Class 15: Pertussis miniproject

PID: A69034741

Pertussis, a.k.a. Whooping Cough, is a highly contagious lung infection caused by the *B. Pertussis* bacteria.

The CDC tracks Pertussis case numbers and they can be accessed here:

We ned to "scrape" this data so we can do stuff with it in R. Let's try the **datapasta** package to do this.

```r
# install.packages("datapasta")
# installs an addin
# copy table from URL - Addins -> Paste as data.frame

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,2022L, 2024L),
                                 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,
                                          6124,2116,3044, 23544)
       )
```

```
cdc
```

```
    year  cases
1    1922 107473
2    1923 164191
3    1924 165418
4    1925 152003
5    1926 202210
6    1927 181411
7    1928 161799
8    1929 197371
9    1930 166914
10   1931 172559
11   1932 215343
12   1933 179135
13   1934 265269
14   1935 180518
15   1936 147237
16   1937 214652
17   1938 227319
18   1939 103188
19   1940 183866
```

```
20  1941 222202
21  1942 191383
22  1943 191890
23  1944 109873
24  1945 133792
25  1946 109860
26  1947 156517
27  1948  74715
28  1949  69479
29  1950 120718
30  1951  68687
31  1952  45030
32  1953  37129
33  1954  60886
34  1955  62786
35  1956  31732
36  1957  28295
37  1958  32148
38  1959  40005
39  1960  14809
40  1961  11468
41  1962  17749
42  1963  17135
43  1964  13005
44  1965   6799
45  1966   7717
46  1967   9718
47  1968   4810
48  1969   3285
49  1970   4249
50  1971   3036
51  1972   3287
52  1973   1759
53  1974   2402
54  1975   1738
55  1976   1010
56  1977   2177
57  1978   2063
58  1979   1623
59  1980   1730
60  1981   1248
61  1982   1895
62  1983   2463
```

63	1984	2276
64	1985	3589
65	1986	4195
66	1987	2823
67	1988	3450
68	1989	4157
69	1990	4570
70	1991	2719
71	1992	4083
72	1993	6586
73	1994	4617
74	1995	5137
75	1996	7796
76	1997	6564
77	1998	7405
78	1999	7298
79	2000	7867
80	2001	7580
81	2002	9771
82	2003	11647
83	2004	25827
84	2005	25616
85	2006	15632
86	2007	10454
87	2008	13278
88	2009	16858
89	2010	27550
90	2011	18719
91	2012	48277
92	2013	28639
93	2014	32971
94	2015	20762
95	2016	17972
96	2017	18975
97	2018	15609
98	2019	18617
99	2020	6124
100	2021	2116
101	2022	3044
102	2024	23544

```
# install.packages("styler")
```

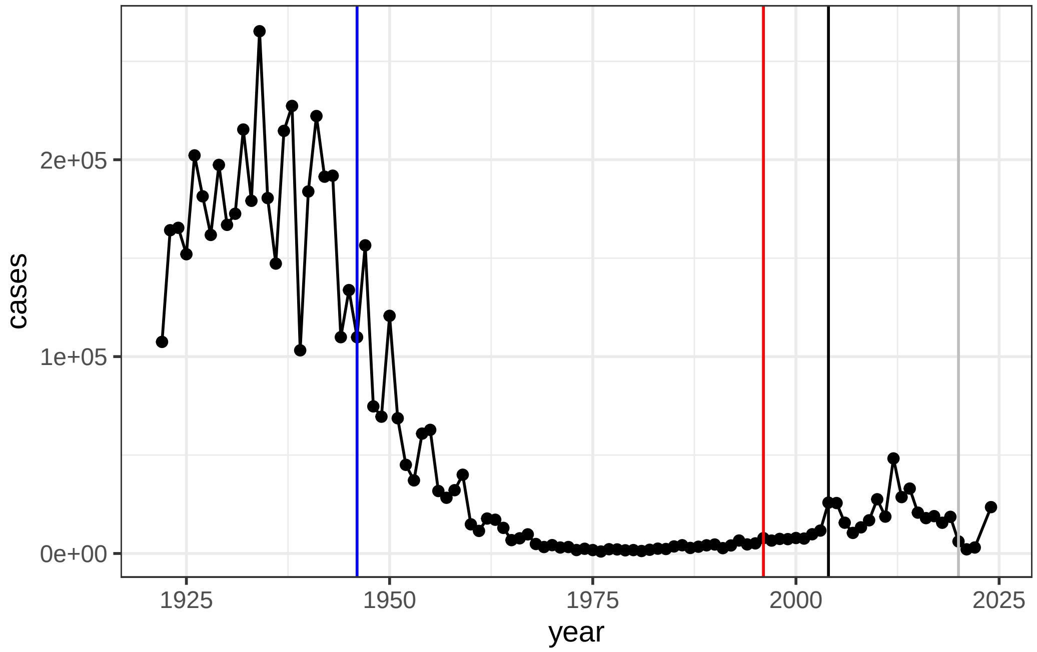
Let's plot year vs cases to see the trend over time in the US.

```
library(ggplot2)

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

Let's add the date of wP vaccine rollout across the US

