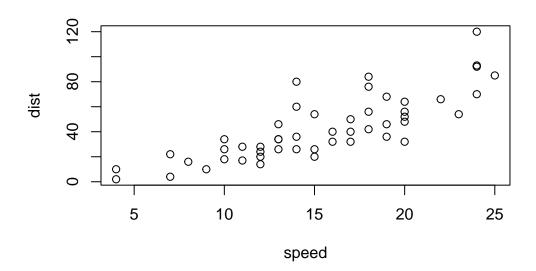
Class 5: Data Viz with ggplot

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Plotting in R

RR has lot's of ways to make plots and figures. This includes so-called **base** graphics and packages like **ggplot**

plot(cars)



This is a base R plot of the in-built cars dataset that has only two columns

head(cars)

```
speed dist
1
             2
            10
2
       4
3
       7
             4
4
       7
            22
5
       8
            16
       9
            10
```

Q. How would we plot this data set with **ggplot2**?

All ggplot figures have at least 3 layers:

-data -aesthetics (how the data map to the plot) - geoms (how we draw the plot, lines, points, etc.)

Before I use any new package I need to download and install it with the install.packages() command.

I never use install.packages() within my quarto document otherwise I will install the package over and over again - which is silly!

Once a package is installed I can load it up with the library() function

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

All the above (Communication of Results, EDA, Detection of Outliers)

Q2. True or False? The ggplot2 package comes already installed with R?

FALSE

Q3. Which plot types are typically NOT used to compare distributions of numeric variables?

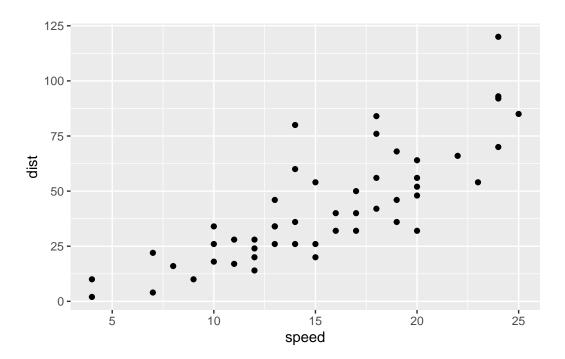
Network Graphs

- 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()

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

Warning: package 'ggplot2' was built under R version 4.3.3

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



Key point: For simple plots (like the one above) ggplot is more verbose (without need to do more typing) but as plots get more complicated ggplot starts to be more clear and simple than base R plot()

Q6. In your own RStudio can you add a trend line layer to help show the relationship between the plot variables with the geom_smooth() function?

Refer to code for scatterplot

Q7. Argue with geom_smooth() to add a straight line from a linear model without the shaded standard error region?

Refer to code for scatterplot

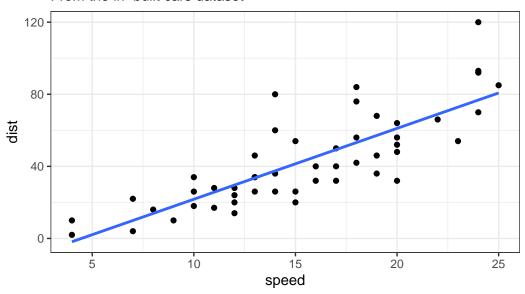
Q8. Can you finish this plot by adding various label annotations with the labs() function and changing the plot look to a more conservative "black & white" theme by adding the theme_bw() function?

