class19

Kai Zhao(PID:A17599942)

```
#1 echo=FALSE

cdc <- data.frame( year = c(1922L,1923L,1924L,1925L,1926L,
                                         1927L,1928L,1929L,1930L,1931L,
                                         1932L,1933L,1934L,1935L,1936L,1937L,
                                         1938L,1939L,1940L,1941L,1942L,
                                         1943L,1944L,1945L,1946L,1947L,1948L,
                                         1949L,1950L,1951L,1952L,1953L,1954L,
                                         1955L,1956L,1957L,1958L,1959L,
                                         1960L,1961L,1962L,1963L,1964L,1965L,
                                         1966L,1967L,1968L,1969L,1970L,
                                         1971L,1972L,1973L,1974L,1975L,1976L,
                                         1977L,1978L,1979L,1980L,1981L,
                                         1982L,1983L,1984L,1985L,1986L,1987L,
                                         1988L,1989L,1990L,1991L,1992L,1993L,
                                         1994L,1995L,1996L,1997L,1998L,
                                         1999L,2000L,2001L,2002L,2003L,2004L,
                                         2005L,2006L,2007L,2008L,2009L,
                                         2010L,2011L,2012L,2013L,2014L,2015L,
                                         2016L,2017L,2018L,2019L,2020L,
                                         2021L), cases = c(107473,164191,165418,152003,
                                         202210,181411,161799,197371,166914,
                                         172559,215343,179135,265269,180518,
                                         147237,214652,227319,103188,183866,
                                         222202,191383,191890,109873,133792,
                                         109860,156517,74715,69479,120718,
                                         68687,45030,37129,60886,62786,
                                         31732,28295,32148,40005,14809,11468,
                                         17749,17135,13005,6799,7717,9718,
                                         4810,3285,4249,3036,3287,1759,
                                         2402,1738,1010,2177,2063,1623,1730,
                                         1248,1895,2463,2276,3589,4195,
                                         2823,3450,4157,4570,2719,4083,6586,
                                         4617,5137,7796,6564,7405,7298,
                                         7867,7580,9771,11647,25827,25616,
                                         15632,10454,13278,16858,27550,18719,
                                         48277,28639,32971,20762,17972,
                                         18975,15609,18617,6124,2116)
      )
```

Lets have a wee look at this table

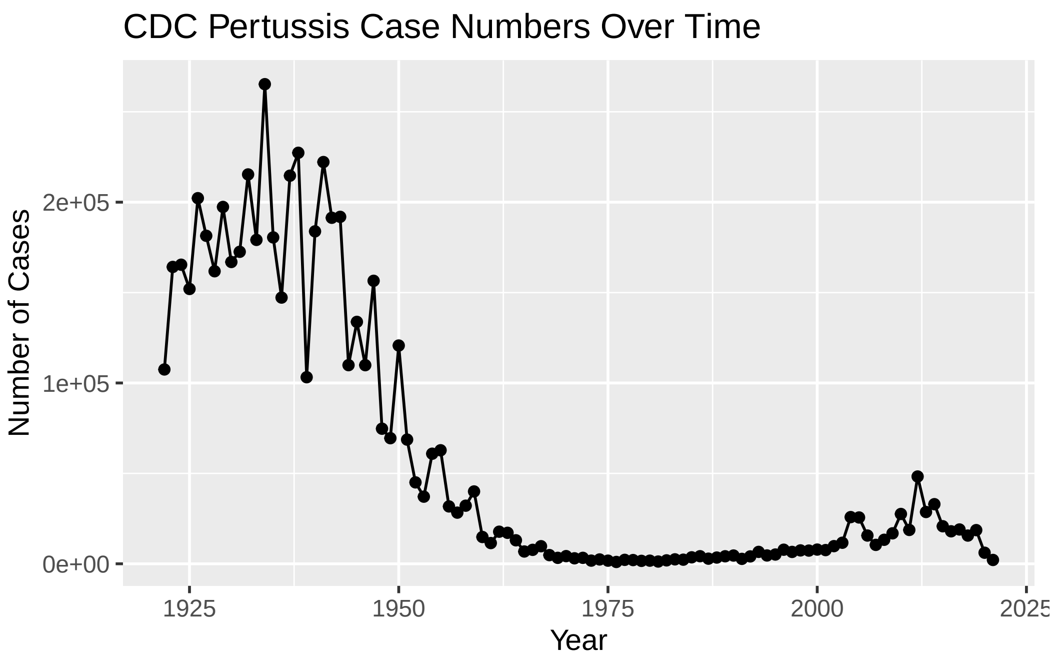
```
head(cdc)
```

```
  year  cases
1 1922 107473
2 1923 164191
3 1924 165418
4 1925 152003
5 1926 202210
6 1927 181411
```

