Class 5 Data Visualization GGPLOT

Varun Durai

Our first ggplot

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

To install any package we use the `install.package()` command.

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

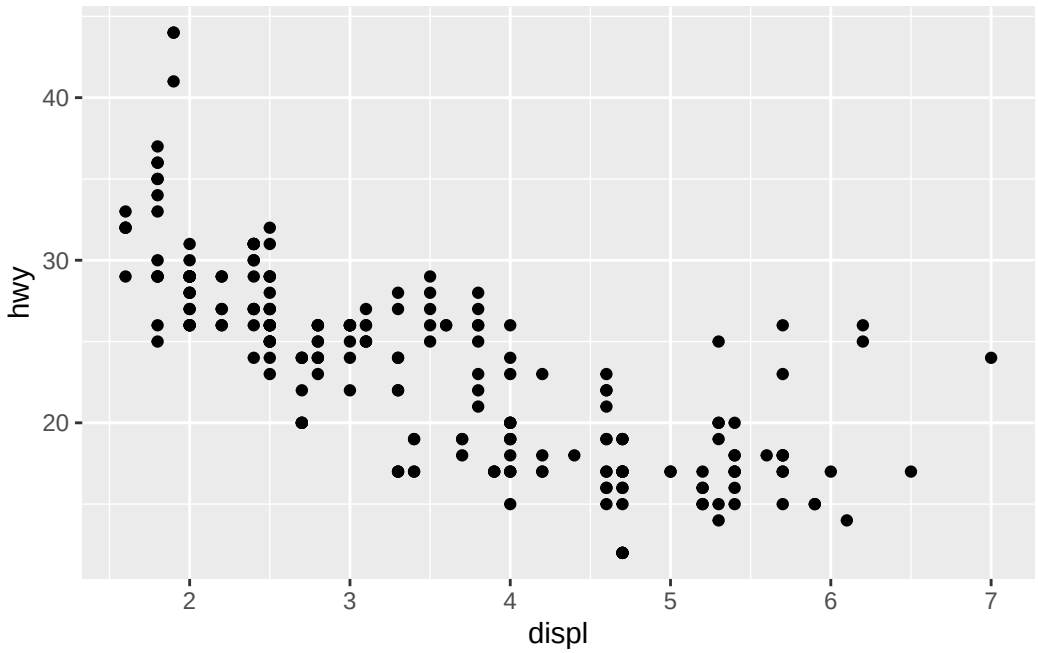
```
library(ggplot2)
ggplot()
```

```
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
```

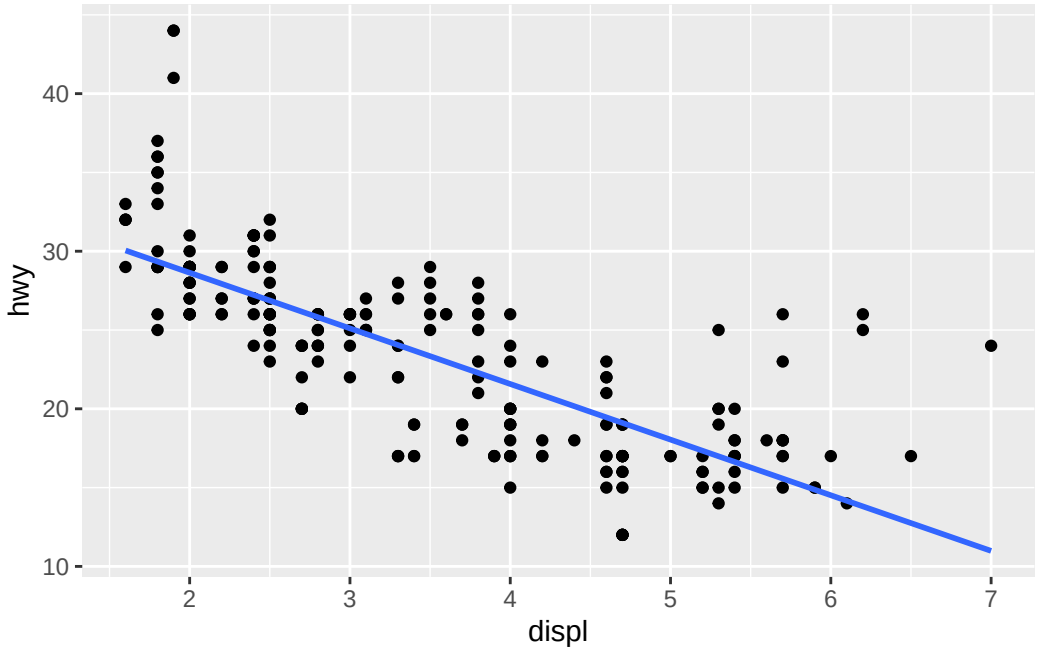
Our first plot of displ vs hwy All ggplot() graphs are made in the same way: data + aes + geoms

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




```
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 may genes are in this dataset?

