Cardiovascular disease worsens the maternal prognosis of COVID-19

Codes and outputs

08/20/2021

Description

This file presents the documentation of the analysis of article "Cardiovascular disease worsens the maternal prognosis of COVID-19" with authors Carolina Testa, Luciana de Godoi, Maria Rita Bortolotto, Nátaly Monroy, Bruna de Mattos, Agatha Rodrigues, and Rossana Francisco.

R packages used, functions and dataset import

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

```
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(
    "dplyr",
    "MatchIt",
    "lubridate",
    "readr",
    "readxl",
    "ggplot2",
    "kableExtra",
    "tables",
    "questionr",
    "car",
    "data.table",
    "magrittr",
    "tidyverse",
    "readxl",
    "summarytools",
    "modelsummary",
    "RColorBrewer",
```

```
    "zoo",
    "WeightIt",
    "jtools",
    "cobalt",
    "weights"
)
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))
```

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

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

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

The search was limited to the first notified case of COVID-19 in February 2020 until the 15th epidemiological week of 2021 (up to April 17, 2021). The datasets were obtained on May 5, 2021, on the site https://opendatasus.saude.gov.br/dataset. The first period (8th to 53rd epidemiological week of 2020) and the second period (1st to 15th epidemiological week of 2021) datasets can be obtained at https://drive.google.com/file/d/1jts4h0ovdwFh86SdKyslMLSG9rOy3UjX/view?usp=sharing and at https://drive.google.com/file/d/1gQSy_dcUkd1UrDEcsrDbyGl4gEvcI8z_/view?usp=sharing, respectively. The data are loaded below:

```
######### loading the datasets ###########
#2021
data_2021 <- read_delim(
  "INFLUD21-03-05-2021.csv",
```

```
  ";",
  escape_double = FALSE,
  locale = locale(encoding = "ISO-8859-2"),
  trim_ws = TRUE
)


#2020
data_2020 <- read_delim(
  "INFLUD-03-05-2021.csv",
  ";",
  escape_double = FALSE,
  locale = locale(encoding = "ISO-8859-2"),
  trim_ws = TRUE
)


sem <- 15 #limit of epidemiological week of 2021

#memory.limit(999999)

#### Concatenating 2020 and 2021 data ###############
data_all <- rbind(data_2020, data_2021)

#Creating the case year variable
data_all <-  data_all %>%
  dplyr::mutate(
    dt_sint = as.Date(DT_SIN_PRI, format = "%d/%m/%Y"),
    year_case = lubridate::year(dt_sint),
  )
```

There are 1905854 observations. The case selection is presented in the following according to the flowchart presented in the article.

Case selection and data treatment

The first filter consists of selecting the cases from 8th epidemiological week of 2020 to 15th epidemiological week of 2021.

```
#Cases from the 8th epidemiological week of 2020 to 15th of 2021
data1 <- data_all %>%
  filter((year_case==2020 & SEM_PRI >=8) | year_case ==2021)
```

There are 12563 cases in 2021 in epidemiological week 53 of 2020. 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 as follows:

```
  data1 <- data1 %>%
  mutate(year_case = ifelse(year_case ==2021 & SEM_PRI ==53, 2020, year_case)) %>%
  filter(year_case==2020 | (year_case ==2021 & SEM_PRI <= sem))
```

There are 1876953 observations.

The next selection consists of selecting only confirmed cases of COVID-19:

```
##Filtering confirmed cases of COVID-19
data2 <- data1 %>%
    filter(CLASSI_FIN == 5)
```

There are 1174350 observations.

The next step is to identify hospitalized cases (`HOSPITAL=1`) and then select only those cases.

```
#Filtering only hospitalized cases
data3 <- data2 %>%
  filter(HOSPITAL == 1)
```

Now we have 1114042 observations.

The next selection consists of selecting females cases:

```
##Filtering female notifications
data4 <- filter(data3, CS_SEXO == "F")
```

There are 495698 observations.

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

```
#Filtering women aged 10-55
data5 <- data4 %>%
  filter(NU_IDADE_N > 9 & NU_IDADE_N <= 55)
```

There are 174525 observations.

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

```
#Creating the classification variable if pregnant, postpartum and not (neither pregnant nor postpartum)
data5 <- data5 %>%
  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",  #puerperium
      CS_GESTANT == 9 & PUERPERA == 1 ~ "puerp", #puerperium
      TRUE ~ "no" #neither pregnant nor postpartum
    )
  )

#Filtering only pregnant and postpartum women
data6 <- data5 %>%
  filter(classi_gesta_puerp != "no")
```

There are 10635 observations.

The variable identified as `EVOLUCAO` is categorized with 1 - cure, 2 - death by SARS, 3 - death by other cause, 9 - ignored.

```
with(data6, freq(EVOLUCAO))
```

```
## Frequencies
## data6$EVOLUCAO
## Type: Numeric
##
##                Freq   % Valid   % Valid Cum.   % Total   % Total Cum.
## ----------- ------- --------- -------------- --------- --------------
##           1    8005     85.38          85.38     75.27          75.27
##           2     979     10.44          95.82      9.21          84.48
##           3      15      0.16          95.98      0.14          84.62
##           9     377      4.02         100.00      3.54          88.16
##        <NA>    1259                                11.84         100.00
##       Total   10635    100.00         100.00    100.00         100.00
```

