

VAERS analysis of COVID-19 vaccines

```
library(readr)
library(magrittr)
library(tidyverse)

## -- Attaching packages ----- tidyverse 1.3.1 --

## v ggplot2 3.3.3    v dplyr 1.0.6
## v tibble 3.1.2     v stringr 1.4.0
## v tidyr 1.1.3      v forcats 0.5.1
## v purrr 0.3.4

## -- Conflicts ----- tidyverse_conflicts() --
## x tidyr::extract() masks magrittr::extract()
## x dplyr::filter()  masks stats::filter()
## x dplyr::lag()      masks stats::lag()
## x purrr::set_names() masks magrittr::set_names()

library(reshape2)

##
## Attaching package: 'reshape2'

## The following object is masked from 'package:tidyr':
##
## smiths

library(ggplot2)
library(openEBGM)

X2021VAERSDATA <- read_csv("../data/2021VAERSDATA.csv",
  col_types = cols(RECVDATE = col_date(format = "%m/%d/%Y"),
    AGE_YRS = col_skip(), CAGE_MO = col_skip(),
    RPT_DATE = col_skip(), SYMPTOM_TEXT = col_skip(),
    DIED = col_skip(), DATEDIED = col_skip(),
    L_THREAT = col_skip(), ER_VISIT = col_skip(),
    HOSPITAL = col_skip(), HOSPDAYS = col_skip(),
    X_STAY = col_skip(), DISABLE = col_skip(),
    RECOVD = col_skip(), VAX_DATE = col_date(format = "%m/%d/%Y"),
    ONSET_DATE = col_skip(), NUMDAYS = col_skip(),
    LAB_DATA = col_skip(), V_ADMINBY = col_skip(),
    V_FUNDBY = col_skip(), OTHER_MEDS = col_skip(),
    CUR_ILL = col_skip(), HISTORY = col_skip(),
    PRIOR_VAX = col_skip(), SPLTTYPE = col_skip(),
    FORM_VERS = col_skip(), TODAYS_DATE = col_skip(),
    BIRTH_DEFECT = col_skip(), OFC_VISIT = col_skip(),
    ER_ED_VISIT = col_skip(), ALLERGIES = col_skip()))

X2021VAERSSYMPTOMS <- read_csv("../data/2021VAERSSYMPTOMS.csv",
  col_types = cols(SYMPTOMVERSION1 = col_skip(),
```

```

SYMPTOMVERSION2 = col_skip(), SYMPTOMVERSION3 = col_skip(),
SYMPTOMVERSION4 = col_skip(), SYMPTOMVERSION5 = col_skip()))

X2021VAERSVAX <- read_csv("../data/2021VAERSVAX.csv",
  col_types = cols(VAX_LOT = col_skip()))

df <- merge(X2021VAERSDATA, X2021VAERSVAX) %>%
  merge(X2021VAERSSYMPTOMS) %>%
  reshape2::melt(measure.vars=c("SYMPTOM1", "SYMPTOM2", "SYMPTOM3", "SYMPTOM4", "SYMPTOM5")) %>%
  select(-variable)

head(df)

##   VAERS_ID  RECVDATE STATE CAGE_YR SEX  VAX_DATE VAX_TYPE      VAX_MANU
## 1  0916600 2021-01-01   TX     33  F 2020-12-28  COVID19      MODERNA
## 2  0916601 2021-01-01   CA     73  F 2020-12-31  COVID19      MODERNA
## 3  0916602 2021-01-01   WA     23  F 2020-12-31  COVID19 PFIZER\\BIONTECH
## 4  0916603 2021-01-01   WA     58  F 2020-12-23  COVID19      MODERNA
## 5  0916604 2021-01-01   TX     47  F 2020-12-22  COVID19      MODERNA
## 6  0916605 2021-01-01   TX     40  M 2020-09-25   FLUC4    SEQIRUS, INC.
##   VAX_DOSE_SERIES VAX_ROUTE VAX_SITE
## 1                1         IM      LA
## 2                1         IM      RA
## 3                1         IM      LA
## 4                UNK      <NA>    <NA>
## 5                1         IM      LA
## 6                1         SYR      LA
##
##               VAX_NAME                value
## 1             COVID19 (COVID19 (MODERNA))      Dysphagia
## 2             COVID19 (COVID19 (MODERNA))      Anxiety
## 3             COVID19 (COVID19 (PFIZER-BIONTECH)) Chest discomfort
## 4             COVID19 (COVID19 (MODERNA))      Dizziness
## 5             COVID19 (COVID19 (MODERNA)) Injection site erythema
## 6 INFLUENZA (SEASONAL) (FLUCELVAX QUADRIVALENT)      Chills

```

Age stratification

```

df$strat_age <- ifelse(is.na(df$CAGE_YR), "unknown",
  ifelse(df$CAGE_YR < 25, "under_25",
    ifelse(df$CAGE_YR < 45, "25-44",
      ifelse(df$CAGE_YR < 65, "45-64", "65_plus"))))

