labweek5.R

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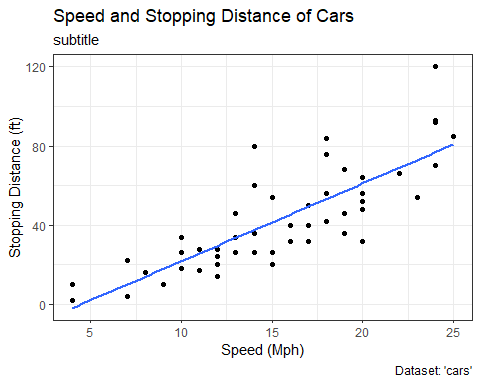
2022-02-06

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'



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()

