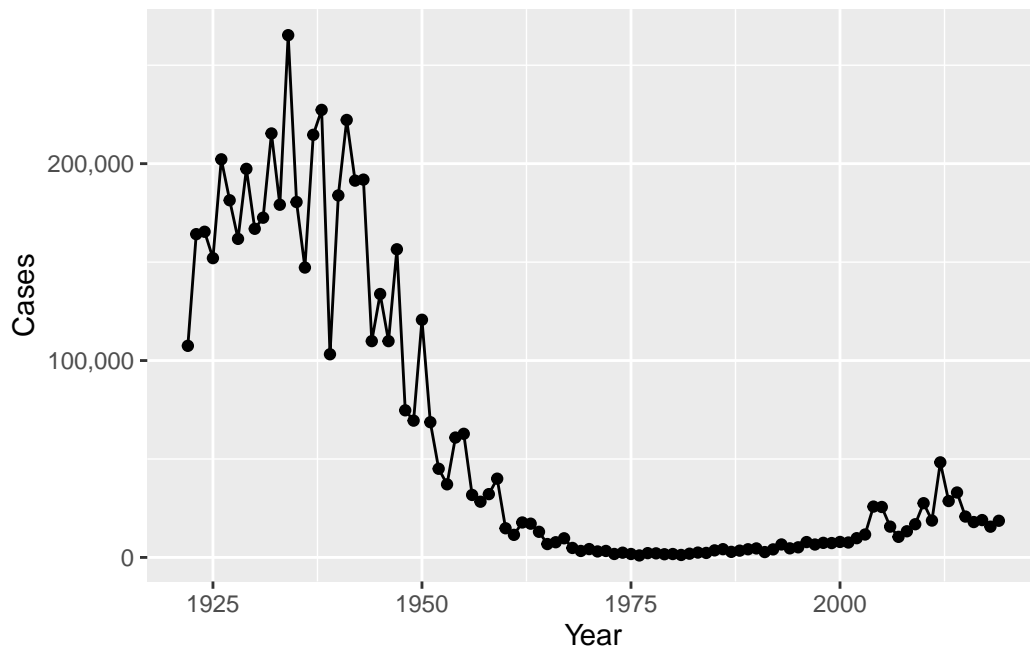
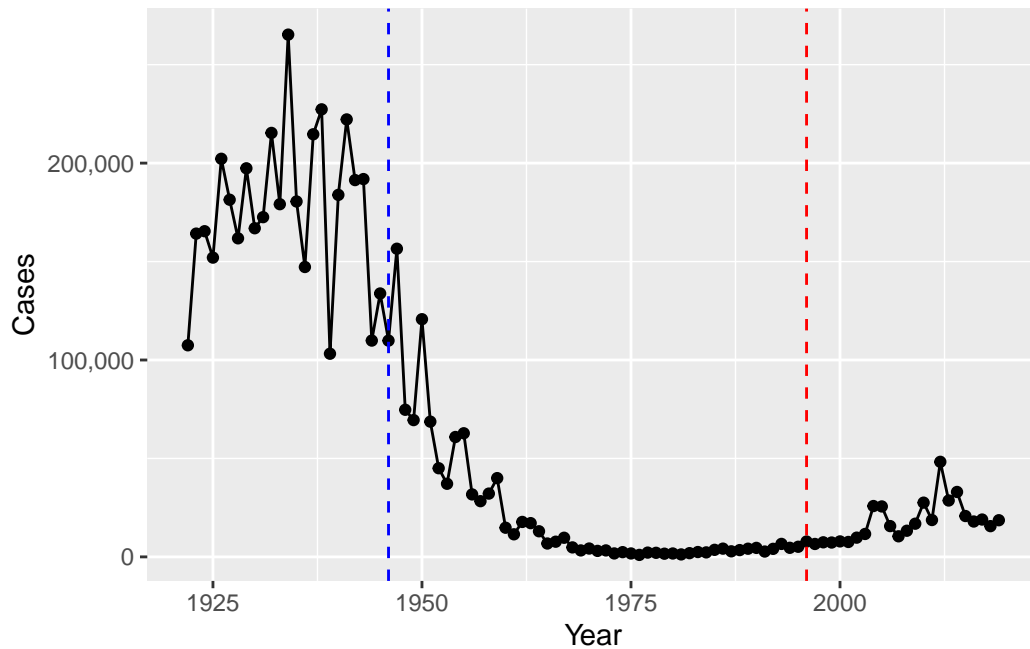


