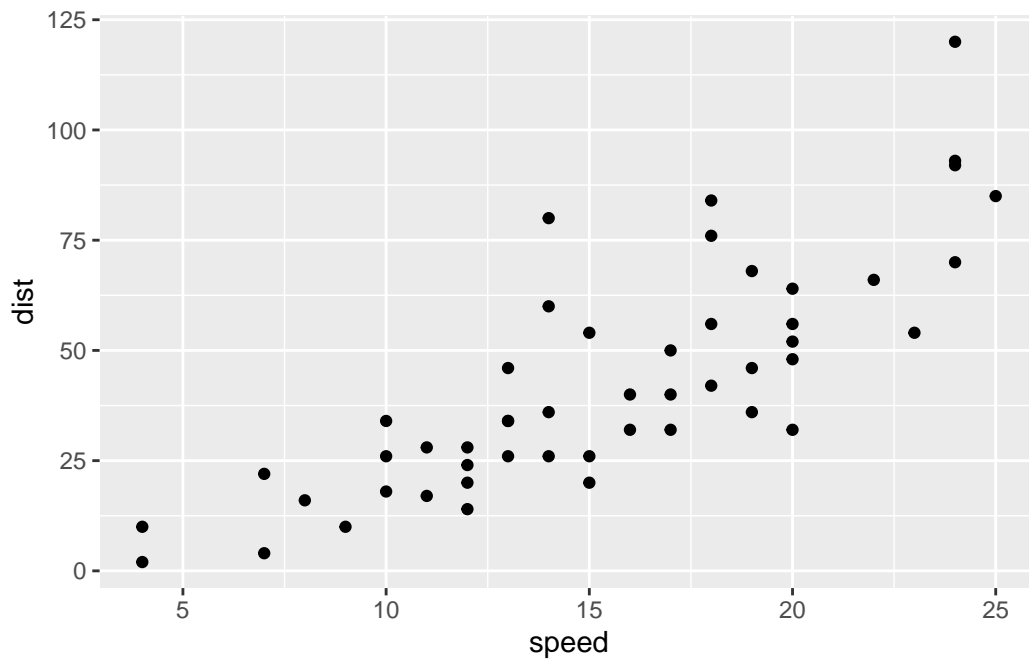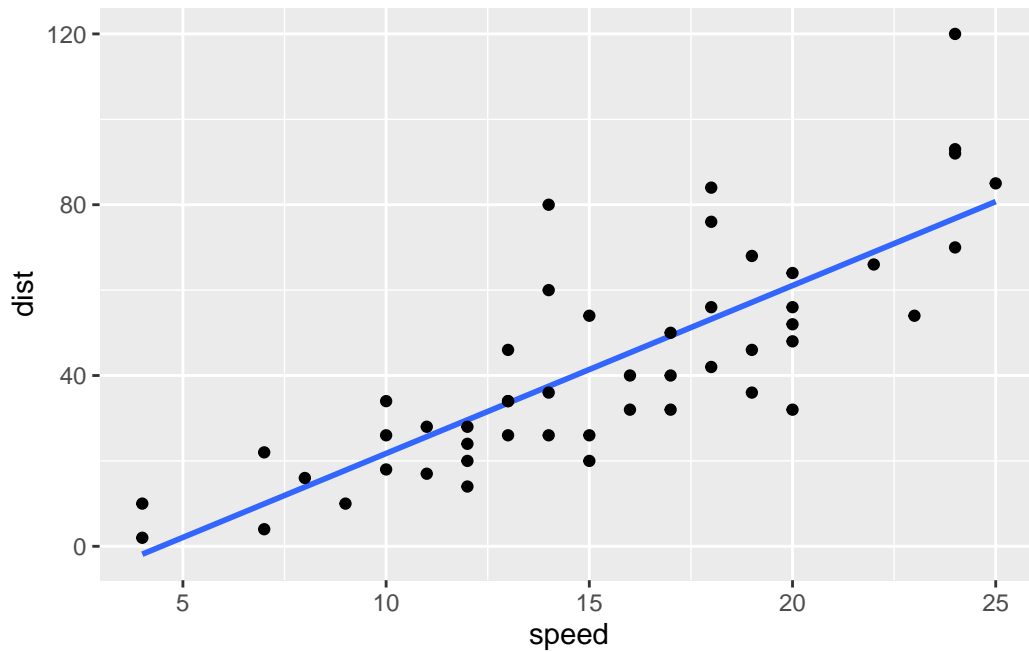# Class 05: Data Visualization with GGPLOT

Jordan Laxa

```r
# Install packages -> install.packages("ggplot2")
# Load packages
library(ggplot2)
```

```r
# Scatterplot of Cars data
ggplot(cars) + aes(x=speed, y=dist) +geom_point()
```



```r
# Cars plot with geom_smooth() and geom_point()
ggplot(cars) + aes(x=speed, y=dist) + geom_smooth(method="lm", se=FALSE) + geom_point()
```

```
`geom_smooth()` using formula = 'y ~ x'
```



```r
# Read an input file
read.delim
```

```
function (file, header = TRUE, sep = "\t", quote = "\"", dec = ".",
    fill = TRUE, comment.char = "", ...)
