Investigating Pertussis Resurgence, Class 15

Janie Chang-Weinberg (A69037446)

Pertussis, aka "whooping cough" is a highly contagious lung infection caused by the *B. Pertussis* bacteria.

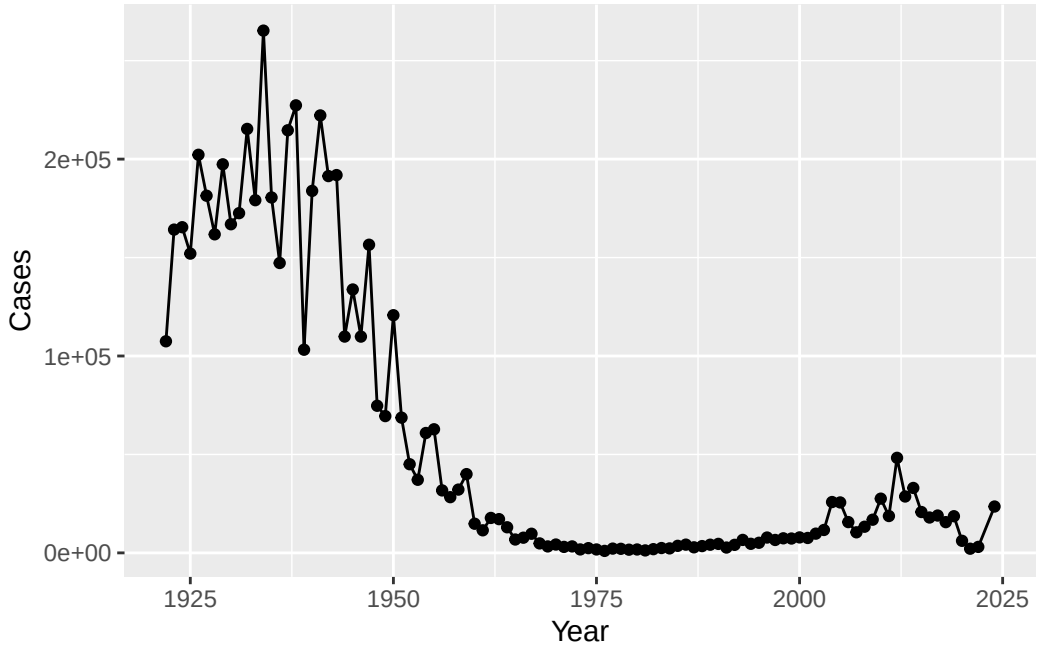
The CDC tracks Pertussis case numbers and they can be accessed here

We need to "scrape" this data so we do stuff with it in R. Let's try the **datapasta** package to do this.

```
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,2022L,2024L),
         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,
```

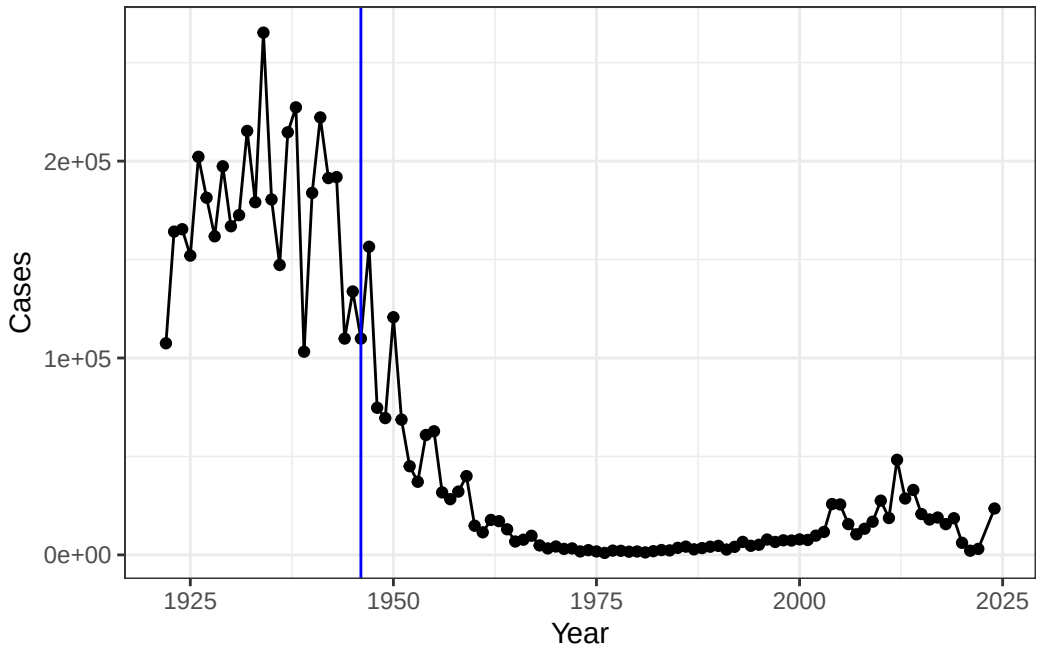
```
                                        133792,109860,156517,74715,69479,
                                        120718,68687,45030,37129,60886,
                                        62786,31732,28295,32148,40005,
                                        14809,11468,17749,17135,13005,6799,
                                        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,
                                        6124,2116,3044, 23544)
       )
```

```
library(ggplot2)

baseplot <- ggplot(cdc, aes(Year, Cases)) +
  geom_point() +
  geom_line()

baseplot
```



