

Brazilian Obstetric Observatory

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Abstract

Covid-19 is responsible for high mortality in all countries, with the maternal population it is no different. Countries with a high rate of maternal mortality have deficiencies in the health care of pregnant women and women who have recently given birth, which will certainly be enhanced in a situation of overload in the health system, as occurred in this pandemic. Understanding the impact of the pandemic on maternal health is essential to discuss public policies and assist in solutions to future crises. With that in mind, we present the Brazilian Obstetric Observatory COVID-19 (OOBr COVID-19). OOBr COVID-19 is a dynamic panel with analyzes of the cases of pregnant and postpartum women with Severe Acute Respiratory Syndrome (SARI) during the pandemic due to the new coronavirus. In this article, we present data loading, case selections, and processing of the variables for the analyzes available in OOBr COVID-19.

1. Introduction

Covid-19 (disease caused by SARS-CoV-2) has been responsible for high mortality in all countries. In November 2020, [1] pointed out that pregnant women would have a higher risk of hospitalization in intensive care units, orotracheal intubation and death than non-pregnant women.

Covid-19 presented many clinical manifestations and has shown inequalities among countries especially with regard to access to healthcare systems. The difference in the mortality rate of pregnant and postpartum women in the world by COVID-19 reflects the differences among countries' maternal death rates observed before the pandemic caused by COVID-19. Countries with a high rate of maternal death have deficiencies in healthcare for pregnant women and women who have recently given birth, which will certainly be enhanced in a situation of overload to the healthcare system, as occurred in this pandemic.

The Brazilian Obstetric Observatory COVID-19 (OOBr COVID-19, in Portuguese: Observatório Obstétrico Brasileiro COVID-19) is a dynamic panel with analyzes of the cases of pregnant and postpartum women with Severe Acute Respiratory Syndrome (SARI) during the pandemic due to the new coronavirus. The OOBr COVID-19 aims to give visibility to the data of this specific public and to offer tools for analysis and reasoning for health care policies for pregnant women and women who have recently given birth.

There are considered the records of reports in the SIVEP Gripe database (Influenza Epidemiological Surveillance Information System), a nationwide surveillance database used to monitor SARI in Brazil. The database is made available by the Ministry of Health of Brazil and updated weekly on the website <https://opendatasus.saude.gov.br/dataset>.

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

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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.

OOBr COVID-19 can be accessed at https://observatorioobstetrico.shinyapps.io/covid_gesta_puerp_br. The analyzed period comprised data from epidemiological weeks 8 to 53 of 2020 (12/29/2019 - 01/02/2021) and from epidemiological weeks 1 to until the last available update of 2021. The OOB COVID-19 is updated weekly depending on the updates made available by the Ministry of Health on the website <https://opendatasus.saude.gov.br/dataset> [2,3].

In this article, we will describe the selections, filters, and data transformations to achieve the information available in OOB COVID-19. Section 2 describes the methods used to select the cases and process the variables for OOB COVID-19 and the results after loading the data and processing the variables are presented in Section 3. Finally, the final remarks are presented in Section 4.

2. Methods

The database from 2020 is downloaded weekly in <https://opendatasus.saude.gov.br/dataset/bd-srag-2020> and the database from 2021 is downloaded weekly in <https://opendatasus.saude.gov.br/dataset/bd-srag-2021>.

The data are analyzed using the R program, version 4.0.3 (<https://www.r-project.org>) and the OOB COVID-19 is available on a Shiny dashboard (<https://www.shinyapps.io>).

The two databases are merged and data are filtered from the 8th epidemiological week of symptoms (when the first confirmed case of COVID-19 was found in the database) to until the last available update of 2021. All data on female cases aged 10 to 55 years old, with information on whether pregnant women (first, second or third gestational period or with ignored gestational age) or in the puerperium period were included. The flowchart is shown in Figure 1.

The variables analyzed and available in OOB COVID-19 are: age, race, education, state of Brazil of residence, region of Brazil of residence, age range, obstetric status, change of municipality for assistance, residence area, SARI diagnosis, laboratory (etiologial) diagnosis, flu syndrome that progresses to SARI, type of antiviral, previous vaccination for influenza, hospital-acquired infection, travel history, contact with swine, signs and symptoms (fever, cough, sore throat, dyspnoea, respiratory distress, O2 saturation less than 95%, diarrhea, vomiting, abdominal pain, fatigue, loss of smell or taste), risk factors/comorbidities (cardiovascular disease, kidney disease, neurological disease, hematological disease, liver disease, diabetes, asthma, pneumopathy, obesity and immunosuppression), hospitalization, admission to the ICU (Intensive Care Unit), use of ventilatory support (invasive and non-invasive) and evolution of the case (cure or death).

