

Text S1. Documentation of the article ‘COVID-19 vaccines confer protection in hospitalized pregnant and postpartum women with severe COVID-19’

Codes and outputs

Feb 10, 2022

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Description

This file presents the documentation of the analysis of article “COVID-19 vaccines confer protection in hospitalized pregnant and postpartum women with severe COVID-19”.

About the database and R packages used

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.

```
#load packages
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",
    "modelsummary",
    "kableExtra",
    "DescTools",
    "effectsize",
    "WeightIt",
    "MatchIt",
    "ggplot2",
    "ggpubr",
    "naniar",
    "mice",
    "miceafter",
    "VIM",
    "miceadds"
  )

lapply(packages, loadlibrary)
```

One can see below the functions that will be used in the data analysis.

```

#functions for summary measures
media <- function(x)
  mean(x, na.rm = TRUE)
mediana <- function(x)
  median(x, na.rm = TRUE)
DP <- function(x)
  sd(x, na.rm = TRUE)
minimo <- function(x)
  base::min(x, na.rm = TRUE)
maximo <- function(x)
  base::max(x, na.rm = TRUE)
q25 <- function(x)
  stats::quantile(x, p = 0.25, na.rm = TRUE)
q75 <- function(x)
  stats::quantile(x, p = 0.75, na.rm = TRUE)
IQR <- function(x)
  round(q75(x) - q25(x), 2)
n <- function(x)
  sum(!is.na(x))

```

This is a retrospective cohort study using the data from the Influenza Epidemiological Surveillance Information System, SIVEP-Gripe (Sistema de Informação de Vigilância Epidemiológica da Gripe) database.

The SIVEP-Gripe is a nationwide surveillance database created to monitor severe acute respiratory infections and data on virus circulation and respiratory infections in Brazil.

The period analyzed comprises epidemiological data from 2021, with a database obtained on December 2, 2021 on the website <https://opendatasus.saude.gov.br>. The dataset can be obtained at <https://www.kaggle.com/agatharodrigues/covid19-vaccine-maternal-population>. It is loaded below:

```

#loading the datasets
#2021
dados <- read_delim(
  "INFLUD21-29-11-2021.csv",
  ";",
  escape_double = FALSE,
  locale = locale(encoding = "ISO-8859-2"),
  trim_ws = TRUE
)

#Create case year variable
dados <- dados %>%
  dplyr::mutate(
    dt_sint = as.Date(DT_SIN_PRI, format = "%d/%m/%Y"), #date of first symptoms
    dt_nasc = as.Date(DT_NASC, format = "%d/%m/%Y"), #date of birth
    dt_vac_gripe = as.Date(DT_UT_DOSE, format = "%d/%m/%Y"), #date of Influenza vaccine
    ano = lubridate::year(dt_sint), #year of the case
  )

```

There are 1625471 observations in the database. To see the dictionary of variables, access (in Portuguese): <https://opendatasus.saude.gov.br/dataset/ae90fa8f-3e94-467e-a33f-94adbb66edf8/resource/8f571374-c555-4ec0-8e44-00b1e8b11c25/download/dicionario-de-dados-srag-hospitalizado-27.07.2020-final.pdf>

Case selection and data treatment

The first filter is to select cases from May 02, 2021 (18th epidemiological week of symptoms of 2021) to November 27, 2021 (epidemiological week 47 of 2021).

```
#selection of cases from 18th epidemiological week of symptoms (May 2, 2021)  
#to November 27, 2021 (week 43 of 2021).  
sem1 <- 18  
sem2 <- 47  
  
dados1 <- dados %>%  
  filter(SEM_PRI >= sem1 & SEM_PRI <= sem2)
```

There are 756681 observations in the database after selection of valid years.

The next selection is female:

```
#filtering F  
dados2 <- filter(dados1, CS_SEXO == "F")
```

There are 338892 observations in the database.

Selection of women of childbearing age (10 to 55 years):

```
#creating the age variable as the difference between dt_sint and dt_nasc.  
#In cases without dt_nasc, we consider  
#the NU_AGE_N field  
dados2 <- dados2 %>%  
  mutate(  
    idade = as.period(interval(start = dt_nasc, end = dt_sint))$year,  
    age = ifelse(is.na(idade), NU_IDADE_N, idade)  
  )  
  
#Filtering of cases aged 55 and under  
dados3 <- dados2 %>%  
  filter(age > 9 & age <= 55)
```

There are 141540 observations in the database.

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  
##neither pregnant nor postpartum  
dados3 <- dados3 %>%  
  mutate(  
    classi_gesta_puerp = case_when(  
      CS_GESTANT == 1 ~ "1tri",  
      CS_GESTANT == 2 ~ "2tri",  
      CS_GESTANT == 3 ~ "3tri",  
      CS_GESTANT == 4 ~ "IG_ig",  
      CS_GESTANT == 5 &  
        PUERPERA == 1 ~ "puerp",  
      CS_GESTANT == 9 & PUERPERA == 1 ~ "puerp",  
    )  
  )
```

```

      TRUE ~ "no"
    )
  )

freq(dados3$classi_gesta_puerp)

```

```

##           n      % val%
## 1tri      800  0.6  0.6
## 2tri     2110  1.5  1.5
## 3tri     4958  3.5  3.5
## IG_ig      368  0.3  0.3
## no     131497 92.9 92.9
## puerp     1807  1.3  1.3

```

```

#filtering only pregnant and postpartum women
dados4 <- dados3 %>%
  filter(classi_gesta_puerp != "no")

```

There are 10043 observations in the database.
We selected only confirmed cases of COVID-19.

```

dados4 <- dados4 %>%
  mutate(
    classi_fin = case_when(
      CLASSI_FIN == 5 ~ "covid",
      TRUE ~ "no"
    )
  )

```

```

#filtering only covid cases
dados5 <- dados4 %>%
  filter(CLASSI_FIN == 5)

```

There are 5806 observations in the database.

Now let's select the cases of COVID by PCR or antigen, but which are also not positive for Influenza.

```

#COVID case diagnosed by PCR
dados5 <- dados5 %>%
  mutate(pcr_covid_SN = case_when(
    (PCR_SARS2 == 1) |
    (
      str_detect(DS_PCR_OUT, "SARS|COVID|COV|CORONA|CIVID")
    ) ~ "yes",
    TRUE ~ "no"
  ))

#Influenza case diagnosed by PCR
dados5 <- dados5 %>%
  mutate(pcr_influenza_SN = case_when(
    (POS_PCRFLU == 1) |

```

```

      (
        str_detect(DS_PCR_OUT, "INFLU|INFLUENZA")
      ) ~ "yes",
      TRUE ~ "no"
    ))

with(dados5, table(pcr_influenza_SN, pcr_covid_SN))

```

```

##                pcr_covid_SN
## pcr_influenza_SN  no  yes
##                no  2806 2999
##                yes   1   0

```

There is no case that is positive for COVID and for Influenza by PCR.

```

#Case of COVID diagnosed by antigen
dados5 <- dados5 %>%
  mutate(antigenio_covid_SN = case_when(
    (AN_SARS2 == 1) |
    (
      str_detect(DS_AN_OUT, "SARS|COVID|COV|CORONA|CIVID")
    ) ~ "yes",
    TRUE ~ "no"
  ))

#Influenza case diagnosed by antigen
dados5 <- dados5 %>%
  mutate(antigenio_influenza_SN = case_when(
    (POS_AN_FLU == 1) |
    (
      str_detect(DS_AN_OUT, "INFLU|INFLUENZA")
    ) ~ "yes",
    TRUE ~ "no"
  ))

with(dados5, table(antigenio_influenza_SN, antigenio_covid_SN))

```

```

##                antigenio_covid_SN
## antigenio_influenza_SN  no  yes
##                no  4306 1499
##                yes    0   1

```

There is one positive case for COVID and for Influenza by antigen.

We will now select the cases of COVID confirmed by PCR or antigen.

```

with(dados5, table(pcr_covid_SN, antigenio_covid_SN))

```

```

##                antigenio_covid_SN
## pcr_covid_SN  no  yes
##                no 1518 1289
##                yes 2788  211

```

```
#filtering only covid cases by PCR or antigen
dados6 <- dados5 %>%
  filter(pcr_covid_SN == "yes" | antigenio_covid_SN == "yes")
```

There are 4288 observations in the database.

Now it's time to remove cases that are also positive for Influenza.

```
with(dados6, table(pcr_influenza_SN, antigenio_influenza_SN))
```

```
##               antigenio_influenza_SN
## pcr_influenza_SN    no    yes
##               no 4287     0
##               yes   0     1
```

```
#filtering only negative cases of Influenza by PCR or antigen
dados7 <- dados6 %>%
  filter(pcr_influenza_SN != "yes" & antigenio_influenza_SN != "yes")
```

There are 4287 observations in the database.

We will only select the finalized cases (death or cure). The variable that indicates the outcome is EVOLUCAO, with the categories: 1-Cure; 2-Death; 3- Death from other causes; 9-Ignored.

```
with(dados7, freq(EVOLUCAO))
```

```
##      n    % val%
## 1 3351 78.2 84.9
## 2  487 11.4 12.3
## 3    8  0.2  0.2
## 9  100  2.3  2.5
## NA  341  8.0  NA
```

Let's select only the finalized cases:

```
#filtering only completed cases
dados8 <- dados7 %>%
  filter((EVOLUCAO == 1 | EVOLUCAO == 2 | EVOLUCAO == 3) & !is.na(EVOLUCAO))
```

```
#creating the evolution variable
dados8 <- dados8 %>%
  mutate(death = case_when(
    EVOLUCAO == 1 ~ "cure",
    EVOLUCAO == 2 ~ "death",
    EVOLUCAO == 3 ~ "death"
  ))
```

```
with(dados8, freq(death))
```

```
##      n    % val%
## cure 3351 87.1 87.1
## death 495 12.9 12.9
```

There are 3846 observations in the database.

The variable that indicates whether the person received a vaccine against COVID-19 is `VACINA_COV`, with categories: 1=yes; 2=no; 9=ignored.

```
#Frequency table for VACINA_COV
with(dados8, freq(VACINA_COV))
```

```
##      n    % val%
## 1   650 16.9 18.7
## 2  2084 54.2 60.0
## 9   738 19.2 21.3
## NA  374  9.7  NA
```

Let's now group "NA" and "9" in the same category (NA - missing data) and label the valid categories.

```
#recoding the vaccine_cov variable
dados8 <- dados8 %>%
  mutate(vaccine_cov = case_when(
    VACINA_COV == 1 ~ "yes",
    VACINA_COV == 2 ~ "no",
    TRUE ~ NA_character_
  ))
#frequency table for vaccine_cov
with(dados8, freq(vaccine_cov))
```

```
##      n    % val%
## no  2084 54.2 76.2
## yes  650 16.9 23.8
## NA  1112 28.9  NA
```

The next step is filtering cases that we have information about COVID-19 vaccination. These data are analyzed in the following.

```
#Filtering cases with information about vaccination
data_final <- dados8 %>%
  filter(!is.na(vaccine_cov))
```

```
with(data_final, freq(vaccine_cov))
```

```
##      n    % val%
## no  2084 76.2 76.2
## yes  650 23.8 23.8
```

The variable `vaccine_cov` only indicates if the pregnant or postpartum women took the vaccine, regardless of the dose. There is no information on whether the person only took the first dose or the second. The closest we come to this is to consider the column `DOSE_2_COV`, which indicates the date of the second dose.

```
#Create second dose date variable
data_final <- data_final %>%
  dplyr::mutate(
```



```

    dt_dose2_cov = as.Date(DOSE_2_COV, format = "%d/%m/%Y")
  )

#Create variable that indicates that it has the date of the second dose
data_final <- data_final %>%
  dplyr::mutate(
    indic_dt_dose2_cov = ifelse(is.na(dt_dose2_cov) & !is.na(vaccine_cov), 0, ifelse(is.na(vaccine_cov)
  )

# first dose date frequency table
with(data_final, freq(indic_dt_dose2_cov, total = TRUE))

```

```

##          n      % val%
## 0      2534  92.7  92.7
## 1        200   7.3   7.3
## Total 2734 100.0 100.0

```

There is only information on the date of the second dose for 200 cases of 650 cases indicated as “yes” for COVID-19 vaccine.

Now we will analyze the not vaccinated group versus two dose vaccinated group.