Now we are going to select only the finalized cases:

```
#Filtering only finalized cases
data7 <- data6 %>%
  filter((EVOLUCAO == 1 | EVOLUCAO == 2 | EVOLUCAO == 3) & !is.na(EVOLUCAO))

#Creating the evolution variable
data7 <- data7 %>%
  mutate(evolution = case_when(
    EVOLUCAO == 1 ~ "cure",
    EVOLUCAO == 2 ~ "death",
    EVOLUCAO == 3 ~ "death"
  ))

with(data7, freq(evolution))
```

```
## Frequencies
## data7$evolution
## Type: Character
##
##               Freq   % Valid   % Valid Cum.   % Total   % Total Cum.
## ----------- ------ --------- -------------- --------- --------------
##        cure   8005     88.95          88.95     88.95          88.95
##       death    994     11.05         100.00     11.05         100.00
##        <NA>      0                                0.00         100.00
##       Total   8999    100.00         100.00    100.00         100.00
```

There are 8999 confirmed and hospitalized cases of COVID-19 in pregnant and postpartum women aged 10 to 55 years. We identify 60.42% of these notifications without any information about the presence or absence of cardiovascular diseases (CVD). The next selection consists of selecting cases where the CVD variable (`CARDIOPATI`) indicates yes or no:

```r
with(data7, freq(CARDIOPATI))
```

```
## Frequencies
## data7$CARDIOPATI
## Type: Numeric
##
##               Freq   % Valid   % Valid Cum.   % Total   % Total Cum.
## ----------- ------ --------- -------------- --------- --------------
##           1    602     16.55          16.55      6.69           6.69
##           2   2960     81.39          97.94     32.89          39.58
##           9     75      2.06         100.00      0.83          40.42
##        <NA>   5362                             59.58         100.00
##       Total   8999    100.00         100.00    100.00         100.00
```

```r
#Creating the CVD variable
data7 <- data7 %>%
  mutate(CVD = case_when(
    CARDIOPATI == 1 ~ "yes",
    CARDIOPATI == 2 ~ "no",
    TRUE ~ NA_character_
  ))
```

Now we present the final dataset.

```r
#Filtering cases with information about CVD
data <- data7 %>%
  filter(!is.na(CVD))
```

```r
questionr::freq(
  data$CVD,
  cum = FALSE,
  total = TRUE,
  na.last = FALSE,
  valid = FALSE
)  %>%
  kable(caption = "Frequency of CVD", digits = 2)  %>%
  kable_styling(latex_options = "HOLD_position")
```

Table 1: Frequency of CVD

	n	%
no	2960	83.1
yes	602	16.9
Total	3562	100.0

Epidemiologic characteristics

Ethnicity

```r
# Ethnicity
data <-  data %>%
  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_
    )
  )
```

```r
with(data, ctable(ethnicity, CVD, prop = "c", useNA = "no", chisq = FALSE))
```

```
## Cross-Tabulation, Column Proportions
## ethnicity * CVD
## Data Frame: data
##
## ------------ ----- --------------- -------------- ---------------
##                CVD              no            yes           Total
##    ethnicity
##        black          167 (  6.5%)    46 (  9.1%)    213 (  6.9%)
##        brown         1375 ( 53.5%)   244 ( 48.1%)   1619 ( 52.6%)
##   indigenous           30 (  1.2%)     1 (  0.2%)     31 (  1.0%)
##        white          975 ( 37.9%)   214 ( 42.2%)   1189 ( 38.6%)
##       yellow           24 (  0.9%)     2 (  0.4%)     26 (  0.8%)
##        Total         2571 (100.0%)   507 (100.0%)   3078 (100.0%)
## ------------ ----- --------------- -------------- ---------------
```

```r
fisher.test(data$ethnicity, data$CVD)
```

```
##
##  Fisher's Exact Test for Count Data
##
## data:  data$ethnicity and data$CVD
## p-value = 0.007096
## alternative hypothesis: two.sided
```

Education

```r
data <- data %>%
     mutate(education = case_when(CS_ESCOL_N == 0 ~ "No schooling",
                          CS_ESCOL_N == 1 ~ "1st to 5th grade",
                          CS_ESCOL_N == 2 ~ "6th to 9th grade",
                          CS_ESCOL_N == 3 ~ "Middle school",
                          CS_ESCOL_N == 4 ~ "Superior",
                            TRUE ~ NA_character_))
```

```r
data$education <- factor(data$education,
levels = c("No schooling","1st to 5th grade", "6th to 9th grade",
"Middle school", "Superior"))
```

```r
with(data, ctable(education, CVD, prop = "c", useNA = "no", chisq = FALSE))
```

```
## Cross-Tabulation, Column Proportions
## education * CVD
## Data Frame: data
##
## ------------------ ----- --------------- -------------- ---------------
##                       CVD              no            yes           Total
##           education
##        No schooling           11 (  0.7%)     2 (  0.7%)     13 (  0.7%)
##    1st to 5th grade          123 (  7.9%)    33 ( 12.2%)    156 (  8.5%)
##    6th to 9th grade          307 ( 19.7%)    52 ( 19.2%)    359 ( 19.6%)
##       Middle school          857 ( 55.0%)   140 ( 51.7%)    997 ( 54.5%)
##            Superior          260 ( 16.7%)    44 ( 16.2%)    304 ( 16.6%)
##               Total         1558 (100.0%)   271 (100.0%)   1829 (100.0%)
## ------------------ ----- --------------- -------------- ---------------
```

```r
fisher.test(data$education, data$CVD)
```

```
##
##  Fisher's Exact Test for Count Data
##
## data:  data$education and data$CVD
## p-value = 0.2405
## alternative hypothesis: two.sided
```