```

Analysis for type of vax

```

processed <- df %>% select(c("VAERS_ID", "VAX_TYPE", "value", "SEX", "strat_age")) %>% set_colnames(c("
## stratification variables used: strat_gender, strat_age
## there were 15 strata: F-25-44, F-45-64, F-65_plus, F-under_25, F-unknown, M-25-44, M-45-64, M-65_plus

```

```
squashed <- processed %>% squashData()
theta_init <- c(alpha1 = 0.2, beta1 = 0.1, alpha2 = 2, beta2 = 4, p = 1/3)
theta_hat <- stats::nlm(negLLsquash, p = theta_init,
  ni = squashed$N, ei = squashed$E, wi = squashed$weight, N_star = 1)$estimate

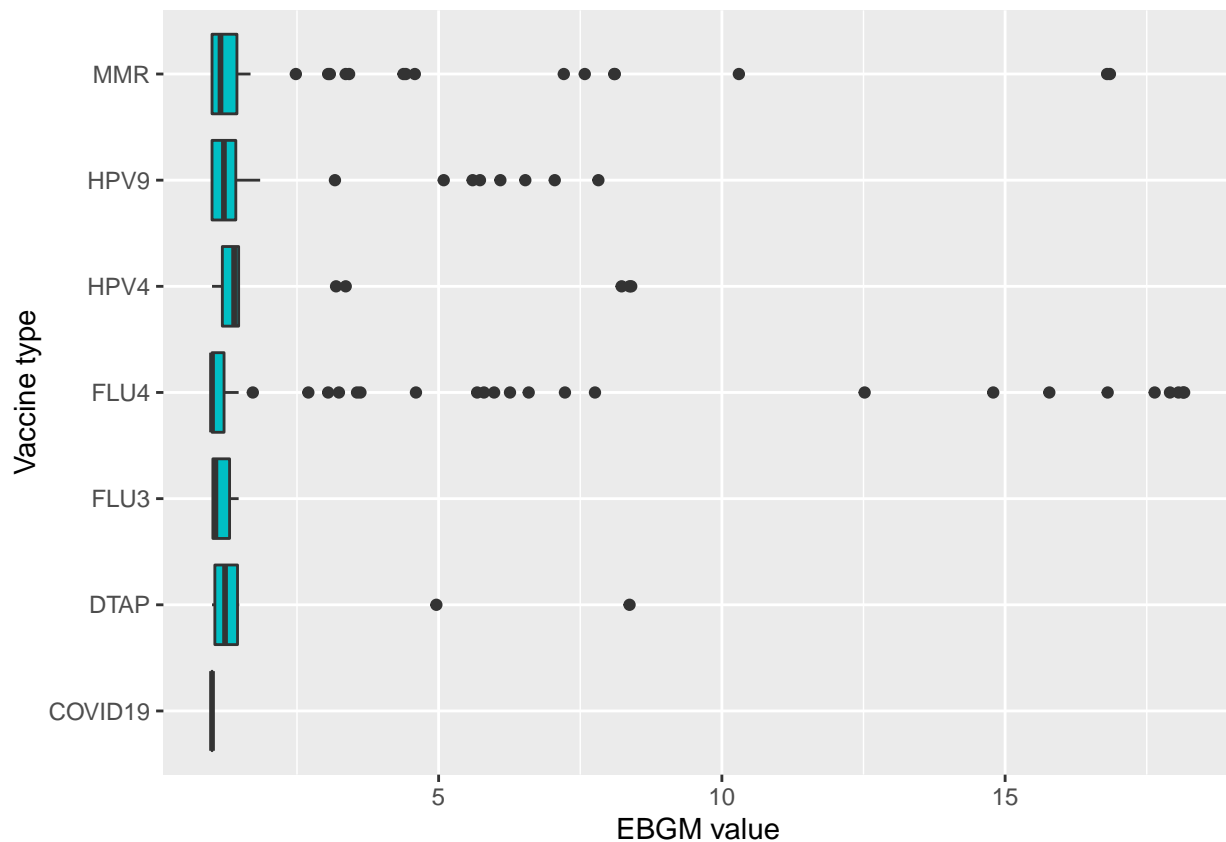
qn <- Qn(theta_hat, N = processed$N, E = processed$E)

processed$ebgm <- ebgm(theta_hat, N = processed$N, E = processed$E, qn = qn)

processed$QUANT_05 <- quantBisect(5, theta_hat = theta_hat,
  N = processed$N, E = processed$E, qn = qn)
processed$QUANT_95 <- quantBisect(95, theta_hat = theta_hat,
  N = processed$N, E = processed$E, qn = qn)
```

