Lab 15

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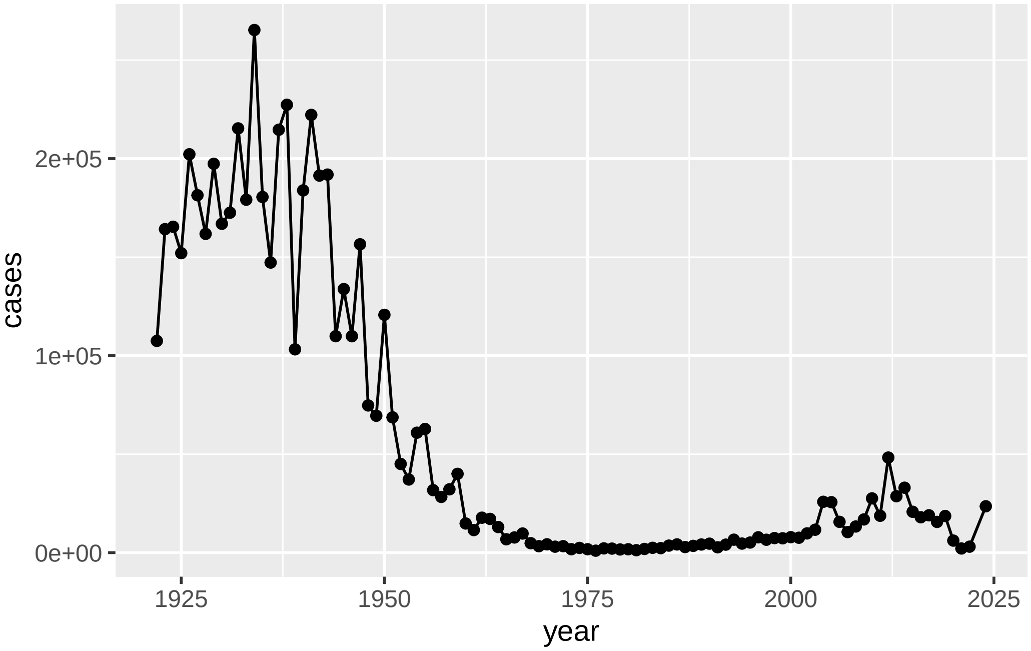
```r
library(datapasta)
```

```r
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))
```

Q1. With the help of the R "addin" package datapasta assign the CDC pertussis case number data to a data frame called cdc and use ggplot to make a plot of cases numbers over time.

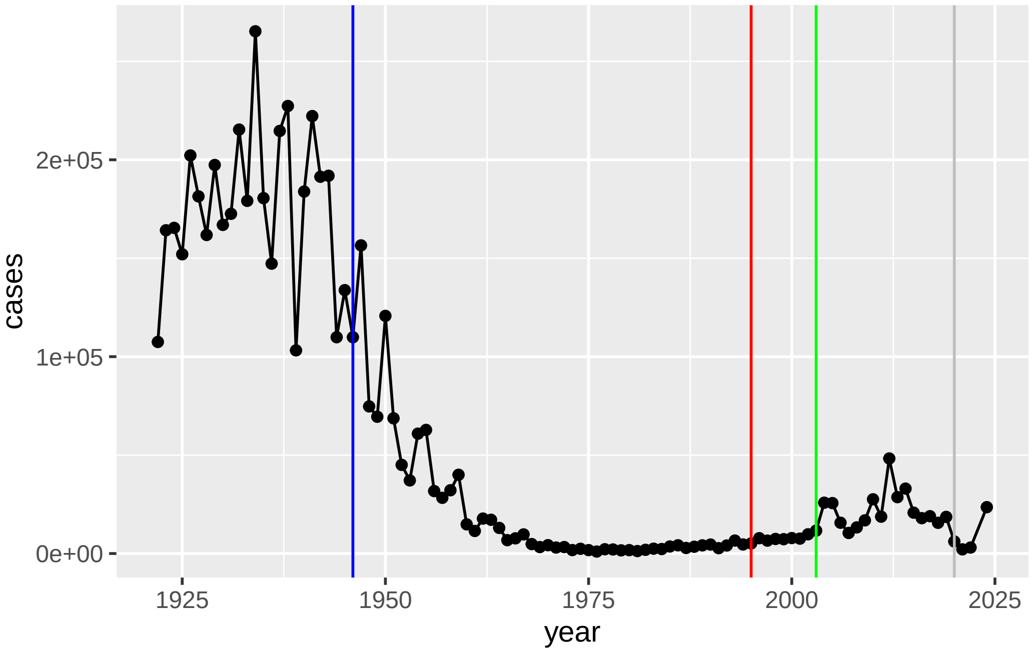
```
library(ggplot2)
baseplot <- ggplot(cdc) +
aes(year, cases) +
geom_point() +
geom_line()
baseplot
```



Q2. 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?