Refer to code for scatterplot

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

Stopping distance of old cars

From the in-built cars dataset



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

```
Gene Condition1 Condition2 State
A4GNT -3.6808610 -3.4401355 unchanging
AAAS 4.5479580 4.3864126 unchanging
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

Q9. Use the nrow() function to find out how many genes are in this dataset. What is your answer?

nrow(genes)

[1] 5196

There are 5196 genes in this dataset

Q10. 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?

colnames(genes)

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

ncol(genes)

[1] 4

I found 4 columns in this dataset

Q11. 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?

table(genes\$State)

down	unchanging	up
72	4997	127

There are 127 upregulated genes

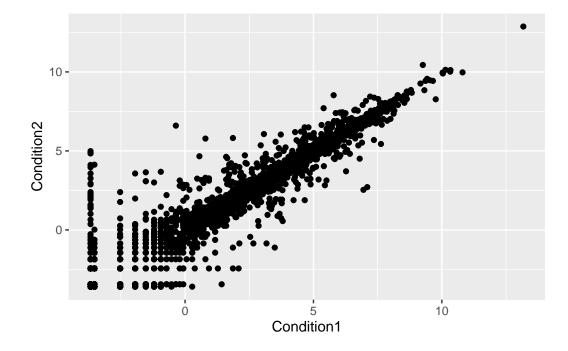
Q12. Using your values above and 2 significant figures. What fraction of total genes is up-regulated in this dataset?

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

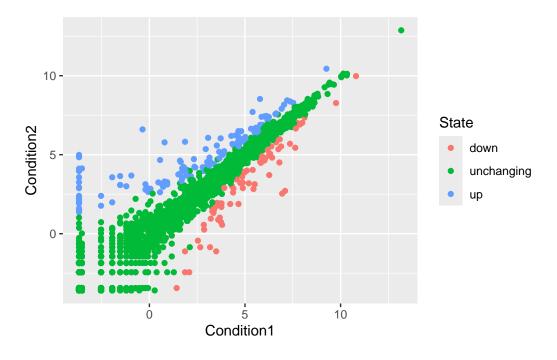
```
down unchanging up
1.39 96.17 2.44
```

- 2.44% of genes are upregulated in this data set
 - Q13. Complete the code below to produce the following plot

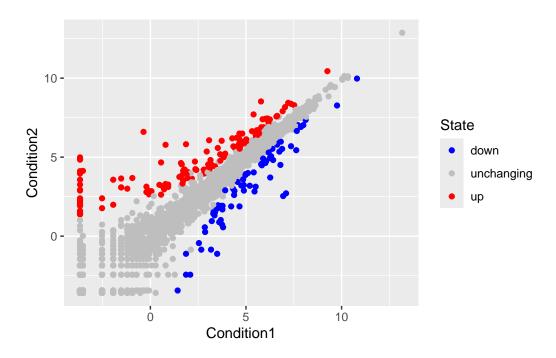
```
ggplot(genes) +
  aes(x=Condition1, y=Condition2) +
  geom_point()
```



```
p <- ggplot(genes) +
    aes(x=Condition1, y=Condition2, col=State) +
    geom_point()
p</pre>
```

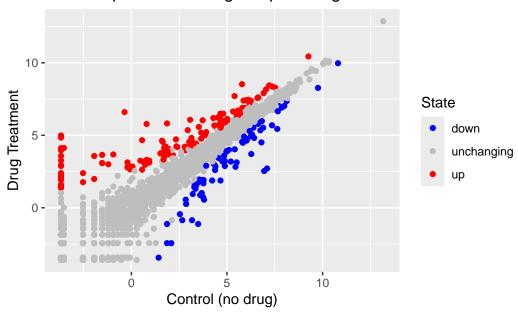


p + scale_colour_manual(values=c("blue", "gray", "red"))



Q14. Nice, now add some plot annotations to the p object with the labs() function so your plot looks like the following:

Gene Expression Changes Upon Drug Treatment



url <- "https://raw.githubusercontent.com/jennybc/gapminder/master/inst/extdata/gapminder.ts
gapminder <- read.delim(url)</pre>

library(dplyr)

