GY7702 Assignment

MSc Satellite Data Science at the University of Leicester

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Introduction

This document was created to meet the requirements of GY7702 R for Data Science at University of Leicester. It was designed and created in R Markdown, a markup language that allows users to create documents that can be formatted to embed code blocks, code outputs and hyperlinks. When the R Markdown file is compiled, the markup language is hidden and the document is displayed in plain text.

This content was created using R, Rstudio, RMarkdown and GitHub

Materials

The libraries used in this assignment:

```
library(tidyverse)
library(palmerpenguins)
library(dplyr)
library(knitr)
library(readr)
library(tinytex)
library(lubridate)
library(ggplot2)
```

For further information regarding the source code, data and libraries used in this assignment, please see the projects GitHub page.

References

Elliot would like to acknowledge that this document includes teaching materials from Dr Stefano De Sabbato for the module GY7702 R for Data Science. Dr Stefanos teaching materials can be found here

R for Data Science by Garrett Grolemund and Hadley Wickham, O'Reilly Media, 2016. See online book

Note to reader

Where a function is mentioned for the **first time**, a brief explanation will be given before the code block. Thereafter, this explanation will be dismissed.

Question 1

A vector of 25 numbers between 1 and 7 are listed below. These values represent answers to a survey question

NA 3 4 4 5 2 4 NA 6 3 5 4 0 5 7 5 NA 5 2 4 NA 3 3 5 NA

- 1 = Completely disagree
- 2 = Disagree
- 3 = Somehow disagree
- 4 = Neither agree or disagree
- 5 = Somehow agree
- 6 = Agree
- 7 = Completely agree
- NA = missing value

Question 1.1

Write the code necessary to check whether all participants to the survey either completely disagree or completely agree, once the missing values are excluded

```
# First, let's create the vector.
num <- c(NA, 3, 4, 4, 5, 2, 4, NA, 6, 3, 5, 4, 0, 5, 7, 5, NA, 5, 2, 4, NA, 3, 3, 5, NA)

# Then, remove missing values.
num <- na.omit(num)

# And finally check whether all students either completely agree (= 7).
students_agree_complete <- all(num == 7)
```

```
## [1] FALSE
```

```
# Or completely disagree (=1).
students_disagree_complete <- all(num == 1)
```

```
## [1] FALSE
```

Question 1.2

Write the code necessary to extract the indexes related to the participants in the survey who at least somehow agree or more.

In the vector `num`, `which` students selected values between 5 and 7.

```
students_agree <- which(num %in% c(5:7))
```

Question 2

Question 2.2

Write the code necessary to create a table showing species, island, bill length and body mass of the 10 Gentoo penguins in the penguins table with the highest body mass

The library `palmerpenguins` was created by Dr. Kristen Gorman and holds 2 data sets. For this assignment, we will work with `penguins`, a table containing 8 measured variables from 344 penguins!

Some of the penguins in `penguins` hold NA values for certain variables. Due to the analysis that we are going to do, these need to be removed

```
pen <- na.omit(penguins)
```

As this task requires multiple steps, it will be more efficient to start a pipe. Lets send the *na omitted* table, `pen` down the pipe.

It is important to note that the functions in the pipe operator do not require the first argument, `pen` because it is being 'fed down' the pipe. For more information on pipes, click here

```
pen %>%
  # First, let's select all the variables that the question asks for
  select(species, island, bill_length_mm, bill_depth_mm, body_mass_g)%>%

  # and select all the 'Gentoo' penguins.
  filter(species == "Gentoo")%>%

  # Order body mass in ascending order
  arrange(-body_mass_g)%>%

  # Return the 10 heaviest Gentoo penguins
  slice_head(n = 10)
```

```
## # A tibble: 10 x 5
##    species island bill_length_mm bill_depth_mm body_mass_g
##    <fct>   <fct>           <dbl>         <dbl>       <int>
##  1 Gentoo  Biscoe           49.2          15.2        6300
##  2 Gentoo  Biscoe           59.6          17          6050
##  3 Gentoo  Biscoe           51.1          16.3        6000
##  4 Gentoo  Biscoe           48.8          16.2        6000
##  5 Gentoo  Biscoe           45.2          16.4        5950
##  6 Gentoo  Biscoe           49.8          15.9        5950
##  7 Gentoo  Biscoe           48.4          14.6        5850
##  8 Gentoo  Biscoe           49.3          15.7        5850
##  9 Gentoo  Biscoe           55.1          16          5850
## 10 Gentoo  Biscoe           49.5          16.2        5800
```

Question 2.3

write the code necessary to create a table showing the average bill length per island, ordered by average bill length.

