Lab18 - Pertussis mini project

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Background

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

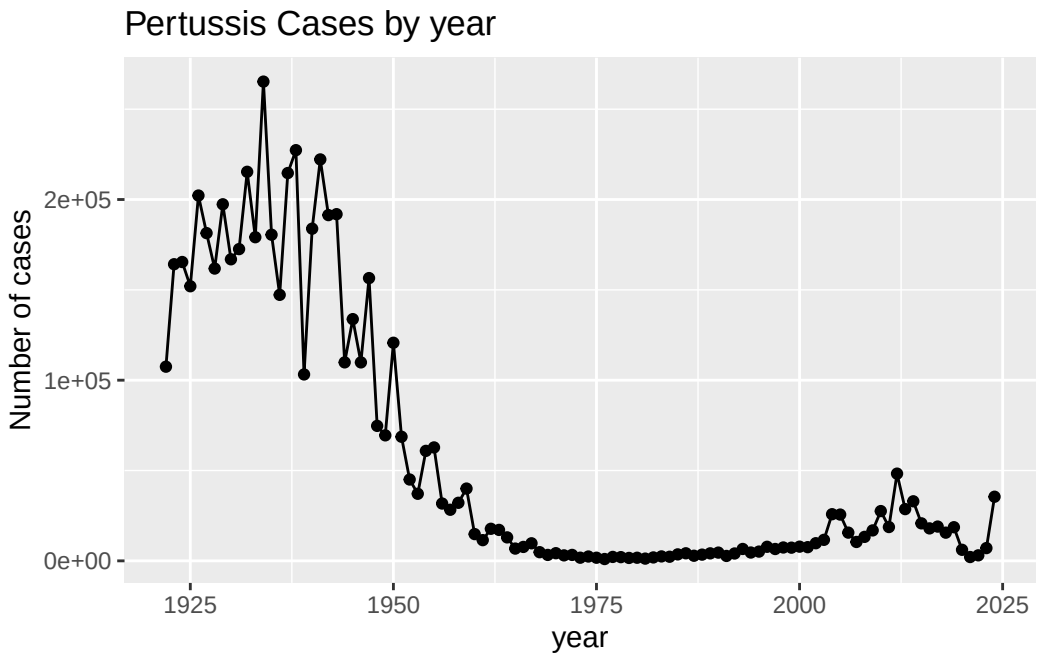
The CDC tracks cases of Pertussis in the US:https://tinyurl.com/pertussiscdc

Examining cases of Pertussis by year

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

Q1. Make a plot of Pertussis cases per year using ggplot.

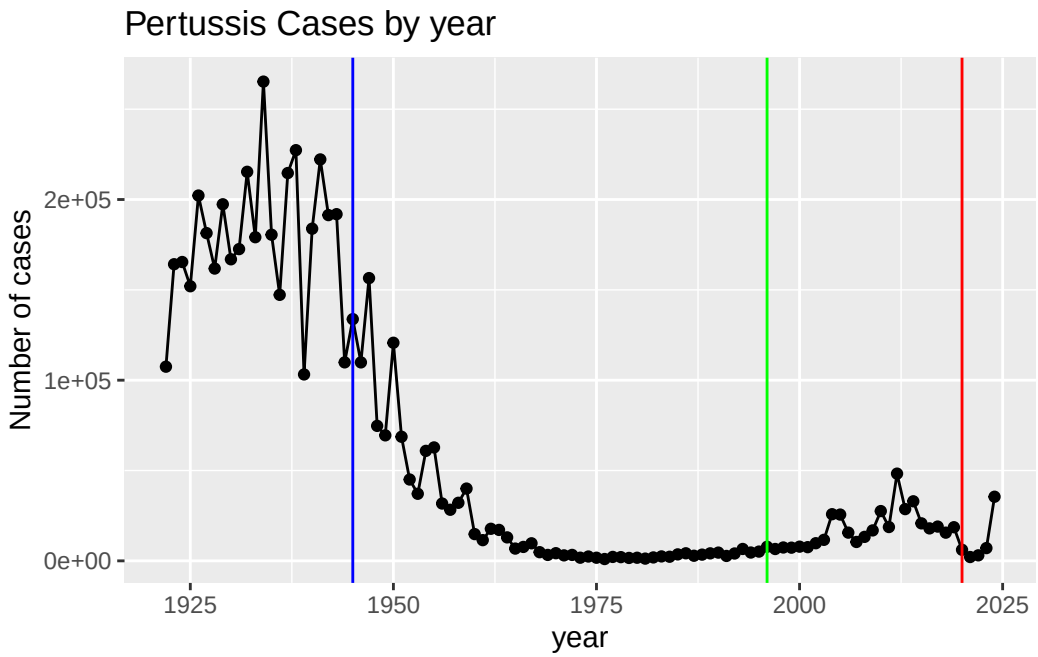
```
library (ggplot2)

cases <- ggplot(cdc) +
  aes(year, cases) +
  geom_point() +
  geom_line() +
  labs(title = "Pertussis Cases by year", y = "Number of cases")

cases
```



