

# class05

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## ggplot Library

Before beginning, the ggplot library must first be loaded into the project environment.

```
#Load ggplot library  
library(ggplot2)
```

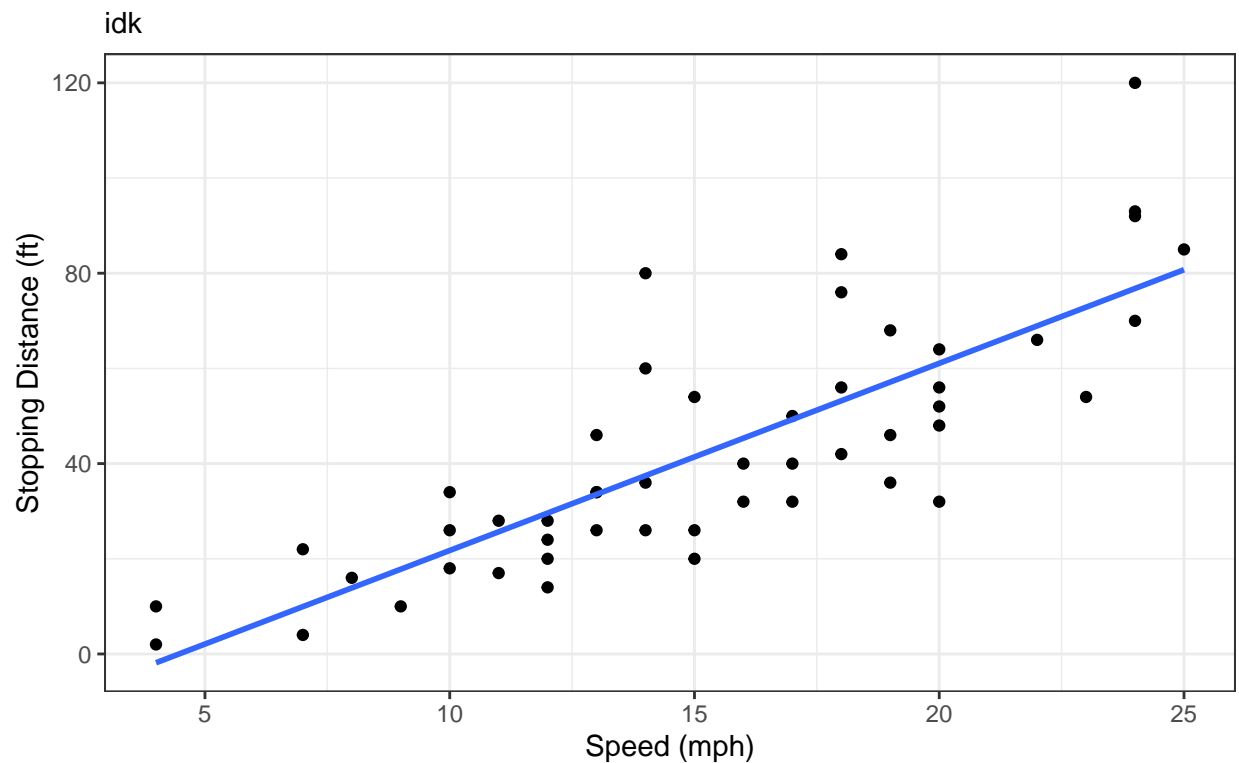
## Using ggplot Layers

In this section, we explored how to construct a ggplot, adding aesthetic and geometric layers, and modifying axis labels / theme.

```
#Plot default cars dataset  
ggplot(cars) +  
  
#Add aesthetic layer w/ axes  
  aes(x = speed, y = dist) +  
  
#Add geometric layer to display points  
  geom_point() +  
  
#Add a trendline  
  geom_smooth(method = "lm", se = FALSE) +  
  
#Add axis labels  
  labs(title = "Speed and Stop Distance in Cars",  
        x = "Speed (mph)",  
        y = "Stopping Distance (ft)",  
        subtitle = "idk",  
        caption = "Dataset: 'cars'") +  
  
#Add conservative black and white theme  
  theme_bw()
```

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

## Speed and Stop Distance in Cars



Dataset: 'cars'

## Exploring Biological Data

In this section, we made calculations based on a large dataset of genes and their reactions to an anti-viral drug. We also plotted this information to further visualize it.

```
#Load in anti-viral drug test data
url <- "https://bioboot.github.io/bimm143_S20/class-material/up_down_expression.txt"
genes <- read.delim(url)
head(genes)
```

```
##      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
```

```
#Find number of genes
nrow(genes)
```

```
## [1] 5196
```

```
#5196 genes
```

```
#Find name/number of columns  
ncol(genes)
```

```
## [1] 4
```

```
colnames(genes)
```