> Q1. With the help of the R “addin” package datapasta assign the CDC pertussis case number data to a data frame called cdc and use ggplot to make a plot of cases numbers over time.

```
library(ggplot2)

ggplot(cdc, aes(x = year, y = cases)) +
  geom_point() +
  geom_line() +
  labs(title = "CDC Pertussis Case Numbers Over Time",
       x = "Year",
       y = "Number of Cases")
```



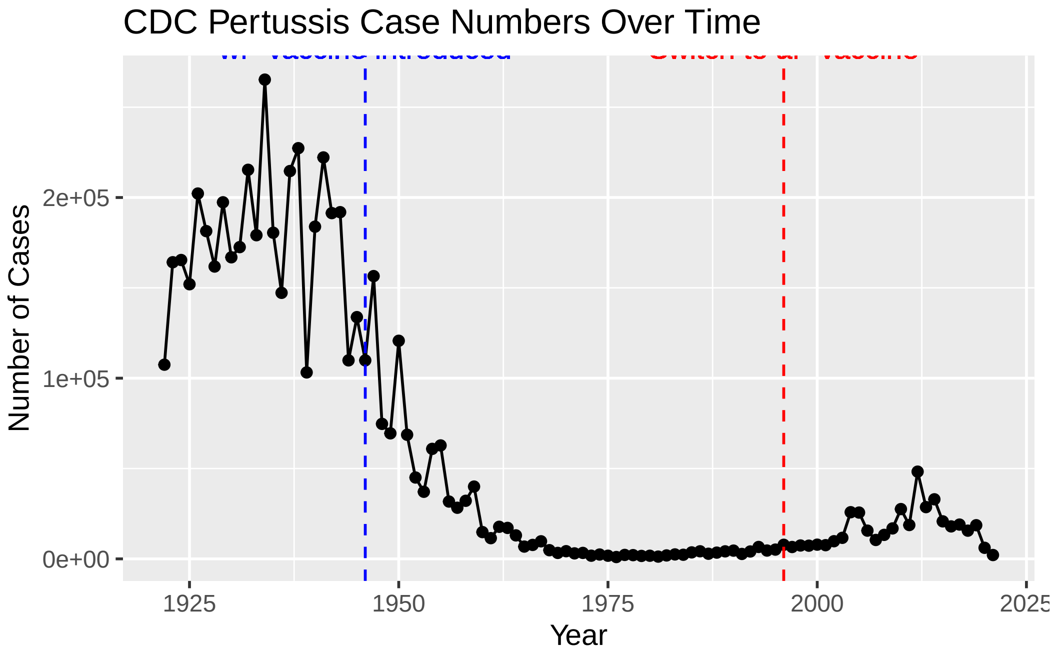
Q2. Using the ggplot geom_vline() function add lines to your previous plot for the 1946 introduction of the wP vaccine and the 1996 switch to aP vaccine (see example in the hint below). What do you notice?

```
library(ggplot2)

# Your existing plot code
ggplot(cdc, aes(x = year, y = cases)) +
  geom_point() +
  geom_line() +
  labs(title = "CDC Pertussis Case Numbers Over Time",
       x = "Year",
       y = "Number of Cases") +

  geom_vline(xintercept = 1946, linetype = "dashed", color = "blue") +
  geom_vline(xintercept = 1996, linetype = "dashed", color = "red") +

  geom_text(aes(x = 1946, y = max(cases), label = "wP vaccine introduced", vjust = -1), co
  geom_text(aes(x = 1996, y = max(cases), label = "Switch to aP vaccine", vjust = -1), col
```



Q3. Describe what happened after the introduction of the aP vaccine? Do you have a possible explanation for the observed trend?

###From the lab hands-on The answer is : It is clear from the CDC data that pertussis cases are once again increasing. For example, we can see that in 2012 the CDC reported 48,277 cases of pertussis in the United States. This is the largest number of cases reported since 1955, when 62,786 cases were reported. The pertussis field has several hypotheses for the resurgence of pertussis including (in no particular order): 1) more sensitive PCR-based testing, 2) vaccination hesitancy 3) bacterial evolution (escape from vaccine immunity), 4) waning of immunity in adolescents originally primed as infants with the newer aP vaccine as compared to the older wP vaccine.

