Class18: Pertussis Mini Project

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

#Getting data from a Webpage:

datapasta package- you don't really use this in the traditional way. It appears in the addins menu in 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)
     )
```

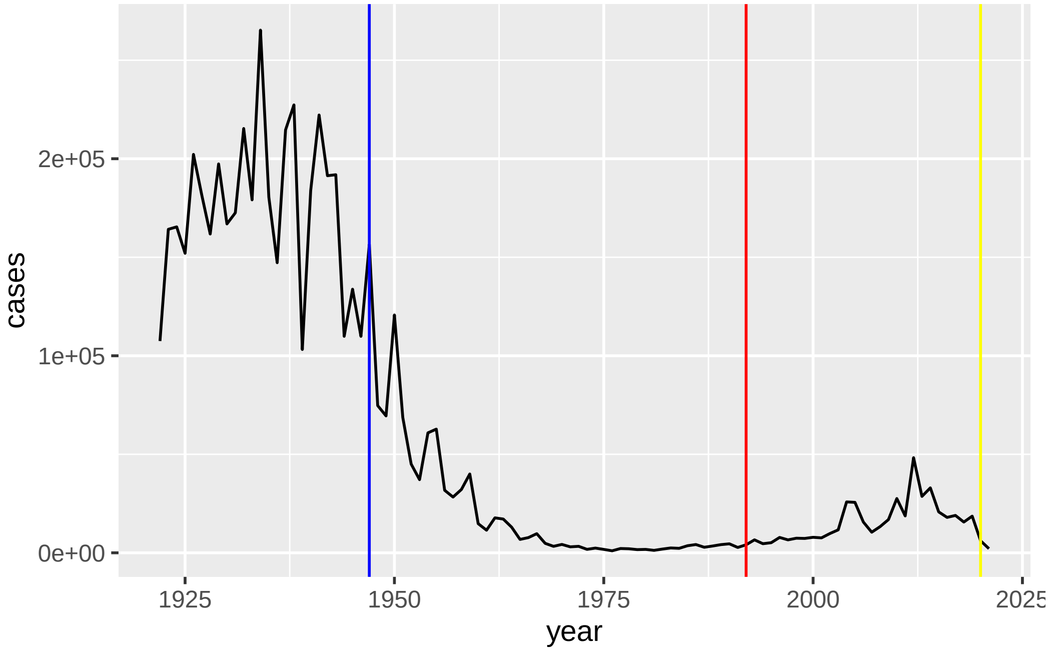
```
head(cdc)
```

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

Q1.

I want a plot of cases per year with ggplot:

```
library(ggplot2)
ggplot(cdc, aes(x=year, y=cases))+
  geom_line()+
  #geom_point()+
  geom_vline(xintercept=1947, col="blue")+
  geom_vline(xintercept=1992, col="red")+
  geom_vline(xintercept=2020, col="yellow")
```



> 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?

There was a resurgence of the disease cases after the 1996 switch to the new vaccine.

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

Cases went up, due to something about the lack of long term protection by the new vaccine.

Access data from the CMI-PB project.

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

We will use the R package `jsonlite`. The simplify vector won't return the key value pair vector, it will reutrn a data frame.

```
library(jsonlite)
```

```
Warning: package 'jsonlite' was built under R version 4.3.3
```

```
subject <- read_json("https://www.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
```

> Q. How many wP(the older whole-cell vaccine) individuals and aP (newer acellular vaccine) individuals are in this dataset?

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

```
[1] 58
```

Alternatively, we could also use `table()`

> Q. What is the number of individuals by biological sex and race?

```
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 path of doing math with dates.

```r
library(lubridate)
```

```
Warning: package 'lubridate' was built under R version 4.3.3
```

```

Attaching package: 'lubridate'

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

    date, intersect, setdiff, union
```

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

```
Time difference of 8832 days
```

```r
time_length(today()-ymd("2002-07-05"), "years")
```