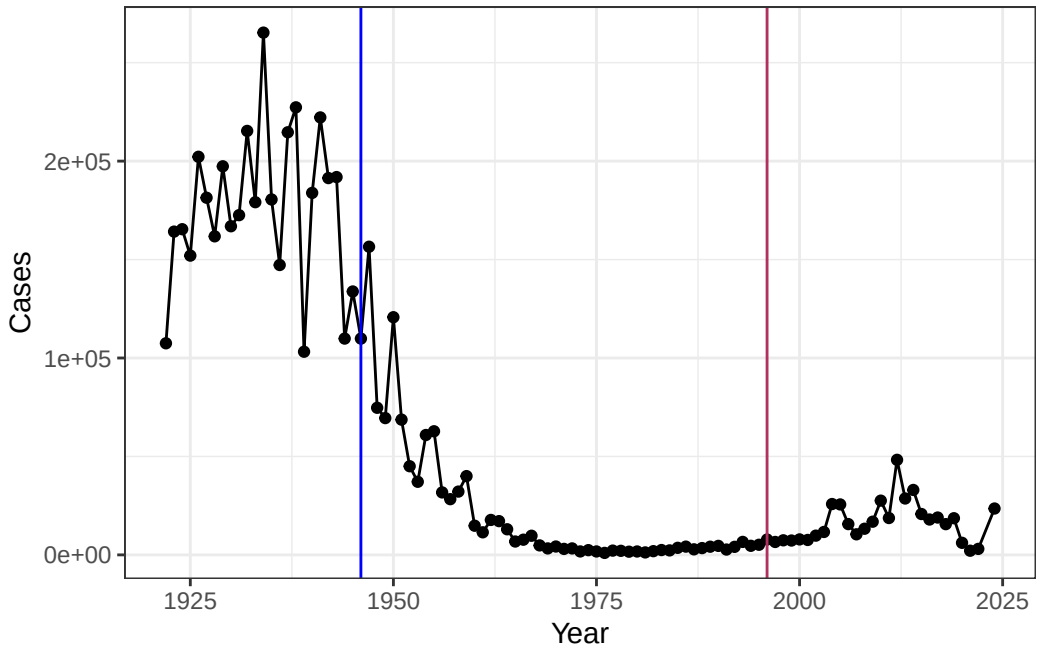
Let's add the date of the wP vaccination introduction.

```
baseplot +
  theme_bw() +
  geom_vline(xintercept = 1946, color = "blue")
```



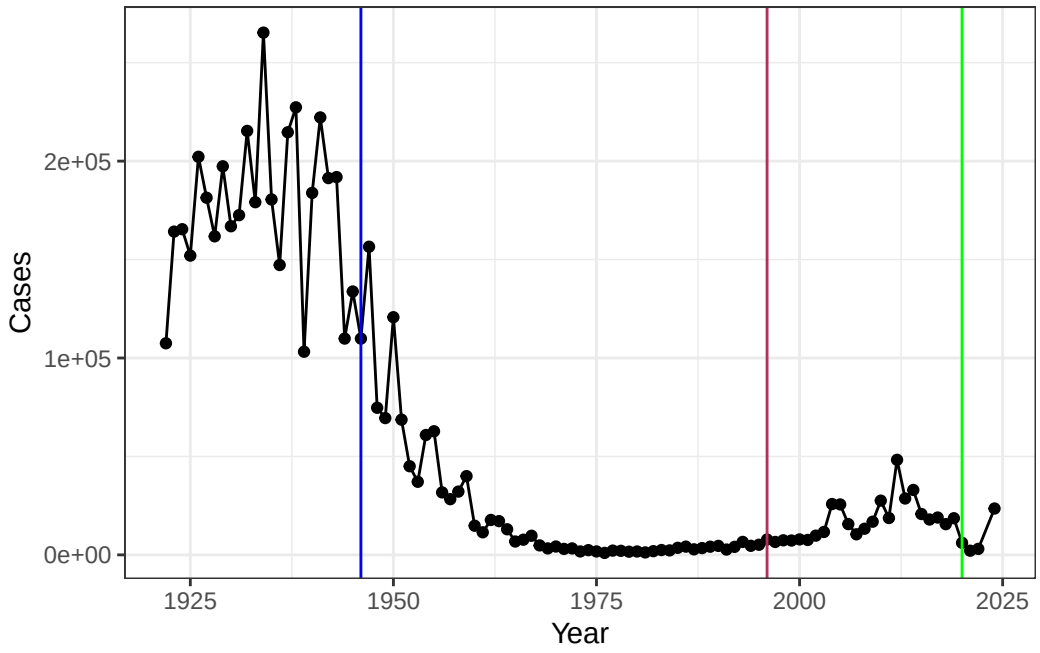
Let's add the date of the switch to the new aP vaccine.

```
baseplot +
  theme_bw() +
  geom_vline(xintercept = 1946, color = "blue") +
  geom_vline(xintercept = 1996, color = "maroon")
```