```
Attaching package: 'dplyr'
```

The following objects are masked from 'package:stats':

filter, lag

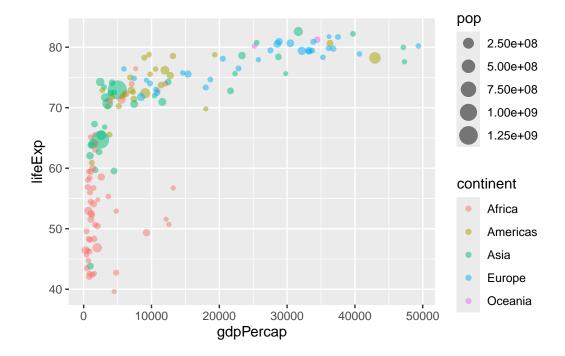
The following objects are masked from 'package:base':

intersect, setdiff, setequal, union

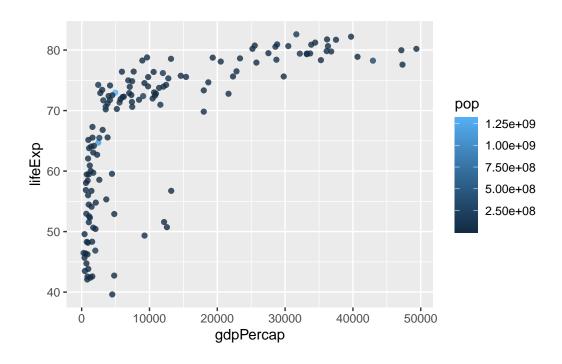
```
gapminder_2007 <- gapminder %>% filter(year==2007)
```

Q15. Complete the code below to produce a first basic scater plot of this gapmin-der_2007 dataset:

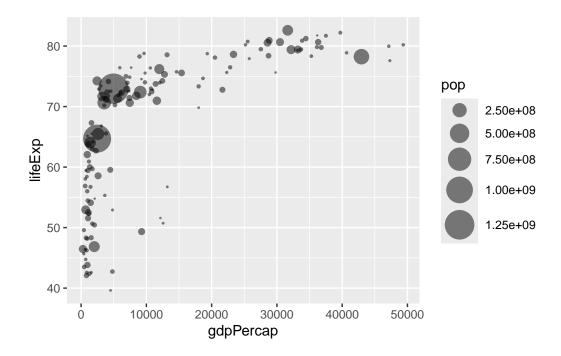
```
library(ggplot2)
ggplot(gapminder_2007) +
  aes(x=gdpPercap, y=lifeExp, color=continent, size=pop) +
  geom_point(alpha=0.5)
```



```
ggplot(gapminder_2007) +
aes(x = gdpPercap, y = lifeExp, color = pop) +
geom_point(alpha=0.8)
```



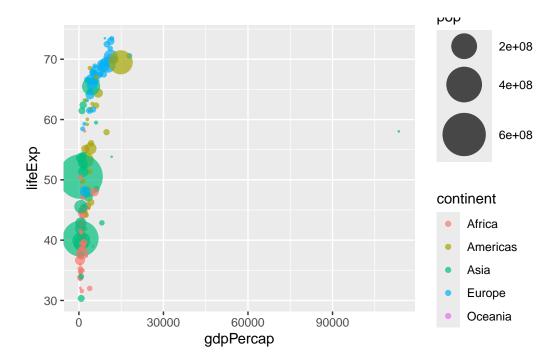
```
ggplot(gapminder_2007) +
  aes(x = gdpPercap, y = lifeExp, size = pop) +
  geom_point(alpha=0.5)+
  scale_size_area(max_size = 10)
```



Q16. Can you adapt the code you have learned thus far to reproduce our gapminder scatter plot for the year 1957? What do you notice about this plot is it easy to compare with the one for 2007?

```
library(dplyr)
gapminder_1957 <- gapminder %>% filter(year==1957)

ggplot(gapminder_1957)+
  aes(x = gdpPercap, y = lifeExp, color=continent, size=pop)+
  geom_point(alpha=0.7)+
  scale_size_area(max_size = 15)
```

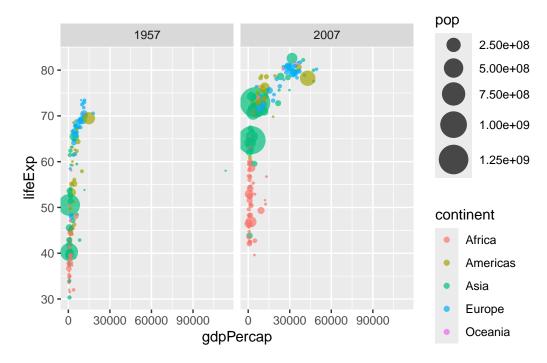


Without having both plots next to each other, or overlapping on the same graph, it is difficult to decipher the small differences between the two years as scrolling up and down to see each graph individually is inefficient and not very precise

Q17. Do the same steps above but include 1957 and 2007 in your input dataset for ggplot(). You should now include the layer facet_wrap(~year) to produce the following plot:

```
gapminder_1957 <- gapminder %>% filter(year==1957 | year==2007)

ggplot(gapminder_1957)+
  aes(x = gdpPercap, y = lifeExp, color=continent, size=pop)+
  geom_point(alpha=0.7)+
  scale_size_area(max_size = 10)+
  facet_wrap(~year)
```



. Q. Extract data for US in 1992

```
country continent year lifeExp pop gdpPercap
1 United States Americas 1992 76.09 256894189 32003.93
```

What was the population of Ireland in the last year we have data for?

```
country continent year lifeExp pop gdpPercap
1 Ireland Europe 2007 78.885 4109086 40676
```

Q. What countries in the data set had pop smaller than Ireland in 2007

```
gap07 <- filter(gapminder, year==2007)
ire_pop <- filter(gap07,country=="Ireland")["pop"]
ire_pop</pre>
```

pop 1 4109086

filter(gap07, pop<4109086)

	country	continent	year	lifeExp	рор	gdpPercap
1	Albania	Europe	•	_	3600523	5937.0295
2	Bahrain	-	2007	75.635	708573	29796.0483
3	Botswana	Africa	2007	50.728	1639131	12569.8518
4	Comoros	Africa	2007	65.152	710960	986.1479
5	Congo, Rep.	Africa	2007	55.322	3800610	3632.5578
6	Djibouti	Africa	2007	54.791	496374	2082.4816
7	Equatorial Guinea	Africa	2007	51.579	551201	12154.0897
8	Gabon	Africa	2007	56.735	1454867	13206.4845
9	Gambia	Africa	2007	59.448	1688359	752.7497
10	Guinea-Bissau	Africa	2007	46.388	1472041	579.2317
11	Iceland	Europe	2007	81.757	301931	36180.7892
12	Jamaica	Americas	2007	72.567	2780132	7320.8803
13	Kuwait	Asia	2007	77.588	2505559	47306.9898
14	Lebanon	Asia	2007	71.993	3921278	10461.0587
15	Lesotho	Africa	2007	42.592	2012649	1569.3314
16	Liberia	Africa	2007	45.678	3193942	414.5073
17	Mauritania	Africa	2007	64.164	3270065	1803.1515
18	Mauritius	Africa	2007	72.801	1250882	10956.9911
19	Mongolia	Asia	2007	66.803	2874127	3095.7723
20	Montenegro	Europe	2007	74.543	684736	9253.8961
21	Namibia	Africa	2007	52.906	2055080	4811.0604
22	Oman	Asia	2007	75.640	3204897	22316.1929
23	Panama	Americas	2007	75.537	3242173	9809.1856
24	Puerto Rico	Americas	2007	78.746	3942491	19328.7090
25	Reunion	Africa	2007	76.442	798094	7670.1226
26	Sao Tome and Principe	Africa	2007	65.528	199579	1598.4351
27	27 Slovenia		2007	77.926	2009245	25768.2576
28	Swaziland	Africa	2007	39.613	1133066	4513.4806
29	O		2007	69.819	1056608	18008.5092
30	Uruguay	Americas	2007	76.384	3447496	10611.4630
31	West Bank and Gaza	Asia	2007	73.422	4018332	3025.3498

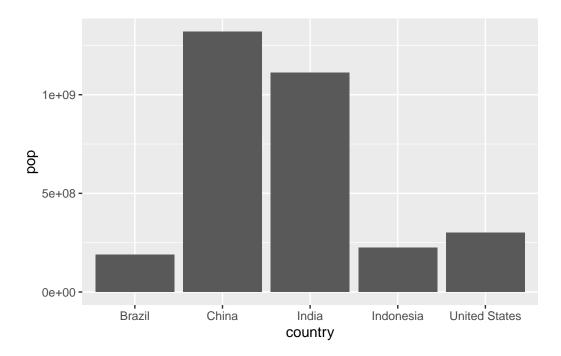
^{**} OPTIONAL BAR CHARTS**

