BGGN213_Class15

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Information

Barry told me that uploading the class lab is enough to get the points. Let me know if you need something else to get the full points.

Mini project

Pertusses, a.k.a. Whoops Caugh, is a highly contagous lung unfection caused by the *B. Pertussis*.

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.

```
# install.packages("datapasta") - do this in console
library(datapasta)

#this package works a bit different. You copy the data that you want including th

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)
        )

head(cdc)
```

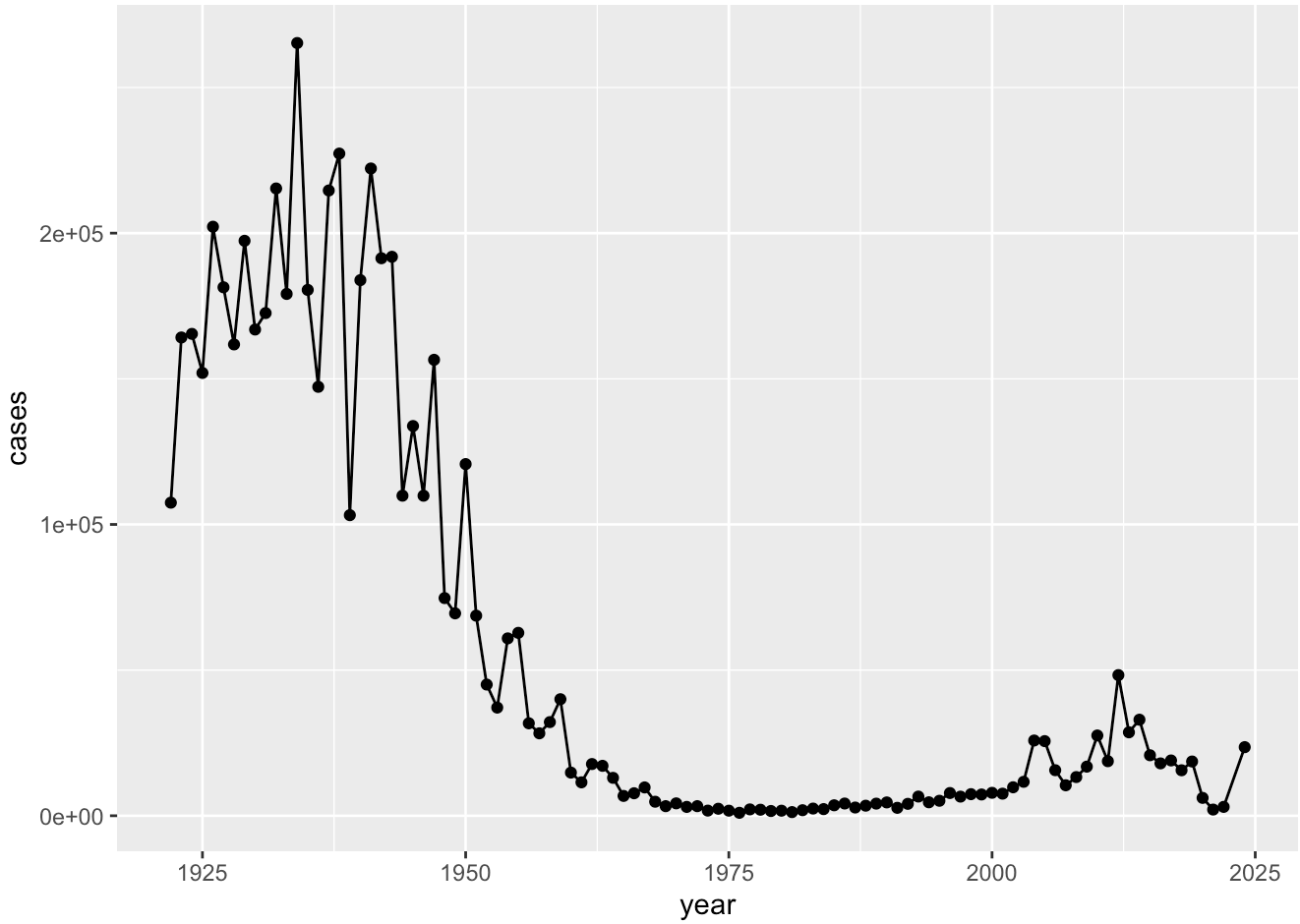
```
  year  cases
1 1922 107473
2 1923 164191
3 1924 165418
4 1925 152003
5 1926 202210
6 1927 181411
```

Make a ggplot (x = year, y = cases)

