Class 19: Pertussis Mini Proj

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Background

Pertussis (aka Whooping cough) is a highly infectious lung infection caused by the bacteria *B. pertussis* .

The CDC tracks case numbers in the US and makes this data available online:

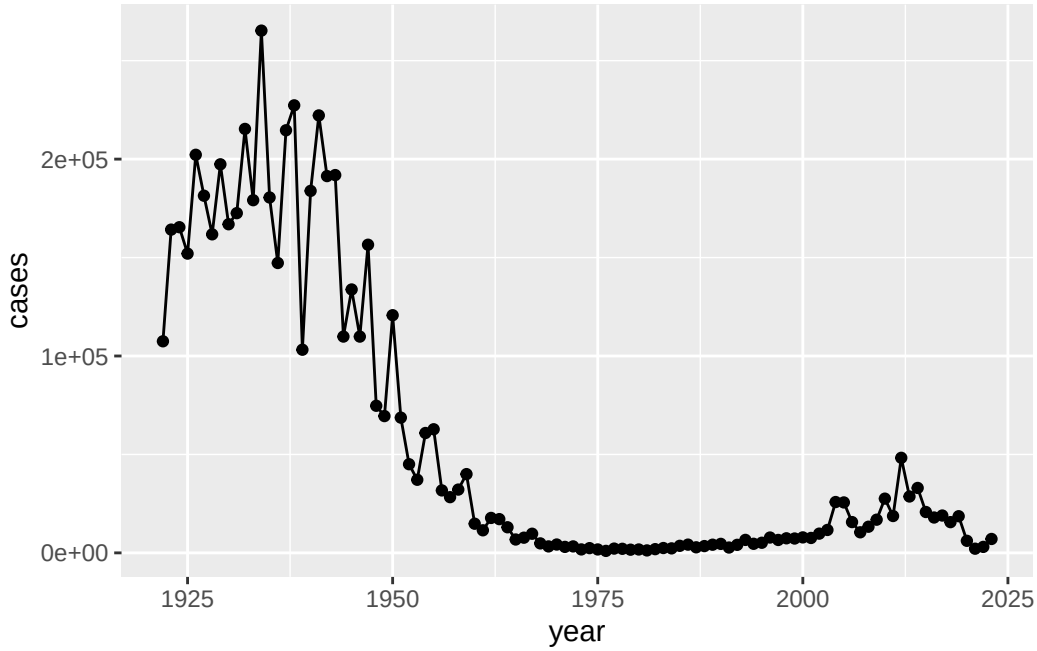
copied table from website initiate variable assign it to Addins>paste as data.frame –> pastes in the table in data.frame format highlight all and go to Code>reformat selection (cmd+shift+A)

Q1. Make a plot of pertussis cases per year with ggplot

```
library(ggplot2)
```

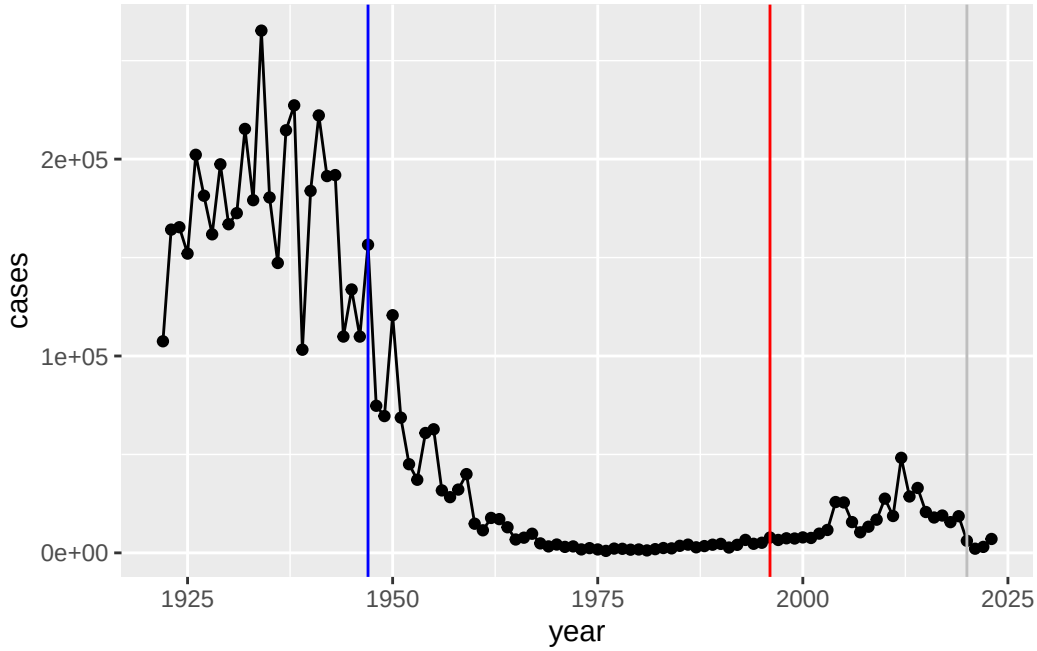
```
Warning: package 'ggplot2' was built under R version 4.5.2
```

```
ggplot(cdc) + aes(x=year, y=cases) + geom_point() + geom_line()
```



