# Class 18: Pertussis mini-project

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First we will examine and explore pertussis case numberss 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 to scrape this data from the the website into 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)
```

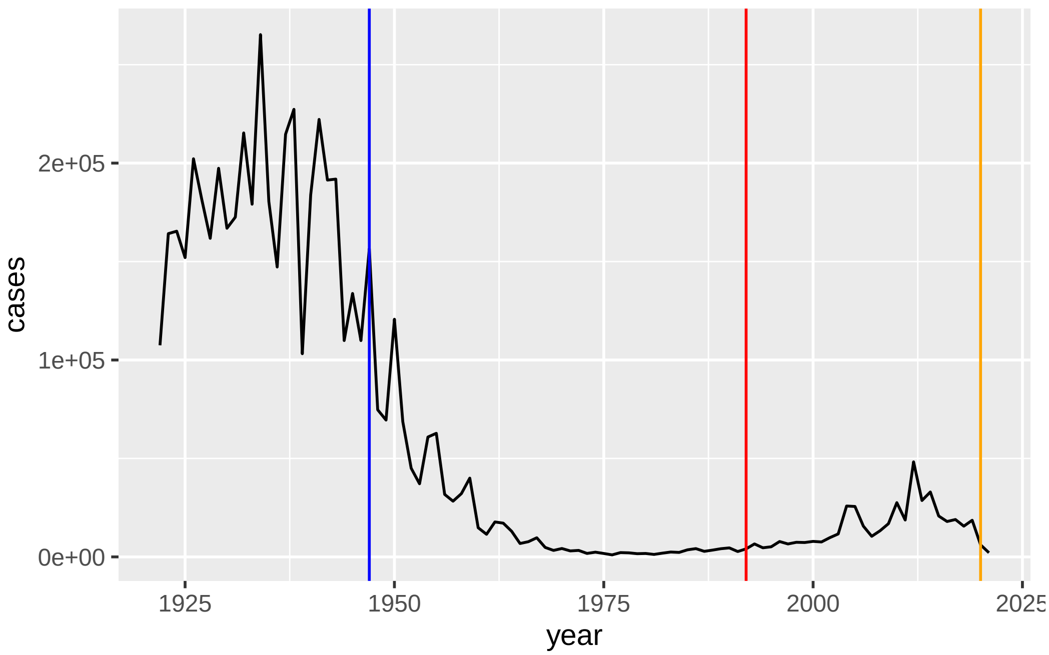
```
  year  cases
1 1922 107473
2 1923 164191
3 1924 165418
4 1925 152003
5 1926 202210
6 1927 181411
```

> 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?

I want to plot of cases per year with ggplot

```
library(ggplot2)

ggplot(cdc)+aes(x=year,y=cases)+geom_line()+geom_vline(xintercept = 1947,col="blue")+geom_
```



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

Pertussis cases began to rise after this point because adap vaccines provide a smaller dosage so the immune system gets smaller effect than before.

##3. Exploring CMI-PB data

acces data from the CMI-PB project

this databas (like many modern projects) uses an API to return JSON format data.

We will use the R package 'jsonlite'

```r
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
```

> Q4. How many aP and wP infancy vaccinated subjects are in the dataset?

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

```

aP wP 
60 58 
```

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

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

```

Female   Male 
    79     39 
```

> Q6. What is the breakdown of race and biological sex (e.g. number of Asian females, White males etc…)?

```r
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
```

```r
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 lubridate package to ease

```r
library(lubridate)
```

```

Attaching package: 'lubridate'

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

    date, intersect, setdiff, union
```

```
today()
```

```
[1] "2024-03-10"
```

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

```
Time difference of 8835 days
```

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

```
Time difference of 8053 days
```

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

```
[1] 22.04791
```

so what is the age of everyone on our dataset.

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

> Q8. Determine the age of all individuals at time of boost?