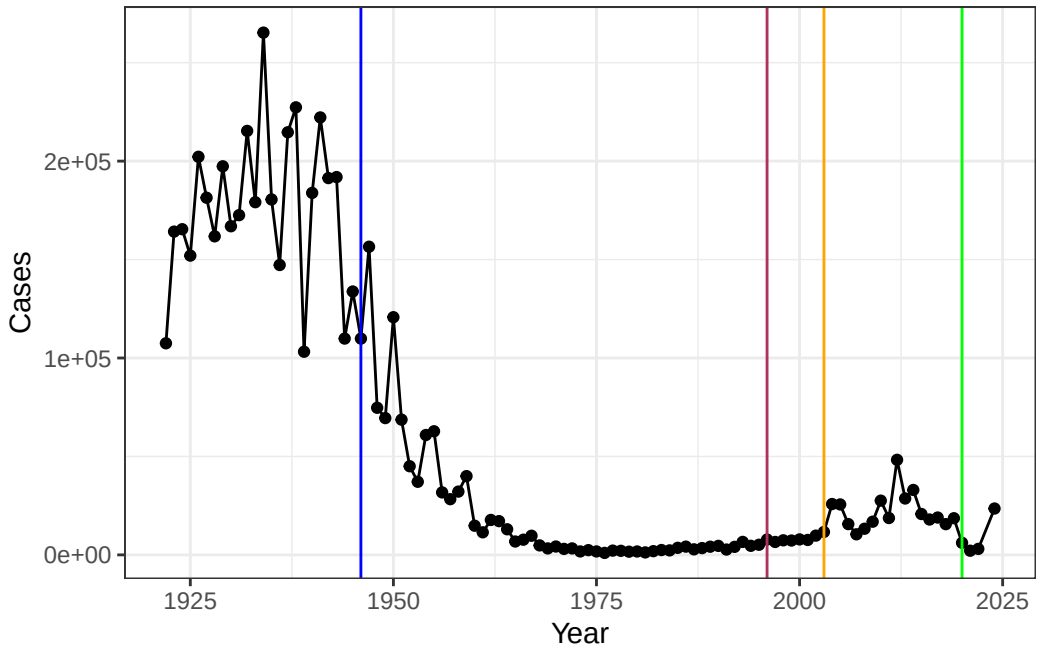
let's add in COVID

```
baseplot +
  theme_bw() +
  geom_vline(xintercept = 1946, color = "blue") +
  geom_vline(xintercept = 1996, color = "maroon") +
  geom_vline(xintercept = 2020, color = "green")
```



There was a pertussis outbreak in Disneyland or something

```
baseplot +
  theme_bw() +
  geom_vline(xintercept = 1946, color = "blue") +
  geom_vline(xintercept = 1996, color = "maroon") +
  geom_vline(xintercept = 2020, color = "green") +
  geom_vline(xintercept = 2003, color = "orange")
```



CMI-PB (Computational Models of Immunity - Pertussis Boost)

This project collects and makes freely available data about the immune response to Pertussis vaccination.

You can access the data via an API which returns JSON format (key:value pairs).

We can use the **jsonlite** package and it's `read_json()` function.

```
library(jsonlite)

subject <- read_json("http://cmi-pb.org/api/v5/subject",
                     simplifyVector = TRUE)

# let's take a gander
head(subject)
```

```
  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
4          4          wP           Male Not Hispanic or Latino Asian
```

```
5          5          wP           Male Not Hispanic or Latino Asian
6          6          wP         Female Not Hispanic or Latino 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
4    1988-01-01    2016-08-29 2020_dataset
5    1991-01-01    2016-08-29 2020_dataset
6    1988-01-01    2016-10-10 2020_dataset
```

How many subjects do we have?

```
nrow(subject)
```

```
[1] 172
```

there are 172 subjects here.