As this question states `per island`, we will use `group_by` to perform an average bill length for each island. We will also see `mean()` to determine average. This is a function built into R.

After the data set is grouped by island, average bill length will be calculated. The result will be appended to `pen` in a column called `avg_bill_length` using the `mutate` function.

```
pen %>%

  # Select the appropriate attributes
  select(species, island, bill_length_mm, bill_depth_mm,)%>%

  # Order by bill_length_mm. By default arrange sorts in ascending order.
  arrange(bill_length_mm)%>%

  # Use group_by to execute the average for each island
  group_by(island)%>%

  # Append the average bill_length_mm to the table pen
  mutate(avg_bill_length_mm = mean(bill_length_mm))%>%

  # Display 3 example average_bill_lengths for each island
  slice_head(n = 3)%>%
kable()
```

species	island	bill_length_mm	bill_depth_mm	avg_bill_length_mm
Adelie	Biscoe	34.5	18.1	45.24847
Adelie	Biscoe	35.0	17.9	45.24847
Adelie	Biscoe	35.0	17.9	45.24847
Adelie	Dream	32.1	15.5	44.22195
Adelie	Dream	33.1	16.1	44.22195
Adelie	Dream	34.0	17.1	44.22195
Adelie	Torgersen	33.5	19.0	39.03830
Adelie	Torgersen	34.4	18.4	39.03830
Adelie	Torgersen	34.6	21.1	39.03830

Question 2.4

Write the code necessary to create a table showing the minimum, median and maximum proportion between bill length and bill depth by species.

The *proportion between bill length and bill depth* will be calculated as `bill_length_mm` / `bill_depth_mm`. This will return a unit-less measure which will be called `bl_bd`

R also contains inbuilt functions for obtaining the minimum, median and maximum values from a vector. So by example after `select()` and `group_by()`, lets take the minimum `bill_length_mm` and minimum `bill_depth_mm` and divide them to get the unit-less measurement `min_bl_bd`.

```
  pen %>%
  # Select the necessary attributes
  select(species, island, bill_length_mm, bill_depth_mm,)%>%

  # Execute the proportions for each species
  group_by(species)%>%
```

```
  # Append the proportions to the table pen, using mutate
  mutate(min_bl_bd = min(bill_length_mm) / min(bill_depth_mm))%>%
```

Then repeat this for the median and maximum values

```
  mutate(med_bl_bd = median(bill_length_mm) / median(bill_depth_mm))%>%
  mutate(max_bl_bd = max(bill_length_mm) / max(bill_depth_mm))%>%

  # Drop bill_length_mm and bill_depth_mm
  subset(select = -c(bill_length_mm, bill_depth_mm))
```

This is a preview of 3 penguins from each island, demonstrating how the proportions are calculated *per island*.

species	island	min_bl_bd	med_bl_bd	max_bl_bd
Adelie	Torgersen	2.070968	2.111413	2.139535
Adelie	Torgersen	2.070968	2.111413	2.139535
Adelie	Torgersen	2.070968	2.111413	2.139535
Chinstrap	Dream	2.493902	2.685637	2.788461
Chinstrap	Dream	2.493902	2.685637	2.788461
Chinstrap	Dream	2.493902	2.685637	2.788461
Gentoo	Biscoe	3.122137	3.160000	3.445087
Gentoo	Biscoe	3.122137	3.160000	3.445087
Gentoo	Biscoe	3.122137	3.160000	3.445087

Question 3

Question 3.1

Write the code necessary to load the data from *covid19_cases_20200301_20201017.csv* to a variable named covid_data

The library `readr` contains the function `read_csv()` which allows us to read .csv (comma-separated value) files into R.

```
# Reading the COVID-19 .csv from a local directory
covid_data <- read_csv("C:/.../data/covid19_cases_20200301_20201017.csv")
```

Question 3.2

Write the code necessary to

- Create a complete table, containing a row for each day and area
- Replace NA values with the value available for the previous date
- Replace the remaining NA values with zero
- Subset only the area assigned to me (Dudley)
- Drop the `area_name` column
- Store the resulting table in a variable named `[Dudley]_complete_covid_data`