We went from around 200,000 cases pre wP to about 1000 cases in 1976.The numbers started to rise again after the introduction of the aP vaccine.

```
baseplot +
geom_vline(xintercept=1946, col="blue") +
geom_vline(xintercept=1995, col="red") +
geom_vline(xintercept=2020, col="gray") +
geom_vline(xintercept=2003, col="green")
```



> Q3. Describe what happened after the introduction of the aP vaccine? Do you have a possible explanation for the observed trend?

There was a gradual increase after the aP vaccine was introduced in 1995. There is a big increase in 2004 to 26,000 cases. Probably the result of bacterial evolution, decreasing immunity, and vaccine skepticism. There is a 10 year lag from the aP roll out to increasing case numbers. This holds true of other countries like Japan, UK, etc.

```
library(jsonlite)
subject <- read_json("https://www.cmi-pb.org/api/v5/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
```

Q. How many subjects are there in this dataset?

```
nrow(subject)
```

```
[1] 172
```

Q4. How many aP and wP infancy vaccinated subjects are in the dataset?

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

```

aP wP 
87 85 
```

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

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

```

Female   Male 
   112     60 
```

Q6. What is the breakdown of race and biological sex (e.g. number of Asian females, White males etc…)?

```
table(subject$biological_sex, subject$race)
```

```
        American Indian/Alaska Native Asian Black or African American
  Female                             0    32                         2
  Male                               1    12                         3

        More Than One Race Native Hawaiian or Other Pacific Islander
  Female                15                                         1
  Male                   4                                         1

        Unknown or Not Reported White
  Female                     14    48
  Male                        7    32
```

```
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 do a good job of representing the US populus?

No!

```
specimen <- read_json("https://www.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
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
```

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

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

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

```r
head (ab)
```

```
  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
```

Q. How many AB antibody measurements do we have?

```r
nrow(ab)
```

```
[1] 52576
```

> Q. How many isotypes are covered in this dataset

```r
table(ab$isotype)
```

```

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

> Q. How many antigens?

```r
table(ab$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 
```

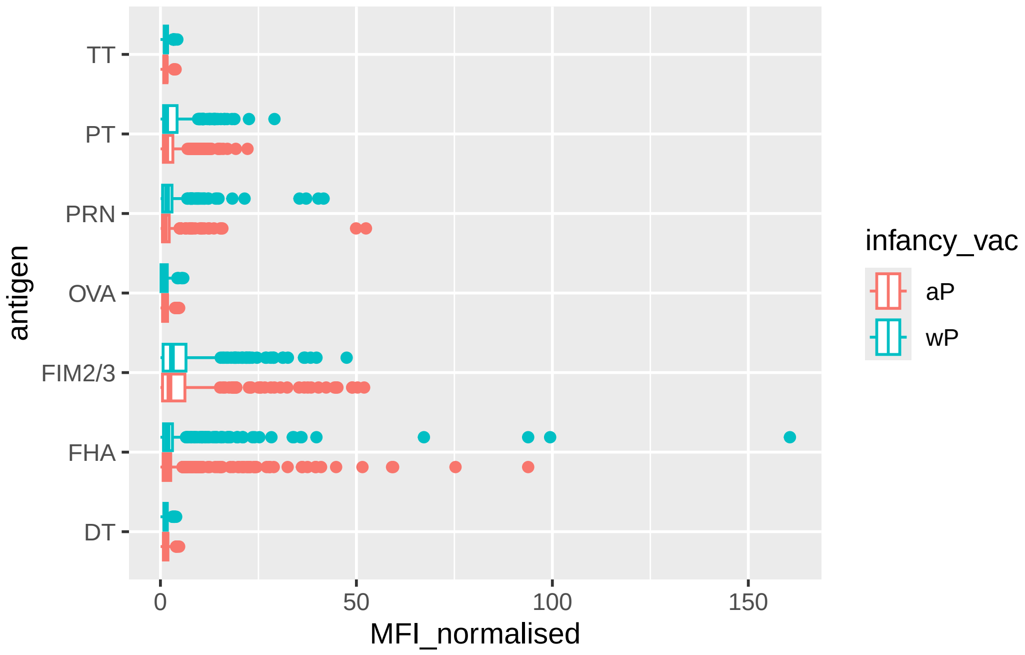
Let's focus in on IgG - one of the main antibodies responsive to bacteria or viral infection

```r
igg <- filter(ab, 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
```

