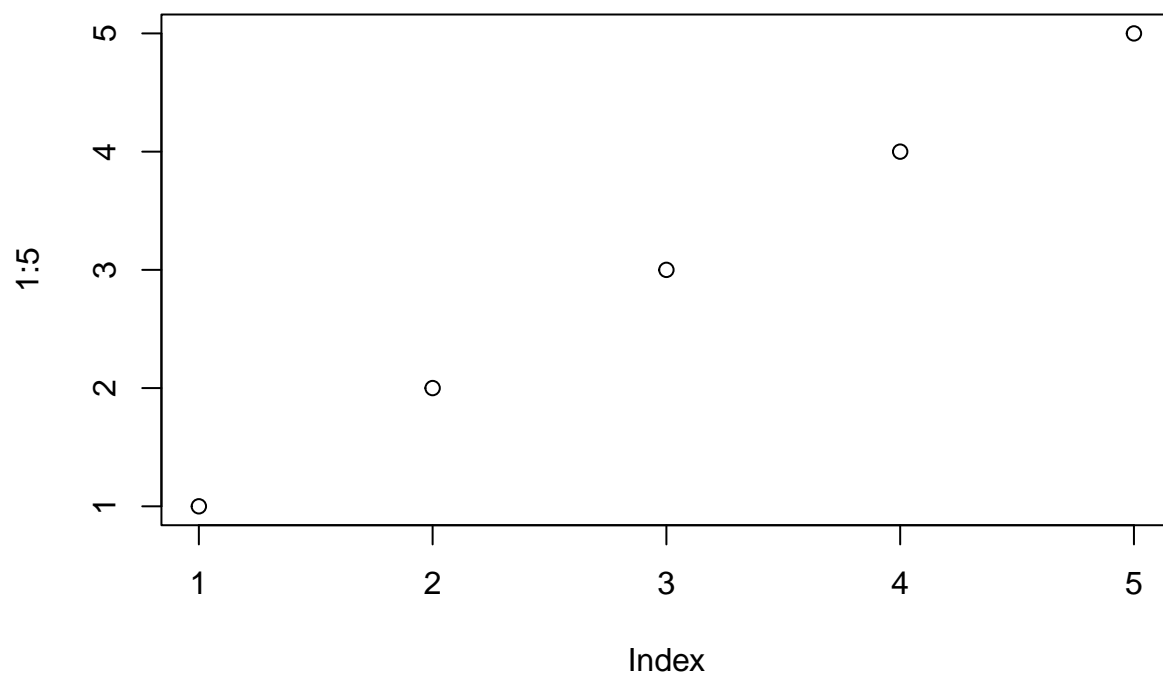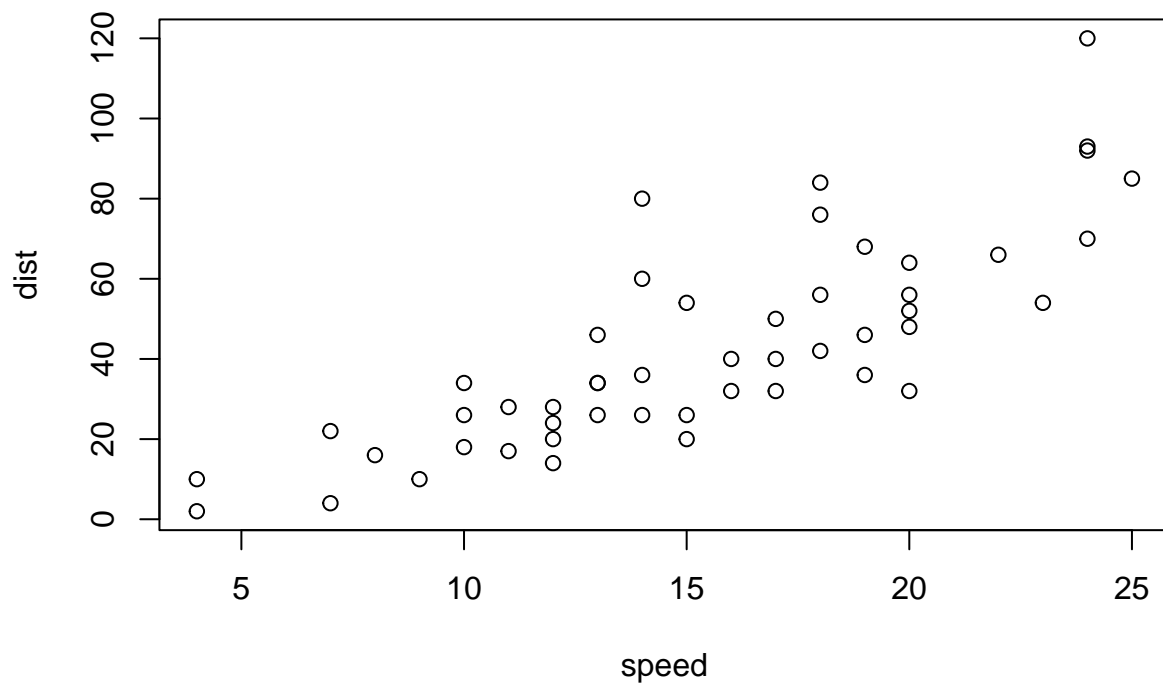# Class5.R