First, lets check how the data is delivered. We want each row to contain a date and an area

```
kable((covid_data[1:10,]), "simple")
```

specimen_date	area_name	newCasesBySpecimenDate	cumCasesBySpecimenDate
2020-03-01	Aberdeen City	0	0
2020-03-01	Aberdeenshire	0	0
2020-03-01	Angus	0	1
2020-03-01	Antrim and Newtownabbey	0	0
2020-03-01	Ards and North Down	0	0
2020-03-01	Argyll and Bute	0	0
2020-03-01	Armagh City, Banbridge and Craigavon	0	0
2020-03-01	Barking and Dagenham	1	1
2020-03-01	Barnet	0	1
2020-03-01	Belfast	0	0

This looks good, a date (`specimen_date`) and an area (`area_name`) is found on one row. A further look at the data shows us that the table runs through all areas (with a case) for `2020-03-01`. This is then repeated for `2020-03-02`

specimen_date	area_name	newCasesBySpecimenDate	cumCasesBySpecimenDate
2020-03-01	Wokingham	0	1
2020-03-01	Wrexham	0	0
2020-03-01	York	0	1
2020-03-02	Aberdeen City	0	0
2020-03-02	Aberdeenshire	0	0
2020-03-02	Angus	0	1

The question also asks for a check for NA values

```
covid_data_na <- any(is.na(covid_data))
```

```
## [1] FALSE
```

So, the table contains no NA values. We can subset the `area_name` column to return only rows that contain the string *Dudley*. After we've subsetted, we can then drop the area_name column entirely.

```
Dudley_complete_covid_data <-
  covid_data %>%
  filter(area_name == "Dudley")%>%
  subset(select = -c(area_name))
```

specimen_date	newCasesBySpecimenDate	cumCasesBySpecimenDate
2020-03-07	1	1
2020-03-08	0	1
2020-03-09	2	3
2020-03-10	1	4
2020-03-11	0	4

specimen_date	newCasesBySpecimenDate	cumCasesBySpecimenDate
2020-03-12	4	8
2020-03-13	1	9
2020-03-14	2	11
2020-03-15	4	15
2020-03-16	3	18

Question 3.3

Starting from the table [area]_complete_covid_data created for Question 3.2 :

- Create a copy of Dudley_complete_covid_data, i.e., as another variable named Dudley_day_before.
- Use the library lubridate to create a new column named day_before in the new table [area]_day_before that reports the day before the day reported in the column specimen_date, as a character value (e.g., if specimen_date is "2020-10-10", day_before should be "2020-10-09")
- Drop the specimen_date and cumCasesBySpecimenDate columns from the [area]_day_before table
- Rename the newCasesBySpecimenDate column of the the [area]_day_before table to newCases_day_before
- Join [area]_day_before with [area]_complete_covid_data, where the column specimen_date of [area]_complete_covid_data is equal to the column day_before of [area]_day_before
- Calculate a new column in the joined table, containing the number of new cases as a percentage of the number of new cases of the day before
- Store the resulting table in a variable named [area]_covid_development.

```
# Duplicate the table Dudley_complete_covid_date
Dudley_day_before <- Dudley_complete_covid_data

# Creating a new column in Dudley_day_before, called 'day_before' that is a duplicate of 'specimen_date
Dudley_day_before$day_before <- Dudley_day_before$specimen_date

# Using lubricate(), subtract 1 day from the day_before column
Dudley_day_before$day_before <- as.Date(Dudley_day_before$day_before)-1
```

If the above section contained one more step, we would have given serious thought of how to put it into a `pipe`. The next section however is a lot more complex, and the `pipe` makes it more readable and more efficient. We'll carry out the operation first and then explain the output below.

```
Dudley_day_before_out <- Dudley_day_before %>%
  # Remove specimen_date and cumcasesbyspecimenDate
  subset(select = -c(specimen_date, cumCasesBySpecimenDate))%>%

  # Rename newCasesBySpecimenDate to newCases_day_before
  rename(newCases_day_before = newCasesBySpecimenDate)%>%

  # Join [area]_day_before with Dudley_complete_covid_data, specimen_date is
  # equal to the day_before
  left_join(Dudley_complete_covid_data, ., by= c("specimen_date" = "day_before"))%>%

  # number of new cases as a percentage of the number of new cases of the day before
  mutate(percentage_of_new_cases = (newCases_day_before/newCasesBySpecimenDate)*100) %>%
```

