Lab 5 Exercises

Jonathan Zau

Genes Dataset Exploration

```
genes = read.delim("https://bioboot.github.io/bimm143_S20/class-material/up_down_expression.t
head(genes, 20) # display first 20 rows
```

```
        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
7       ABCA7  3.4484220  3.8266509 unchanging
8    ABCA9-AS1 -3.6808610 -3.5921390 unchanging
9      ABCC11 -3.5288580 -1.8551732 unchanging
10      ABCC3  0.9305738  3.2603040         up
11      ABCC5  4.6004252  5.4994435         up
12   ABCC5-AS1 -3.6808610 -3.4401355 unchanging
13     ABCC6P1 -0.7215031 -0.2702107 unchanging
14      ABCD1  2.6805956  3.3800430 unchanging
15     ABHD11  4.4136560  3.9521816 unchanging
16     ABI3BP -1.2069298 -3.5921390 unchanging
17       ABL1  6.3583620  6.0814650 unchanging
18     ABLIM2 -1.9438953 -1.1182077 unchanging
19        ABO -3.6808610 -3.5921390 unchanging
20       ABP1 -3.6808610 -3.5921390 unchanging
```

```
nrow(genes) # display how many rows (i.e. genes) are in this dataset
```

```
[1] 5196
```

```
ncol(genes) # display how many columns (i.e. data points) are in this dataset
```

```
[1] 4
```

```
colnames(genes) # display the names of the columns (i.e. data points)
```

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

```
table(genes$State) # Displays number of each unique value in the "State" column
```

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

```
table(genes$State)/nrow(genes) # Calculates fraction of all genes that are upregulated, down
```

```
      down unchanging         up
0.01385681 0.96170131 0.02444188
```

Plotting Genes Dataset

```
library(ggplot2) # Dont forget to call ggplot2 first!
ggplot(data = genes, mapping = aes(x = Condition1, y = Condition2, col = State))+
  geom_point()+ # Plots data as points
  scale_color_manual(values = c("blue", "gray", "red"))+ # Changes color for levels in the da
  labs(
    title = "Gene Expression Changes Upon Drug Treatment",
    x = "Control (no drug)",
    y = "Drug Treatment")
```

Gene Expression Changes Upon Drug Treatment
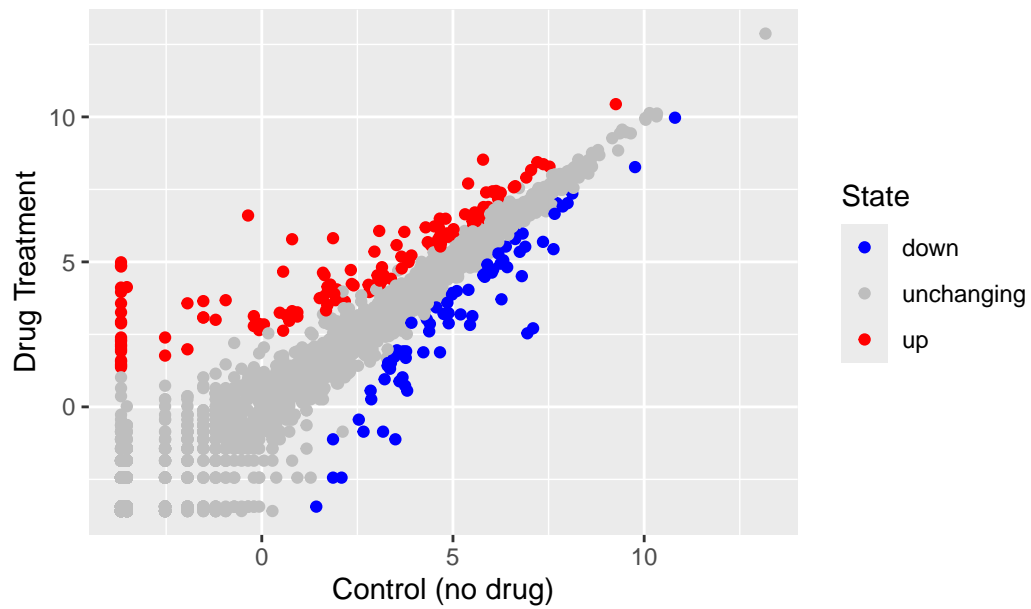

```
ggsave("genes.pdf")
```

```
Saving 5.5 x 3.5 in image
```