tforman

2022-02-02
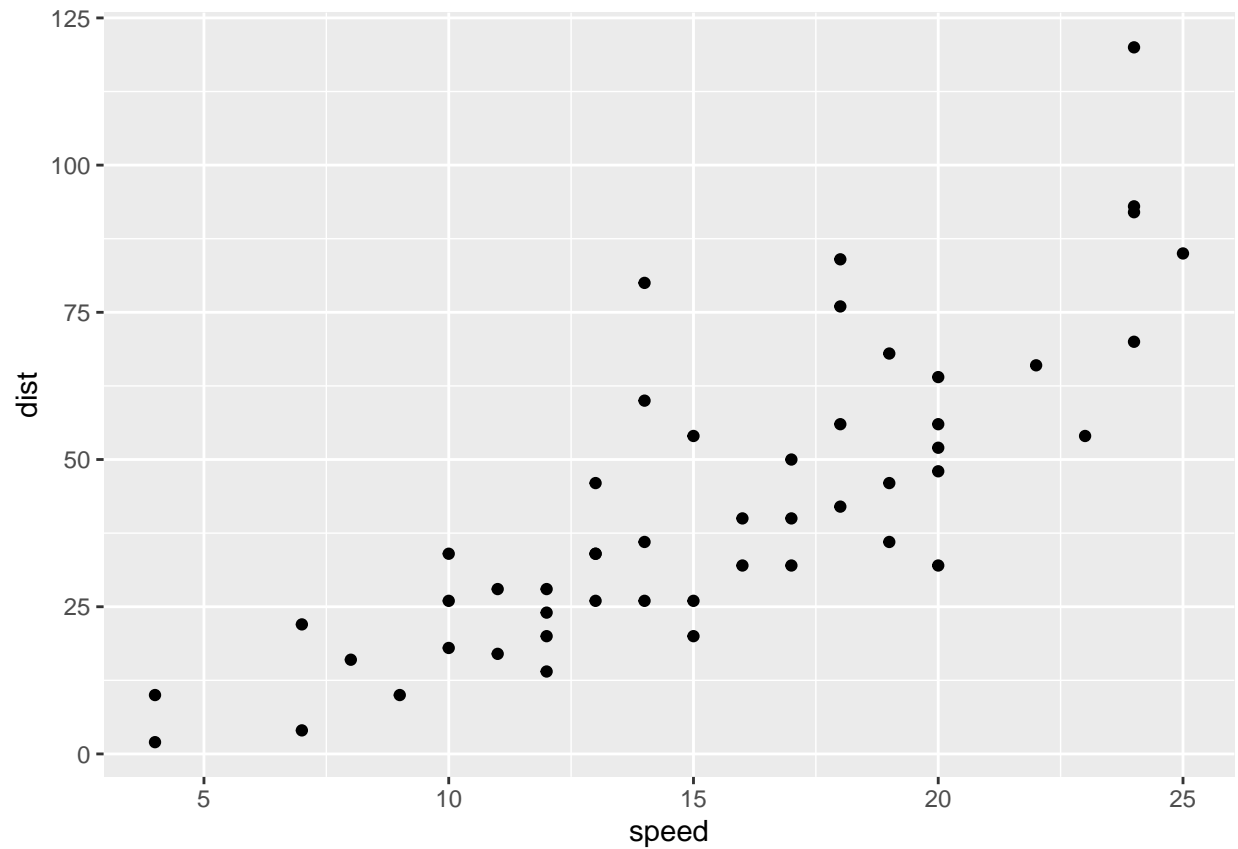
```r
plot(1:5)

# To load a package: install.packages("package_name")

#install.packages("ggplot2")

# Must load the package before using: library(package_name)

library(ggplot2)
```
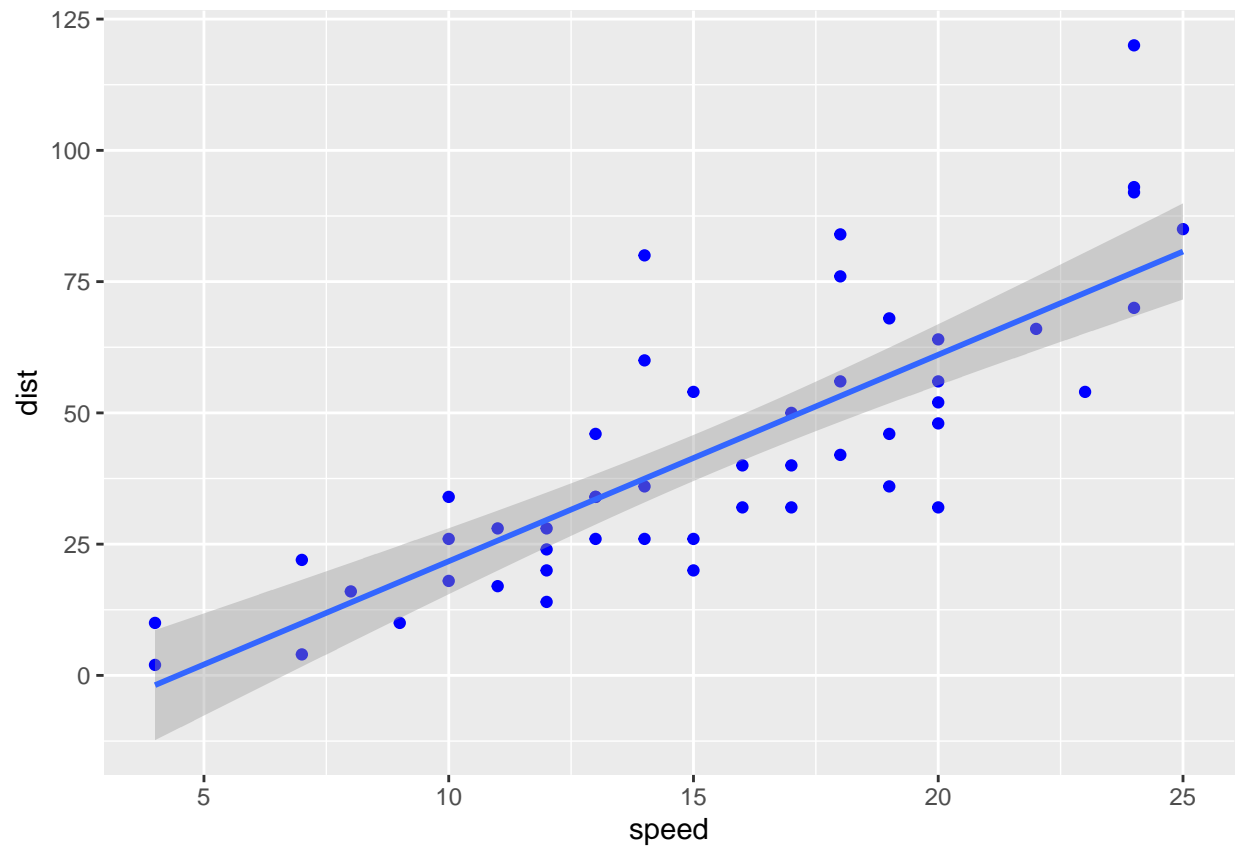


```r
plot(cars)
```

```
# Every ggplot has at least 3 layers
# data + aes(thetics) + geom(etries)

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

```
# Change the color of the points

#ggplot(data=cars) + aes(x=speed, y=dist) + geom_point(col="blue")

carplot <- ggplot(data=cars) + aes(x=speed, y=dist) + geom_point(col="blue")

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

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

```
carplot + labs(title="Speed Over Distance")
```