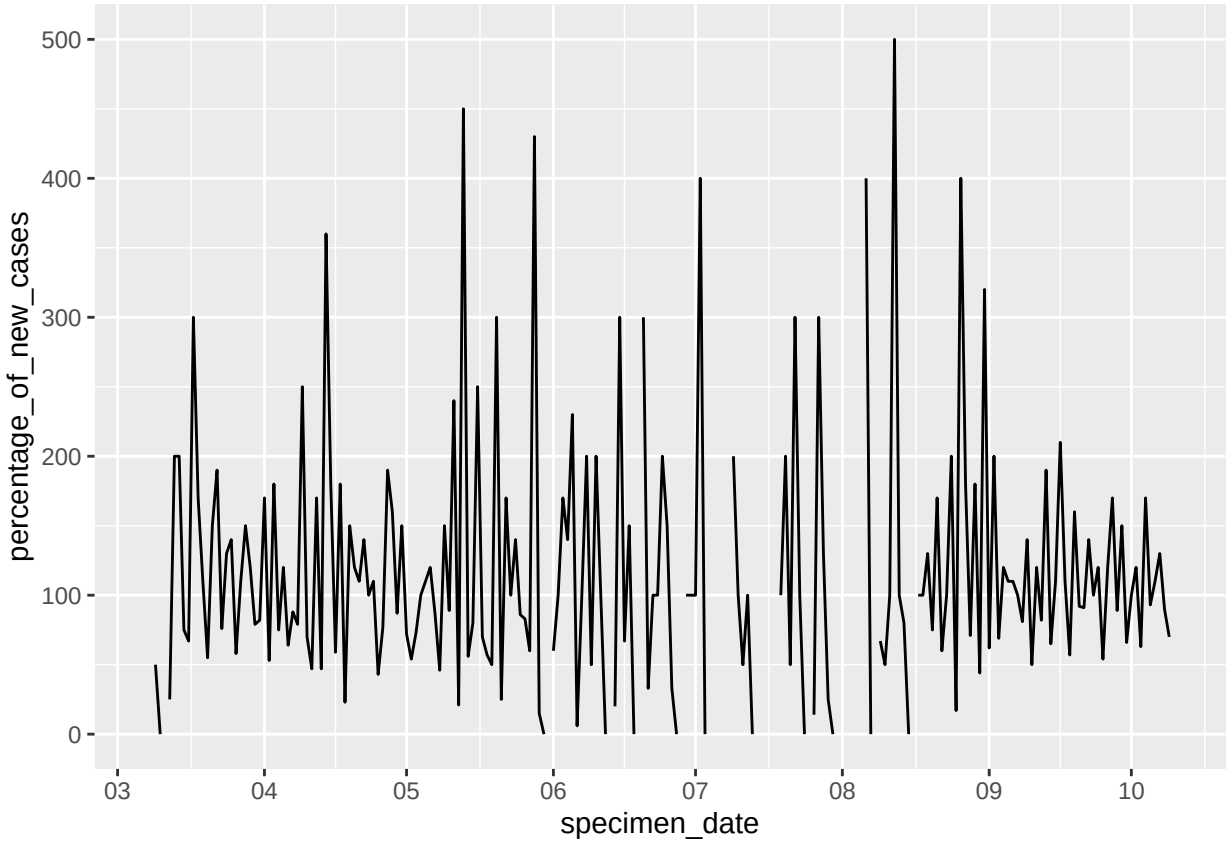
```
  # Set percentage_of_new_cases to 2 significant digits
  mutate(percentage_of_new_cases = signif(percentage_of_new_cases, 2)) %>%

  # Remove any trailing 0's from percentage_of_new_cases
  mutate(percentage_of_new_cases = round(percentage_of_new_cases, 0)) %>%

  # If there is any infinite values in the table, set these to NA
  mutate_if(is.numeric, list(~na_if(., Inf)))

  # and then replace all NA values with 0
  # mutate_if(is.numeric, replace_na, 0)

kable(Dudley_day_before_out[1:10,], "simple")
```

specimen_date	newCasesBySpecimenDate	cumCasesBySpecimenDate	newCases_day_before	percentage_of
2020-03-07	1	1	0	
2020-03-08	0	1	2	
2020-03-09	2	3	1	
2020-03-10	1	4	0	
2020-03-11	0	4	4	
2020-03-12	4	8	1	
2020-03-13	1	9	2	
2020-03-14	2	11	4	
2020-03-15	4	15	3	
2020-03-16	3	18	2	
By way of an exp	lanation, “‘newCases_day	_before“‘		
states the cases	on the following day. “	‘newCasesBySpecimenDate“	‘	
states the cases	on the “specimen_date	“. This allows		
“‘newCases_day_	before/newCasesBySpecimen	Date“‘		
to efficiently c	alculate change in COVID	cases over 2 days, across	1 row.	