How many male/female do we have?

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

```
Female   Male
   112     60
```

There are 112 females and 60 males

How many wP and aP do we have?

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

```
aP wP
87 85
```

There are 85 wP and 87 aP.

Breakdown of biological sex and race?

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

```
                                        Female Male
  American Indian/Alaska Native              0    1
  Asian                                     32   12
  Black or African American                  2    3
  More Than One Race                        15    4
  Native Hawaiian or Other Pacific Islander  1    1
  Unknown or Not Reported                   14    7
  White                                     48   32
```

Does this breakdown reflect the US population?

```
table(subject$dataset)
```

```
2020_dataset 2021_dataset 2022_dataset 2023_dataset
          60           36           22           54
```

NO!

These data are still useful, however.

```
specimen <- read_json("http://cmi-pb.org/api/v5/specimen",
                      simplifyVector = TRUE)

ab_titer <- read_json("http://cmi-pb.org/api/v5/plasma_ab_titer",
                      simplifyVector = TRUE)
```

```
head(specimen)
```

```
  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
1                             0         Blood     1
2                             1         Blood     2
3                             3         Blood     3
4                             7         Blood     4
5                            14         Blood     5
6                            30         Blood     6
```

```
head(ab_titer)
```

```
  specimen_id isotype is_antigen_specific antigen        MFI MFI_normalised
1           1     IgE               FALSE   Total 1110.21154       2.493425
2           1     IgE               FALSE   Total 2708.91616       2.493425
3           1     IgG                TRUE      PT   68.56614       3.736992
4           1     IgG                TRUE     PRN  332.12718       2.602350
5           1     IgG                TRUE     FHA 1887.12263      34.050956
6           1     IgE                TRUE     ACT    0.10000       1.000000
   unit lower_limit_of_detection
1 UG/ML                2.096133
2 IU/ML               29.170000
3 IU/ML                0.530000
4 IU/ML                6.205949
5 IU/ML                4.679535
6 IU/ML                2.816431
```

We want to join `subject` and `specimen` together! Using dplyer, there are two modes of joining– innerjoining or full joining. Inerjoining only merges data frame values for which there are no values missing from either dataset.

For this, we only want those who both were vaccinated and also had their titers recorded, so we will use innerjoining.

```
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
```

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

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

```
head(meta)
```

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

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

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

```
head(abdata)
```

```
  specimen_id isotype is_antigen_specific antigen        MFI MFI_normalised
1           1     IgE               FALSE   Total 1110.21154       2.493425
2           1     IgE               FALSE   Total 2708.91616       2.493425
3           1     IgG                TRUE      PT   68.56614       3.736992
4           1     IgG                TRUE     PRN  332.12718       2.602350
5           1     IgG                TRUE     FHA 1887.12263      34.050956
6           1     IgE                TRUE     ACT    0.10000       1.000000
   unit lower_limit_of_detection subject_id infancy_vac biological_sex
1 UG/ML                 2.096133          1          wP         Female
2 IU/ML                29.170000          1          wP         Female
3 IU/ML                 0.530000          1          wP         Female
4 IU/ML                 6.205949          1          wP         Female
5 IU/ML                 4.679535          1          wP         Female
6 IU/ML                 2.816431          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 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
  actual_day_relative_to_boost planned_day_relative_to_boost specimen_type
1                           -3                             0         Blood
2                           -3                             0         Blood
3                           -3                             0         Blood
4                           -3                             0         Blood
5                           -3                             0         Blood
6                           -3                             0         Blood
  visit
1     1
2     1
3     1
4     1
5     1
6     1
```

```
nrow(abdata)
```

```
[1] 52576
```

wow !

```
head(abdata)
```

```
  specimen_id isotype is_antigen_specific antigen        MFI MFI_normalised
1           1     IgE               FALSE   Total 1110.21154       2.493425
2           1     IgE               FALSE   Total 2708.91616       2.493425
3           1     IgG                TRUE      PT   68.56614       3.736992
4           1     IgG                TRUE     PRN  332.12718       2.602350
5           1     IgG                TRUE     FHA 1887.12263      34.050956
6           1     IgE                TRUE     ACT    0.10000       1.000000
   unit lower_limit_of_detection subject_id infancy_vac biological_sex
1 UG/ML                2.096133          1          wP         Female
2 IU/ML               29.170000          1          wP         Female
3 IU/ML                0.530000          1          wP         Female
4 IU/ML                6.205949          1          wP         Female
5 IU/ML                4.679535          1          wP         Female
6 IU/ML                2.816431          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 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
  actual_day_relative_to_boost planned_day_relative_to_boost specimen_type
1                           -3                             0         Blood
2                           -3                             0         Blood
3                           -3                             0         Blood
4                           -3                             0         Blood
5                           -3                             0         Blood
6                           -3                             0         Blood
  visit
1     1
2     1
3     1
4     1
```

```
5     1
6     1
```

