Lab 15

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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 need to "scrape" this data so we do stuff with it in R. Let's try the **datapasta** package to do this. We will not be using a function from this package, but rather an "addin" to copy the data and paste as a `data.frame`.

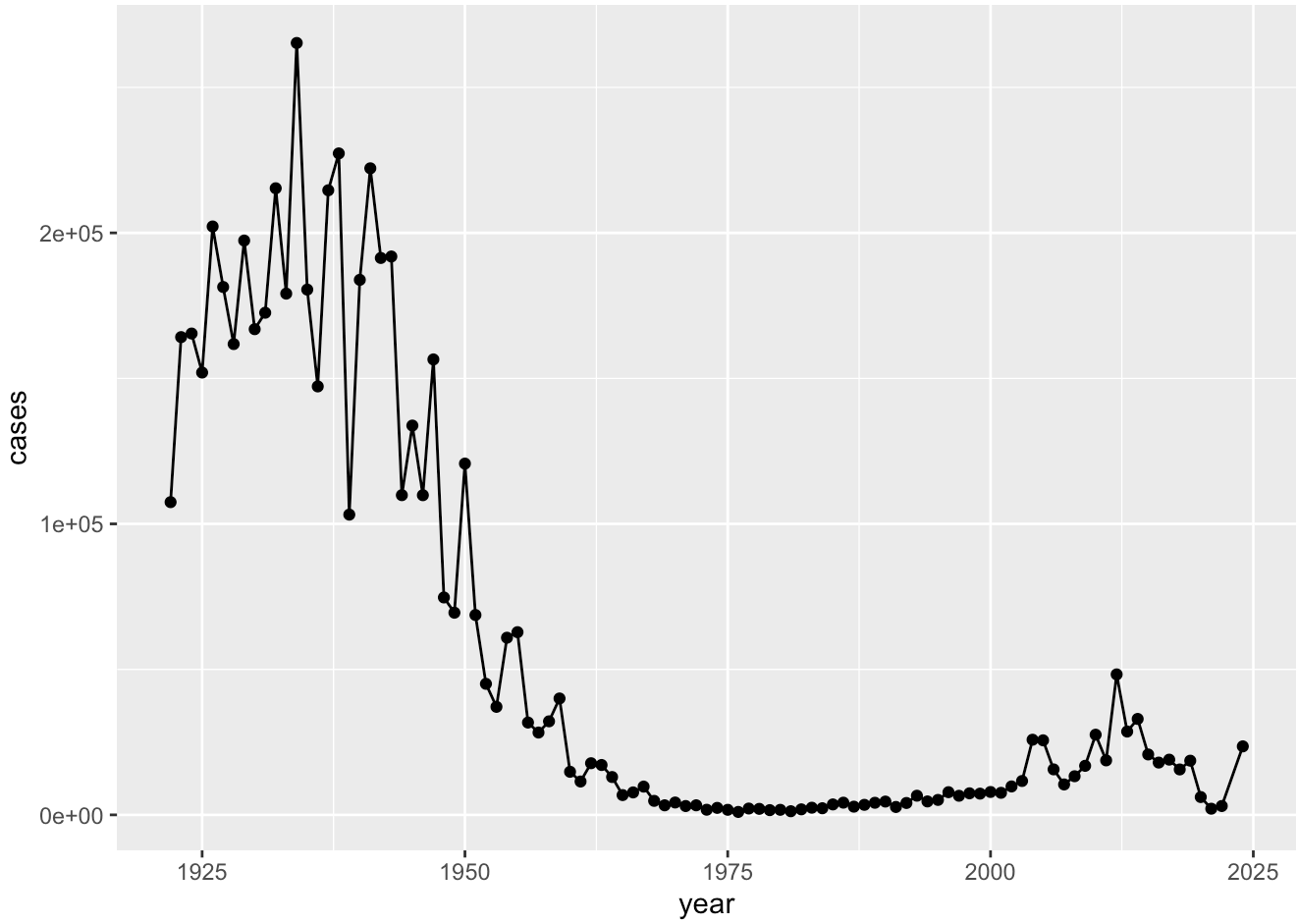
#install.packages("datapasta")

```
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)
        )
```