```

#Create second dose date variable
data_final <- data_final %>%
  filter(vaccine_cov == "no" | (vaccine_cov == "yes" & indic_dt_dose2_cov == 1))

with(data_final, freq(vaccine_cov))

```

```

##          n      % val%
## no    2084  91.2  91.2
## yes     200   8.8   8.8

```

#Analysis

Epidemiologic characteristics

```

# Ethnicity
data_final <- data_final %>%
  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_
    ),
    white_color = case_when(
      ethnicity == "white" ~ "yes",
      is.na(ethnicity) ~ NA_character_,

```

```

    TRUE ~ "no"
  )
)

# Education
data_final <- data_final %>%
  mutate(
    education2 = case_when(
      CS_ESCOL_N <= 2 ~ "up to 9 years",
      CS_ESCOL_N == 3 ~ "from 9 to 12 years",
      CS_ESCOL_N == 4 ~ "over 12 years",
      TRUE ~ NA_character_
    )
  )
data_final$education2 <-
  factor(data_final$education2, levels = c("up to 9 years", "from 9 to 12 years", "over 12 years"))

# residence area
data_final <- data_final %>%
  mutate(
    residence = case_when(
      CS_ZONA == 1 ~ "urban",
      CS_ZONA == 2 ~ "rural",
      CS_ZONA == 3 ~ "periurban",
      TRUE ~ NA_character_
    )
  )

# residence area 2 (grouping the categories urban and periurban)
data_final <- data_final %>%
  mutate(
    residence2 = case_when(
      CS_ZONA == 1 ~ "urban/periurban",
      CS_ZONA == 2 ~ "rural",
      CS_ZONA == 3 ~ "urban/periurban",
      TRUE ~ NA_character_
    )
  )
data_final$residence2 <-
  factor(data_final$residence2, levels = c("rural", "urban/periurban"))

```

Ethnicity

```
with(data_final, ctable(ethnicity, vaccine_cov, prop = "c", useNA = "no", chisq = FALSE, OR = FALSE))
```

```
## Cross-Tabulation, Column Proportions
```

```
## ethnicity * vaccine_cov
```

```
## Data Frame: data_final
```

```
##
```

```
## -----
##               vaccine_cov              no              yes              Total
```

```
## ethnicity
## black 96 ( 5.1%) 6 ( 3.3%) 102 ( 4.9%)
## brown 753 ( 39.9%) 61 ( 33.3%) 814 ( 39.3%)
## indigenous 5 ( 0.3%) 4 ( 2.2%) 9 ( 0.4%)
## white 1022 ( 54.1%) 111 ( 60.7%) 1133 ( 54.7%)
## yellow 12 ( 0.6%) 1 ( 0.5%) 13 ( 0.6%)
## Total 1888 (100.0%) 183 (100.0%) 2071 (100.0%)
## -----
```

```
fisher.test(data_final$ethnicity, data_final$vaccine_cov)
```

```
##
## Fisher's Exact Test for Count Data
##
## data: data_final$ethnicity and data_final$vaccine_cov
## p-value = 0.007548
## alternative hypothesis: two.sided
```

White color

```
with(data_final, ctable(white_color, vaccine_cov, prop = "c", useNA = "no", chisq = TRUE, OR = TRUE))
```

```
## Cross-Tabulation, Column Proportions
## white_color * vaccine_cov
## Data Frame: data_final
##
## -----
## vaccine_cov      no      yes      Total
## white_color
## no      866 ( 45.9%)  72 ( 39.3%)  938 ( 45.3%)
## yes    1022 ( 54.1%) 111 ( 60.7%) 1133 ( 54.7%)
## Total  1888 (100.0%) 183 (100.0%) 2071 (100.0%)
## -----
##
## -----
## Chi.squared  df  p.value
## -----
## 2.6088      1  0.1063
## -----
##
## -----
## Odds Ratio  Lo - 95%  Hi - 95%
## -----
## 1.31        0.96     1.78
## -----
```

Education (years)

```
with(data_final, ctable(education2, vaccine_cov, prop = "c", useNA = "no", chisq = TRUE))
```

```
## Cross-Tabulation, Column Proportions
## education2 * vaccine_cov
## Data Frame: data_final
##
## -----
##               vaccine_cov              no              yes              Total
##      education2
##      up to 9 years              279 ( 26.7%)       20 ( 19.8%)       299 ( 26.1%)
##      from 9 to 12 years          573 ( 54.9%)       55 ( 54.5%)       628 ( 54.8%)
##      over 12 years              192 ( 18.4%)       26 ( 25.7%)       218 ( 19.0%)
##      Total                    1044 (100.0%)       101 (100.0%)      1145 (100.0%)
## -----
##
## -----
##      Chi.squared    df    p.value
##      -----
##      4.3072         2     0.1161
## -----
```

Age

```
datasummary((vaccine_cov) ~ age*(n+media+DP+mediana+q25+q75+IQR),
            data = data_final, output = 'markdown')
```

	n	media	DP	mediana	q25	q75	IQR
no	2084.00	29.72	7.09	30.00	25.00	35.00	10.00
yes	200.00	31.44	7.72	31.00	25.00	37.00	12.00

```
#t-test
t.test(age ~ vaccine_cov, data = data_final)
```

```
##
## Welch Two Sample t-test
##
## data: age by vaccine_cov
## t = -3.0298, df = 232.39, p-value = 0.002724
## alternative hypothesis: true difference in means between group no and group yes is not equal to 0
## 95 percent confidence interval:
## -2.8372657 -0.6012756
## sample estimates:
## mean in group no mean in group yes
##      29.72073      31.44000
```

```
#effect size
c_cohen <- cohens_d(age ~ as.factor(vaccine_cov), data=data_final)
c_cohen
```

```
## Cohen's d |          95% CI
## -----
## -0.24      | [-0.39, -0.10]
##
## - Estimated using pooled SD.
```

```
interpret_d(c_cohen$Cohens_d, rules="cohen1988")
```

```
## [1] "small"
## (Rules: cohen1988)
```

Residence area

```
with(data_final, ctable(residence, vaccine_cov, prop = "c", useNA = "no", chisq = FALSE))
```

```
## Cross-Tabulation, Column Proportions
## residence * vaccine_cov
## Data Frame: data_final
##
## -----
##          vaccine_cov          no          yes          Total
## residence
## periurban          6 ( 0.3%)          0 ( 0.0%)          6 ( 0.3%)
##      rural         113 ( 5.8%)          9 ( 4.8%)         122 ( 5.7%)
##      urban        1838 (93.9%)        179 (95.2%)       2017 (94.0%)
##      Total        1957 (100.0%)       188 (100.0%)       2145 (100.0%)
## -----
```

```
fisher.test(data_final$residence, data_final$vaccine_cov)
```

```
##
## Fisher's Exact Test for Count Data
##
## data: data_final$residence and data_final$vaccine_cov
## p-value = 0.8508
## alternative hypothesis: two.sided
```

Residence area 2 (grouping the categories urban and periurban)

```
with(data_final, ctable(residence2, vaccine_cov, prop = "c", useNA = "no", chisq = TRUE, OR = TRUE))
```

```
## Cross-Tabulation, Column Proportions
## residence2 * vaccine_cov
```

```
## Data Frame: data_final
##
##
## -----
##          vaccine_cov          no          yes          Total
## residence2
##      rural          113 ( 5.8%)          9 ( 4.8%)          122 ( 5.7%)
## urban/periurban          1844 ( 94.2%)          179 ( 95.2%)          2023 ( 94.3%)
##      Total          1957 (100.0%)          188 (100.0%)          2145 (100.0%)
## -----
##
## -----
## Chi.squared   df   p.value
## -----
##      0.1546      1   0.6941
## -----
##
## -----
## Odds Ratio   Lo - 95%   Hi - 95%
## -----
##      1.22      0.61      2.44
## -----
```

Comorbidities

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

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

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

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

#Diabetes
data_final <- data_final %>%
  mutate(diabetes = case_when(DIABETES == 1 ~ "yes",
```

```

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

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

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

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

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

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

```

Cardiac

```
with(data_final, ctable(vaccine_cov, cardiac, prop = "r", useNA = "no", chisq = TRUE, OR = TRUE))
```

```
## Cross-Tabulation, Row Proportions
```

```
## vaccine_cov * cardiac
```

```
## Data Frame: data_final
```

```
##
```

```
##
```

```
## -----
```

	cardiac	no	yes	Total
vaccine_cov				
no	738 (87.6%)	104 (12.4%)	842 (100.0%)	
yes	71 (76.3%)	22 (23.7%)	93 (100.0%)	
Total	809 (86.5%)	126 (13.5%)	935 (100.0%)	

```
## -----
```

```
##
```

```
##
```

```
## -----
```

```
## Chi.squared  df  p.value
## -----
##      8.2348    1  0.0041
## -----
##
## -----
## Odds Ratio   Lo - 95%   Hi - 95%
## -----
##      2.20      1.31      3.70
## -----
```

Hematologic

```
with(data_final, ctable(vaccine_cov, hematologic, prop = "r", useNA = "no", chisq = FALSE, OR = TRUE))
```

```
## Cross-Tabulation, Row Proportions
## vaccine_cov * hematologic
## Data Frame: data_final
##
## -----
##           hematologic           no           yes           Total
## vaccine_cov
##           no           807 (99.1%)    7 (0.9%)    814 (100.0%)
##           yes           87 (97.8%)    2 (2.2%)    89 (100.0%)
##           Total        894 (99.0%)    9 (1.0%)    903 (100.0%)
## -----
##
## -----
## Odds Ratio   Lo - 95%   Hi - 95%
## -----
##      2.65      0.54      12.96
## -----
```

```
fisher.test(data_final$hematologic, data_final$vaccine_cov)
```

```
##
## Fisher's Exact Test for Count Data
##
## data: data_final$hematologic and data_final$vaccine_cov
## p-value = 0.2198
## alternative hypothesis: true odds ratio is not equal to 1
## 95 percent confidence interval:
##  0.2642886 14.1850125
## sample estimates:
## odds ratio
##  2.646116
```


Diabetes

```
ctable(data_final$vaccine_cov, data_final$diabetes, chisq=TRUE, prop="r", useNA = "no", OR = TRUE)
```

```
## Cross-Tabulation, Row Proportions
## vaccine_cov * diabetes
## Data Frame: data_final
##
## -----
##          diabetes          no          yes          Total
## vaccine_cov
##          no          708 (83.1%)    144 (16.9%)    852 (100.0%)
##          yes          73 (77.7%)     21 (22.3%)     94 (100.0%)
##          Total        781 (82.6%)    165 (17.4%)    946 (100.0%)
## -----
##
## -----
## Chi.squared  df    p.value
## -----
##          1.382      1    0.2398
## -----
##
## -----
## Odds Ratio   Lo - 95%   Hi - 95%
## -----
##          1.41         0.84     2.37
## -----
```

Obesity

```
ctable(data_final$vaccine_cov, data_final$obesity, chisq=TRUE, prop="r", useNA = "no", OR = TRUE)
```

```
## Cross-Tabulation, Row Proportions
## vaccine_cov * obesity
## Data Frame: data_final
##
## -----
##          obesity          no          yes          Total
## vaccine_cov
##          no          680 (78.1%)    191 (21.9%)    871 (100.0%)
##          yes          76 (84.4%)     14 (15.6%)     90 (100.0%)
##          Total        756 (78.7%)    205 (21.3%)    961 (100.0%)
## -----
##
## -----
## Chi.squared  df    p.value
## -----
##          1.6129      1    0.2041
```

```
## -----
##
## -----
## Odds Ratio    Lo - 95%    Hi - 95%
## -----
##      0.66      0.36      1.19
## -----
```

Asthma

```
ctable(data_final$vaccine_cov, data_final$asthma, chisq=TRUE, prop="r", useNA = "no", OR = TRUE)
```

```
## Cross-Tabulation, Row Proportions
## vaccine_cov * asthma
## Data Frame: data_final
##
## -----
##          asthma          no          yes          Total
## vaccine_cov
##      no          767 (92.2%)    65 ( 7.8%)    832 (100.0%)
##      yes          81 (90.0%)     9 (10.0%)    90 (100.0%)
##      Total        848 (92.0%)    74 ( 8.0%)    922 (100.0%)
## -----
##
## -----
## Chi.squared    df    p.value
## -----
##      0.2718      1    0.6021
## -----
##
## -----
## Odds Ratio    Lo - 95%    Hi - 95%
## -----
##      1.31      0.63      2.73
## -----
```

Hepatic

```
ctable(data_final$vaccine_cov, data_final$hepatic, chisq=FALSE, prop="r", useNA = "no", OR = TRUE)
```

```
## Cross-Tabulation, Row Proportions
## vaccine_cov * hepatic
## Data Frame: data_final
##
## -----
##          hepatic          no          yes          Total
## vaccine_cov
```

```
##           no           807 ( 99.6%)   3 (0.4%)   810 (100.0%)
##           yes           88 ( 98.9%)   1 (1.1%)    89 (100.0%)
##          Total          895 ( 99.6%)   4 (0.4%)   899 (100.0%)
## -----
##
## -----
## Odds Ratio   Lo - 95%   Hi - 95%
## -----
##      3.06      0.31     29.70
## -----
```

```
fisher.test(data_final$vaccine_cov, data_final$hepatic)
```

```
##
## Fisher's Exact Test for Count Data
##
## data: data_final$vaccine_cov and data_final$hepatic
## p-value = 0.3415
## alternative hypothesis: true odds ratio is not equal to 1
## 95 percent confidence interval:
##  0.05758056 38.46642499
## sample estimates:
## odds ratio
##  3.050859
```

Neurologic

```
ctable(data_final$vaccine_cov, data_final$neurologic, chisq=FALSE, prop="r", useNA = "no", OR = TRUE)
```

```
## Cross-Tabulation, Row Proportions
## vaccine_cov * neurologic
## Data Frame: data_final
##
## -----
##           neurologic           no           yes           Total
## vaccine_cov
##      no           802 (98.9%)    9 (1.1%)    811 (100.0%)
##      yes           86 (97.7%)    2 (2.3%)    88 (100.0%)
##      Total          888 (98.8%)   11 (1.2%)   899 (100.0%)
## -----
##
## -----
## Odds Ratio   Lo - 95%   Hi - 95%
## -----
##      2.07      0.44     9.75
## -----
```

```
fisher.test(data_final$vaccine_cov, data_final$neurologic)
```

```
##
## Fisher's Exact Test for Count Data
##
## data: data_final$vaccine_cov and data_final$neurologic
## p-value = 0.2936
## alternative hypothesis: true odds ratio is not equal to 1
## 95 percent confidence interval:
## 0.2143274 10.2318114
## sample estimates:
## odds ratio
## 2.070139
```

