Class 18: Pertussis Mini-Project

Michael McClellan (PID: A169692395)

Table of contents

Background

Pertussis (aka whooping cough) is a common lung infection caused by the bacteria *B. Pertussis*.

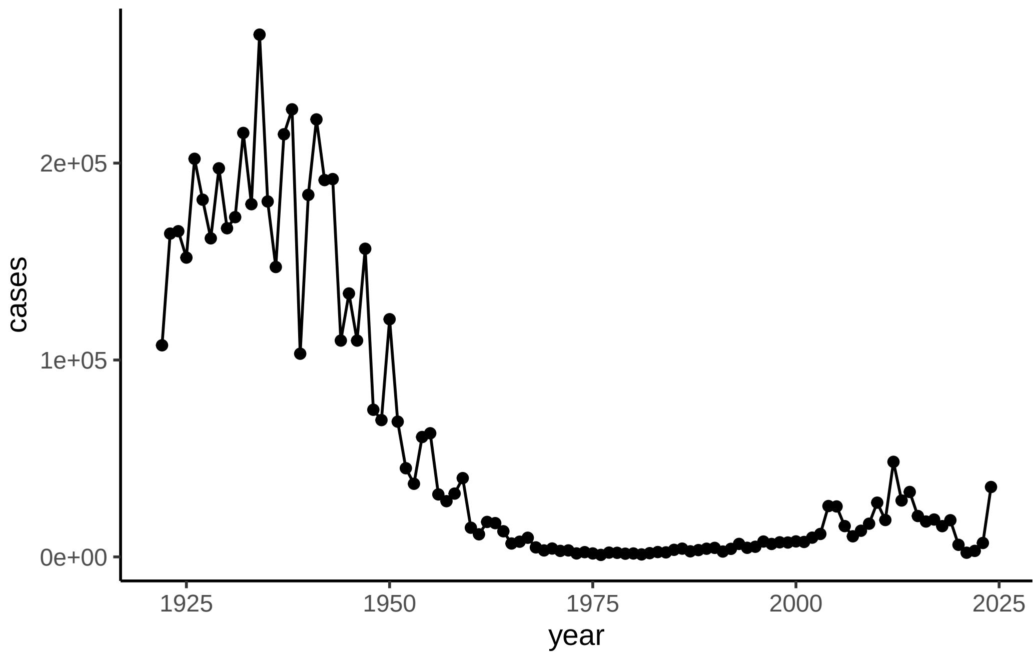
The CDC tracks cases of Pertussis in the US: https://www.cdc.gov/pertussis/php/surveillance/pertussis-cases-by-year.html

Examining cases of Pertussis by year

We can use the **datapasta** package to scrape case numbers from the CDC website.

> Q1. Make a plot of pertussis cases per year using ggplot.

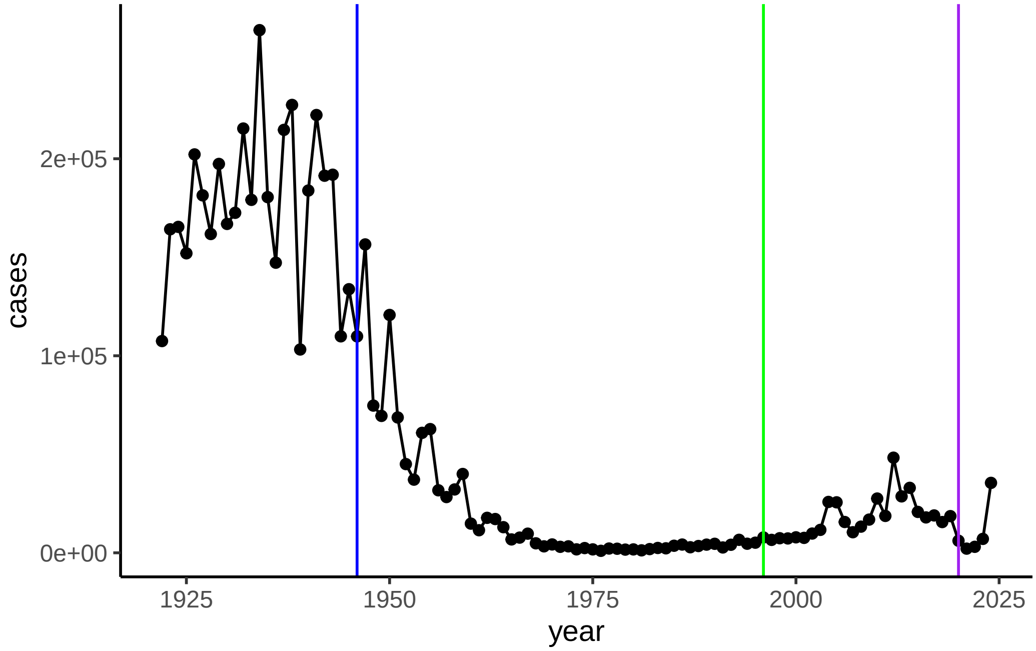
```
library(ggplot2)

cases <- ggplot(cdc) +
  aes(x=year, y=cases) +
  geom_line() +
  geom_point() +
  theme_classic()

cases
```