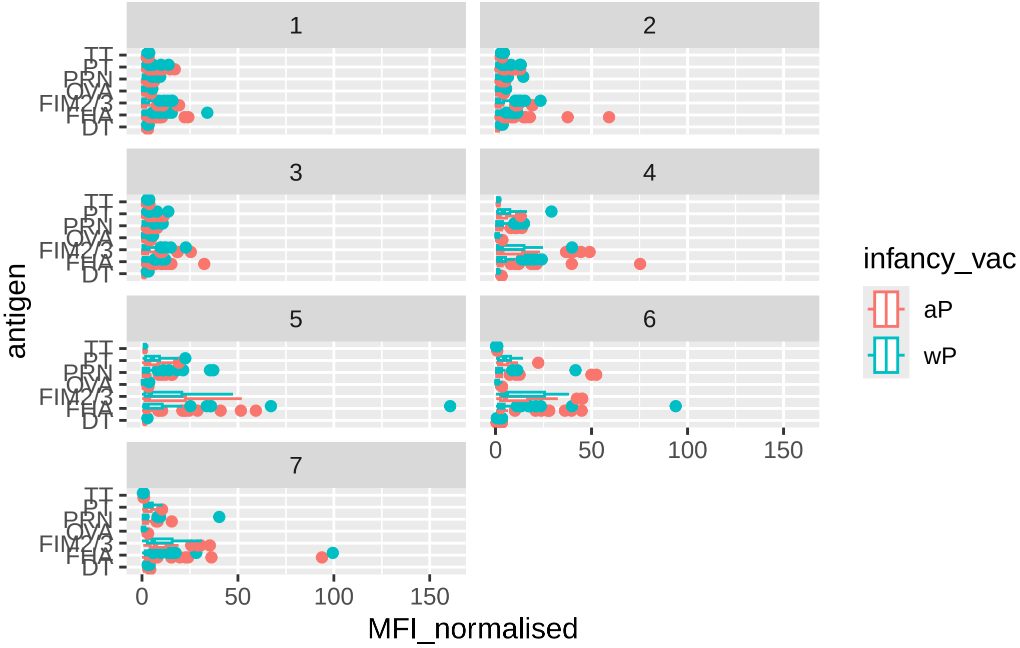
```
ggplot(igg) + aes(MFI_normalised, antigen, col=infancy_vac) + geom_boxplot()
```



