

Week 5 Data Visualization Lab

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Install ggplot2 package

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

***Any time I want to use**

this package I need to load it!*

```
library(ggplot2)
```

View Cars data

```
View(cars)
```

Plot Cars data (base R plot)

```
plot(cars)
```

ggplot graph

We need data + aes + geoms

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

Saves in p

```
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 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)
```

Questions for gene analysis

Q. How many genes are in this dataset?

```
nrow(genes)
```

Q. Column names and number of rows?

```
ncol(genes) colnames(genes)
```

Q. How many up regulated genes there are?

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

Q. Fraction of genes up-regulated (2 SF)

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

First plot attempt!

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

Add some color

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