

COVID-19: impact of original, Gamma, Delta, and Omicron
variants of SARS-CoV-2 in vaccinated and unvaccinated pregnant
and postpartum women

Codes and outputs

25/07/22

Description

This file presents the documentation of the analysis of article “Demographic and epidemiological characteristics of pregnant and postpartum women who died from Severe Acute Respiratory Syndrome in Brazil: a comparison between COVID-19 and nonspecific etiologic causes”.

R packages used, functions and dataset import

The data are analyzed using the free-software R (<https://www.R-project.org>) in version 4.0.3. Next, we present and load the libraries used in the data analysis process.

```
#carregar pacotes
loadlibrary <- function(x) {
  if (!require(x, character.only = TRUE)) {
    install.packages(x, dependencies = T)
    if (!require(x, character.only = TRUE))
      stop("Package not found")
  }
}

packages <-
  c(
    "readr",
    "readxl",
    "janitor",
    "dplyr",
    "forcats",
    "stringr",
    "lubridate",
    "summarytools",
    "magrittr",
    "questionr",
    "knitr",
    "data.table",
    "writexl",
    "modelsummary"
  )
lapply(packages, loadlibrary)
```

The Influenza Epidemiological Surveillance Information System, SIVEP-Gripe (Sistema de Informação de Vigilância Epidemiológica da Gripe), is a nationwide surveillance database used to monitor severe acute respiratory infections in Brazil.

Notification is mandatory for Influenza Syndrome (characterized by at least two of the following signs and symptoms: fever, even if referred, chills, sore throat, headache, cough, runny nose, olfactory or taste disorders) and who has dyspnea/respiratory discomfort or persistent pressure in the chest or O₂ saturation less than 95% in room air or bluish color of the lips or face. Asymptomatic individuals with laboratory confirmation by molecular biology or immunological examination for COVID-19 infection are also reported.

For notifications in Sivep-Gripe, hospitalized cases in both public and private hospitals and all deaths due to severe acute respiratory infections regardless of hospitalization must be considered.

The search was limited to the first notified case of COVID-19 in February 2020 until the 28th epidemiological week of 2022 (up to July 16, 2021). The datasets were obtained on May 25, 2022, on the site <https://>

//opendatasus.saude.gov.br/dataset. The first period (8th to 53rd epidemiological week of 2020), the second period (1st to 53rd epidemiological week of 2021) and the third period (1st to 28th epidemiological week of 2022) datasets can be obtained as below:

```
##### load data base in opendatasus #####
ckanr::ckanr_setup("https://opendatasus.saude.gov.br")

arqs <- ckanr::package_search("srag 2020")$results %>%
  purrr::map("resources") %>%
  purrr::map(purrr::keep, ~ .x$mimetype == "text/csv") %>%
  purrr::map_chr(purrr::pluck, 1, "url")

arqs2 <- ckanr::package_search("srag 2021")$results %>%
  purrr::map("resources") %>%
  purrr::map(purrr::keep, ~ .x$mimetype == "text/csv") %>%
  purrr::map_chr(purrr::pluck, 2, "url")

dados_a <- fread(arqs[1], sep = ";")

dados_b <- fread(arqs[2], sep = ";")

dados_c <- fread(arqs2[1], sep = ";")

#### merge datas 2020, 2021 e 2022 #####
dados_a <- dados_a %>%
  mutate(FATOR_RISC = case_when(FATOR_RISC == 1 ~ "S",
                                FATOR_RISC == 2 ~ "N"))

dados_b <- dados_b %>%
  mutate(FATOR_RISC = case_when(FATOR_RISC == 1 ~ "S",
                                FATOR_RISC == 2 ~ "N"))

dados_c <- dados_c %>%
  mutate(FATOR_RISC = case_when(FATOR_RISC == 1 ~ "S",
                                FATOR_RISC == 2 ~ "N"))

# same class cod_idade

dados_c$COD_IDADE <- as.character(dados_c$COD_IDADE)

dados1 <- dados_a %>%
  full_join(dados_b) %>%
  full_join(dados_c)

rm(dados_a,dados_b,dados_c,arqs,arqs2)

#Criar variavel de ano do caso
data_all <- dados1 %>%
  dplyr::mutate(
    dt_sint = as.Date(DT_SIN_PRI, format = "%d/%m/%Y"),
    dt_nasc = as.Date(DT_NASC, format = "%d/%m/%Y"),
    year_case = lubridate::year(dt_sint),
  ) %>%
  filter(
    dt_sint >= as.Date("16-02-2020", format = "%d-%m-%Y") &
```

```
dt_sint <- as.Date("16-07-2022", format = "%d-%m-%Y")
)
```