```
nrow(genes)
```

```
[1] 5196
```

What are the column names?

```
colnames(genes)
```

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

```
ncol(genes)
```

```
[1] 4
```

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

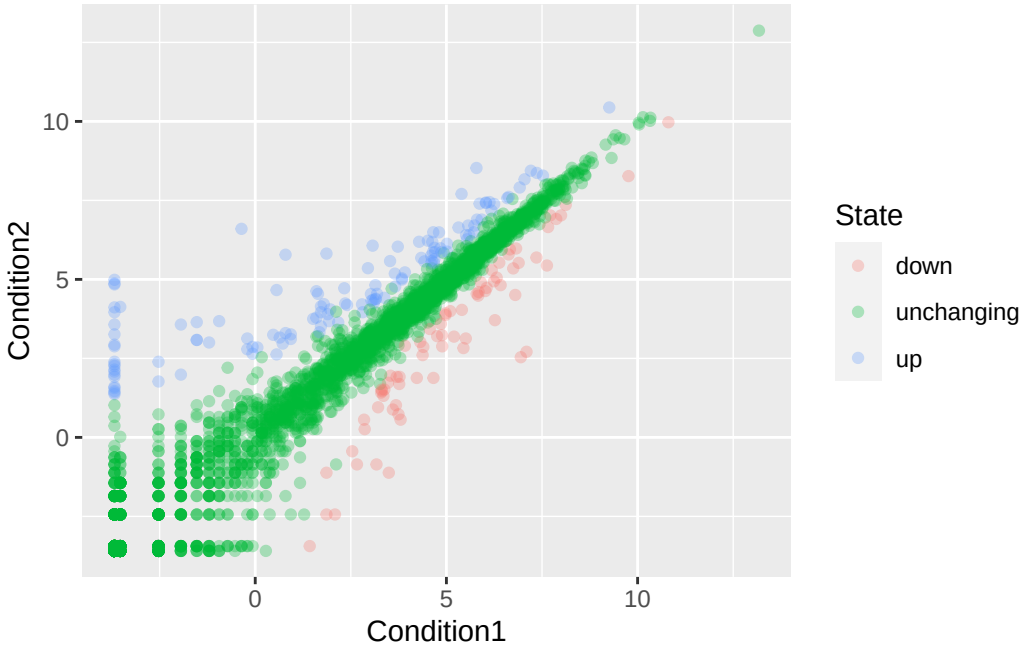
```
      down unchanging         up
        72       4997        127
```