Q2. Add some annotation (lines on the plot) for some major milestones in our interaction with pertussis. The original wP deployment in 1947 and the newer aP vaccine roll-out in 1996. Finally a line for 2020

```
ggplot(cdc) + aes(x=year, y=cases) + geom_point() + geom_line() + geom_vline(xintercept = 194
```



This red line seems to precede a spike in cases. This is likely related to a few different factors, including anti-vaccine movements, slight changes in pertussis strain (and the vaccine needing to catch up), and most importantly how the aP vaccine was shown to require boosters for continued efficacy. aP is the cell-free vaccine, which was an improvement on the wP vaccine which used the whole bacterial cell to inoculate.

The CMI-PB Project

The CMI-Pertussis Boost (PB) porject focuses on gathering data on this same topic. What is distinct between aP and wP individuals. aP induced protection wanes faster than wP…Why?

CMI-PB makes their data available via a JSON format returning API. We can read JSON format with the `read_json()` function from the **jsonlite** package

```
# install.packages("jsonlite")
library(jsonlite)

subject <- read_json("http://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" are in this db?

```
nrow(subject)
```

```
[1] 172
```

Q4. How many wP and aP primed subjects are there in the dataset?

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

```
aP wP
87 85
```

Q5. What is the `biological sex` and `race` breakdown of these subjects? Ie, is this a representative population?

```
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
```

Not a representative sample :(

Let's read in more tables from the CMI-PB database API (go to website and get some more links)

```
specimen <- read_json("http://cmi-pb.org/api/v5_1/specimen", simplifyVector = TRUE)
ab_titer <- read_json("http://cmi-pb.org/api/v5_1/plasma_ab_titer", simplifyVector = TRUE)
```

A wee peak at 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
```

```
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
```

Join using the `inner_join()` function from **dplyr**

```
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
```

```
ab_data <- inner_join(meta, ab_titer)
```

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

```
head(ab_data)
```

```
  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           1
3    1986-01-01    2016-09-12 2020_dataset           1
4    1986-01-01    2016-09-12 2020_dataset           1
5    1986-01-01    2016-09-12 2020_dataset           1
6    1986-01-01    2016-09-12 2020_dataset           1
  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 isotype is_antigen_specific antigen        MFI MFI_normalised  unit
1     1     IgE              FALSE   Total 1110.21154       2.493425 UG/ML
2     1     IgE              FALSE   Total 2708.91616       2.493425 IU/ML
3     1     IgG               TRUE      PT   68.56614       3.736992 IU/ML
```

```
4     1     IgG                TRUE     PRN  332.12718       2.602350 IU/ML
5     1     IgG                TRUE     FHA 1887.12263      34.050956 IU/ML
6     1     IgE                TRUE     ACT    0.10000       1.000000 IU/ML
  lower_limit_of_detection
1                 2.096133
2                29.170000
3                 0.530000
4                 6.205949
5                 4.679535
6                 2.816431
```

Q6. How many different Ab isotypes are there?

```
unique(ab_data$isotype)
```

```
[1] "IgE"  "IgG"  "IgG1" "IgG2" "IgG3" "IgG4"
```

2 major isotypes (6 including IgG subtypes)

Q7. How many different antigens are there in the dataset?

