```r
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
```

```r
library(ggplot2)
library(readr)
library(broom)
library(testthat)
```

```
##
## Attaching package: 'testthat'
```

```
## The following objects are masked from 'package:readr':
##
##     edition_get, local_edition
```

```
## The following object is masked from 'package:dplyr':
##
##     matches
```

Question 1 [2 marks] The first part of our PPDAC framework is to identify the problem you are addressing with these data. State the question you are trying to answer and let us know what type of question this is in terms of the PPDAC framework. A question statement should be as specific as possible. For example: Do students who regularly get 8 hours of sleep have fewer visits to the health center? This question is an example of an etiologic or causal question.

Our question is as follows: does influenza A have a higher prevalence in the northern or southern hemisphere? This is an etiological/causal question that aims to see whether a country will have a higher prevalence of influenza (response variable) depending on whether they are in the northern or southern hemisphere (explanatory variable).

Question 2 [2 marks] Why is this question interesting or important? You could talk here about how existing data/studies suggest this might be important, how the findings might make an impact, how the findings might be used, or why you are personally interested in this question.

Part of the reason we are interested in this question is because of the historical context of "third world countries" and the modern discourse on "the Global South." The history of imperialism in the global south has led to the majority of countries being classified by international ranking organizations as "poor" and "developing." Given this knowledge, it is valuable to consider how the health of people today is affected by their geographic location, and if it indeed corresponds to the historical exploitation of peoples and comparative lack of resources. Each country comes with its own history of infectious disease, and it will be interesting to see how this develops into the current trends. Another aspect of this question is how the findings can show where the virus frequents and reveal more about its genetic disposition and what climate it prefers to proliferate in, allowing scientists to advance antiviral drugs and vaccines to combat Influenza. Additionally, this question is important given that the data we analyze can also be used to guide fund allocation for influenza treatment around the world. Like any other disease, influenza's spread is highly relevant to the hygiene and economic conditions of different countries.

Question 3 [2 marks] What is the target population for your project? Why was this target chosen? (i.e., what was your rationale for wanting to answer this question in this specific population?)

Our target population is the entire world. This population was chosen to shed light on hemispheric differences to create an understanding of our world as a whole. Taking data from a city, country, or one region would not be enough to generalize to the world.

Question 4 [2 marks] What is the sampling frame used to collect the data you are using? It may be helpful here to read any protocol papers, trial registration records, '.Readme' files or documentation that are associated with your dataset. If you have trouble identifying how the records/individuals were sampled, confirm with your supporting GSI that your dataset will be usable for the purposes of the class. Describe why you think this sampling strategy is appropriate for your question. To what group(s) would you feel comfortable generalizing the findings of your study and why?

As the WHO explains, "The data are provided remotely by National Influenza Centres (NICs) of the Global Influenza Surveillance and Response System (GISRS) and other national influenza reference laboratories collaborating actively with GISRS, or are uploaded from WHO regional databases."

According to FluNet, "FluNet is a global web-based tool for influenza virological surveillance first launched in 1997 [...].The data is provided remotely by National Influenza Centres (NICs) of the Global Influenza Surveillance and Response System (GISRS) and other national influenza reference laboratories collaborating actively with GISRS, or are uploaded from WHO regional databases."

Overall, the sampling method used by FluNet resembles convenience sampling, where the data is voluntarily reported by the national institutions registered with WHO. This sampling method is appropriate as it is the most cost-effective and timely approach to acquire such large quantities of data across a vast geographic landscape.

This sampling strategy also creates bias where only severe cases of influenza that reports to governmental institutions are recorded in the data. There's also the bias that the governments which do not work with WHO (like DPRK) would not be registered on the dataset. With this in mind, we can comfortably generalize our findings to the tested cases of influenza in countries that are WHO members.

Question 5 [2 marks] Write a brief description (1-4 sentences) of the source and contents of your dataset. Provide a URL to the original data source if applicable. If not (e.g., the data came from your internship), provide 1-2 sentences saying where the data came from. If you completed a web form to access the data and selected a subset, describe these steps (including any options you selected) and the date you accessed the data

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The data is publically available at https://www.who.int/tools/flunet under the view/download filtered data section.

