nov_20

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Pertussis (more commonly known as whooping cough) is a highly contagious respiratory disease caused by the bacterium Bordetella pertussis

The United States Centers for Disease Control and Prevention (CDC) has been compiling reported pertussis case numbers since 1922 in their National Notifiable Diseases Surveillance System (NNDSS). We can view this data on the CDC website [here]:(https://www.cdc.gov/pertussis/php/surveillance/pertussis-cases-by-year.html?CDC_AAref_Val=https
reporting/cases-by-year.html)

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.

we need to scrape this data so we can do stuff with it in R. let's try the datapasta package

```
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
```

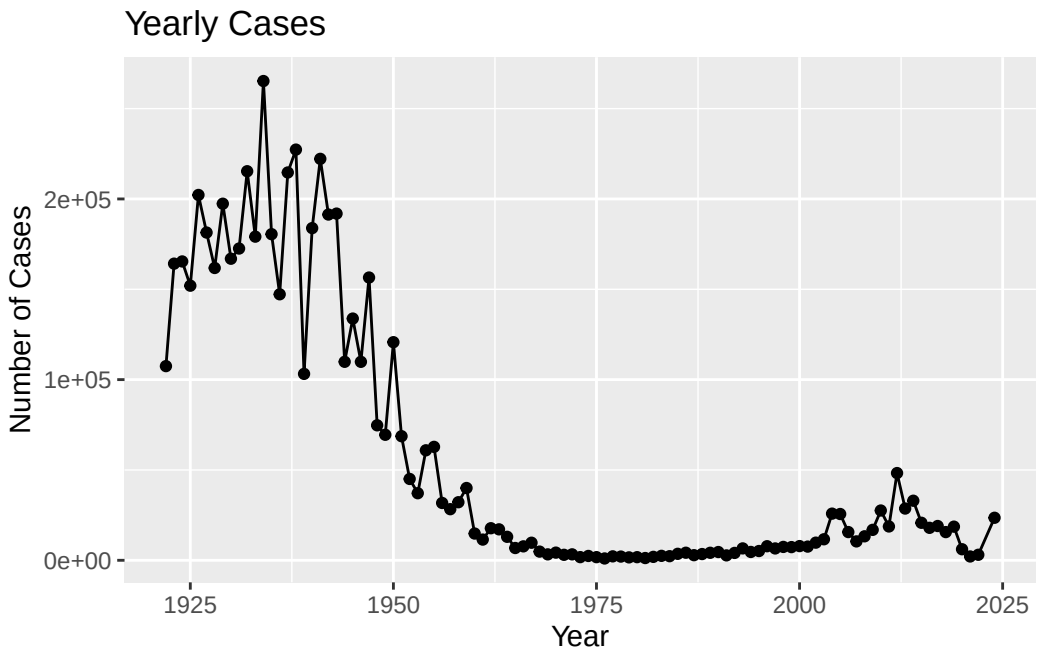
```
    year  cases
1   1922 107473
2   1923 164191
3   1924 165418
4   1925 152003
5   1926 202210
6   1927 181411
7   1928 161799
8   1929 197371
9   1930 166914
10  1931 172559
11  1932 215343
12  1933 179135
13  1934 265269
14  1935 180518
```