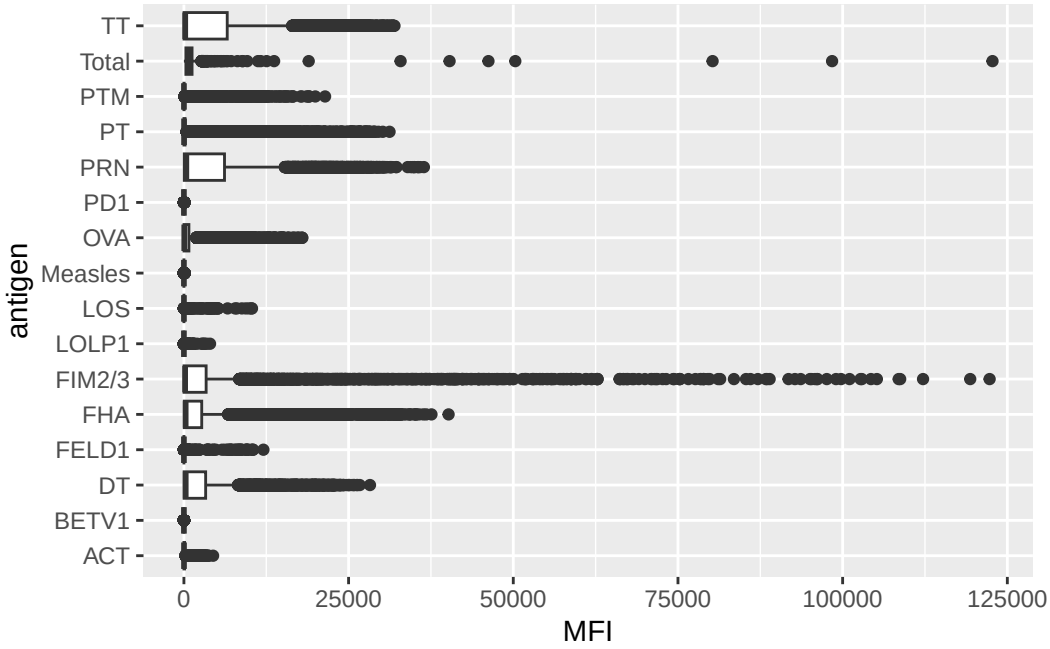
```
unique(ab_data$antigen)
```

```
 [1] "Total"   "PT"      "PRN"     "FHA"     "ACT"     "LOS"     "FELD1"
 [8] "BETV1"   "LOLP1"   "Measles" "PTM"     "FIM2/3"  "TT"      "DT"
[15] "OVA"     "PD1"
```

Q8. Let's plot MFI vs antigen

```
ggplot(ab_data) + aes(x=MFI, y=antigen) + geom_boxplot()
```