Pneumologic

```
ctable(data_final$vaccine_cov, data_final$pneumologic, chisq=FALSE, prop="r", useNA = "no", OR = TRUE)
```

```
## Cross-Tabulation, Row Proportions
## vaccine_cov * pneumologic
## Data Frame: data_final
##
## -----
##      pneumologic      no      yes      Total
## vaccine_cov
##      no      805 (98.9%)      9 (1.1%)      814 (100.0%)
##      yes      86 (96.6%)      3 (3.4%)      89 (100.0%)
##      Total      891 (98.7%)      12 (1.3%)      903 (100.0%)
## -----
##
## -----
## Odds Ratio  Lo - 95%  Hi - 95%
## -----
##      3.12      0.83      11.74
## -----
```

```
fisher.test(data_final$vaccine_cov, data_final$pneumologic)
```

```
##
## Fisher's Exact Test for Count Data
##
## data: data_final$vaccine_cov and data_final$pneumologic
## p-value = 0.1059
## alternative hypothesis: true odds ratio is not equal to 1
## 95 percent confidence interval:
## 0.5323484 12.7897697
## sample estimates:
## odds ratio
## 3.114462
```

Imunossupression

```
ctable(data_final$vaccine_cov, data_final$imuno, chisq=FALSE, prop="r", useNA = "no", OR = TRUE)
```

```
## Cross-Tabulation, Row Proportions
## vaccine_cov * imuno
## Data Frame: data_final
##
## -----
##           imuno          no          yes          Total
## vaccine_cov
##           no          801 (98.6%)    11 (1.4%)    812 (100.0%)
##           yes          84 (94.4%)     5 (5.6%)     89 (100.0%)
##           Total        885 (98.2%)    16 (1.8%)    901 (100.0%)
## -----
##
## -----
## Odds Ratio   Lo - 95%   Hi - 95%
## -----
##           4.33         1.47        12.77
## -----
```

```
fisher.test(data_final$imuno, data_final$vaccine_cov)
```

```
##
## Fisher's Exact Test for Count Data
##
## data: data_final$imuno and data_final$vaccine_cov
## p-value = 0.01526
## alternative hypothesis: true odds ratio is not equal to 1
## 95 percent confidence interval:
##  1.149292 13.896222
## sample estimates:
## odds ratio
##  4.32279
```

Renal

```
ctable(data_final$vaccine_cov, data_final$renal, chisq=FALSE, prop="r", useNA = "no", OR = TRUE)
```

```
## Cross-Tabulation, Row Proportions
## vaccine_cov * renal
## Data Frame: data_final
##
## -----
##           renal          no          yes          Total
## vaccine_cov
```

```
##           no           797 (98.9%)    9 (1.1%)    806 (100.0%)
##           yes           87 (97.8%)    2 (2.2%)    89 (100.0%)
##          Total          884 (98.8%)   11 (1.2%)   895 (100.0%)
## -----
##
## -----
## Odds Ratio    Lo - 95%    Hi - 95%
## -----
##      2.04         0.43      9.57
## -----
```

```
fisher.test(data_final$renal, data_final$vaccine_cov)
```

```
##
## Fisher's Exact Test for Count Data
##
## data: data_final$renal and data_final$vaccine_cov
## p-value = 0.3002
## alternative hypothesis: true odds ratio is not equal to 1
## 95 percent confidence interval:
##  0.21058 10.04877
## sample estimates:
## odds ratio
##  2.033657
```

Symptoms

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

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

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

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

```

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

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

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

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

# Abdominal pain
data_final <- data_final %>%
  mutate(abd_pain = case_when(DOR_ABD == 1 ~ "yes",
                                DOR_ABD == 2 ~ "no",
                                TRUE ~ NA_character_))

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

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

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

# Any respiratory symptom
df <- data_final %>%
  select(dyspnea, fatigue, desaturation, resp_disc)

soma <- function(x){

```

```

if (sum(is.na(x))==4)
  return(NA_character_)
else
  return(sum(!is.na(x) & x=="yes"))
}
data_final$qt_sintomas_resp_aux <- apply(df,1,soma)

data_final <- data_final %>%
  mutate(resp_symp = case_when(qt_sintomas_resp_aux >=1 ~ "yes",
                                qt_sintomas_resp_aux ==0 ~ "no",
                                TRUE ~ NA_character_))

# Any symptom
df <- data_final %>%
  select(dyspnea,fatigue,desaturation,resp_disc,
         fever,cough,sore_throat,diarrhea,vomit,abd_pain,olfac_loss,loss_taste)
soma <- function(x){
  if (sum(is.na(x))==12)
    return(NA_character_)
  else
    return(sum(!is.na(x) & x=="yes"))
}
data_final$qt_sintomas_aux <- apply(df,1,soma)

data_final <- data_final %>%
  mutate(symptom = case_when(qt_sintomas_aux >= 1 ~ "yes",
                              qt_sintomas_aux == 0 ~ "no",
                              TRUE ~ NA_character_))

```

Fever

```
with(data_final, ctable(vaccine_cov, fever, prop = "r", useNA = "no", chisq = TRUE, OR=TRUE))
```

```
## Cross-Tabulation, Row Proportions
## vaccine_cov * fever
## Data Frame: data_final
##
##
## -----
##          fever          no          yes          Total
## vaccine_cov
##          no      783 (42.1%)  1077 (57.9%)  1860 (100.0%)
##          yes       94 (53.4%)    82 (46.6%)   176 (100.0%)
##          Total    877 (43.1%)  1159 (56.9%)  2036 (100.0%)
## -----
##
## -----
## Chi.squared  df  p.value
## -----
##      7.9362    1  0.0048
## -----
##
```



```
## -----
## Odds Ratio   Lo - 95%   Hi - 95%
## -----
##      0.63      0.47      0.86
## -----
```

Cough

```
with(data_final, ctable(vaccine_cov, cough, prop = "r", useNA = "no", chisq = TRUE, OR=TRUE))
```

```
## Cross-Tabulation, Row Proportions
## vaccine_cov * cough
## Data Frame: data_final
##
## -----
##      vaccine_cov      cough      no      yes      Total
##      no      406 (20.9%)  1532 (79.1%)  1938 (100.0%)
##      yes      45 (24.7%)   137 (75.3%)   182 (100.0%)
##      Total    451 (21.3%)  1669 (78.7%)  2120 (100.0%)
## -----
##
## -----
##      Chi.squared   df   p.value
## -----
##      1.1998        1   0.2734
## -----
##
## -----
##      Odds Ratio   Lo - 95%   Hi - 95%
## -----
##      0.81         0.57       1.15
## -----
```

Sore throat

```
with(data_final, ctable(vaccine_cov, sore_throat, prop = "r", useNA = "no", chisq = TRUE, OR=TRUE))
```

```
## Cross-Tabulation, Row Proportions
## vaccine_cov * sore_throat
## Data Frame: data_final
##
## -----
##      vaccine_cov      sore_throat      no      yes      Total
##      no      1263 (73.9%)  447 (26.1%)  1710 (100.0%)
##      yes      126 (79.2%)   33 (20.8%)   159 (100.0%)
```

```
##           Total           1389 (74.3%)   480 (25.7%)   1869 (100.0%)
## -----
##
## -----
## Chi.squared   df   p.value
## -----
##      1.9375      1   0.1639
## -----
##
## -----
## Odds Ratio   Lo - 95%   Hi - 95%
## -----
##      0.74      0.50      1.10
## -----
```

Dyspnea

```
with(data_final, ctable(vaccine_cov, dyspnea, prop = "r", useNA = "no", chisq = TRUE, OR=TRUE))
```

```
## Cross-Tabulation, Row Proportions
## vaccine_cov * dyspnea
## Data Frame: data_final
##
## -----
##           dyspnea           no           yes           Total
## vaccine_cov
##      no           565 (29.5%)   1349 (70.5%)   1914 (100.0%)
##      yes           76 (43.9%)    97 (56.1%)    173 (100.0%)
##      Total         641 (30.7%)   1446 (69.3%)   2087 (100.0%)
## -----
##
## -----
## Chi.squared   df   p.value
## -----
##      14.8145      1   1e-04
## -----
##
## -----
## Odds Ratio   Lo - 95%   Hi - 95%
## -----
##      0.53      0.39      0.73
## -----
```

Respiratory discomfort

```
with(data_final, ctable(vaccine_cov, resp_disc, prop = "r", useNA = "no", chisq = TRUE, OR=TRUE))
```

```
## Cross-Tabulation, Row Proportions
```

```
## vaccine_cov * resp_disc
## Data Frame: data_final
##
##
## -----
##           resp_disc           no           yes           Total
## vaccine_cov
##           no           792 (43.5%)   1028 (56.5%)   1820 (100.0%)
##           yes           95 (55.2%)    77 (44.8%)    172 (100.0%)
##           Total        887 (44.5%)   1105 (55.5%)   1992 (100.0%)
## -----
##
## -----
## Chi.squared  df    p.value
## -----
##      8.2652    1      0.004
## -----
##
## -----
## Odds Ratio   Lo - 95%   Hi - 95%
## -----
##      0.62      0.46      0.86
## -----
```

Desaturation

```
with(data_final, ctable(vaccine_cov, desaturation, prop = "r", useNA = "no", chisq = TRUE, OR=TRUE))
```

```
## Cross-Tabulation, Row Proportions
## vaccine_cov * desaturation
## Data Frame: data_final
##
##
## -----
##           desaturation           no           yes           Total
## vaccine_cov
##           no           815 (44.3%)   1025 (55.7%)   1840 (100.0%)
##           yes           103 (59.9%)    69 (40.1%)    172 (100.0%)
##           Total        918 (45.6%)   1094 (54.4%)   2012 (100.0%)
## -----
##
## -----
## Chi.squared  df    p.value
## -----
##     14.7886    1      1e-04
## -----
##
## -----
## Odds Ratio   Lo - 95%   Hi - 95%
## -----
##      0.53      0.39      0.73
## -----
```

Diarrhea

```
with(data_final, ctable(vaccine_cov, diarrhea, prop = "r", useNA = "no", chisq = TRUE, OR=TRUE))
```

```
## Cross-Tabulation, Row Proportions
## vaccine_cov * diarrhea
## Data Frame: data_final
##
## -----
##      vaccine_cov      diarrhea      no      yes      Total
##      no      1488 (88.7%)      189 (11.3%)      1677 (100.0%)
##      yes      143 (89.9%)      16 (10.1%)      159 (100.0%)
##      Total      1631 (88.8%)      205 (11.2%)      1836 (100.0%)
## -----
##
## -----
##      Chi.squared      df      p.value
## -----
##      0.109      1      0.7412
## -----
##
## -----
##      Odds Ratio      Lo - 95%      Hi - 95%
## -----
##      0.88      0.51      1.51
## -----
```

Vomit

```
with(data_final, ctable(vaccine_cov, vomit, prop = "r", useNA = "no", chisq = TRUE, OR=TRUE))
```

```
## Cross-Tabulation, Row Proportions
## vaccine_cov * vomit
## Data Frame: data_final
##
## -----
##      vaccine_cov      vomit      no      yes      Total
##      no      1480 (88.0%)      202 (12.0%)      1682 (100.0%)
##      yes      143 (89.9%)      16 (10.1%)      159 (100.0%)
##      Total      1623 (88.2%)      218 (11.8%)      1841 (100.0%)
## -----
##
## -----
##      Chi.squared      df      p.value
## -----
##      0.3573      1      0.55
```

```
## -----
##
## -----
## Odds Ratio    Lo - 95%    Hi - 95%
## -----
##      0.82      0.48      1.40
## -----
```

Abdominal pain

```
with(data_final, ctable(vaccine_cov, abd_pain, prop = "r", useNA = "no", chisq = TRUE, OR=TRUE))
```

```
## Cross-Tabulation, Row Proportions
## vaccine_cov * abd_pain
## Data Frame: data_final
##
##
## -----
##      vaccine_cov    abd_pain      no      yes      Total
##      no      1494 (90.1%)    164 ( 9.9%)    1658 (100.0%)
##      yes      138 (88.5%)     18 (11.5%)     156 (100.0%)
##      Total    1632 (90.0%)    182 (10.0%)    1814 (100.0%)
## -----
##
## -----
##      Chi.squared    df    p.value
## -----
##      0.2655        1    0.6064
## -----
##
## -----
##      Odds Ratio    Lo - 95%    Hi - 95%
## -----
##      1.19          0.71        1.99
## -----
```

Fatigue

```
with(data_final, ctable(vaccine_cov, fatigue, prop = "r", useNA = "no", chisq = TRUE, OR=TRUE))
```

```
## Cross-Tabulation, Row Proportions
## vaccine_cov * fatigue
## Data Frame: data_final
##
##
## -----
##      vaccine_cov    fatigue      no      yes      Total
## -----
```

```
##           no           1147 (66.0%)   590 (34.0%)   1737 (100.0%)
##           yes           110 (67.5%)    53 (32.5%)    163 (100.0%)
##          Total          1257 (66.2%)   643 (33.8%)   1900 (100.0%)
## -----
##
## -----
##  Chi.squared   df   p.value
## -----
##    0.0829      1   0.7735
## -----
##
## -----
##  Odds Ratio   Lo - 95%   Hi - 95%
## -----
##    0.94       0.67      1.32
## -----
```

