Class 18: Pertussis Mini-Project

Emily Chen (PID: A16925878)

Background

Pertussis, also known as Whooping Cough, is a common lung infection causes by the bacteria *B. Pertussis.*

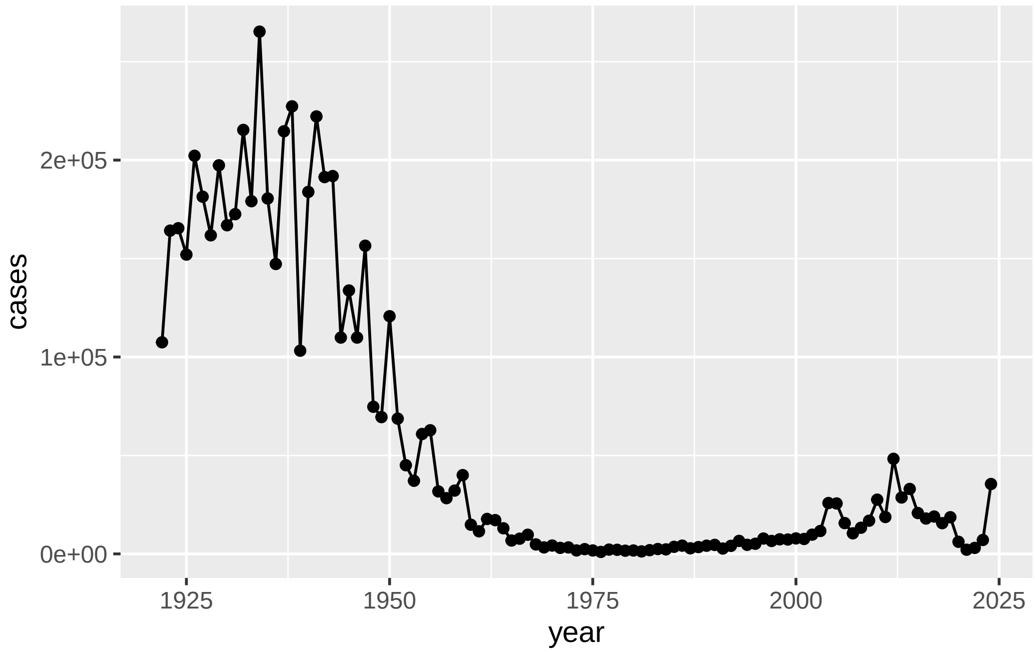
The CDC tracks cases of Pertussis in the US: https://tinyurl.com/pertussuscdc

##Examine cases of PErtussis by year

We can use the **datapaste** to

> Q. Make a plot of pertussis cases per year usign ggplot

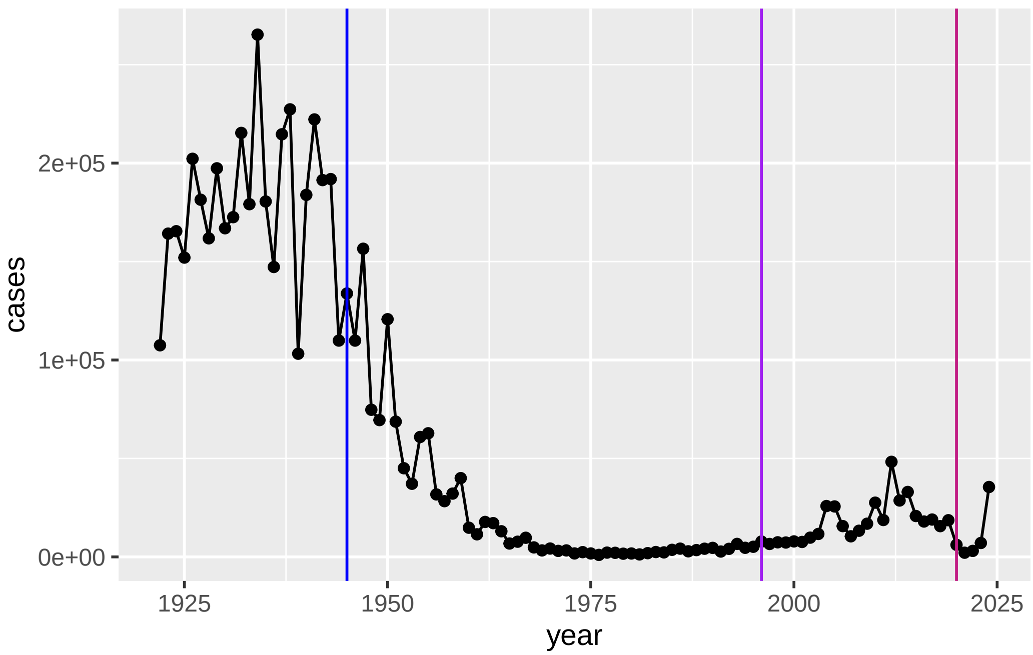
```
library(ggplot2)

ggplot(cdc)+
  aes(year, cases)+
  geom_point()+
  geom_line()
```



Q2. Add some key time points in our history of interactions with Pertussis. These include wP roll-out (the first vaccine) in 1945 and teh swrich to aP in 1996.