lab18

```
library(ggplot2)
base <- ggplot(cdc) +
  aes(Year,Cases) +
  geom_point() +
  geom_line() +
  scale_y_continuous(labels = scales::label_comma())
base
```



```
base + geom_vline(xintercept=1946, col="blue", linetype=2) +
  geom_vline(xintercept=1996, col="red", linetype=2)
```



```
library(jsonlite)
subject <- read_json("http://cmi-pb.org/api/subject",simplifyVector = T)
```

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

	Female	Male
American Indian/Alaska Native	0	1
Asian	18	9
Black or African American	2	0
More Than One Race	8	2
Native Hawaiian or Other Pacific Islander	1	1
Unknown or Not Reported	10	4
White	27	13

```
specimen <- read_json("http://cmi-pb.org/api/specimen",simplifyVector = T)
dim(specimen)
```

```
[1] 729 6
```

```
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(specimen,subject)
```

Joining with `by = join_by(subject_id)`

```
dim(subject)
```

```
[1] 96  8
```

```
dim(meta)
```

```
[1] 729 13
```

```
titer <- read_json("http://cmi-pb.org/api/ab_titer",simplifyVector = T)
table(titer$isotype)
```

```
 IgE  IgG IgG1 IgG2 IgG3 IgG4
6698 1413 6141 6141 6141 6141
```

```
abmeta <- inner_join(titer,meta)
```

Joining with `by = join_by(specimen_id)`

```
head(abmeta)
```

	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	actual_day_relative_to_boost
1	UG/ML	2.096133	1	-3
2	IU/ML	29.170000	1	-3
3	IU/ML	0.530000	1	-3
4	IU/ML	6.205949	1	-3
5	IU/ML	4.679535	1	-3
6	IU/ML	2.816431	1	-3

	planned_day_relative_to_boost	specimen_type	visit	infancy_vac	biological_sex
1	0	Blood	1	wP	Female
2	0	Blood	1	wP	Female
3	0	Blood	1	wP	Female
4	0	Blood	1	wP	Female
5	0	Blood	1	wP	Female
6	0	Blood	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

```
table(abmeta$visit)
```

```

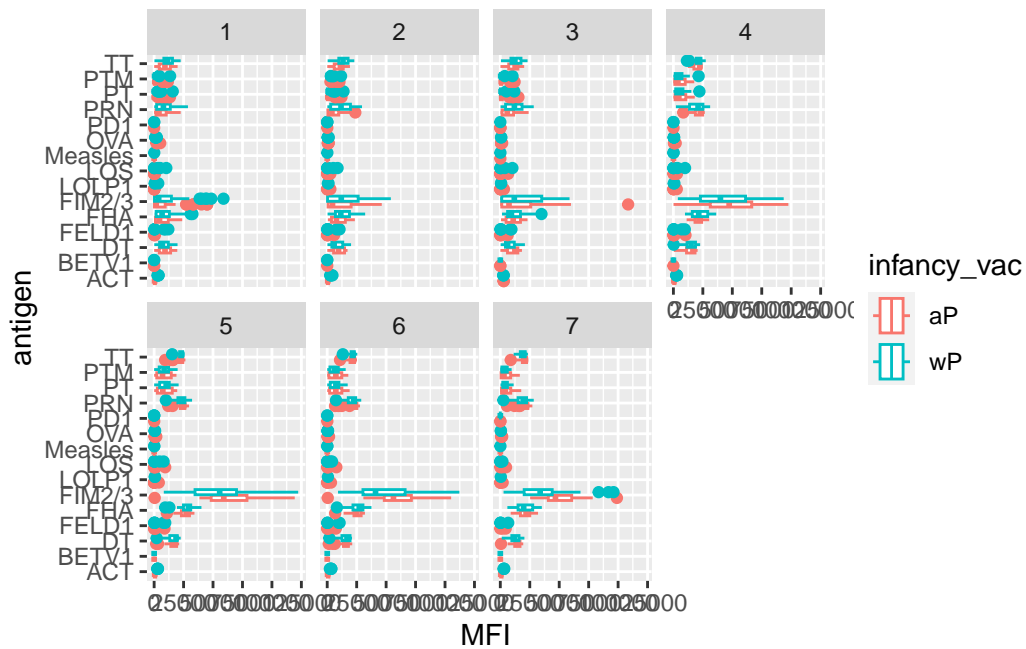
  1    2    3    4    5    6    7    8
5795 4640 4640 4640 4640 4320 3920  80

