Class 18: Mini Project - Investigating Pertussis Resurgence

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First we will examine and explore Pertussis case numbers in the US as tracked by the CDC: https://www.cdc.gov/pertussis/surv-reporting/cases-by-year.html

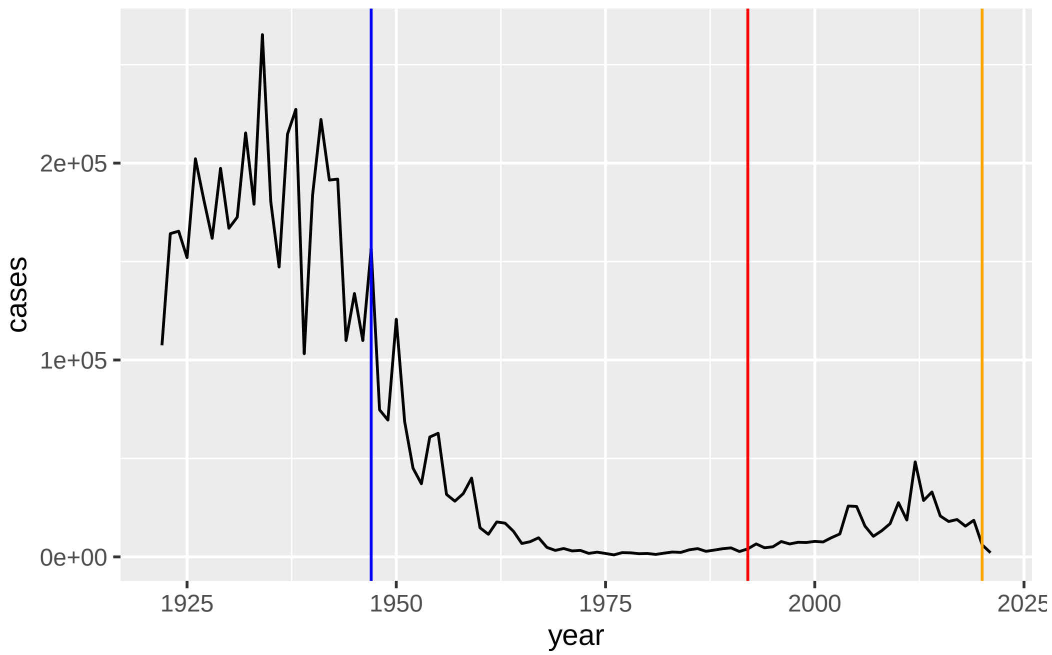
We can use the datapasta package package to scrape

```r
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)
       )
```

I want a plot of cases per year

```
library(ggplot2)

ggplot(cdc) +
  aes(year, cases) +
  geom_line() +
  geom_vline(xintercept = 1947, col="blue" ) +
  geom_vline(xintercept = 1992, col="red") +
  geom_vline(xintercept = 2020, col="orange")
```



Access data from CMI-PB project

This database (like many modern projects) uses an API to return JSON format data.

We will use the R package `jsonlite`

```
library(jsonlite)

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

```
sum(subject$infancy_vac == "wP")
```

```
[1] 58
```

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

```

aP wP 
60 58 
```

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

```

Female   Male 
    79     39 
```

```
table(subject$race)
```

```

            American Indian/Alaska Native 
                                        1 
                                    Asian 
                                       32 
                Black or African American 
                                        2 
                       More Than One Race 
                                       11 
Native Hawaiian or Other Pacific Islander 
                                        2 
                  Unknown or Not Reported 
                                       15 
                                    White 
                                       55 
```

