Class 05: Data Visualization with GGPLOT

Aishwarya

Our first ggplot

To use the ggplot2 package I first need to have it installed on my computer.

To install packages we use the `install.packages()` command.

Now can I use it? NO! First need to call `library(ggplot2)`

```
library(ggplot2)
ggplot()
```

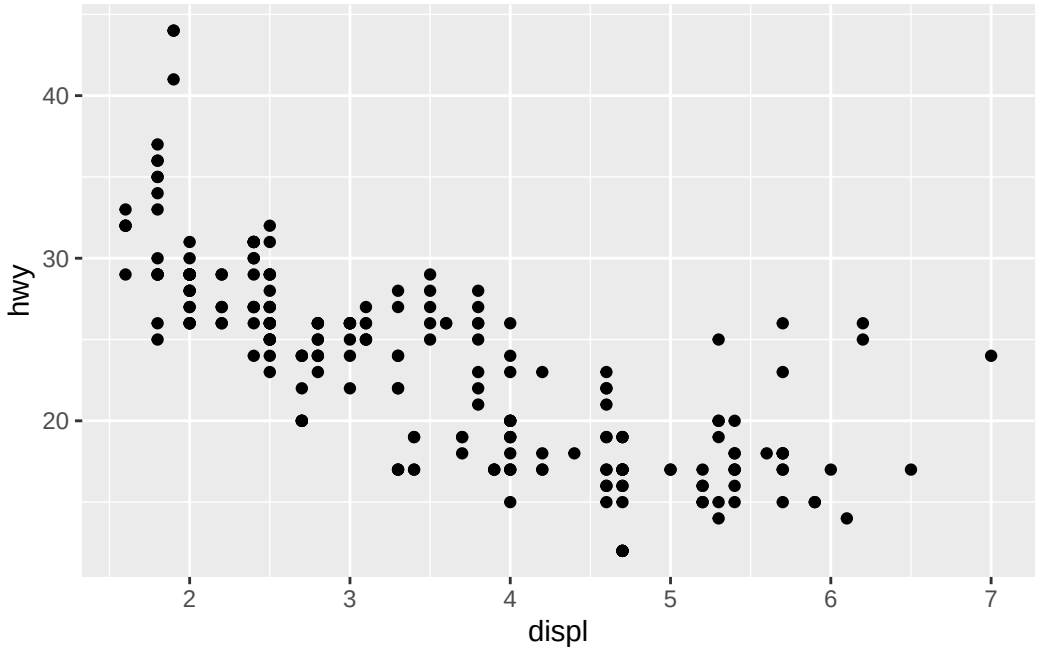
```
mpg
```

```
# A tibble: 234 x 11
   manufacturer model      displ  year   cyl trans drv     cty   hwy fl    class
   <chr>        <chr>      <dbl> <int> <int> <chr> <chr> <int> <int> <chr> <chr>
 1 audi         a4           1.8  1999     4 auto~ f        18    29 p     comp~
 2 audi         a4           1.8  1999     4 manu~ f        21    29 p     comp~
 3 audi         a4           2    2008     4 manu~ f        20    31 p     comp~
 4 audi         a4           2    2008     4 auto~ f        21    30 p     comp~
 5 audi         a4           2.8  1999     6 auto~ f        16    26 p     comp~
 6 audi         a4           2.8  1999     6 manu~ f        18    26 p     comp~
 7 audi         a4           3.1  2008     6 auto~ f        18    27 p     comp~
 8 audi         a4 quattro   1.8  1999     4 manu~ 4        18    26 p     comp~
 9 audi         a4 quattro   1.8  1999     4 auto~ 4        16    25 p     comp~
10 audi         a4 quattro   2    2008     4 manu~ 4        20    28 p     comp~
# ... with 224 more rows
```

Our first plot of displ vs hwy All ggplot() graphs are made in the same way:

- data + aes + geoms

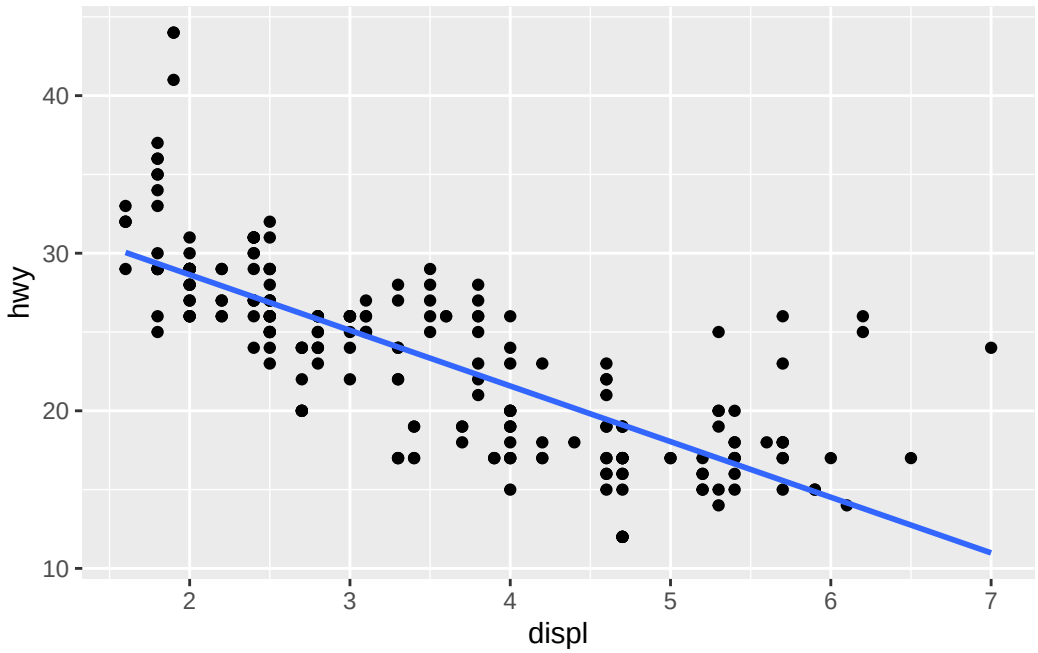
```
ggplot(mpg) +
  aes(x=displ, y=hwy) +
  geom_point()
```



I can add more layers

```
ggplot(mpg) +
  aes(x=displ, y=hwy) +
  geom_point() +
  geom_smooth(method=lm, se=FALSE)
```

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



Plot of gene expression data

First read the data from online.

```
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
```

Q. How many genes are in this dataset?

```
nrow(genes)
```

```
[1] 5196
```

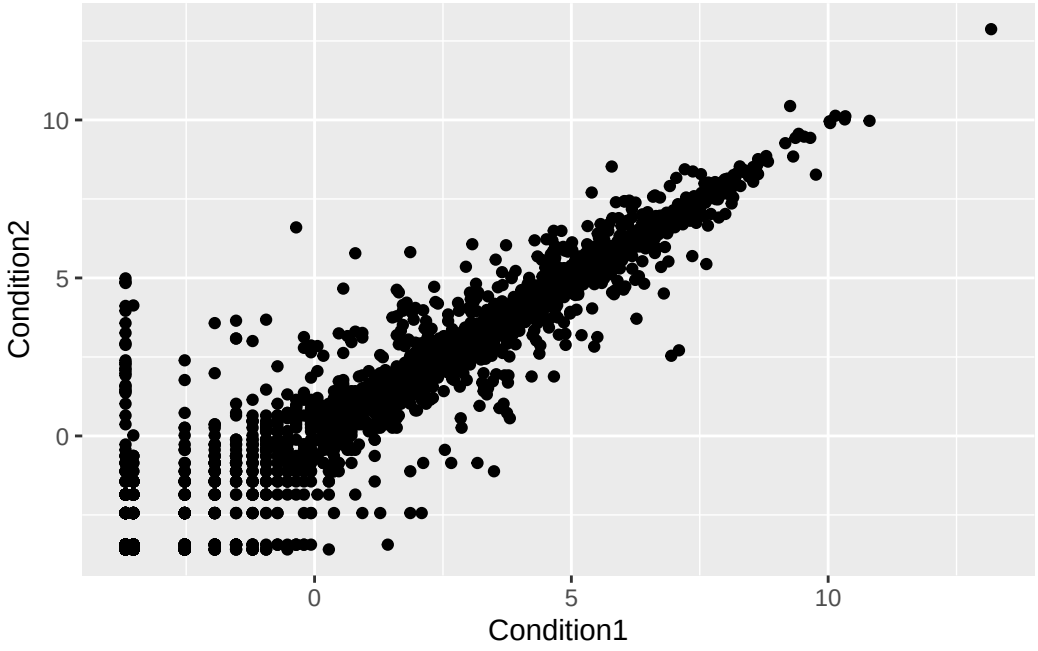
What are the colnames?

```
colnames(genes)
```

