

class15

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Pertussis, aka Whooping Cough, is a highly contagious lung infection 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.

In the console, type `#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)
)

```

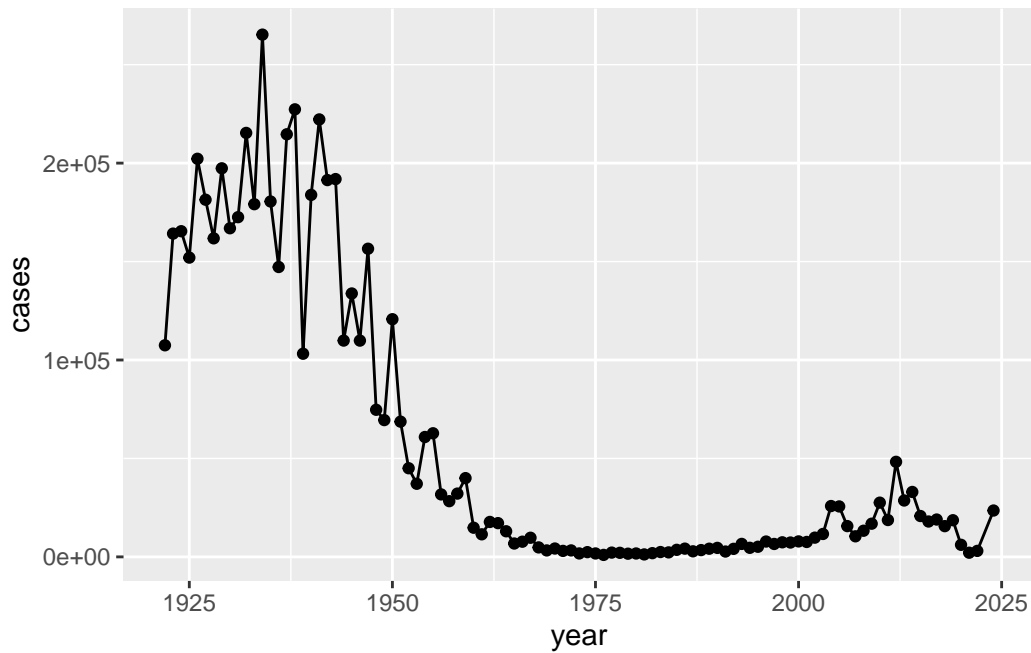
```

library(ggplot2)

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

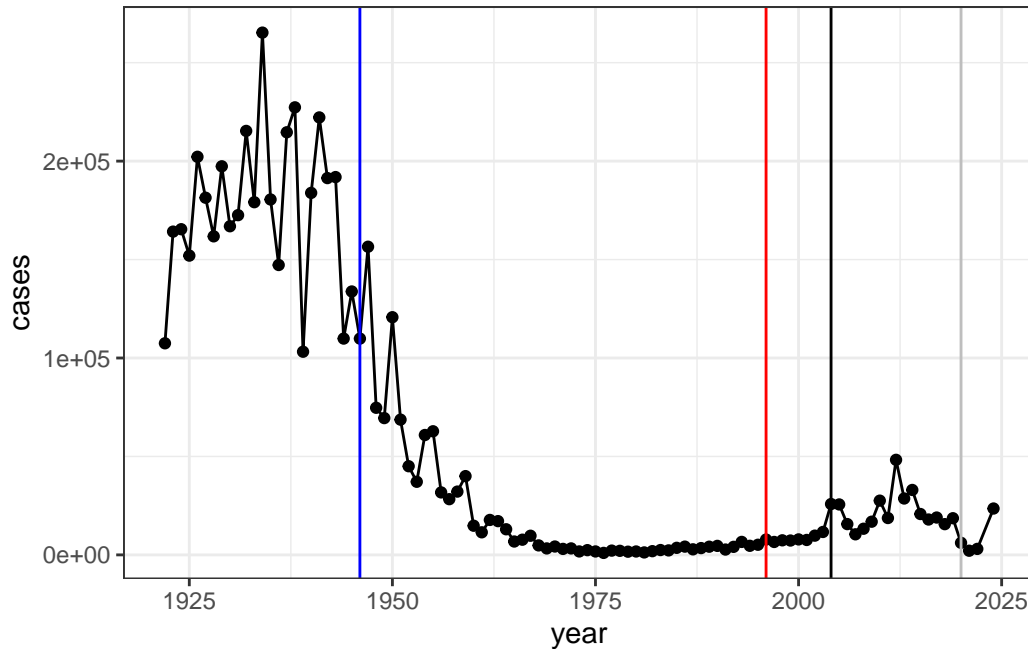
baseplot

```



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

```
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 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:value pairs).