```
gapminder_top5 <- gapminder %>%
  filter(year==2007) %>%
  arrange(desc(pop)) %>%
  top_n(5, pop)

gapminder_top5
```

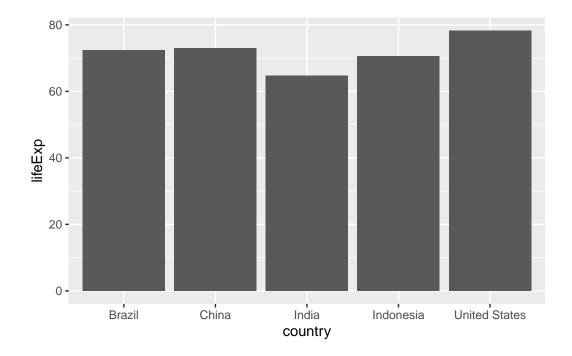
```
pop gdpPercap
       country continent year lifeExp
                    Asia 2007 72.961 1318683096 4959.115
1
         China
2
         India
                    Asia 2007 64.698 1110396331
                                                  2452.210
3 United States Americas 2007 78.242 301139947 42951.653
     Indonesia
                    Asia 2007 70.650
                                       223547000
                                                  3540.652
        Brazil Americas 2007 72.390 190010647
5
                                                  9065.801
```

```
ggplot(gapminder_top5) +
geom_col(aes(x = country, y = pop))
```

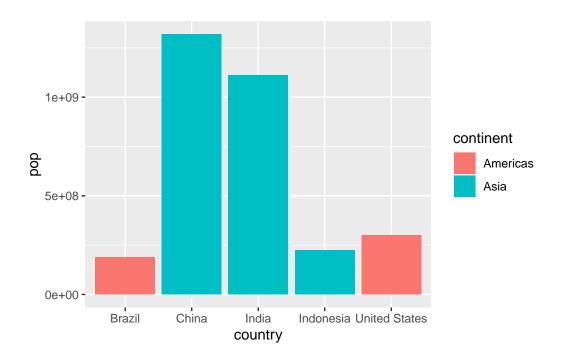


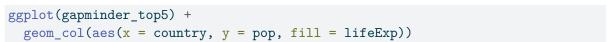
Q18. Create a bar chart showing the life expectancy of the five biggest countries by population in 2007.

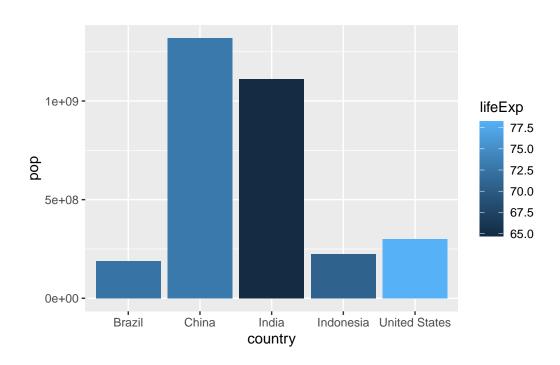
```
ggplot(gapminder_top5) +
geom_col(aes(x = country, y = lifeExp))
```



```
ggplot(gapminder_top5) +
geom_col(aes(x = country, y = pop, fill = continent))
```







Q19. Plot population size by country. Create a bar chart showing the population (in millions) of the five biggest countries by population in 2007.

```
ggplot(gapminder_top5) +
  aes(x=reorder(country, -pop), y=pop, fill=country) +
  geom_col(col="gray30") +
  guides(fill="none")
```