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

Creating a scatterplot of Condition1 and Condition2:

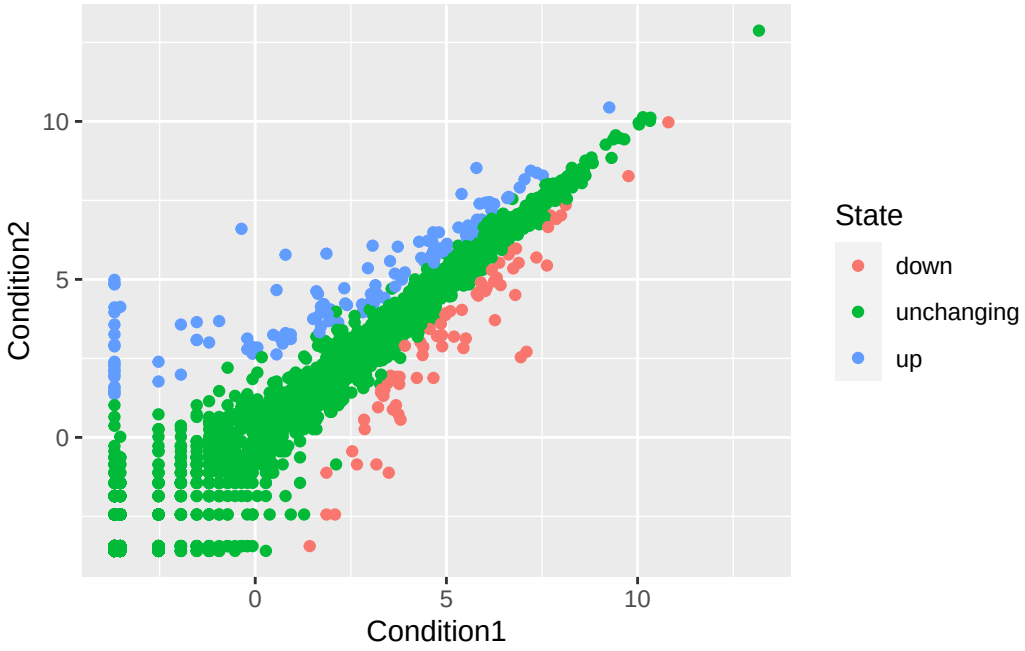
```
ggplot(genes) +
  aes(x=Condition1, y=Condition2) +
  geom_point() #+
```




```
  #geom_smooth(method=lm, se=FALSE)
```

Adding color now:

```
p <- ggplot(genes) +
  aes(x=Condition1, y=Condition2, col=State) +
  geom_point()
p
```



Q: How many genes are up regulated and down regulated?

```
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
```