Each row of the data represents a reported outbreak from the aforementioned influenza centers, containing crucial information like the country the outbreak occurred in, the specific break down of the influenza genotypes, as well as the time stamp of the outbreak event.

We accessed this data on Oct 5 2023.

Question 6 [1 mark] Write code below to import your data into R. Assign your dataset to an object. Make sure to include and annotate this code in your submission (you can use a # to comment out regular text within code chunks to annotate).

```
fluA <- read_csv("VIW_FNT.csv") %>%
  select(COUNTRY_AREA_TERRITORY, WHOREGION, HEMISPHERE, ISO_YEAR, AH1N12009,
         AH1, AH3, AH5, AH7N9, AOTHER_SUBTYPE, INF_A)
```

```
## Rows: 147936 Columns: 49
## -- Column specification --------------------------------------------------------
## Delimiter: ","
## chr  (12): WHOREGION, FLUSEASON, HEMISPHERE, ITZ, COUNTRY_CODE, COUNTRY_AREA...
## dbl  (35): ISO_YEAR, ISO_WEEK, MMWR_YEAR, MMWR_WEEK, SPEC_PROCESSED_NB, SPEC...
## date  (2): ISO_WEEKSTARTDATE, MMWR_WEEKSTARTDATE
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

```
#From our influenza data, we pick out region data and country as well as the
#year the data was collected. For simplicity sake, we are only importing
#relevant data for the influenza A virus (and not B strains).

flu.metaA <- read_csv("VIW_FLU_METADATA.csv") %>%
  select(-DatasetName,-TableName,-Comments) %>%
  filter(FieldName %in% c("COUNTRY_AREA_TERRITORY","WHOREGION", "HEMISPHERE",
                          "ISO_YEAR", "AH1N12009", "AH1","AH3", "AH5", "AH7N9",
                          "AOTHER_SUBTYPE", "INF_A"))
```

```
## Rows: 89 Columns: 6
## -- Column specification --------------------------------------------------------
## Delimiter: ","
## chr (6): DatasetName, TableName, FieldName, DataType, Description, Comments
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

```
#Variable descriptions for the fluA dataset. WHO region codes can be found
#online on the WHO website.

fluA
```

```
## # A tibble: 147,936 x 11
##    COUNTRY_AREA_TERRITORY    WHOREGION HEMISPHERE ISO_YEAR AH1N12009   AH1   AH3
##    <chr>                     <chr>     <chr>         <dbl>     <dbl> <dbl> <dbl>
##  1 Democratic Republic of t~ AFR       SH             2010         0     0    10
##  2 Honduras                  AMR       NH             2012         1     0     0
##  3 Malta                     EUR       NH             2016         0     0     1
##  4 Bangladesh                SEAR      NH             2014         0     0    21
##  5 United Kingdom, Northern~ EUR       NH             2016         0     0     0
##  6 Netherlands (Kingdom of ~ EUR       NH             2015         0     0     1
##  7 United Republic of Tanza~ AFR       SH             2009        30     1     0
##  8 Cameroon                  AFR       NH             2019        13    NA     0
##  9 Malaysia                  WPR       NH             2014         0     0     1
## 10 Mongolia                  WPR       NH             2022         0     0     1
## # i 147,926 more rows
## # i 4 more variables: AH5 <dbl>, AH7N9 <dbl>, AOTHER_SUBTYPE <dbl>, INF_A <dbl>
```

```
flu.metaA
```

```
## # A tibble: 15 x 3
##    FieldName              DataType Description
##    <chr>                  <chr>    <chr>
##  1 WHOREGION              string   WHO regions (AFR, AMR, EMR, EUR, SEAR, WPR)
##  2 HEMISPHERE             string   Hemisphere (NH=northern hemisphere, SH=south~
##  3 COUNTRY_AREA_TERRITORY string   Country, area or territory name
##  4 ISO_YEAR               integer  Year  (ISO 8601)
##  5 AH1N12009              integer  Number of A(H1N1)pdm09 detections
##  6 AH1                    integer  Number of A(H1) detections (other than A(H1N~
##  7 AH3                    integer  Number of A(H3) detections
##  8 AH5                    integer  Number of A(H5) detections
##  9 AH7N9                  integer  Number of A(H7N9) detections
## 10 AOTHER_SUBTYPE         integer  Number of other influenza A subtype detectio~
## 11 INF_A                  integer  Number of influenza A detections (all subtyp~
## 12 WHOREGION              string   WHO regions (AFR, AMR, EMR, EUR, SEAR, WPR)
## 13 HEMISPHERE             string   Hemisphere (NH=northern hemisphere, SH=south~
## 14 COUNTRY_AREA_TERRITORY string   Country, area or territory name
## 15 ISO_YEAR               integer  Year  (ISO 8601)
```