Using `library(ggplot2)` we can visualise the change in cases over `specimen_date` .The syntax here is quite self-explanatory, `geom_line` just specifies that it is a line plot, instead of a scatter (`geom_point`) for example.

```
ggplot(data = Dudley_day_before_out, mapping = aes(x = specimen_date,
format = "%Y-%m-%d", y = percentage_of_new_cases)) + geom_path() +
  scale_x_date(date_breaks ="1 month", date_labels = "%m")
```

```
## Warning: Removed 1 row(s) containing missing values (geom_path).
```



The first cases for Dudley were reported on 07/03/2020. From this date, the percentage of new cases fluctuated, when compared to the previous day fluctuated 50-200%. There are outliers in this period on 17/03/2020 and 14/04/2020 where cases increased 300% and 360% respectively. This pattern continues throughout May, with a significant rise on 13/05/2020 to a 450% increase. The data in June and July presents a very different pattern. The percentage of new cases decreased below 100% more frequently, demonstrating that there were less cases on the following day. This continues until mid-way through August when the percentage of new cases increases again. The largest increase occured on 12/08/2020 when cases increased 500% the following day. This leads to a gradual rise in cases again throught September, to a level similar to that of April.

Some issues arose when the next day (`newcases_day_before`) contained 0 cases. Dividing by 0 is `inf` or undefined, so these results were set to `NA` . These were not converted to 0 because `inf != 0` . This is the source of the gaps in the date seen throughout July, August and September.

Question 4

Analyse COVID and population data as you see fit

First, lets read in the population data

```
# Read in population data
pop <- read_csv("C:/Users/44792/Desktop/R for data science/lad19_population.csv")
```

```
##
## -- Column specification --------------------------------------------------------
```

```
## cols(
##   lad19_area_name = col_character(),
##   lad19_area_code = col_character(),
##   area_population = col_double()
## )
```

For a suitable comparison, we need join `pop` and `covid_data`. They hold 2 common columns that state the name of the area. However in `covid_data` this column is called `area_name` and in `pop` it's called `lad19_area_name`. Lets rename `lad19_area_name` to `area_name` for an easier join

Note: Generally, renaming variables is bad practice. However, because this is a relatively small data set and this is a fairly *heuristic* study a `rename` serves it's purpose

```
# Renaming lad19_area_name in pop to area_name
names(pop)[names(pop) == "lad19_area_name"] <- "area_name"

# Joining covid_data and pop, using area_name
cov_pop <- left_join(covid_data, pop)
```

```
## Joining, by = "area_name"
```

This is looking good! Covid data for an area, alongside its associated population data. Next, lets extract some areas from this dataset `cov_pop` and called it `places`.

```
places <- c("Dudley","Plymouth")
```

Using a `pipe` , we can extract the data for the areas in `places` , normalize cumulative cases by the population of an area and drop any columns we don't need.

