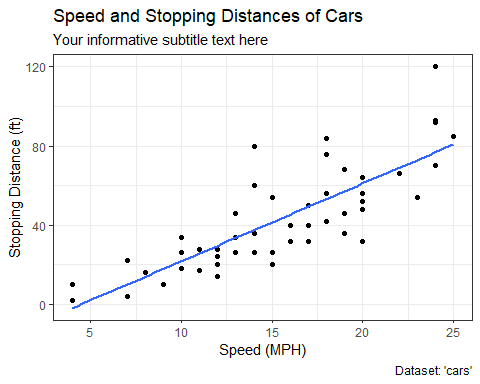
1.R

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

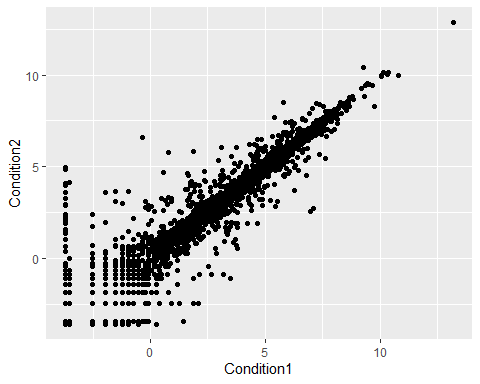
table(genes$State)

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

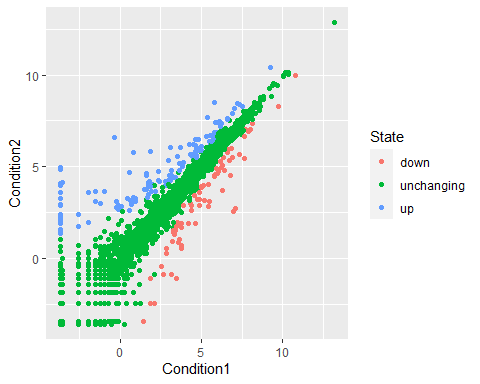
round(table(genes$State)/nrow(genes)\*100,2)

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

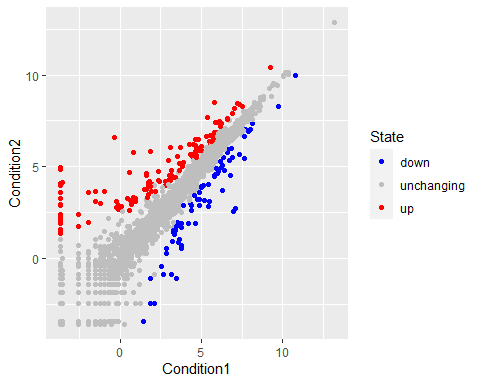
ggplot(genes)+  
 aes(x=Condition1, y=Condition2)+  
 geom\_point()



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 Expresion Changes Upon Drug Treatment",  
 x="Control (no drug) ",  
 y="Drug Treatment")