Olfactory loss

```
with(data_final, ctable(vaccine_cov, olfac_loss, prop = "r", useNA = "no", chisq = TRUE, OR=TRUE))
```

```
## Cross-Tabulation, Row Proportions
## vaccine_cov * olfac_loss
## Data Frame: data_final
##
## -----
##           olfac_loss           no           yes           Total
##  vaccine_cov
##           no           1372 (81.6%)   310 (18.4%)   1682 (100.0%)
##           yes           127 (79.4%)    33 (20.6%)    160 (100.0%)
##          Total          1499 (81.4%)   343 (18.6%)   1842 (100.0%)
## -----
##
## -----
##  Chi.squared   df   p.value
## -----
##    0.3308      1   0.5652
## -----
##
## -----
##  Odds Ratio   Lo - 95%   Hi - 95%
## -----
##    1.15       0.77      1.72
## -----
```

Loss of taste

```
with(data_final, ctable(vaccine_cov, loss_taste, prop = "r", useNA = "no", chisq = TRUE, OR=TRUE))
```

```
## Cross-Tabulation, Row Proportions
## vaccine_cov * loss_taste
## Data Frame: data_final
##
##
## -----
##           loss_taste           no           yes           Total
## vaccine_cov
##           no           1403 (83.2%)    284 (16.8%)    1687 (100.0%)
##           yes           129 (81.1%)     30 (18.9%)     159 (100.0%)
##           Total        1532 (83.0%)    314 (17.0%)    1846 (100.0%)
## -----
##
## -----
## Chi.squared  df    p.value
## -----
##      0.2937    1    0.5879
## -----
##
## -----
## Odds Ratio   Lo - 95%   Hi - 95%
## -----
##      1.15      0.76      1.74
## -----
```

Any respiratory symptom

```
with(data_final, ctable(vaccine_cov, resp_symp, prop = "r", useNA = "no", chisq = TRUE, OR=TRUE))
```

```
## Cross-Tabulation, Row Proportions
## vaccine_cov * resp_symp
## Data Frame: data_final
##
##
## -----
##           resp_symp           no           yes           Total
## vaccine_cov
##           no           361 (18.2%)    1618 (81.8%)    1979 (100.0%)
##           yes           56 (30.6%)     127 (69.4%)     183 (100.0%)
##           Total        417 (19.3%)    1745 (80.7%)    2162 (100.0%)
## -----
##
## -----
## Chi.squared  df    p.value
## -----
##     15.6528    1    1e-04
## -----
##
## -----
## Odds Ratio   Lo - 95%   Hi - 95%
## -----
##      0.51      0.36      0.71
## -----
```

```
## -----
```

Any symptom

```
with(data_final, ctable(vaccine_cov, symptom, prop = "r", useNA = "no", chisq = TRUE, OR=TRUE))
```

```
## Cross-Tabulation, Row Proportions
```

```
## vaccine_cov * symptom
```

```
## Data Frame: data_final
```

```
##
```

```
##
```

```
## -----  
##          symptom          no          yes          Total  
## vaccine_cov  
##      no          78 (3.8%)    1980 (96.2%)    2058 (100.0%)  
##      yes          16 (8.2%)    178 (91.8%)     194 (100.0%)  
##      Total         94 (4.2%)    2158 (95.8%)    2252 (100.0%)  
## -----
```

```
##
```

```
## -----  
## Chi.squared  df  p.value  
## -----
```

```
##      7.727      1    0.0054  
## -----
```

```
##
```

```
## -----  
## Odds Ratio  Lo - 95%  Hi - 95%  
## -----
```

```
##      0.44      0.25      0.77  
## -----
```

```
##
```

Outcome

```
# ICU
```

```
data_final <- data_final %>%
```

```
  mutate(icu = case_when(UTI == 1 ~ "yes",  
                          UTI == 2 ~ "no",  
                          TRUE ~ NA_character_))
```

```
# Length time in ICU
```

```
data_final<- data_final%>%
```

```
  mutate(dt_enticu = as.Date(DT_ENTUTI, format = "%d/%m/%Y"),  
         dt_exicu = as.Date(DT_SAIDUTI, format = "%d/%m/%Y"),  
         time_icu = as.numeric(dt_exicu - dt_enticu)
```

```
)
```

```
# ventilatory support
```

```
data_final <- data_final %>%
```

```
  mutate(ventilatory_support = case_when(SUPPORT_VEN == 1 ~ "invasive",
```



```

      SUPPORT_VEN == 2 ~ "non-invasive",
      SUPPORT_VEN == 3 ~ "no",
      TRUE ~ NA_character_)

# Intubation
data_final <- data_final %>%
  mutate(intubation = case_when(SUPPORT_VEN == 1 ~ "yes",
                                SUPPORT_VEN == 2 | SUPPORT_VEN == 3 ~ "no",
                                TRUE ~ NA_character_))

```

ICU

```
with(data_final, ctable(vaccine_cov, icu, prop = "r", useNA = "no", chisq = TRUE, OR=TRUE))
```

```

## Cross-Tabulation, Row Proportions
## vaccine_cov * icu
## Data Frame: data_final
##
##
## -----
##           icu           no           yes           Total
## vaccine_cov
##           no       1239 (62.6%)       740 (37.4%)       1979 (100.0%)
##           yes        143 (76.5%)         44 (23.5%)        187 (100.0%)
##           Total     1382 (63.8%)       784 (36.2%)       2166 (100.0%)
## -----
##
## -----
## Chi.squared   df   p.value
## -----
##      13.6244    1    2e-04
## -----
##
## -----
## Odds Ratio   Lo - 95%   Hi - 95%
## -----
##           0.52         0.36         0.73
## -----

```

Length time in ICU

```

data_final_aux <- data_final %>%
  filter (icu == "yes")

```

```

datasummary((vaccine_cov) ~ time_icu*(n+media+DP+mediana+q25+q75+IQR),
  data = data_final_aux, output = 'markdown')

```

	n	media	DP	mediana	q25	q75	IQR
no	548.00	13.09	12.22	10.00	5.00	18.00	13.00
yes	21.00	9.38	9.30	5.00	3.00	13.00	10.00

```
#t-test
t.test(time_icu ~ vaccine_cov, data = data_final_aux)

##
## Welch Two Sample t-test
##
## data: time_icu by vaccine_cov
## t = 1.7692, df = 22.727, p-value = 0.09028
## alternative hypothesis: true difference in means between group no and group yes is not equal to 0
## 95 percent confidence interval:
## -0.6305326 8.0474599
## sample estimates:
## mean in group no mean in group yes
## 13.089416 9.380952
```

Ventilatory support

```
with(data_final, ctable(vaccine_cov, ventilatory_support, prop = "r", useNA = "no", chisq = TRUE, OR=TRUE))

## Cross-Tabulation, Row Proportions
## vaccine_cov * ventilatory_support
## Data Frame: data_final
##
##
## -----
##      vaccine_cov      ventilatory_support      invasive      no      non-invasive      Total
##      no      368 (18.8%)      711 (36.3%)      880 (44.9%)      1959 (100.0%)
##      yes      9 ( 4.8%)      99 (52.4%)      81 (42.9%)      189 (100.0%)
##      Total      377 (17.6%)      810 (37.7%)      961 (44.7%)      2148 (100.0%)
## -----
##
## -----
##      Chi.squared      df      p.value
## -----
##      31.3063      2      0
## -----
```

Intubation

```
with(data_final, ctable(vaccine_cov, intubation, prop = "r", useNA = "no", chisq = TRUE, OR=TRUE))

## Cross-Tabulation, Row Proportions
```

```
## vaccine_cov * intubation
## Data Frame: data_final
##
##
## -----
##           intubation           no           yes           Total
## vaccine_cov
##           no           1591 (81.2%)   368 (18.8%)   1959 (100.0%)
##           yes           180 (95.2%)    9 ( 4.8%)    189 (100.0%)
##           Total        1771 (82.4%)   377 (17.6%)   2148 (100.0%)
## -----
##
## -----
## Chi.squared  df  p.value
## -----
##      22.4651   1      0
## -----
##
## -----
## Odds Ratio   Lo - 95%   Hi - 95%
## -----
##      0.22      0.11      0.43
## -----
```

Death

```
with(data_final, ctable(vaccine_cov, death, prop = "r", useNA = "no", chisq = TRUE, OR=TRUE))
```

```
## Cross-Tabulation, Row Proportions
## vaccine_cov * death
## Data Frame: data_final
##
##
## -----
##           death           cure           death           Total
## vaccine_cov
##           no           1790 (85.9%)   294 (14.1%)   2084 (100.0%)
##           yes           194 (97.0%)    6 ( 3.0%)    200 (100.0%)
##           Total        1984 (86.9%)   300 (13.1%)   2284 (100.0%)
## -----
##
## -----
## Chi.squared  df  p.value
## -----
##      18.7715   1      0
## -----
##
## -----
## Odds Ratio   Lo - 95%   Hi - 95%
## -----
##      0.188      0.083      0.428
## -----
```

Propensity Scoring Method (PSM) - information about date of second dose

```
data_final <- data_final %>%
  mutate(vaccine1 = ifelse(vaccine_cov == "yes", 1, 0),
         id = 1:dim(data_final)[1])

data_final1 <- data_final %>%
  select(id, vaccine1, age, cardiac)

data_final1 <- data_final1 %>%
  mutate(
    cardiac1 = ifelse(is.na(cardiac) == TRUE, "na", cardiac)
  )

#PSM
psm1 <- matchit(vaccine1 ~ age + cardiac1, data = data_final1, method = "nearest", ratio = 1)

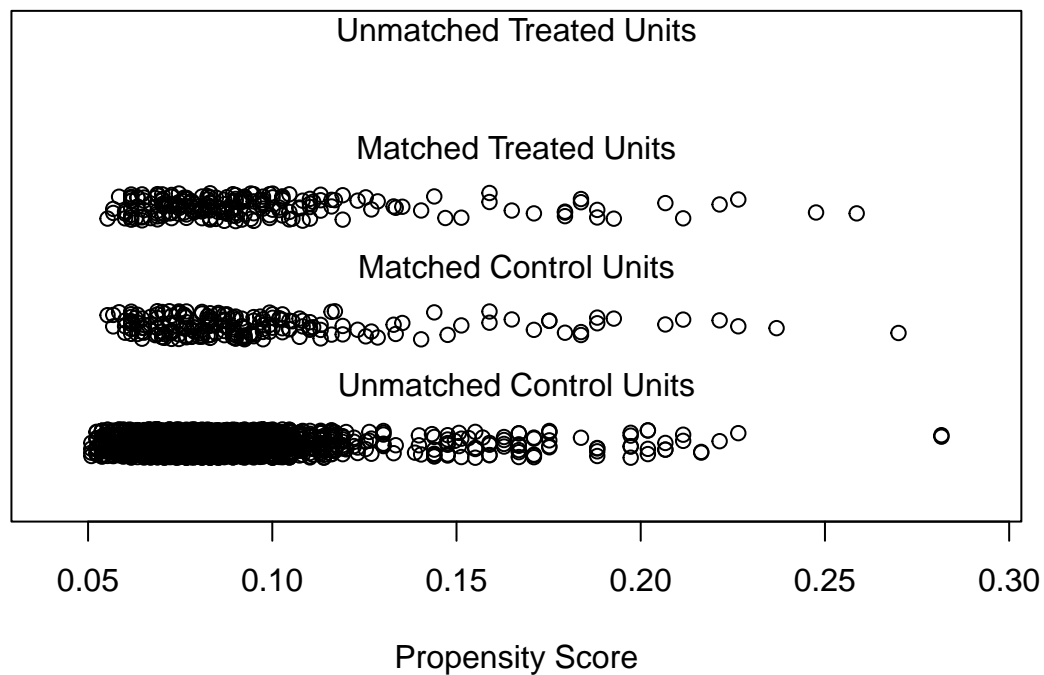
summary(psm1)
```

```
##
## Call:
## matchit(formula = vaccine1 ~ age + cardiac1, data = data_final1,
##         method = "nearest", ratio = 1)
##
## Summary of Balance for All Data:
##           Means Treated Means Control Std. Mean Diff. Var. Ratio eCDF Mean
## distance           0.0965          0.0867           0.2648    1.9872  0.0595
## age                31.4400          29.7207           0.2227    1.1850  0.0409
## cardiac1na          0.5350          0.5960          -0.1222         .  0.0610
## cardiac1no          0.3550          0.3541           0.0018         .  0.0009
## cardiac1yes         0.1100          0.0499           0.1921         .  0.0601
##           eCDF Max
## distance           0.1179
## age                0.1056
## cardiac1na          0.0610
## cardiac1no          0.0009
## cardiac1yes         0.0601
##
##
## Summary of Balance for Matched Data:
##           Means Treated Means Control Std. Mean Diff. Var. Ratio eCDF Mean
## distance           0.0965          0.0965           0.0010    1.0023  0.0002
## age                31.4400          31.2950           0.0188    1.0431  0.0035
## cardiac1na          0.5350          0.5300           0.0100         .  0.0050
## cardiac1no          0.3550          0.3550           0.0000         .  0.0000
## cardiac1yes         0.1100          0.1150          -0.0160         .  0.0050
##           eCDF Max Std. Pair Dist.
## distance           0.010          0.0042
## age                0.015          0.0214
## cardiac1na          0.005          0.0100
## cardiac1no          0.000          0.0000
```

```
## cardiac1yes    0.005      0.0160
##
## Percent Balance Improvement:
##           Std. Mean Diff. Var. Ratio eCDF Mean eCDF Max
## distance           99.6      99.7      99.6      91.5
## age                91.6      75.2      91.6      85.8
## cardiac1na         91.8          .      91.8      91.8
## cardiac1no        100.0          .     100.0     100.0
## cardiac1yes        91.7          .      91.7      91.7
##
## Sample Sizes:
##           Control Treated
## All           2084      200
## Matched        200      200
## Unmatched     1884         0
## Discarded         0         0
```

```
plot(psm1, type = "jitter", interactive = FALSE)
```