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

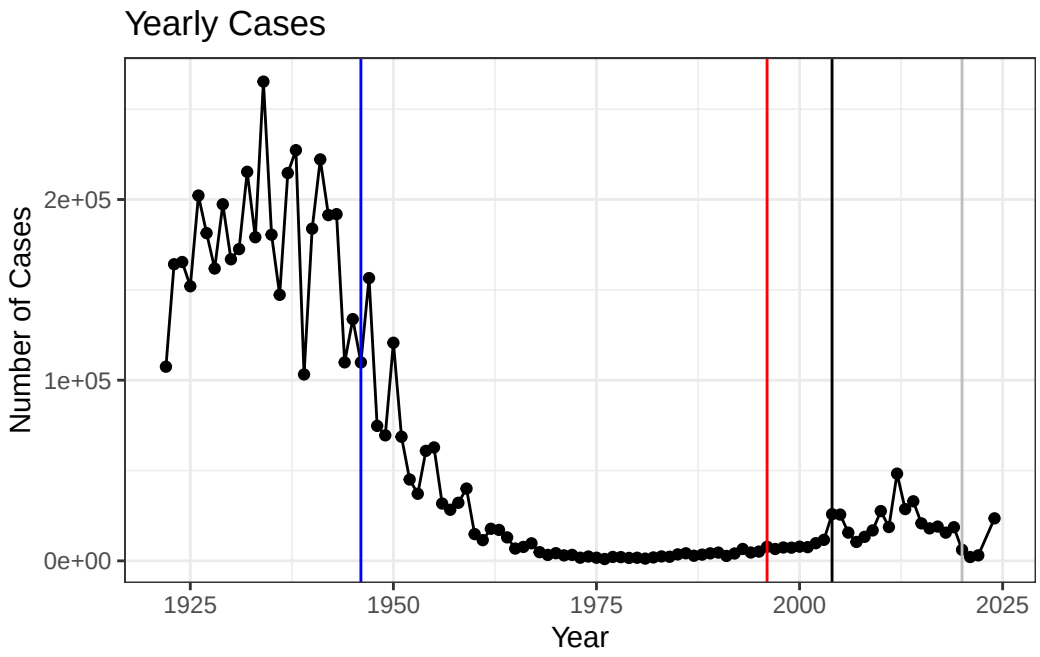
```
101 2022   3044
102 2024  23544
```

```
library(ggplot2)
baseplot <- ggplot(cdc) +
  aes(year, cases) +
  geom_point() +
  geom_line() +
  labs(title = "Yearly Cases", x = "Year", y = "Number of Cases")
baseplot
```



let's add the date of wP, and the switch to 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=2004,col="black")
```



##CMI-PB(computational models of immunity-Pertussis Boost)

this projects collects and makes freely available data about the immune response to pertussis vaccination

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

you cna use the jsonlite package and its read_json function

```
library(jsonlite)

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

kets 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
```

Q how many subjects do we have?

```
nrow(subject)
```

```
[1] 172
```

Q how many male/female do we have?

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

```
Female   Male
   112     60
```

how many wP and aP do we have?

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

```
aP wP
87 85
```

break down of biological sex and race?

```
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
```

does this break down reflect US population,no

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

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

```
library(jsonlite)

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

```
library(jsonlite)

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

```
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
```

and add one last join of ab_titer and meta

```
library(dplyr)