> Q2. Add some key time points in our history of interaction with Pertussis. These include wP rollout (the first vaccine) in 1946 and the switch to aP in 1996.

We can use `geom_vline()` for this.

```
cases +
  geom_vline(xintercept = 1946, col = "blue") +
  geom_vline(xintercept = 1996, col = "green") +
  geom_vline(xintercept = 2020, col = "purple")
```



After the introduction of the wP vaccine, the number of cases decreased significantly. After the introduction of the aP vaccine, the number of cases remained relatively the same, but eventually increased in the years leading up to Covid (2020). The initial decrease in cases can be attributed to lockdowns and masking, but this number has since increased since national preventative orders have been lifted.

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 (efficacy) wanes more rapidly with ap than wP.

Enter the CMI-PB project

CMI-PB (Computational Models of Immunity - Pertussis Booster shot) 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 these.

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

```r
library(jsonlite)

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

```r
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 there in this dataset?

```r
nrow(subject)
```

```
[1] 172
```

Q. How many “aP” and “wP” subjects are there?

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

```

aP wP 
87 85 
```

Q. How many Male/Female are in the dataset?

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

```

Female   Male 
   112     60 
```

Q. 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?

No, but the data is representative of the UCSD population.

Let's read another database table 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 = TRU
```

Wee peak at these:

```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 to get all our information together. For this we’ll 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
```

We'll do one more "join" to get ab_data and meta all together.

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

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

```
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
```

```r
dim(abdata)
```

```
[1] 61956    20
```

Q. How many Ab isotypes are there in the dataset?

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

```

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

Q. How many different antigens are measured in the dataset?

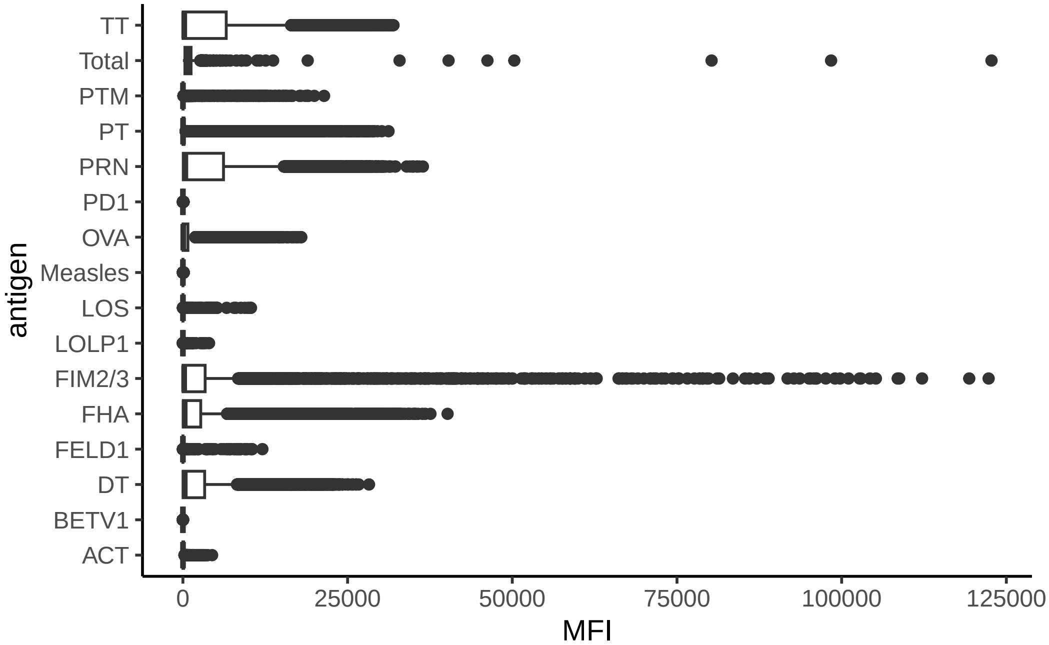
```r
table(abdata$antigen)
```

```

    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 boxplot of antigen levels across the whole dataset (MFI vs. antigen).

