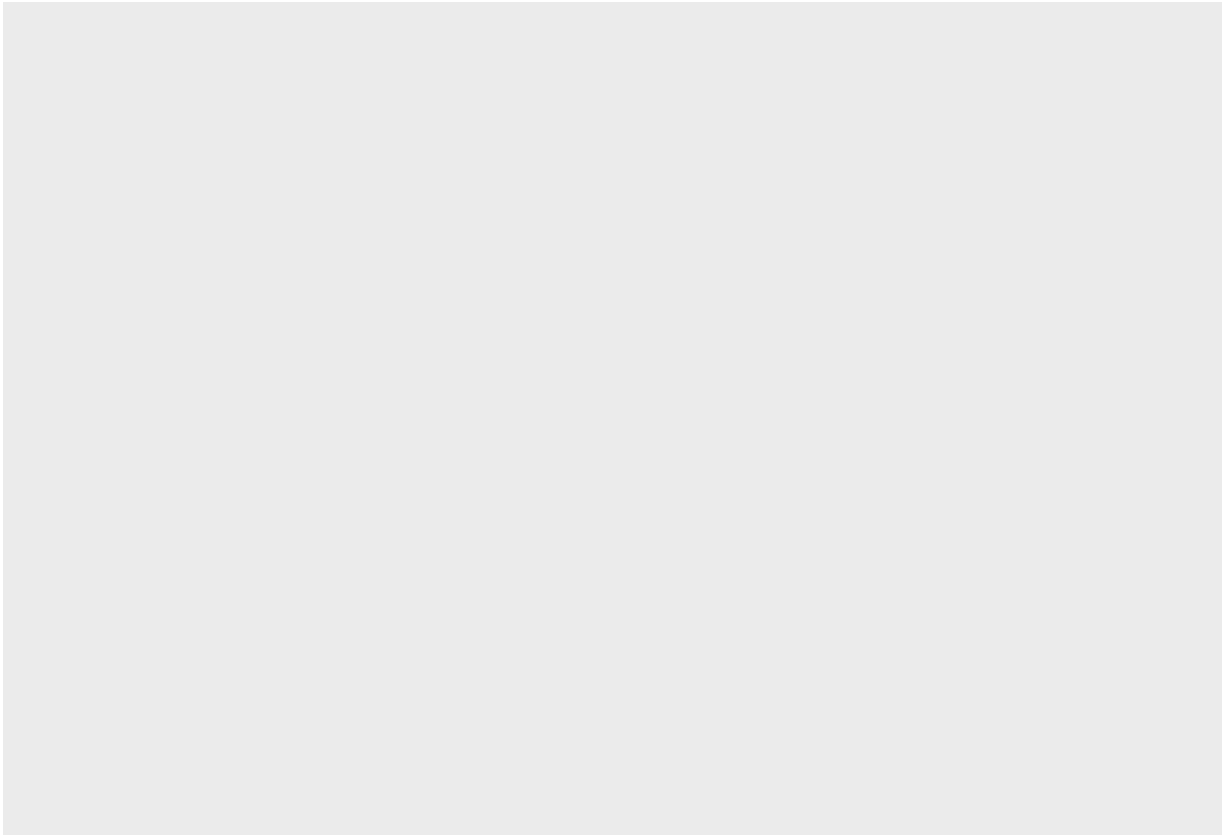
```
##  
##      down  unchanging      up  
## 1.385681 96.170131 2.444188
```

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

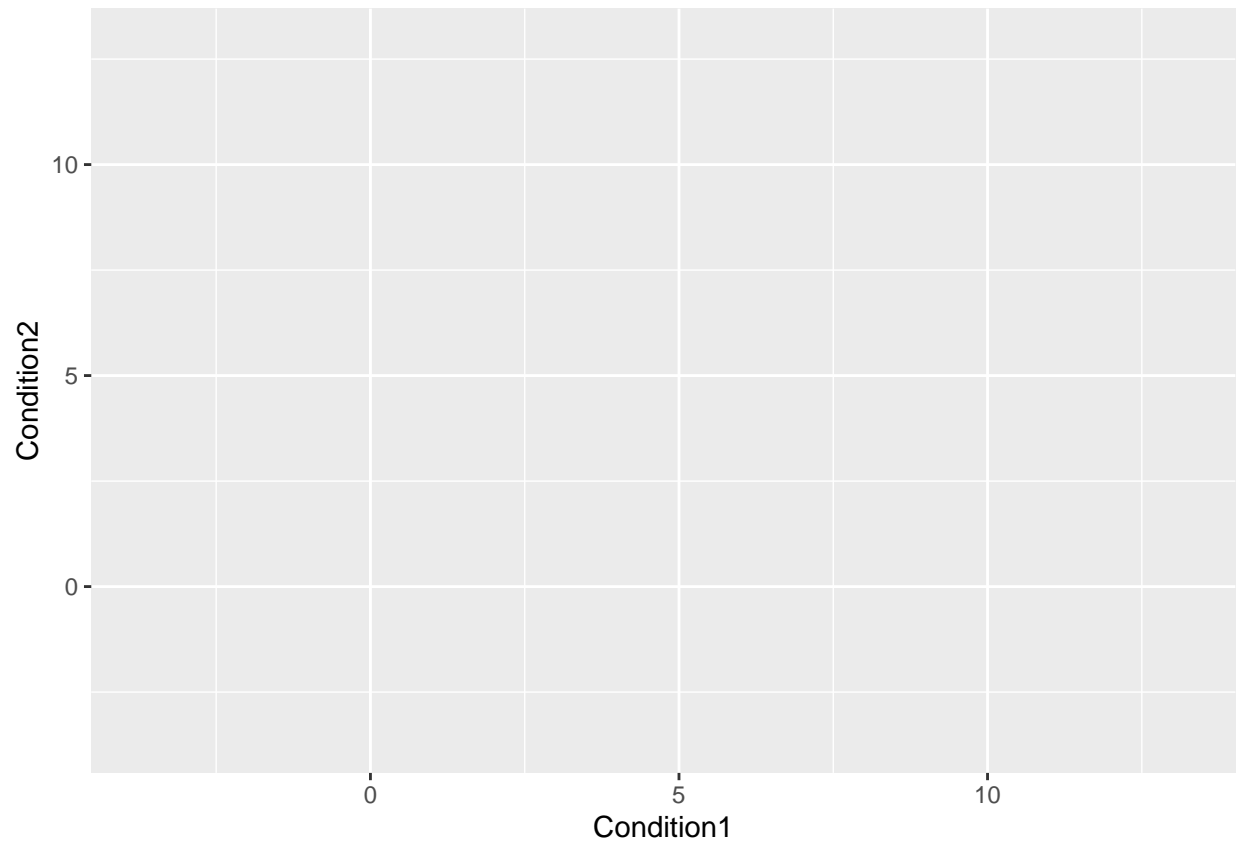
```
##  
##      down  unchanging      up  
## 1.39      96.17      2.44
```

```
# Start graphing data
```