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

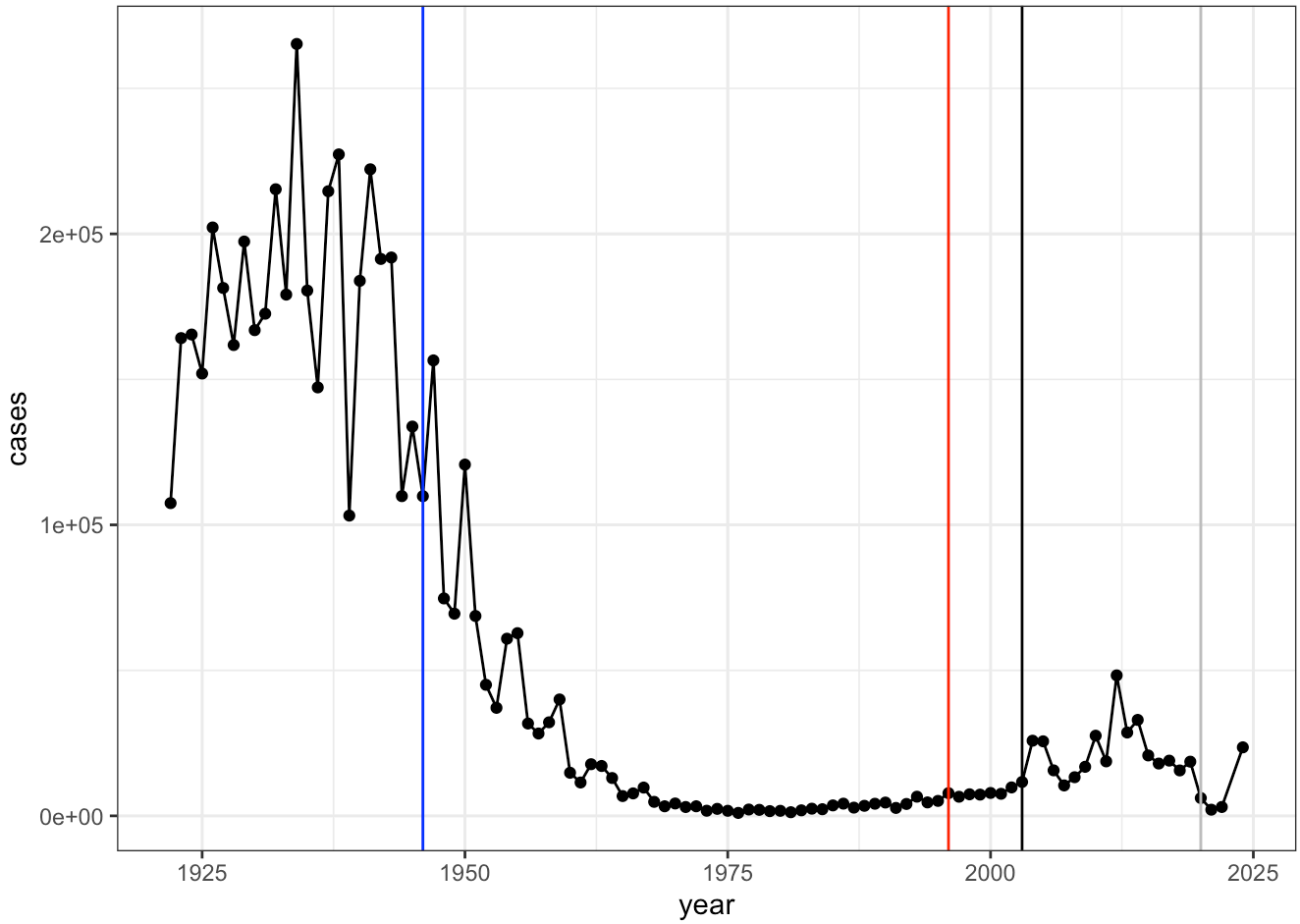
```
library(ggplot2)
baseplot <- ggplot(cdc) +
  aes(year, cases) +
  geom_point() +
  geom_line()
baseplot
```




```
#now we can add more layers to baseplot so we don't have to keep copying the entire chunk
```