Age (Years)

```r
datasummary((CVD) ~ NU_IDADE_N*(n+media+DP+mediana+minimo+maximo+q25+q75+IQR),
            data = data, output = 'markdown')
```

	n	media	DP	mediana	minimo	maximo	q25	q75	IQR
no	2960.00	30.00	7.43	30.00	13.00	55.00	24.00	35.00	11.00
yes	602.00	34.76	8.52	34.00	15.00	55.00	29.00	39.75	10.75

```r
t.test(NU_IDADE_N ~ CVD, data = data)
```

```
##
##  Welch Two Sample t-test
##
## data:  NU_IDADE_N by CVD
## t = -12.745, df = 797.4, p-value < 2.2e-16
## alternative hypothesis: true difference in means is not equal to 0
```

```
## 95 percent confidence interval:
##  -5.485124 -4.021042
## sample estimates:
##  mean in group no mean in group yes
##          30.00439          34.75748
```

Age group

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

```
with(data, ctable(age_group, CVD, prop = "c", useNA = "no", chisq = FALSE))
```

```
## Cross-Tabulation, Column Proportions
## age_group * CVD
## Data Frame: data
##
## ----------- ----- --------------- -------------- ---------------
##                CVD              no            yes           Total
##   age_group
##         <20          237 (  8.0%)    10 (  1.7%)    247 (  6.9%)
##       20-34         1895 ( 64.0%)   292 ( 48.5%)   2187 ( 61.4%)
##        >=35          828 ( 28.0%)   300 ( 49.8%)   1128 ( 31.7%)
##       Total         2960 (100.0%)   602 (100.0%)   3562 (100.0%)
## ----------- ----- --------------- -------------- ---------------
```

```
with(data,fisher.test(age_group, CVD))
```

```
##
##  Fisher's Exact Test for Count Data
##
## data:  age_group and CVD
## p-value < 2.2e-16
## alternative hypothesis: two.sided
```

Residence area

```r
data <-  data %>%
  mutate(zone = case_when(CS_ZONA ==1  ~ "Urban",
                          CS_ZONA == 2 ~ "Rural",
                          CS_ZONA == 3 ~ "Periurban",
                            TRUE ~ NA_character_))
```

```r
with(data, ctable( zone, CVD, prop = "c", useNA = "no", chisq = FALSE))
```

```
## Cross-Tabulation, Column Proportions
## zone * CVD
## Data Frame: data
##
## ----------- ----- --------------- -------------- ----------------
##                CVD              no            yes            Total
##         zone
##    Periurban           10 (  0.4%)     3 (  0.5%)     13 (  0.4%)
##        Rural          159 (  5.7%)    24 (  4.4%)    183 (  5.5%)
##        Urban         2618 ( 93.9%)   522 ( 95.1%)   3140 ( 94.1%)
##        Total         2787 (100.0%)   549 (100.0%)   3336 (100.0%)
## ----------- ----- --------------- -------------- ----------------
```

```r
fisher.test(data$zone, data$CVD)
```

```
##
##  Fisher's Exact Test for Count Data
##
## data:  data$zone and data$CVD
## p-value = 0.3673
## alternative hypothesis: two.sided
```

Gestational moment

```r
ctable(data$classi_gesta_puerp, data$CVD, prop="c", OR=TRUE, useNA = "no", chisq = TRUE)
```

```
## Cross-Tabulation, Column Proportions
## classi_gesta_puerp * CVD
## Data Frame: data
##
##
## -------------------- ----- --------------- -------------- ----------------
##                        CVD              no            yes            Total
##   classi_gesta_puerp
##                 1tri          161 (  5.4%)    34 (  5.6%)    195 (  5.5%)
##                 2tri          471 ( 15.9%)   120 ( 19.9%)    591 ( 16.6%)
##                 3tri         1199 ( 40.5%)   248 ( 41.2%)   1447 ( 40.6%)
##               IG_ig           84 (  2.8%)    30 (  5.0%)    114 (  3.2%)
##               puerp         1045 ( 35.3%)   170 ( 28.2%)   1215 ( 34.1%)
##               Total         2960 (100.0%)   602 (100.0%)   3562 (100.0%)
## -------------------- ----- --------------- -------------- ----------------
```

```
##
## ----------------------------
##  Chi.squared   df   p.value
## ------------- ---- ---------
##    19.4898     4     6e-04
## ----------------------------
```

Hospital-acquired infection

```
data <-  data %>%
  mutate(hospital_infection = case_when(NOSOCOMIAL ==1  ~ "yes",
                              NOSOCOMIAL == 2 ~ "no",
                                TRUE ~ NA_character_))
```

```
with(data, ctable( hospital_infection, CVD, prop = "c", useNA = "no", chisq = FALSE))
```

```
## Cross-Tabulation, Column Proportions
## hospital_infection * CVD
## Data Frame: data
##
## -------------------- ----- --------------- -------------- ---------------
##                         CVD              no            yes           Total
##   hospital_infection
##                    no         2551 ( 98.0%)   448 ( 98.0%)   2999 ( 98.0%)
##                   yes           53 (  2.0%)     9 (  2.0%)     62 (  2.0%)
##                 Total         2604 (100.0%)   457 (100.0%)   3061 (100.0%)
## -------------------- ----- --------------- -------------- ---------------
```

```
fisher.test(data$hospital_infection, data$CVD)
```

```
##
##  Fisher's Exact Test for Count Data
##
## data:  data$hospital_infection and data$CVD
## p-value = 1
## alternative hypothesis: true odds ratio is not equal to 1
## 95 percent confidence interval:
##  0.4163122 1.9955578
## sample estimates:
## odds ratio
##  0.9669453
```