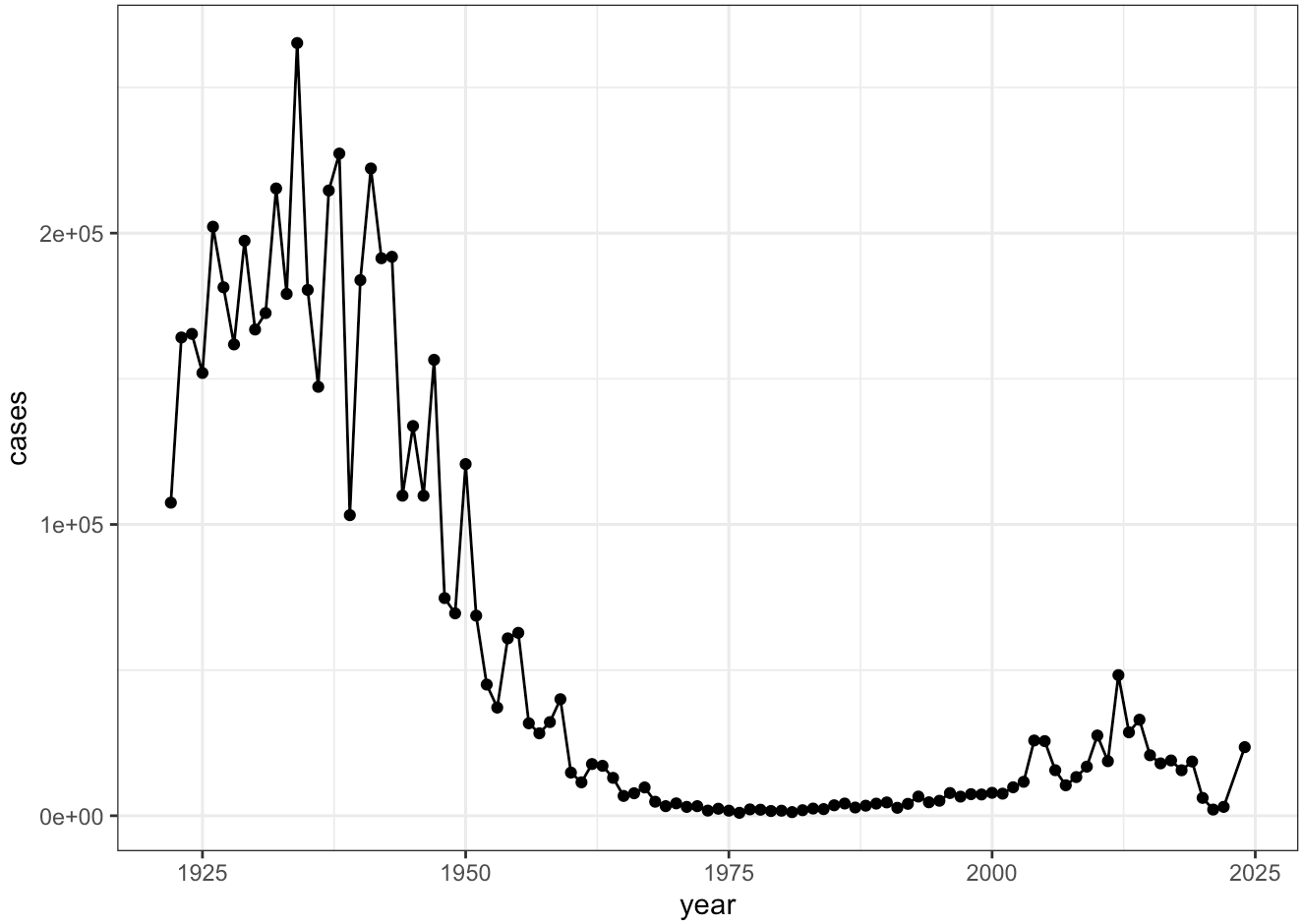
```
library(ggplot2)

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

baseplot #so you can easily add more layers
```

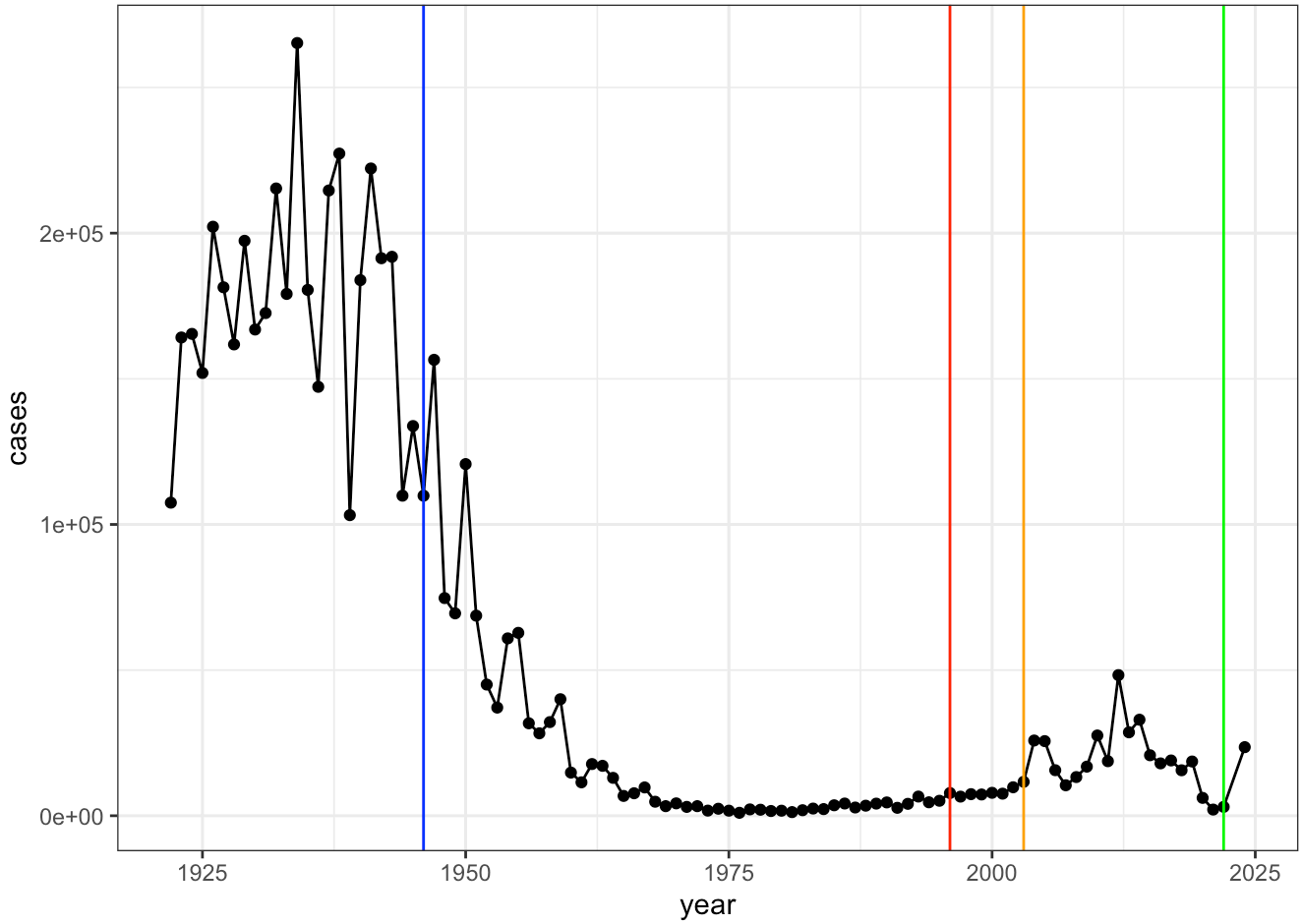



```
baseplot +
  theme_bw()
```



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?

```
baseplot +
  theme_bw() +
  geom_vline(xintercept = 1946, col="blue") +
  geom_vline(xintercept = 1996, col="red") +
  geom_vline(xintercept = 2022, col="green") +
  geom_vline(xintercept = 2003, col="orange")
```




```
        #it is lower in 2022, because there was less social interaction, because of COVID
        #2004, there was an outbreak in Disney California
```