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

```
  IgE   IgG  IgG1  IgG2  IgG3  IgG4
 6698  5389 10117 10124 10124 10124
```

```
table(abdata$antigen)
```

```
    ACT   BETV1      DT   FELD1     FHA  FIM2/3   LOLP1     LOS Measles     OVA
   1970    1970    4978    1970    5372    4978    1970    1970    1970    4978
    PD1     PRN      PT     PTM   Total      TT
   1970    5372    5372    1970     788    4978
```

Let's look at IgG.

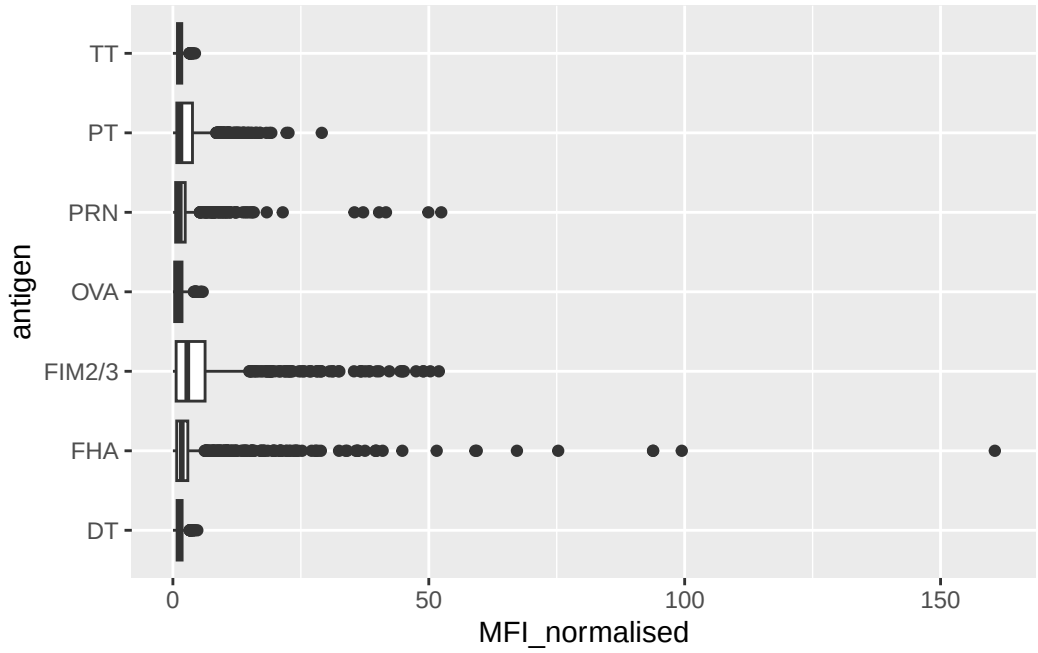
```
igg <- filter(abdata, isotype=="IgG")
head(igg)
```

```
  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 infancy_vac biological_sex
1 IU/ML                0.530000          1          wP         Female
2 IU/ML                6.205949          1          wP         Female
3 IU/ML                4.679535          1          wP         Female
4 IU/ML                0.530000          3          wP         Female
5 IU/ML                6.205949          3          wP         Female
6 IU/ML                4.679535          3          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
```

