Lab 19: Pertussis and the CMI-PB project

Lauren Waters

Pertussis is a severe lung infection also known as whooping cough.

We will begin by investigation the number of Pertussis cases per year in the US.

This data is available on the CDC website here

```
#/ 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 look at the data frame

```
head(cdc)
```

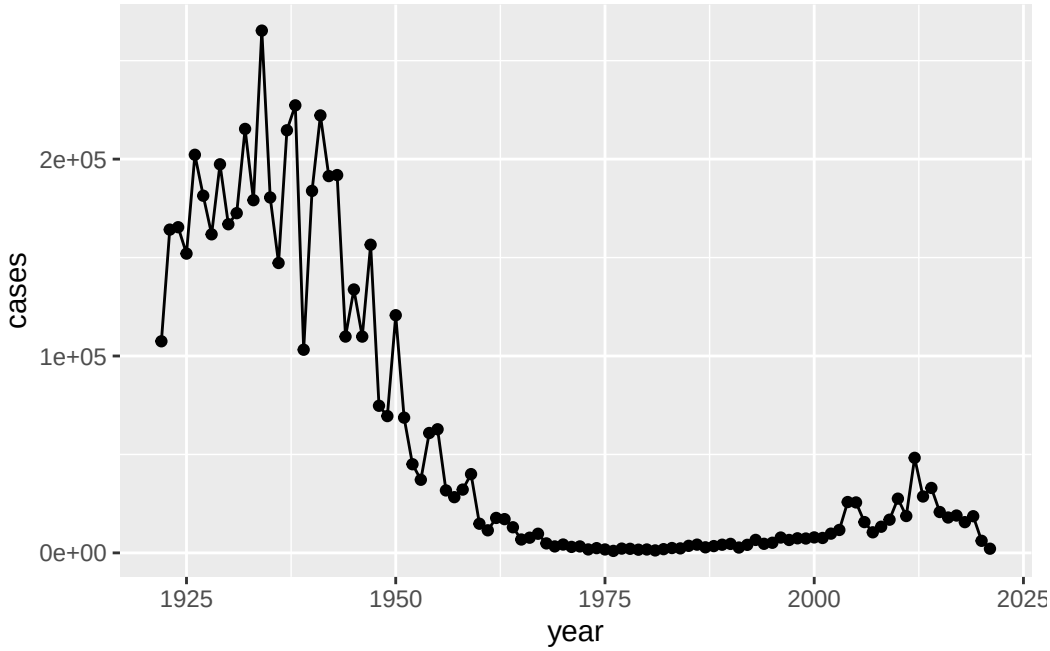
```
  year  cases
1 1922 107473
2 1923 164191
3 1924 165418
4 1925 152003
5 1926 202210
6 1927 181411
```

Q1.

I want a nice plot of the number of cases per year.

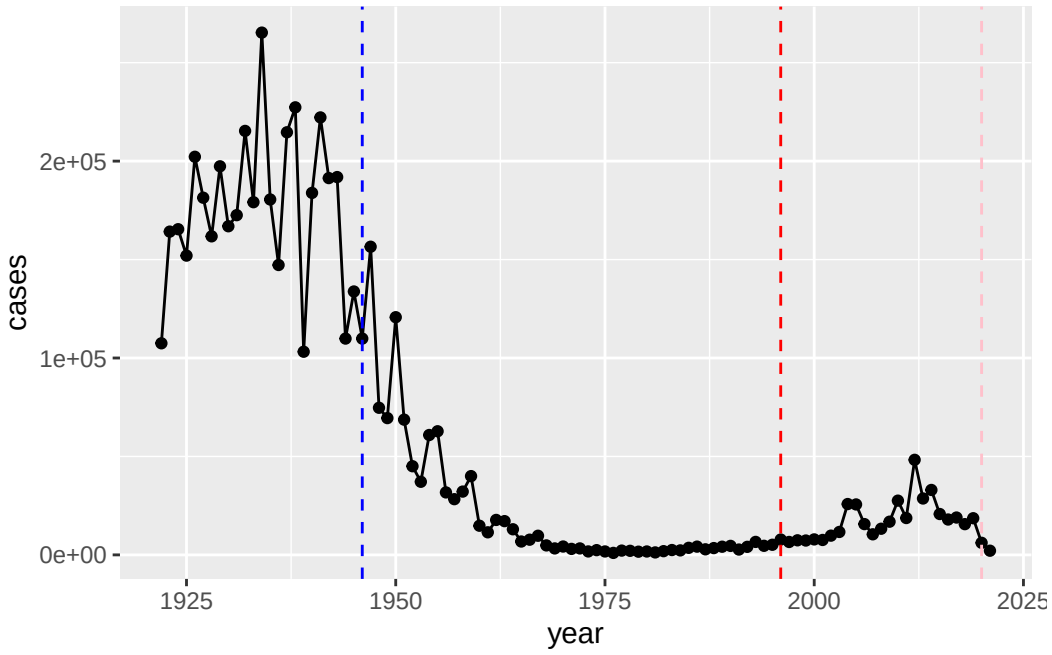
```
library(ggplot2)