Question 7 [3 marks] Write code in R (included in your submission with annotation) to answer the following questions:

7i) What are the dimensions of the dataset?

```
dim(fluA)
```

```
## [1] 147936     11
```

7ii) What are the variable names of the variables in your dataset?

```
names(fluA)
```

```
##  [1] "COUNTRY_AREA_TERRITORY" "WHOREGION"              "HEMISPHERE"
##  [4] "ISO_YEAR"               "AH1N12009"              "AH1"
##  [7] "AH3"                    "AH5"                    "AH7N9"
## [10] "AOTHER_SUBTYPE"         "INF_A"
```

7iii) Print the first six rows of the dataset.

```
fluA %>% head(6)
```

```
## # A tibble: 6 x 11
##   COUNTRY_AREA_TERRITORY     WHOREGION HEMISPHERE ISO_YEAR AH1N12009   AH1   AH3
##   <chr>                      <chr>     <chr>         <dbl>     <dbl> <dbl> <dbl>
## 1 Democratic Republic of th~ AFR       SH             2010         0     0    10
## 2 Honduras                   AMR       NH             2012         1     0     0
## 3 Malta                      EUR       NH             2016         0     0     1
## 4 Bangladesh                 SEAR      NH             2014         0     0    21
## 5 United Kingdom, Northern ~ EUR       NH             2016         0     0     0
## 6 Netherlands (Kingdom of t~ EUR       NH             2015         0     0     1
## # i 4 more variables: AH5 <dbl>, AH7N9 <dbl>, AOTHER_SUBTYPE <dbl>, INF_A <dbl>
```