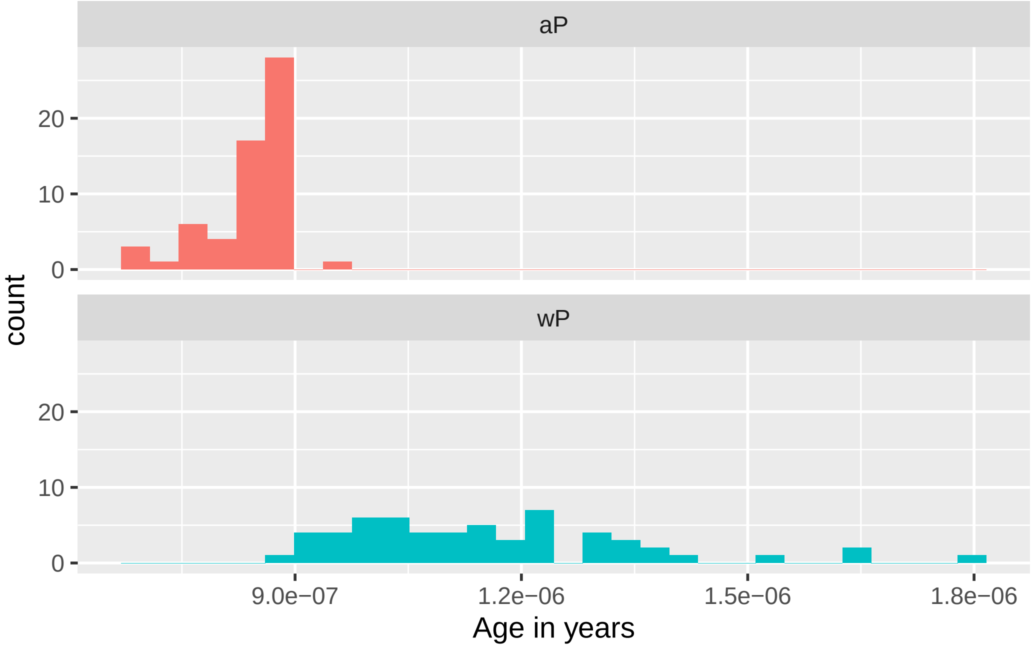
```
int <- ymd(subject$date_of_boost) - ymd(subject$year_of_birth)
age_at_boost <- time_length(int, "year")
head(age_at_boost)
```

```
[1] 30.69678 51.07461 33.77413 28.65982 25.65914 28.77481
```

> Q9. With the help of a faceted boxplot or histogram (see below), do you think these two groups are significantly different?

```
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`.
```



##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
```

> Q9. Complete the code to join specimen and subject tables to make a new merged data frame containing all specimen records along with their associated subject details:

```
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 38.18754           1
2    1986-01-01    2016-09-12 2020_dataset 38.18754           2
```

```
3    1986-01-01    2016-09-12 2020_dataset 38.18754           3
4    1986-01-01    2016-09-12 2020_dataset 38.18754           4
5    1986-01-01    2016-09-12 2020_dataset 38.18754           5
6    1986-01-01    2016-09-12 2020_dataset 38.18754           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 = 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
```

> Q10. Now using the same procedure join meta with titer data so we can further analyze this data in terms of time of visit aP/wP, male/female etc.

```
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
       age actual_day_relative_to_boost planned_day_relative_to_boost
1 38.18754                           -3                             0
2 38.18754                           -3                             0
3 38.18754                           -3                             0
4 38.18754                           -3                             0
5 38.18754                           -3                             0
6 38.18754                           -3                             0
  specimen_type visit
1         Blood     1
2         Blood     1
3         Blood     1
4         Blood     1
5         Blood     1
6         Blood     1
```

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 
```