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

Website here Click on: access data -> data composition

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.

```
        # install.packages("jsonlite") -> dont do this in here, but do it in console
        library(jsonlite)
```

```
Warning: package 'jsonlite' was built under R version 4.3.3
```

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

Let's have a wee peak and explore of 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
```

How many subjects do we have? How many wP and aP do we have?

```
nrow(subject)
```

```
[1] 172
```

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

```
aP wP
87 85
```

How many male/female do we have?

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

```
Female   Male
   112     60
```

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

```
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
```

Does this break down reflect the US population?

```
# no
```

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

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

```
specimen <- read_json("https://www.cmi-pb.org/api/v5/specimen", simplifyVector =
ab_titer <- read_json("https://www.cmi-pb.org/api/v5/plasma_ab_titer", simplifyVe

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 want to merge or “join” these tables, so we can have all the info we need about a give 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
```

```
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) #52576 big, a lot of antibody measurements
```

```
[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 (look at this specific isotype)

```
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
```

```
#check if it is correct
table(igg$isotype)
```

```
 IgG
5389
```

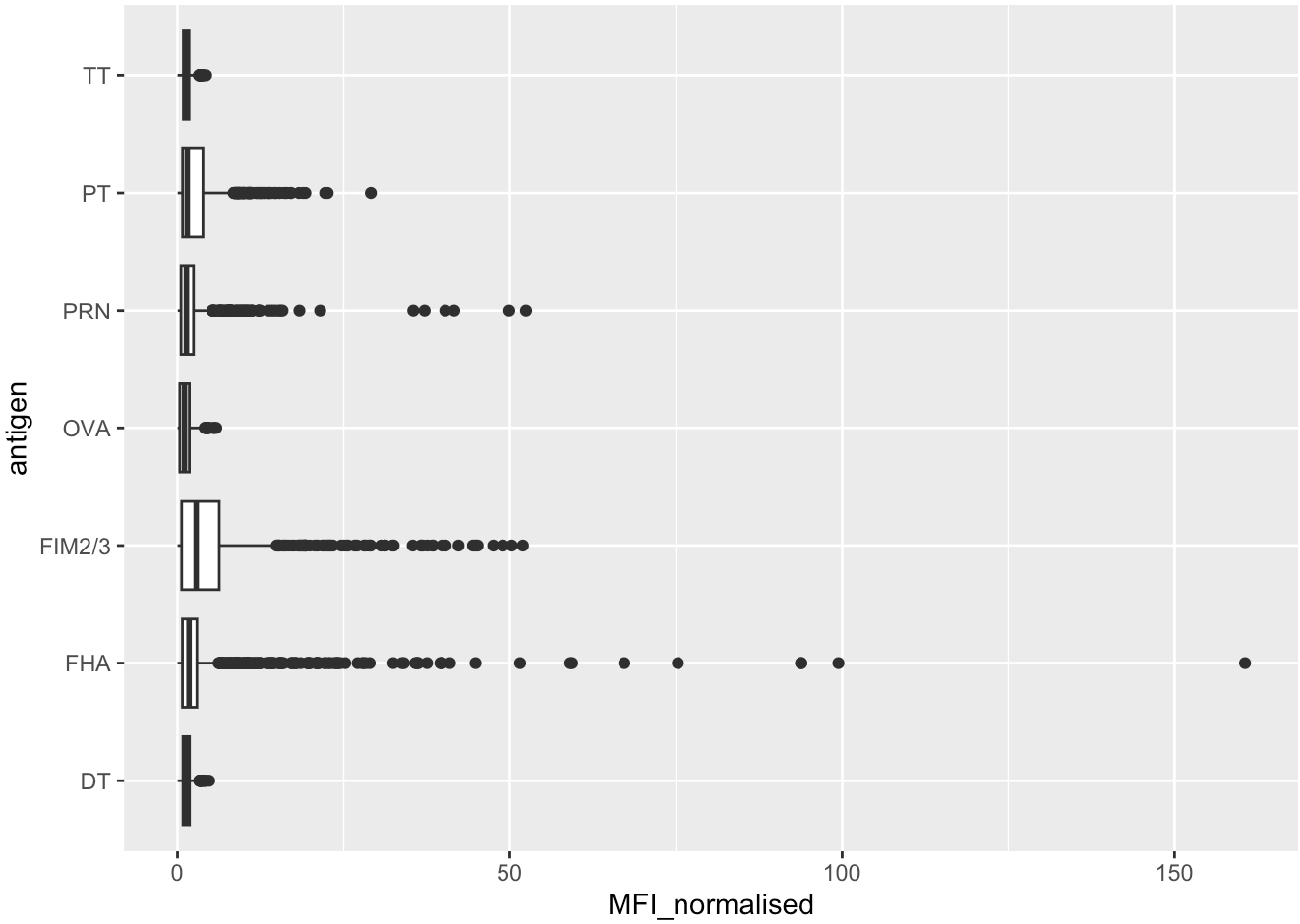
```
nrow(igg)
```

```
[1] 5389
```

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

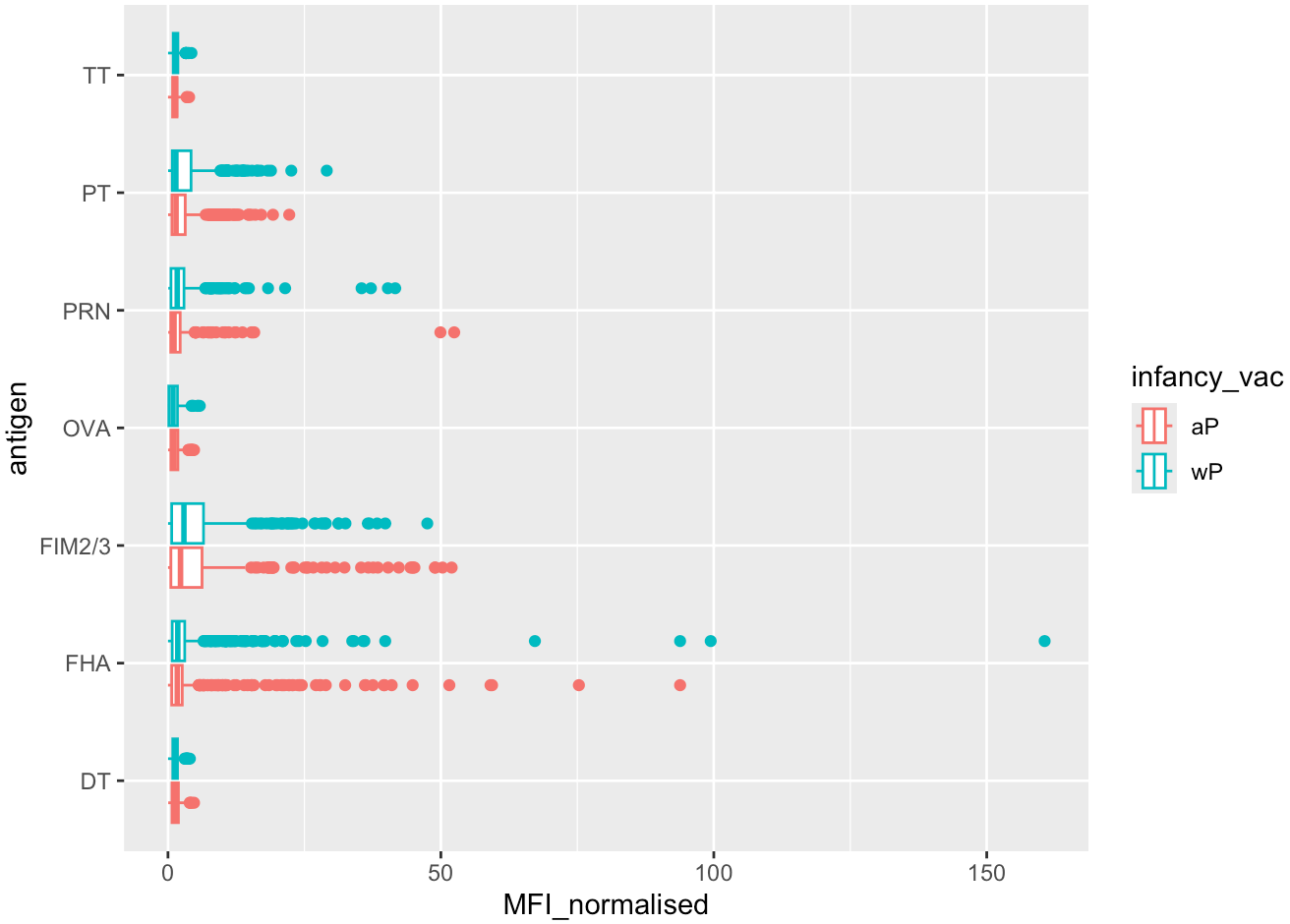
```
library(ggplot2)

ggplot(igg) +
  aes(x = MFI_normalised, y = antigen) +
  geom_boxplot()
```