We can uses `geom_vline()` which will give us a vertical line

```
ggplot(cdc)+
  aes(year, cases)+
  geom_point()+
  geom_line()+
  geom_vline(xintercept=1945, col="blue")+
  geom_vline(xintercept=1996, col="purple")+
  geom_vline(xintercept=2020, col="#C11C84")
```



Q3. Describe what happened after the introduction of the aP vaccine?

According to the graph, we can see that the aP vaccine seemed efficient as there was a decrease in the number of cases after. One of the reasons why we see any increase in the number of cases is due to anti-vaccine parents not vaccinating their children, and the virus evolving and growing resistance to the vaccine. Thailand never switched to aP vaccine and kept administering the wP vaccine and they never had a surge of cases like we see in our case.

Mounting evidence suggests that the newer **aP** vaccine is less effective over the long term than the older **wP** vaccine that it replaced. In other words, vaccine protection wanes more rapidly with the aP than the wP.

Enter the CMI-PB Project

CMI-PB (Computational Models of Immunity- Pertussis boost) major goal is to investigate how the immune system responds differently to aP vs wP vaccinated individuals and be able to predict this at an early stage.

CMI-PB makes all their collected data freely available, and they store it in a database composed of different tables. Here we will access a few of them.

We can use the **jsonlite** package to read this data

```
library(jsonlite)
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 subjects (i.e. enrolled people) are in this dataset?

```
nrow(subject)
```

```
[1] 172
```

There are 172 subjects in this dataset.

> Q4. How many "aP" and "wP" subjects are there

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

```

aP wP 
87 85 
```

Ther are 87 subject who got the aP vaccine and 85 subject got the wP vaccine.

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

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

```
Female   Male 
   112     60 
```

There are 112 females and 60 males in this dataset

> Q6. How about gender and race numbers

```r
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
```

> Q. Is this representative of the US population?

NOPE! But this looks like UCSD population

Lets read another database from CMI-PB

```r
specimen <- read_json("https://www.cmi-pb.org/api/v5_1/specimen",
                      simplifyVector = TRUE)
ab_data <- read_json("https://www.cmi-pb.org/api/v5_1/plasma_ab_titer",
                     simplifyVector = TRUE)
```

```r
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 want to "join" these tables together all our information together. For this we will use the **dplyr** package and the `inner_join()` function.

"

```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(subject, specimen)
```

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

```r
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
```

```
head(ab_data)
```

```
  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 “join” to get ab_data and meta all together into one dataset

```r
abdata <- inner_join(ab_data, 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
  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
```

```
dim(abdata)
```

```
[1] 61956    20
```

Q11. How many antibody isotypes are there in the dataset?

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

```

  IgE   IgG  IgG1  IgG2  IgG3  IgG4 
 6698  7265 11993 12000 12000 12000 
```

Q.How any different antigen are measured in the dataset?

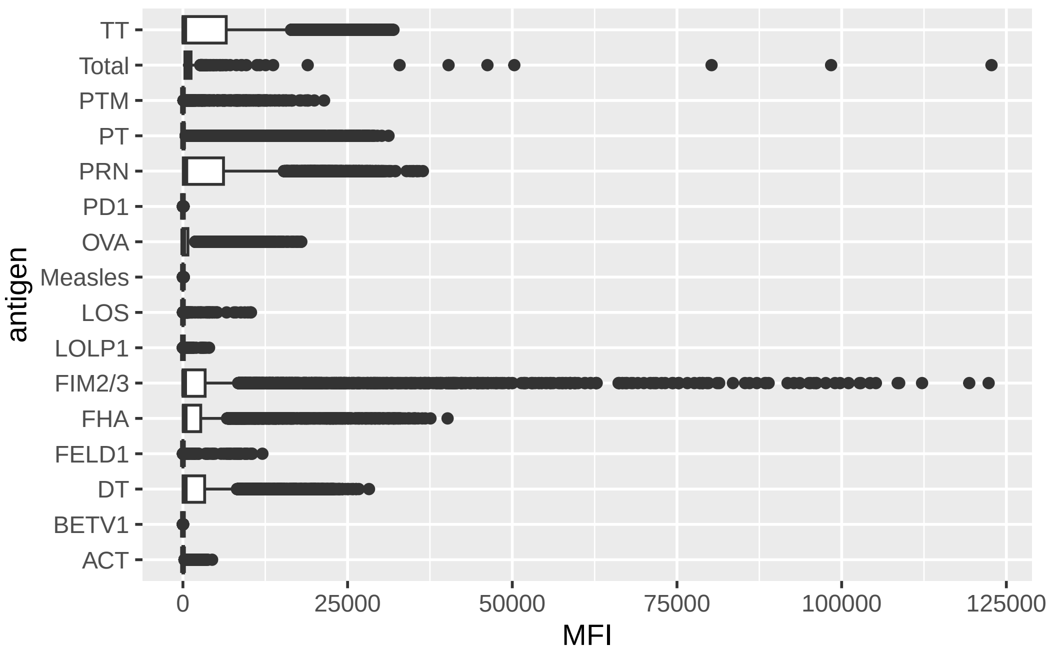
```
table(abdata$antigen)
```