We can use the **jsonlite** package and its `read_json()` function.

Install **jsonlite** using `install.packages()`.

```
library(jsonlite)
```

Warning: package 'jsonlite' was built under R version 4.4.2

```
subject <- read_json("http://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 do we have?

```
nrow(subject)
```

```
[1] 172
```

We have 172 subjects.

Q. How many male/female?

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

Female	Male
112	60

There are 112 females and 60 males.

Q. How many wP and aP do we have?

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

aP	wP
87	85

We have 87 aP and 85 wP.

Q. Break down 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 break down 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=TRUE)
```

```
ab_titer <- read_json("http://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 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

```
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				

```
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

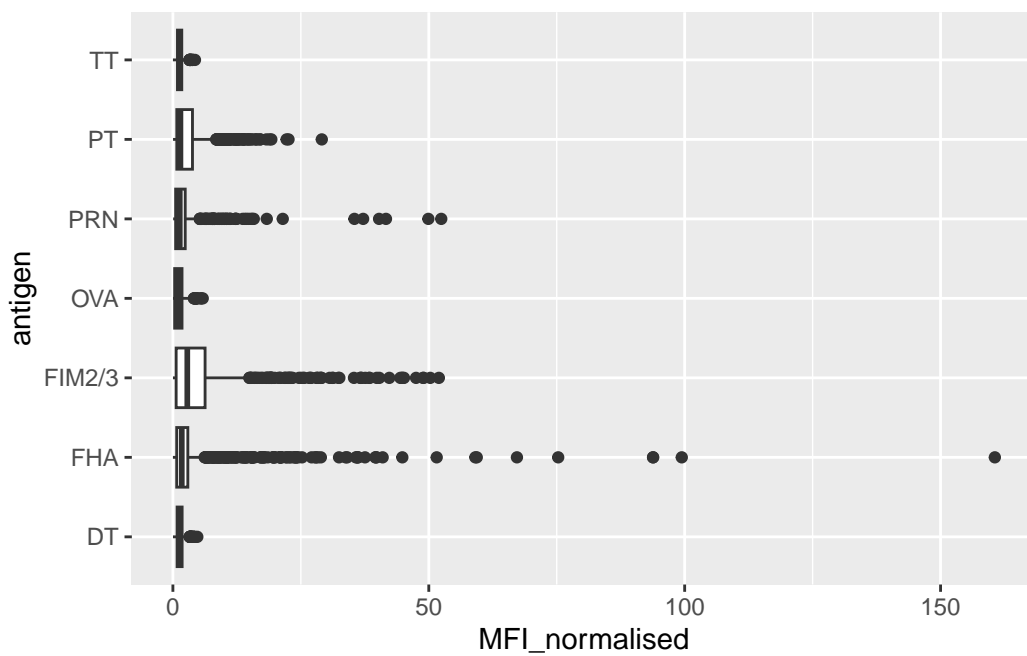
	actual_day_relative_to_boost	planned_day_relative_to_boost	specimen_type
1	-3	0	Blood
2	-3	0	Blood
3	-3	0	Blood
4	-3	0	Blood
5	-3	0	Blood
6	-3	0	Blood

	visit
1	1

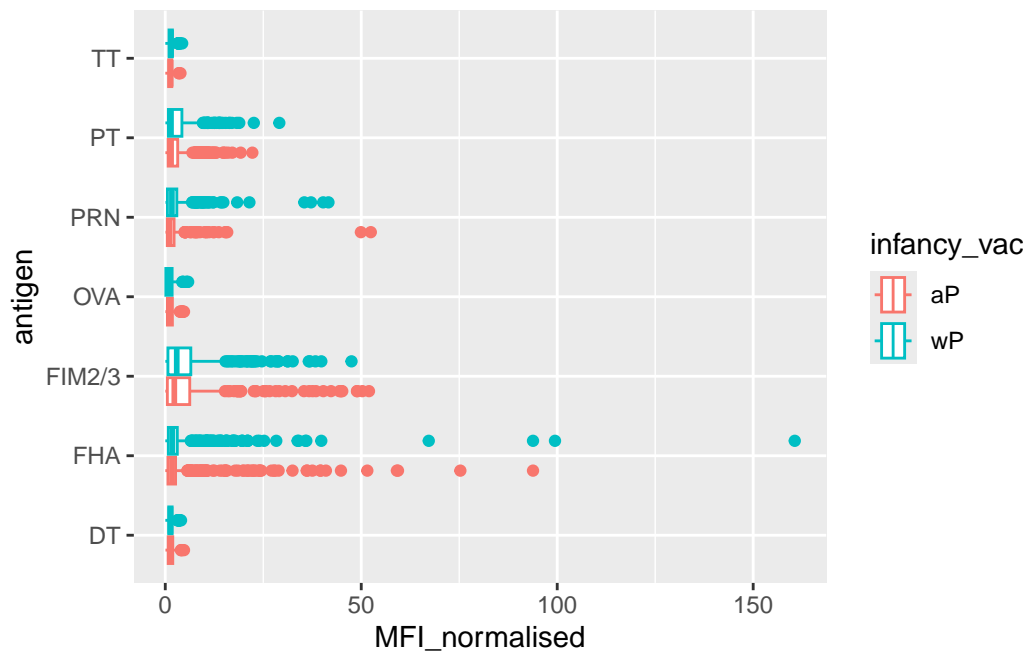
2	1
3	1
4	1
5	1
6	1

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

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



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

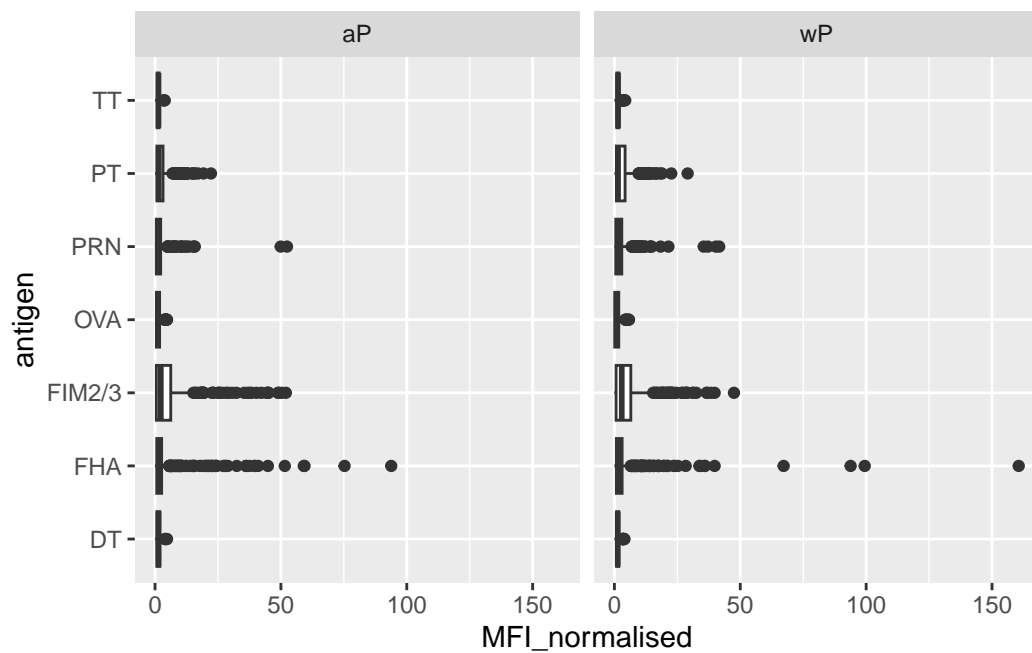