Speed Over Distance
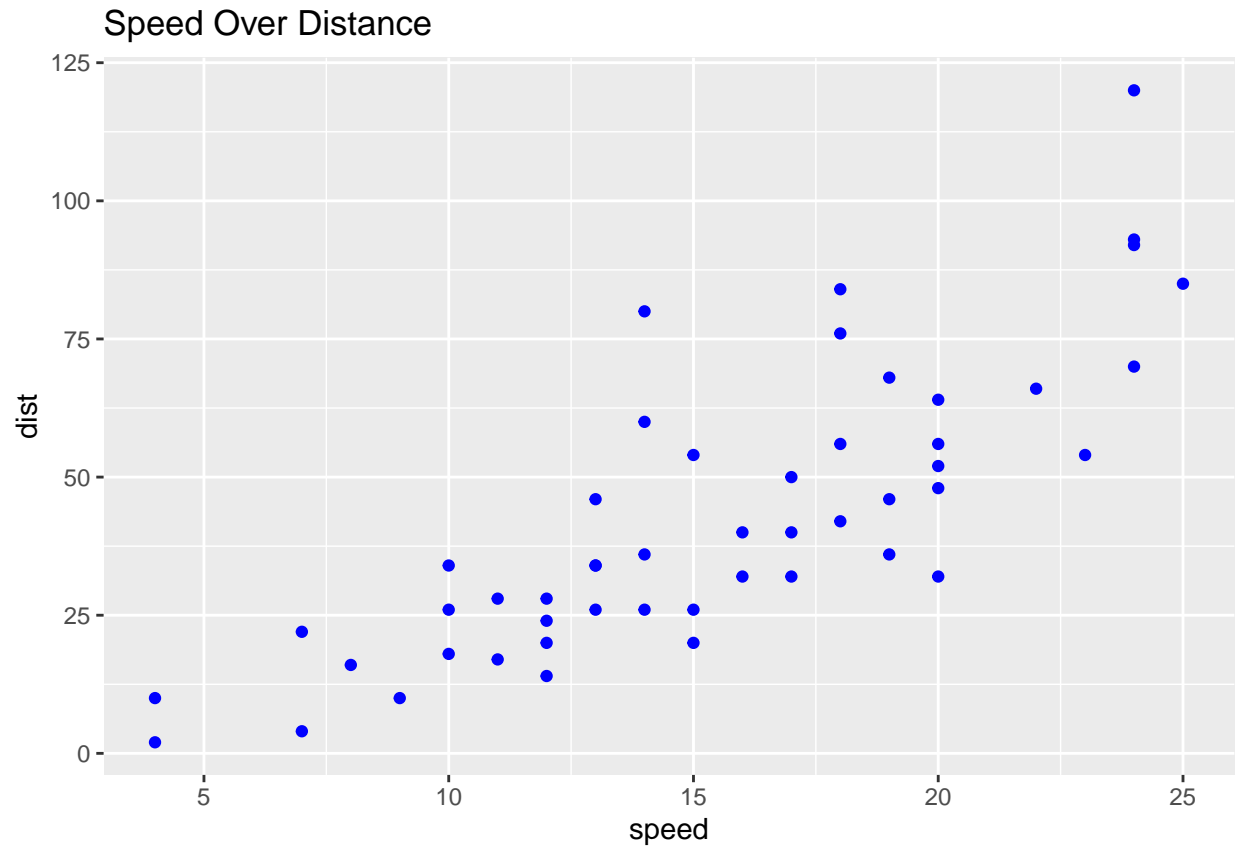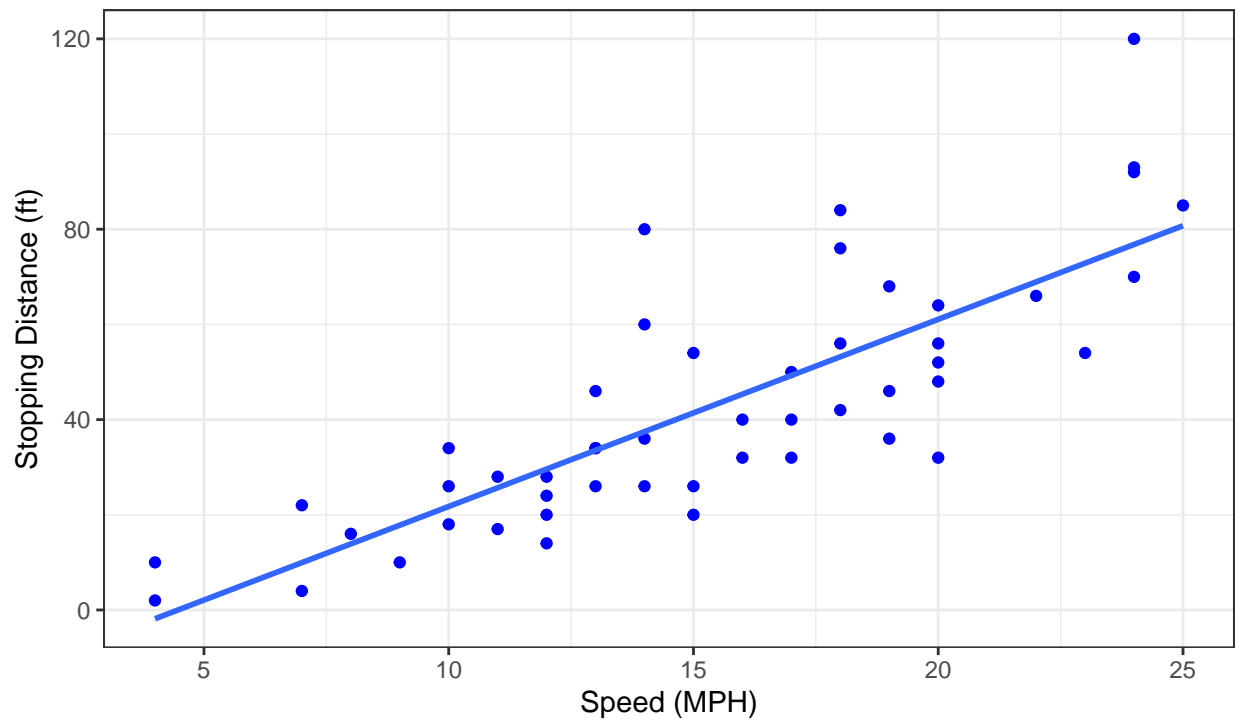


```r
carplot + labs(title="Speed and Stopping Distances of Cars",
               x="Speed (MPH)",
               y="Stopping Distance (ft)",
               subtitle = "More Relevant Information if I Had Some",
               caption="Dataset: 'cars' preloaded in RStudio") +
  geom_smooth(method="lm", se=FALSE) +
  theme_bw()
```