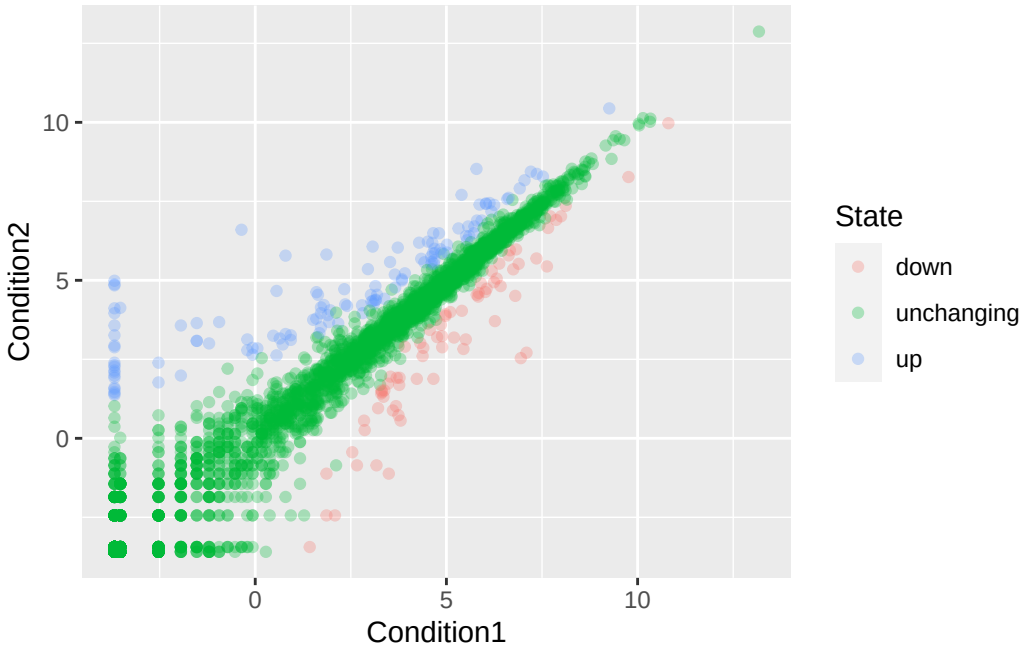
To get at just the State column

```
table(genes$State)
```

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

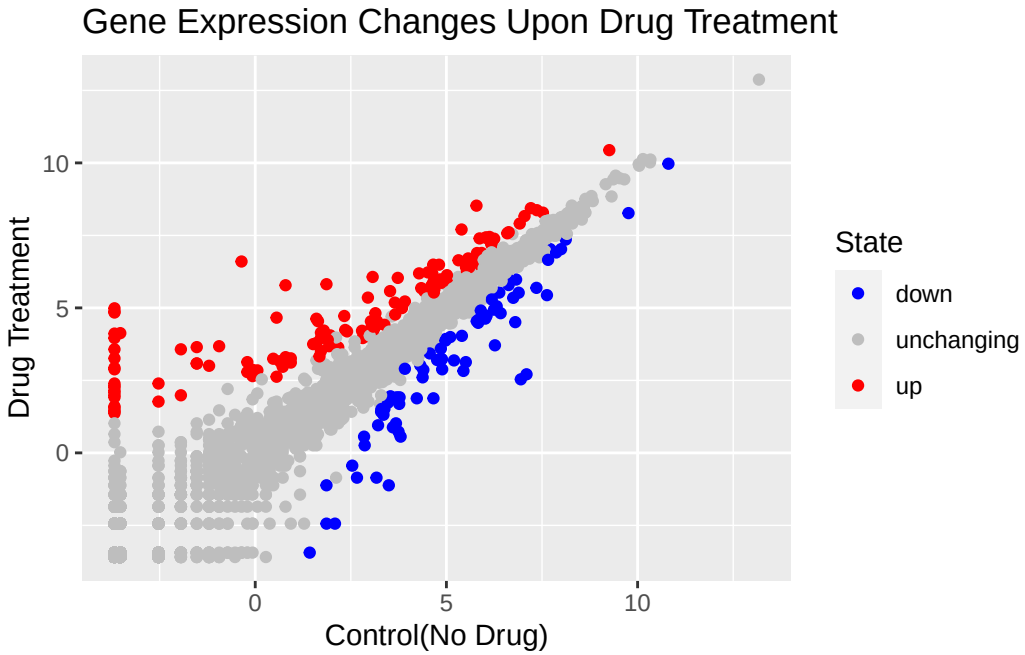
Another plot

```
q <- ggplot(genes) +
  aes(x=Condition1, y=Condition2, col=State) +
  geom_point(alpha=0.3)
q
```



Making plot more colorful:

```
p <- p + scale_colour_manual( values=c("blue","gray","red") ) + labs(title='Gene Expressio
p
```


Gene Expression Changes Upon Drug Treatment
Drug Treatment
10
5
0
0
5
10
Control(No Drug)
State
down
unchanging
up