Symptoms

Fever

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

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

```
## Cross-Tabulation, Row Proportions
## CVD * fever
## Data Frame: data
##
##
## ------- ------- -------------- -------------- ----------------
##           fever             no            yes            Total
##     CVD
##      no           1289 (44.2%)   1625 (55.8%)   2914 (100.0%)
##     yes            209 (38.3%)    337 (61.7%)    546 (100.0%)
##   Total           1498 (43.3%)   1962 (56.7%)   3460 (100.0%)
## ------- ------- -------------- -------------- ----------------
##
## ----------------------------
##  Chi.squared   df   p.value
## ------------- ---- ---------
##    6.4048      1    0.0114
## ----------------------------
##
## ----------------------------------
##  Odds Ratio   Lo - 95%   Hi - 95%
## ------------ ---------- ----------
##     1.28        1.06       1.54
## ----------------------------------
##
## --------------------------------
##  Risk Ratio   Lo - 0%   Hi - 0%
## ------------ --------- ---------
##     1.16       1.16      1.16
## --------------------------------
```

Cough

```r
data <-  data %>%
  mutate(cough = case_when(TOSSE == 1 ~ "yes",
                           TOSSE == 2 ~ "no",
                           TRUE ~ NA_character_))
```

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

```
## Cross-Tabulation, Row Proportions
## CVD * cough
```

```
## Data Frame: data
##
##
## ------- ------- -------------- -------------- ----------------
##           cough              no             yes            Total
##     CVD
##      no           1002 (34.4%)   1913 (65.6%)   2915 (100.0%)
##     yes            138 (24.6%)    424 (75.4%)    562 (100.0%)
##   Total           1140 (32.8%)   2337 (67.2%)   3477 (100.0%)
## ------- ------- -------------- -------------- ----------------
##
## ----------------------------
##  Chi.squared   df   p.value
## ------------ ---- ---------
##    20.1693     1       0
## ----------------------------
##
## ----------------------------------
##  Odds Ratio   Lo - 95%   Hi - 95%
## ------------ ---------- ----------
##     1.61        1.31       1.98
## ----------------------------------
##
## --------------------------------
##  Risk Ratio   Lo - 0%   Hi - 0%
## ------------ --------- ---------
##     1.40        1.40      1.40
## --------------------------------
```

Sore throat

```
data <-  data %>%
  mutate(sore_throat = case_when(GARGANTA == 1 ~ "yes",
                                 GARGANTA  == 2 ~ "no",
                                 TRUE ~ NA_character_))
```

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

```
## Cross-Tabulation, Row Proportions
## CVD * sore_throat
## Data Frame: data
##
##
## ------- ------------- -------------- ------------- ----------------
##           sore_throat             no           yes            Total
##     CVD
##      no                 2245 (78.5%)   616 (21.5%)   2861 (100.0%)
##     yes                  367 (74.7%)   124 (25.3%)    491 (100.0%)
##   Total                 2612 (77.9%)   740 (22.1%)   3352 (100.0%)
## ------- ------------- -------------- ------------- ----------------
##
```

```
## ----------------------------
##  Chi.squared   df   p.value
## ------------- ---- ---------
##    3.1648      1    0.0752
## ----------------------------
##
## ---------------------------------
##  Odds Ratio   Lo - 95%   Hi - 95%
## ------------ ---------- ----------
##     1.23        0.99       1.54
## ---------------------------------
##
## --------------------------------
##  Risk Ratio   Lo - 0%   Hi - 0%
## ------------ --------- ---------
##     1.05        1.05      1.05
## --------------------------------
```

Dyspnea

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

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

```
## Cross-Tabulation, Row Proportions
## CVD * dyspnea
## Data Frame: data
##
##
## ------- --------- -------------- -------------- ---------------
##           dyspnea             no            yes           Total
##     CVD
##      no             1361 (46.7%)   1553 (53.3%)   2914 (100.0%)
##     yes              154 (27.7%)    401 (72.3%)    555 (100.0%)
##   Total             1515 (43.7%)   1954 (56.3%)   3469 (100.0%)
## ------- --------- -------------- -------------- ---------------
##
## ----------------------------
##  Chi.squared   df   p.value
## ------------- ---- ---------
##    67.3439     1       0
## ----------------------------
##
## ---------------------------------
##  Odds Ratio   Lo - 95%   Hi - 95%
## ------------ ---------- ----------
##     2.28        1.87       2.79
## ---------------------------------
```

```
##
## -------------------------------
##  Risk Ratio   Lo - 0%   Hi - 0%
## ------------ --------- ---------
##     1.68       1.68      1.68
## -------------------------------
```

Respiratory distress

```
data <-  data %>%
  mutate(resp_dist = case_when(DESC_RESP == 1 ~ "yes",
                               DESC_RESP == 2 ~ "no",
                               TRUE ~ NA_character_))
```

```
with(data, ctable(CVD, resp_dist, prop = "r", useNA = "no", chisq = TRUE, OR=TRUE))
```

```
## Cross-Tabulation, Row Proportions
## CVD * resp_dist
## Data Frame: data
##
##
## ------- ----------- -------------- -------------- ----------------
##           resp_dist             no            yes            Total
##     CVD
##      no               1541 (53.1%)   1361 (46.9%)   2902 (100.0%)
##     yes                213 (40.3%)    316 (59.7%)    529 (100.0%)
##   Total               1754 (51.1%)   1677 (48.9%)   3431 (100.0%)
## ------- ----------- -------------- -------------- ----------------
##
## ----------------------------
##  Chi.squared   df   p.value
## ------------- ---- ---------
##    28.9948     1       0
## ----------------------------
##
## ---------------------------------
##  Odds Ratio   Lo - 95%   Hi - 95%
## ------------ ---------- ----------
##     1.68        1.39       2.03
## ---------------------------------
##
## -------------------------------
##  Risk Ratio   Lo - 0%   Hi - 0%
## ------------ --------- ---------
##     1.32       1.32      1.32
## -------------------------------
```