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

Speed and Stopping Distances of Cars
More Relevant Information if I Had Some

Dataset: 'cars' preloaded in RStudio

```
# 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
```

```
nrow(genes)
```

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

```
ncol(genes)
```

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

```
colnames(genes)
```

```
## [1] "Gene"       "Condition1" "Condition2" "State"
```
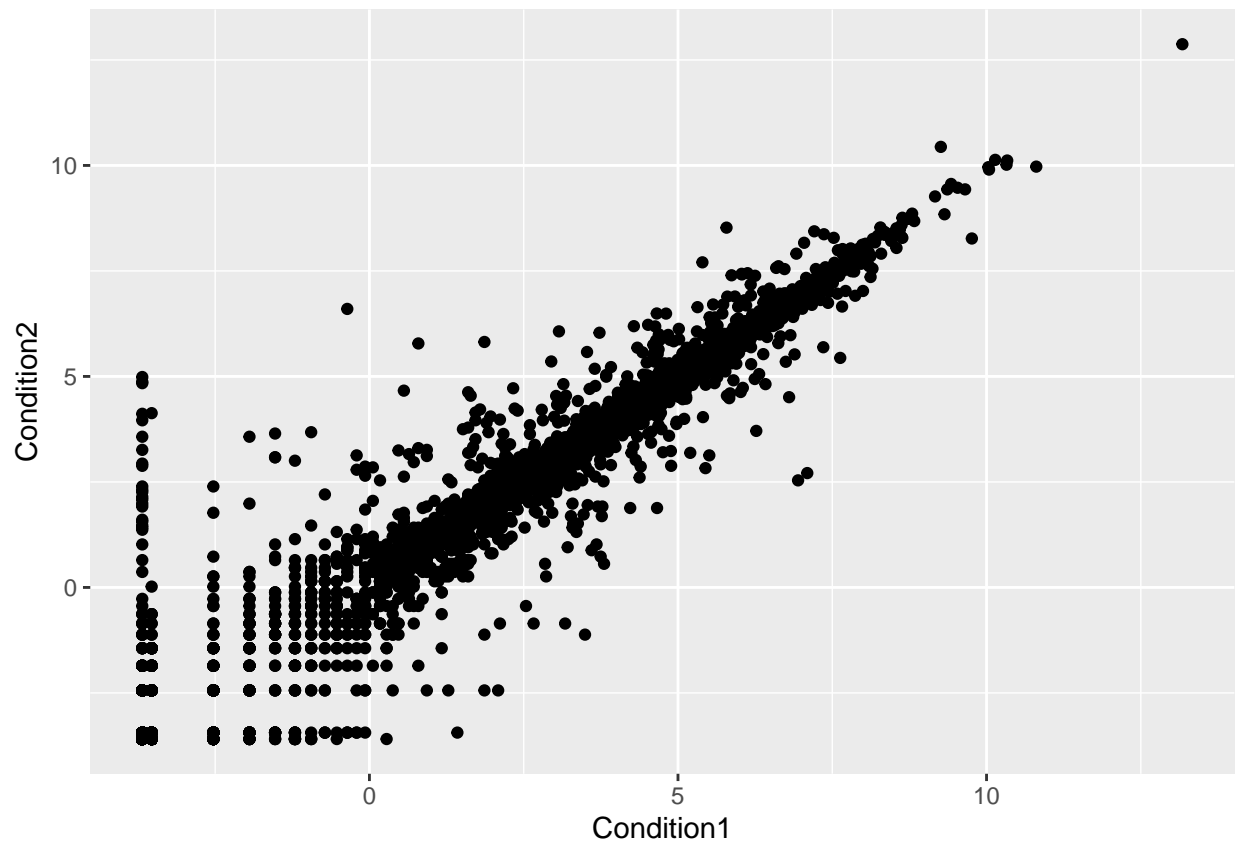
```
table(genes$State)
```

```
##
##      down unchanging         up
##        72       4997        127
```