```
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
```

```
subject$year_of_birth
```

```
  [1] "1986-01-01" "1968-01-01" "1983-01-01" "1988-01-01" "1991-01-01"
  [6] "1988-01-01" "1981-01-01" "1985-01-01" "1996-01-01" "1982-01-01"
 [11] "1986-01-01" "1982-01-01" "1997-01-01" "1993-01-01" "1989-01-01"
 [16] "1987-01-01" "1980-01-01" "1997-01-01" "1994-01-01" "1981-01-01"
 [21] "1983-01-01" "1985-01-01" "1991-01-01" "1992-01-01" "1988-01-01"
 [26] "1983-01-01" "1997-01-01" "1982-01-01" "1997-01-01" "1988-01-01"
 [31] "1989-01-01" "1997-01-01" "1990-01-01" "1983-01-01" "1991-01-01"
 [36] "1997-01-01" "1998-01-01" "1997-01-01" "1985-01-01" "1994-01-01"
 [41] "1985-01-01" "1997-01-01" "1998-01-01" "1998-01-01" "1997-01-01"
 [46] "1998-01-01" "1996-01-01" "1998-01-01" "1997-01-01" "1997-01-01"
 [51] "1997-01-01" "1998-01-01" "1998-01-01" "1997-01-01" "1997-01-01"
 [56] "1997-01-01" "1996-01-01" "1997-01-01" "1997-01-01" "1997-01-01"
 [61] "1987-01-01" "1993-01-01" "1995-01-01" "1993-01-01" "1990-01-01"
 [66] "1976-01-01" "1972-01-01" "1972-01-01" "1990-01-01" "1998-01-01"
 [71] "1998-01-01" "1991-01-01" "1995-01-01" "1995-01-01" "1998-01-01"
 [76] "1998-01-01" "1988-01-01" "1993-01-01" "1987-01-01" "1992-01-01"
 [81] "1993-01-01" "1998-01-01" "1999-01-01" "1997-01-01" "2000-01-01"
 [86] "1998-01-01" "2000-01-01" "2000-01-01" "1997-01-01" "1999-01-01"
 [91] "1998-01-01" "2000-01-01" "1996-01-01" "1999-01-01" "1998-01-01"
 [96] "2000-01-01" "1986-01-01" "1993-01-01" "1999-01-01" "2001-01-01"
[101] "2003-01-01" "2003-01-01" "1994-01-01" "1989-01-01" "1994-01-01"
[106] "1996-01-01" "1998-01-01" "1995-01-01" "1989-01-01" "1997-01-01"
[111] "1996-01-01" "1996-01-01" "1996-01-01" "1990-01-01" "2002-01-01"
[116] "2000-01-01" "1994-01-01" "1998-01-01"
```

Side-Note: Working with dates

We can use the `lubridate` package to ease the pain of working with dates

```r
library(lubridate)
```

```

Attaching package: 'lubridate'