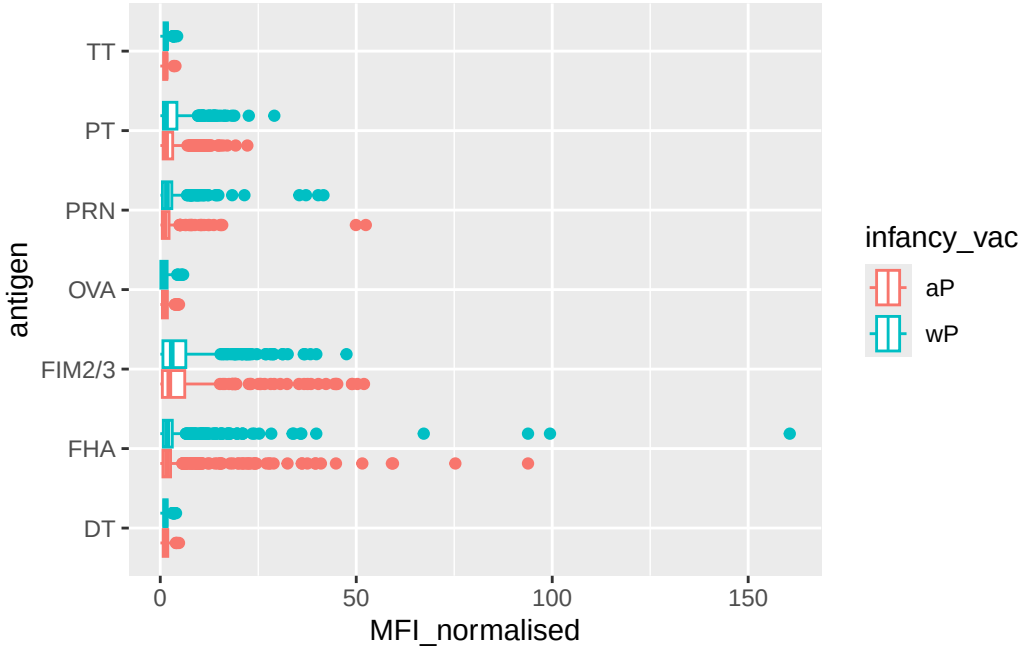
```
4                 Unknown White    1983-01-01    2016-10-10 2020_dataset
5                 Unknown White    1983-01-01    2016-10-10 2020_dataset
6                 Unknown White    1983-01-01    2016-10-10 2020_dataset
  actual_day_relative_to_boost planned_day_relative_to_boost specimen_type
1                           -3                             0         Blood
2                           -3                             0         Blood
3                           -3                             0         Blood
4                           -3                             0         Blood
5                           -3                             0         Blood
6                           -3                             0         Blood
  visit
1     1
2     1
3     1
4     1
5     1
6     1
```

Make a boxplot of IgG antigen levels. This will be a plot of MFI vs antigen.

```
ggplot(igg, aes(MFI_normalised, antigen)) +
  geom_boxplot()
```



```
ggplot(igg, aes(MFI_normalised, antigen, color = infancy_vac)) +
  geom_boxplot()
```

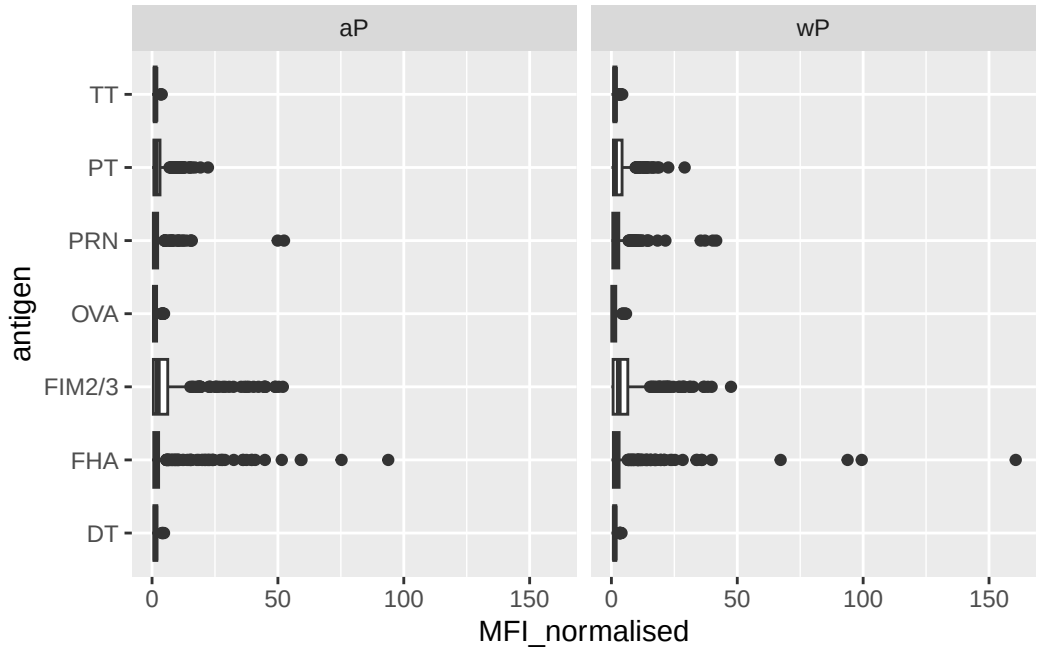


Ideally, we would like to see how these Ab levels change over time relative to the booster shot.