```r
ggplot(abdata) +
  aes(x=MFI, y=antigen) +
  geom_boxplot() +
  theme_classic()
```

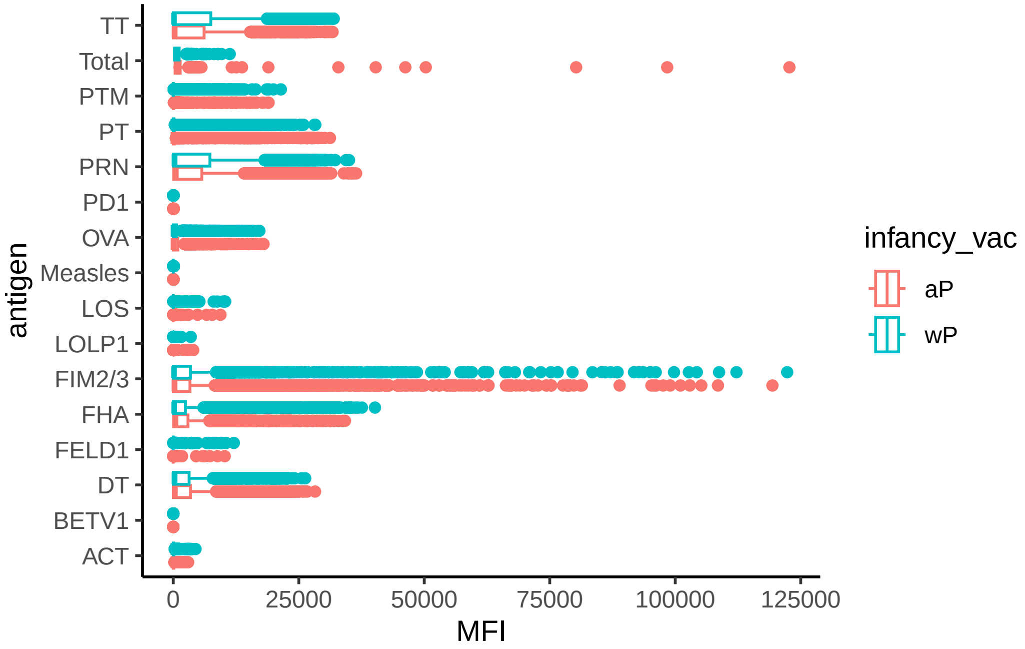
```
Warning: Removed 1 row containing non-finite outside the scale range
(`stat_boxplot()`).
```



Q. Are there obvious differences between aP and wP values?

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

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



Focus on IgG levels

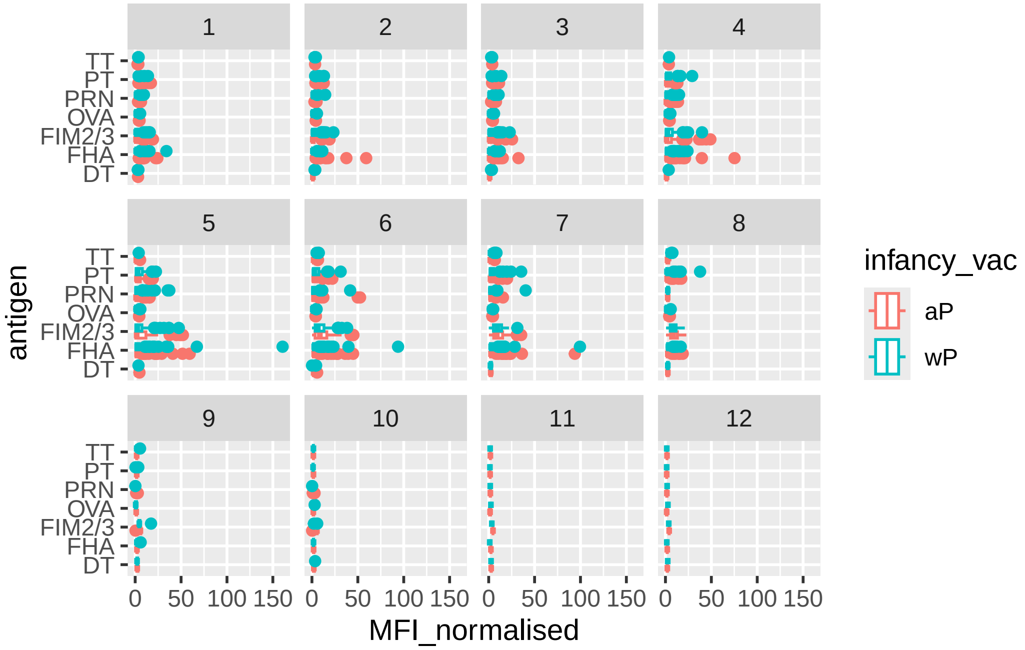
```
igg <- abdata |> filter(isotype == "IgG")

