class05.R

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```
# Class 05: Data Visualization
# Author: Jocelyn Olvera
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# Description: Today we are going to use ggplot2 package

# First we need to loud the package!
# Install.packages("ggplot2")
library(ggplot2)

# We will use this inbuilt "cars" dataset first
# "head" allows viewing of only a small subset of the data
head(cars)
```
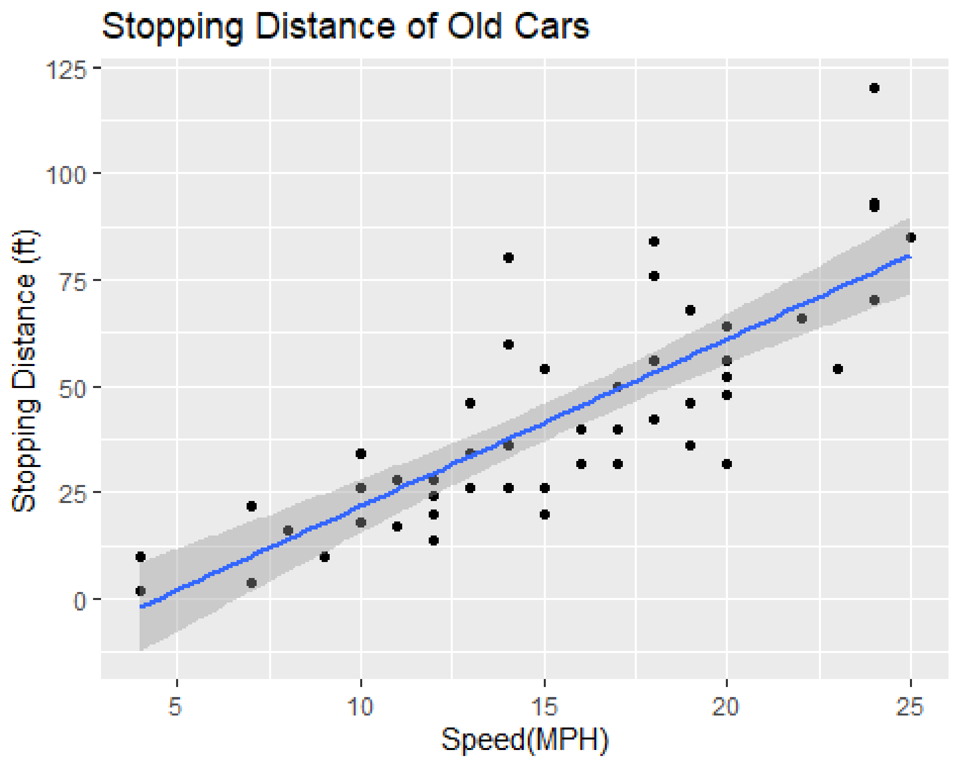
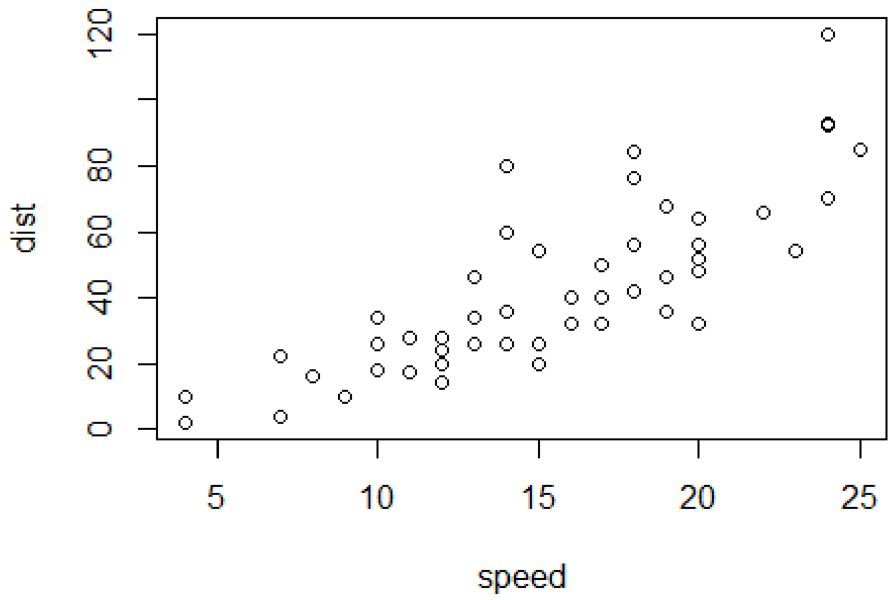

```
##   speed dist
## 1     4    2
## 2     4   10
## 3     7    4
## 4     7   22
## 5     8   16
## 6     9   10
```