Q2. Add some key timepoints in our history of interaction with Pertussis. These include wP roll-out (the first vaccine) in 1945 and switch to aP in 1996.

We can use `geom_vline()` for this.

```
cases +
  geom_vline(xintercept = 1945, col = "blue") +
  geom_vline(xintercept = 1996, col = "green") +
  geom_vline(xintercept = 2020, col = "Red")
```



After the aP vaccine, the data displays a decrease in pertussis. The increase seen can be inffered from possible immunological escape (virus evolves) and potential anti-vaxxers. Mounting evidence suggests that the newer **aP** vaccine is less effective over the long term than the older **wP** vaccine that is replaced. In other words, vaccine protection wanes more rappidly with aP than with 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 with aP vs wP vaccinated individuals and be able to predict this

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 those.

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

```
library(jsonlite)

subject <- read_json("https://www.cmi-pb.org/api/v5_1/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
```

Q3. How many subjects (i.e enrolled people) are there in this dataset

```
nrow(subject)
```

```
[1] 172
```

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

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

```
aP wP
87 85
```

Q5. How many Male/Female are in the dataset?

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

```
Female   Male
   112     60
```

Q6. How about gender and race numbers?

```
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
```

Q7. Is this representative of the US population?

NO

Let's read another database table from the CMI-PB.

```
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 of these

```
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 use the **Dplyr** package and the `inner_join()` function.

```
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 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

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

Q8. How many antibody isotypes are there in the dataset>

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

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

Q9. How many different antigens are measured in the dataset?

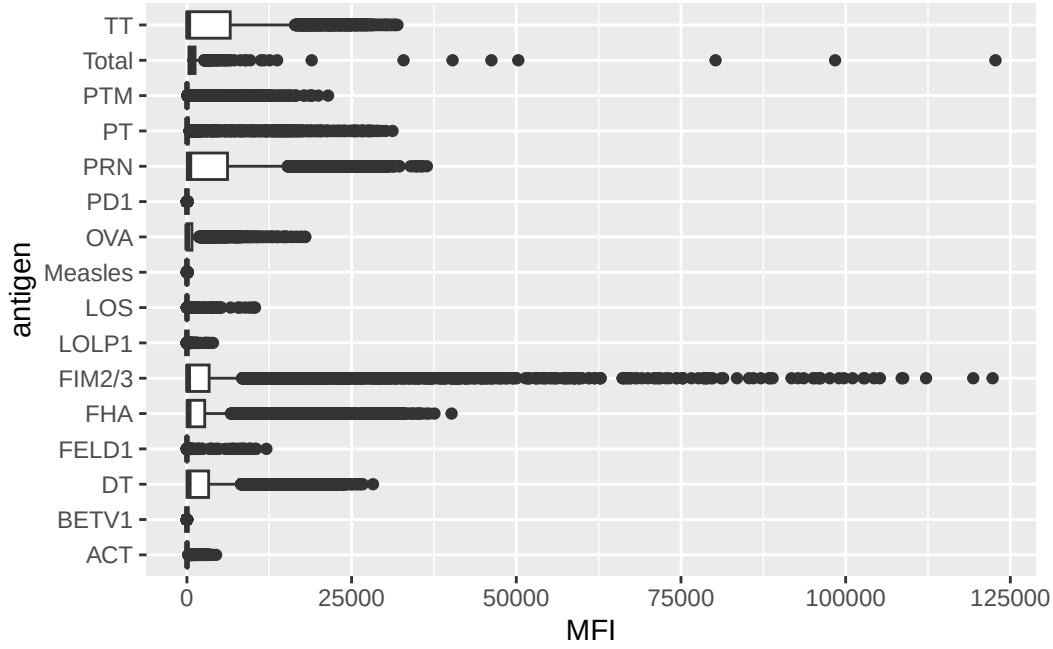
```
table(abdata$antigen)
```