```
baseplot +
  theme_bw() +
  geom_vline(xintercept=1946, col="blue") +
  geom_vline(xintercept=1996, col="red") +
  geom_vline(xintercept=2020, col="gray") +
  geom_vline(xintercept=2004, col="black")
```



CMI-PB (Computational Models of Immunity - Pertussis Boost)

This project collects and makes freely available doata about the immune response to Pertussis vaccination.

You can access the data via an API which returns JSON format (key:value pairs).

We can use the **jsonlite** package and it's `read_json()` function.

```
# API - application programming interface - way to access data
# install.packages("jsonlite")

library(jsonlite)

subject <- read_json("https://www.cmi-pb.org/api/v5/subject", simplifyVector=TRUE)
```

Let's have a wee peak ad explore this

```
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 do we have?

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

```

Female   Male 
   112     60 
```

Q. How many wP and aP do we have?

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

```

aP wP 
87 85 
```

Q. Break down of biological sex and race?

```
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. Does this break down reflect the US population?

```
table(subject$dataset)
```

```

2020_dataset 2021_dataset 2022_dataset 2023_dataset 
          60           36           22           54 
```

```
specimen <- read_json("http://cmi-pb.org/api/v5/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
```

```r
ab_titer <- read_json("http://cmi-pb.org/api/v5/plasma_ab_titer", simplifyVector = TRUE)
```

```r
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
```

We want to merge or “join” these tables so we can have all the info we need about a given antibody measurement.

```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
```

```
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
```

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

```r
nrow(abdata)
```

```
[1] 52576
```

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

```

  IgE   IgG  IgG1  IgG2  IgG3  IgG4 
 6698  5389 10117 10124 10124 10124 
```

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

```

    ACT   BETV1      DT   FELD1     FHA  FIM2/3   LOLP1     LOS Measles     OVA 
   1970    1970    4978    1970    5372    4978    1970    1970    1970    4978 
    PD1     PRN      PT     PTM   Total      TT 
   1970    5372    5372    1970     788    4978 
```

Let's begin with IgG