There are 3296533 cases in the complete dataset. The case selection is presented in the following according to the flowchart presented in the article.

Case selection and data treatment

We are going to select only the cases hospitalized confirmed by COVID-19 (CLASSI_FIN = 5) and hospitalized cases. The other cases are influenza (CLASSI_FIN = 1), other virus (CLASSI_FIN = 2), other etiologic agent (CLASSI_FIN = 3) and unspecified (CLASSI_FIN = 4).

Now are going select the hospitalized cases.

```
data_all <- data_all %>%
  filter(HOSPITAL == 1)
```

There are 3118036 cases.

Now we are going to select only the cases confirmed by COVID-19 (CLASSI_FIN = 5).

```
data_all <- data_all %>%
  filter(CLASSI_FIN == 5)
```

There are 1989953 observations.

The next step consists in selecting cases with positive TR-PCR.

```
# case with PCR
data_all <- data_all %>%
  mutate(pcr_SN = case_when(
    (PCR_SARS2 == 1) |
    (
      str_detect(DS_PCR_OUT, "SARS|COVID|COV|CORONA|CIVID")
    ) ~ "yes",
    TRUE ~ "no"
  ))

# identify sorology
data_all$res_igg <-
  ifelse(is.na(data_all$RES_IGG) == TRUE, 0, data_all$RES_IGG)

data_all$res_igm <-
  ifelse(is.na(data_all$RES_IGM) == TRUE, 0, data_all$RES_IGM)

data_all$res_iga <-
  ifelse(is.na(data_all$RES_IGA) == TRUE, 0, data_all$RES_IGA)

data_all$sorologia_SN <-
  ifelse(data_all$res_igg == 1 |
    data_all$res_igm == 1 | data_all$res_iga == 1,
```

```

      "yes",
      "no")

# identify antígeno
data_all <- data_all %>%
  mutate(antigeno_SN = case_when(
    (AN_SARS2 == 1) | #positivo
    (
      str_detect(DS_AN_OUT, "SARS|COVID|COV|CORONA|CONA")
    ) ~ "yes",
    TRUE ~ "no"
  ))

#Criação da variável de classificação da covid-19
data_all <- data_all %>%
  mutate(
    classi_covid = case_when(
      CLASSI_FIN == 5 & pcr_SN == "yes" ~ "pcr",
      CLASSI_FIN == 5 & pcr_SN == "no" &
        antigeno_SN == "yes" ~ "antigenio",
      CLASSI_FIN == 5 & sorologia_SN == "yes" &
        antigeno_SN == "no" &
        pcr_SN == "no" ~ "sorologia",
      CLASSI_FIN != 5 ~ "no", #não é outro agente etiológico ou não especificado
      TRUE ~ "outro"
    )
  )

```

Now we are filter positive RT-PCR cases.

```

data_all <- data_all %>%
  filter(classi_covid == "pcr")

```

There are 1223248 observations.