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
```

```
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
```

```
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
```

lets begin with IgG

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

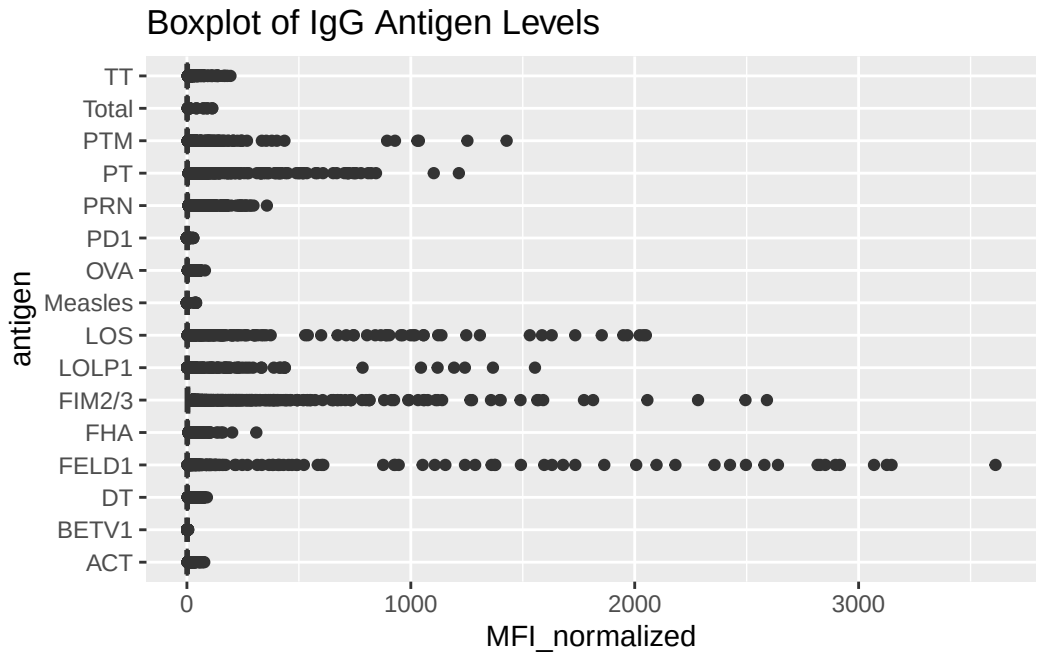
```
  specimen_id isotype is_antigen_specific antigen        MFI MFI_normalised
1           1     IgG                TRUE      PT   68.56614       3.736992
2           1     IgG                TRUE     PRN  332.12718       2.602350
3           1     IgG                TRUE     FHA 1887.12263      34.050956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

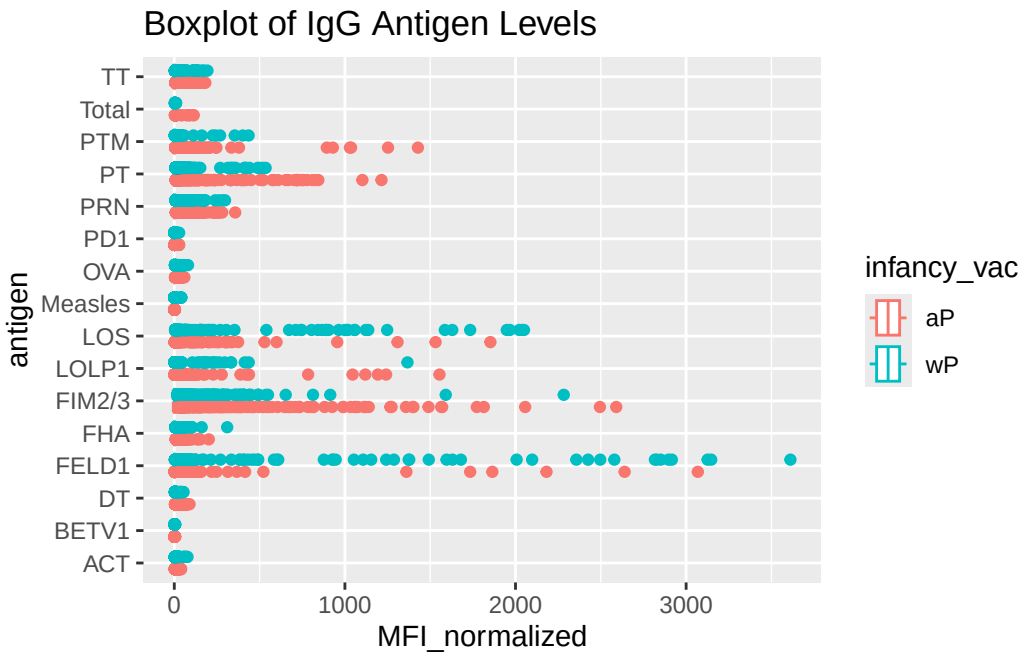
```
library(ggplot2)

ggplot(abdata) +
  aes(x = MFI_normalised, y = antigen) +
  geom_boxplot() +
  labs(
    title = "Boxplot of IgG Antigen Levels",
    x = "MFI_normalized",
    y = "antigen"
  )
```



```
library(ggplot2)

ggplot(abdata) +
  aes(x = MFI_normalised, y = antigen,col=infancy_vac) +
  geom_boxplot() +
  labs(
    title = "Boxplot of IgG Antigen Levels",
    x = "MFI_normalized",
    y = "antigen"
  )
```