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



Q2.

```
ggplot(cdc) +
  aes(x=year, y=cases) +
  geom_point() +
  geom_line() +
  geom_vline(xintercept = 1946, linetype = "dashed", color = "blue") +
  geom_vline(xintercept = 1996, linetype = "dashed", color = "red") +
  geom_vline(xintercept = 2020, linetype = "dashed", color = "pink")
```



Q3.

There is an increase in cases after the aP vaccine is introduced.

We will use the **jsonlite** package to access this data. The main function in this package is `read_json()`.

```
library(jsonlite)
```

```
Warning: package 'jsonlite' was built under R version 4.3.2
```

```
#Suject table
subject <- read_json("http://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)
```

```
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
```

Q4.

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

```
aP wP
60 58
```

Q5.

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

```
Female   Male
    79     39
```

Q6.

```
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
```

```
library(tidyverse)
```

```
Warning: package 'tidyverse' was built under R version 4.3.2
```

```
Warning: package 'readr' was built under R version 4.3.2
```

```
Warning: package 'stringr' was built under R version 4.3.2
```

```
Warning: package 'forcats' was built under R version 4.3.2
```

```
Warning: package 'lubridate' was built under R version 4.3.2
```

```
-- Attaching core tidyverse packages ------------------------ tidyverse 2.0.0 --
v dplyr     1.1.3     v readr     2.1.4
v forcats   1.0.0     v stringr   1.5.1
v lubridate 1.9.3     v tibble    3.2.1
v purrr     1.0.2     v tidyr     1.3.0
-- Conflicts ------------------------------------------ tidyverse_conflicts() --
x dplyr::filter()  masks stats::filter()
x purrr::flatten() masks jsonlite::flatten()
x dplyr::lag()     masks stats::lag()
i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to becor
```

```
today()
```

```
[1] "2023-12-05"
```

```
today() - mdy("12-05-2001")
```

```
Time difference of 8035 days
```

```
time_length( today() - ymd("2001-12-05"), "years")
```

```
[1] 21.99863
```

Q8.

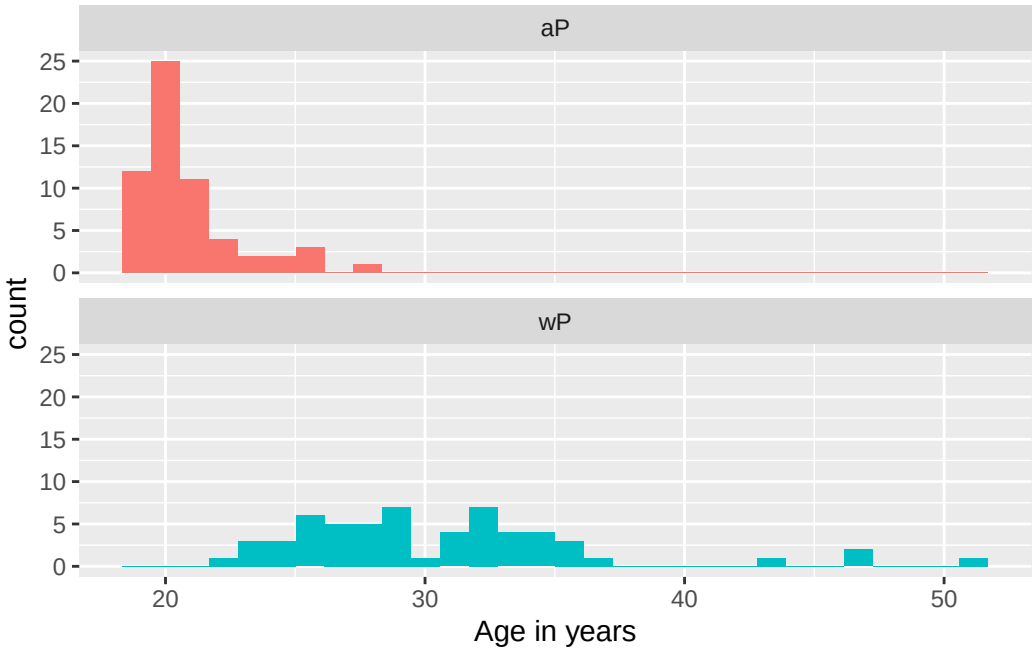
```
subject$age <-  ymd(subject$date_of_boost) - ymd(subject$year_of_birth)
subject$age_years <-  time_length(subject$age, "years")

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        age age_years
1    1986-01-01    2016-09-12 2020_dataset 11212 days  30.69678
2    1968-01-01    2019-01-28 2020_dataset 18655 days  51.07461
3    1983-01-01    2016-10-10 2020_dataset 12336 days  33.77413
4    1988-01-01    2016-08-29 2020_dataset 10468 days  28.65982
5    1991-01-01    2016-08-29 2020_dataset  9372 days  25.65914
6    1988-01-01    2016-10-10 2020_dataset 10510 days  28.77481
```

```
ggplot(subject) +
  aes(age_years,
      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`.
```