The next step is to identify pregnant and postpartum people (variable `classi_gesta_puerp`) and then select only those cases.

```

#Creating the classification variable if pregnant, postpartum and not (neither pregnant nor postpartum)
data_all <- data_all %>%
  mutate(
    classi_gesta_puerp = case_when(
      CS_GESTANT == 1 ~ "1tri", #1st trimester
      CS_GESTANT == 2 ~ "2tri", #2st trimester
      CS_GESTANT == 3 ~ "3tri", #3st trimester
      CS_GESTANT == 4 ~ "GA_ig", #ignored gestational Age
      CS_GESTANT == 5 &
        PUERPERA == 1 ~ "puerp", #puerperium
      CS_GESTANT == 9 & PUERPERA == 1 ~ "puerp", #puerperium
      TRUE ~ "no" #neither pregnant nor postpartum
    )
  )

```

The next selection consists of selecting females cases:

```
# Filter females cases
data_all <- data_all %>%
  filter(CS_SEX0 == "F")
```

There are 543558 observations.

The next selection consists of selecting women between 10 and 55 years old.

```
data_all <- data_all %>%
  mutate(
    age = as.period(interval(start = dt_nasc, end = dt_sint))$year,
    age_year = ifelse(is.na(age), NU_IDADE_N, age)
  )

# filter cases
data_all <- data_all %>%
  filter(age_year > 9 & age_year <= 49)
```

There are 149243 observations.

Now we are going filter only pregnant and postpartum women.

```
#Filtering only pregnant and postpartum women
data_all <- data_all %>%
  filter(classi_gesta_puerp != "no")
```

There are 12364 observations.

Now let's create a variant identifier.

```
#variable variants
in_gama <- as.Date("01-02-2021",format="%d-%m-%Y")
in_delta <- as.Date("01-08-2021",format="%d-%m-%Y")
in_ommi <- as.Date("01-01-2022",format="%d-%m-%Y")

data_all <- data_all %>%
  mutate(variants = case_when(dt_sint < in_gama ~ "original",
                              dt_sint >= in_gama & dt_sint < in_delta ~ "gama",
                              dt_sint >= in_delta & dt_sint < in_ommi ~ "delta",
                              dt_sint >= in_ommi ~ "omicron"))
```

```
data_all <- data_all %>%
  mutate(
    group = case_when(
      CS_GESTANT == 1 | CS_GESTANT == 2 | CS_GESTANT == 3 | CS_GESTANT == 4 ~ "pregnant",
      CS_GESTANT == 5 &
        PUERPERA == 1 ~ "puerp",
      CS_GESTANT == 9 & PUERPERA == 1 ~ "puerp",
      TRUE ~ "no"
    )
  )
ctable(data_all$variante,data_all$group)
```

```
## Cross-Tabulation, Row Proportions
## variants * group
## Data Frame: data_1
##
## -----
##      group      pregnant      puerp      Total
## variants
##      delta      576 (83.4%)    115 (16.6%)    691 (100.0%)
##      gama      4603 (81.8%)    1025 (18.2%)    5628 (100.0%)
##      omicron    1020 (78.2%)    284 (21.8%)    1304 (100.0%)
##      original   3804 (80.2%)    937 (19.8%)    4741 (100.0%)
##      Total     10003 (80.9%)    2361 (19.1%)    12364 (100.0%)
## -----
```

Regions of Brazil:

```
#Criação da variável de região
regions <- function(state) {
  southeast <- c("SP", "RJ", "ES", "MG")
  south <- c("PR", "SC", "RS")
  central <- c("GO", "MT", "MS", "DF")
  northeast <-
    c("AL", "BA", "CE", "MA", "PB", "PE", "PI", "RN", "SE")
  north <- c("AC", "AP", "AM", "PA", "RO", "RR", "TO")
  out <-
    ifelse(any(state == southeast),
           "southeast",
           ifelse(any(state == south),
                  "south",
                  ifelse(
                    any(state == central),
                    "central",
                    ifelse(any(state == northeast),
                           "northeast", "north")
                  )))
  return(out)
}

data_all$region <- sapply(data_all$SG_UF, regions)
data_all$region <-
  ifelse(is.na(data_all$region) == TRUE, 0, data_all$region)
```