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

    date, intersect, setdiff, union
```

```r
today()
```

```
[1] "2024-03-07"
```

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

```
Time difference of 8832 days
```

```r
today() - ymd("2002-02-21")
```

```
Time difference of 8050 days
```

```r
time_length(today() - ymd("2002-02-21"), "years")
```

```
[1] 22.0397
```

So what is the age of everyone in our dataset

```r
time_length(today() - ymd(subject$year_of_birth), "years")
```

```
 [1] 38.17933 56.18070 41.18001 36.18070 33.18001 36.18070 43.17864 39.17864
 [9] 28.18070 42.17933 38.17933 42.17933 27.17864 31.17864 35.17864 37.18001
[17] 44.18070 27.17864 30.17933 43.17864 41.18001 39.17864 33.18001 32.18070
[25] 36.18070 41.18001 27.17864 42.17933 27.17864 36.18070 35.17864 27.17864
[33] 34.17933 41.18001 33.18001 27.17864 26.17933 27.17864 39.17864 30.17933
[41] 39.17864 27.17864 26.17933 26.17933 27.17864 26.17933 28.18070 26.17933
[49] 27.17864 27.17864 27.17864 26.17933 26.17933 27.17864 27.17864 27.17864
[57] 28.18070 27.17864 27.17864 27.17864 37.18001 31.17864 29.18001 31.17864
```

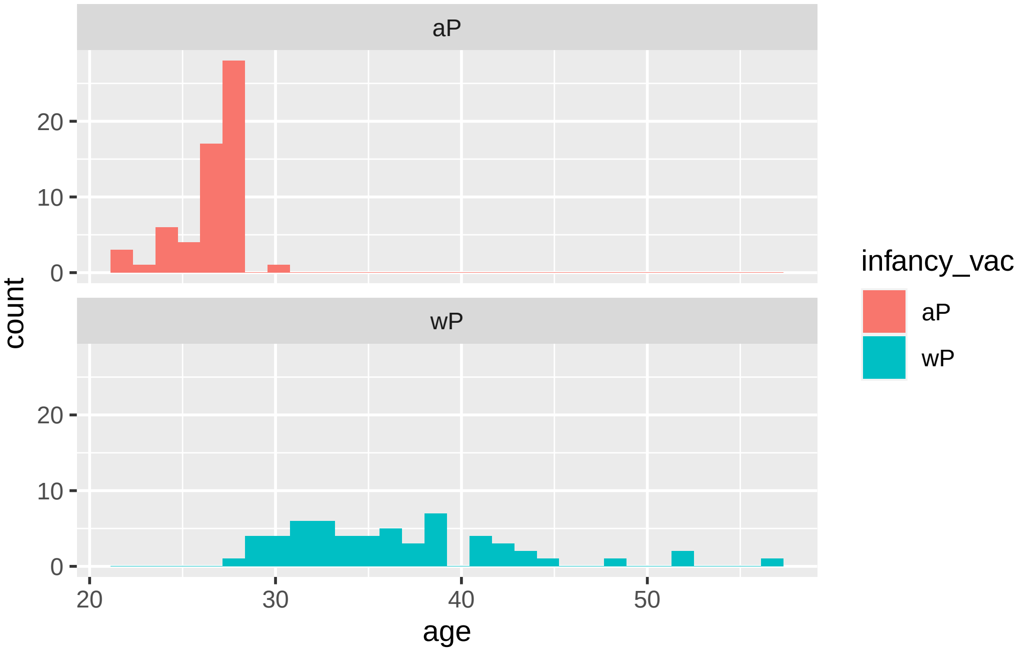
```
 [65] 34.17933 48.18070 52.18070 52.18070 34.17933 26.17933 26.17933 33.18001
 [73] 29.18001 29.18001 26.17933 26.17933 36.18070 31.17864 37.18001 32.18070
 [81] 31.17864 26.17933 25.18001 27.17864 24.18070 26.17933 24.18070 24.18070
 [89] 27.17864 25.18001 26.17933 24.18070 28.18070 25.18001 26.17933 24.18070
 [97] 38.17933 31.17864 25.18001 23.17864 21.18001 21.18001 30.17933 35.17864
[105] 30.17933 28.18070 26.17933 29.18001 35.17864 27.17864 28.18070 28.18070
[113] 28.18070 34.17933 22.17933 24.18070 30.17933 26.17933
```

```r
subject$age <- time_length(today() - ymd(subject$year_of_birth), "years")
```

plot of ages

```r
ggplot(subject) +
  aes(age, fill=infancy_vac) +
  geom_histogram() +
  facet_wrap(vars(infancy_vac), nrow=2)
```

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



Get more data from CMI-PB

```
specimen <- read_json("http://cmi-pb.org/api/specimen", 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
```

```
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      age specimen_id
1    1986-01-01    2016-09-12 2020_dataset 38.17933           1
2    1986-01-01    2016-09-12 2020_dataset 38.17933           2
3    1986-01-01    2016-09-12 2020_dataset 38.17933           3
4    1986-01-01    2016-09-12 2020_dataset 38.17933           4
5    1986-01-01    2016-09-12 2020_dataset 38.17933           5
6    1986-01-01    2016-09-12 2020_dataset 38.17933           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
```

Now we can read some of the other data from CMI-PB

```
ab_titer <- read_json("http://cmi-pb.org/api/v4/plasma_ab_titer", simplifyVector = T)
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
```

One more `inner_join()` to add all our metadata in `meta` on to our `abdata` table:

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

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

```r
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
       age actual_day_relative_to_boost planned_day_relative_to_boost
1 38.17933                           -3                             0
```