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



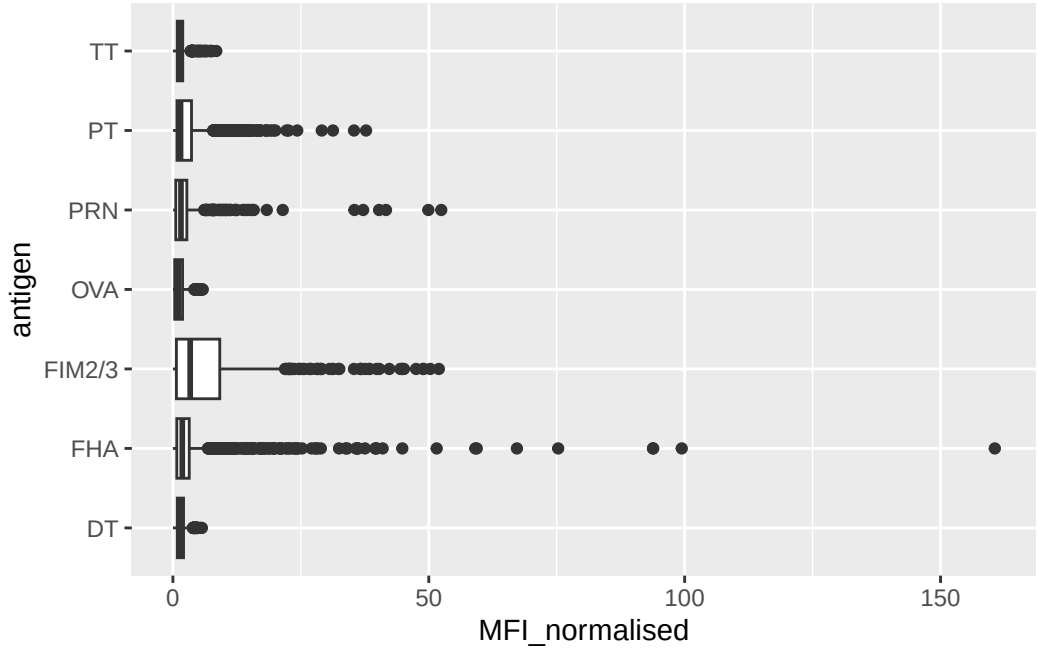
Focus in IgG

IgG is crucial for long-term immunity and responding to the bacterial and viral infections.

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

Plot of antigen levels again but for IgG only

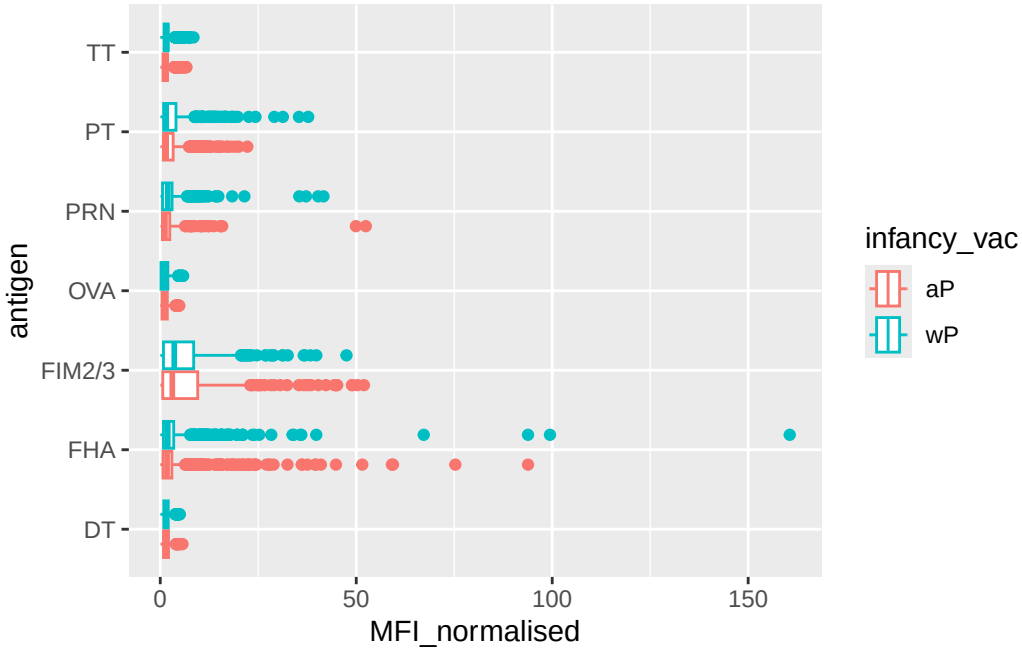
```
ggplot(igg) + aes(MFI_normalised, antigen) + geom_boxplot()
```



Differences between aP and wP?