Epidemiologic characteristics

```
# Ethnicity
data_all <- data_all %>%
  mutate(
    ethnicity = case_when(
      CS_RACA == 1 ~ "white",
      CS_RACA == 2 ~ "black",
      CS_RACA == 3 ~ "yellow",
      CS_RACA == 4 ~ "brown",
```

```

    CS_RACA == 5 ~ "indigenous",
    TRUE ~ NA_character_
  )
)

# Education
data_all <- data_all %>%
  mutate(education = case_when(CS_ESCOL_N == 0 ~ "No education",
                                CS_ESCOL_N == 1 | CS_ESCOL_N == 2 ~ "Up to high school",
                                CS_ESCOL_N == 3 ~ "High school",
                                CS_ESCOL_N == 4 ~ "College",
                                TRUE ~ NA_character_))

data_all$education <- factor(data_all$education,
                             levels = c("No education", "Up to high school",
                                           "High school", "College"))

# Age group
data_all <- data_all %>%
  mutate(
    age_group = case_when(
      NU_IDADE_N <= 19 ~ "<20",
      NU_IDADE_N >= 20
      & NU_IDADE_N <= 34 ~ "20-34",
      NU_IDADE_N >= 35 ~ ">=35",
      TRUE ~ NA_character_
    )
  )
data_all$age_group <-
  factor(data_all$age_group, levels = c("<20", "20-34", ">=35"))

# Residence area
data_all <- data_all %>%
  mutate(zone = case_when(CS_ZONA == 1 | CS_ZONA == 3 ~ "urban",
                           CS_ZONA == 2 ~ "rural",
                           TRUE ~ NA_character_))

# flu vaccine
data_all <- data_all %>%
  mutate(vaccine = case_when(VACINA == 1 ~ "sim",
                              VACINA == 2 ~ "não",
                              TRUE ~ NA_character_))

# covid-19 vaccine
data_all <- data_all %>%
  mutate(vaccine_cov = case_when(VACINA_COV == 1 ~ "sim",
                                  VACINA_COV == 2 ~ "não",
                                  variants == "original" ~ "não",
                                  TRUE ~ NA_character_))

```


Symptoms

```
# Fever
data_all <- data_all %>%
  mutate( fever = case_when(FEBRE == 1 ~ "yes",
                             FEBRE == 2 ~ "no",
                             TRUE ~ NA_character_))

# Cough
data_all <- data_all %>%
  mutate( cough = case_when(TOSSE == 1 ~ "yes",
                             TOSSE == 2 ~ "no",
                             TRUE ~ NA_character_))

# Sore throat
data_all <- data_all %>%
  mutate( sore_throat = case_when(GARGANTA == 1 ~ "yes",
                                   GARGANTA == 2 ~ "no",
                                   TRUE ~ NA_character_))

# Dyspnea
data_all <- data_all %>%
  mutate( dyspnea = case_when(DISPNEIA == 1 ~ "yes",
                              DISPNEIA == 2 ~ "no",
                              TRUE ~ NA_character_))

# Respiratory discomfort
data_all <- data_all %>%
  mutate( resp_disc = case_when(DESC_RESP == 1 ~ "yes",
                                 DESC_RESP == 2 ~ "no",
                                 TRUE ~ NA_character_))

# Desaturation SpO2 <95%
data_all <- data_all %>%
  mutate( desaturation = case_when(SATURACAO == 1 ~ "yes",
                                    SATURACAO == 2 ~ "no",
                                    TRUE ~ NA_character_))

# Diarrhea
data_all <- data_all %>%
  mutate( diarrhea = case_when(DIARREIA == 1 ~ "yes",
                                DIARREIA == 2 ~ "no",
                                TRUE ~ NA_character_))

# Vomit
data_all <- data_all %>%
  mutate( vomit = case_when(VOMITO == 1 ~ "yes",
                             VOMITO == 2 ~ "no",
                             TRUE ~ NA_character_))

# Abdominal pain
data_all <- data_all %>%
  mutate( abd_pain = case_when(DOR_ABD == 1 ~ "yes",
```

```

DOR_ABD == 2 ~ "no",
TRUE ~ NA_character_))

# Fatigue
data_all <- data_all %>%
  mutate(fatigue = case_when(FADIGA == 1 ~ "yes",
                             FADIGA == 2 ~ "no",
                             TRUE ~ NA_character_))

# Olfactory loss
data_all <- data_all %>%
  mutate(olfac_loss = case_when(PERD_OLFT == 1 ~ "yes",
                                PERD_OLFT == 2 ~ "no",
                                TRUE ~ NA_character_))

# Loss of taste
data_all <- data_all %>%
  mutate(loss_taste = case_when(PERD_PALA == 1 ~ "yes",
                                PERD_PALA == 2 ~ "no",
                                TRUE ~ NA_character_))