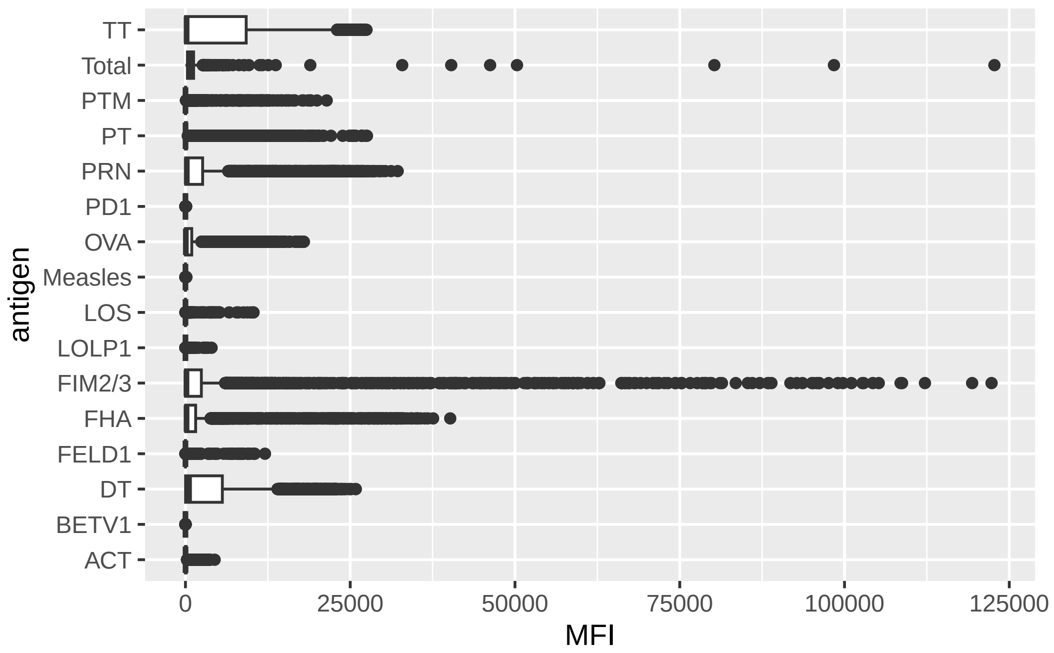
Our first exploratory plot:

```
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 
```

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

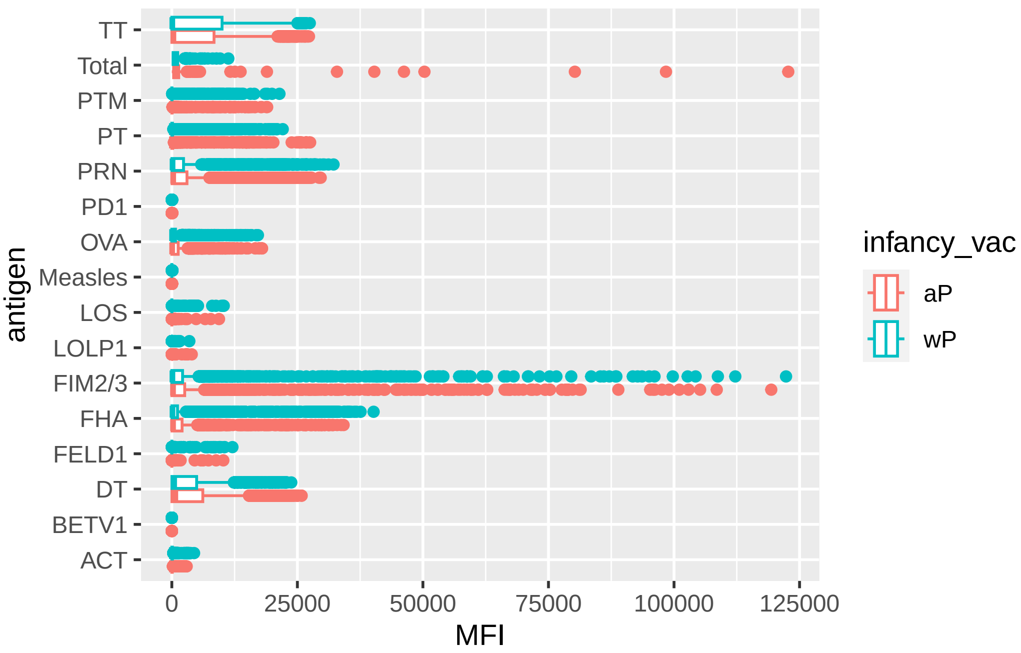
```
Warning: Removed 1 rows containing non-finite values (`stat_boxplot()`).
```



Q14. What antigens show differences in the level of IgG antibody titers recognizing them over time? Why these and not others?

```r
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…

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

```

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

lets focus in on just the 2021_dataset.

