Class05: Data Visualization with GGPLOT

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#Our first ggplot

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

To install nay package we use the 'install.packages()' command.

Now can I use it? No! first we need to call 'library(ggplot2)'

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



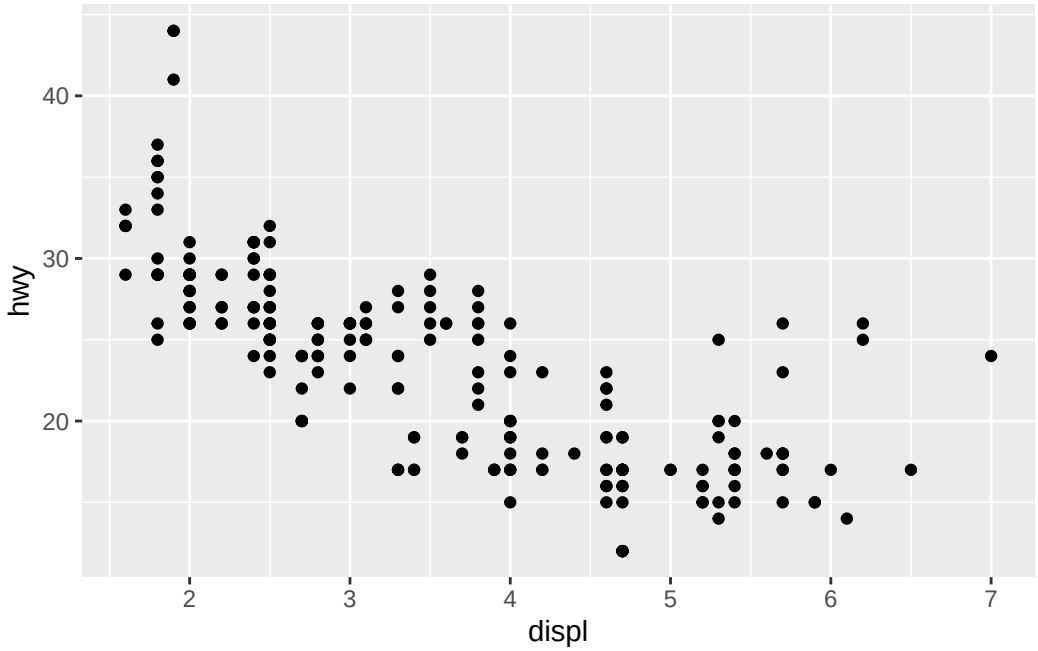
```
mpg
```

```
# 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

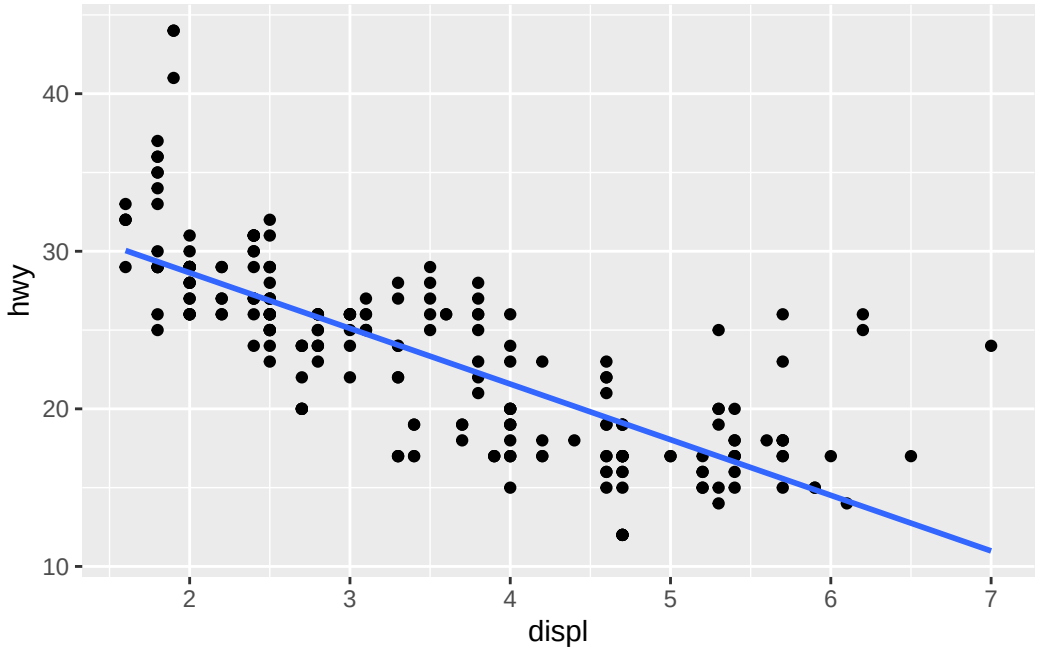
```
ggplot(mpg) +
  aes(x=displ, y=hwy) +
  geom_point()
```



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
```