Saturation

```r
data <-  data %>%
  mutate(saturation = case_when(SATURACAO == 1 ~ "yes",
                                SATURACAO == 2 ~ "no",
                                TRUE ~ NA_character_))
```

```r
with(data, ctable(CVD, saturation, prop = "r", useNA = "no", chisq = TRUE, OR=TRUE))
```

```
## Cross-Tabulation, Row Proportions
## CVD * saturation
## Data Frame: data
##
##
## ------- ------------ -------------- -------------- ----------------
##           saturation             no            yes            Total
##     CVD
##      no                1873 (65.1%)   1003 (34.9%)   2876 (100.0%)
##     yes                 231 (43.4%)    301 (56.6%)    532 (100.0%)
##   Total                2104 (61.7%)   1304 (38.3%)   3408 (100.0%)
## ------- ------------ -------------- -------------- ----------------
##
## ----------------------------
##  Chi.squared   df   p.value
## ------------- ---- ---------
##    88.612      1       0
## ----------------------------
##
## ----------------------------------
##  Odds Ratio   Lo - 95%   Hi - 95%
## ------------ ---------- ----------
##     2.43        2.02       2.94
## ----------------------------------
##
## --------------------------------
##  Risk Ratio   Lo - 0%   Hi - 0%
## ------------ --------- ---------
##     1.50        1.50      1.50
## --------------------------------
```

Diarrhea

```r
data <-  data %>%
  mutate(diarrhea = case_when(DIARREIA == 1 ~ "yes",
                                DIARREIA == 2 ~ "no",
                                TRUE ~ NA_character_))
```

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

```
## Cross-Tabulation, Row Proportions
## CVD * diarrhea
```

```
## Data Frame: data
##
##
## ------- ---------- -------------- ------------- ---------------
##           diarrhea             no           yes           Total
##     CVD
##      no              2557 (88.8%)   324 (11.2%)   2881 (100.0%)
##     yes               421 (87.0%)    63 (13.0%)    484 (100.0%)
##   Total              2978 (88.5%)   387 (11.5%)   3365 (100.0%)
## ------- ---------- -------------- ------------- ---------------
##
## ----------------------------
##  Chi.squared   df   p.value
## ------------ ---- ---------
##    1.1081      1    0.2925
## ----------------------------
##
## ----------------------------------
##  Odds Ratio   Lo - 95%   Hi - 95%
## ------------ ---------- ----------
##     1.18        0.88       1.58
## ----------------------------------
##
## --------------------------------
##  Risk Ratio   Lo - 0%   Hi - 0%
## ------------ --------- ---------
##     1.02        1.02      1.02
## --------------------------------
```

Vomit

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

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

```
## Cross-Tabulation, Row Proportions
## CVD * vomit
## Data Frame: data
##
##
## ------- ------- -------------- ------------- ---------------
##           vomit             no           yes           Total
##     CVD
##      no           2589 (90.2%)   282 ( 9.8%)   2871 (100.0%)
##     yes            423 (87.9%)    58 (12.1%)    481 (100.0%)
##   Total           3012 (89.9%)   340 (10.1%)   3352 (100.0%)
## ------- ------- -------------- ------------- ---------------
##
```

```
## ----------------------------
##  Chi.squared   df   p.value
## ------------- ---- ---------
##     2.021      1    0.1551
## ----------------------------
##
## ----------------------------------
##  Odds Ratio   Lo - 95%   Hi - 95%
## ------------ ---------- ----------
##     1.26        0.93       1.70
## ----------------------------------
##
## --------------------------------
##  Risk Ratio   Lo - 0%   Hi - 0%
## ------------ --------- ---------
##     1.03       1.03      1.03
## --------------------------------
```

Abdominal pain

```
data <-  data %>%
  mutate(abd_pain = case_when(DOR_ABD == 1 ~ "yes",
                              DOR_ABD == 2 ~ "no",
                              TRUE ~ NA_character_))
```

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

```
## Cross-Tabulation, Row Proportions
## CVD * abd_pain
## Data Frame: data
##
##
## ------- ---------- -------------- ------------- ---------------
##           abd_pain             no           yes           Total
##     CVD
##      no              1877 (91.1%)   183 ( 8.9%)   2060 (100.0%)
##     yes               291 (89.0%)    36 (11.0%)    327 (100.0%)
##   Total              2168 (90.8%)   219 ( 9.2%)   2387 (100.0%)
## ------- ---------- -------------- ------------- ---------------
##
## ----------------------------
##  Chi.squared   df   p.value
## ------------- ---- ---------
##    1.2858      1    0.2568
## ----------------------------
##
## ----------------------------------
##  Odds Ratio   Lo - 95%   Hi - 95%
## ------------ ---------- ----------
##     1.27        0.87       1.85
## ----------------------------------
```

```
##
## -------------------------------
##  Risk Ratio   Lo - 0%   Hi - 0%
## ------------ --------- ---------
##     1.02       1.02      1.02
## -------------------------------
```

Fatigue

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

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

```
## Cross-Tabulation, Row Proportions
## CVD * fatigue
## Data Frame: data
##
##
## ------- --------- -------------- ------------- ----------------
##           fatigue              no           yes            Total
##     CVD
##      no              1609 (77.8%)   460 (22.2%)   2069 (100.0%)
##     yes               238 (69.6%)   104 (30.4%)    342 (100.0%)
##   Total              1847 (76.6%)   564 (23.4%)   2411 (100.0%)
## ------- --------- -------------- ------------- ----------------
##
## ----------------------------
##  Chi.squared   df   p.value
## ------------ ---- ---------
##    10.4972     1    0.0012
## ----------------------------
##
## ---------------------------------
##  Odds Ratio   Lo - 95%   Hi - 95%
## ------------ ---------- ----------
##     1.53        1.19       1.97
## ---------------------------------
##
## -------------------------------
##  Risk Ratio   Lo - 0%   Hi - 0%
## ------------ --------- ---------
##     1.12       1.12      1.12
## -------------------------------
```