```
2 38.17933                           -3                            0
3 38.17933                           -3                            0
4 38.17933                           -3                            0
5 38.17933                           -3                            0
6 38.17933                           -3                            0
  specimen_type visit
1         Blood     1
2         Blood     1
3         Blood     1
4         Blood     1
5         Blood     1
6         Blood     1
```

Our first exploratory plot:

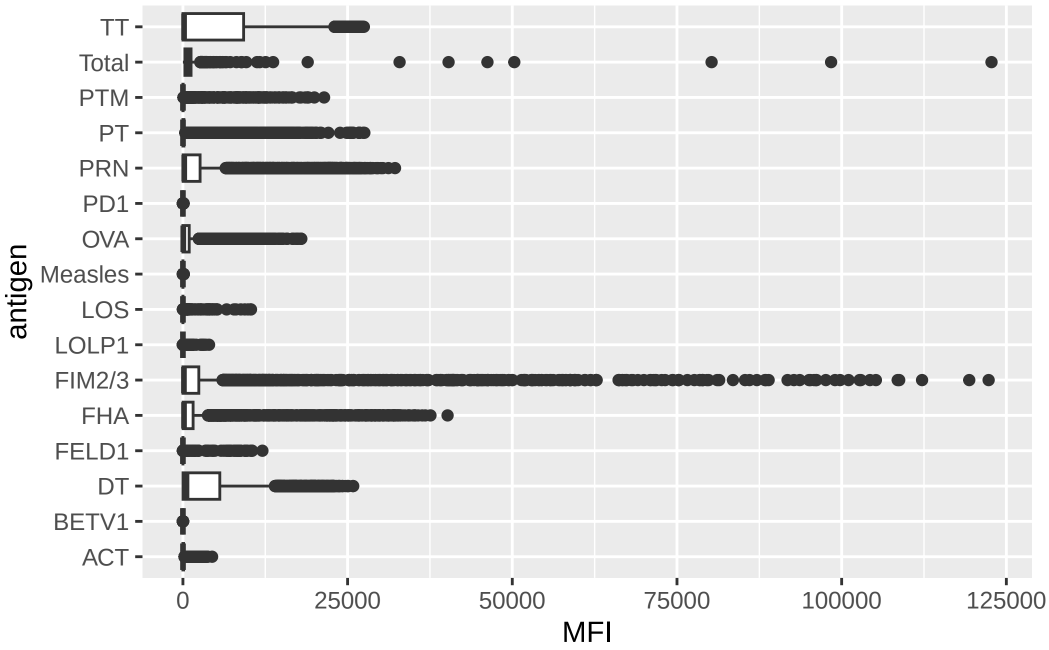
```r
table(abdata$antigen)
```

```

    ACT   BETV1      DT   FELD1     FHA  FIM2/3   LOLP1     LOS Measles     OVA 
   1970    1970    3435    1970    3829    3435    1970    1970    1970    3435 
    PD1     PRN      PT     PTM   Total      TT 
   1970    3829    3829    1970     788    3435 
```

```r
ggplot(abdata) +
  aes(MFI, antigen) +
  geom_boxplot()
```

```
Warning: Removed 1 rows containing non-finite values (`stat_boxplot()`).
```

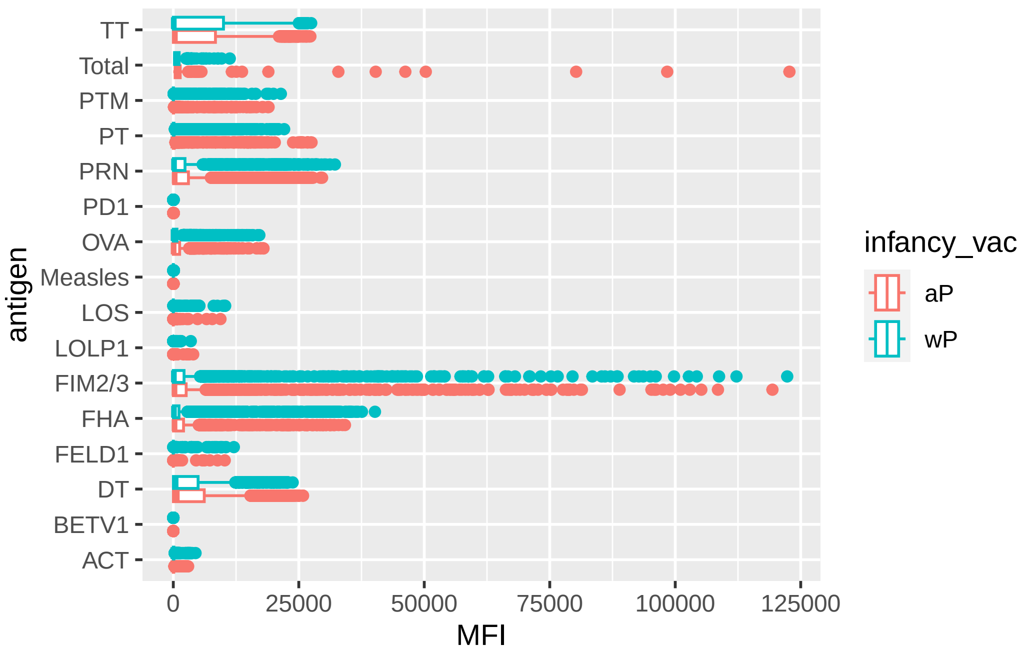


Why are certain antigens and not other very variable in their detected levels here?

Can you facet or even just color by infancy_vac? Is there some difference?