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

```
#4 columns, named "Gene" "Condition 1" "Condition2" "State"
```

```
#Find number of upregulated genes  
table(genes$State)
```

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

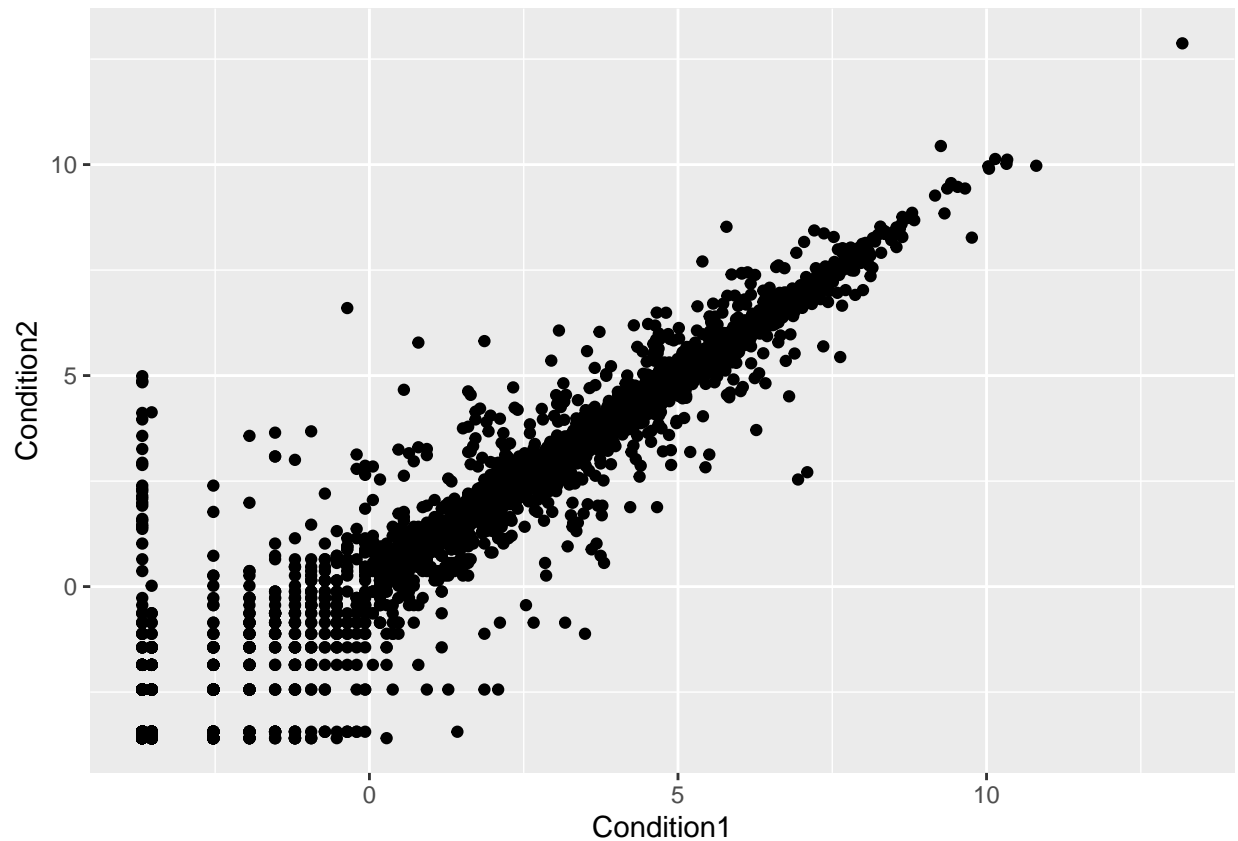
```
#127 genes
```

```
#Find fraction of upregulated genes  
round(table(genes$State)[3] / nrow(genes) * 100, 2)
```

```
## up  
## 2.44
```

```
#2.44%
```

```
#Gene plot  
ggplot(genes) +  
  aes(x = Condition1, y = Condition2) +  
  geom_point()
```



## Combining Plots

Below was the example given for combining multiple plots into one figure.

```
#Combining plots example
library(patchwork)

# Setup some example plots
p1 <- ggplot(mtcars) + geom_point(aes(mpg, disp))
p2 <- ggplot(mtcars) + geom_boxplot(aes(gear, disp, group = gear))
p3 <- ggplot(mtcars) + geom_smooth(aes(disp, qsec))
p4 <- ggplot(mtcars) + geom_bar(aes(carb))

# Use patchwork to combine them here:
(p1 | p2 | p3) /
  p4
```

```
## 'geom_smooth()' using method = 'loess' and formula 'y ~ x'
```