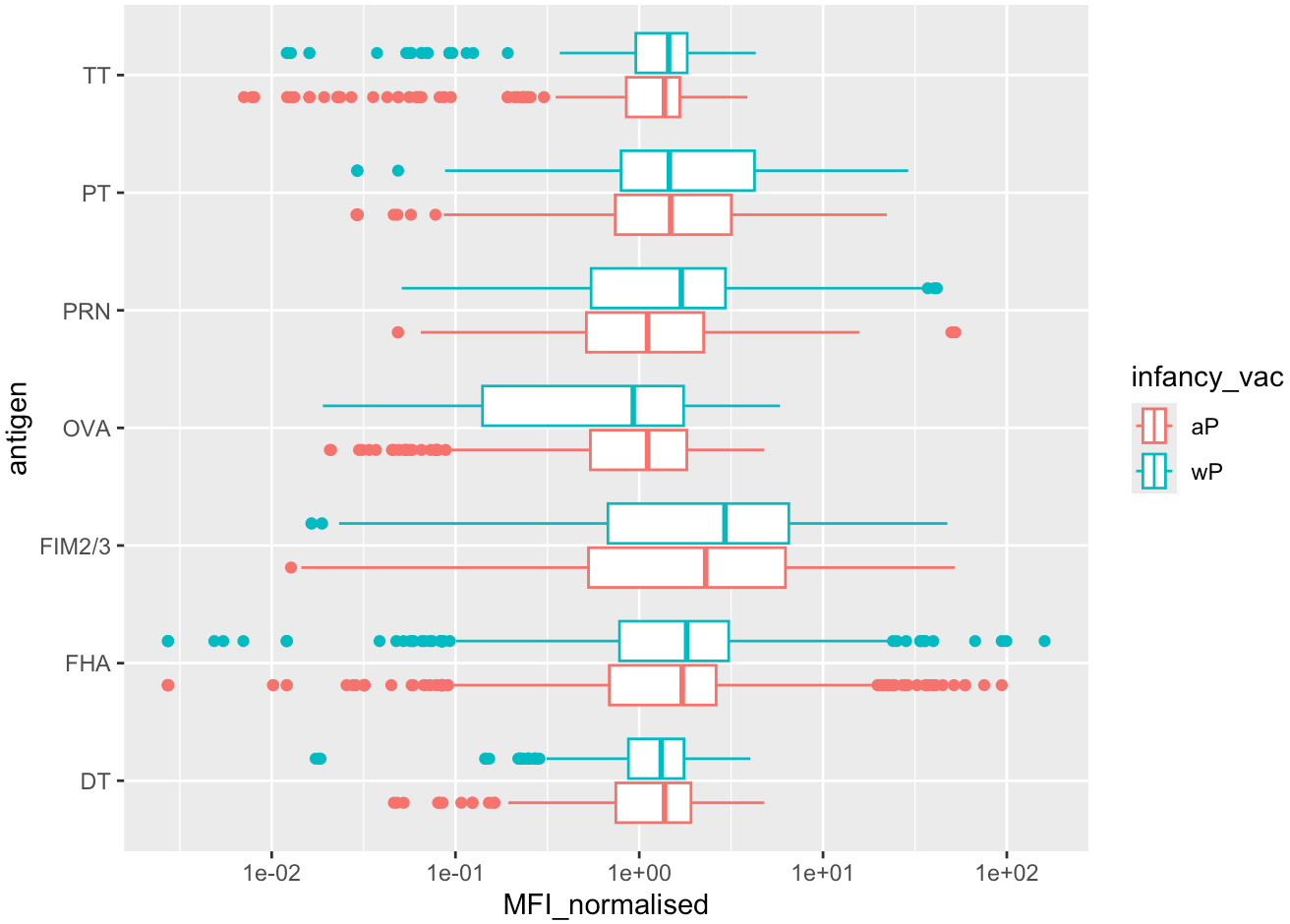


Colour it by aP and wP

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




```
ggplot(igg) +
  aes(x = MFI_normalised, y = antigen, col=infancy_vac) +
  geom_boxplot() +
  scale_x_log10()
```



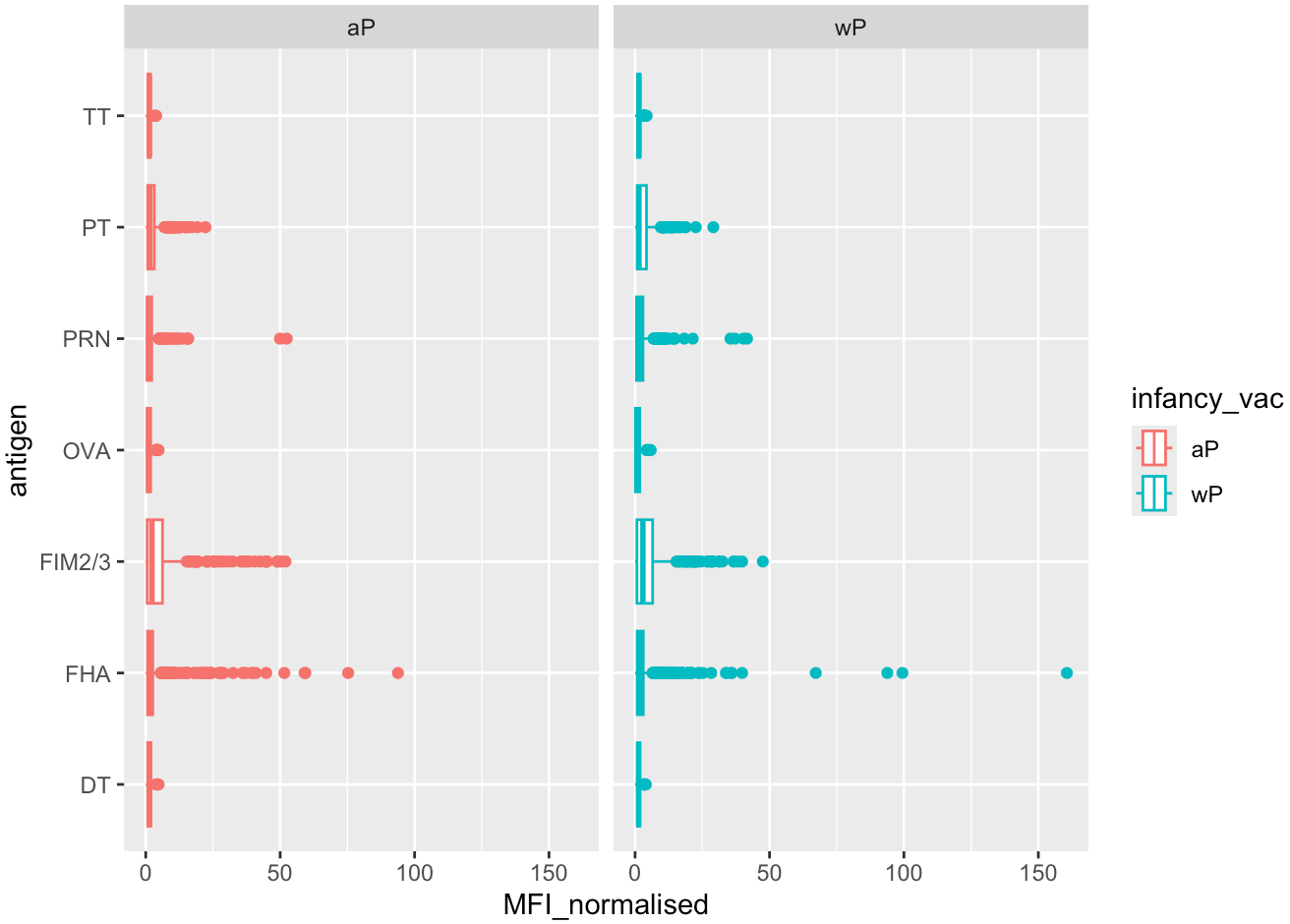
Ideally I would like to see how these Ab levels change over time relative to the booster shot.

