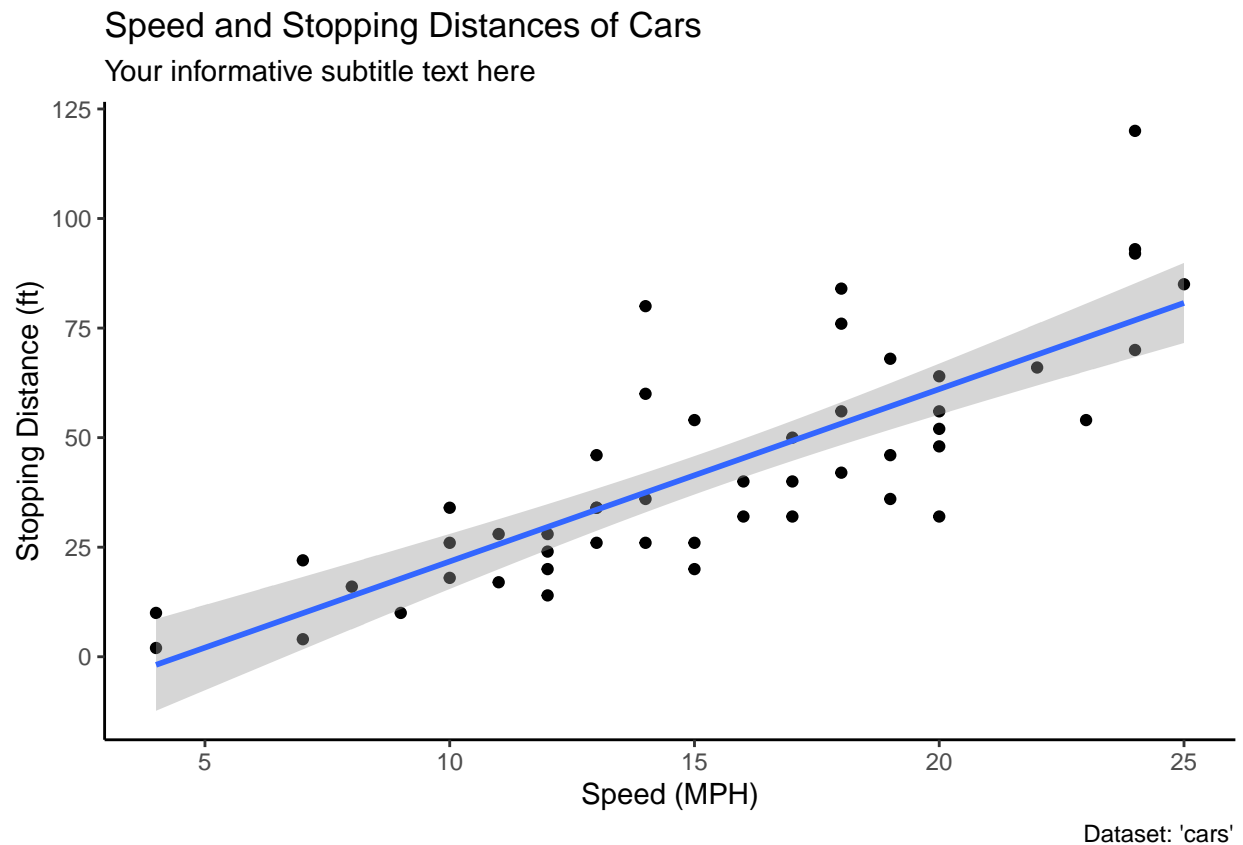# class5.R

astro

2021-10-12

```r
library(ggplot2)
# every ggplot has a data +aes + geoms
p1 <- ggplot(data=cars)+
  aes(x=speed, y=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'")
 p1+ geom_smooth(method="lm", se=TRUE) +
   theme_classic()
```

```
## '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
```

```
# How many genes
nrow(genes)
```

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

```
#how many collumns
ncol(genes)
```

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

```
#Q How to access state col
table(genes$State)
```

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

```
#Q amount of up genes 2 sig figs
round( table(genes$State)/nrow(genes) * 100, 2 )
```