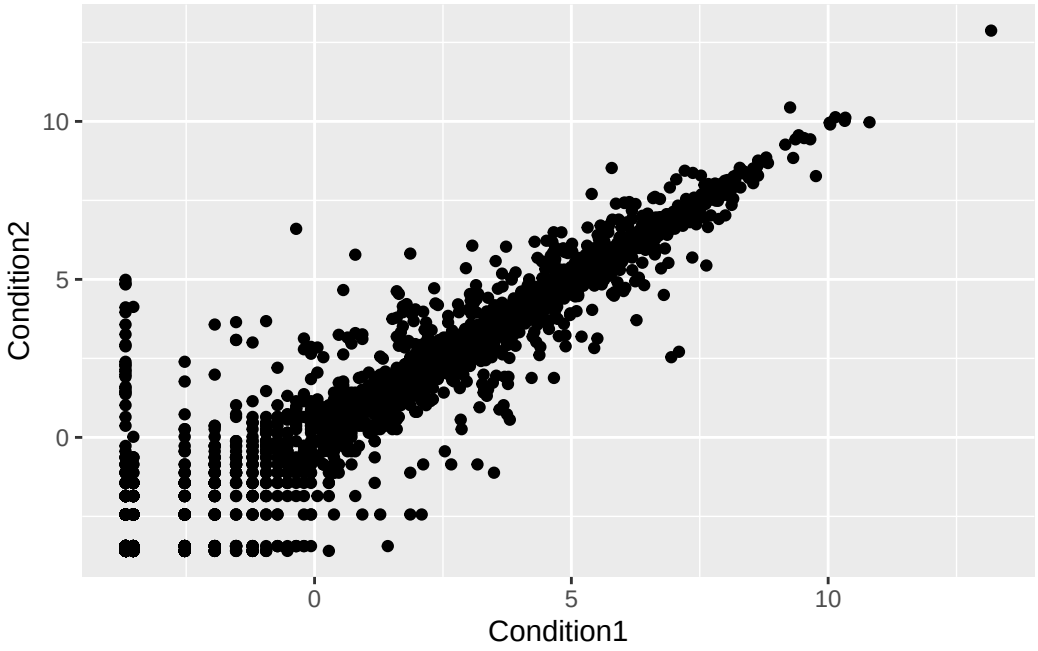
What are the colnames?

```
colnames(genes)
```

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

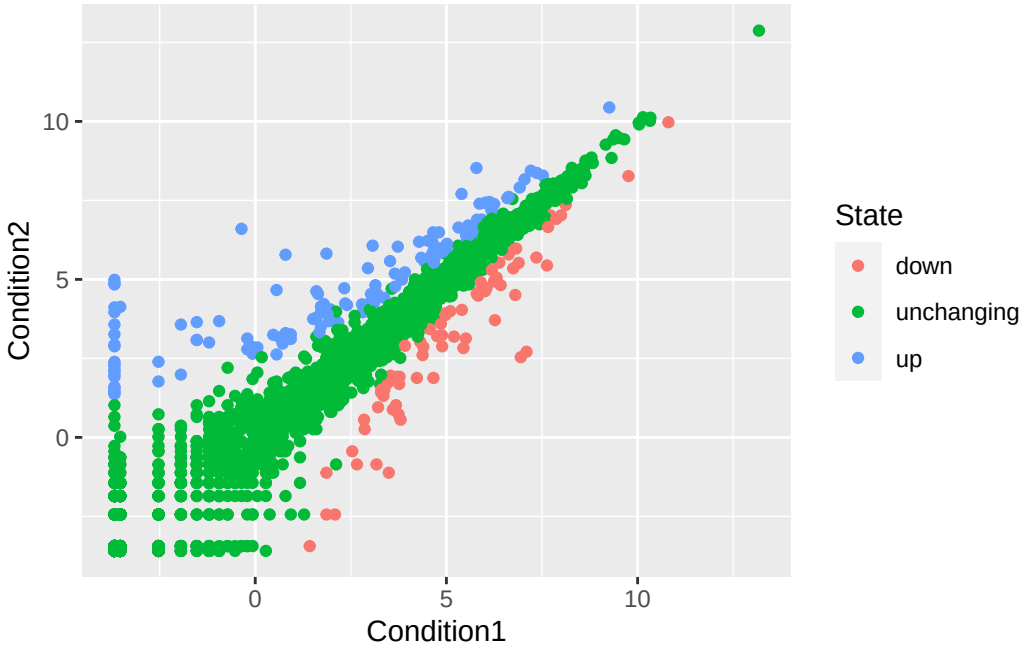
A first version plot of this data Condition1 vs Condition2

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



Let's add some color. To do this we can add another aes() mapping of color to the 'State' column in our data.