```

    ACT   BETV1      DT   FELD1     FHA  FIM2/3   LOLP1     LOS Measles     OVA 
   1970    1970    6318    1970    6712    6318    1970    1970    1970    6318 
    PD1     PRN      PT     PTM   Total      TT 
   1970    6712    6712    1970     788    6318 
```

Q. Make a box plot od antigen levels across the whole dataset. MFI vs antigen MFI refers to the mean fluorescent intensity

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

```
Warning: Removed 1 row containing non-finite outside the scale range
(`stat_boxplot()`).
```

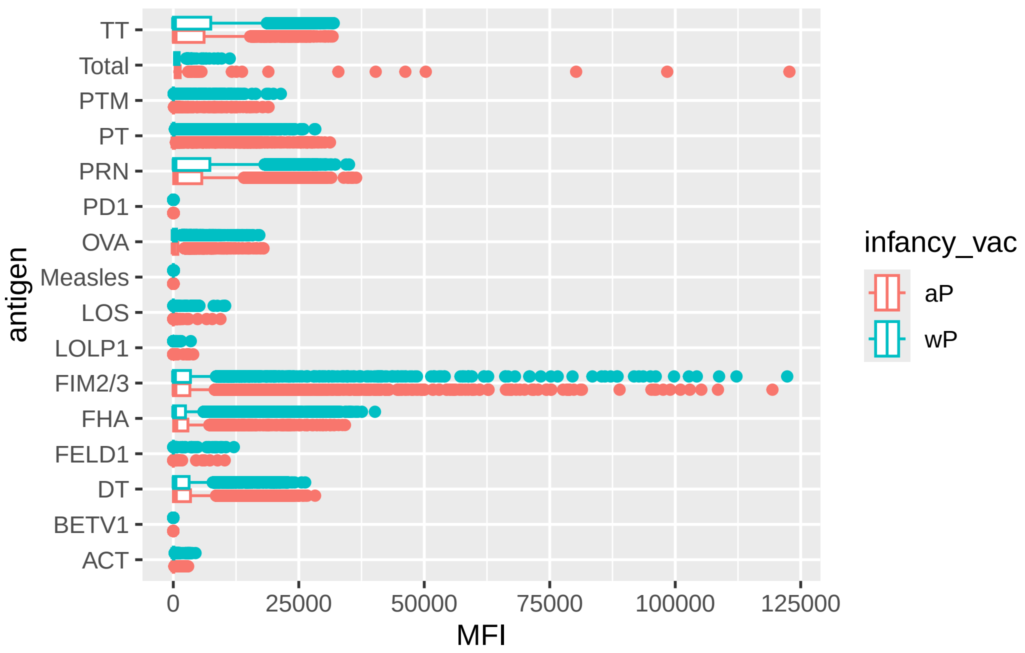


We should not see any MFI for the measles row, as that is our control

> Q. Are there obvious difference between aP and wP values

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