```r
igg <- filter(abdata, isotype=="IgG")
head(igg)
```

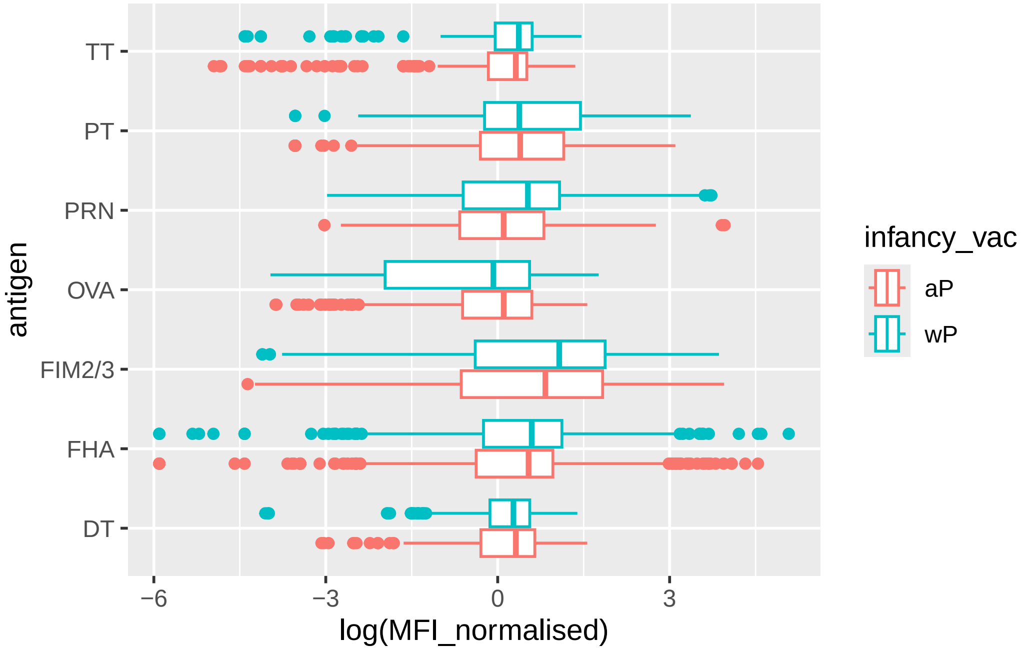
```
  specimen_id isotype is_antigen_specific antigen        MFI MFI_normalised
1           1     IgG                TRUE      PT   68.56614       3.736992
2           1     IgG                TRUE     PRN  332.12718       2.602350
3           1     IgG                TRUE     FHA 1887.12263      34.050956
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
```

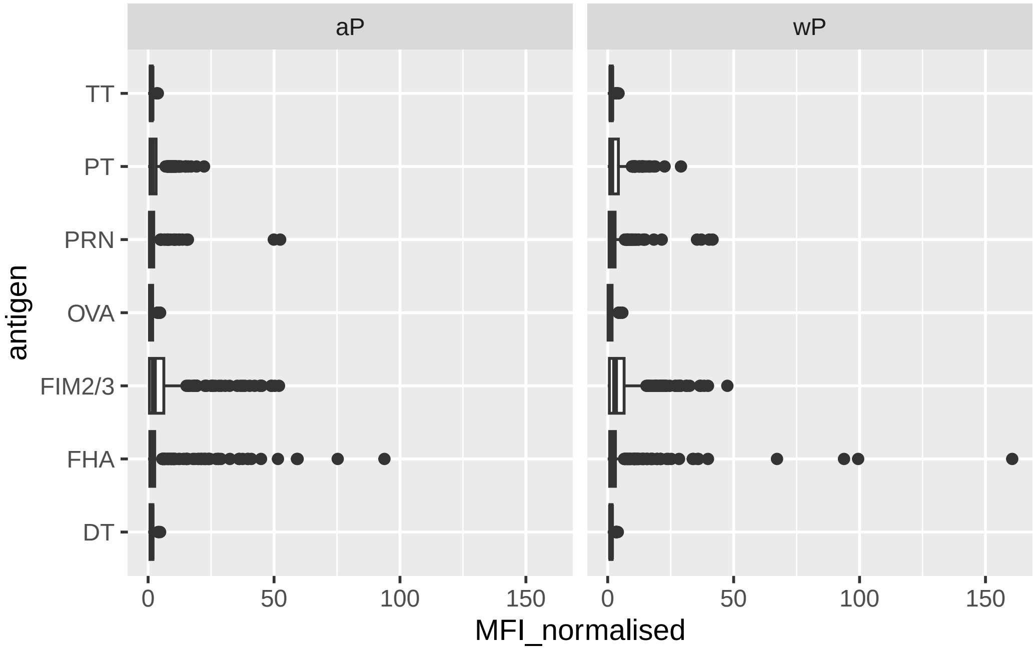
Make a boxplot of IgG antigen levels - this will be a plot of MFI vs antigen

```r
library(ggplot2)