Results by vaccine type

```
processed %>% mutate(type=ifelse(var1=="COVID19", "Highlighted", "Normal")) %>%
  dplyr::filter(var1 %in% c("COVID19", "DTAP", "FLU4", "FLU3", "MMR", "HPV4", "HPV9")) %>%
  ggplot() +
  geom_boxplot(aes(ebgm, var1, fill=type)) +
  xlab("EBGM value") +
  ylab("Vaccine type") +
  theme(legend.position = "none")
```



```
## Saving 6.5 x 4.5 in image
```

```
processed <- df %>% select(c("VAERS_ID", "VAX_NAME", "value", "SEX", "strat_age")) %>% set_colnames(c("VAERS_ID", "VAX_NAME", "value", "SEX", "strat_age"))
```

```
## there were 15 strata:  F-25-44, F-45-64, F-65_plus, F-under_25, F-unknown, M-25-44, M-45-64, M-65_pl
```

```
squashed <- processed %>% squashData()
```

```
theta_init <- c(alpha1 = 0.2, beta1 = 0.1, alpha2 = 2, beta2 = 4, p = 1/3)
```

```
qn <- Qn(theta_hat, N = processed$N, E = processed$E)
```

[illegible]

```
processed$QUANT_95 <- quantBisect(95, theta_hat = theta_hat,  
                                  N = processed$N, E = processed$E, qn = qn)
```

```
processed %>%
```

```
dplyr::filter(var1 %in% c(c("COVID19 (COVID19 (JANSSEN))", "COVID19 (COVID19 (MODERNA))", "COVID19 (COVID19 (PFIZER))"))
```

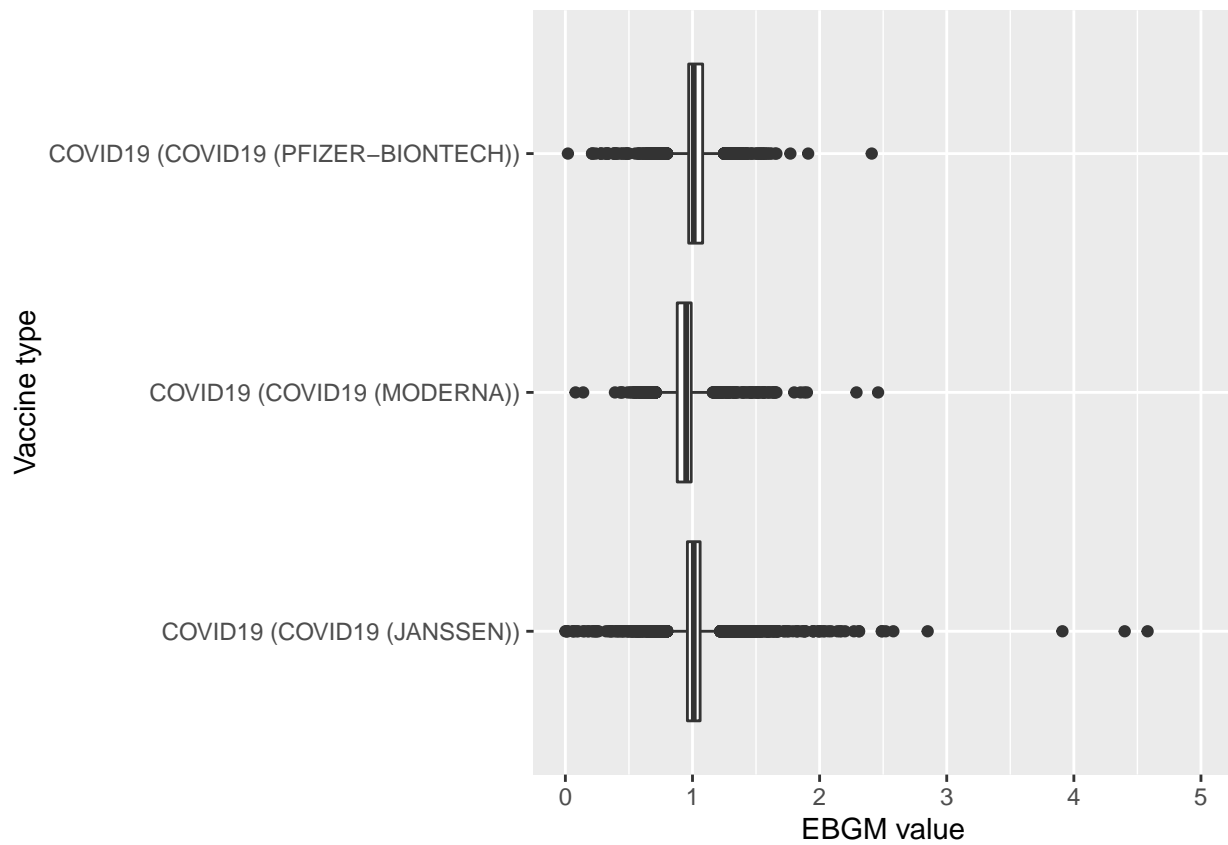
```
ggplot() +
```

```
geom_boxplot(aes(ebgm, var1)) +
```

```
xlab("EBGM value") +
```

```
ylab("Vaccine type") +
```

```
xlim(c(0, 5.0))
```



```
ggsave("covid_vax.pdf")
```

```
## Saving 6.5 x 4.5 in image
```