```
   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
```

Q10. make a boxplot of antigen levels across the whole dataset? (MFI vs antigen)

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

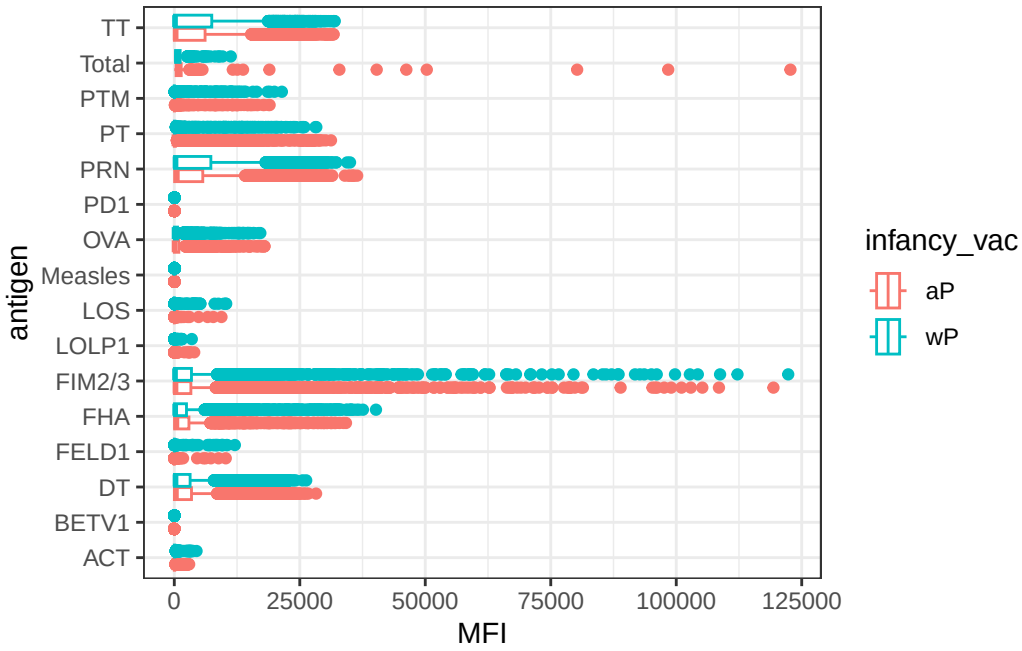
```
Warning: Removed 1 row containing non-finite outside the scale range
(`stat_boxplot()`).
```



Q11. Are there obvious differences between aP and wP values?

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

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



Focus on IgG levels

IgG is the most abundant antibody levels in blood. With four sub-classes (IgG1-4) crucial for long-term — viral infections.

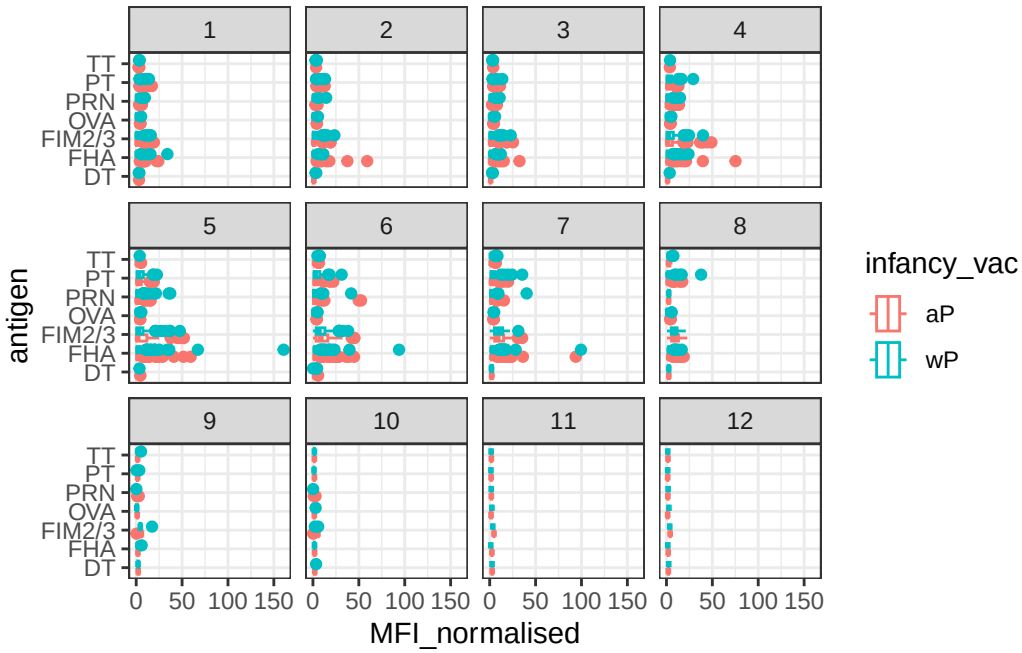
```
igg <- abdata |>
  filter(isotype == "IgG")