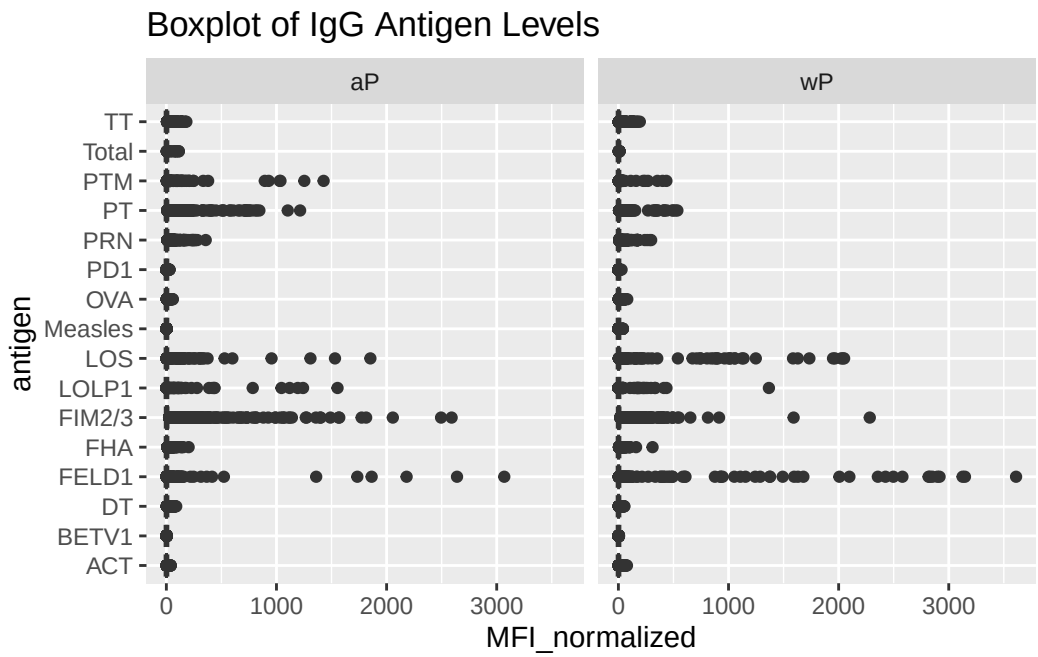
ideally I would like to see how these ab levels change over time relative to the booster shot

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

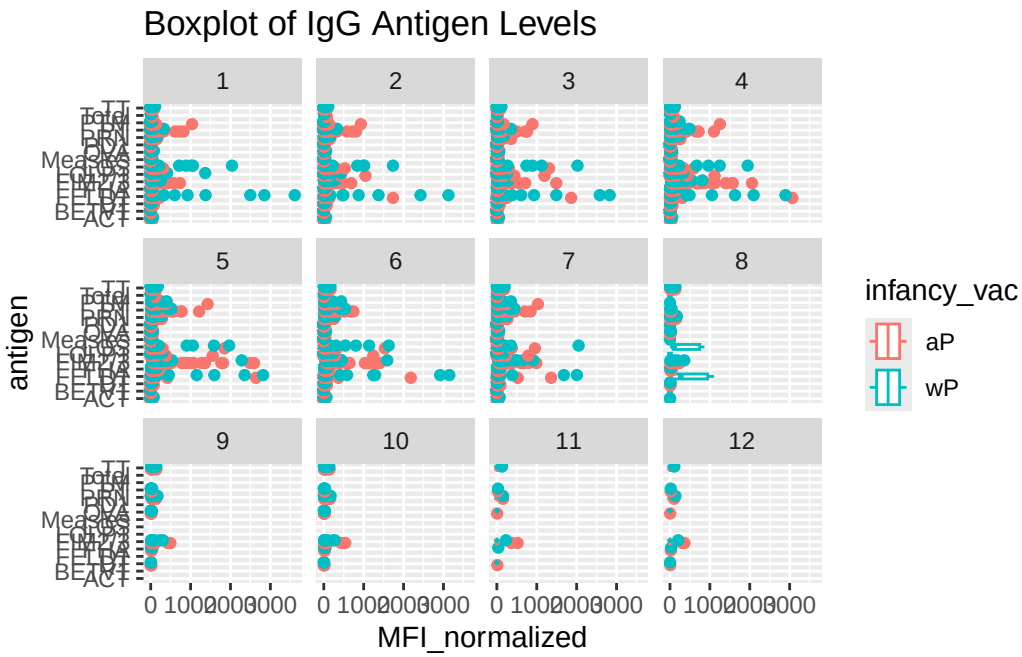
```
   1    2    3    4    5    6    7    8    9   10   11   12
8280 8280 8420 6565 6565 6210 5810  815  735  686  105  105
```