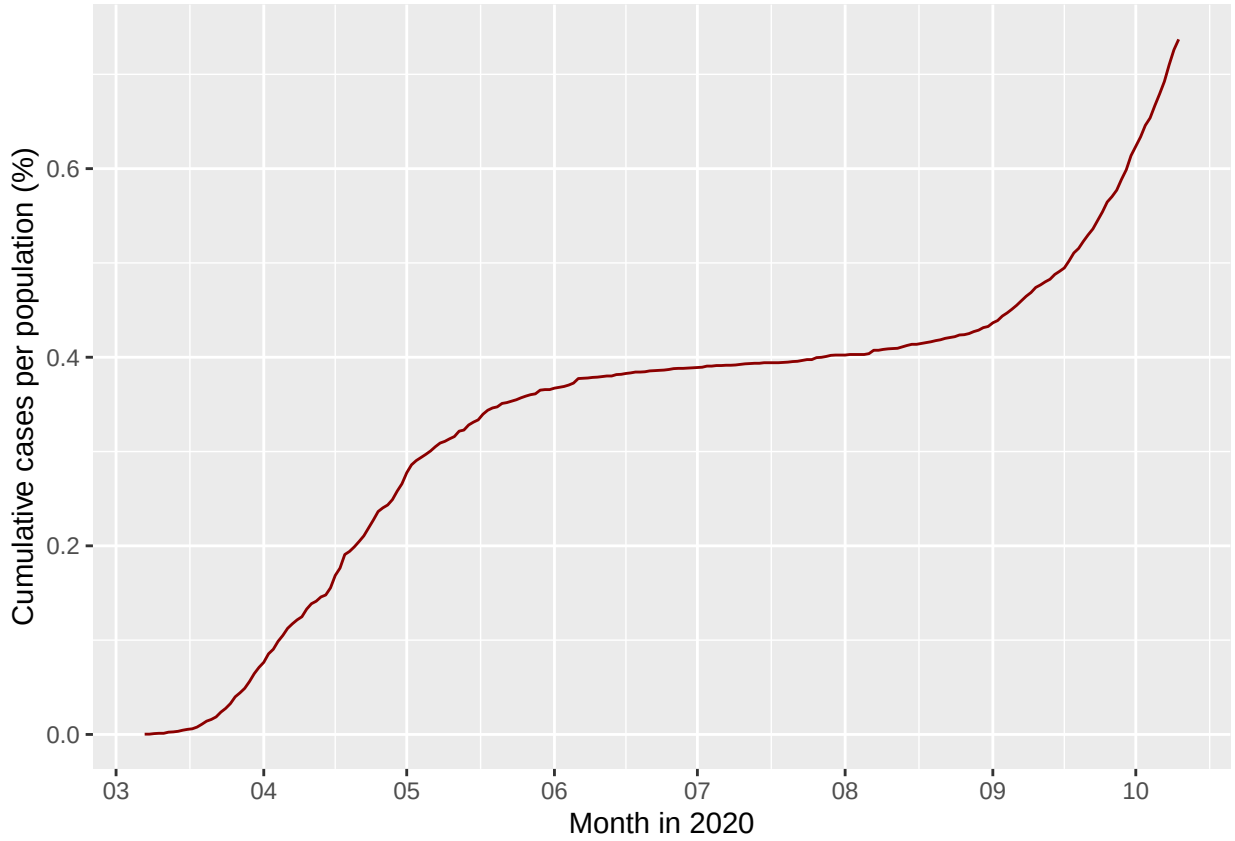
```
Dudley_Plymouth_covid_data <-
  cov_pop %>%

  # Filtering rows out of cov_pop that match the values in places
  filter(area_name %in% places) %>%

  # Remove area_name and newcasesbyspeciendate
  subset(select = -c(lad19_area_code, newCasesBySpecimenDate))%>%

  # Show cumulative cases as a percentage of the population of an area
  mutate(CumCases_percentage_of_pop = (cumCasesBySpecimenDate / area_population)*100)%>%

  # Remove the area_population
  subset(select = -c(area_population, cumCasesBySpecimenDate))
```

We can then show the cumulative cases for Dudley as a proportion of the population.

To show just Dudley, we need to `pivot_wider` to get `Dudley` in it's own column.