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

```
p2 <- (ggplot(genes)+
  aes(x=Condition1, y=Condition2, col=State)+
  geom_point())
p2 + labs(title="Gene Expresion Changes Upon Drug Treatment",
        x="Control (no drug) ",
        y="Drug Treatment")+geom_smooth(method="lm", se=FALSE,colour="orange") +
  theme_classic()+scale_colour_manual( values=c("blue","purple","green"))
```

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

## Gene Expresion Changes Upon Drug Treatment
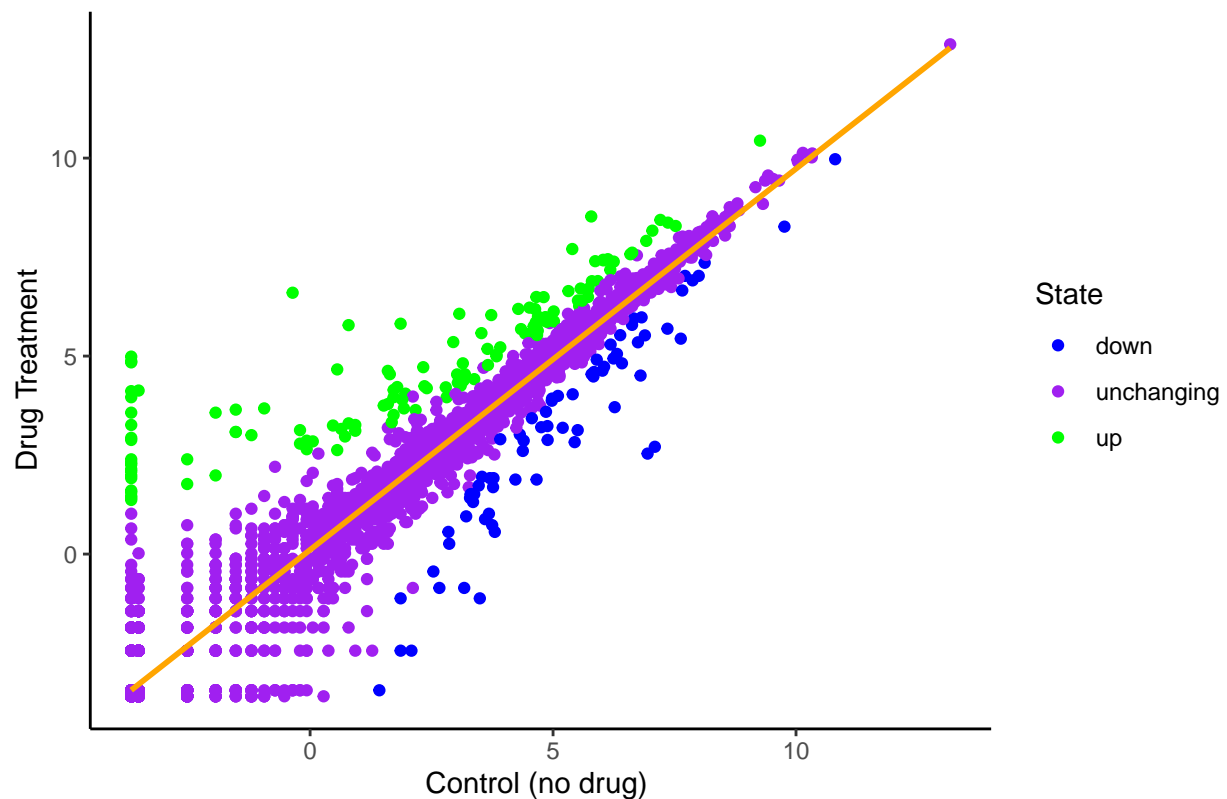


```
###
#install.packages("gapminder")
library(gapminder)
# File location online
#url <- "https://raw.githubusercontent.com/jennybc/gapminder/master/inst/extdata/gapminder.tsv"
#gapminder <- read.delim(url)

#install.packages("dplyr")
# install.packages("dplyr")  ## uncoment to install if needed
library(dplyr)
```

```
##
## Attaching package: 'dplyr'
```

```
## The following objects are masked from 'package:stats':
##
##     filter, lag
```

```
## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
```

```
gapminder_2007 <- gapminder %>% filter(year==2007)
```

```
ggplot(gapminder_2007) +
  aes(x=gdpPercap, y=lifeExp, color=continent, size=pop) +
  geom_point(alpha=0.5)
```