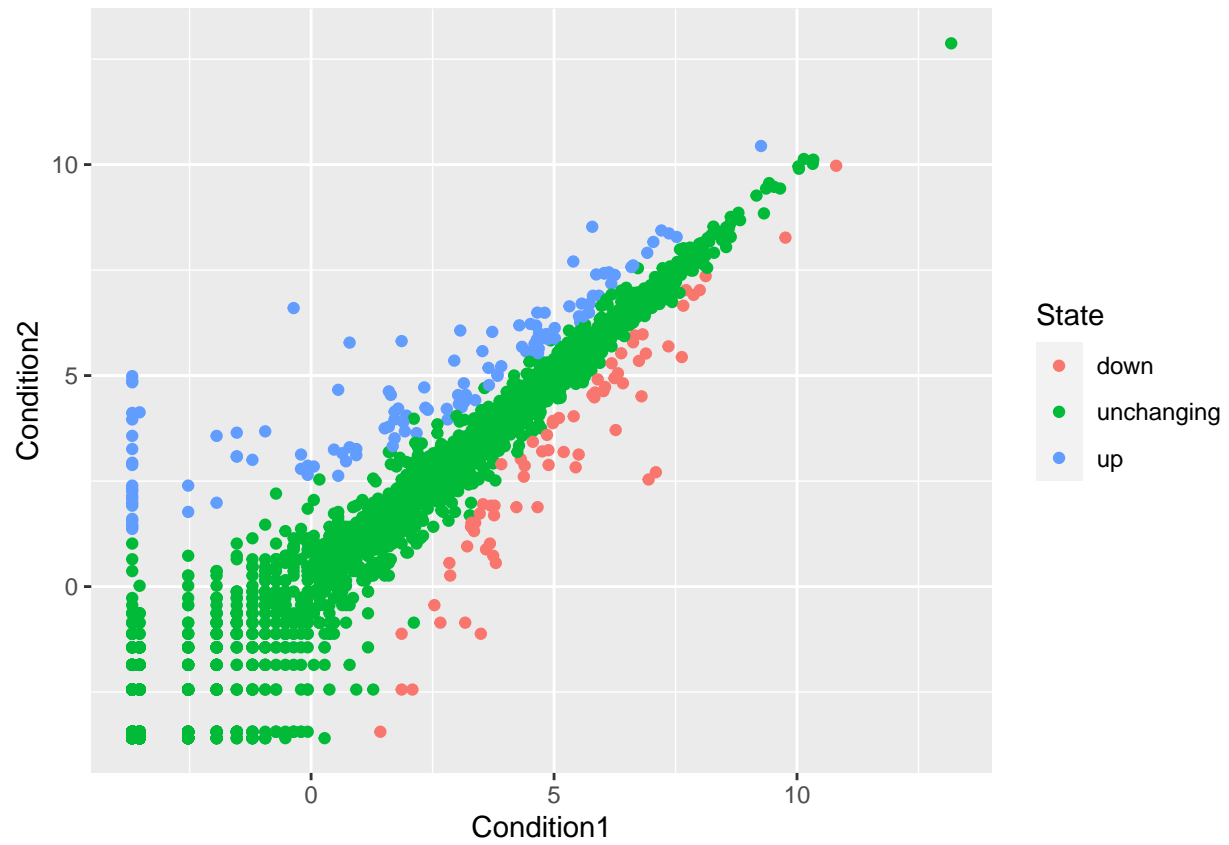
```
round( table(genes$State)/nrow(genes) * 100, 2 )
```

```
##
##      down unchanging         up
##      1.39      96.17       2.44
```
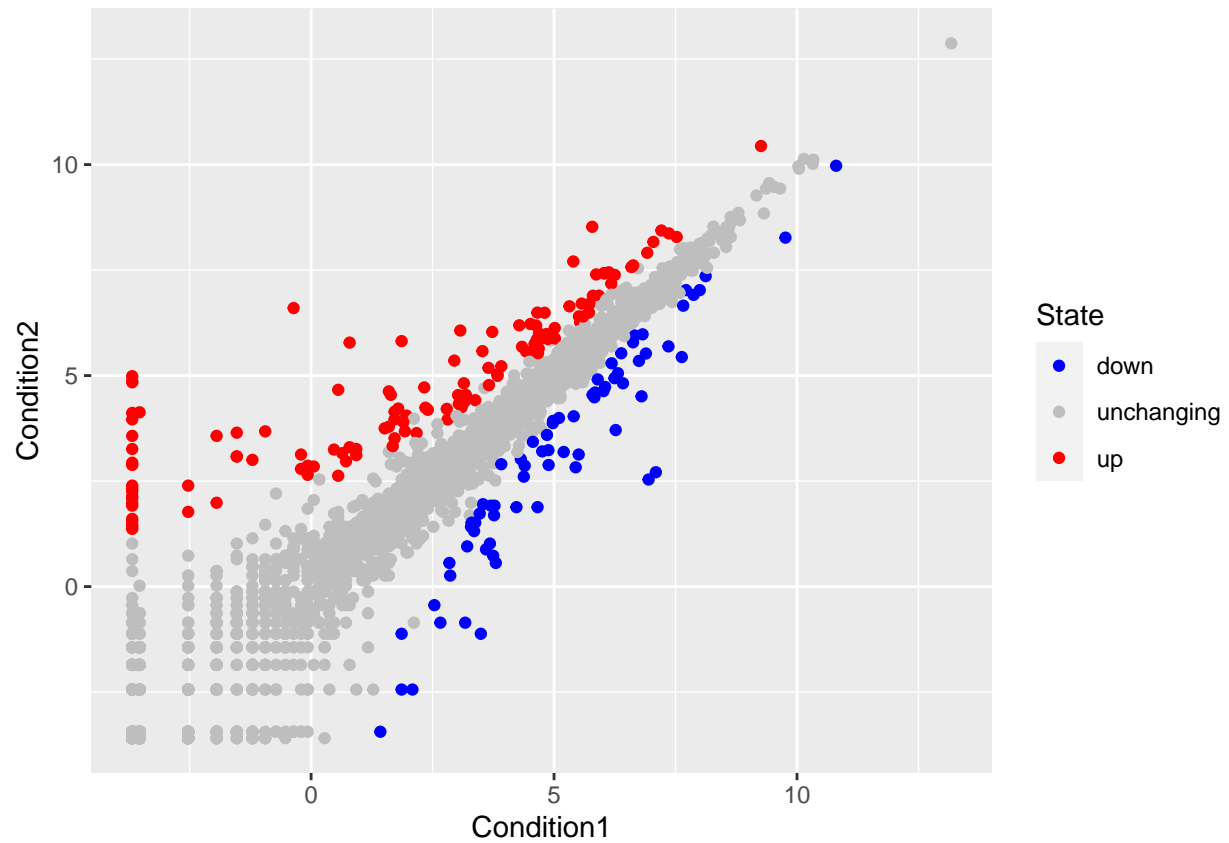
```
ggplot(genes) + aes(x=Condition1, y=Condition2) + geom_point()
```



```
ggplot(genes) + aes(x=Condition1, y=Condition2, col=State) + geom_point()
```
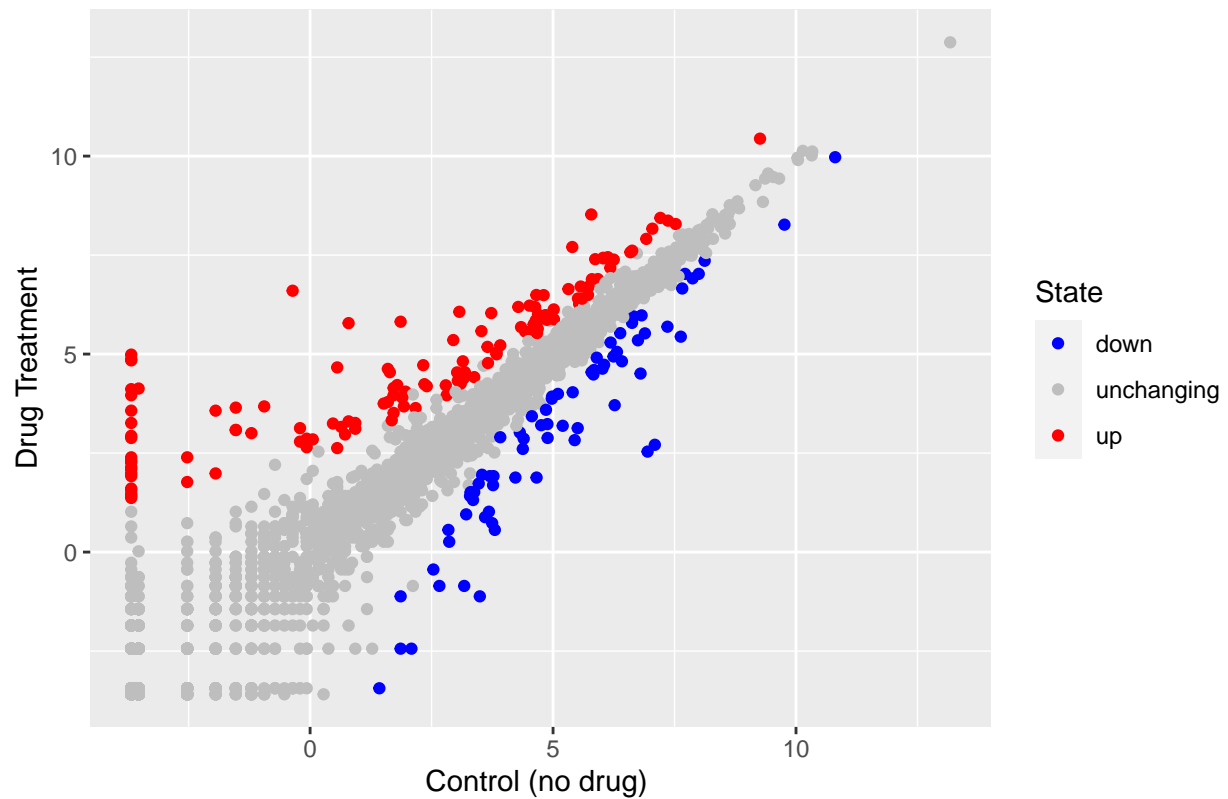
```
reg_plot <- ggplot(genes) +
  aes(x=Condition1, y=Condition2, col=State) +
  geom_point()
reg_plot + scale_colour_manual( values=c("blue","gray","red") )
```

```
reg_plot + scale_colour_manual(values=c("blue","gray","red")) +
  labs(title="Gene Expresion Changes Upon Drug Treatment",
       x="Control (no drug) ",
       y="Drug Treatment")
```

Gene Expresion Changes Upon Drug Treatment


```
reg_plot2 <- ggplot(genes) +
  aes(x=Condition1, y=Condition2, col=State) +
  geom_point(alpha = 0.4)
reg_plot2 + scale_colour_manual(values=c("blue","gray","red")) +
  labs(title="Gene Expression Changes Upon Drug Treatment",
       x="Control (no drug) ",
       y="Drug Treatment")
```

Gene Expresion Changes Upon Drug Treatment