Class 5: Data visualization with GGPlot

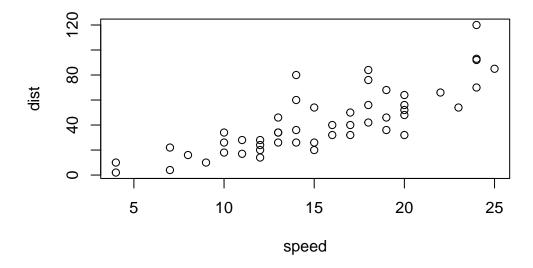
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Base R plotting

We are going to start by generating the plot of class 04. This code is plotting the **cars** dataset: plot(cars)

plot(cars)



Ggplot2

First, we need to install the package (this is a one time thing!)

```
# install.packages('ggplot2')
```

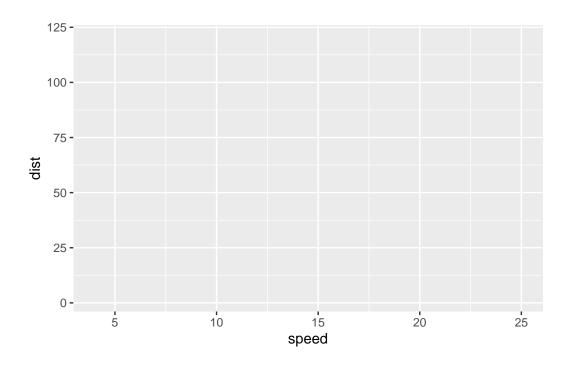
After that, we need to load the package

```
library(ggplot2)
```

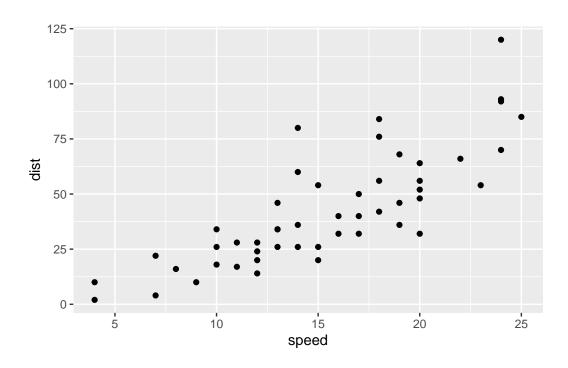
Using the **cars** dataframe, we can generate a scatterplot using ggplot2

```
ggplot(data = cars)
```

```
# add the aesthetics (labeling the x and y axis)
ggplot(data = cars) + aes(x=speed, y=dist)
```

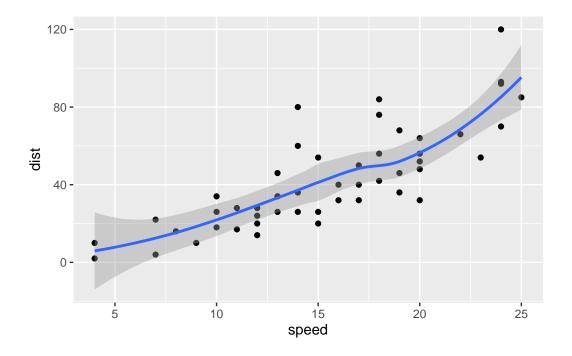


now add the geometry points to generate points in the graph, making sure to leave the ()
ggplot(data = cars) + aes(x=speed, y=dist) + geom_point()



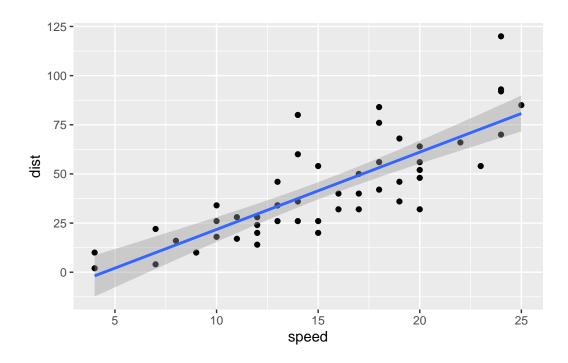
```
# add a trendline
ggplot(data = cars) + aes(x=speed, y=dist) + geom_point() + geom_smooth()
```

 $\ensuremath{\text{`geom_smooth()`}}\ \ensuremath{\text{using method}}\ = \ensuremath{\text{'loess'}}\ \ensuremath{\text{and formula}}\ = \ensuremath{\text{'y}}\ \sim \ensuremath{\text{x'}}$



```
# using geom_smooth(method = 'lm'), this better fits the data
ggplot(data = cars) + aes(x=speed, y=dist) + geom_point() + geom_smooth(method = 'lm')
```