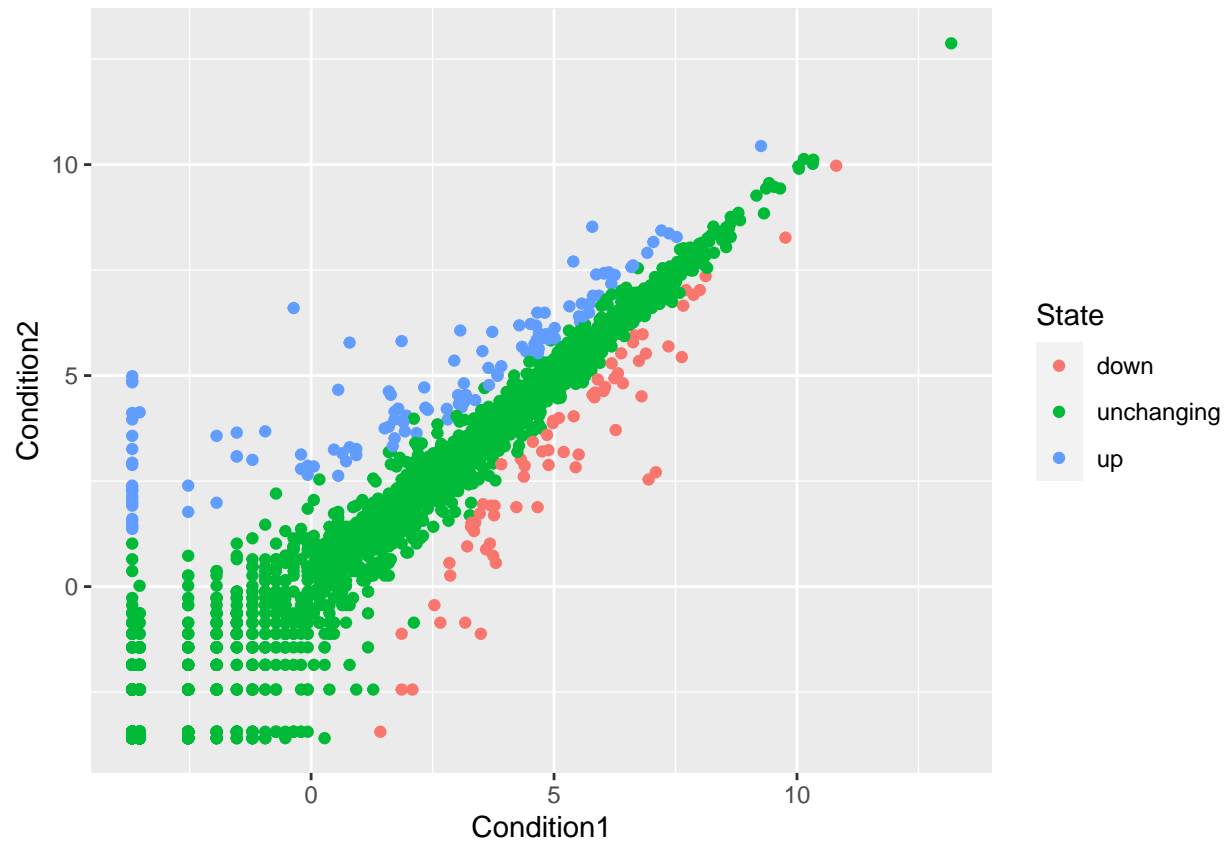
```
ggplot(genes)
```



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

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



```
g <- ggplot(genes) + aes(x=Condition1, y=Condition2, col=State) + geom_point()
g + scale_color_manual(values=c("purple", "grey", "pink"))
```



```
# Add additional labels
g + scale_color_manual(values=c("purple", "grey", "pink")) + labs(title="Gene Expression Changes Upon D
```

Gene Expression Changes Upon Drug Treatment

