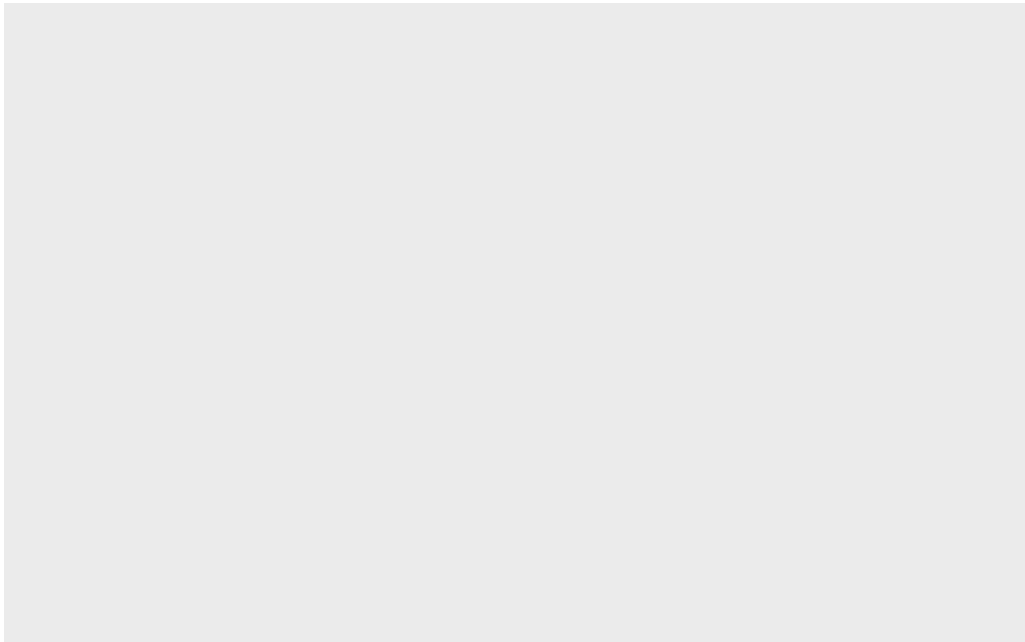# Class 05: Data Visualization with GGPLOT

Forrest Wang

```
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
```
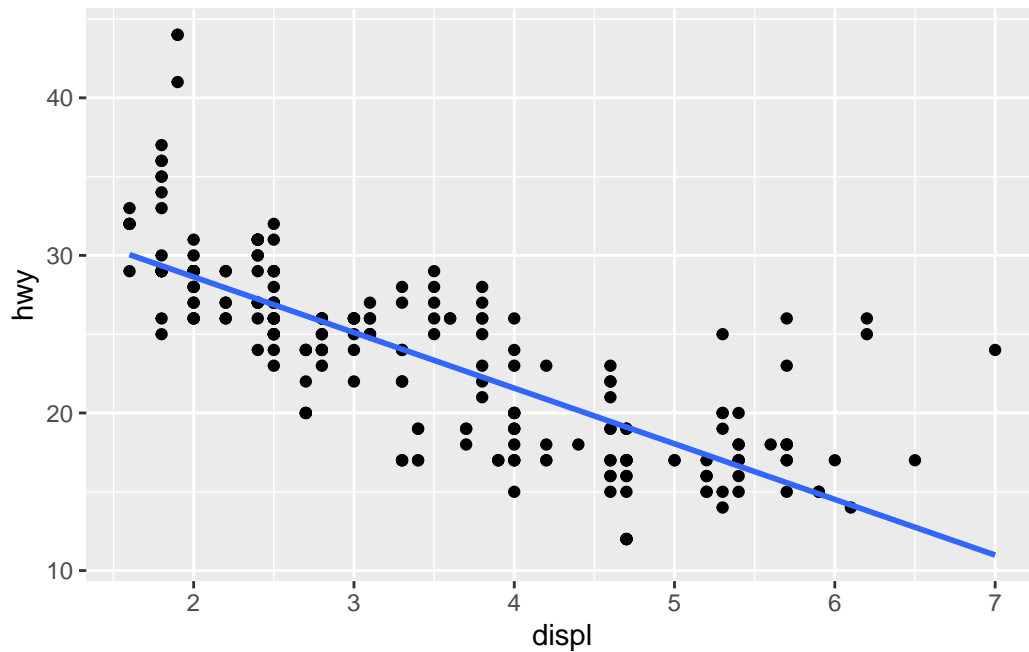
Our fist plot of displ vs hwy All ggplot() graphs are made in the same way. data + aes + geoms

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

How many genes are in the dataset?

```
nrow(genes)
```

```
[1] 5196
```
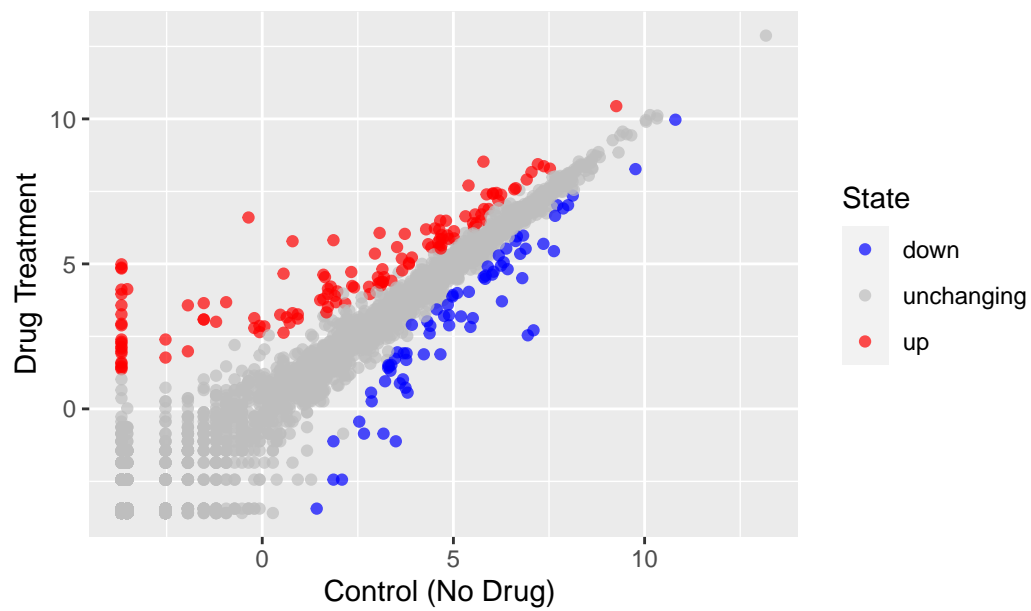
Whata re the colnames?

```
colnames(genes)
```

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

A first version of this data Condition1 vs Condition2

```
p <- ggplot(genes) +
  aes(x=Condition1, y=Condition2, color=State) +
  geom_point(alpha=0.7)
p + scale_colour_manual(values=c("blue","gray","red")) +
    labs(title="Gene Expression Changes Upon Drug Treatment", x="Control (No Drug) ", y="D
```

Gene Expression Changes Upon Drug Treatment

To get a just the state columne:

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

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