3. Results

The analyzes that result in observatory https://observatorioobstetrico.shinyapps.io/covid_gesta_puerp_br are described in this section. At first, the R packages used are presented, the data are loaded, the selections and filters are made and, finally, the characterization variables, symptoms, comorbidities, and outcome variables are processed.

3.1 Database load and R packages used

The R packages used for filtering and data processing are presented in this subsection.

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

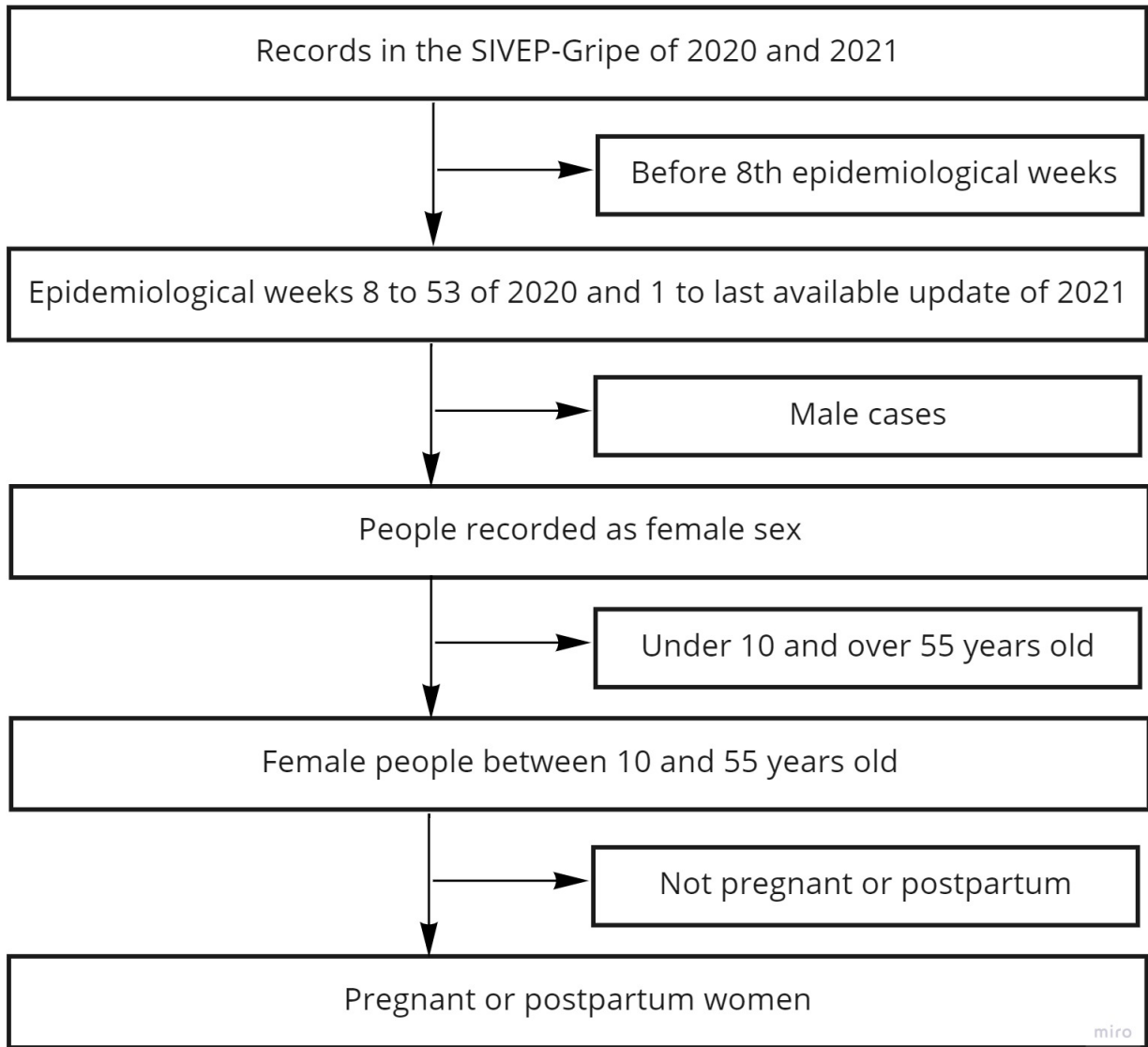


Figure 1: Flowchart of case selection

```

}

packages <-
  c(
    "readr",
    "readxl",
    "janitor",
    "dplyr",
    "forcats",
    "stringr",
    "lubridate",
    "summarytools",
    "magrittr",
    "questionr",
    "knitr"
  )
lapply(packages, loadlibrary)