Q9.

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

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

```
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.

```
abdata <-  inner_join(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 actual_day_relative_to_boost
1 UG/ML                 2.096133          1                           -3
2 IU/ML                29.170000          1                           -3
3 IU/ML                 0.530000          1                           -3
4 IU/ML                 6.205949          1                           -3
5 IU/ML                 4.679535          1                           -3
6 IU/ML                 2.816431          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 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
```

Q. How many isotypes are we measuring for all these individuals?

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

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

Lets focus on one of these (IgG)

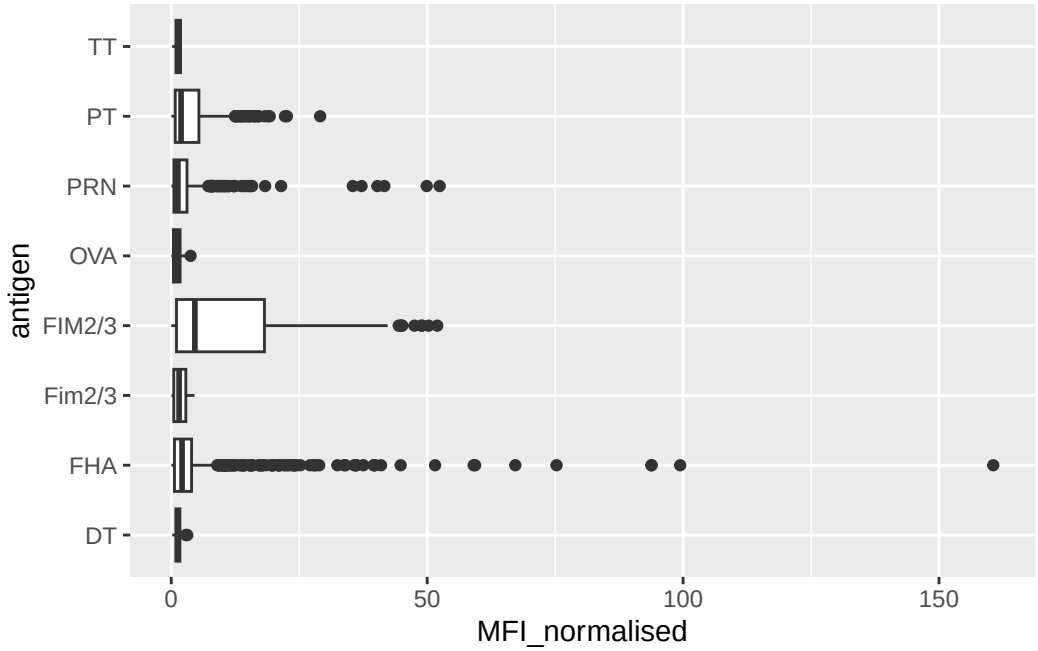
```
igg <- abdata %>% filter(isotype == "IgG")
head(igg)
```