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

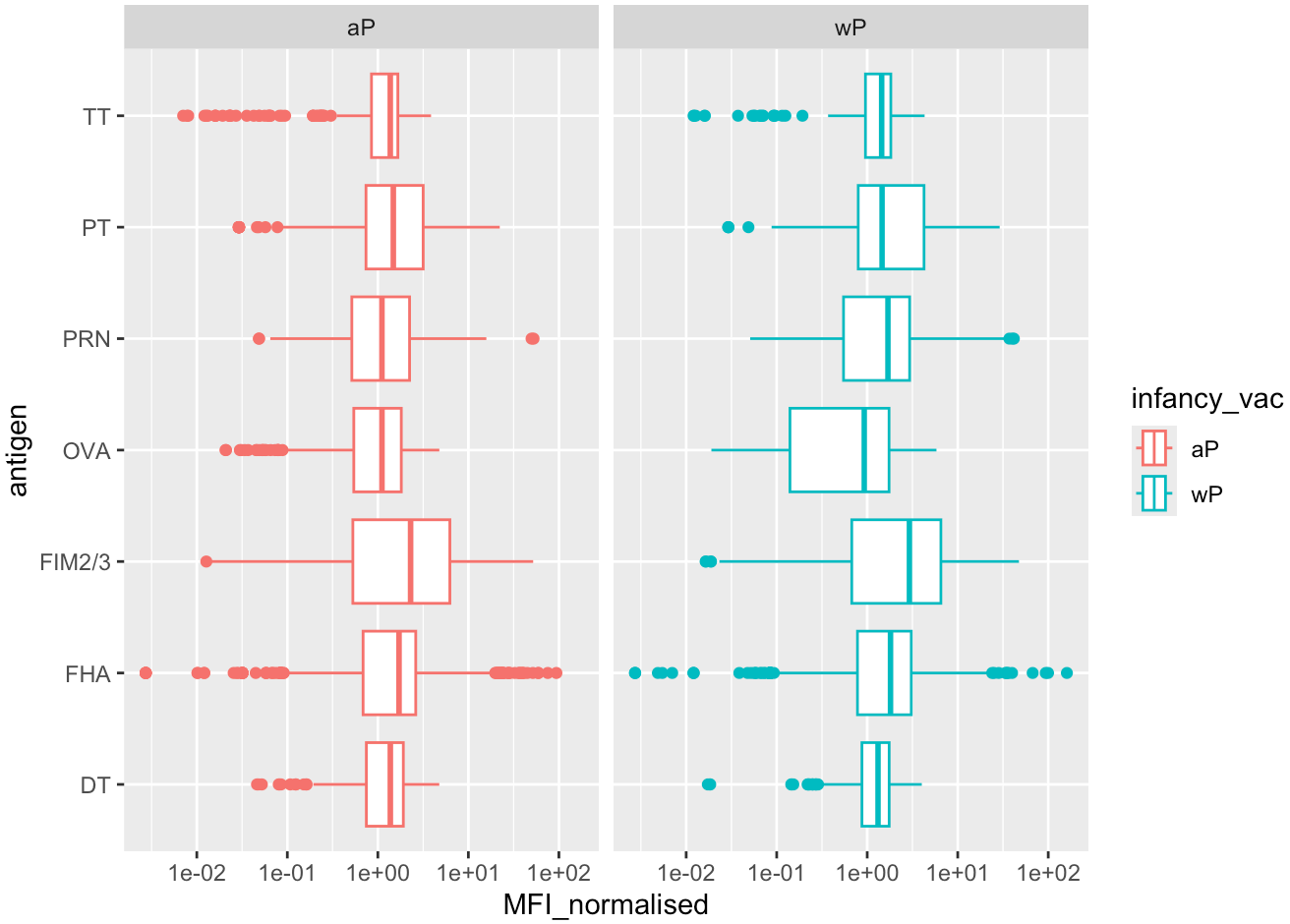
```
   1    2    3    4    5    6    7    8    9   10   11   12
8280 8280 8420 6565 6565 6210 5810  815  735  686  105  105
```

Try facet-wrap, to split the graphs. Here are different graphs.

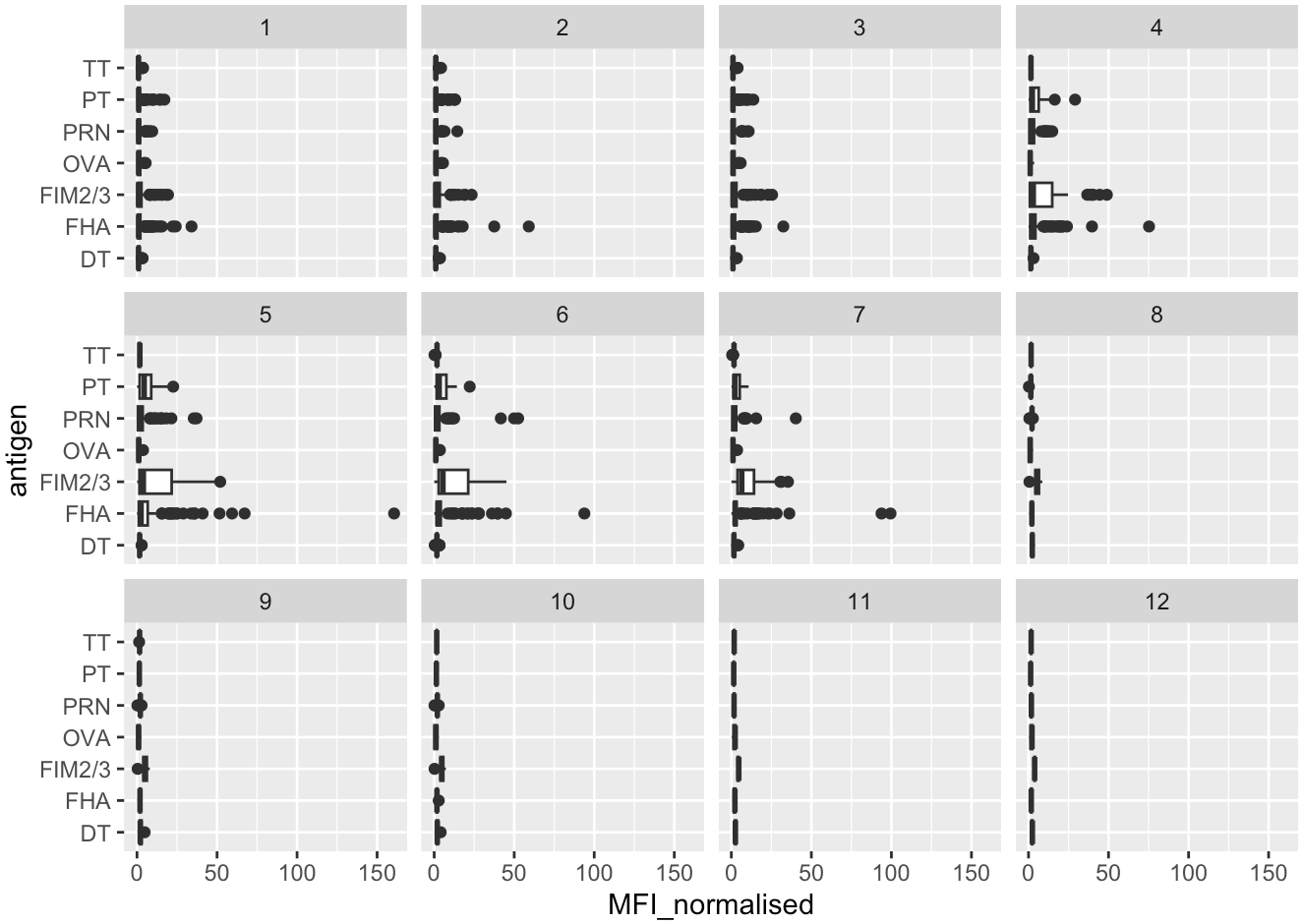
```
ggplot(igg) +
  aes(x = MFI_normalised, y = antigen, col=infancy_vac) +
  geom_boxplot() +
  facet_wrap(~infancy_vac)
```