Loss of smell

```r
data <-  data %>%
  mutate(loss_smell = case_when(PERD_OLFT == 1 ~ "yes",
                                PERD_OLFT == 2 ~ "no",
                                TRUE ~ NA_character_))
```

```r
with(data, ctable(CVD, loss_smell, prop = "r", useNA = "no", chisq = TRUE, OR=TRUE))
```

```
## Cross-Tabulation, Row Proportions
## CVD * loss_smell
## Data Frame: data
##
##
## ------- ------------ -------------- ------------- ----------------
##           loss_smell             no           yes            Total
##     CVD
##      no                1683 (81.4%)   384 (18.6%)   2067 (100.0%)
##     yes                 250 (74.2%)    87 (25.8%)    337 (100.0%)
##   Total                1933 (80.4%)   471 (19.6%)   2404 (100.0%)
## ------- ------------ -------------- ------------- ----------------
##
## ----------------------------
##  Chi.squared   df   p.value
## ------------- ---- ---------
##    9.1828      1    0.0024
## ----------------------------
##
## ---------------------------------
##  Odds Ratio   Lo - 95%   Hi - 95%
## ------------ ---------- ----------
##     1.53        1.17       1.99
## ---------------------------------
##
## --------------------------------
##  Risk Ratio   Lo - 0%   Hi - 0%
## ------------ --------- ---------
##     1.10        1.10      1.10
## --------------------------------
```

Loss of taste

```r
data <-  data %>%
  mutate(loss_taste = case_when(PERD_PALA == 1 ~ "yes",
                                PERD_PALA == 2 ~ "no",
                                TRUE ~ NA_character_))
```

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

```
## Cross-Tabulation, Row Proportions
## CVD * loss_taste
```

```
## Data Frame: data
##
##
## ------- ------------ -------------- ------------- ---------------
##           loss_taste             no           yes           Total
##     CVD
##      no                1694 (82.1%)   369 (17.9%)   2063 (100.0%)
##     yes                 250 (74.0%)    88 (26.0%)    338 (100.0%)
##   Total                1944 (81.0%)   457 (19.0%)   2401 (100.0%)
## ------- ------------ -------------- ------------- ---------------
##
## ----------------------------
##  Chi.squared   df   p.value
## ------------ ---- ---------
##    11.9908     1     5e-04
## ----------------------------
##
## ---------------------------------
##  Odds Ratio   Lo - 95%   Hi - 95%
## ------------ ---------- ----------
##     1.62        1.24       2.11
## ---------------------------------
##
## -------------------------------
##  Risk Ratio   Lo - 0%   Hi - 0%
## ------------ --------- ---------
##     1.11        1.11      1.11
## -------------------------------
```

Any respiratory symptom

Now we are going to create the variable `resp_symp` indicating the presence of at least one respiratory symptom (Dyspnea, Fadigue, Saturation, Respiratory distress). Empty cells are considered missing data (<NA>). The variable `qt_resp_symp` indicates the number of respiratory symptoms of each case.

```
df <- select(data,dyspnea,fatigue,saturation,resp_dist )
soma <- function(x){
  if (sum(is.na(x))==4)
    return(NA_character_)
  else
   return(sum(!is.na(x) & x=="yes"))
}
data$qt_sintomas_resp_aux <- apply(df,1,soma)

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

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

```
## Cross-Tabulation, Row Proportions
## CVD * resp_symp
```

```
## Data Frame: data
##
##
## ------- ----------- -------------- -------------- ---------------
##           resp_symp             no            yes           Total
##     CVD
##      no                935 (31.9%)   1992 (68.1%)   2927 (100.0%)
##     yes                 94 (16.3%)    484 (83.7%)    578 (100.0%)
##   Total               1029 (29.4%)   2476 (70.6%)   3505 (100.0%)
## ------- ----------- -------------- -------------- ---------------
##
## ----------------------------
##  Chi.squared   df   p.value
## ------------ ---- ---------
##    56.4759     1       0
## ----------------------------
##
## ---------------------------------
##  Odds Ratio   Lo - 95%   Hi - 95%
## ------------ ---------- ----------
##     2.42        1.91       3.05
## ---------------------------------
##
## -------------------------------
##  Risk Ratio   Lo - 0%   Hi - 0%
## ------------ --------- ---------
##     1.96       1.96      1.96
## -------------------------------
```

```
data <-  data %>%
  mutate(qt_resp_symp = case_when(qt_sintomas_resp_aux == 4  ~ "4 symptoms",
                                  qt_sintomas_resp_aux == 3  ~ "3 symptoms",
                                  qt_sintomas_resp_aux == 2  ~ "2 symptoms",
                                  qt_sintomas_resp_aux == 1  ~ "1 symptom",
                                  qt_sintomas_resp_aux == 0  ~ "No respiratory symptom",
                                TRUE ~ NA_character_))

with(data, ctable(qt_resp_symp, CVD, prop="c", useNA = "no", chisq = TRUE))
```

```
## Cross-Tabulation, Column Proportions
## qt_resp_symp * CVD
## Data Frame: data
##
##
## ----------------------- ----- -------------- -------------- ---------------
##                             CVD             no            yes           Total
##             qt_resp_symp
##                1 symptom          640 ( 21.9%)   116 ( 20.1%)    756 ( 21.6%)
##               2 symptoms          528 ( 18.0%)   151 ( 26.1%)    679 ( 19.4%)
##               3 symptoms          615 ( 21.0%)   164 ( 28.4%)    779 ( 22.2%)
##               4 symptoms          209 (  7.1%)    53 (  9.2%)    262 (  7.5%)
##   No respiratory symptom          935 ( 31.9%)    94 ( 16.3%)   1029 ( 29.4%)
##                    Total         2927 (100.0%)   578 (100.0%)   3505 (100.0%)
## ----------------------- ----- -------------- -------------- ---------------
```