Ideally, I would like to see how these Ab levels change over time relative to the booster shot.

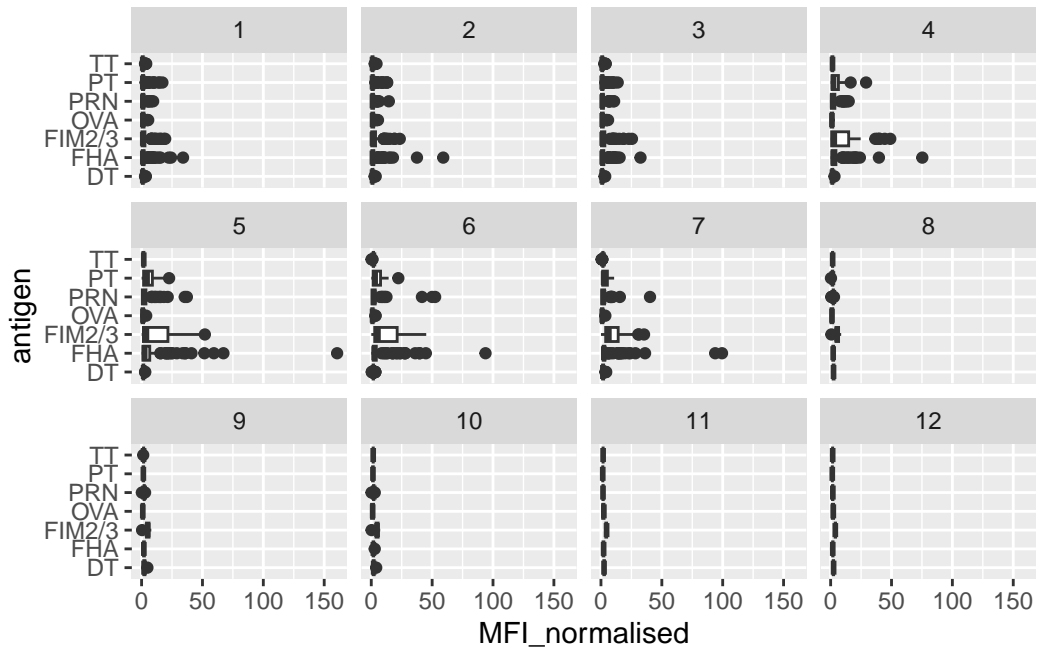
```
table(abdata$visit)
```

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

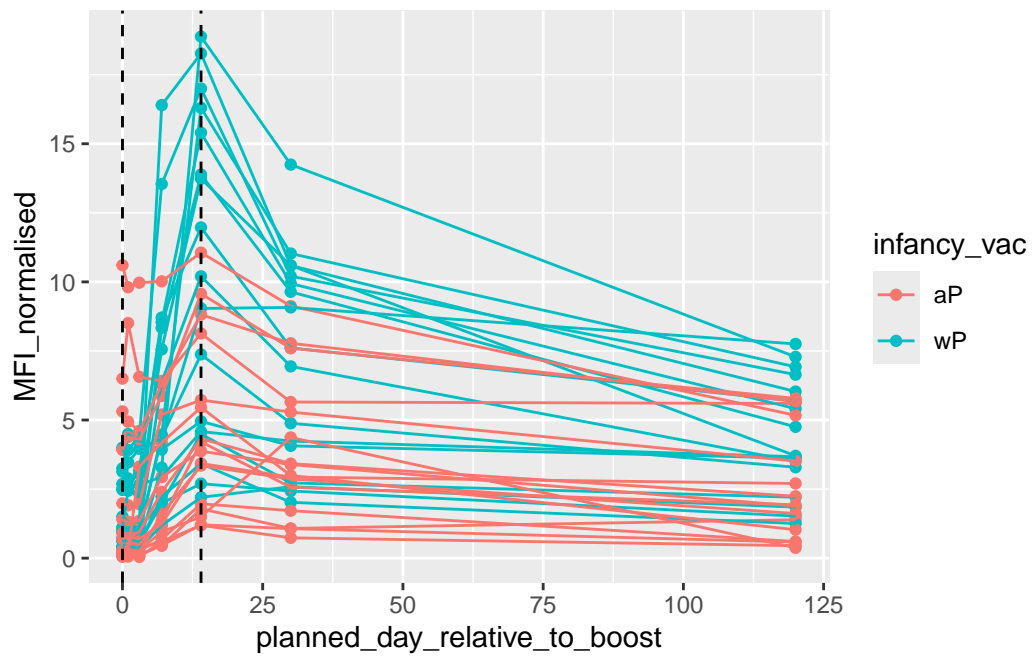


```
ggplot(igg) +
  aes(MFI_normalised, antigen) +
  geom_boxplot() +
  facet_wrap(~visit)
```



```
pt_2021 <- filter(igg, dataset=="2021_dataset")
data_2021 <- filter(pt_2021, antigen=="PT")
```

```
ggplot(data_2021) +
  aes(planned_day_relative_to_boost, MFI_normalised, col=infancy_vac, group=subject_id) +
  geom_point() +
  geom_line() +
  geom_vline(xintercept=0, linetype="dashed") +
  geom_vline(xintercept=14, linetype="dashed")
```



```
table(igg$dataset)
```

2020_dataset	2021_dataset	2022_dataset	2023_dataset
1182	1617	1456	1134