```

The 2020 and 2021 databases are loaded and they are also merged. Below are the databases updated on April 26, 2021, the last update available at the time of writing this article.

```

##### Importing databases
#2021
dados_2021 <- read_delim(
  "INFLUD21-26-04-2021.csv",
  ";",
  escape_double = FALSE,
  locale = locale(encoding = "ISO-8859-2"),
  trim_ws = TRUE
)

#2020
dados_2020 <- read_delim(
  "INFLUD-26-04-2021.csv",
  ";",
  escape_double = FALSE,
  locale = locale(encoding = "ISO-8859-2"),
  trim_ws = TRUE
)

##### Merging 2020 and 2021 databases
dados1 <- rbind(dados_2020, dados_2021)

```

3.2 Selecting cases and data processing

We will filter only the cases from the 8th epidemiological week of 2020 (first confirmed case of COVID-19) until the current epidemiological week of 2021.

```

#### Current epidemiological week
sem <- 16

#### Create year variable (ano)
dados1 <- dados1 %>%
  dplyr::mutate(
    dt_sint = as.Date(DT_SIN_PRI, format = "%d/%m/%Y"),

```

```

ano = lubridate::year(dt_sint),
)

#### Case filtering from the 8th epidemiological week of 2020
dados2 <- dados1 %>%
  filter((ano==2020 & SEM_PRI >=8) | ano ==2021)

```

The table in the following presents the distribution of cases by year and by epidemiological week.

```

#### Cross table of epidemiological year and week
ctable(dados2$SEM_PRI, dados2$ano, prop="n")

```

```

## Cross-Tabulation
## SEM_PRI * ano
## Data Frame: dados2
##
## -----
##      ano      2020      2021      Total
## SEM_PRI
##      1           0     35122     35122
##      2           0     33809     33809
##      3           0     31044     31044
##      4           0     28985     28985
##      5           0     34670     34670
##      6           0     37745     37745
##      7           0     47328     47328
##      8          923     50091     51014
##      9         1164     68575     69739
##     10         1980     68057     70037
##     11         5136     65397     70533
##     12        12826     50657     63483
##     13        14974     45334     60308
##     14        16289     37006     53295
##     15        19583     19824     39407
##     16        24872      4445     29317
##     17        30828         19     30847
##     18        34864         0     34864
##     19        34566         0     34566
##     20        37172         0     37172
##     21        33824         0     33824
##     22        31256         0     31256
##     23        35643         0     35643
##     24        34162         0     34162
##     25        36694         0     36694
##     26        32968         0     32968
##     27        37444         0     37444
##     28        37041         0     37041
##     29        34440         0     34440
##     30        33704         0     33704
##     31        32184         0     32184
##     32        30028         0     30028
##     33        31070         0     31070
##     34        28271         0     28271
##     35        26337         0     26337

```

```

##      36      26459      0      26459
##      37      24047      0      24047
##      38      22222      0      22222
##      39      21579      0      21579
##      40      22451      0      22451
##      41      21026      0      21026
##      42      18999      0      18999
##      43      19464      0      19464
##      44      18719      0      18719
##      45      23302      0      23302
##      46      25802      0      25802
##      47      29289      0      29289
##      48      29162      0      29162
##      49      32940      0      32940
##      50      30540      0      30540
##      51      28405      0      28405
##      52      30304      0      30304
##      53      21559     12514     34073
## Total     1176512     670622     1847134
## -----

```

Note that there are 12514 cases in 2021 in week 53. These are cases from the first two days of 2021, which are still part of the last epidemiological week of 2020 (<http://portalsinan.saude.gov.br/calendario-epidemiologico?layout=edit&id=168>). However, these cases belong to the 53rd week of 2020 and we corrected in the following:

```

#### Correcting year variable (ano) from 53rd epidemiological week
dados2 <- dados2 %>%
  mutate(ano = ifelse(ano ==2021 & SEM_PRI ==53, 2020, ano)) %>%
  filter(ano==2020 | (ano == 2021 & SEM_PRI <= sem))

```

The distribution of epidemiological week by year of the pandemic after correction is presented in the following.

```

#### Cross table of epidemiological year and week
ctable(dados2$SEM_PRI, dados2$ano, prop="n")