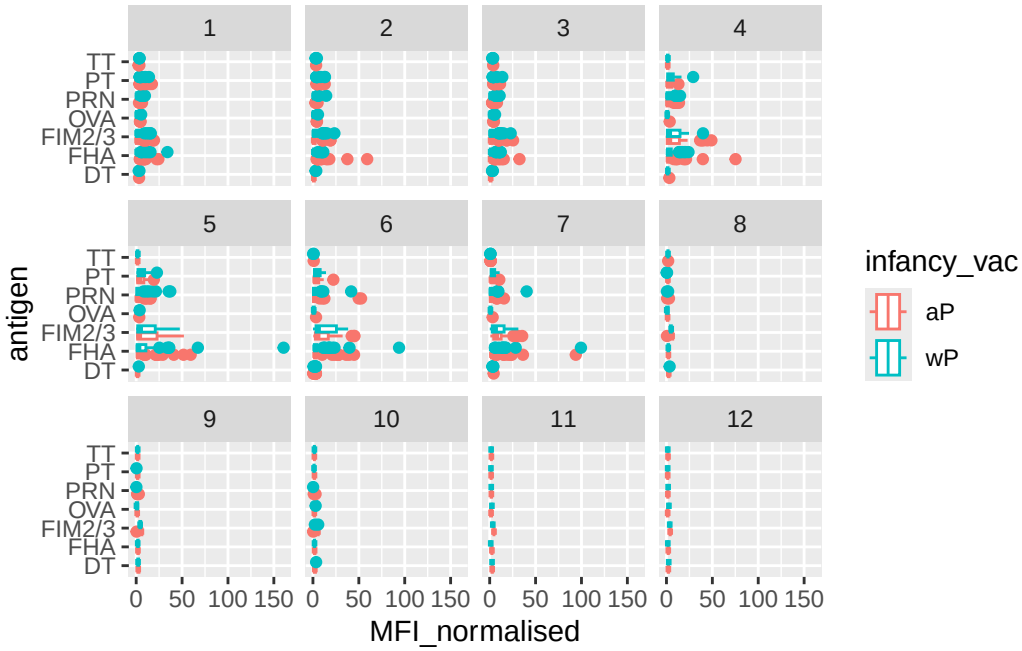
```
table(abdata$visit)
```

```
   1    2    3    4    5    6    7    8    9   10   11   12
8280 8280 8420 6565 6565 6210 5810  815  735  686  105  105
```

```
ggplot(igg)+
  aes(MFI_normalised, antigen) +
  geom_boxplot() +
  facet_wrap(~infancy_vac)
```




```
ggplot(igg)+
  aes(MFI_normalised, antigen, color = infancy_vac) +
  geom_boxplot() +
  facet_wrap(~visit)
```




```
iggpt <- filter(igg, antigen=="PT")
head(iggpt)
```

```
  specimen_id isotype is_antigen_specific antigen       MFI MFI_normalised
1           1     IgG                TRUE      PT 68.566139      3.7369917
2          19     IgG                TRUE      PT 20.116067      1.0963659
3          27     IgG                TRUE      PT 37.552222      2.0466712
4          37     IgG                TRUE      PT 69.685645      3.7980070
5          45     IgG                TRUE      PT  3.914130      0.2133279
6          55     IgG                TRUE      PT  9.139656      0.4981295
   unit lower_limit_of_detection subject_id infancy_vac biological_sex
1 IU/ML                     0.53          1          wP         Female
2 IU/ML                     0.53          3          wP         Female
3 IU/ML                     0.53          4          wP           Male
4 IU/ML                     0.53          5          wP           Male
5 IU/ML                     0.53          6          wP         Female
6 IU/ML                     0.53          7          wP         Female
              ethnicity              race year_of_birth date_of_boost
1 Not Hispanic or Latino             White    1986-01-01    2016-09-12
2               Unknown              White    1983-01-01    2016-10-10
3 Not Hispanic or Latino             Asian    1988-01-01    2016-08-29
4 Not Hispanic or Latino             Asian    1991-01-01    2016-08-29
```