```
##
## ----------------------------
##  Chi.squared   df   p.value
## ------------- ---- ---------
##    71.8703     4       0
## ----------------------------
```

Any symptom

```
df <- select(data, dyspnea, fatigue, saturation, resp_dist, fever, cough, sore_throat, diarrhea, vomit,

soma <- function(x){
  if (sum(is.na(x)) == 12)
    return(NA_character_)
  else
    return(sum(!is.na(x) & x=="yes"))
}
data$qt_symp_aux <- apply(df,1,soma)

data <-  data %>%
  mutate(symp = case_when(qt_symp_aux >= 1 ~ "yes",
                          qt_symp_aux == 0 ~ "no",
                          TRUE ~ NA_character_))

with(data, ctable(CVD, symp,  prop="r", useNA = "no", chisq = TRUE, OR=TRUE))
```

```
## Cross-Tabulation, Row Proportions
## CVD * symp
## Data Frame: data
##
##
## ------- ------ ------------ -------------- ---------------
##           symp           no            yes           Total
##     CVD
##      no          256 (8.7%)   2685 (91.3%)   2941 (100.0%)
##     yes           22 (3.7%)    574 (96.3%)    596 (100.0%)
##   Total          278 (7.9%)   3259 (92.1%)   3537 (100.0%)
## ------- ------ ------------ -------------- ---------------
##
## ----------------------------
##  Chi.squared   df   p.value
## ------------- ---- ---------
##    16.513      1       0
## ----------------------------
##
## ---------------------------------
##  Odds Ratio   Lo - 95%   Hi - 95%
## ------------ ---------- ----------
##     2.49        1.59       3.88
## ---------------------------------
##
## -------------------------------
```

```
##  Risk Ratio   Lo - 0%   Hi - 0%
## ------------ --------- ---------
##     2.36       2.36      2.36
## --------------------------------
```

Comorbities

```
#Hematologic
data <-  data %>%
mutate(hematologic = case_when(HEMATOLOGI == 1 ~ "yes",
                               HEMATOLOGI == 2 ~ "no",
                               TRUE ~ NA_character_))
#Immunodepression
data <-  data %>%
mutate(imunodepre = case_when(IMUNODEPRE == 1 ~ "yes",
                               IMUNODEPRE == 2 ~ "no",
                               TRUE ~ NA_character_))
#Hepatic
data <-  data %>%
mutate(hepatic = case_when(HEPATICA == 1 ~ "yes",
                           HEPATICA== 2 ~ "no",
                           TRUE ~ NA_character_))
#Asthma
data <-  data %>%
mutate(asthma = case_when(ASMA == 1 ~ "yes",
                       ASMA == 2 ~ "no",
                       TRUE ~ NA_character_))
#Diabetes
data <-  data %>%
mutate(diabetes = case_when(DIABETES == 1 ~ "yes",
                           DIABETES == 2 ~ "no",
                           TRUE ~ NA_character_))
#Neurologic
data <-  data %>%
mutate(neurologic = case_when(NEUROLOGIC == 1 ~ "yes",
                               NEUROLOGIC == 2 ~ "no",
                               TRUE ~ NA_character_))
#Pneumologic
data <-  data %>%
mutate(pneumologic = case_when(PNEUMOPATI == 1 ~ "yes",
                               PNEUMOPATI == 2 ~ "no",
                               TRUE ~ NA_character_))
#Renal
data <-  data %>%
mutate(renal = case_when(RENAL == 1 ~ "yes",
                         RENAL == 2 ~ "no",
                         TRUE ~ NA_character_))
#Obesity
data <-  data %>%
mutate(obesity = case_when(OBESIDADE == 1 ~ "yes",
                               OBESIDADE == 2 ~ "no",
                               TRUE ~ NA_character_))
```

Hematologic

```
with(data, ctable(CVD, hematologic, prop = "r", useNA = "no", chisq = TRUE, OR=TRUE))
```

```
## Cross-Tabulation, Row Proportions
## CVD * hematologic
## Data Frame: data
##
##
## ------- ------------- -------------- ----------- ---------------
##           hematologic             no         yes           Total
##     CVD
##      no                 2919 (98.9%)   31 (1.1%)   2950 (100.0%)
##     yes                  428 (97.9%)    9 (2.1%)    437 (100.0%)
##   Total                 3347 (98.8%)   40 (1.2%)   3387 (100.0%)
## ------- ------------- -------------- ----------- ---------------
##
## ----------------------------
##  Chi.squared   df   p.value
## ------------ ---- ---------
##    2.5101      1    0.1131
## ----------------------------
##
## ---------------------------------
##  Odds Ratio   Lo - 95%   Hi - 95%
## ------------ ---------- ----------
##     1.98        0.94       4.19
## ---------------------------------
##
## -------------------------------
##  Risk Ratio   Lo - 0%   Hi - 0%
## ------------ --------- ---------
##     1.01       1.01      1.01
## -------------------------------
```

Diabetes

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

```
## Cross-Tabulation, Row Proportions
## CVD * diabetes
## Data Frame: data
##
##
## ------- ---------- -------------- ------------- ---------------
##           diabetes             no           yes           Total
##     CVD
```