```

Comorbidades

```

#Cardiac
data_all <- data_all %>%
  mutate(cardiac = case_when(CARDIOPATI == 1 ~ "yes",
                             CARDIOPATI == 2 ~ "no",
                             TRUE ~ NA_character_))

#Hematologic
data_all <- data_all %>%
  mutate(hematologic = case_when(HEMATOLOGI == 1 ~ "yes",
                                 HEMATOLOGI == 2 ~ "no",
                                 TRUE ~ NA_character_))

#Hepatic
data_all <- data_all %>%
  mutate(hepatic = case_when(HEPATICA == 1 ~ "yes",
                             HEPATICA == 2 ~ "no",
                             TRUE ~ NA_character_))

#Asthma
data_all <- data_all %>%
  mutate(asthma = case_when(ASMA == 1 ~ "yes",
                            ASMA == 2 ~ "no",
                            TRUE ~ NA_character_))

#Diabetes
data_all <- data_all %>%
  mutate(diabetes = case_when(DIABETES == 1 ~ "yes",
                              DIABETES == 2 ~ "no",
                              TRUE ~ NA_character_))

```

```

#Neurologic
data_all <- data_all %>%
  mutate(neurologic = case_when(NEUROLOGIC == 1 ~ "yes",
                                NEUROLOGIC == 2 ~ "no",
                                TRUE ~ NA_character_))

#Pneumologic
data_all <- data_all %>%
  mutate(pneumologic = case_when(PNEUMOPATI == 1 ~ "yes",
                                  PNEUMOPATI == 2 ~ "no",
                                  TRUE ~ NA_character_))

#Imunossupression
data_all <- data_all %>%
  mutate(imuno = case_when(IMUNODEPRE == 1 ~ "yes",
                           IMUNODEPRE == 2 ~ "no",
                           TRUE ~ NA_character_))

#Renal
data_all <- data_all %>%
  mutate(renal = case_when(RENAL == 1 ~ "yes",
                          RENAL == 2 ~ "no",
                          TRUE ~ NA_character_))

#Obesity
data_all <- data_all %>%
  mutate(obesity = case_when(OBESIDADE == 1 ~ "yes",
                             OBESIDADE == 2 ~ "no",
                             TRUE ~ NA_character_))

```

Outcome

```

# Hospital-acquired infection
data_all <- data_all %>%
  mutate(hospital_infection = case_when(NOSOCOMIAL == 1 ~ "yes",
                                          NOSOCOMIAL == 2 ~ "no",
                                          TRUE ~ NA_character_))

# ICU admission
data_all <- data_all %>%
  mutate(icu = case_when(UTI == 1 ~ "yes",
                        UTI == 2 ~ "no",
                        TRUE ~ NA_character_))

# Invasive respiratory support
data_all <- data_all %>%
  mutate(intubation = case_when(SUPPORT_VEN == 1 ~ "yes",
                                SUPPORT_VEN == 2 | SUPPORT_VEN == 3 ~ "no",
                                TRUE ~ NA_character_))

# Death
data_all <- data_all %>%

```

```
mutate(death = case_when(  
  EVOLUCAO == 1 ~ "cure",  
  EVOLUCAO == 2 ~ "death",  
  EVOLUCAO == 3 ~ "death",  
  TRUE ~ NA_character_  
))
```

Export data base

```
saveRDS(data_all, "data_paper.rds")
```