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 box plot of antigens as before

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

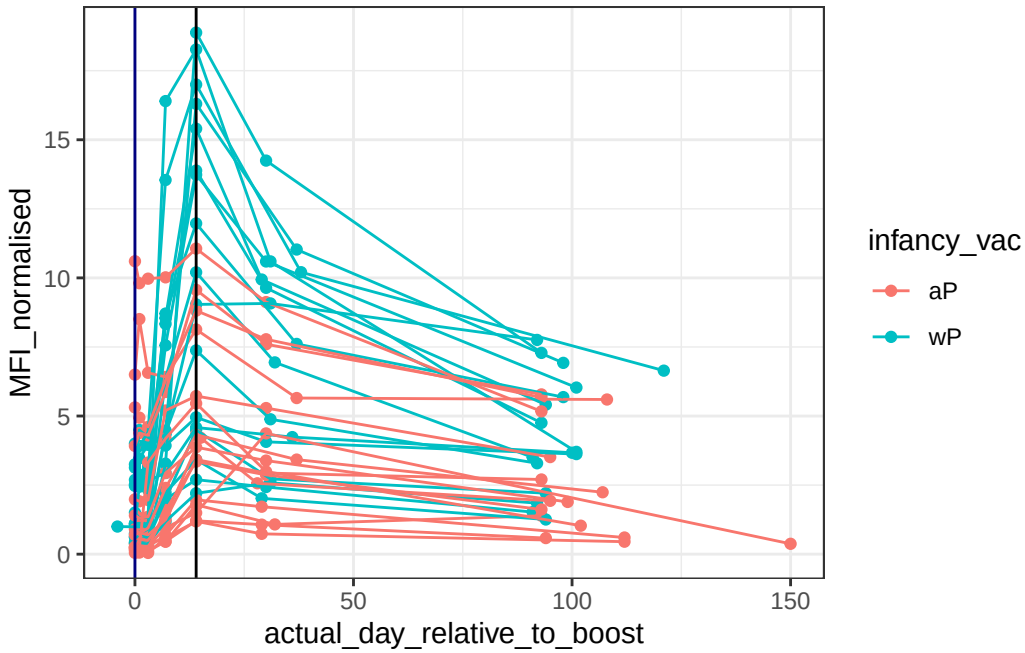
```
  specimen_id isotype is_antigen_specific antigen    MFI MFI_normalised unit
1         468     IgG                FALSE      PT 112.75      1.0000000  MFI
2         469     IgG                FALSE      PT 111.25      0.9866962  MFI
3         470     IgG                FALSE      PT 125.50      1.1130820  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
```

```
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 = "navy") +
  geom_vline(xintercept = 14)
```


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