More people get the diseases.

```
library(jsonlite)
subject <- read_json("https://www.cmi-pb.org/api/subject", simplifyVector = TRUE)
head(subject, 3)
```

```
  subject_id infancy_vac biological_sex              ethnicity  race
1          1          wP         Female Not Hispanic or Latino White
2          2          wP         Female Not Hispanic or Latino White
```

```
3          3          wP         Female                Unknown White
  year_of_birth date_of_boost      dataset
1    1986-01-01    2016-09-12 2020_dataset
2    1968-01-01    2019-01-28 2020_dataset
3    1983-01-01    2016-10-10 2020_dataset
```

> Q4. How many aP and wP infancy vaccinated subjects are in the dataset?

```r
table(subject$infancy_vac)
```

```

aP wP 
60 58 
```

```r
library(jsonlite)

# Subject table
subject <- read_json("https://www.cmi-pb.org/api/subject", simplifyVector = TRUE)
specimen <- read_json("http://cmi-pb.org/api/specimen", simplifyVector = TRUE)
titer <- read_json("http://cmi-pb.org/api/v4/plasma_ab_titer", simplifyVector = TRUE )
```

> Q5. How many Male and Female subjects/patients are in the dataset?

```r
table(subject$biological_sex)
```

```

Female   Male 
    79     39 
```

> Q6. What is the breakdown of race and biological sex (e.g. number of Asian females, White males etc…)?

```r
table(subject$race, subject$biological_sex)
```

```
                                               
                                            Female Male
  American Indian/Alaska Native                  0    1
  Asian                                         21   11
  Black or African American                      2    0
  More Than One Race                                 9    2
  Native Hawaiian or Other Pacific Islander          1    1
  Unknown or Not Reported                           11    4
  White                                             35   20
```

```r
library(lubridate)
```

```

Attaching package: 'lubridate'

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

    date, intersect, setdiff, union
```

```r
today()
```

```
[1] "2023-12-07"
```

```r
today() - ymd("2000-01-01")
```

```
Time difference of 8741 days
```

```r
time_length( today() - ymd("2000-01-01"),  "years")
```

```
[1] 23.93155
```

> Q7. Using this approach determine (i) the average age of wP individuals, (ii) the average age of aP individuals; and (iii) are they significantly different?

```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(lubridate)

subject$age <- ymd(subject$date_of_boost) - ymd(subject$year_of_birth)

subject$age_years <- time_length(subject$age,"years")
```

```r
ap <- subject %>% filter(infancy_vac == "aP")
round(summary(time_length(ap$age, "years")))
```

```
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max. 
     19      20      20      21      21      28 
```

```r
wp <- subject %>% filter(infancy_vac == "wP")
round(summary(time_length(wp$age, "years")))
```

```
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max. 
     23      26      29      31      34      51 
```

> Q8. Determine the age of all individuals at time of boost?

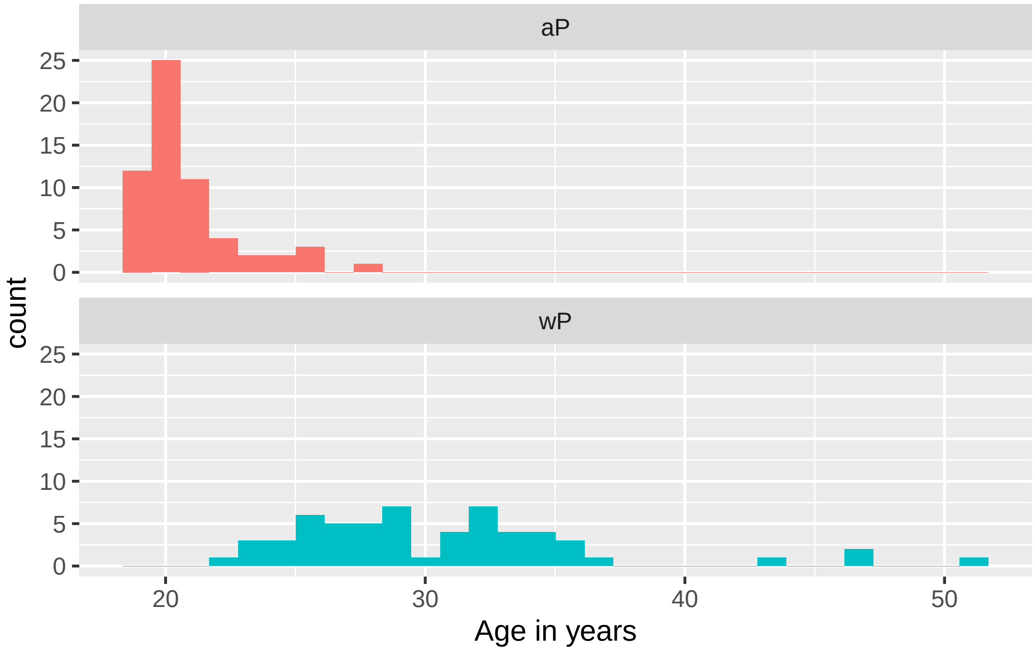
```r
int <- ymd(subject$date_of_boost) - ymd(subject$year_of_birth)
age_at_boost <- time_length(int, "year")
head(age_at_boost)
```

```
[1] 30.69678 51.07461 33.77413 28.65982 25.65914 28.77481
```