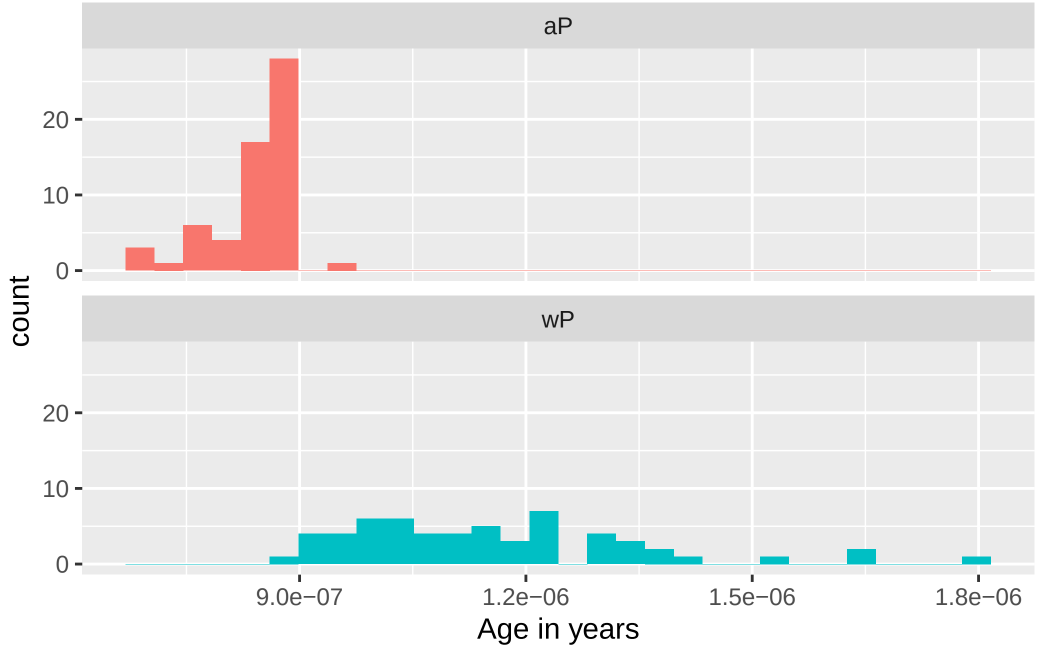
```
[1] 21.67283
```

So what is the age of everyone on our dataset.

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

```
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`.
```



```
specimen<-read_json("https://www.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
```

We need to **join** these two tables (subject and specimen) to make a single new “meta” table with all our metadata. We will use the dplyrjoin functions to do this. We will use the inner_join function because we are dropping subjects that did not show up for further trials.

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

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

```r
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
1 38.17933
2 38.17933
3 38.17933
4 38.17933
5 38.17933
6 38.17933
```

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

```r
ab_titer<- read_json("https://www.cmi-pb.org/api/v4/plasma_ab_titer",simplifyVector=TRUE)
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` onto our `abdata` table:

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

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

```
head(abdata)
```

```
  specimen_id subject_id actual_day_relative_to_boost
1           1          1                           -3
2           1          1                           -3
3           1          1                           -3
4           1          1                           -3
5           1          1                           -3
6           1          1                           -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 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 isotype is_antigen_specific antigen        MFI MFI_normalised  unit
1 38.17933     IgE               FALSE   Total 1110.21154       2.493425 UG/ML
2 38.17933     IgE               FALSE   Total 2708.91616       2.493425 IU/ML
3 38.17933     IgG                TRUE      PT   68.56614       3.736992 IU/ML
4 38.17933     IgG                TRUE     PRN  332.12718       2.602350 IU/ML
5 38.17933     IgG                TRUE     FHA 1887.12263      34.050956 IU/ML
6 38.17933     IgE                TRUE     ACT    0.10000       1.000000 IU/ML
  lower_limit_of_detection
1                 2.096133
2                29.170000
3                 0.530000
4                 6.205949
```

```
5                   4.679535
6                   2.816431
```

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

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

```
 IgE  IgG IgG1 IgG2 IgG3 IgG4 
6698 3233 7961 7961 7961 7961 
```

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

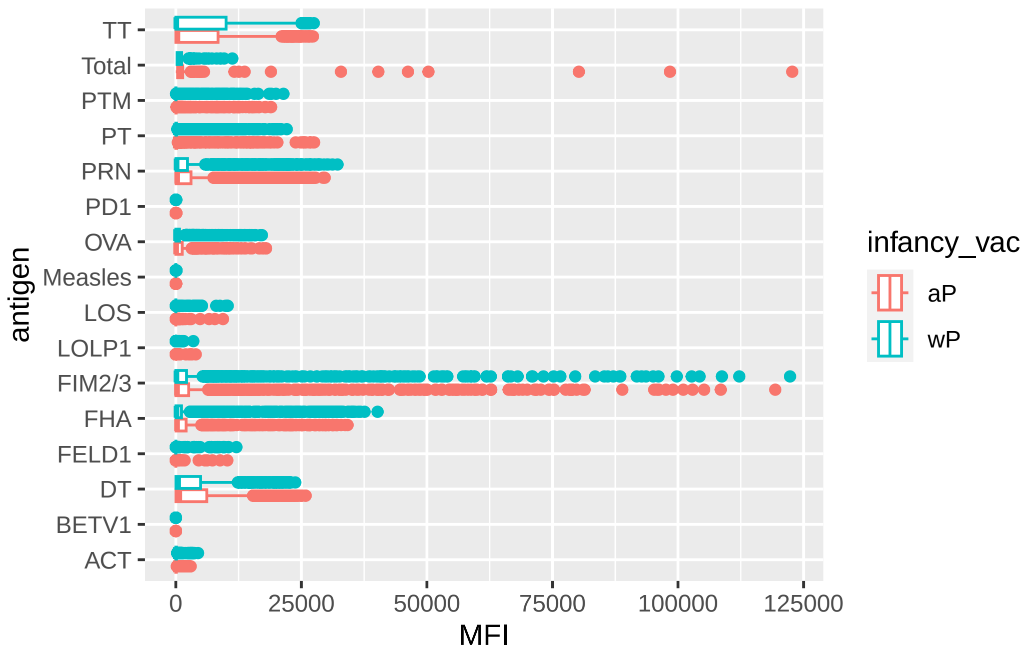
```
table(abdata$dataset)
```

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

Our first exploratory plot: We have MFI (In various fields such as immunology, virology, and microbiology, "titer level" typically refers to the concentration of a substance, such as antibodies or infectious agents, in a biological sample.)

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

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



> Q. why are certain antigens and not others very variable in their detected levels here?

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 on just the 2021 dataset

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