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

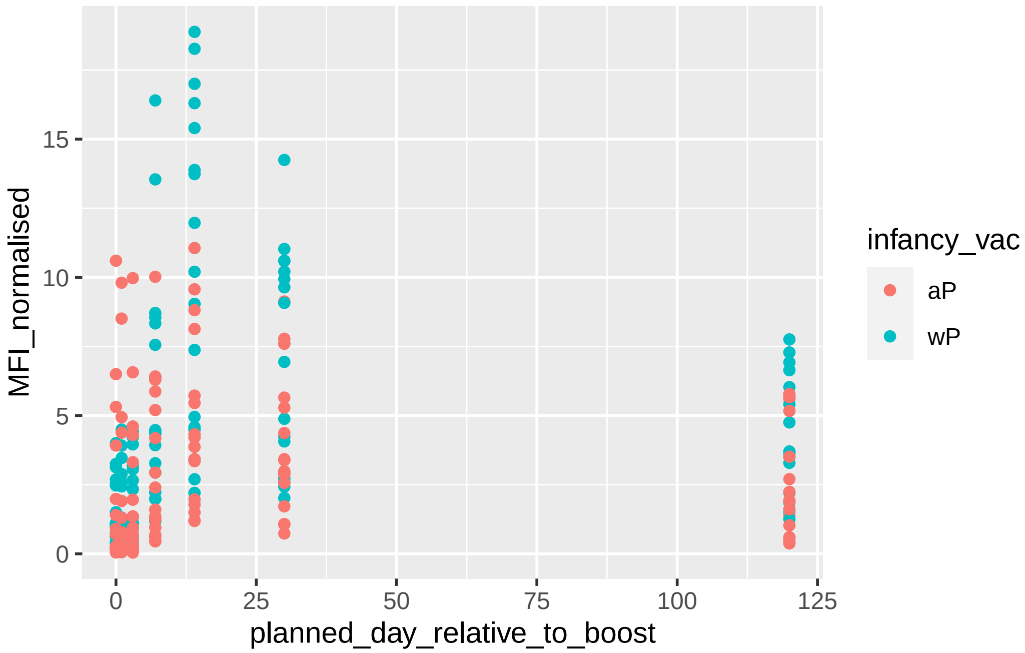
```

2021_dataset 
        8085 
```

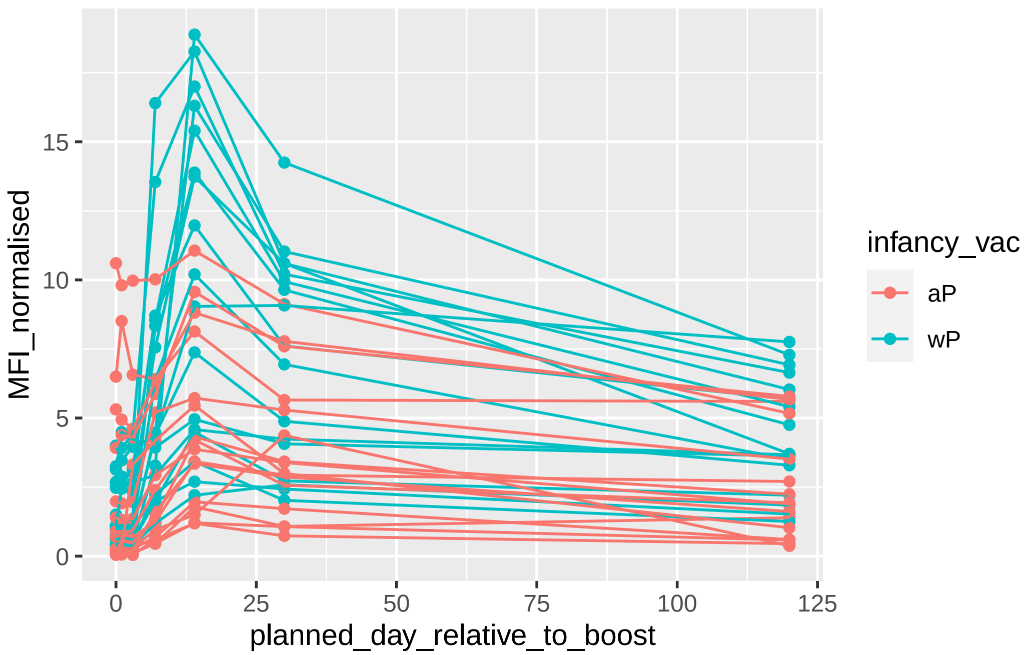
```r
pt.21<-filter(abdata.21, isotype == "IgG",  antigen == "PT")
```

plot

```
ggplot(pt.21)+aes(x=planned_day_relative_to_boost, y=MFI_normalised, col=infancy_vac)+geom
```



```
ggplot(pt.21)+aes(x=planned_day_relative_to_boost, y=MFI_normalised, col=infancy_vac,group
```


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