Distribution of Propensity Scores



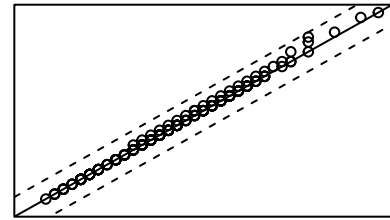
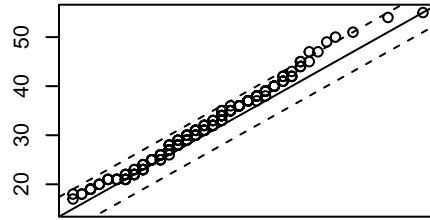
```
plot(psm1, type = "qq", interactive = FALSE,
      which.xs = c("age", "cardiac1"))
```

eQQ Plots

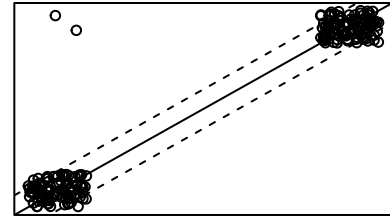
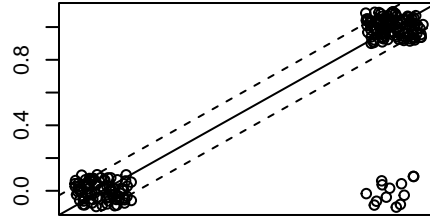
All

Matched

age

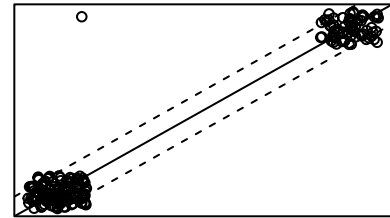
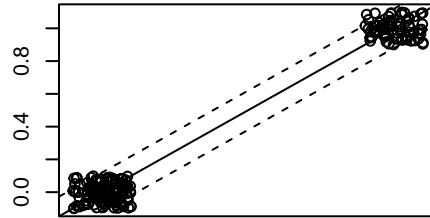


cardiac1na

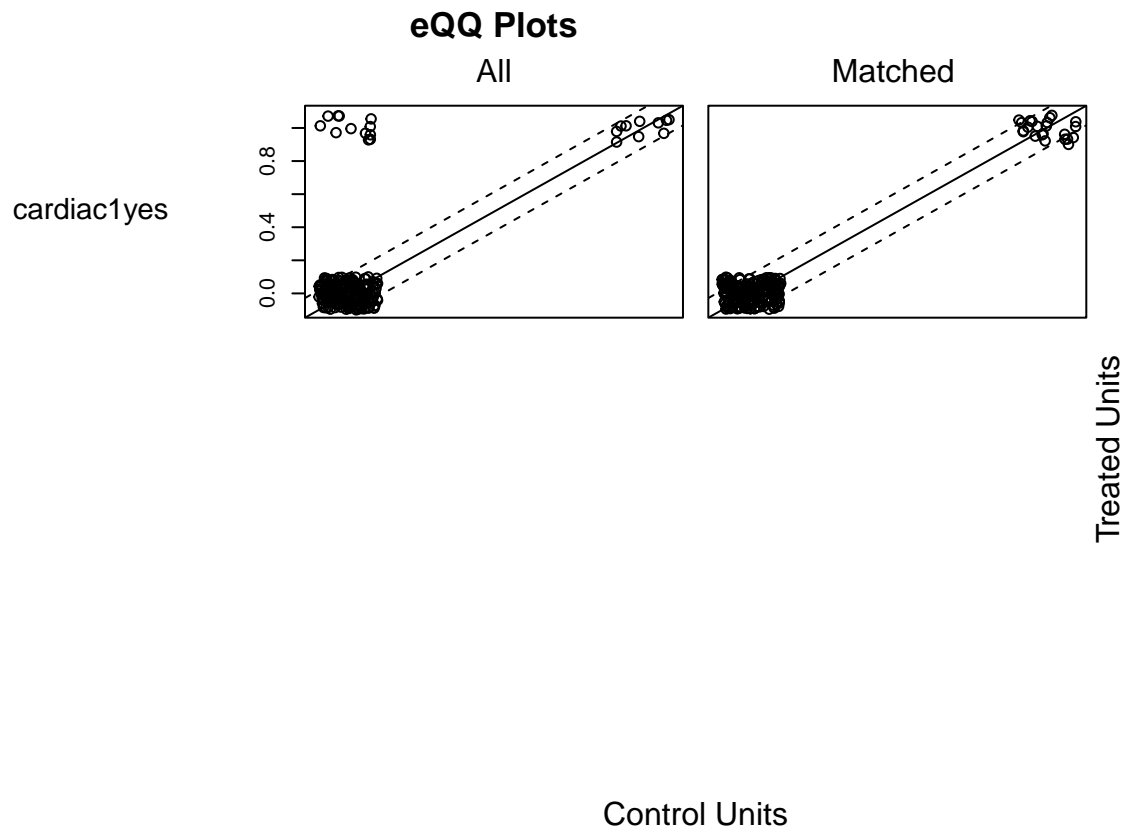


Treated Units

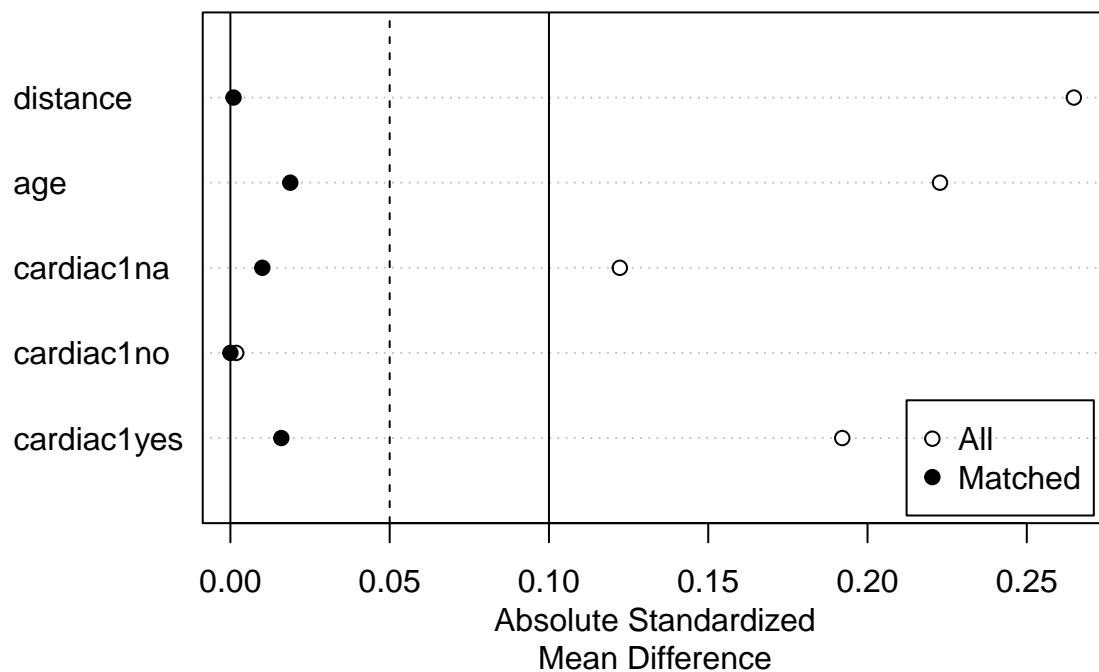
cardiac1no



Control Units



```
plot(summary(psm1))
```



```
#Selecting only the selected observations
data_aux <- data_final1[psm1$weights==1, ]

#Now let's join data_aux with data_final

data_psm <- right_join(data_final, data_aux, by= c("id", "vaccine1", "age", "cardiac"))
freq(data_psm$vaccine_cov)
```

```
##      n  % val%
## no  200 50   50
## yes 200 50   50
```

For outcomes

ICU

```
with(data_psm, ctable(vaccine_cov, icu, prop = "r", useNA = "no", chisq = TRUE, OR=TRUE))

## Cross-Tabulation, Row Proportions
## vaccine_cov * icu
## Data Frame: data_psm
##
```



```
##
## -----
##           icu           no           yes           Total
## vaccine_cov
##           no           121 (63.7%)    69 (36.3%)    190 (100.0%)
##           yes           143 (76.5%)    44 (23.5%)    187 (100.0%)
##           Total        264 (70.0%)    113 (30.0%)    377 (100.0%)
## -----
##
## -----
## Chi.squared   df   p.value
## -----
##      6.7444      1   0.0094
## -----
##
## -----
## Odds Ratio   Lo - 95%   Hi - 95%
## -----
##      0.54      0.34      0.85
## -----
```

Length time in ICU

```
data_psm_aux <- data_psm %>%
  filter (icu == "yes")
```

```
datasummary((vaccine_cov) ~ time_icu*(n+media+DP+mediana+q25+q75+IQR),
  data = data_psm_aux, output = 'markdown')
```

	n	media	DP	mediana	q25	q75	IQR
no	57.00	14.09	11.67	12.00	5.00	18.00	13.00
yes	21.00	9.38	9.30	5.00	3.00	13.00	10.00

```
#teste t
t.test(time_icu ~ vaccine_cov, data = data_psm_aux)
```

```
##
## Welch Two Sample t-test
##
## data: time_icu by vaccine_cov
## t = 1.8447, df = 44.556, p-value = 0.07173
## alternative hypothesis: true difference in means between group no and group yes is not equal to 0
## 95 percent confidence interval:
## -0.4335558 9.8470897
## sample estimates:
## mean in group no mean in group yes
##      14.087719      9.380952
```

Ventilatory support

```
with(data_psm, ctable(vaccine_cov, ventilatory_support, prop = "r", useNA = "no", chisq = TRUE, OR=TRUE))
```

```
## Cross-Tabulation, Row Proportions
## vaccine_cov * ventilatory_support
## Data Frame: data_psm
##
## -----
##      ventilatory_support      invasive      no      non-invasive      Total
## vaccine_cov
##      no      39 (20.6%)      68 (36.0%)      82 (43.4%)      189 (100.0%)
##      yes      9 ( 4.8%)      99 (52.4%)      81 (42.9%)      189 (100.0%)
##      Total      48 (12.7%)      167 (44.2%)      163 (43.1%)      378 (100.0%)
## -----
##
## -----
##      Chi.squared      df      p.value
## -----
##      24.5106      2      0
## -----
```

Intubation

```
with(data_psm, ctable(vaccine_cov, intubation, prop = "r", useNA = "no", chisq = TRUE, OR=TRUE))
```

```
## Cross-Tabulation, Row Proportions
## vaccine_cov * intubation
## Data Frame: data_psm
##
## -----
##      intubation      no      yes      Total
## vaccine_cov
##      no      150 (79.4%)      39 (20.6%)      189 (100.0%)
##      yes      180 (95.2%)      9 ( 4.8%)      189 (100.0%)
##      Total      330 (87.3%)      48 (12.7%)      378 (100.0%)
## -----
##
## -----
##      Chi.squared      df      p.value
## -----
##      20.0693      1      0
## -----
##
## -----
##      Odds Ratio      Lo - 95%      Hi - 95%
## -----
##      0.19      0.09      0.41
## -----
```

Death

```
with(data_psm, ctable(vaccine_cov, death, prop = "r", useNA = "no", chisq = TRUE, OR=TRUE))
```

```
## Cross-Tabulation, Row Proportions
## vaccine_cov * death
## Data Frame: data_psm
##
## -----
##      vaccine_cov      death      cure      death      Total
##      no      174 (87.0%)    26 (13.0%)    200 (100.0%)
##      yes      194 (97.0%)     6 ( 3.0%)    200 (100.0%)
##      Total    368 (92.0%)    32 ( 8.0%)    400 (100.0%)
## -----
##
## -----
##      Chi.squared    df    p.value
## -----
##      12.2622        1      5e-04
## -----
##
## -----
##      Odds Ratio    Lo - 95%    Hi - 95%
## -----
##      0.207          0.083        0.515
## -----
```

Multivariate Imputation by Chained Equations (MICE)