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

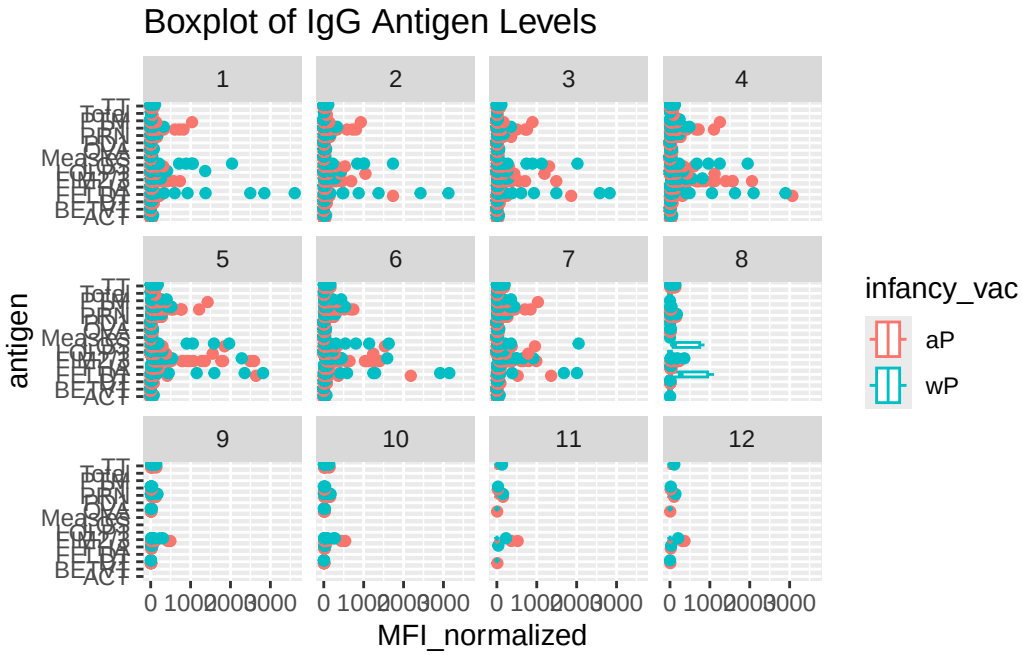
```
  labs(
    title = "Boxplot of IgG Antigen Levels",
    x = "MFI_normalized",
    y = "antigen"
  )+
  facet_wrap(~infancy_vac)
```