```

```

## Cross-Tabulation
## SEM_PRI * ano
## Data Frame: dados2
##
## -----
##      ano      2020      2021      Total
## SEM_PRI
##      1          0     35122     35122
##      2          0     33809     33809
##      3          0     31044     31044
##      4          0     28985     28985
##      5          0     34670     34670
##      6          0     37745     37745
##      7          0     47328     47328
##      8         923     50091     51014
##      9        1164     68575     69739
##     10        1980     68057     70037
##     11        5136     65397     70533
##     12       12826     50657     63483
##     13       14974     45334     60308

```

##	14	16289	37006	53295
##	15	19583	19824	39407
##	16	24872	4445	29317
##	17	30828	0	30828
##	18	34864	0	34864
##	19	34566	0	34566
##	20	37172	0	37172
##	21	33824	0	33824
##	22	31256	0	31256
##	23	35643	0	35643
##	24	34162	0	34162
##	25	36694	0	36694
##	26	32968	0	32968
##	27	37444	0	37444
##	28	37041	0	37041
##	29	34440	0	34440
##	30	33704	0	33704
##	31	32184	0	32184
##	32	30028	0	30028
##	33	31070	0	31070
##	34	28271	0	28271
##	35	26337	0	26337
##	36	26459	0	26459
##	37	24047	0	24047
##	38	22222	0	22222
##	39	21579	0	21579
##	40	22451	0	22451
##	41	21026	0	21026
##	42	18999	0	18999
##	43	19464	0	19464
##	44	18719	0	18719
##	45	23302	0	23302
##	46	25802	0	25802
##	47	29289	0	29289
##	48	29162	0	29162
##	49	32940	0	32940
##	50	30540	0	30540
##	51	28405	0	28405
##	52	30304	0	30304
##	53	34073	0	34073
##	Total	1189026	658089	1847115
##	-----	-----	-----	-----

The next step is to identify pregnant women. For this, we will analyze the variable CS_GESTANT. This variable assumes the values: 1-1st trimester; 2-2nd trimester; 3-3rd trimester; 4-Ignored Gestational Age; 5-No; 6-Does not apply; 9-Ignored.

```
##### Frequency table for gestational information
questionr::freq(
  dados2$CS_GESTANT,
  cum = FALSE,
  total = TRUE,
  na.last = FALSE,
  valid = FALSE
) %>%
```

```
kable(caption = "Frequency table for variable
  about pregnancy", digits = 2)
```

Table 1: Frequency table for variable about pregnancy

	n	%
0	371	0.0
1	1938	0.1
2	4475	0.2
3	9593	0.5
4	978	0.1
5	574545	31.1
6	1163859	63.0
9	91356	4.9
Total	1847115	100.0

There are 371 cases with CS_GESTANT=0, where category 0 has no code in the database dictionary.

The next step is to check if there is any inconsistency when analyzing this variable together with sex (CS_SEXO), with categories F-female, M-male and I-ignored.

```
#### Cross table of gestation and sex
ctable(dados2$CS_GESTANT, dados2$CS_SEXO, prop="n")
```

```
## Cross-Tabulation
## CS_GESTANT * CS_SEXO
## Data Frame: dados2
##
## -----
##          CS_SEXO      F      I      M      Total
## CS_GESTANT
##          0          115    177      79      371
##          1          1938      0       0      1938
##          2          4474      1       0      4475
##          3          9592      1       0      9593
##          4           977      1       0       978
##          5          573354    51     1140     574545
##          6          165319    279    998261    1163859
##          9           91108     94      154     91356
##          Total          846877    604    999634    1847115
## -----
```

There are 0 cases of CS_SEXO=M with CS_GESTANT=1,2,3 ou 4, hopefully.

The puerperium indicator variable is PUERPERA, with categories 1=yes, 2=no and 9-Ignored.

```
#Frequency table for puerperium
questionr::freq(
  dados2$PUERPERA,
  cum = FALSE,
  total = TRUE,
  na.last = FALSE,
  valid = FALSE
) %>%
  kable(caption = "Frequency table for puerperium", digits = 2)
```


Table 2: Frequency table for puerperium

	n	%
1	6648	0.4
2	682995	37.0
9	18082	1.0
NA	1139390	61.7
Total	1847115	100.0

The next step is to check if there is any inconsistency when analyzing this variable together with sex (CS_SEXO), with categories F-female, M-male and I-ignored.

```
#### Cross table of puerperium and sex
ctable(dados2$PUERPERA, dados2$CS_SEXO, prop="n")
```

```
## Cross-Tabulation
## PUERPERA * CS_SEXO
## Data Frame: dados2
##
## -----
##          CS_SEXO      F      I      M      Total
## PUERPERA
##      1           6647      1      0      6648
##      2          327159     174    355662    682995
##      9           8345     10     9727     18082
##      <NA>         504726    419    634245    1139390
##      Total         846877    604    999634    1847115
## -----
```

There are 0 cases of CS_SEXO=M with PUERPERA = 1, that is, puerperium and male sex cases, hopefully.