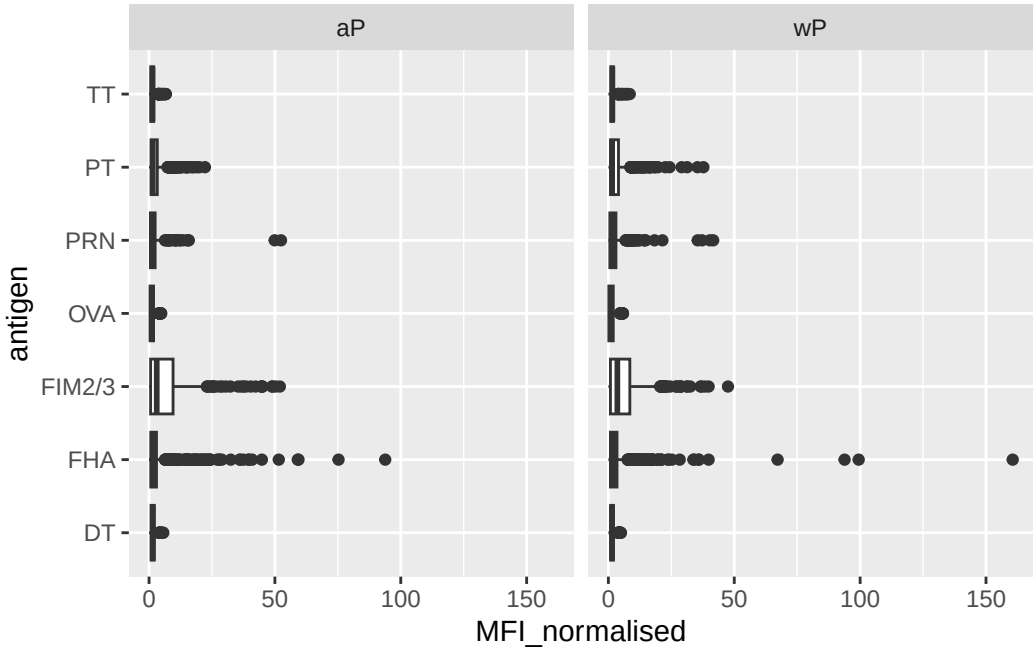
We can color up by the `infancy_vac` values of "wP" or "aP"

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



We could also "facet" by the "aP" vs "wP" column

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



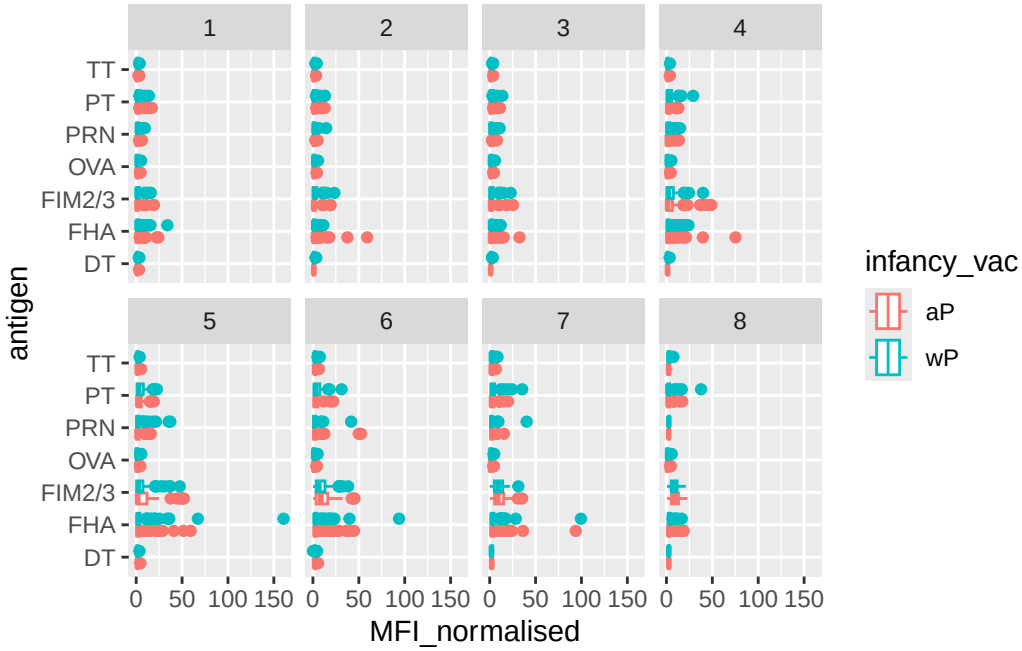
Time course analysis

We can use 'visit as a proxy for time and facet our plots by this value 1 to 8 ...

```
table(ab_data$visit) # it's an ongoing study so more recent visits are still collecting data
```

```
   1    2    3    4    5    6    7    8    9   10   11   12
8280 8280 8420 8420 8420 8100 7700 2670  770  686  105  105
```