A total of 2284 patients were analyzed and divided into two groups, according to their COVID-19 vaccination status: unvaccinated (n = 2084; 91.2%) and vaccinated (n = 200; 8.8%) groups. With respect to this dataset, to deal with possible nonresponse bias, we explore the missing values and we conduct a multiple imputation.

```
data_na <- data_final %>%
  select(
    vaccine_cov,
    age,
    white_color,
    cardiac,
    diabetes,
    hematologic,
    obesity,
    asthma,
    hepatic,
    neurologic,
    pneumologic,
    imuno,
    renal,
    education2,
```

```

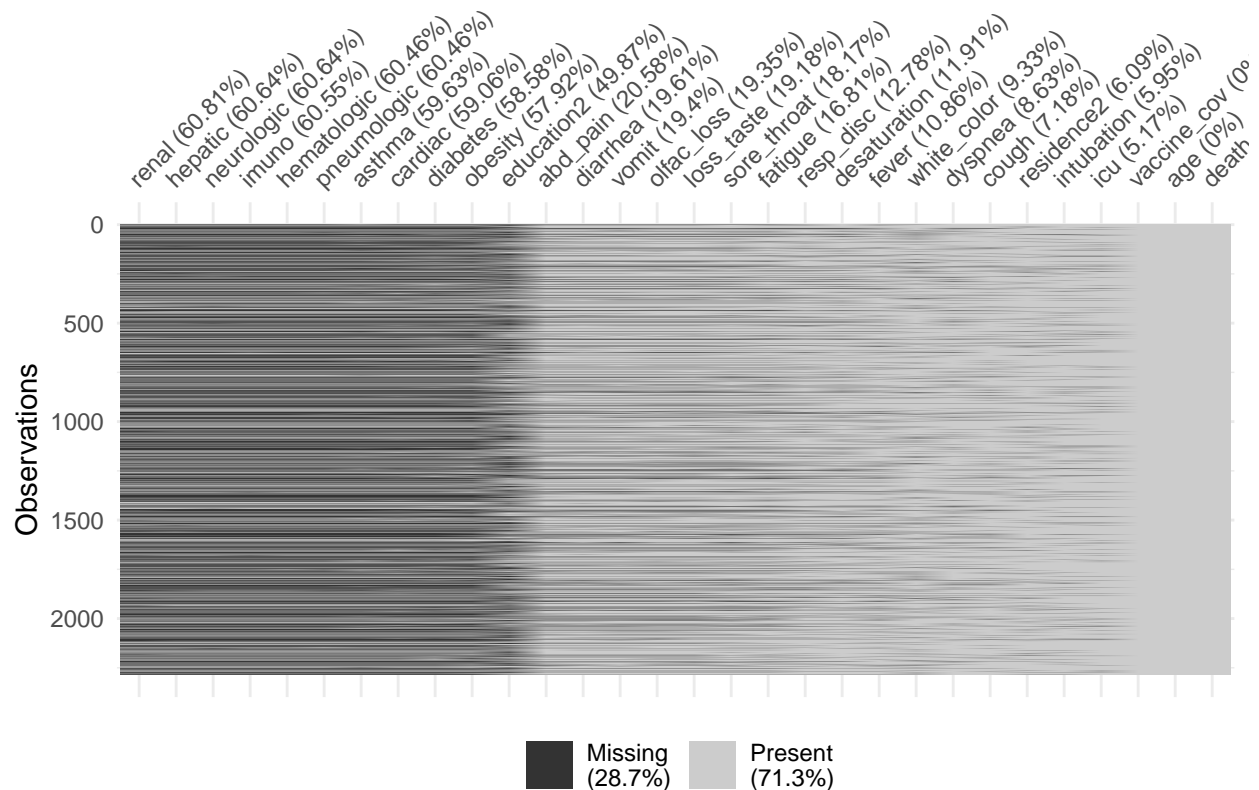
    residence2,
    fever,
    cough,
    sore_throat,
    dyspnea,
    resp_disc,
    desaturation,
    diarrhea,
    vomit,
    abd_pain,
    fatigue,
    olfac_loss,
    loss_taste,
    icu,
    intubation,
    death
  )

data_na$vaccine_cov <- as.factor(data_na$vaccine_cov)
data_na$white_color <- as.factor(data_na$white_color)
data_na$cardiac <- as.factor(data_na$cardiac)
data_na$diabetes <- as.factor(data_na$diabetes)
data_na$hematologic <- as.factor(data_na$hematologic)
data_na$obesity <- as.factor(data_na$obesity)
data_na$asthma <- as.factor(data_na$asthma)
data_na$hepatic <- as.factor(data_na$hepatic)
data_na$neurologic <- as.factor(data_na$neurologic)
data_na$pneumologic <- as.factor(data_na$pneumologic)
data_na$imuno <- as.factor(data_na$imuno)
data_na$renal <- as.factor(data_na$renal)
data_na$residence2 <- as.factor(data_na$residence2)
data_na$fever <- as.factor(data_na$fever)
data_na$cough <- as.factor(data_na$cough)
data_na$sore_throat <- as.factor(data_na$sore_throat)
data_na$dyspnea <- as.factor(data_na$dyspnea)
data_na$resp_disc <- as.factor(data_na$resp_disc)
data_na$desaturation <- as.factor(data_na$desaturation)
data_na$diarrhea <- as.factor(data_na$diarrhea)
data_na$vomit <- as.factor(data_na$vomit)
data_na$abd_pain <- as.factor(data_na$abd_pain)
data_na$fatigue <- as.factor(data_na$fatigue)
data_na$olfac_loss <- as.factor(data_na$olfac_loss)
data_na$loss_taste <- as.factor(data_na$loss_taste)
data_na$icu <- as.factor(data_na$icu)
data_na$intubation <- as.factor(data_na$intubation)
data_na$death <- as.factor(data_na$death)

print(dfSummary(data_na, varnumbers = FALSE), method = "render")

```

Note that all comorbidities variables and the education variable have high proportions of missing data. The percentage of valid responses is, at least, of 79,4% for variables related to the symptoms.



To deal with missing data, we consider a multiple imputation by fully conditional specification. The mice package implements this method, where each incomplete variable is imputed by a separate model. According to the previously analysis, the most of the variables with missing data are binary. The variables “hematologic”, “hepatic”, “neurologic”, “pneumologic”, “renal” and “imuno” present categories extremely unbalanced, with approximately 60% missing data each one. For this reason and to avoid problems of bias and efficiency, these variables will not be considered in the process of multiple imputation. The “residence” variable was recategorized in two levels, urban/periurban and rural because the periurban level has only 6 observations. We considered as a imputation method for dichotomous variable the logistic regression (logreg), except when the percentage of missing values for the variable is greater than 50%. In this situation, we consider a bootstrapped logistic regression model (logreg.boot). For education variable, we considered a proportional odds model (polr). Following, because of high percentage of missing data on some variables, we present 100 imputed datasets e the trace plots to investigate the convergence of the method.

```
cols.dont.want <- c("hematologic", "hepatic", "neurologic", "pneumologic", "renal", "imuno")
data_na2 <- data_na[, ! names(data_na) %in% cols.dont.want, drop = F]

mice.impute.logreg <- function (y, ry, x, wy = NULL, ...)
{
  if (is.null(wy))
    wy <- !ry
  aug <- augment(y, ry, x, wy)
  x <- aug$x
  y <- aug$y
  ry <- aug$ry
  wy <- aug$wy
  w <- aug$w
}
```

```

x <- cbind(1, as.matrix(x))
expr <- expression(glm.fit(x = x[ry, , drop = FALSE], y = y[ry],
                           family = binomial(link = logit), weights = w[ry], maxit = 150))

fit <- eval(expr)
fit.sum <- summary.glm(fit)
beta <- coef(fit)
rv <- t(chol(sym(fit.sum$cov.unscaled)))
beta.star <- beta + rv %*% rnorm(ncol(rv))
p <- 1/(1 + exp(-(x[wy, , drop = FALSE] %*% beta.star)))
vec <- (runif(nrow(p)) <= p)
vec[vec] <- 1
if (is.factor(y)) {
  vec <- factor(vec, c(0, 1), levels(y))
}
vec
}

imputed_Data <- mice(data_na2, m=100, maxit = 60, method = c("", "", "logreg", rep("logreg.boot", 4), "logreg",
rep("logreg", 16)), printFlag = FALSE, seed = 300)

summary(imputed_Data)

```

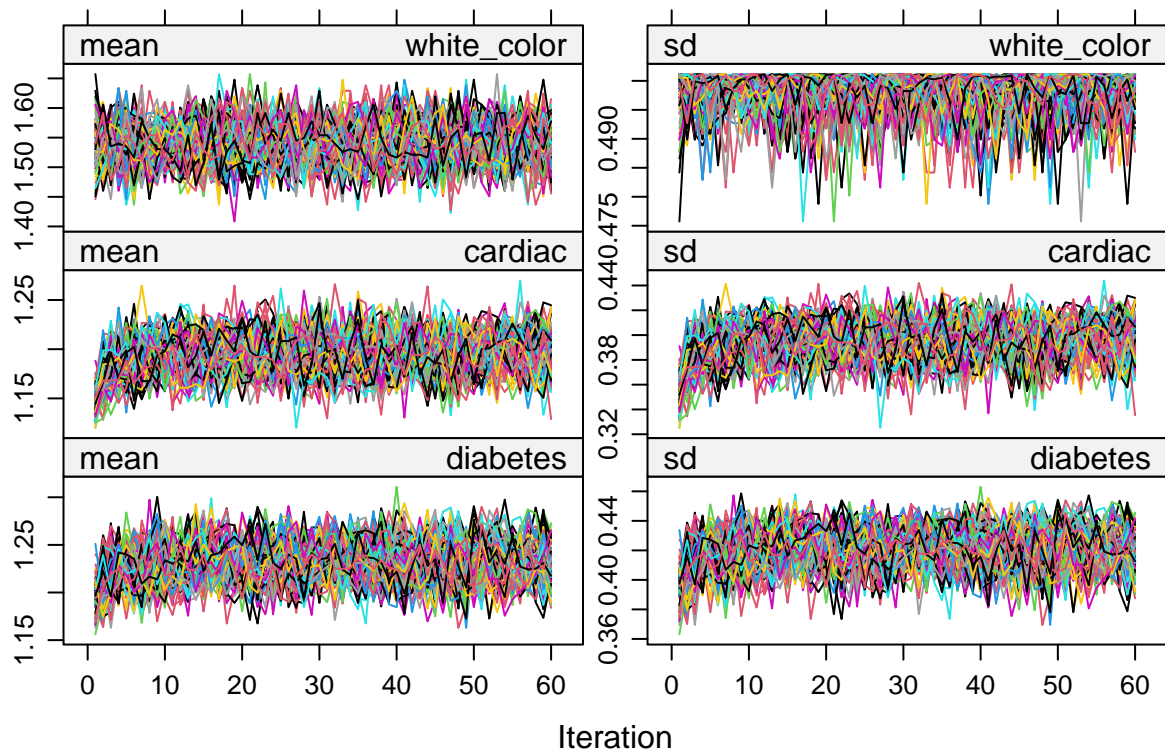
```

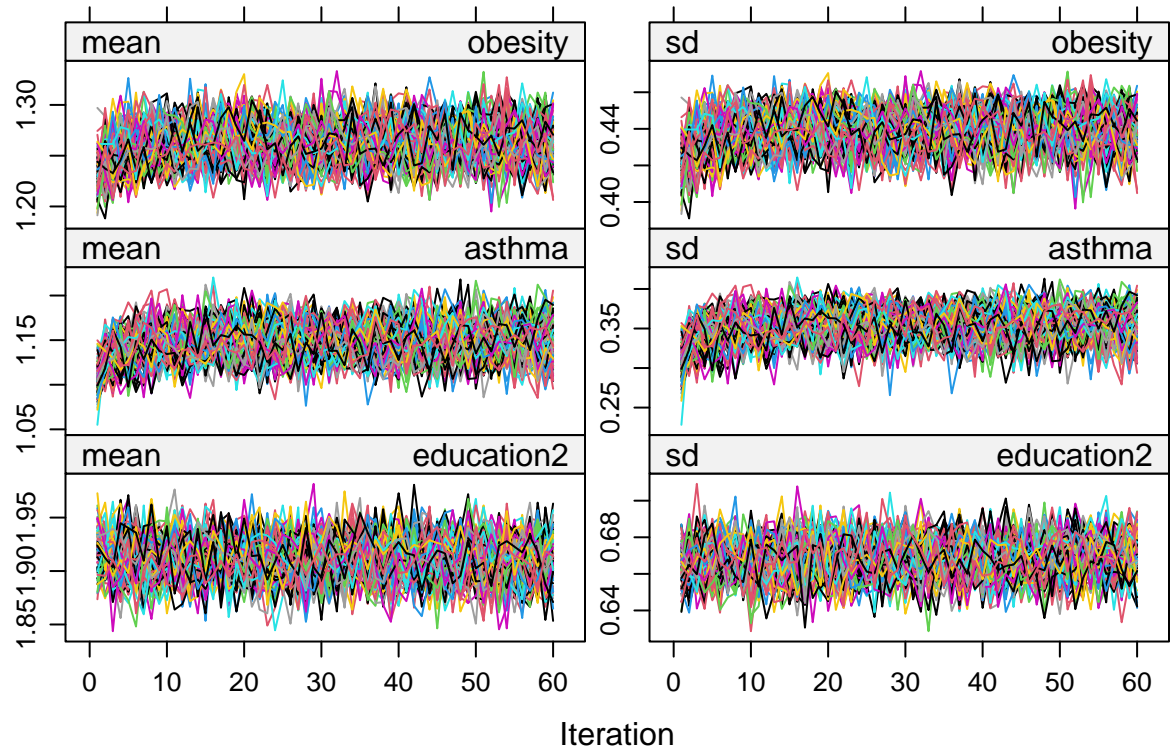
## Class: mids
## Number of multiple imputations: 100
## Imputation methods:
##   vaccine_cov      age  white_color      cardiac      diabetes
##   ""              ""    "logreg" "logreg.boot" "logreg.boot"
##   obesity          asthma  education2    residence2      fever
## "logreg.boot" "logreg.boot"  "polyreg"    "logreg"      "logreg"
##   cough      sore_throat    dyspnea      resp_disc  desaturation
##   "logreg"    "logreg"      "logreg"    "logreg"      "logreg"
##   diarrhea    vomit      abd_pain      fatigue      olfac_loss
##   "logreg"    "logreg"    "logreg"    "logreg"      "logreg"
##   loss_taste      icu      intubation      death
##   "logreg"    "logreg"    "logreg"      ""
## PredictorMatrix:
##   vaccine_cov age white_color cardiac diabetes obesity asthma
## vaccine_cov      0  1          1      1      1      1      1
## age              1  0          1      1      1      1      1
## white_color      1  1          0      1      1      1      1
## cardiac          1  1          1      0      1      1      1
## diabetes         1  1          1      1      0      1      1
## obesity          1  1          1      1      1      0      1
##   education2 residence2 fever cough sore_throat dyspnea resp_disc
## vaccine_cov      1      1      1      1      1      1      1
## age              1      1      1      1      1      1      1
## white_color      1      1      1      1      1      1      1
## cardiac          1      1      1      1      1      1      1
## diabetes         1      1      1      1      1      1      1
## obesity          1      1      1      1      1      1      1
##   desaturation diarrhea vomit abd_pain fatigue olfac_loss loss_taste
## vaccine_cov      1      1      1      1      1      1      1
## age              1      1      1      1      1      1      1

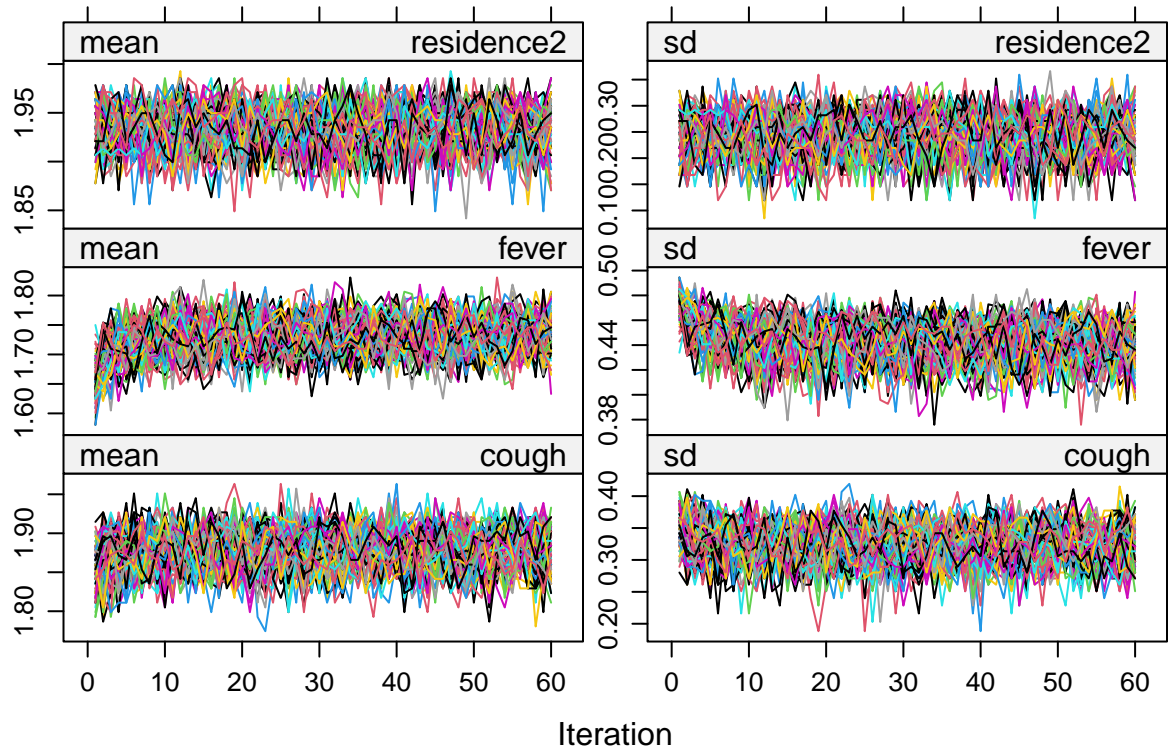
```