The next selection is to consider only female people and aged over 10 and under or equal to 55 years.

```
#### Filtering only female cases
dados3 <- dados2 %>%
  filter(CS_SEXO == "F")

#### Filtering of cases aged 55 years or less
dados4 <- dados3 %>%
  filter(NU_IDADE_N > 9 & NU_IDADE_N <= 55)
```

Now we are going to create the variable of gestational trimester or puerperium. Note that for puerperium (puerp), nonpregnant or ignored cases with PUERPERA = 1 are considered.

```
#### Creation of the classi_gesta_puerp variable for the gestational or postpartum period
dados4 <- dados4 %>%
  mutate(
    classi_gesta_puerp = case_when(
      CS_GESTANT == 1 ~ "1tri", # 1st trimester
      CS_GESTANT == 2 ~ "2tri", # 2nd trimester
      CS_GESTANT == 3 ~ "3tri", # 3rd trimester
      CS_GESTANT == 4 ~ "IG_ig", # Ignored gestational age
      CS_GESTANT == 5 &
        PUERPERA == 1 ~ "puerp", # puerperal woman
      CS_GESTANT == 9 & PUERPERA == 1 ~ "puerp", # puerperal woman
      TRUE ~ "nãõ" # 'nãõ' means not pregnant
    )
  )
```

```
)  
)
```

The last filtering consists of selecting the cases of pregnant or postpartum women.

```
### Selection only of pregnant or postpartum cases
```

```
dados5 <- dados4 %>%  
  filter(classi_gesta_puerp != "nãõ")
```

```
### Frequency table for gestational group
```

```
questionr::freq(  
  dados5$classi_gesta_puerp,  
  cum = FALSE,  
  total = TRUE,  
  na.last = FALSE,  
  valid = FALSE  
) %>%  
  kable(caption = "Frequency table for gestational trimester or postpartum variable",  
        digits = 2)
```

Table 3: Frequency table for gestational trimester or postpartum variable

	n	%
1tri	1914	8.9
2tri	4407	20.5
3tri	9575	44.6
IG_ig	917	4.3
puerp	4661	21.7
Total	21474	100.0

In the following, we deal with other variables considered at the OOB Covid-19.

3.3 Variables processing

The variable that indicates the SARI diagnosis is CLASSI_FIN, with categories: 1-SARI by influenza, 2-SARI by another respiratory virus, 3-SARI by another etiologic agent, 4-SARI not specified, 5-SARI by COVID-19.

```
#frequency table for SARI diagnosis
```

```
questionr::freq(  
  dados5$CLASSI_FIN,  
  cum = FALSE,  
  total = TRUE,  
  na.last = FALSE,  
  valid = FALSE  
) %>%  
  kable(caption = "Frequency table for SARI diagnosis", digits = 2)
```