```
# All ggplots have at least 3 layers
# data + aes + geoms

ggplot(data=cars) +
  aes(x=speed, y=dist) +
  geom_point()+
# Side-Note: geom_line()+ draws lines connecting data points
  geom_smooth(method="lm")+
  labs(title="Stopping Distance of Old Cars",
    x="Speed(MPH)",
    y="Stopping Distance (ft)")
```

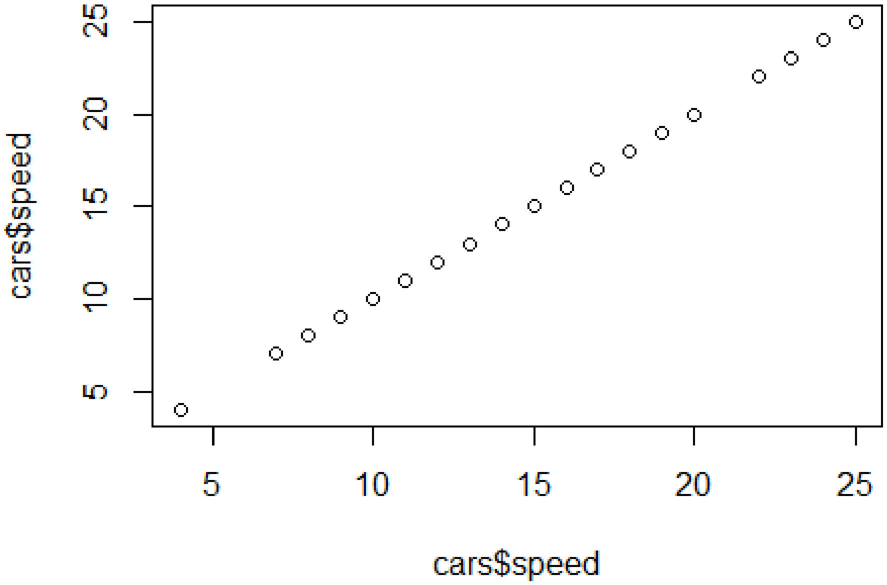
```
## `geom_smooth()` using formula 'y ~ x'
```



```
# Side-Note: ggplot is not the only graphics system
# A very popular is a good old "base" R graphics
plot(cars)
```

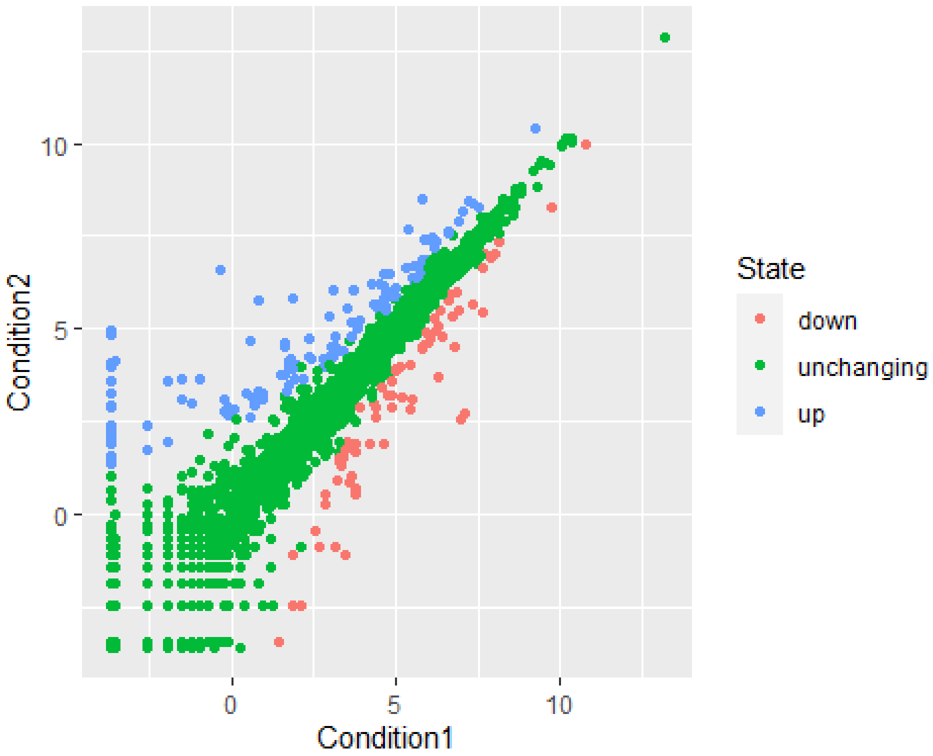