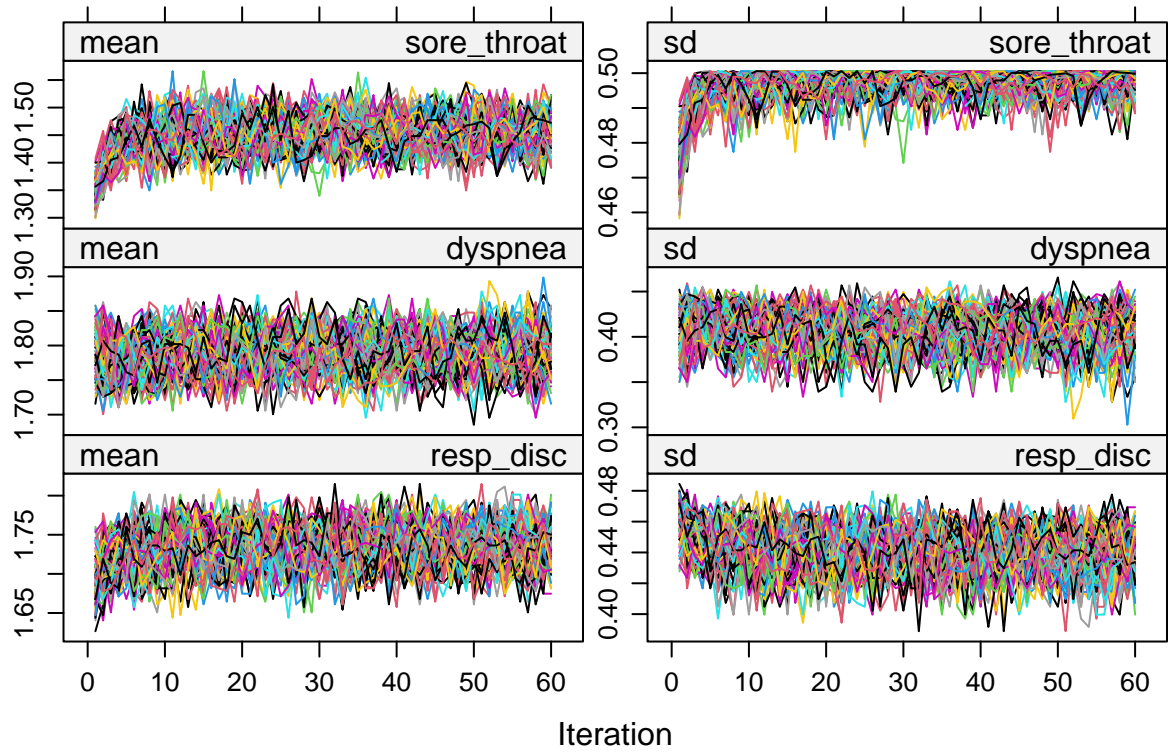
```
## white_color      1      1      1      1      1      1      1
## cardiac          1      1      1      1      1      1      1
## diabetes         1      1      1      1      1      1      1
## obesity          1      1      1      1      1      1      1
##               icu intubation death
## vaccine_cov     1          1      1
## age             1          1      1
## white_color     1          1      1
## cardiac         1          1      1
## diabetes        1          1      1
## obesity         1          1      1
```

