

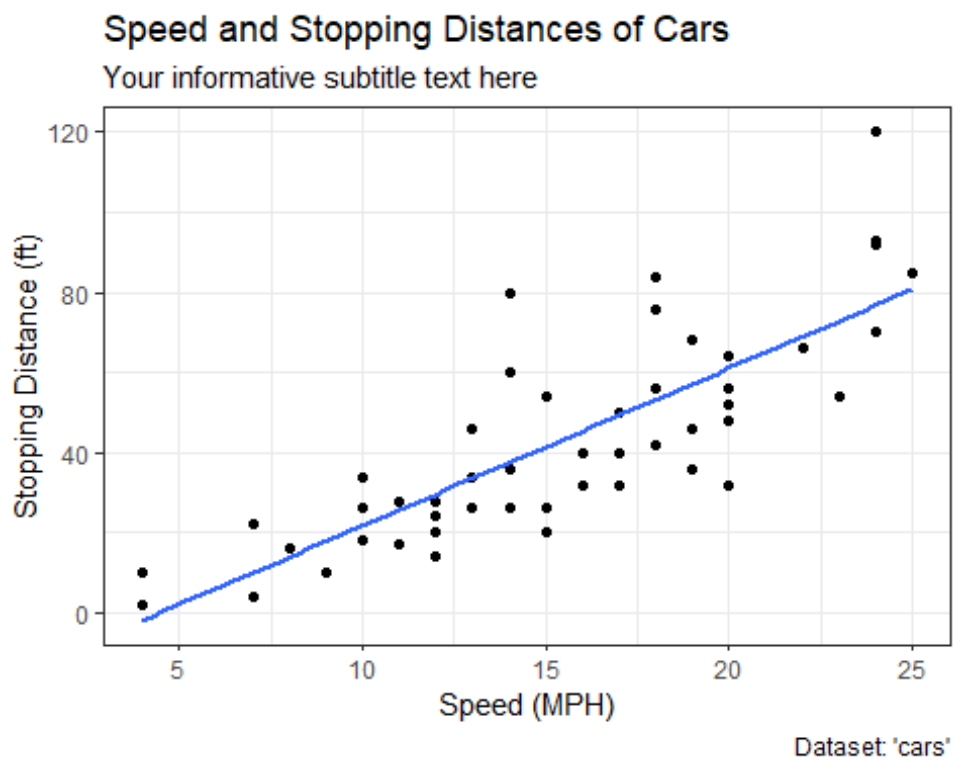
1.R

Noah

2022-02-06

```
library(ggplot2)
ggplot(cars)+
  aes(speed,dist)+
  geom_point()+
  labs(title="Speed and Stopping Distances of Cars",
       x="Speed (MPH)",
       y="Stopping Distance (ft)",
       subtitle = "Your informative subtitle text here",
       caption="Dataset: 'cars'") +
  geom_smooth(method="lm", se=FALSE) +
  theme_bw()

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



```
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

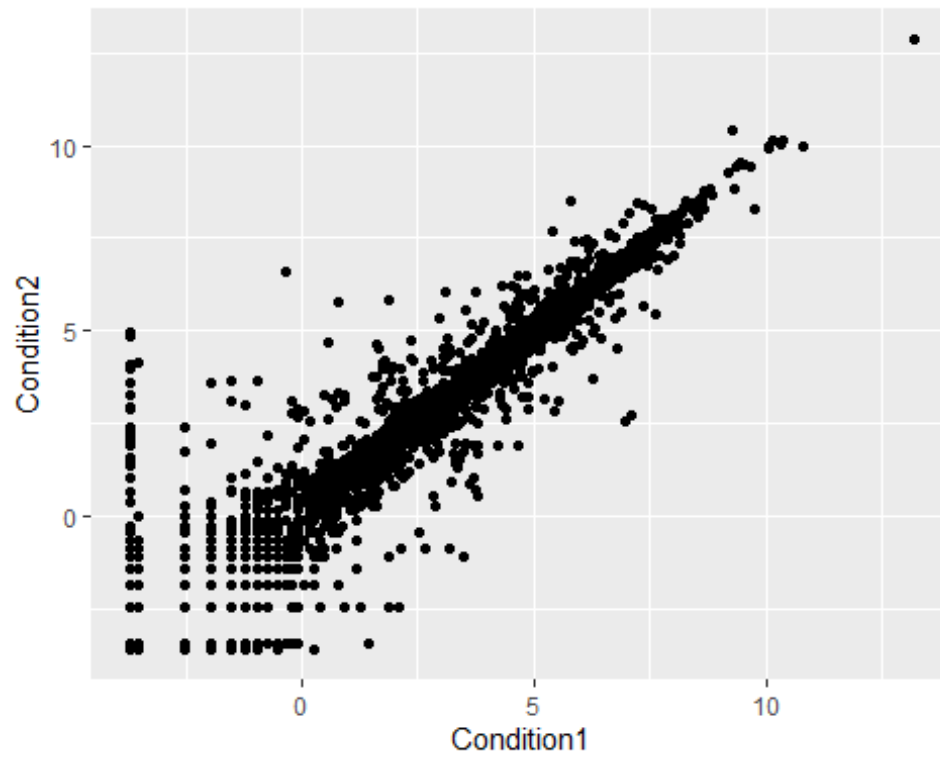
table(genes$State)