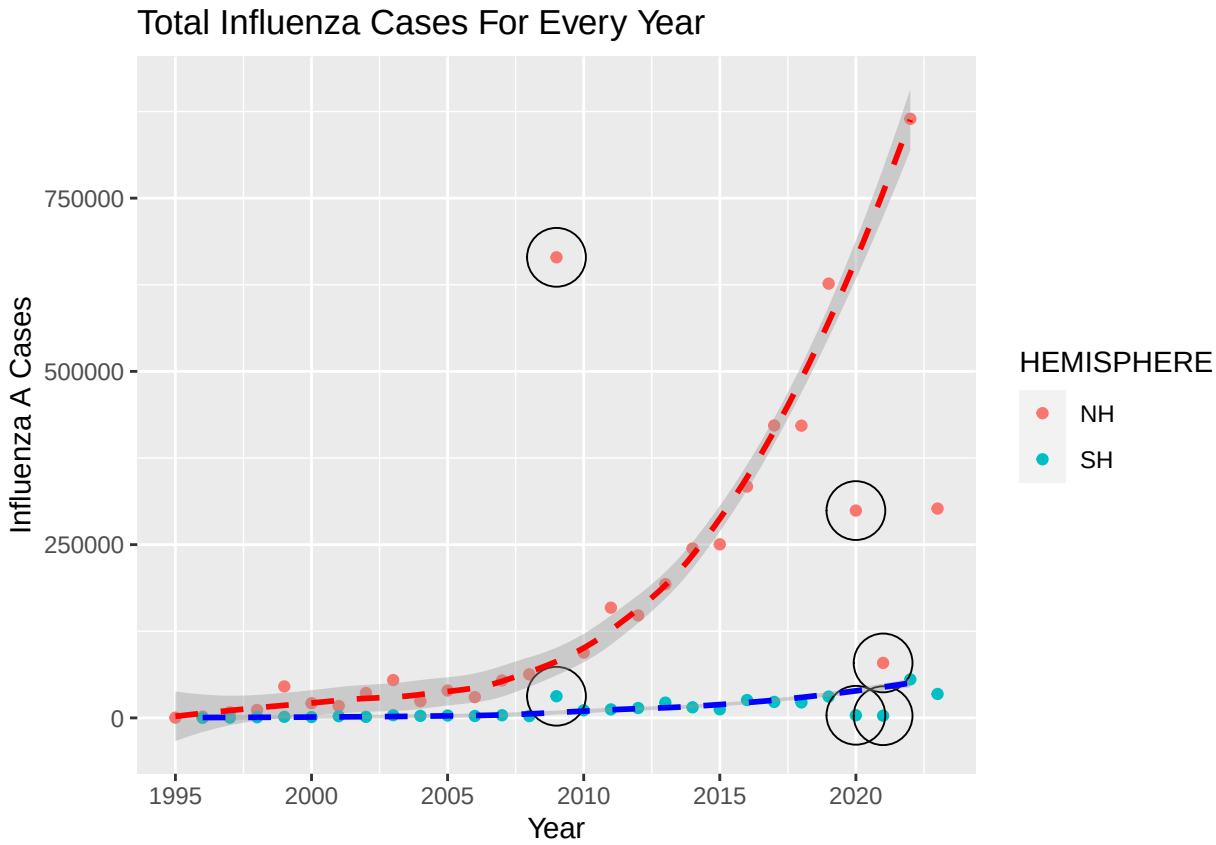
Question 8 [2 marks] Use the data to demonstrate a data visualization skill we have covered during Part I of the course. Choose a visualization relevant to your stated problem. Include your code in your submission. For example, you could visualize the distribution of our outcome with a histogram, or use a bar graph to represent the distribution of your exposure variable.

```
plotA <- fluA %>% group_by(ISO_YEAR,HEMISPHERE) %>%
  summarise(INFA_CASES = sum(na.omit(INF_A)))
```

```
## `summarise()` has grouped output by 'ISO_YEAR'. You can override using the
## `.groups` argument.
```

```
ggplot(plotA,aes(x=ISO_YEAR,y=INFA_CASES,col=HEMISPHERE)) +
  geom_point() +
  geom_point(data=plotA %>% filter(ISO_YEAR %in% c(2009,2020,2021)),
             pch=21,
             size=10,
             colour="black") +
  geom_smooth(data=plotA %>% filter(HEMISPHERE=="NH") %>%
                filter(!(ISO_YEAR %in% c(2009,2020,2021,2023))),
              colour="red",linetype="dashed") +
  geom_smooth(data=plotA %>% filter(HEMISPHERE=="SH") %>%
                filter(!(ISO_YEAR %in% c(2009,2020,2021,2023))),
              colour="blue",linetype="dashed") +
  labs(title="Total Influenza Cases For Every Year") +
  xlab("Year") +
  ylab("Influenza A Cases")
```

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



Question 9 [2 marks] Describe the skill that you are demonstrating and interpret your findings. For example, if you have created a histogram, describe the central tendency, shape of the distribution, etc.

Since our question is etiological, it is useful to divide our visualization between the northern and southern hemispheres as a form of comparison. In our visualization, we can observe some key events such as the 2009 influenza pandemic and the 2020 COVID-19 quarantine. We may consider these events outliers to the general trend of Influenza A and, as such, we will omit them in our loess line computation. Beyond these events, the general trend for influenza in the 21th century shows a positive and curved increase in influenza A over time in the Northern hemisphere. In the Southern hemisphere, the the number of influenza cases has not had the same rapid increase over time and has remained mostly constant relative to Northern hemisphere levels.