```
127/5196 * 100
```

```
[1] 2.444188
```

A first version plot of this data Condition1 vs Condition2

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



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

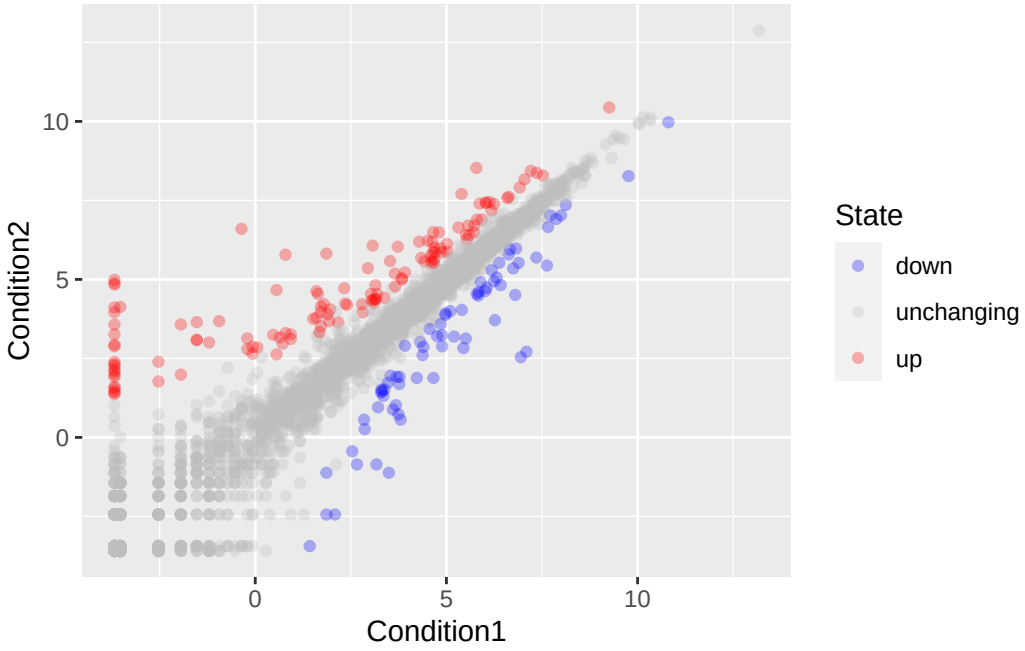
```
head(genes)
```

```
        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
```

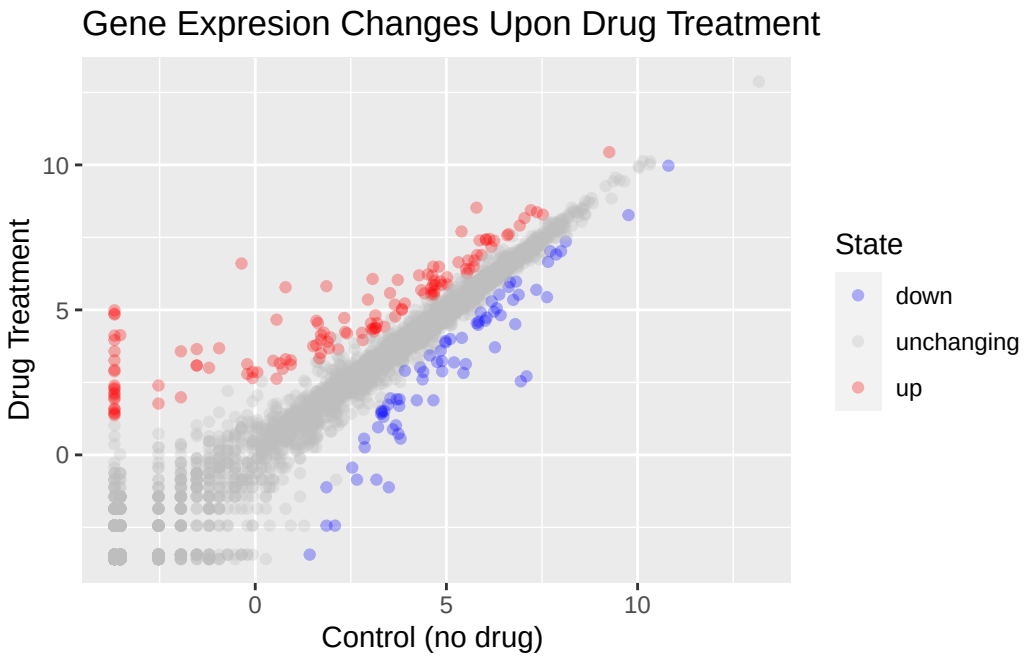
```
table(genes$State)
```

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

```
p <- p + scale_colour_manual( values=c("blue","gray","red") )
p
```




```
p + labs(title="Gene Expresion Changes Upon Drug Treatment",
         x="Control (no drug) ",
         y="Drug Treatment")
```



Going Further

```
url <- "https://raw.githubusercontent.com/jennybc/gapminder/master/inst/extdata/gapminder.

gapminder <- read.delim(url)
library(dplyr)
```

```
Attaching package: 'dplyr'

The following objects are masked from 'package:stats':

    filter, lag

The following objects are masked from 'package:base':

    intersect, setdiff, setequal, union
```

```r
gapminder_2007 <- gapminder %>% filter(year==2007)

ggplot(gapminder_2007) +
  aes(x = gdpPercap, y = lifeExp, color = continent, size = pop) +
  geom_point(alpha = 0.5)
```