Let's add the date of wP vaccine roll out completion (1946) and the switch to the new aP vaccine (1996).

```
baseplot +
  theme_bw() +
  geom_vline(xintercept=1946, col = "blue") +
  geom_vline(xintercept=1996, col = "red") +
  geom_vline(xintercept=2020, col = "gray") +
  geom_vline(xintercept=2003)
```



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

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

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

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

```
library(jsonlite)

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

Let's have a wee peek and 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 are in this dataset?

```
nrow(subject)
```

```
[1] 172
```

> Q. How many male/female 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. Breakdown 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 breakdown reflect the US population?

Not really.

```
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 = T)

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

```
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
```

```
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 will want to merge or "join" these data.frames together using dplyr. This is so we can have all the info we need about a given antibody measurement.

```
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
```

And one last join of `ab_titer` and `meta`.

```
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
  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
```

```
nrow(abdata)
```

```
[1] 52576
```

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

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

```
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

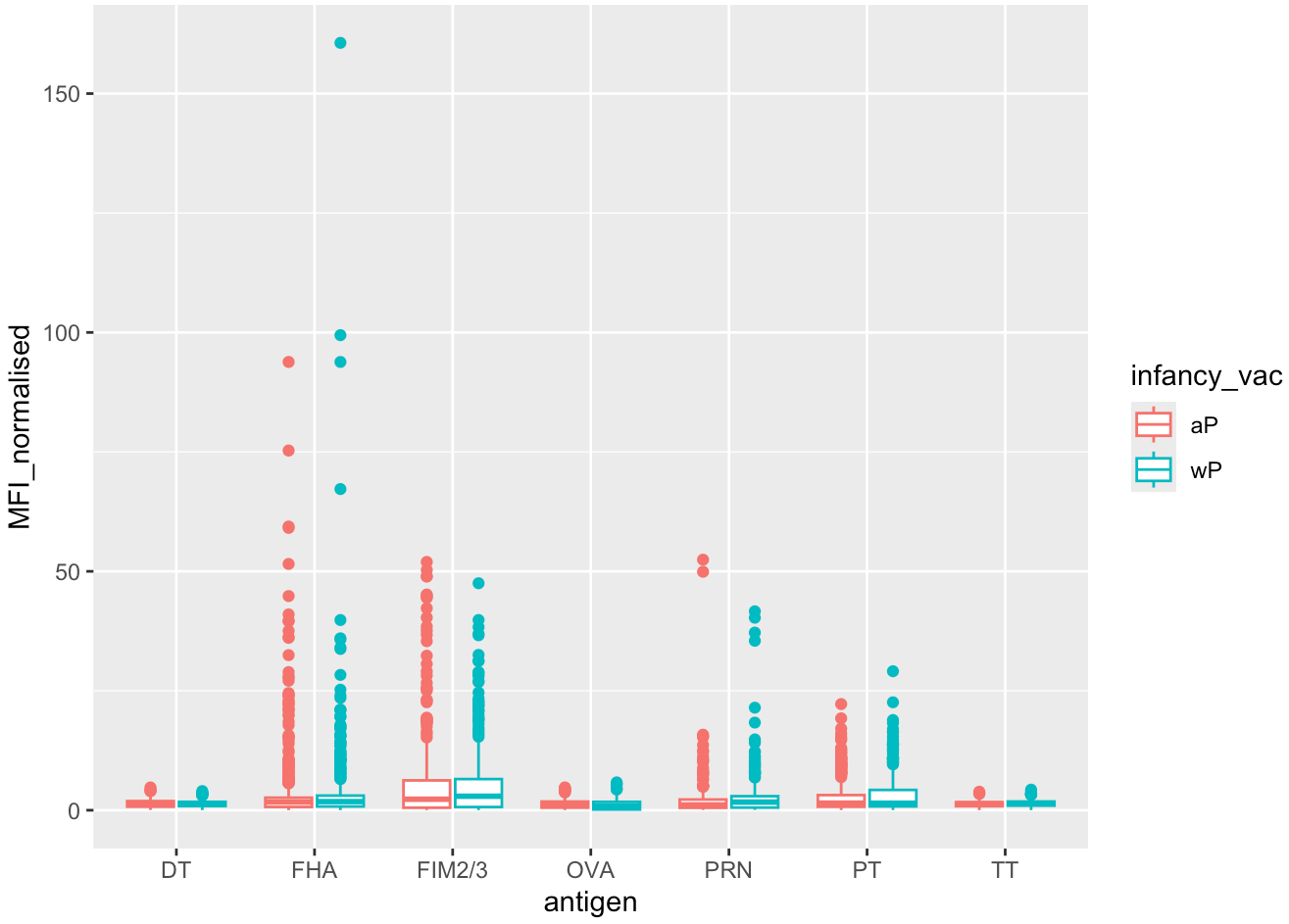
```
igg <- filter(abdata, isotype=="IgG")
head(igg)
```

```
  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_normalized vs. antigen

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

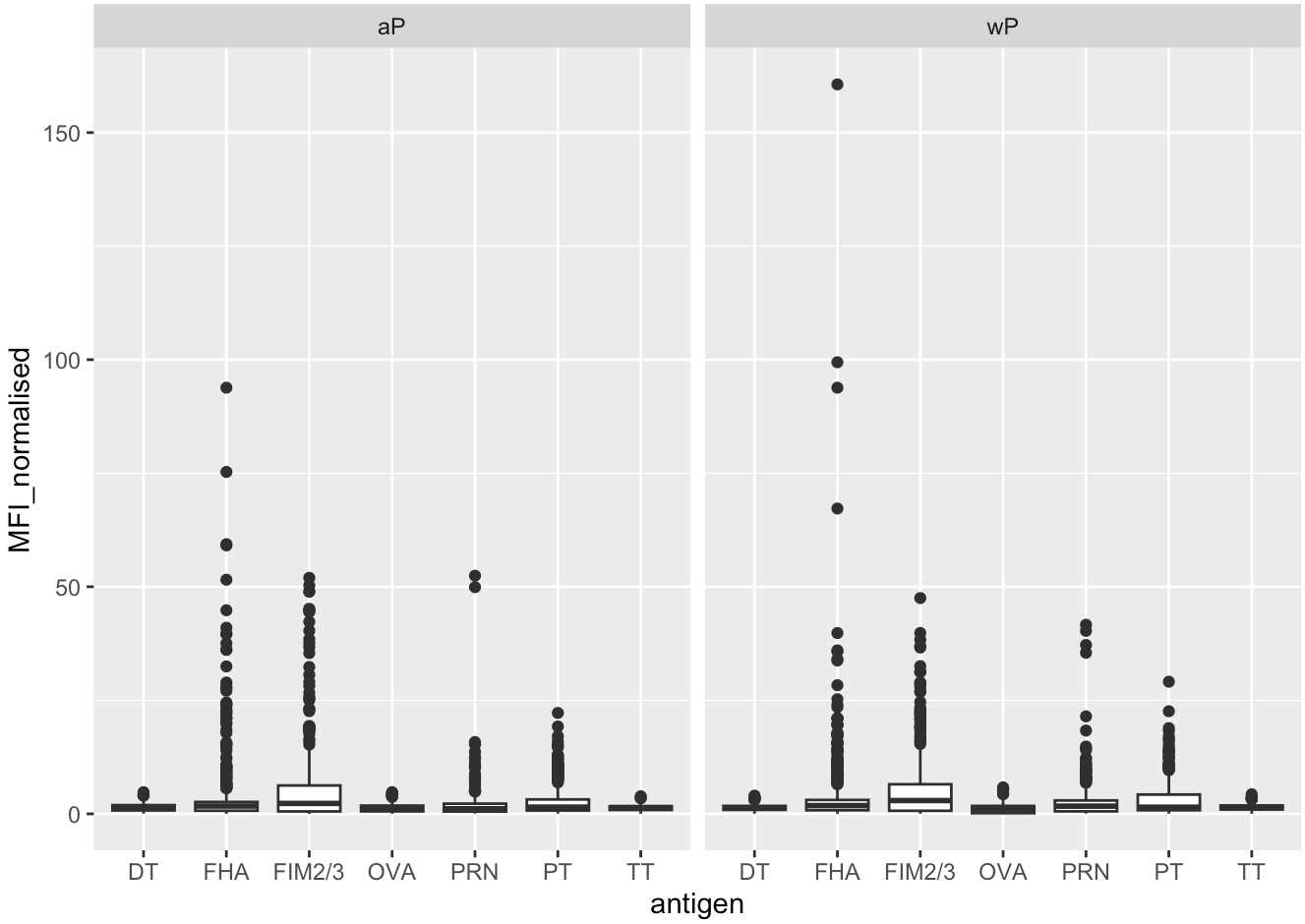


Ideally I would like to see how these Ab levels change over time relative to the booster shot.

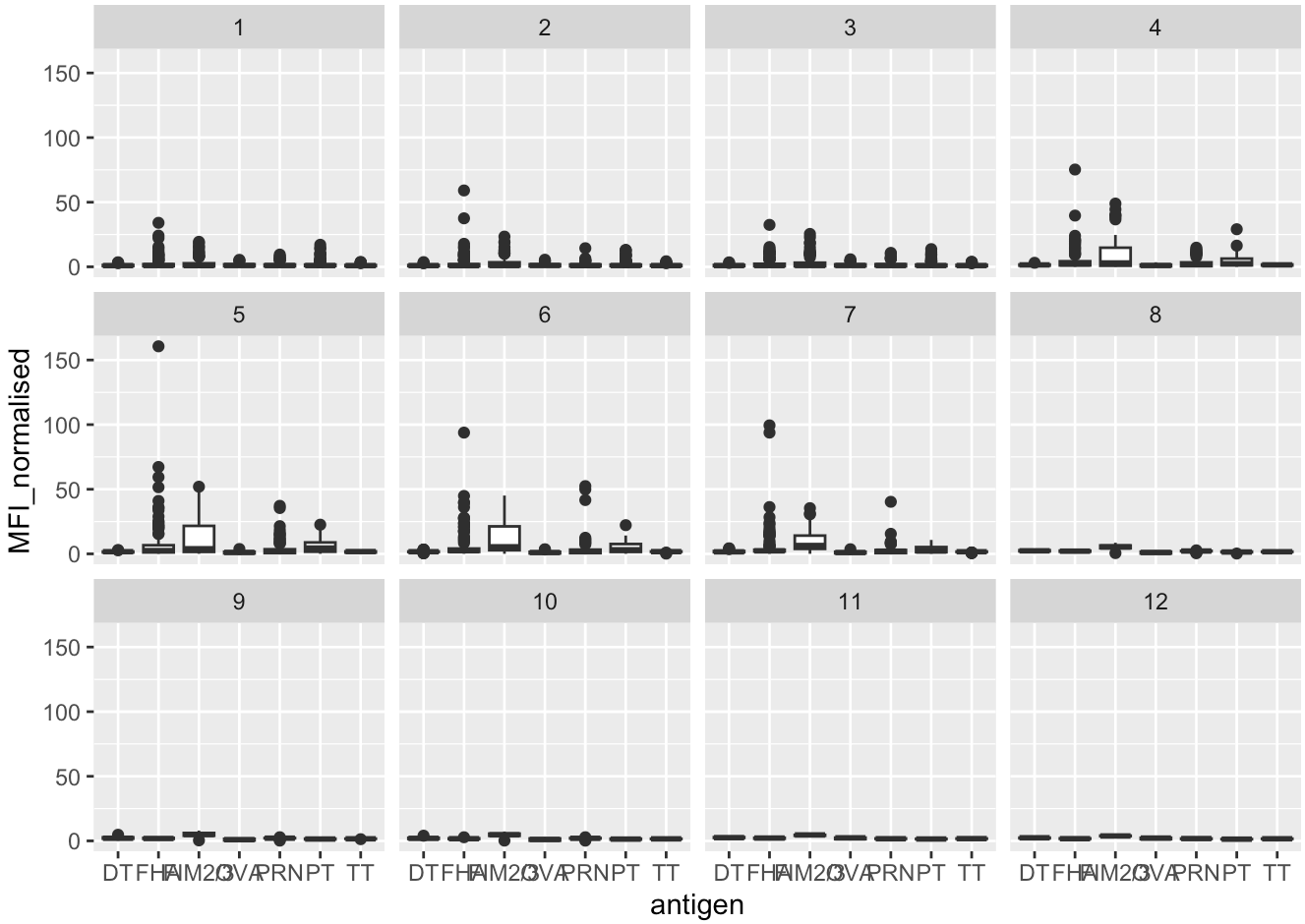
```
table(abdata$visit)
```

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