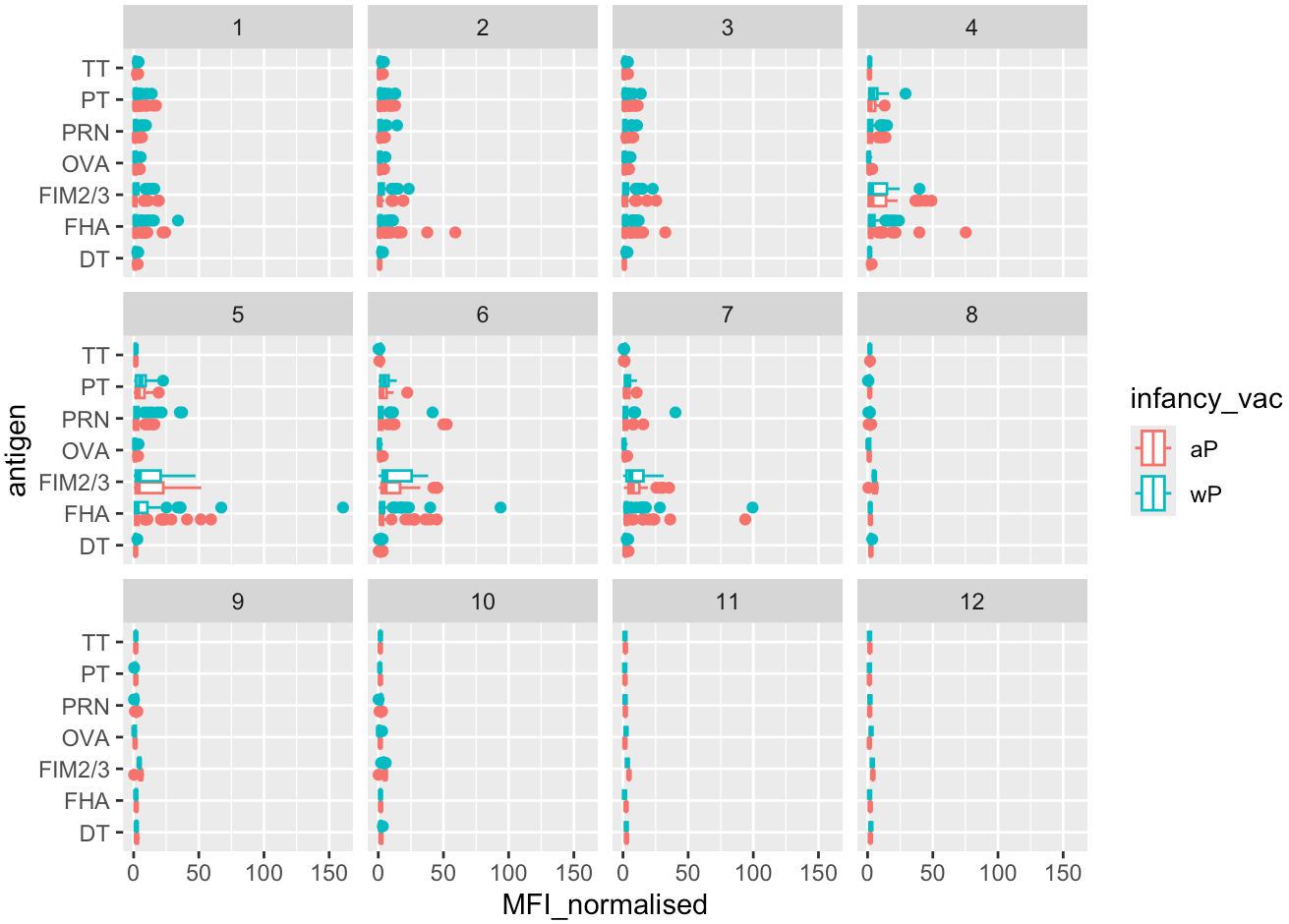

```
# log variant
ggplot(igg) +
  aes(x = MFI_normalised, y = antigen, col=infancy_vac) +
  geom_boxplot() +
  scale_x_log10() +
  facet_wrap(~infancy_vac)
```