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



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
```

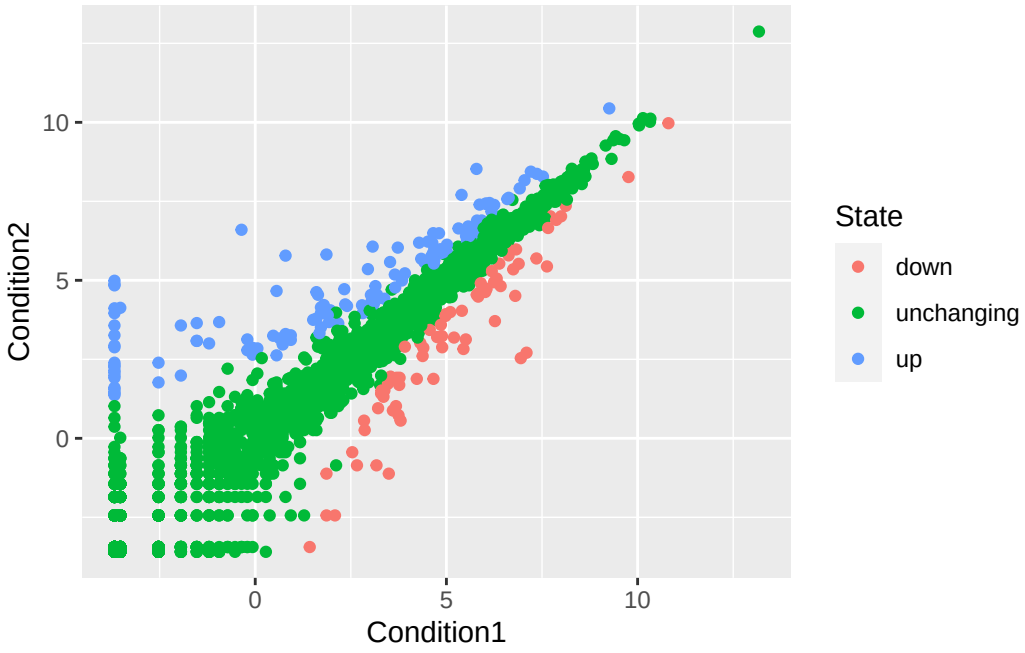
To get at just the State column

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

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

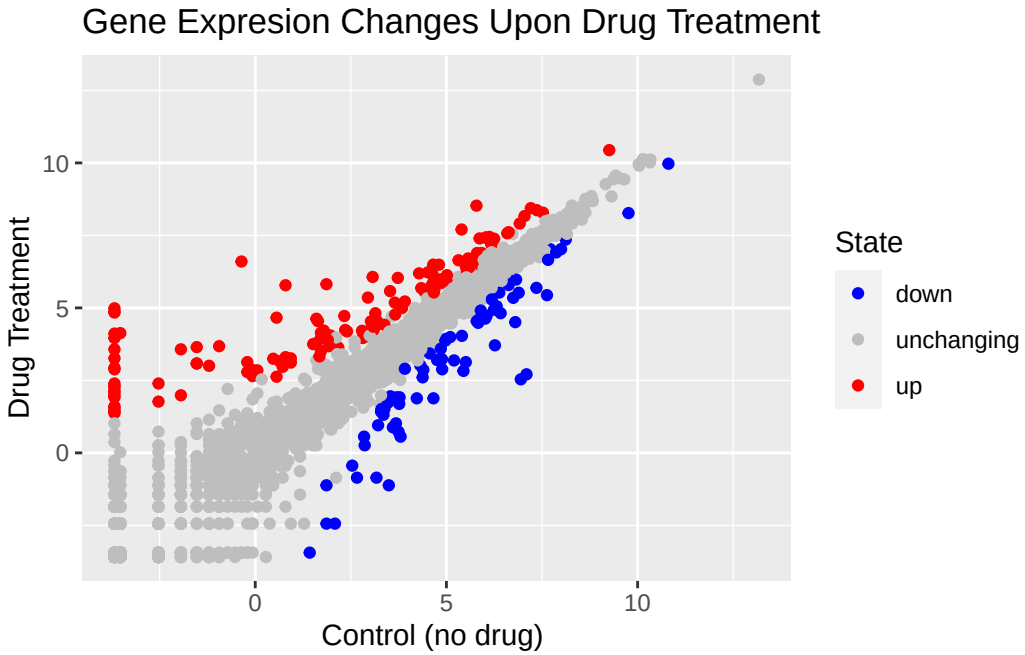
Save our plot as the object 'p' to use it to add more layers

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



Then just add to our object 'p'

```
p + scale_colour_manual(values=c("blue","gray","red")) +
    labs(title="Gene Expresion Changes Upon Drug Treatment",
         x="Control (no drug) ",
         y="Drug Treatment")
```


Gene Expresion Changes Upon Drug Treatment
Drug Treatment
10
5
0
0
5
10
Control (no drug)
State
down
unchanging
up