

# **Class 05: Data Visualization with GGLOT**

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## **Week 4 Data Visualization Lab**

### **Install the package ggplot2**

**`install.packages("ggplot2")`**

### **Anytime I want to use this package I need to load it**

`library(ggplot2)`

`View(cars)`

### **A quick base R plot - this is not a ggplot2**

`plot(cars)`

### **Our first ggplot**

### **We need data + aes + geoms**

`ggplot(data=cars) + aes(x=speed, y=dist) + geom_point()`

`p <- ggplot(data=cars) + aes(x=speed, y=dist) + geom_point()`

## Add a line geom with geom\_line()

```
p + geom_line()
```

## Add a trend line close to the data

```
p + geom_smooth()
```

```
p + geom_smooth(method= "lm")
```

```
#—————#
```

## Read in our drug expression data

```
url <- "https://bioboot.github.io/bimm143_S20/class-material/up_down_expression.txt"
genes <- read.delim(url) head(genes)
```

## Q. How many genes are in this dataset

```
nrow(genes)
```

```
ncol(genes)
```

## Q. how many 'up' regulated genes

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

## Q. What fraction of genes is up-regulated

```
round((table(genes$State) / nrow(genes)) * 100, 2)
```

## Let's make a first plot attempt

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

## Add some color

```
g + scale_color_manual(values=c("blue", "gray", "red")) + labs(title = "Gene Expression  
changes", x = "Control (no drug)") + theme_bw()
```