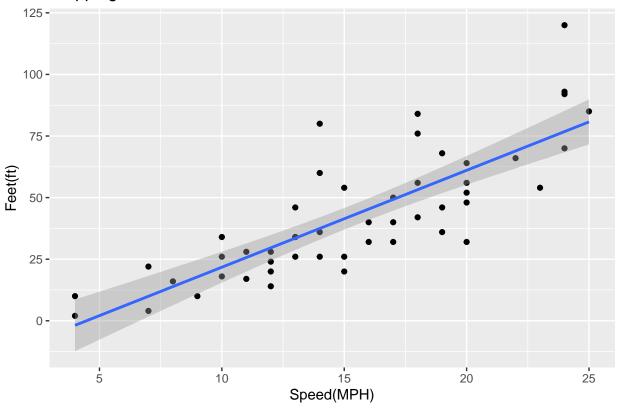
class5.R

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```
#import
library(ggplot2)
# #beginning
head(cars)
   speed dist
##
## 1 4
## 2
       4 10
## 3
       7 4
       7 22
## 4
## 5
      8 16
      9 10
## 6
# Layers of my Plot(DATA, Aesthetic, Geometry, Trend)
ggplot(cars) + aes(x=speed, y=dist)+geom_point() + geom_smooth(method="lm") +
labs(title="Stopping Distance of Old Cars", x="Speed(MPH)", y="Feet(ft)")
## 'geom_smooth()' using formula 'y ~ x'
```

Stopping Distance of Old Cars



#GENES url <- "https://bioboot.github.io/bimm143_S20/class-material/up_down_expression.txt" genes <- read.delim(url) head(genes)</pre>

```
## 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)

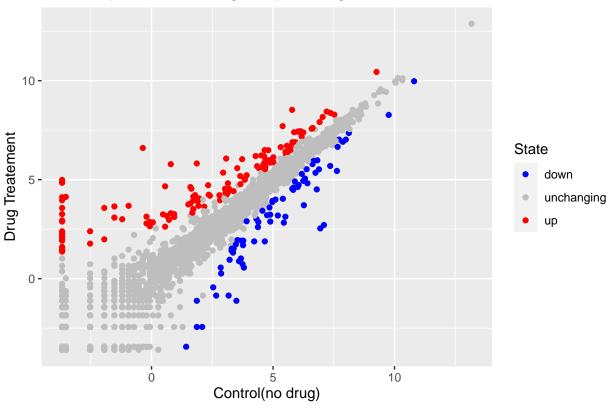
```
## [1] "Gene" "Condition1" "Condition2" "State"

ncol(genes)
```

[1] 4

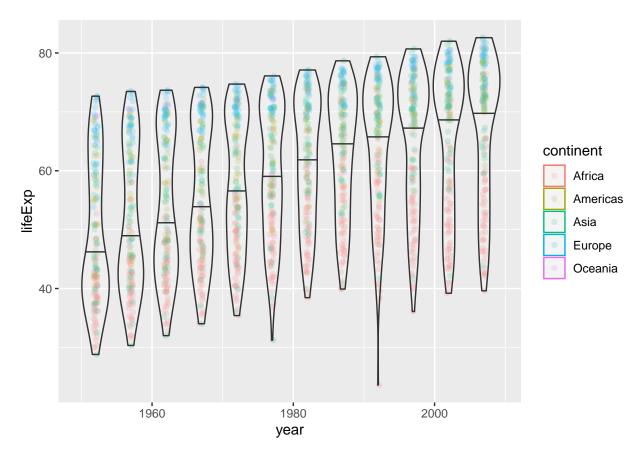
```
table(genes$State)
##
##
         down unchanging
                     4997
                                  127
round( table(genes$State)/nrow(genes) * 100, 2 )
##
##
         down unchanging
                    96.17
         1.39
                                 2.44
##
p <- ggplot(genes) +</pre>
  aes(x=Condition1, y=Condition2, col=State) +
  geom_point()
p<-p+ scale_colour_manual( values=c("blue", "gray", "red") )</pre>
p<-p+labs(title="Gene Expressions Changes Upon Drug Treatment ", x="Control(no drug)", y="Drug Treatement</pre>
```

Gene Expressions Changes Upon Drug Treatment



```
#Gapminder with plotly
library(gapminder)
library(plotly)
```

```
##
## Attaching package: 'plotly'
## The following object is masked from 'package:ggplot2':
##
##
       last_plot
## The following object is masked from 'package:stats':
##
##
       filter
## The following object is masked from 'package:graphics':
##
##
       layout
head(gapminder)
## # A tibble: 6 x 6
     country
                continent year lifeExp
                                              pop gdpPercap
##
     <fct>
                <fct> <int> <dbl>
                                            <int>
                                                      <dbl>
## 1 Afghanistan Asia
                          1952
                                    28.8 8425333
                                                       779.
                                    30.3 9240934
                                                       821.
## 2 Afghanistan Asia
                           1957
## 3 Afghanistan Asia
                           1962
                                    32.0 10267083
                                                       853.
                                                       836.
## 4 Afghanistan Asia
                           1967
                                    34.0 11537966
## 5 Afghanistan Asia
                                    36.1 13079460
                                                       740.
                            1972
## 6 Afghanistan Asia
                            1977
                                    38.4 14880372
                                                       786.
ggplot(gapminder) + aes(x=year,y=lifeExp, col=continent) + geom_jitter(width=0.3,alpha=0.2) +
 geom_violin(aes(group=year),alpha=0.2,draw_quantiles = 0.5)
```



```
#ggplotly()

#Combining Plots
library(patchwork)
p1 <- ggplot(mtcars) + geom_point(aes(mpg, disp))
p2 <- ggplot(mtcars) + geom_boxplot(aes(gear, disp, group = gear))
p3 <- ggplot(mtcars) + geom_smooth(aes(disp, qsec))
p4 <- ggplot(mtcars) + geom_bar(aes(carb))
r=(p1 | p2 | p3) /p4
r</pre>
```

'geom_smooth()' using method = 'loess' and formula 'y ~ x'