```
ggplot(igg) +
  aes(antigen, MFI_normalised) +
  geom_boxplot() +
  facet_wrap(~visit)
```




```
year <- filter(abdata, dataset=="2021_dataset")
head(year)
```

```
  specimen_id isotype is_antigen_specific antigen        MFI MFI_normalised
1         468     IgG                FALSE     PRN   700.1375      0.1105807
2         468     IgG                FALSE      DT  8924.4547      0.7060561
3         468     IgG                FALSE     FHA  2362.4022     10.6423728
4         468     IgG                FALSE  FIM2/3   755.7511      1.4246015
5         468     IgG                FALSE      TT 14727.5902      1.1090932
6         468     IgG                FALSE      PT   112.7500      1.0000000
  unit lower_limit_of_detection subject_id infancy_vac biological_sex
1  MFI               502.263892         61          wP         Female
2  MFI              2448.250000         61          wP         Female
3  MFI                 7.071092         61          wP         Female
4  MFI                13.875962         61          wP         Female
5  MFI              2557.146899         61          wP         Female
6  MFI                 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                           -4                             0
3 2021_dataset                           -4                             0
4 2021_dataset                           -4                             0
5 2021_dataset                           -4                             0
6 2021_dataset                           -4                             0
  specimen_type visit
1         Blood     1
2         Blood     1
3         Blood     1
4         Blood     1
5         Blood     1
6         Blood     1
```

```
igg_2021 <- filter(year, isotype == "IgG")
head(igg_2021)
```

```
  specimen_id isotype is_antigen_specific antigen        MFI MFI_normalised
1         468     IgG               FALSE     PRN   700.1375      0.1105807
2         468     IgG               FALSE      DT  8924.4547      0.7060561
3         468     IgG               FALSE     FHA  2362.4022     10.6423728
4         468     IgG               FALSE  FIM2/3   755.7511      1.4246015
5         468     IgG               FALSE      TT 14727.5902      1.1090932
6         468     IgG               FALSE      PT   112.7500      1.0000000
  unit lower_limit_of_detection subject_id infancy_vac biological_sex
1  MFI              502.263892         61          wP         Female
2  MFI             2448.250000         61          wP         Female
3  MFI                7.071092         61          wP         Female
4  MFI               13.875962         61          wP         Female
5  MFI             2557.146899         61          wP         Female
6  MFI                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                           -4                             0
3 2021_dataset                           -4                             0
4 2021_dataset                           -4                             0
5 2021_dataset                           -4                             0
6 2021_dataset                           -4                             0
  specimen_type visit
1         Blood     1
2         Blood     1
```

```
3         Blood     1
4         Blood     1
5         Blood     1
6         Blood     1
```

```
pt_2021 <- filter(igg_2021, antigen == "PT")
head(pt_2021)
```

```
  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
```

```
ggplot(pt_2021) +
  aes(planned_day_relative_to_boost, MFI_normalised, col = infancy_vac, group = subject_i
  geom_point() +
  geom_line() +
  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)"
```