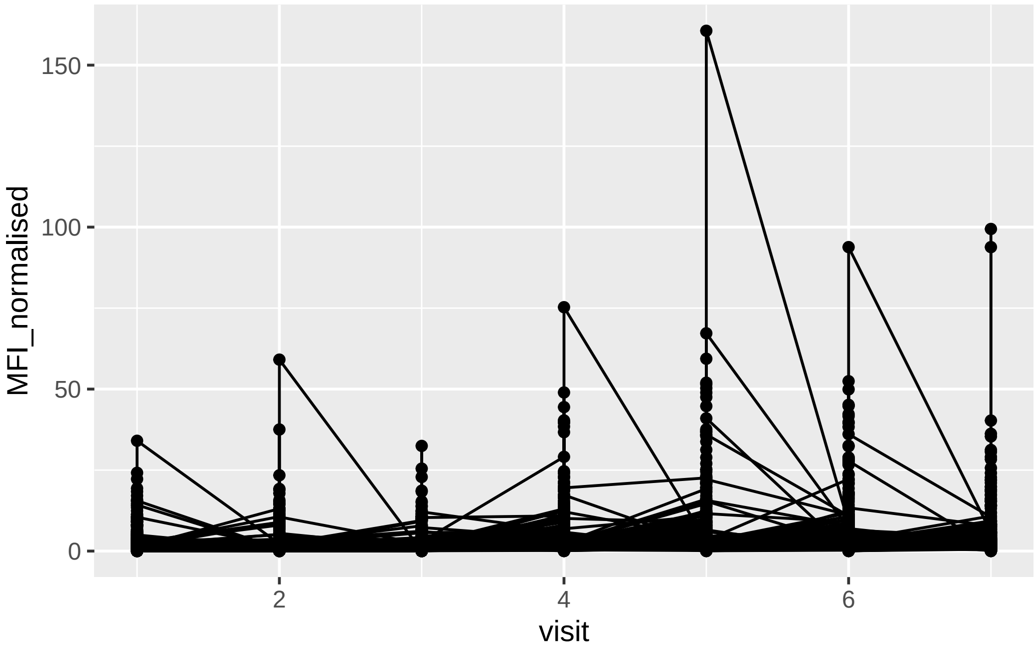
```
igg_7 <- filter(igg, visit %in% 1:7)
table(igg_7$visit)
```

```
  1   2   3   4   5   6   7 
902 902 930 559 559 540 525 
```

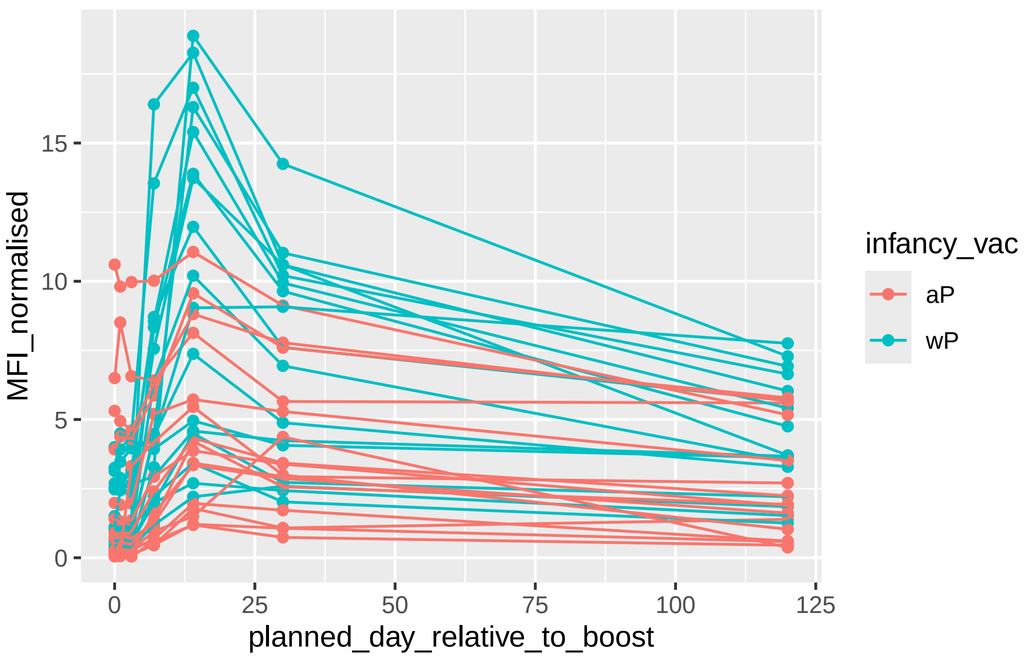
```
ggplot(igg_7) +
aes(MFI_normalised, antigen, col=infancy_vac) +
geom_boxplot() +
facet_wrap(~visit, ncol=2)
```



```
ggplot(igg_7) +
aes(visit, MFI_normalised, group=subject_id) +
geom_point() +
geom_line()
```



```r
abdata.21 <- ab %>% filter(dataset == "2021_dataset")
abdata.21 %>%
filter(isotype == "IgG", antigen == "PT") %>%
ggplot() +
aes(x=planned_day_relative_to_boost,
y=MFI_normalised,
col=infancy_vac,
group=subject_id) +
geom_point() +
geom_line()
```


MFI_normalised
0
5
10
15
planned_day_relative_to_boost
0
25
50
75
100
125
infancy_vac
aP
wP