```
  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
```

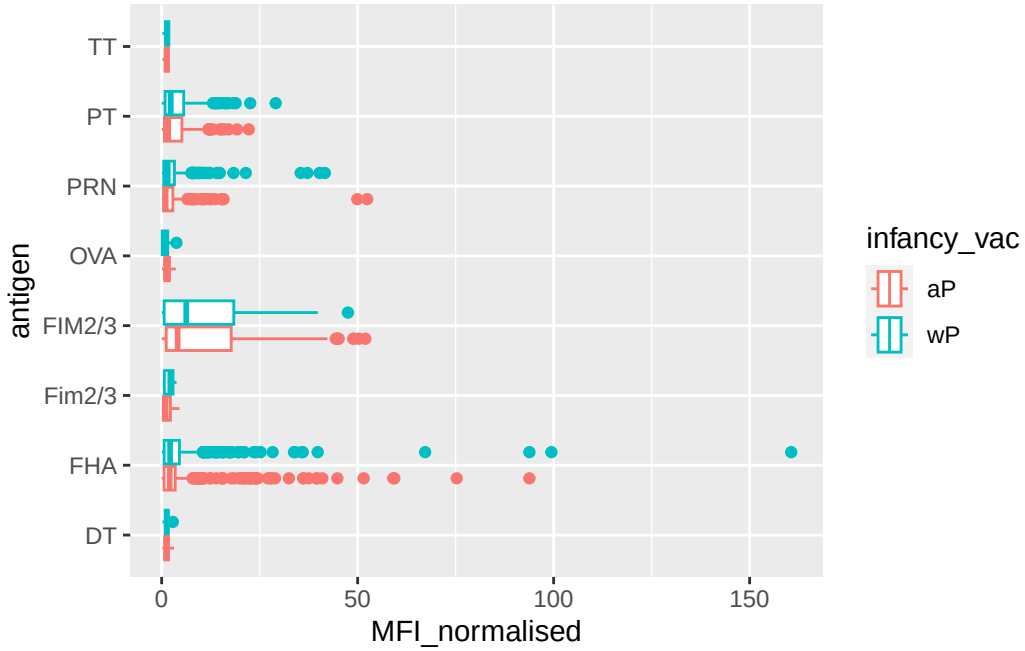
```
2 IU/ML                 6.205949          1                          -3
3 IU/ML                 4.679535          1                          -3
4 IU/ML                 0.530000          3                          -3
5 IU/ML                 6.205949          3                          -3
6 IU/ML                 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
```

Boxplot of MFI_normalized vs antigen

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



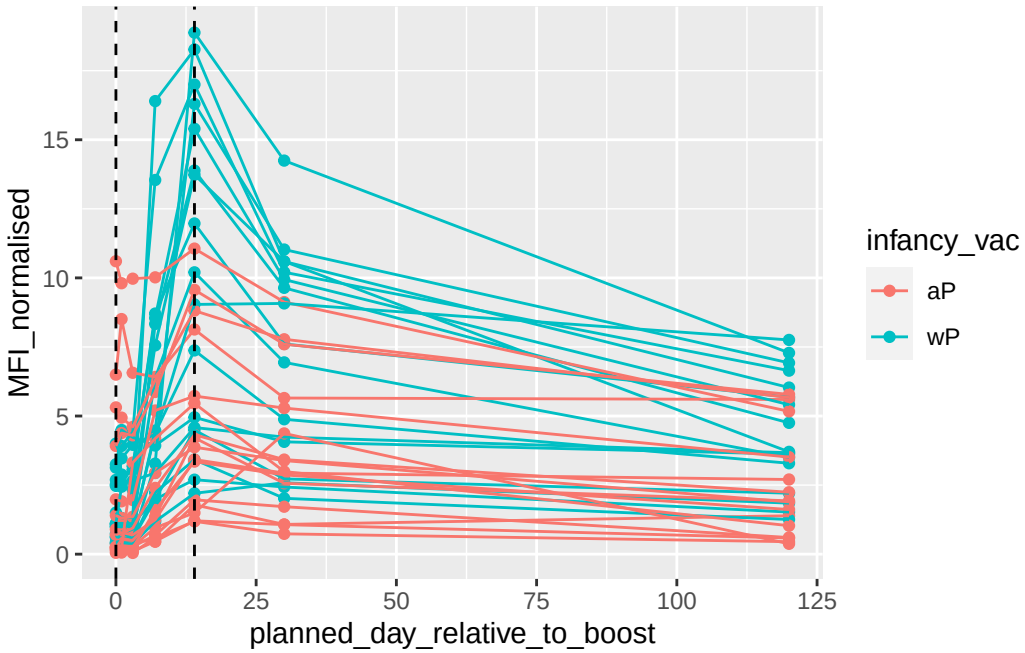

```
ggplot(igg) +
  aes(MFI_normalised, antigen, col = infancy_vac) +
  geom_boxplot()
```



Focus in on IgG to the Pertussis Toxin (PT) antigen in the 2021 dataset.

```
igg.pt <- igg %>% filter(antigen == "PT", dataset=="2021_dataset")
```

```
ggplot(igg.pt) +
  aes(planned_day_relative_to_boost,
      MFI_normalised,
      col = infancy_vac,
      group = subject_id) +
  geom_point() +
  geom_line() +
  geom_vline(xintercept = 0, linetype = "dashed", col = "black") +
  geom_vline(xintercept = 14, linetype = "dashed", col = "black")
```


MFI_normalised
15
10
5
0
0
25
50
75
100
125
planned_day_relative_to_boost
infancy_vac
aP
wP