```
ggplot(abdata) +
  aes(MFI, antigen, col=infancy_vac) +
  geom_boxplot()
```

```
Warning: Removed 1 rows containing non-finite values (`stat_boxplot()`).
```



There are potentially some differences here but in general it is hard to tell with this whole dataset overview…

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

```
2020_dataset 2021_dataset 2022_dataset 
       31520         8085         2170 
```

Let's focus in on just the 2021_dataset.

```
abdata.21 <- filter(abdata, dataset == "2021_dataset")
table(abdata.21$dataset)
```

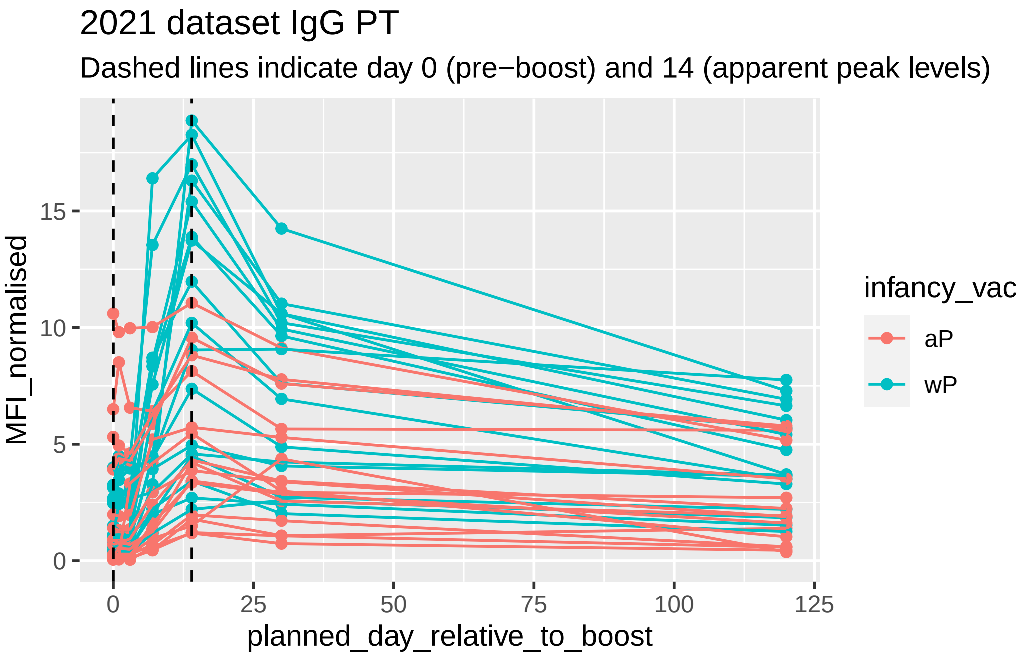
```
2021_dataset 
        8085 
```

Focus on PT antigen IgG levels

```
pt.21 <- filter(abdata.21, isotype == "IgG", antigen == "PT")
```

plot of

```
ggplot(pt.21) +
  aes(x=planned_day_relative_to_boost,
      y=MFI_normalised,
      col=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 14 (apparent peak levels)")
```


2021 dataset IgG PT
Dashed lines indicate day 0 (pre−boost) and 14 (apparent peak levels)
MFI_normalised
planned_day_relative_to_boost
infancy_vac
aP
wP