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



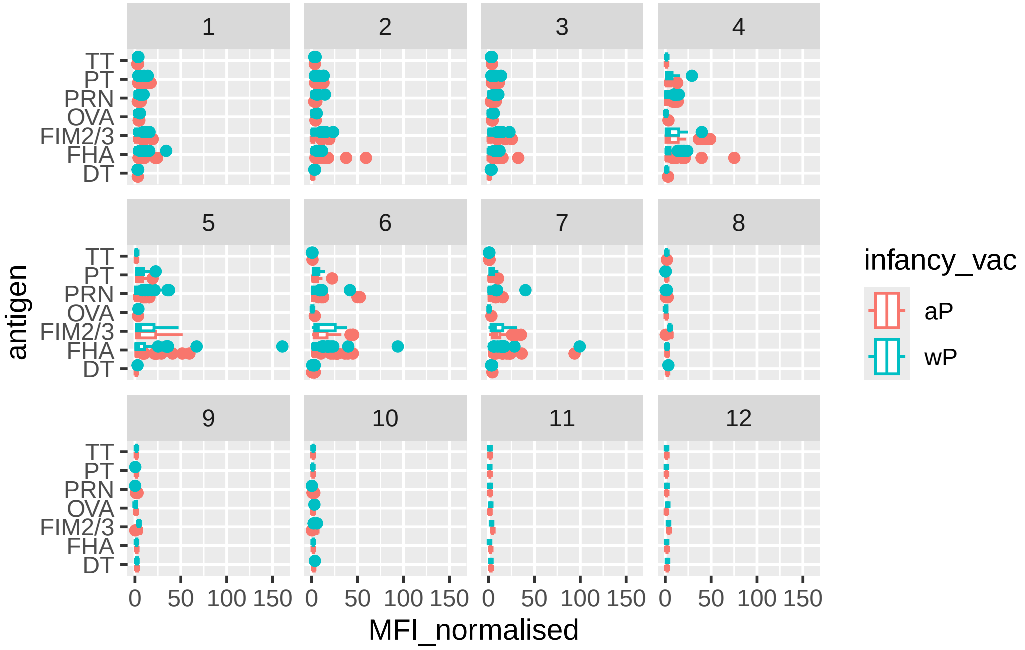
```
ggplot(data=igg) +
  aes (MFI_normalised, antigen) +
  geom_boxplot() +
  facet_wrap(~infancy_vac)
```



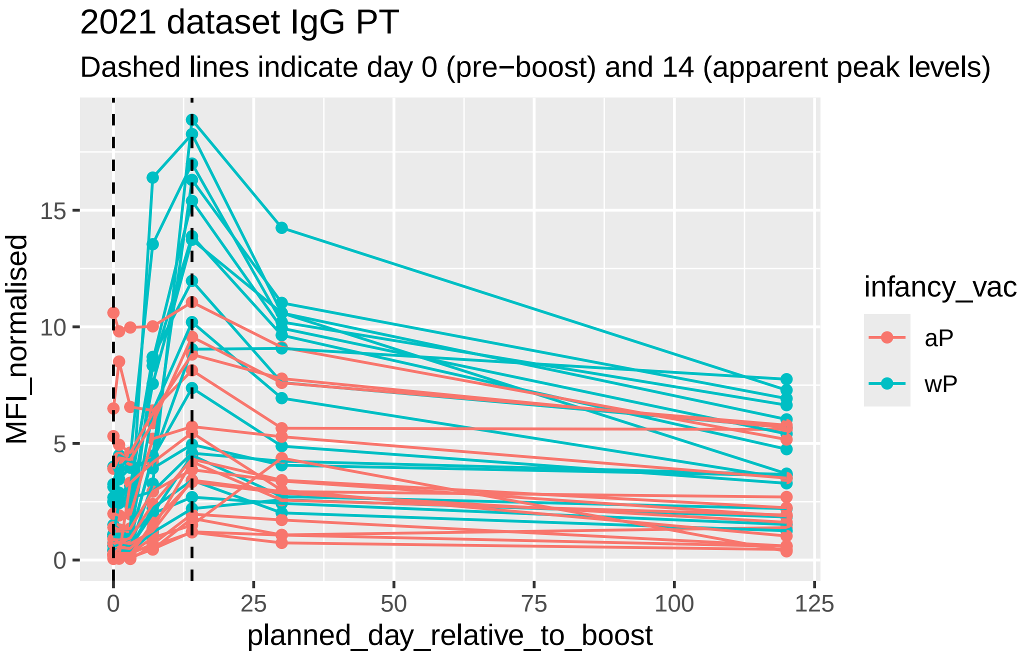
```
table(abdata$visit)
```

```
   1    2    3    4    5    6    7    8    9   10   11   12
8280 8280 8420 6565 6565 6210 5810  815  735  686  105  105
```