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:

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



Focus in 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 **IgG** antibody isotypes.

```
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")

head(pt_igg)
```

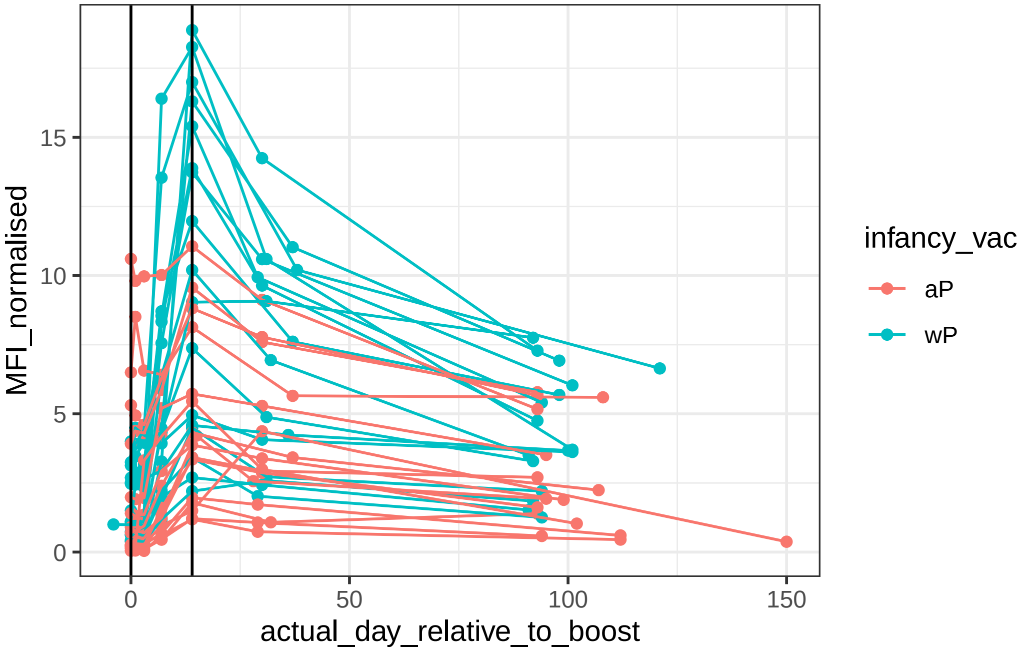
```
  specimen_id isotype is_antigen_specific antigen    MFI MFI_normalised unit
1         468     IgG               FALSE      PT 112.75      1.0000000  MFI
2         469     IgG               FALSE      PT 111.25      0.9866962  MFI
3         470     IgG               FALSE      PT 125.50      1.1130820  MFI
4         471     IgG               FALSE      PT 224.25      1.9889135  MFI
5         472     IgG               FALSE      PT 304.00      2.6962306  MFI
6         473     IgG               FALSE      PT 274.00      2.4301552  MFI
```

```
  lower_limit_of_detection subject_id infancy_vac biological_sex
1                 5.197441         61          wP         Female
2                 5.197441         61          wP         Female
3                 5.197441         61          wP         Female
4                 5.197441         61          wP         Female
5                 5.197441         61          wP         Female
6                 5.197441         61          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 actual_day_relative_to_boost planned_day_relative_to_boost
1 2021_dataset                           -4                              0
2 2021_dataset                            1                              1
3 2021_dataset                            3                              3
4 2021_dataset                            7                              7
5 2021_dataset                           14                             14
6 2021_dataset                           30                             30
  specimen_type visit
1         Blood     1
2         Blood     2
3         Blood     3
4         Blood     4
5         Blood     5
6         Blood     6
```

```r
dim(pt_igg)
```

```
[1] 231  20
```

```r
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) +
  geom_vline(xintercept=14)
```


MFI_normalised
0
5
10
15
actual_day_relative_to_boost
0
50
100
150
infancy_vac
aP
wP