```
plot(cars$speed, cars$speed)
```

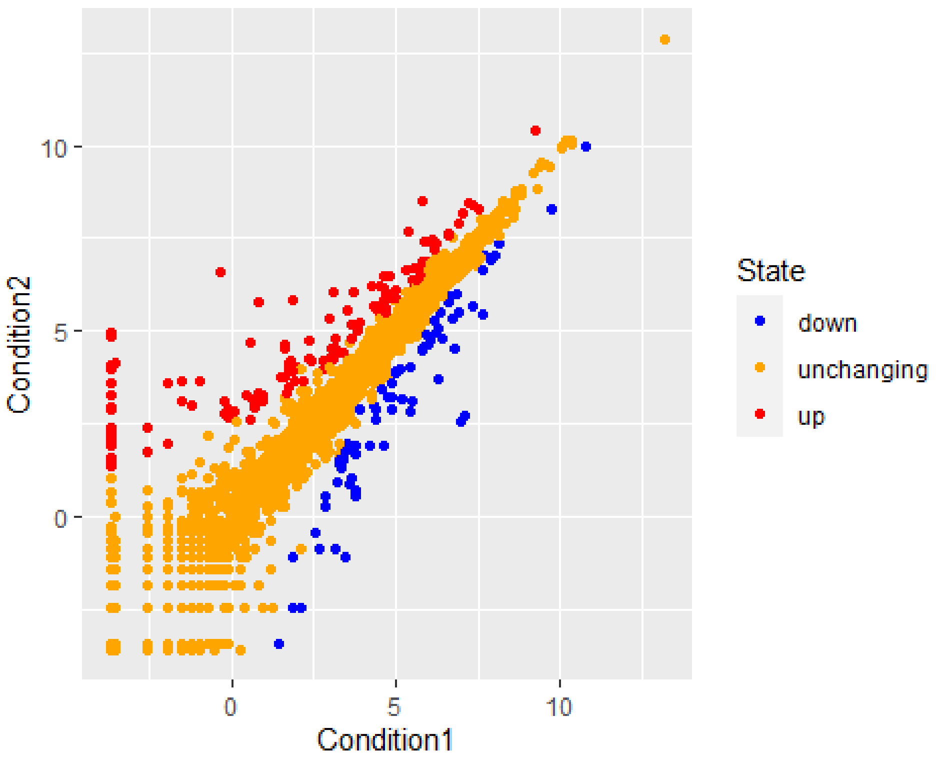


```
url <- "https://bioboot.github.io/bimm143_S20/class-material/up_down_expressi
on.txt"
genes <- read.delim(url)
head(genes)

##         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

# Q1.how many genes are in this dataset?
nrow(genes)

## [1] 5196

# Q2. how many genes are "up"?
# this function list all genes: genes$State
table(genes$State)

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

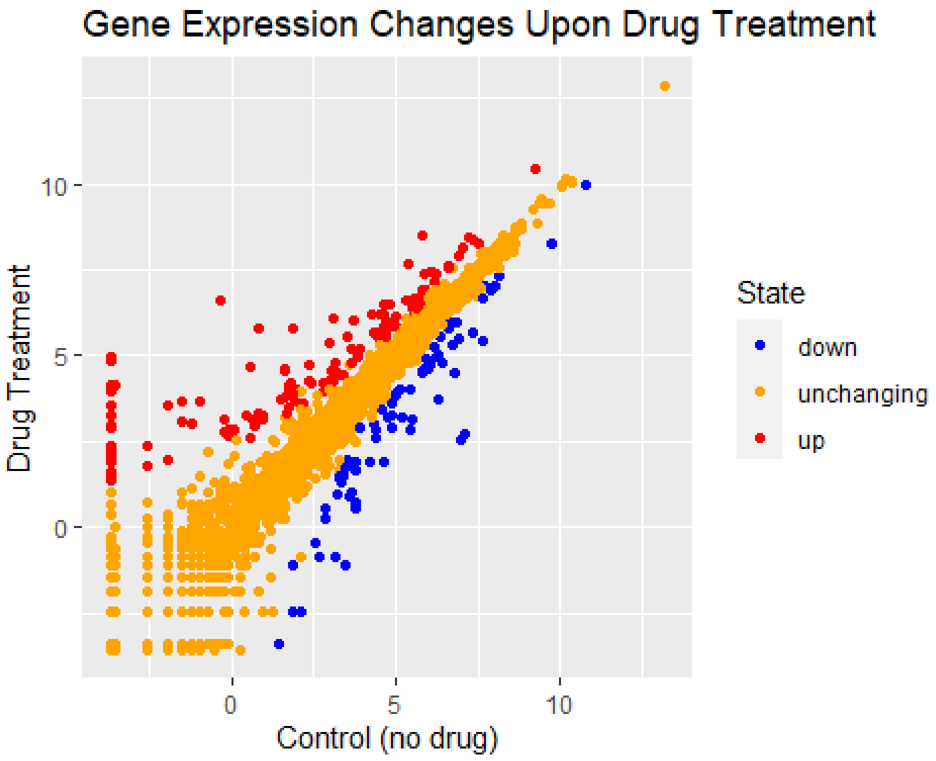
```r
# Q3. What % are up?
# this updates as data updates, adding sig-figs is the #3
# round=rounding up percentage
round(table(genes$State)/nrow(genes)*100,2)

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

# Lets make a figure
# Sates are the down/up/unchanging gene expressions
p <- ggplot(genes) +
  aes(x=Condition1, y=Condition2, col=State) +
  geom_point()

p
```



```r
# I like it but not the default colors, lets change them
# reminder to re-assign p in orde to keep the color change
p <- p + scale_colour_manual(values=c("blue", "orange", "red"))
p
```