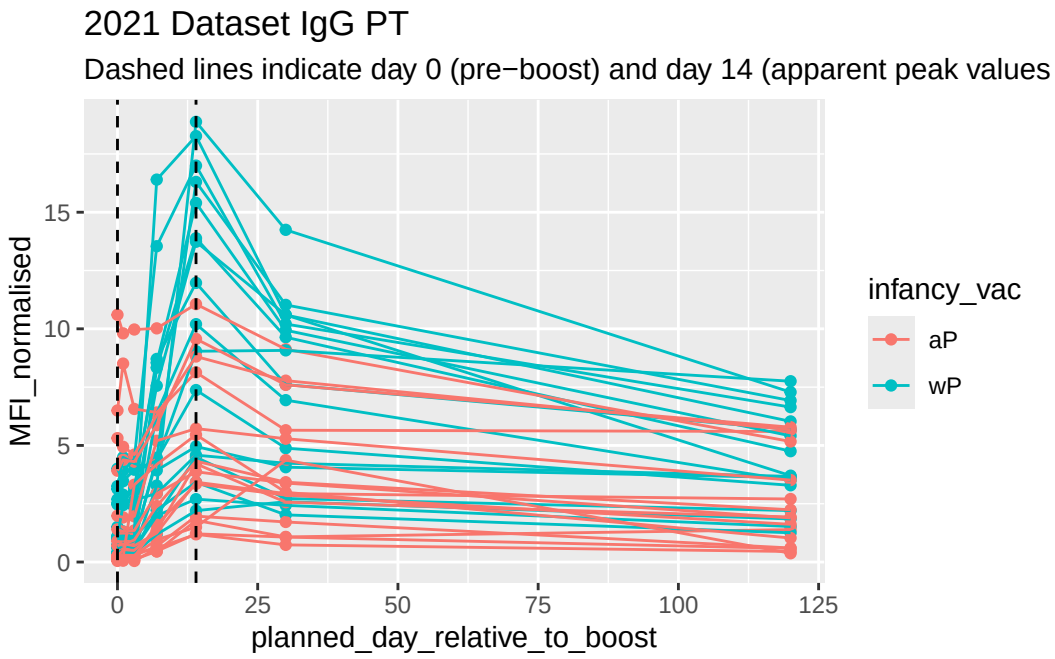
```
5 Not Hispanic or Latino              White    1988-01-01    2016-10-10
6     Hispanic or Latino More Than One Race    1981-01-01    2016-11-07
       dataset actual_day_relative_to_boost planned_day_relative_to_boost
1 2020_dataset                           -3                             0
2 2020_dataset                           -3                             0
3 2020_dataset                           -7                             0
4 2020_dataset                           -5                             0
5 2020_dataset                           -6                             0
6 2020_dataset                           -6                             0
  specimen_type visit
1         Blood     1
2         Blood     1
3         Blood     1
4         Blood     1
5         Blood     1
6         Blood     1
```

```r
iggpt21 <- filter(iggpt, dataset=="2021_dataset")
head(iggpt21)
```

```
  specimen_id isotype is_antigen_specific antigen    MFI MFI_normalised unit
1         468     IgG               FALSE      PT 112.75      1.0000000  MFI
2         469     IgG               FALSE      PT 111.25      0.9866962  MFI
3         470     IgG               FALSE      PT 125.50      1.1130820  MFI
4         471     IgG               FALSE      PT 224.25      1.9889135  MFI
5         472     IgG               FALSE      PT 304.00      2.6962306  MFI
6         473     IgG               FALSE      PT 274.00      2.4301552  MFI
  lower_limit_of_detection subject_id infancy_vac biological_sex
1                 5.197441         61          wP         Female
2                 5.197441         61          wP         Female
3                 5.197441         61          wP         Female
4                 5.197441         61          wP         Female
5                 5.197441         61          wP         Female
6                 5.197441         61          wP         Female
              ethnicity                   race year_of_birth date_of_boost
1 Not Hispanic or Latino Unknown or Not Reported    1987-01-01    2019-04-08
2 Not Hispanic or Latino Unknown or Not Reported    1987-01-01    2019-04-08
3 Not Hispanic or Latino Unknown or Not Reported    1987-01-01    2019-04-08
4 Not Hispanic or Latino Unknown or Not Reported    1987-01-01    2019-04-08
5 Not Hispanic or Latino Unknown or Not Reported    1987-01-01    2019-04-08
6 Not Hispanic or Latino Unknown or Not Reported    1987-01-01    2019-04-08
       dataset actual_day_relative_to_boost planned_day_relative_to_boost
```

```
1 2021_dataset                          -4                           0
2 2021_dataset                           1                           1
3 2021_dataset                           3                           3
4 2021_dataset                           7                           7
5 2021_dataset                          14                          14
6 2021_dataset                          30                          30
  specimen_type visit
1         Blood     1
2         Blood     2
3         Blood     3
4         Blood     4
5         Blood     5
6         Blood     6
```

```r
ggplot(iggpt21) +
  aes(x= planned_day_relative_to_boost,
      y= MFI_normalised,
      color = infancy_vac,
      group = subject_id)+
  geom_point()+
  geom_line()+
  geom_vline(xintercept=0, linetype="dashed")+
  geom_vline(xintercept=14, linetype="dashed")+
  labs(title="2021 Dataset IgG PT", subtitle="Dashed lines indicate day 0 (pre-boost) and day
```


2021 Dataset IgG PT
Dashed lines indicate day 0 (pre−boost) and day 14 (apparent peak values
MFI_normalised
15
10
5
0
0
25
50
75
100
125
planned_day_relative_to_boost
infancy_vac
aP
wP

yayy