> Q9. With the help of a faceted boxplot or histogram (see below), do you think these two groups are significantly different?

```r
library(ggplot2)
ggplot(subject) +
  aes(time_length(age, "year"),
      fill=as.factor(infancy_vac)) +
  geom_histogram(show.legend=FALSE) +
  facet_wrap(vars(infancy_vac), nrow=2) +
  xlab("Age in years")
```

```
`stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```



```
# Or use wilcox.test()
x <- t.test(time_length( wp$age, "years" ),
       time_length( ap$age, "years" ))

x$p.value
```

```
[1] 9.121472e-19
```

Q9. Complete the code to join specimen and subject tables to make a new merged data frame containing all specimen records along with their associated subject details:

```
meta <- inner_join(specimen,subject)
```

```
Joining with `by = join_by(subject_id)`
```

```
dim(meta)
```

```
[1] 939  15
```

```
head(meta)
```

```
  specimen_id subject_id actual_day_relative_to_boost
1           1          1                           -3
2           2          1                            1
3           3          1                            3
4           4          1                            7
5           5          1                           11
6           6          1                           32
  planned_day_relative_to_boost specimen_type visit infancy_vac biological_sex
1                             0         Blood     1          wP         Female
2                             1         Blood     2          wP         Female
3                             3         Blood     3          wP         Female
4                             7         Blood     4          wP         Female
5                            14         Blood     5          wP         Female
6                            30         Blood     6          wP         Female
               ethnicity  race year_of_birth date_of_boost      dataset
1 Not Hispanic or Latino White    1986-01-01    2016-09-12 2020_dataset
2 Not Hispanic or Latino White    1986-01-01    2016-09-12 2020_dataset
3 Not Hispanic or Latino White    1986-01-01    2016-09-12 2020_dataset
4 Not Hispanic or Latino White    1986-01-01    2016-09-12 2020_dataset
5 Not Hispanic or Latino White    1986-01-01    2016-09-12 2020_dataset
6 Not Hispanic or Latino White    1986-01-01    2016-09-12 2020_dataset
         age age_years
1 11212 days  30.69678
2 11212 days  30.69678
3 11212 days  30.69678
4 11212 days  30.69678
5 11212 days  30.69678
6 11212 days  30.69678
```

> Q10. Now using the same procedure join meta with titer data so we can further analyze this data in terms of time of visit aP/wP, male/female etc.

```
abdata <- inner_join(titer, meta)
```

```
Joining with `by = join_by(specimen_id)`
```

```r
dim(abdata)
```

```
[1] 41810    22
```

> Q11. How many specimens (i.e. entries in abdata) do we have for each isotype?

```r
table(abdata$isotype)
```

```

 IgE  IgG IgG1 IgG2 IgG3 IgG4 
6698 3240 7968 7968 7968 7968 
```

> Q12. What are the different $dataset values in abdata and what do you notice about the number of rows for the most "recent" dataset?