Part II

11. [2 marks] Calculate a marginal probability based on your outcome variable. Provide an equation (using probability notation) that describes this probability. For example, if my outcome variable is height in inches, I might calculate the probability that an individual in the dataset has a height of greater than 60 inches. $P(height >= 60)$. This would be a marginal probability. You may need to first add a new variable to your dataset to calculate your probability of interest, such as a binary variable indicating whether height is greater than 60 inches. There is a resource video about how to code such variables that could be helpful!

We calculated the probability that a randomly chosen country in the 2009 flu epidemic had a total number of influenza cases larger than 30. In probability notation this is given by P(INF_A > 30)

```
prob_over_30 <- (fluA %>% filter(ISO_YEAR == 2009, INF_A > 30) %>% nrow())/(
  fluA %>% filter(ISO_YEAR == 2009) %>% nrow())
prob_over_30
```

```
## [1] 0.3250173
```

12. [2 marks] Using any two variables in your dataset (or derived variables), calculate a conditional probability. Provide an equation (using probability notation) that describes this probability and then use R to calculate it.

We calculated the probability that a randomly chosen country in the 2009 flu epidemic had a total number of influenza cases larger than 30, given that the country is in the southern hemisphere.In probability notation this is given by P(INF_A > 30 | HEMISPHERE = SH)

```
prob_over_30_SH <- (fluA %>% filter(ISO_YEAR == 2009,
                                    HEMISPHERE == "SH",
                                    INF_A > 30) %>% nrow())/
  (fluA %>% filter(ISO_YEAR == 2009,
                   HEMISPHERE == "SH") %>% nrow())
prob_over_30_SH
```

```
## [1] 0.2717584
```

13. [2 marks] Does your dataset contain a continuous variable? If it does, does the distribution of that variable appear to be normal? Justify your answer using a plot. If your data does not contain a continous variable, give an example related to your dataset of a hypothetical variable that is continuous. That is, imagine what a continuous variable could be in relation to your dataset and topic of interest. For this hypothetical variable, describe what you imagine its shape might be, and how you would check whether or not it is normally distributed.

We could include a hypotehtical variable that measures the average temperature of that country for that particular ISO_YEAR. This measurement would be continuous because these temperatures can be measured to arbitrary accuracy. This measurement would be relevant because we are trying to see if there is higher prevalence of Influenza A in the northern vs southern hemispheres and temperature/weather patterns are a key difference between these two regions. If we plotted this temperature data on a histogram, and if it's Q-Q plot showed a linear line, we would consider the data to be normally distributed. We believe this data would be approximately normal because average temperatures for each country would include countries that are both colder and warmer. We have no reason to believe there would be a particular skew for warmer or colder countries, so the data would be approximately normal.

14. [4 marks] Does your dataset contain a binary variable? If so, does this variable meet the criteria to be considered binomially distributed? If so, describe this variable in terms of n and p. Calculate a probability based on this variable, first write the formula for the probability and then using R to calculate the probability (you do not need to calculate the probability by hand). If your data does not contain a binary variable, you can create one based on an underlying continuous variable or a categorical variable with > 2 levels to answer this question.

Yes our data set contains a a binary variable. The column Hemisphere has two possible outcomes either you are a country in the Northern Hemisphere or the Southern Hemisphere, which can be binomially distributed with our chances of success being either a country in the NH or SH, therefore our n would be the number of countries chosen and p would be the probability of the country being in the NH or vice versa p could be the probability of a country lying in the SH.If we choose, the probability of success to be country in the Nh then the formula for our probability would be NH/total # countries

```
knitr::include_graphics("partII_binomial expression.png")
```

$$P(X > 40) = 1 - P(X \leq 40) = 1 - \sum_{i=0}^{40} \text{nCr}(50,i)\,(0.85)^{(i)}\,(1-0.85)^{(50-i)}$$

```
p_NH <- round(filter(fluA, HEMISPHERE=='NH')%>%nrow()/(fluA%>%nrow()),2)
p_greater30 <- pbinom(q = 40,size = 50, prob = p_NH,lower.tail=F)
p_greater30
```

```
## [1] 0.7910937
```