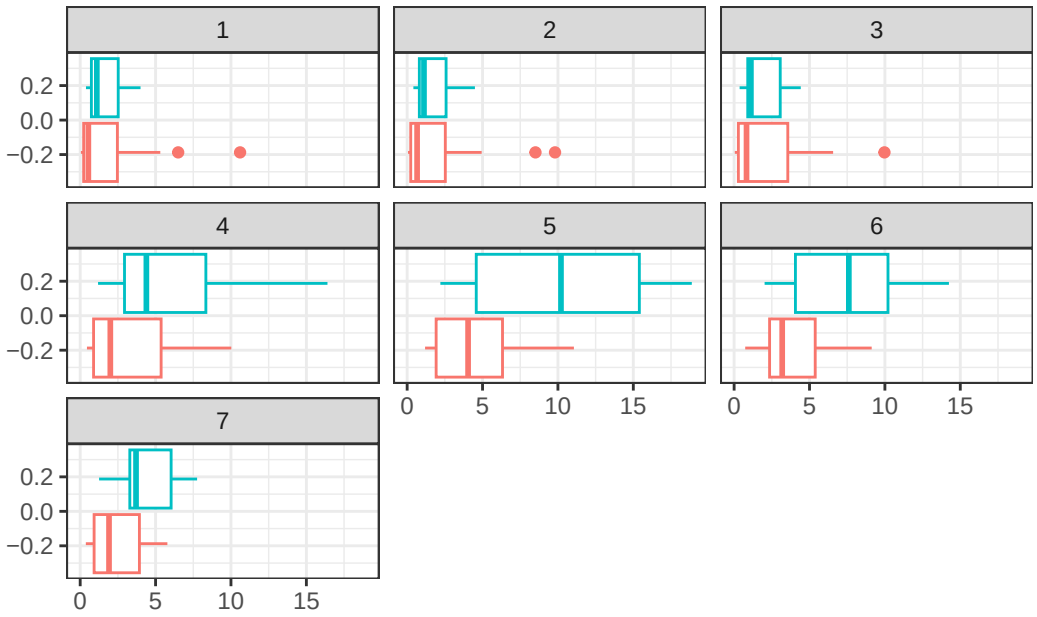

```
ggplot(abdata) +
  aes(x = MFI_normalised, y = antigen,col=infancy_vac) +
  geom_boxplot() +
  labs(
    title = "Boxplot of IgG Antigen Levels",
    x = "MFI_normalized",
    y = "antigen"
  )+
  facet_wrap(~visit)
```




```
ggplot(abdata) +
  aes(x = MFI_normalised, y = antigen,col=infancy_vac) +
  geom_boxplot() +
  labs(
    title = "Boxplot of IgG Antigen Levels",
    x = "MFI_normalized",
    y = "antigen"
  )+
  facet_wrap(~visit)
```




```
filter(igg, antigen=="PT",dataset=="2021_dataset") %>%
  ggplot() +
  aes(MFI_normalised, col=infancy_vac) +
  geom_boxplot(show.legend = FALSE) +
  facet_wrap(vars(visit)) +
  theme_bw()
```




```
abdata.21 <- abdata %>% filter(dataset == "2021_dataset")

library(dplyr)
library(ggplot2)

average_data <- abdata.21 %>%
  filter(isotype == "IgG", antigen == "PT") %>%
  group_by(infancy_vac, planned_day_relative_to_boost) %>%
  summarise(avg_MFI_normalised = mean(MFI_normalised, na.rm = TRUE), .groups = "drop")

abdata.21 %>%
  filter(isotype == "IgG", antigen == "PT") %>%
  ggplot(aes(x = planned_day_relative_to_boost, y = MFI_normalised, col = infancy_vac, group
  geom_point() +
  geom_line() +
  # Average curves
  geom_line(
    data = average_data,
    aes(x = planned_day_relative_to_boost, y = avg_MFI_normalised, col = infancy_vac),
    size = 1.5, inherit.aes = FALSE
  ) +
  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)",
    x = "Planned Day Relative to Boost",
    y = "MFI Normalised"
  ) +
  theme_minimal()
```

```
Warning: Using `size` aesthetic for lines was deprecated in ggplot2 3.4.0.
i Please use `linewidth` instead.
```