

class05

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```
View(cars)
```

```
install.packages("ggplot2") library(ggplot2) p <- ggplot(cars) + aes(x=speed, y=dist) +  
geom_point()
```

```
p
```

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

```
url <- "https://bioboot.github.io/bimm143\_S20/class-material/up\_down\_expression.txt"  
genes <- read.delim(url)
```

```
#Look at first 6 lines head(genes)
```

```
View(genes)
```

```
#Q. how many genes are there in the list? nrow(genes)
```

```
#Q. how many genes are upregulated? table(genes$State)
```

```
#Q. What fraction of genes are up, down etc.  
round((table(genes$State)/nrow(genes))*100, 2)
```

```
#Q. Generate a publication figure
```

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

```
g
```

```
#Add more custom layers
```

```
g + theme_bw() + scale_color_manual(values=c("blue", "gray", "red")) + labs(x="Control(no  
drug)", y="Drug treated", title="Gene expression changes example plot")
```