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

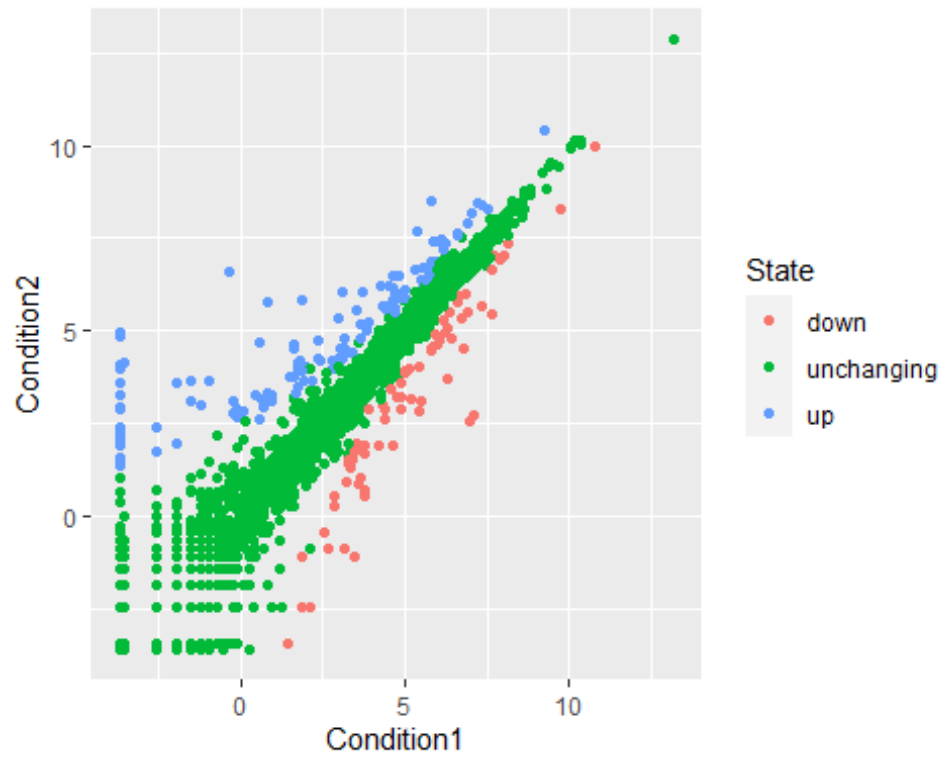
round(table(genes$State)/nrow(genes)*100,2)

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

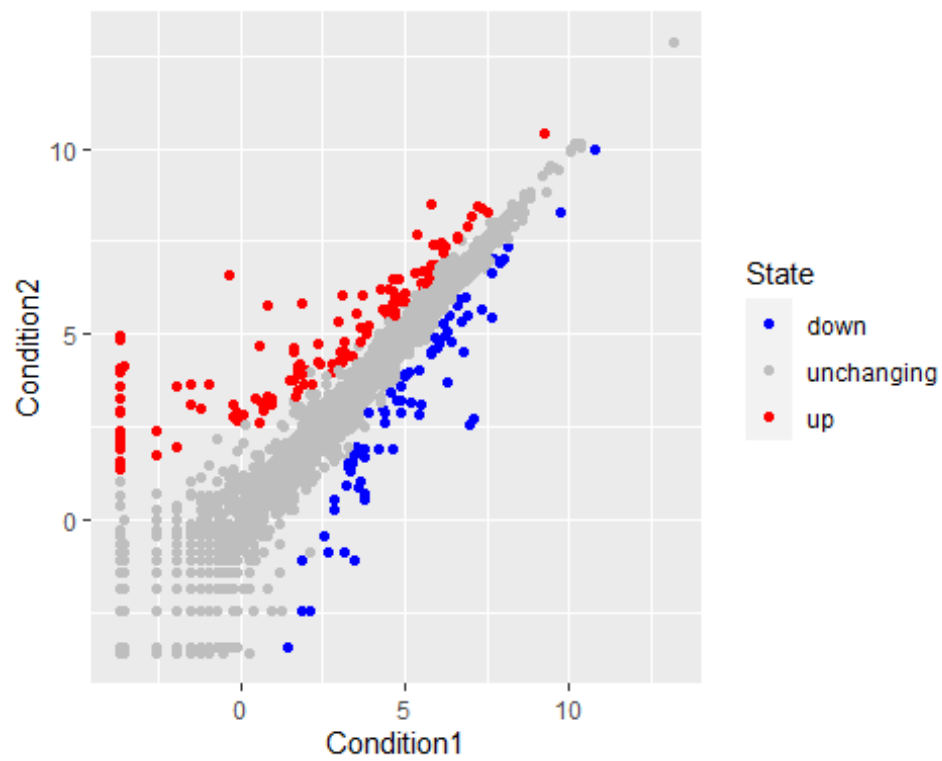
ggplot(genes)+
  aes(x=Condition1, y=Condition2)+
  geom_point()
```



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



```
p + scale_colour_manual( values=c("blue","gray","red") )
```



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