```
  specimen_id subject_id actual_day_relative_to_boost
1         468         61                           -4
2         468         61                           -4
3         468         61                           -4
4         468         61                           -4
```

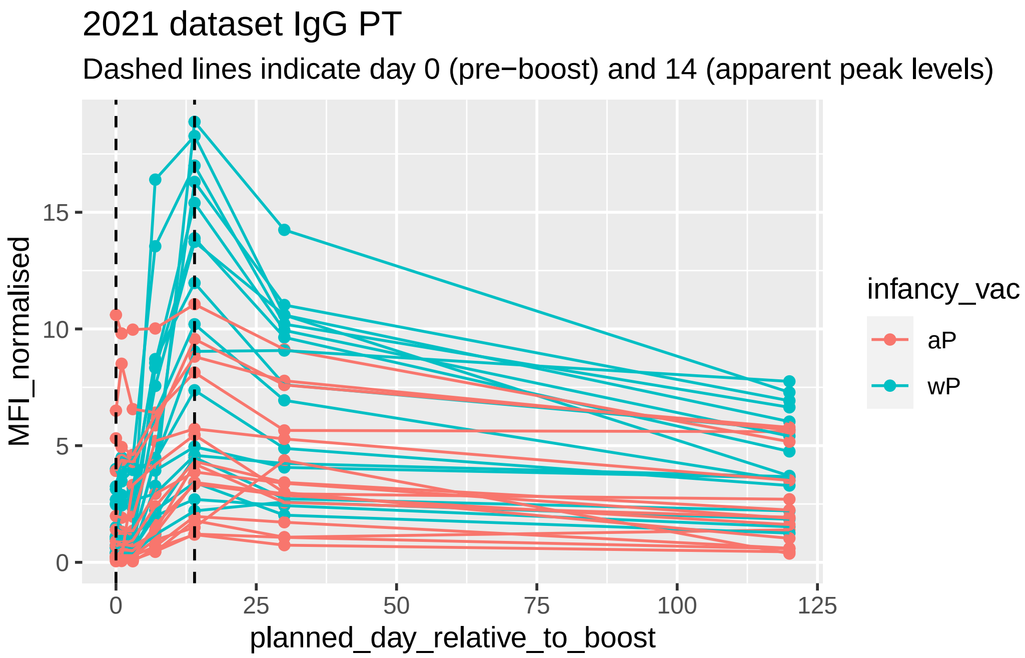
```
5         468         61                            -4
6         468         61                            -4
  planned_day_relative_to_boost specimen_type visit infancy_vac biological_sex
1                             0         Blood     1          wP         Female
2                             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
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      age isotype is_antigen_specific antigen        MFI
1 2021_dataset 37.18001     IgG               FALSE     PRN   700.1375
2 2021_dataset 37.18001     IgG               FALSE      DT  8924.4547
3 2021_dataset 37.18001     IgG               FALSE     FHA  2362.4022
4 2021_dataset 37.18001     IgG               FALSE  FIM2/3   755.7511
5 2021_dataset 37.18001     IgG               FALSE      TT 14727.5902
6 2021_dataset 37.18001     IgG               FALSE      PT   112.7500
  MFI_normalised unit lower_limit_of_detection
1      0.1105807  MFI               502.263892
2      0.7060561  MFI              2448.250000
3     10.6423728  MFI                 7.071092
4      1.4246015  MFI                13.875962
5      1.1090932  MFI              2557.146899
6      1.0000000  MFI                 5.197441
```

Focus on PT antigen IgG levels

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

plot

```
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)")
```



There is a clear difference in the aP vs wP response, there is something different related to the antigen “PT”.