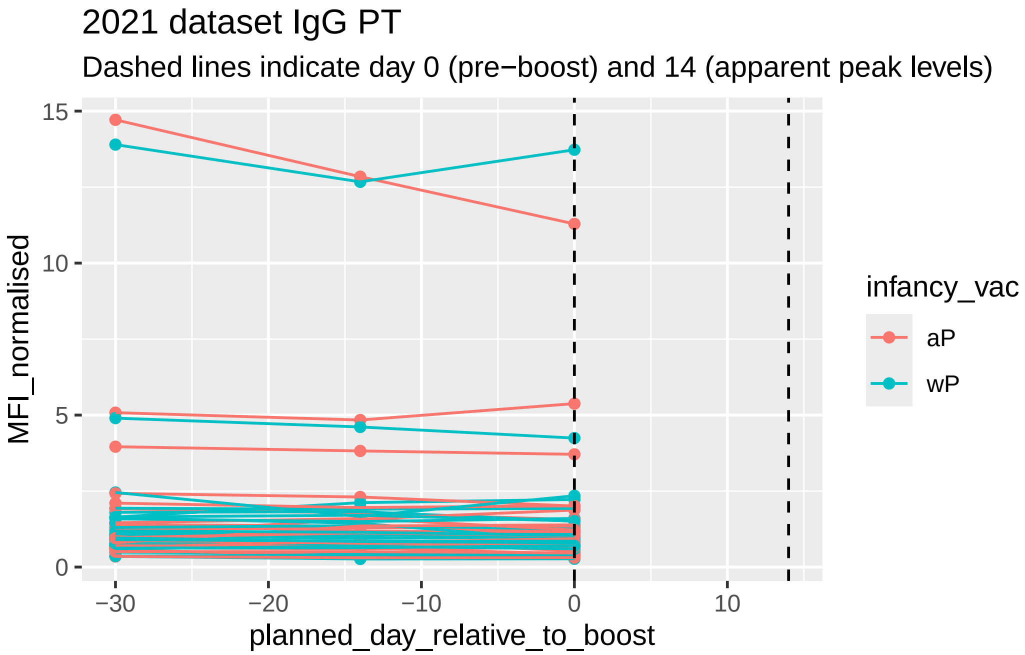
```
ggplot(data=igg) +
  aes (MFI_normalised, antigen, col=infancy_vac) +
  geom_boxplot() +
  facet_wrap(~visit)
```



```
filter(igg, antigen=="PT", dataset=="2021_dataset") %>%
ggplot() +
  aes (planned_day_relative_to_boost, MFI_normalised, col=infancy_vac, group=subject_id) +
  geom_point() +
  geom_line() +
  #geom_smooth(aes(group=infancy_vac), method = loess, se = TRUE) +
  geom_vline(xintercept=0, linetype="dashed") +
  geom_vline(xintercept=14, linetype="dashed") +
  labs(title="2021 dataset IgG PT",
       subtitle = "Dashed lines indicate day 0 (pre-boost) and 14 (apparent peak levels)")
```



```
filter(igg, antigen=="PT", dataset=="2023_dataset") %>%
ggplot() +
  aes (planned_day_relative_to_boost, MFI_normalised, col=infancy_vac, group=subject_id) +
  geom_point() +
  geom_line() +
 # geom_smooth() +
  geom_vline(xintercept=0, linetype="dashed") +
  geom_vline(xintercept=14, linetype="dashed") +
  labs(title="2021 dataset IgG PT",
       subtitle = "Dashed lines indicate day 0 (pre-boost) and 14 (apparent peak levels)")
```


2021 dataset IgG PT
Dashed lines indicate day 0 (pre−boost) and 14 (apparent peak levels)
MFI_normalised
15
10
5
0
−30
−20
−10
0
10
planned_day_relative_to_boost
infancy_vac
aP
wP