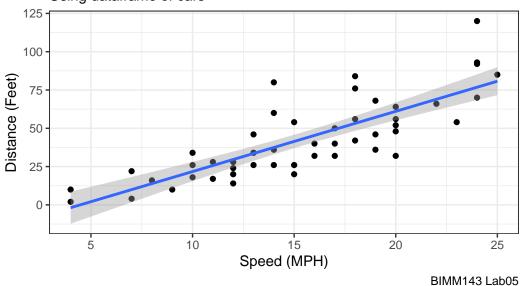
 $geom_smooth() using formula = 'y ~ x'$



```
# polish up the graph by adding labels and changing the theme
ggplot(data = cars) + aes(x=speed, y=dist) + geom_point() + geom_smooth(method = 'lm') + l
```

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

Distance vs. Speed Using dataframe of cars



Q1. For which phases is data visualization important in our scientific workflows?

Communication of Results, Exploratory Data Analysis, Detection of Outliers

All of the above

Q2. True or False? The ggplot2 package comes already installed with R?
False, using the install.packages command, ggplot2 will need to be installed in R
Q3. Which plot types are typically NOT used to compare distributions of numeric variables?
Network graphs

Q4. Which statement about data visualization with ggplot2 is incorrect? ggplot2 is the only way to create plots in R

Q5. Which geometric layer should be used to create scatter plots in ggplot2? geom_point()

Plotting gene expression data

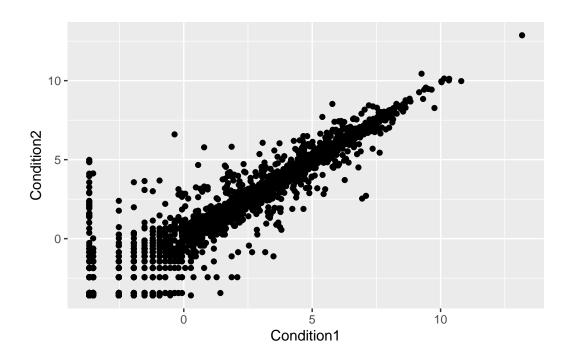
Loading the data from the URL

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

```
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
```

Generate ggplot

```
#an initial ggplot
ggplot(data = genes) + aes(x=Condition1, y=Condition2) + geom_point()
```

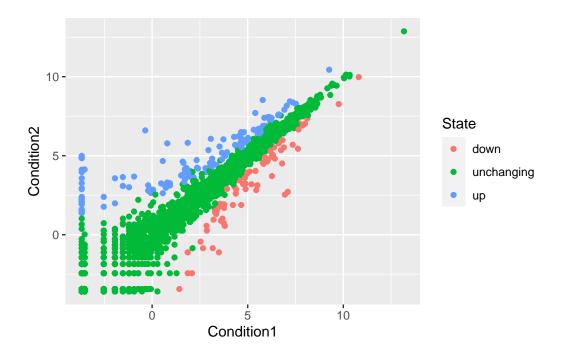


Q6. Use the nrow() function to find out how many genes are in this dataset. What is your answer 5196

- Q7. Use the colnames() function and the ncol() function on the genes data frame to find out what the column names are (we will need these later) and how many columns there are. How many columns did you find? 4
- Q8. Use the table() function on the State column of this data frame to find out how many 'up' regulated genes there are. What is your answer? 127 up regulated genes
- **Q9.** Using your values above and 2 significant figures. What fraction of total genes is upregulated in this dataset? **2.44**

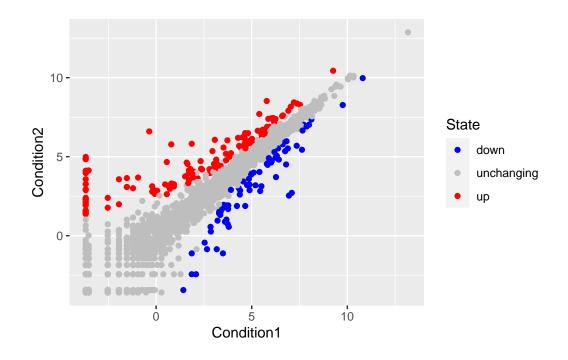
Figuring out the amounts of data in the gene expression data

```
nrow(genes)
[1] 5196
  ncol(genes)
[1] 4
  colnames (genes)
[1] "Gene"
                  "Condition1" "Condition2" "State"
  table(genes[,'State'])
      down unchanging
                               up
        72
                  4997
                              127
Adding color to the plot
  p1 <- ggplot(data = genes) + aes(x=Condition1, y=Condition2, col=State) + geom_point()
  р1
```



Changing the color scheme, adding some labels

```
p2 <- p1 + scale_color_manual(values = c('blue', 'gray', 'red'))
p2</pre>
```



```
\# adding labels p2 + labs(title = 'Differential Gene Expression', <math>x = 'Control (no drug)', y = 'Drug Tream'
```