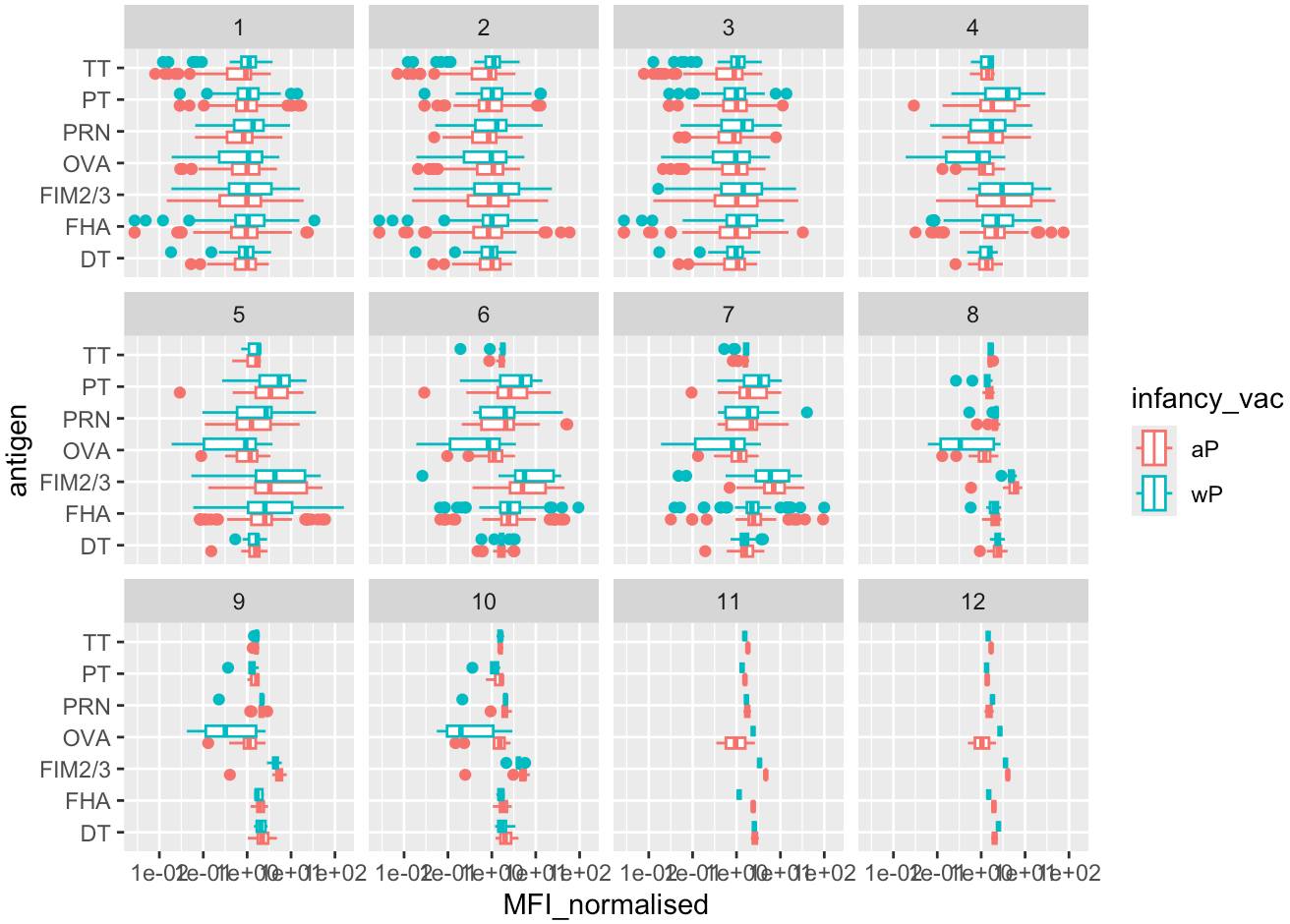

```
# facet by visit
ggplot(igg) +
  aes(x = MFI_normalised, y = antigen) +
  geom_boxplot() +
  facet_wrap(~visit)
```




```
# facet by visit, with col
ggplot(igg) +
  aes(x = MFI_normalised, y = antigen, col=infancy_vac) +
  geom_boxplot() +
  facet_wrap(~visit)
```




```
# facet by visit, with col and log
ggplot(igg) +
  aes(x = MFI_normalised, y = antigen, col=infancy_vac) +
  geom_boxplot() +
  scale_x_log10() +
  facet_wrap(~visit)
```



Lets look at the 2021 dataset IgG PT antigen levels time-course

```
library(ggplot2)

#first get the 2021 data filtered out
abdata_2021 <- abdata %>% filter(dataset == "2021_dataset")
head(abdata_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
```

```
#second get the IgG data filtered out
abdata_2021_igg <- abdata_2021 %>% filter(isotype == "IgG")
head(abdata_2021_igg)
```

```
  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
```

```
nrow(abdata_2021_igg)
```

```
[1] 1617
```

```
#third get the PT data filtered out
abdata_2021_igg_pt <- abdata_2021_igg %>% filter(antigen == "PT")
head(abdata_2021_igg_pt)
```

```
  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
```

```
nrow(abdata_2021_igg_pt)
```

```
[1] 231
```

```
#fourth make the graph
ggplot(abdata_2021_igg_pt) +
  aes(x = planned_day_relative_to_boost, y = MFI_normalised, col=infancy_vac, grc
  geom_point() +
  geom_line() +
  geom_vline(xintercept = 0, col="orange", linetype="dashed") +
  geom_vline(xintercept = 14, col="orange", linetype="dashed") +
  geom_smooth(aes(group=NULL), se=F) +
  labs(title="2021 dataset IgG PT",
       subtitle = "Dashed lines indicate day 0 (pre-boost) and 14 (apparent peak
```

```
`geom_smooth()` using method = 'loess' and formula = 'y ~ x'
```