Table 4: Frequency table for SARI diagnosis

	n	%
1	74	0.3
2	105	0.5
3	61	0.3

	n	%
4	8104	37.7
5	10818	50.4
NA	2312	10.8
Total	21474	100.0

The variable that identify the diagnostic type of COVID-19 is `classi_covid`, with categories: pcr (RT-PCR), antigenio (antigen), sorologia (serology) and outro (other). This variable only has valid categories for cases confirmed by SARI by COVID-19 (`CLASSI_FIN=5`).

```
#Case diagnosed by RT-PCR
dados5 <- dados5 %>%
  mutate(pcr_SN = case_when(
    (PCR_SARS2 == 1) |
      (
        str_detect(DS_PCR_OUT, "SARS|COVID|COV|CORONA|CIVID")
      ) ~ "sim",
    TRUE ~ "nãõ"
  ))

#Identify if diagnosed by serology
dados5$res_igg <-
  ifelse(is.na(dados5$RES_IGG) == TRUE, 0, dados5$RES_IGG)

dados5$res_igm <-
  ifelse(is.na(dados5$RES_IGM) == TRUE, 0, dados5$RES_IGM)

dados5$res_iga <-
  ifelse(is.na(dados5$RES_IGA) == TRUE, 0, dados5$RES_IGA)

dados5$sorologia_SN <-
  ifelse(dados5$res_igg == 1 |
    dados5$res_igm == 1 | dados5$res_iga == 1,
    "sim",
    "nãõ")

#Identify if diagnosed by antigen
dados5 <- dados5 %>%
  mutate(antigeno_SN = case_when(
    (AN_SARS2 == 1) | #positivo
      (
        str_detect(DS_AN_OUT, "SARS|COVID|COV|CORONA|CONA")
      ) ~ "sim",
    TRUE ~ "nãõ"
  ))

#Creation of the covid-19 classification variable
dados5 <- dados5 %>%
  mutate(
    classi_covid = case_when(
      CLASSI_FIN == 5 & pcr_SN == "sim" ~ "pcr",
      CLASSI_FIN == 5 & pcr_SN == "nãõ" &
        antigeno_SN == "sim" ~ "antigenio",
```

```

CLASSI_FIN == 5 & sorologia_SN == "sim" &
  antigeno_SN == "não" &
  pcr_SN == "não" ~ "sorologia",
CLASSI_FIN != 5 ~ "não", #is not another etiologic agent or unspecified
TRUE ~ "outro"
)
)

#frequency table for COVID-19 diagnostic type
questionr::freq(
  dados5$classi_covid,
  cum = FALSE,
  total = TRUE,
  na.last = FALSE,
  valid = FALSE
) %>%
  kable(caption = "Frequency table for the COVID-19 diagnostic type", digits = 2)

```

Table 5: Frequency table for the COVID-19 diagnostic type

	n	%
antigenio	827	3.9
não	8344	38.9
outro	4354	20.3
pcr	6908	32.2
sorologia	1041	4.8
Total	21474	100.0

The variable that indicates the state of Brazil is `SG_UF`. The variable that indicates the region of Brazil (North, Northeast, Central, Southeast and South) is `region`, created in the following.

```

#Creation of the region variable
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)
}

```

```

dados5$region <- sapply(dados5$SG_UF, regions)
dados5$region <-
  ifelse(is.na(dados5$region) == TRUE, 0, dados5$region)

#Frequency table for region
questionr::freq(
  dados5$region,
  cum = FALSE,
  total = TRUE,
  na.last = FALSE,
  valid = FALSE
) %>%
  kable(caption = "Frequency table for the region of Brazil", digits = 2)

```

Table 6: Frequency table for the region of Brazil

	n	%
0	4	0.0
central	2384	11.1
north	2363	11.0
northeast	5394	25.1
south	2671	12.4
southeast	8658	40.3
Total	21474	100.0

Note that there are 4 cases without information for the region of the country (encoded as 0).

The processing of the characterization variables is presented in the following.

```

#Race
dados5 <- dados5 %>%
  mutate(
    raca = case_when(
      CS_RACA == 1 ~ "branca", #white
      CS_RACA == 2 ~ "preta", #black
      CS_RACA == 3 ~ "amarela", #yellow
      CS_RACA == 4 ~ "parda", #brown
      CS_RACA == 5 ~ "indigena", #indigenous
      TRUE ~ NA_character_
    )
  )

#Education
dados5 <- dados5 %>%
  mutate(
    escol = case_when(
      CS_ESCOL_N == 0 ~ "sem escol", #no school
      CS_ESCOL_N == 1 ~ "fund1", #1st elementary school
      CS_ESCOL_N == 2 ~ "fund2", #2nd elementary school
      CS_ESCOL_N == 3 ~ "medio", #high school
      CS_ESCOL_N == 4 ~ "superior", #university education
      TRUE ~ NA_character_
    )
  )