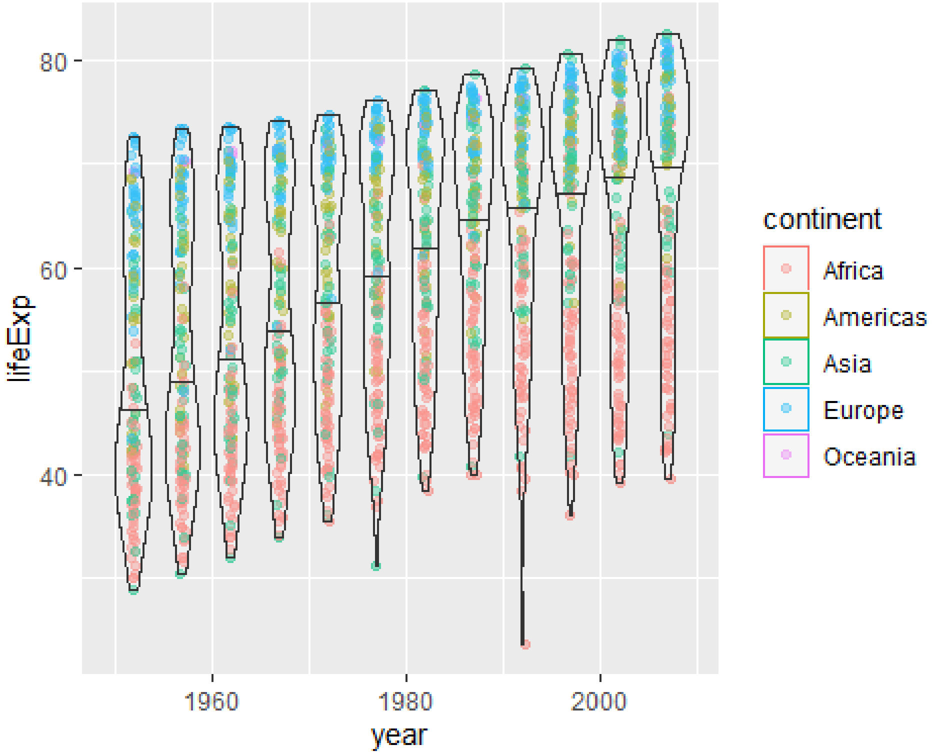
```
# Changing the main title and titles of the X and Y axis
p + labs(title="Gene Expression Changes Upon Drug Treatment", x="Control (no
drug)", y="Drug Treatment")
```



```
# Lets explore the gapminder dataset
# install.packages("gapminder")
library(gapminder)
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.
## 2 Afghanistan Asia       1957    30.3  9240934      821.
## 3 Afghanistan Asia       1962    32.0 10267083      853.
## 4 Afghanistan Asia       1967    34.0 11537966      836.
## 5 Afghanistan Asia       1972    36.1 13079460      740.
## 6 Afghanistan Asia       1977    38.4 14880372      786.
```

```
# Lets make a new plot of year vs lifeExp
# running first 2 lines just displays plot layout
# alpha is transparency
# reminder "aes" aesthetics
ggplot(gapminder) +
  aes(x=year, y=lifeExp, col=continent) +
  geom_jitter(width=0.3, alpha=0.4) +
#  geom_boxplot(aes(group=year), alpha=0.4)
# mean line = quantiles
  geom_violin(aes(group=year),alpha=0.2,
              draw_quantiles = 0.5)
```



```
# Install the plotly
# install.packages("plotly")
# plotly is an interactive plot function (AMAZING!)
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

# adding (#) to ggplotly to be able to save as PDF
# ggplotly()
```