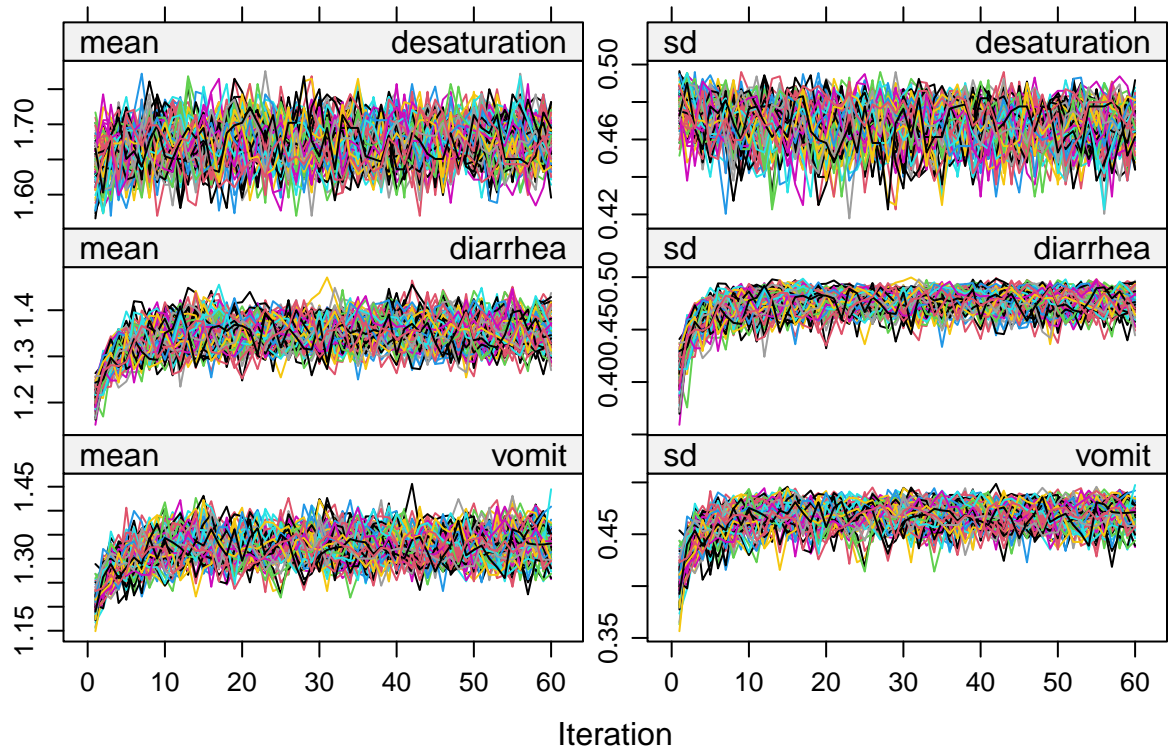
```
plot(imputed_Data)
```

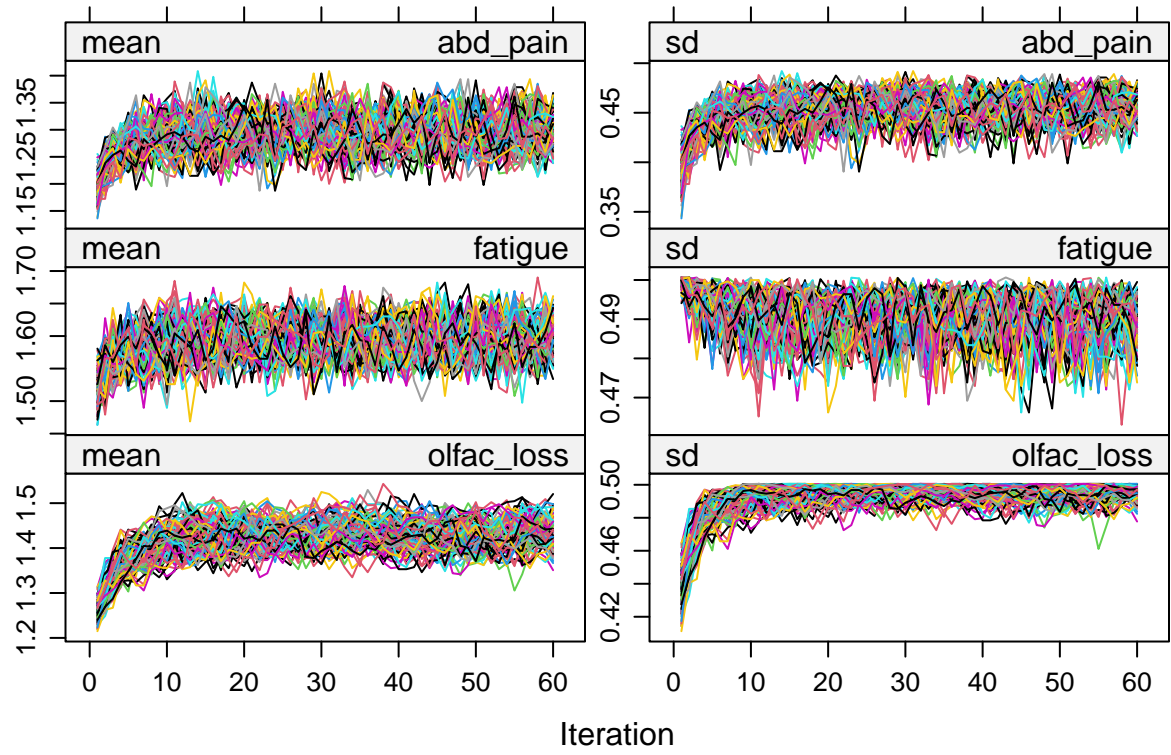


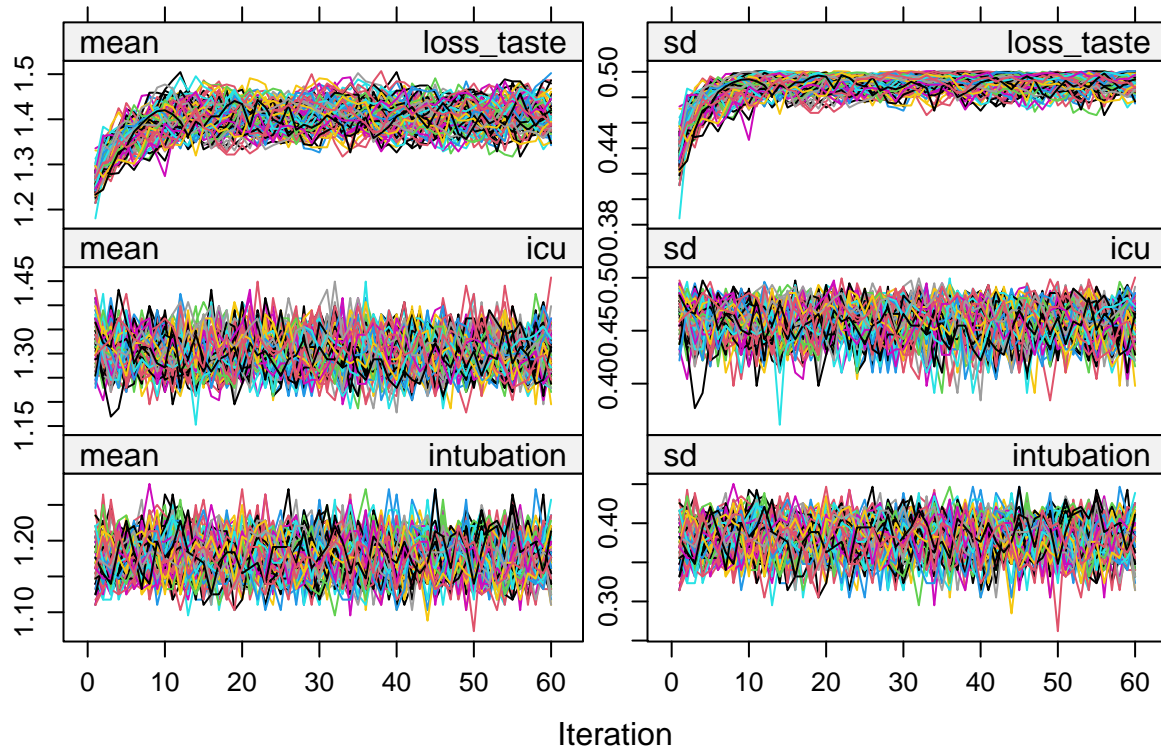












```
dat_imp <- mids2milst(imputed_Data)
```

Each one of these 100 imputed datasets were analysed using the function `with()`, and including an expression for the statistical analysis approach. Procedures to pool Chi-square values are available in the `miceadds` package. To combine the 100 odds ratios, we use the `miceafter` package.

Baseline characteristics of the subjects according to vaccination status

White color

```
fit_w <- with(dat_imp, exp = chisq.test(vaccine_cov, white_color))
Stat_w <- numeric()
for (i in 1:imputed_Data$m) Stat_w[i] <- fit_w$statistics[[i]]$statistic
micombine.chisquare(Stat_w, 1, display = TRUE, version=1)
```

```
## Combination of Chi Square Statistics for Multiply Imputed Data
## Using 100 Imputed Data Sets
## F(1, 18484.24)=3.054      p=0.08054
```

Cardiac

```
fit_c <- with(dat_imp, exp = chisq.test(vaccine_cov, cardiac))
Stat_c <- numeric()
for (i in 1:imputed_Data$m) Stat_c[i] <- fit_c$statistics[[i]]$statistic
micombine.chisquare(Stat_c, 1, display = TRUE, version=1)
```

```
## Combination of Chi Square Statistics for Multiply Imputed Data
## Using 100 Imputed Data Sets
## F(1, 270.94)=4.983      p=0.02642
```

Diabetes

```
fit_d <- with(dat_imp, exp = chisq.test(vaccine_cov, diabetes))
Stat_d <- numeric()
for (i in 1:imputed_Data$m) Stat_d[i] <- fit_d$statistics[[i]]$statistic
micombine.chisquare(Stat_d, 1, display = TRUE, version=1)
```

```
## Combination of Chi Square Statistics for Multiply Imputed Data
## Using 100 Imputed Data Sets
## F(1, 394.63)=0.892      p=0.34539
```

Obesity

```
fit_o <- with(dat_imp, exp = chisq.test(vaccine_cov, obesity))
Stat_o <- numeric()
for (i in 1:imputed_Data$m) Stat_o[i] <- fit_o$statistics[[i]]$statistic
micombine.chisquare(Stat_o, 1, display = TRUE, version=1)
```

```
## Combination of Chi Square Statistics for Multiply Imputed Data
## Using 100 Imputed Data Sets
## F(1, 439.29)=1.475      p=0.22518
```

Asthma

```
fit_a <- with(dat_imp, exp = chisq.test(vaccine_cov, asthma))
Stat_a <- numeric()
for (i in 1:imputed_Data$m) Stat_a[i] <- fit_a$statistics[[i]]$statistic
micombine.chisquare(Stat_a, 1, display = TRUE, version=1)
```

```
## Combination of Chi Square Statistics for Multiply Imputed Data
## Using 100 Imputed Data Sets
## F(1, 273.82)=1.085      p=0.29841
```

Education

```
fit_e <- with(dat_imp, exp = chisq.test(vaccine_cov, education2))
Stat_e <- numeric()
for (i in 1:imputed_Data$m) Stat_e[i] <- fit_e$statistics[[i]]$statistic
micombine.chisquare(Stat_e, 2, display = TRUE, version=1)
```

```
## Combination of Chi Square Statistics for Multiply Imputed Data
## Using 100 Imputed Data Sets
## F(2, 755.7)=2.461      p=0.08601
```

Residence area 2 (grouping the categories urban and periurban)

```
fit_res <- with(dat_imp, exp = chisq.test(vaccine_cov, residence2))
Stat_res <- numeric()
for (i in 1:imputed_Data$m) Stat_res[i] <- fit_res$statistics[[i]]$statistic
micombine.chisquare(Stat_res, 2, display = TRUE, version=1)
```

```
## Combination of Chi Square Statistics for Multiply Imputed Data
## Using 100 Imputed Data Sets
## F(2, 44650.47)=0.07    p=0.93195
```

Characteristics of COVID-19 symptoms by vaccination status

Fever

```
pool_odds_ratio(with(dat_imp, expr=odds_ratio(vaccine_cov ~ fever)))
```

```
##      pooled OR 95 CI low 95 CI high
## [1,] 0.6434665 0.4735422 0.8743657
## attr(,"class")
## [1] "mipool"
```

Cough

```
pool_odds_ratio(with(dat_imp, expr=odds_ratio(vaccine_cov ~ cough)))
```

```
##      pooled OR 95 CI low 95 CI high
## [1,] 0.8208345 0.5776051 1.166488
## attr(,"class")
## [1] "mipool"
```

Sore throat


```
pool_odds_ratio(with(dat_imp, expr=odds_ratio(vaccine_cov ~ sore_throat)))
```

```
##      pooled OR 95 CI low 95 CI high  
## [1,] 0.7729552 0.5312457  1.124639  
## attr(,"class")  
## [1] "mipool"
```

Dyspnea

```
pool_odds_ratio(with(dat_imp, expr=odds_ratio(vaccine_cov ~ dyspnea)))
```

```
##      pooled OR 95 CI low 95 CI high  
## [1,] 0.562676 0.412656 0.7672355  
## attr(,"class")  
## [1] "mipool"
```

Respiratory discomfort

```
pool_odds_ratio(with(dat_imp, expr=odds_ratio(vaccine_cov ~ resp_disc)))
```

```
##      pooled OR 95 CI low 95 CI high  
## [1,] 0.6371953 0.4682167 0.867158  
## attr(,"class")  
## [1] "mipool"
```

Desaturation

```
pool_odds_ratio(with(dat_imp, expr=odds_ratio(vaccine_cov ~ desaturation)))
```

```
##      pooled OR 95 CI low 95 CI high  
## [1,] 0.5412815 0.3945068 0.7426633  
## attr(,"class")  
## [1] "mipool"
```

Diarrhea

```
pool_odds_ratio(with(dat_imp, expr=odds_ratio(vaccine_cov ~ diarrhea)))
```

```
##      pooled OR 95 CI low 95 CI high  
## [1,] 0.9370858 0.5794052 1.515571  
## attr(,"class")  
## [1] "mipool"
```


Vomit

```
pool_odds_ratio(with(dat_imp, expr=odds_ratio(vaccine_cov ~ vomit)))
```

```
##      pooled OR 95 CI low 95 CI high
## [1,] 0.8352794 0.5083313  1.372514
## attr(,"class")
## [1] "mipool"
```

Abdominal pain

```
pool_odds_ratio(with(dat_imp, expr=odds_ratio(vaccine_cov ~ abd_pain)))
```

```
##      pooled OR 95 CI low 95 CI high
## [1,]  1.169572 0.7296263  1.874794
## attr(,"class")
## [1] "mipool"
```

Fatigue

```
pool_odds_ratio(with(dat_imp, expr=odds_ratio(vaccine_cov ~ fatigue)))
```

```
##      pooled OR 95 CI low 95 CI high
## [1,] 0.9631591 0.6867503  1.350819
## attr(,"class")
## [1] "mipool"
```

Loss of smell

```
pool_odds_ratio(with(dat_imp, expr=odds_ratio(vaccine_cov ~ olfac_loss)))
```

```
##      pooled OR 95 CI low 95 CI high
## [1,]  1.137034 0.7773557  1.663132
## attr(,"class")
## [1] "mipool"
```

Loss of taste

```
pool_odds_ratio(with(dat_imp, expr=odds_ratio(vaccine_cov ~ loss_taste)))
```

```
##      pooled OR 95 CI low 95 CI high
## [1,]  1.181084 0.8003242  1.742992
## attr(,"class")
## [1] "mipool"
```

Any respiratory symptom

```
for (i in 1:imputed_Data$m){
df <- dat_imp[[i]] %>%
  select(dyspnea,fatigue,desaturation,resp_disc)

soma <- function(x){
  if (sum(is.na(x))==4)
    return(NA_character_)
  else
    return(sum(!is.na(x) & x=="yes"))
}
dat_imp[[i]]$qt_sintomas_resp_aux <- apply(df,1,soma)

dat_imp[[i]] <- dat_imp[[i]] %>%
  mutate(resp_symp = case_when(qt_sintomas_resp_aux >=1 ~ "yes",
                               qt_sintomas_resp_aux ==0 ~ "no",
                               TRUE ~ NA_character_))
}

pool_odds_ratio(with(dat_imp, expr=odds_ratio(vaccine_cov ~ resp_symp)))

##      pooled OR 95 CI low 95 CI high
## [1,] 0.5210252 0.3724448 0.7288791
## attr(,"class")
## [1] "mipool"
```

Any symptom

```
for (i in 1:imputed_Data$m){
df <- dat_imp[[i]] %>%
  select(dyspnea,fatigue,desaturation,resp_disc,
         fever,cough,sore_throat,diarrhea,vomit,abd_pain,olfac_loss,loss_taste)
soma <- function(x){
  if (sum(is.na(x))==12)
    return(NA_character_)
  else
    return(sum(!is.na(x) & x=="yes"))
}
dat_imp[[i]]$qt_sintomas_aux <- apply(df,1,soma)

dat_imp[[i]] <- dat_imp[[i]] %>%
  mutate(symptom = case_when(qt_sintomas_aux >= 1 ~ "yes",
                             qt_sintomas_aux == 0 ~ "no",
                             TRUE ~ NA_character_))
}

pool_odds_ratio(with(dat_imp, expr=odds_ratio(vaccine_cov ~ symptom)))

##      pooled OR 95 CI low 95 CI high
```

```
## [1,] 0.4706185 0.2644071 0.8376544
## attr(,"class")
## [1] "mipool"
```

Characteristics of COVID-19 symptoms by vaccination status

ICU

```
pool_odds_ratio(with(dat_imp, expr=odds_ratio(vaccine_cov ~ icu)))
```

```
##      pooled OR 95 CI low 95 CI high
## [1,] 0.5361446 0.3789471 0.7585517
## attr(,"class")
## [1] "mipool"
```

Intubation

```
pool_odds_ratio(with(dat_imp, expr=odds_ratio(vaccine_cov ~ intubation)))
```

```
##      pooled OR 95 CI low 95 CI high
## [1,] 0.2267073 0.1160312 0.4429518
## attr(,"class")
## [1] "mipool"
```

Death

```
pool_odds_ratio(with(dat_imp, expr=odds_ratio(vaccine_cov ~ death)))
```

```
##      pooled OR 95 CI low 95 CI high
## [1,] 0.1883021 0.08279405 0.4282638
## attr(,"class")
## [1] "mipool"
```