```

```

)

#Age range
dados5 <- dados5 %>%
  mutate(
    faixa_et = 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_
    )
  )
dados5$faixa_et <-
  factor(dados5$faixa_et, levels = c("<20", "20-34", ">=35"))

#Hospitalization
dados5 <- dados5 %>%
  mutate(hospital = case_when(HOSPITAL == 1 ~ "sim", #yes
                              HOSPITAL == 2 ~ "não", #no
                              TRUE ~ NA_character_))

#Travel history
dados5 <- dados5 %>%
  mutate(hist_viagem = case_when(HISTO_VGM == 1 ~ "sim", #yes
                                 HISTO_VGM == 2 ~ "não", #no
                                 TRUE ~ NA_character_))

#Influenza syndrome evolved to SARI
dados5 <- dados5 %>%
  mutate(sg_para_srag = case_when(SURTO_SG == 1 ~ "sim", #yes
                                  SURTO_SG == 2 ~ "não", #no
                                  TRUE ~ NA_character_))

#Hospital acquired infection
dados5 <- dados5 %>%
  mutate(inf_inter = case_when(NOSOCOMIAL == 1 ~ "sim", #yes
                               NOSOCOMIAL == 2 ~ "não", #no
                               TRUE ~ NA_character_))

#Contact with poultry or swine
dados5 <- dados5 %>%
  mutate(cont_ave_suino = case_when(AVE_SUINO == 1 ~ "sim", #yes
                                    AVE_SUINO == 2 ~ "não", #no
                                    TRUE ~ NA_character_))

#Influenza vaccine
dados5 <- dados5 %>%
  mutate(vacina = case_when(VACINA == 1 ~ "sim", #yes
                            VACINA == 2 ~ "não", #no
                            TRUE ~ NA_character_))

#Antiviral

```

```

dados5 <- dados5 %>%
  mutate(
    antiviral = case_when(
      ANTIVIRAL == 1 ~ "Oseltamivir",
      ANTIVIRAL == 2 ~ "Zanamivir",
      TRUE ~ NA_character_ ))

#Residence zone
dados5 <- dados5 %>%
  mutate(zona = case_when(CS_ZONA == 1 ~ "urbana", #urban
                          CS_ZONA == 2 ~ "rural", #rural
                          CS_ZONA == 3 ~ "periurbana", #periurban
                          TRUE ~ NA_character_))

#If change of municipality for care
dados5 <- dados5 %>%
  mutate(mudou_muni = case_when(CO_MUN_RES==CO_MU_INTE & !is.na(CO_MU_INTE) &
                                !is.na(CO_MUN_RES) ~ "não", #no
                                CO_MUN_RES!=CO_MU_INTE & !is.na(CO_MU_INTE) &
                                !is.na(CO_MUN_RES) ~ "sim", #yes
                                TRUE ~ NA_character_
                                )
  )

```

The processing of symptom variables is presented below.

```

#Fever
dados5 <- dados5 %>%
  mutate(febre = case_when(FEBRE == 1 ~ "sim", #yes
                           FEBRE == 2 ~ "não", #no
                           TRUE ~ NA_character_))

#Cough
dados5 <- dados5 %>%
  mutate(tosse = case_when(TOSSE == 1 ~ "sim", #yes
                            TOSSE == 2 ~ "não", #no
                            TRUE ~ NA_character_))

#Sore throat
dados5 <- dados5 %>%
  mutate(garganta = case_when(GARGANTA == 1 ~ "sim", #yes
                              GARGANTA == 2 ~ "não", #no
                              TRUE ~ NA_character_))

#Dyspnea
dados5 <- dados5 %>%
  mutate(dispnéia = case_when(DISPNEIA == 1 ~ "sim", #yes
                              DISPNEIA == 2 ~ "não", #no
                              TRUE ~ NA_character_))

#Respiratory distress
dados5 <- dados5 %>%
  mutate(desc_resp = case_when(DESC_RESP == 1 ~ "sim", #yes
                                DESC_RESP == 2 ~ "não", #no

```

```

TRUE ~ NA_character_))

#O2 saturation less than 95%
dados5 <- dados5 %>%
  mutate(saturacao = case_when(SATURACAO == 1 ~ "sim", #yes
                                SATURACAO == 2 ~ "não", #no
                                TRUE ~ NA_character_))

#Diarrhea
dados5 <- dados5 %>%
  mutate(diarreia = case_when(DIARREIA == 1 ~ "sim", #yes
                                DIARREIA == 2 ~ "não", #no
                                TRUE ~ NA_character_))

#Vomiting
dados5 <- dados5 %>%
  mutate(vomito = case_when(VOMITO == 1 ~ "sim", #yes
                              VOMITO == 2 ~ "não", #no
                              TRUE ~ NA_character_))

#Abdominal pain
dados5 <- dados5 %>%
  mutate(dor_abd = case_when(DOR_ABD == 1 ~ "sim",
                              DOR_ABD == 2 ~ "não",
                              TRUE ~ NA_character_))

#Fatigue
dados5 <- dados5 %>%
  mutate(fadiga = case_when(FADIGA == 1 ~ "sim", #yes
                              FADIGA == 2 ~ "não", #no
                              TRUE ~ NA_character_))

#Olfactory loss
dados5 <- dados5 %>%
  mutate(perd_olft = case_when(PERD_OLFT == 1 ~ "sim", #yes
                                PERD_OLFT == 2 ~ "não", #no
                                TRUE ~ NA_character_))

#Loss of taste
dados5 <- dados5 %>%
  mutate(perd_pala = case_when(PERD_PALA == 1 ~ "sim", #yes
                                PERD_PALA == 2 ~ "não", #no
                                TRUE ~ NA_character_))