```
Warning: Removed 1 row containing non-finite outside the scale range
(`stat_boxplot()`).
```



Focus on IgG levels

IgG is the most abundant antibody in blood. With four sub-classes (IgG1 to IgG4) for crucial for long-term immunity and responding to bacterial and viral infection.

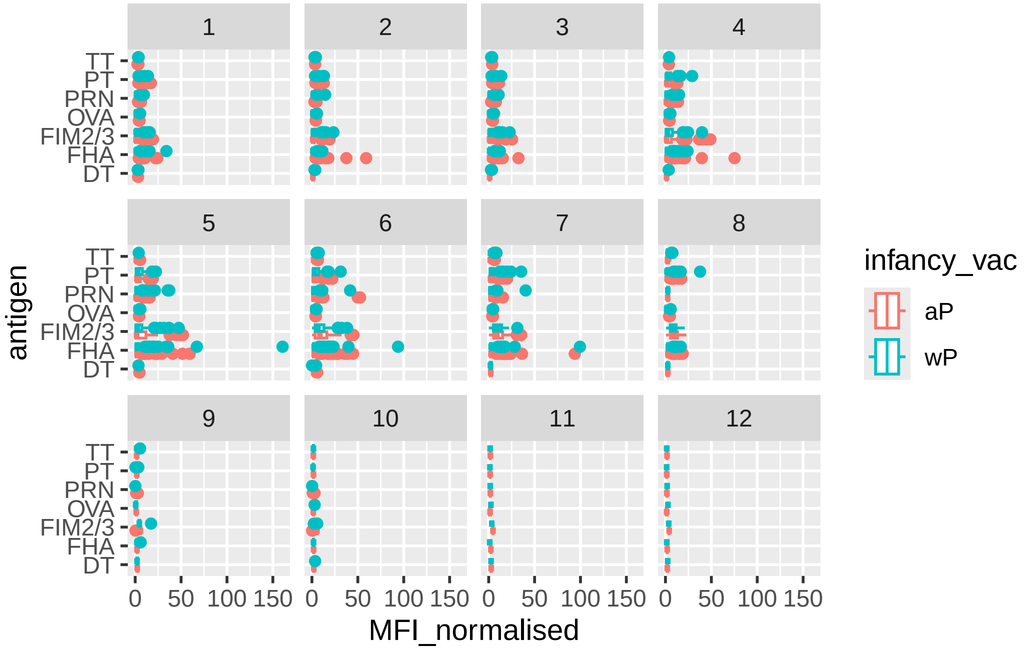
```
igg<-abdata |> filter(isotype== "IgG")
head(igg)
```

```
  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 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
```

Same boxplot of antigens as before

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



Focus further on just one of these antigens- let's pick **PT** (Pertussis Toxin, one of the main toxins of the bacteria) in the **2021 dataset** again for the **IgG** antibody isotype.

```
table(igg$dataset)
```

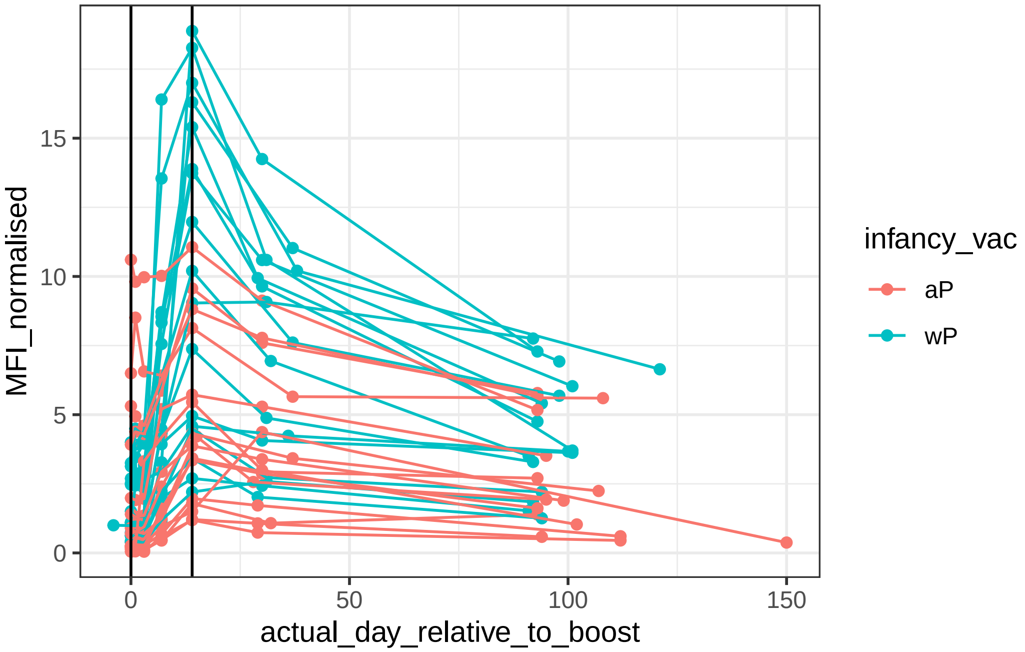
```
2020_dataset 2021_dataset 2022_dataset 2023_dataset
        1182         1617         1456         3010
```

```
pt_igg<- abdata |>
  filter(isotype=="IgG", antigen== "PT", dataset=="2021_dataset")
```

```
dim(pt_igg)
```

```
[1] 231  20
```

```
ggplot(pt_igg)+
  aes(actual_day_relative_to_boost, MFI_normalised, col=infancy_vac, group=subject_id)+
  geom_point()+
  geom_line()+
  theme_bw()+
  geom_vline(xintercept=0, col="black")+
  geom_vline(xintercept=14, col="black")
```



At day 14, we see that we had peak levels and a distinctive difference between the aP and wP vaccines