read.table(file = file, header = header, sep = sep, quote = quote,
    dec = dec, fill = fill, comment.char = comment.char, ...)
<bytecode: 0x000001e0b4025ea0>
<environment: namespace:utils>
```

```r
# Accessing Gene data
url <- "https://bioboot.github.io/bimm143_S20/class-material/up_down_expression.txt"
genes <- read.delim(url)
```

```r
# Plot with custom settings
p <- ggplot(genes) + aes(x=Condition1, y=Condition2, col=State) + geom_point() + scale_col
p
```
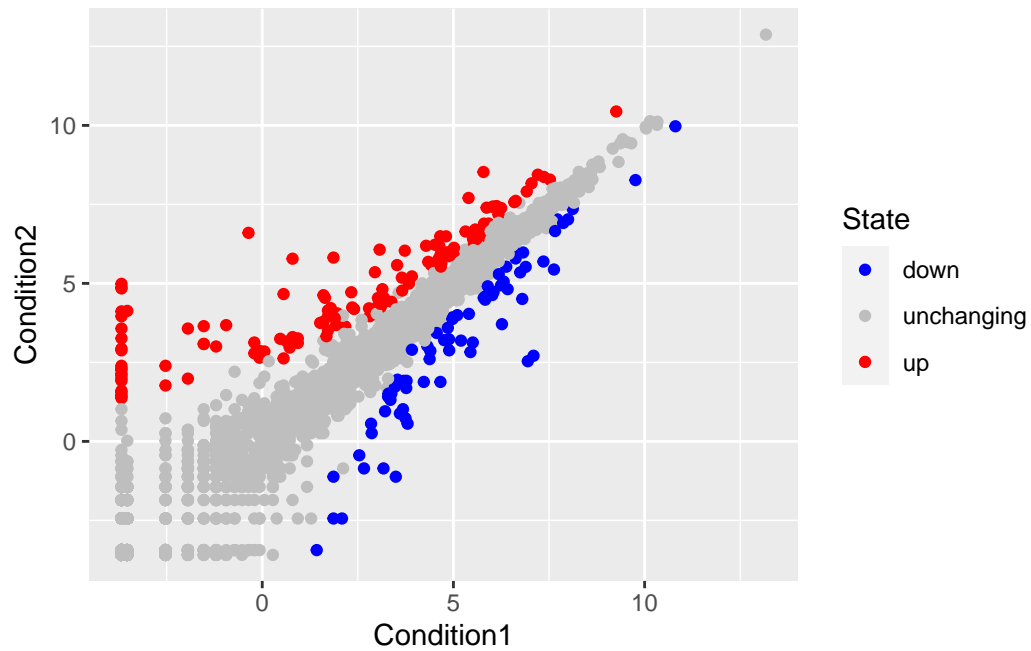
```
# Plot with labs setting
p + labs(title="Gene Expression Changes Upon Drug Treament", x="Control (no drug)", y="Dru
```

Gene Expression Changes Upon Drug Treament