```r
table(abdata$dataset)
```

```

2020_dataset 2021_dataset 2022_dataset 
       31520         8085         2205 
```

```r
igg <- abdata %>% filter(isotype == "IgG")
head(igg)
```

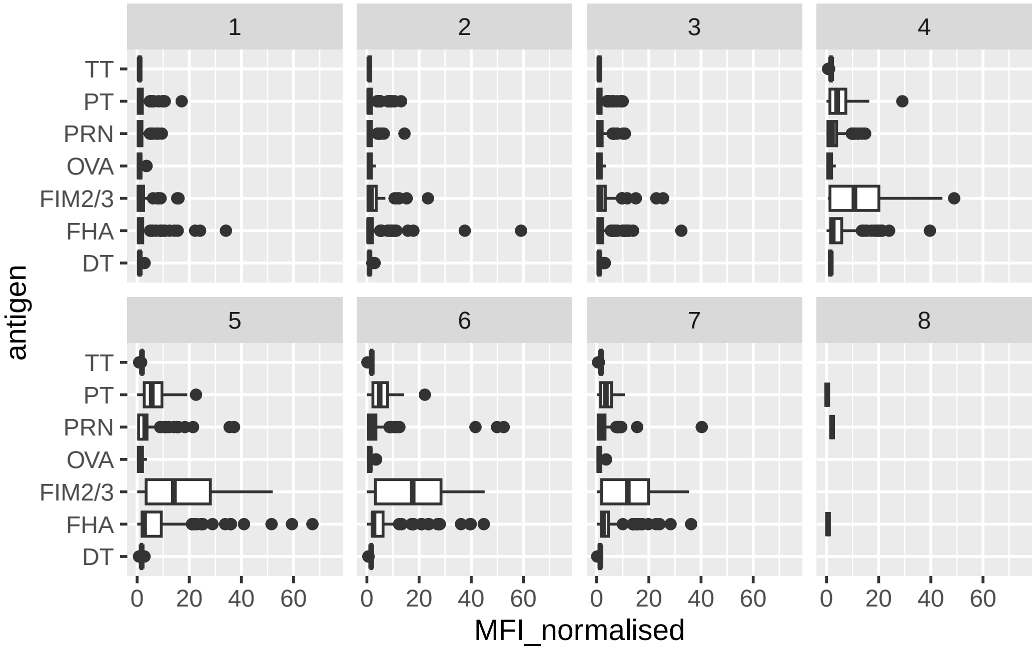
```
  specimen_id isotype is_antigen_specific antigen        MFI MFI_normalised
1           1     IgG                TRUE      PT   68.56614       3.736992
2           1     IgG                TRUE     PRN  332.12718       2.602350
3           1     IgG                TRUE     FHA 1887.12263      34.050956
4          19     IgG                TRUE      PT   20.11607       1.096366
5          19     IgG                TRUE     PRN  976.67419       7.652635
6          19     IgG                TRUE     FHA   60.76626       1.096457
   unit lower_limit_of_detection subject_id actual_day_relative_to_boost
1 IU/ML                 0.530000          1                           -3
2 IU/ML                 6.205949          1                           -3
3 IU/ML                 4.679535          1                           -3
4 IU/ML                 0.530000          3                           -3
5 IU/ML                 6.205949          3                           -3
```

```
6 IU/ML                 4.679535          3                            -3
  planned_day_relative_to_boost specimen_type visit infancy_vac biological_sex
1                             0         Blood     1          wP         Female
2                             0         Blood     1          wP         Female
3                             0         Blood     1          wP         Female
4                             0         Blood     1          wP         Female
5                             0         Blood     1          wP         Female
6                             0         Blood     1          wP         Female
               ethnicity  race year_of_birth date_of_boost      dataset
1 Not Hispanic or Latino White    1986-01-01    2016-09-12 2020_dataset
2 Not Hispanic or Latino White    1986-01-01    2016-09-12 2020_dataset
3 Not Hispanic or Latino White    1986-01-01    2016-09-12 2020_dataset
4                Unknown White    1983-01-01    2016-10-10 2020_dataset
5                Unknown White    1983-01-01    2016-10-10 2020_dataset
6                Unknown White    1983-01-01    2016-10-10 2020_dataset
         age age_years
1 11212 days  30.69678
2 11212 days  30.69678
3 11212 days  30.69678
4 12336 days  33.77413
5 12336 days  33.77413
6 12336 days  33.77413
```

Q13. Complete the following code to make a summary boxplot of Ab titer levels (MFI) for all antigens:

```
ggplot(igg)+
  aes(MFI_normalised ,
      antigen) +
  geom_boxplot() +
  xlim(0,75) +
 facet_wrap(vars(visit),nrow = 2)
```

```
Warning: Removed 5 rows containing non-finite values (`stat_boxplot()`).
```


1
2
3
4
5
6
7
8
antigen
TT
PT
PRN
OVA
FIM2/3
FHA
DT
0
20
40
60
MFI_normalised