```

The processing of comorbidity variables is presented below.

```

#Cardiovascular disease
dados5 <- dados5 %>%
  mutate(cardiopati = case_when(CARDIOPATI == 1 ~ "sim", #yes
                                CARDIOPATI == 2 ~ "não", #no
                                TRUE ~ NA_character_))

#Hematological disease
dados5 <- dados5 %>%

```



```

mutate(hematologi = case_when(HEMATOLOGI == 1 ~ "sim", #yes
                              HEMATOLOGI == 2 ~ "não", #no
                              TRUE ~ NA_character_))

#Liver disease
dados5 <- dados5 %>%
  mutate(hepatica = case_when(HEPATICA == 1 ~ "sim", #yes
                              HEPATICA == 2 ~ "não", #no
                              TRUE ~ NA_character_))

#Asthma
dados5 <- dados5 %>%
  mutate(asma = case_when(ASMA == 1 ~ "sim", #yes
                          ASMA == 2 ~ "não", #no
                          TRUE ~ NA_character_))

#Diabetes
dados5 <- dados5 %>%
  mutate(diabetes = case_when(DIABETES == 1 ~ "sim", #yes
                              DIABETES == 2 ~ "não", #no
                              TRUE ~ NA_character_))

#Neurological disease
dados5 <- dados5 %>%
  mutate(neuro = case_when(NEUROLOGIC == 1 ~ "sim", #yes
                           NEUROLOGIC == 2 ~ "não", #no
                           TRUE ~ NA_character_))

#Pneumopathy
dados5 <- dados5 %>%
  mutate(pneumopati = case_when(PNEUMOPATI == 1 ~ "sim", #yes
                                 PNEUMOPATI == 2 ~ "não", #no
                                 TRUE ~ NA_character_))

#Immunosuppression
dados5 <- dados5 %>%
  mutate(imunodepre = case_when(IMUNODEPRE == 1 ~ "sim", #yes
                                 IMUNODEPRE == 2 ~ "não", #no
                                 TRUE ~ NA_character_))

#Kidney disease
dados5 <- dados5 %>%
  mutate(renal = case_when(RENAL == 1 ~ "sim", #yes
                           RENAL == 2 ~ "não", #no
                           TRUE ~ NA_character_))

#Obesity
dados5 <- dados5 %>%
  mutate(obesidade = case_when(OBESIDADE == 1 ~ "sim", #yes
                                OBESIDADE == 2 ~ "não", #no
                                TRUE ~ NA_character_))

```

The processing of the variables admission to the ICU, use of ventilatory support and evolution (death or cure) is done as follows

```

#ICU
dados5 <- dados5 %>%
  mutate(uti = case_when(UTI == 1 ~ "sim", #yes
                        UTI == 2 ~ "não", #no
                        TRUE ~ NA_character_))

#Use of ventilatory support
dados5 <- dados5 %>%
  mutate(
    suport_ven = case_when(
      SUPPORT_VEN == 1 ~ "invasivo", #invasive
      SUPPORT_VEN == 2 ~ "não invasivo", #non-invasive
      SUPPORT_VEN == 3 ~ "não", #no
      TRUE ~ NA_character_
    )
  )

dados5$suport_ven <- factor(dados5$suport_ven,
                          levels = c("invasivo", "não invasivo", "não"))

#Evolution
dados5 <-
  dados5 %>% mutate(
    evolucao = case_when(
      EVOLUCAO == 1 ~ "Cura", #cure
      EVOLUCAO == 2 ~ "Obito", #death
      EVOLUCAO == 3 ~ "Obito", #death
      TRUE ~ NA_character_
    )
  )

```

The analyzes obtained after the processes described above are presented in https://observatorioobstetrico.shinyapps.io/covid_gesta_puerp_br.

4. Final remarks

In this article we present the documentation for loading the data, merge data from the years 2020 and 2021, selection and filtering cases and processing the variables to obtain the analyzes in OOB COVID-19, available in https://observatorioobstetrico.shinyapps.io/covid_gesta_puerp_br.

With OOB COVID-19 we hope that information about COVID-19 in the Brazilian maternal population will be accessible so that society is aware of the pandemic situation in the country and that public policy decisions are based on reliable data.

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