```

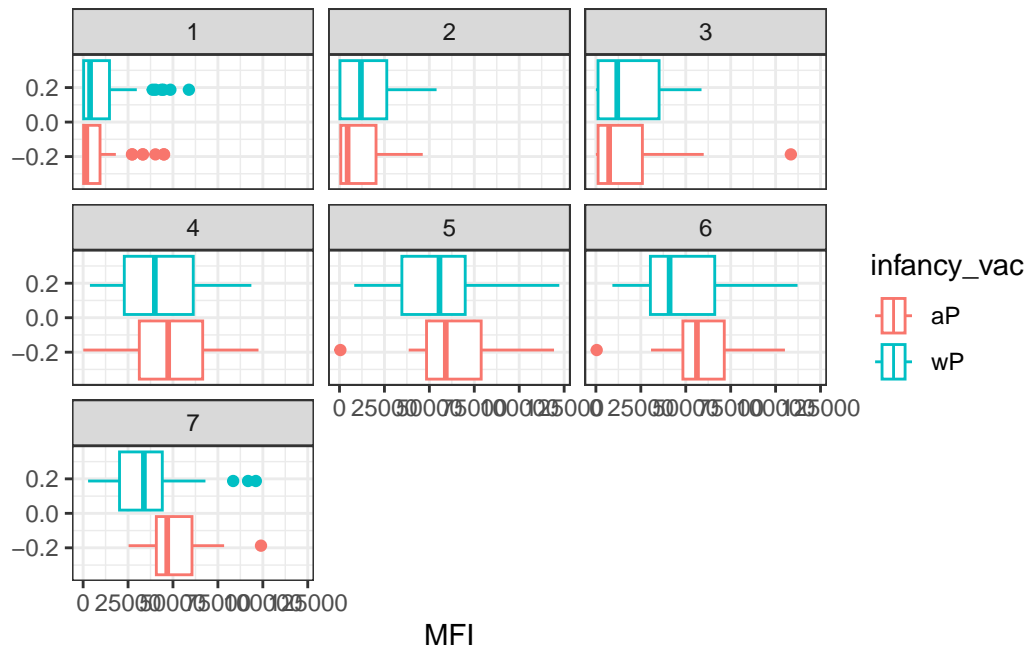
```
ig1 <- filter(abmeta, isotype == "IgG1", visit!=8)
table(ig1$antigen)
```

ACT	BETV1	DT	FELD1	FHA	FIM2/3	LOLP1	LOS	Measles	OVA
393	393	426	393	426	426	393	393	393	426
PD1	PRN	PT	PTM	TT					
393	426	426	393	426					

```
ggplot(ig1) +
  aes(MFI, antigen, col=infancy_vac) +
  geom_boxplot() +
  facet_wrap(vars(visit), nrow=2)
```



```
ggplot(filter(ig1, antigen=="FIM2/3")) +
  aes(MFI, col=infancy_vac) +
  geom_boxplot() +
  facet_wrap(vars(visit)) +
  theme_bw()
```



```
url <- "https://www.cmi-pb.org/api/v2/rnaseq?versioned_ensembl_gene_id=eq.ENSOG00000211896."
rna <- read_json(url, simplifyVector = TRUE)

ssrna <- inner_join(rna, meta)
```

Joining with `by = join_by(specimen_id)`

```
ggplot(ssrna) +
  aes(visit, tpm, group=subject_id) +
  geom_point() +
  geom_line(alpha=0.2)
```