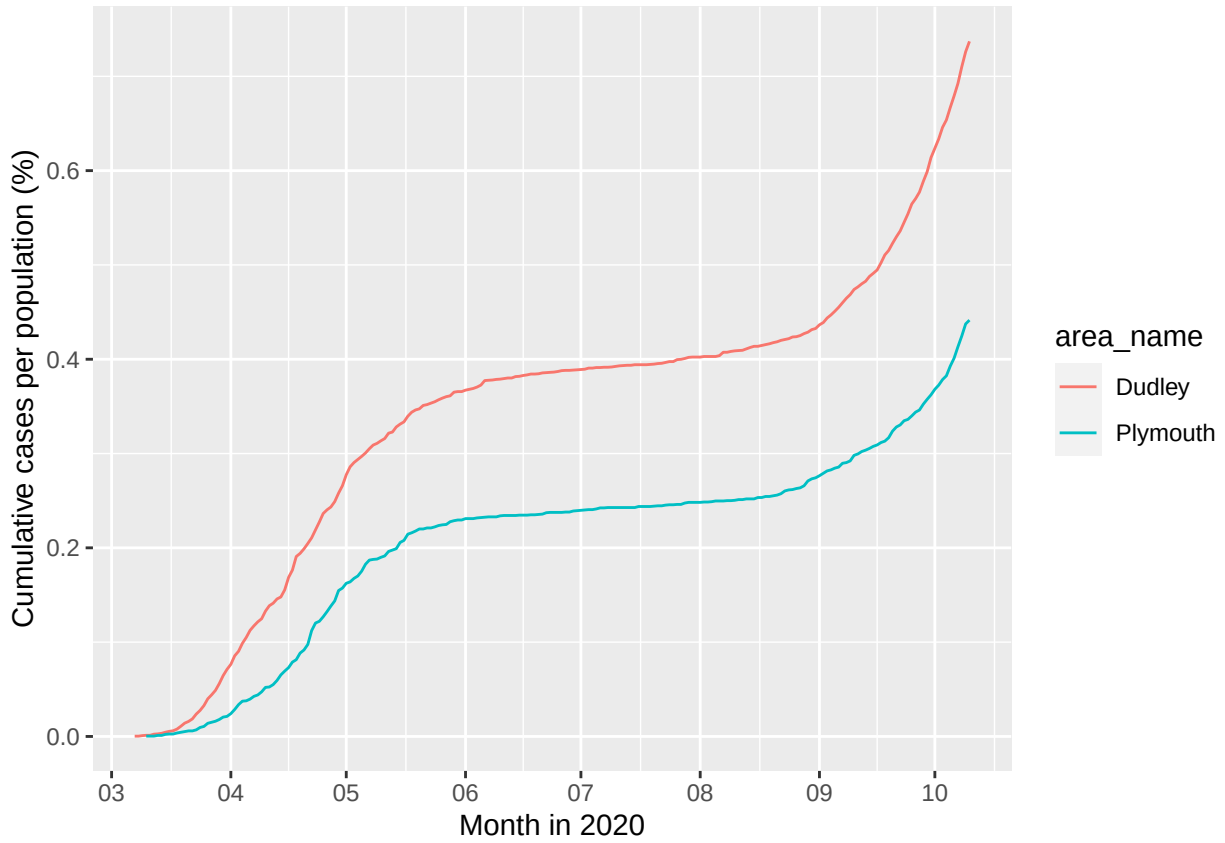
`ggplot` then takes `Dudley_Plymouth_wide` as the data and the new column `Dudley` from the pivot to form the figure seen below.

```
Dudley_Plymouth_wide <- pivot_wider(Dudley_Plymouth_covid_data, names_from = area_name, values_from = c

ggplot(data = Dudley_Plymouth_wide, mapping = aes(x = specimen_date, format = "%Y-%m-%d")) + geom_line(a
```



Interestingly, the original data set `Dudley_Plymouth_covid_data` was formatted perfectly for `ggplot` to visualise multiple areas on the same plot. This works because `ggplot` takes all the data and colours it by the `area_name`. `ggplot` is recognising 2 unique area names, and so they are coloured uniquely and displayed in an inbuilt legend.

```
Dudley_Plymouth_long <- pivot_longer(Dudley_Plymouth_wide, cols = -specimen_date, names_to = c("CumCases

ggplot(Dudley_Plymouth_covid_data, aes(x = specimen_date, format = "%Y-%m-%d", y = CumCases_percentage_
```



The analysis above displays cumulative cases for Dudley and Plymouth as a percentage of the areas population. This is important as Dudley has a population of 333,334 while Plymouth has a population of 272,728. This was performed for a more honest assessment between the 2 areas. Dudley and Plymouth display cases in March. Dudley's first case is 07/03/10, compared to Plymouths later date of 10/03/2020. From this point, both areas display a very similar pattern in the rise of cases. That is, a sharp increase until the middle of May, followed by a flattened curve throughout June, July and August until cases increase again in September. A sharper rise, similar to March occur in October. Though the pattern for both areas are the same, the proportion of cases when compared to the populations are very different. After the initial rise in April, 0.3% of Dudleys population has had a case. This is compared to 0.15% for Plymouth. Additionally, when the curve is flattened in the Summer months, ~0.4% of Dudley has has a case, compared to Plymouths ~0.25%. The second 'spike' in October only serves to widen this gap. The last data from both areas was 10/10/2020 where there was a ~0.3% difference between cumulative cases in Plymouth and Dudley.