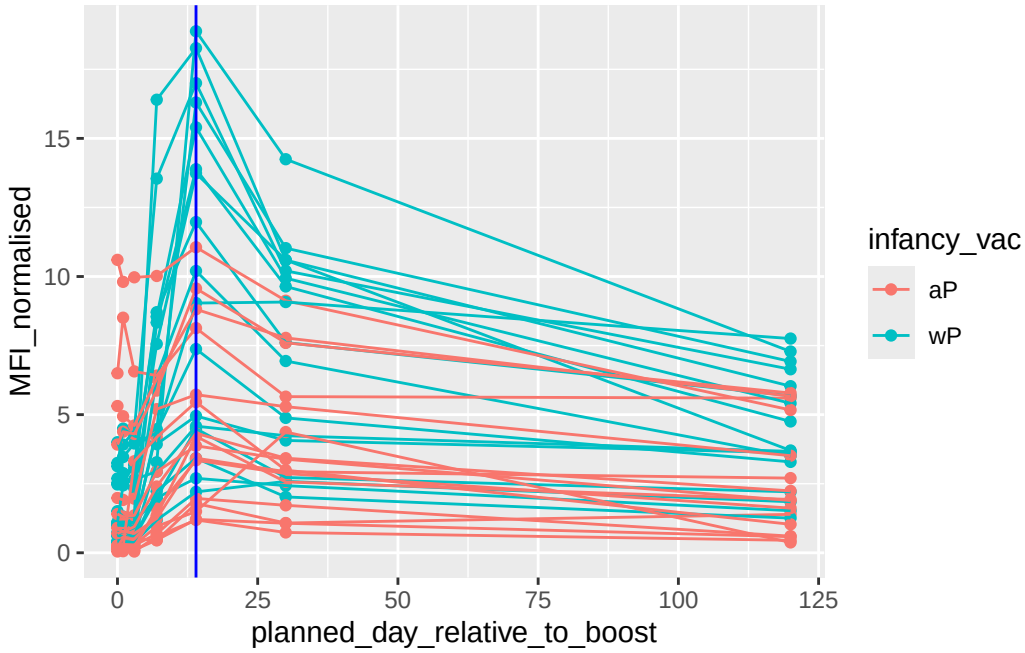
```
igg |>
  filter(visit %in% 1:8) |>
  ggplot() + aes(MFI_normalised, antigen, col=infancy_vac) + geom_boxplot() + facet_wrap(~vis
```



Time course of PT (Virulence Factor: Persussis Toxin)

```
pt <- igg |>
  filter(antigen == "PT") |>
  filter(dataset == "2021_dataset")
```

```
ggplot(pt) +
  aes(planned_day_relative_to_boost,
      MFI_normalised,
      col=infancy_vac,
      group=subject_id) +
  geom_point() +
  geom_line() +
  geom_vline(xintercept = 14, col="blue")
```



System setup

```
sessionInfo()
```

```
R version 4.5.1 (2025-06-13)
Platform: aarch64-apple-darwin20
Running under: macOS Sonoma 14.6.1

Matrix products: default
BLAS:   /Library/Frameworks/R.framework/Versions/4.5-arm64/Resources/lib/libRblas.0.dylib
LAPACK: /Library/Frameworks/R.framework/Versions/4.5-arm64/Resources/lib/libRlapack.dylib;
```

```
locale:
[1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8

time zone: America/Los_Angeles
tzcode source: internal

attached base packages:
[1] stats     graphics  grDevices utils     datasets  methods   base

other attached packages:
[1] dplyr_1.1.4    jsonlite_2.0.0 ggplot2_4.0.1

loaded via a namespace (and not attached):
 [1] vctrs_0.6.5        cli_3.6.5          knitr_1.50         rlang_1.1.6
 [5] xfun_0.54          generics_0.1.4     S7_0.2.1           labeling_0.4.3
 [9] glue_1.8.0         htmltools_0.5.8.1  scales_1.4.0       rmarkdown_2.30
[13] grid_4.5.1         evaluate_1.0.5     tibble_3.3.0       fastmap_1.2.0
[17] yaml_2.3.11        lifecycle_1.0.4    compiler_4.5.1     RColorBrewer_1.1-3
[21] pkgconfig_2.0.3    rstudioapi_0.17.1  farver_2.1.2       digest_0.6.39
[25] R6_2.6.1           tidyselect_1.2.1   pillar_1.11.1      magrittr_2.0.4
[29] withr_3.0.2        tools_4.5.1        gtable_0.3.6
```