```
##      no              2610 (88.6%)   337 (11.4%)   2947 (100.0%)
##     yes               312 (66.4%)   158 (33.6%)    470 (100.0%)
##   Total              2922 (85.5%)   495 (14.5%)   3417 (100.0%)
## ------- ---------- -------------- ------------- ---------------
##
## ----------------------------
##  Chi.squared   df   p.value
## ------------- ---- ---------
##   159.2143     1       0
## ----------------------------
##
## ---------------------------------
##  Odds Ratio   Lo - 95%   Hi - 95%
## ------------ ---------- ----------
##     3.92        3.14       4.90
## ---------------------------------
##
## -------------------------------
##  Risk Ratio   Lo - 0%   Hi - 0%
## ------------ --------- ---------
##     1.33        1.33      1.33
## -------------------------------
```

Obesity

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

```
## Cross-Tabulation, Row Proportions
## CVD * obesity
## Data Frame: data
##
##
## ------- --------- -------------- ------------- ---------------
##           obesity             no           yes           Total
##     CVD
##      no             2651 (91.2%)   255 ( 8.8%)   2906 (100.0%)
##     yes              344 (76.6%)   105 (23.4%)    449 (100.0%)
##   Total             2995 (89.3%)   360 (10.7%)   3355 (100.0%)
## ------- --------- -------------- ------------- ---------------
##
## ----------------------------
##  Chi.squared   df   p.value
## ------------- ---- ---------
##    85.149      1       0
## ----------------------------
##
## ---------------------------------
##  Odds Ratio   Lo - 95%   Hi - 95%
## ------------ ---------- ----------
##     3.17        2.46       4.09
## ---------------------------------
##
```

```
## --------------------------------
##  Risk Ratio   Lo - 0%   Hi - 0%
## ------------ --------- ---------
##     1.19       1.19      1.19
## --------------------------------
```

Asthma

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

```
## Cross-Tabulation, Row Proportions
## CVD * asthma
## Data Frame: data
##
##
## ------- -------- -------------- ------------ ---------------
##           asthma              no          yes           Total
##     CVD
##      no            2734 (93.2%)   199 (6.8%)   2933 (100.0%)
##     yes             396 (90.8%)    40 (9.2%)    436 (100.0%)
##   Total            3130 (92.9%)   239 (7.1%)   3369 (100.0%)
## ------- -------- -------------- ------------ ---------------
##
## ----------------------------
##  Chi.squared   df   p.value
## ------------- ---- ---------
##    2.9356      1    0.0866
## ----------------------------
##
## ---------------------------------
##  Odds Ratio   Lo - 95%   Hi - 95%
## ------------ ---------- ----------
##     1.39        0.97       1.98
## ---------------------------------
##
## --------------------------------
##  Risk Ratio   Lo - 0%   Hi - 0%
## ------------ --------- ---------
##     1.03       1.03      1.03
## --------------------------------
```

Hepatic

```
ctable(data$CVD, data$hepatic, chisq=TRUE, prop="r", OR=TRUE, useNA = "no")
```

```
## Cross-Tabulation, Row Proportions
## CVD * hepatic
## Data Frame: data
##
```

```
##
## ------- --------- --------------- ----------- ---------------
##           hepatic              no         yes           Total
##     CVD
##      no             2921 ( 99.6%)   12 (0.4%)   2933 (100.0%)
##     yes              426 ( 98.8%)    5 (1.2%)    431 (100.0%)
##   Total             3347 ( 99.5%)   17 (0.5%)   3364 (100.0%)
## ------- --------- --------------- ----------- ---------------
##
## ----------------------------
##  Chi.squared   df   p.value
## ------------- ---- ---------
##    2.8535      1    0.0912
## ----------------------------
##
## ---------------------------------
##  Odds Ratio   Lo - 95%   Hi - 95%
## ------------ ---------- ----------
##     2.86        1.00       8.15
## ---------------------------------
##
## --------------------------------
##  Risk Ratio   Lo - 0%   Hi - 0%
## ------------ --------- ---------
##     1.01       1.01      1.01
## --------------------------------
```

```
fisher.test(data$hepatic, data$CVD)
```

```
##
##  Fisher's Exact Test for Count Data
##
## data:  data$hepatic and data$CVD
## p-value = 0.05627
## alternative hypothesis: true odds ratio is not equal to 1
## 95 percent confidence interval:
##  0.7841874 8.7612195
## sample estimates:
## odds ratio
##   2.855734
```

Neurologic

```
ctable(data$CVD, data$neurologic, chisq=TRUE, prop="r", OR=TRUE, useNA = "no")
```

```
## Cross-Tabulation, Row Proportions
## CVD * neurologic
## Data Frame: data
##
##
## ------- ------------ -------------- ----------- ---------------
```

```
##           neurologic             no         yes           Total
##     CVD
##      no                2915 (99.0%)   28 (1.0%)   2943 (100.0%)
##     yes                 422 (97.9%)    9 (2.1%)    431 (100.0%)
##   Total                3337 (98.9%)   37 (1.1%)   3374 (100.0%)
## ------- ------------ -------------- ----------- ---------------
##
## ----------------------------
##  Chi.squared   df   p.value
## ------------- ---- ---------
##    3.4923      1    0.0617
## ----------------------------
##
## ---------------------------------
##  Odds Ratio   Lo - 95%   Hi - 95%
## ------------ ---------- ----------
##     2.22        1.04       4.74
## ---------------------------------
##
## --------------------------------
##  Risk Ratio   Lo - 0%   Hi - 0%
## ------------ --------- ---------
##     1.01       1.01      1.01
## --------------------------------
```

```
fisher.test(data$neurologic, data$CVD)
```

```
##
##  Fisher's Exact Test for Count Data
##
## data:  data$neurologic and data$CVD
## p-value = 0.04511
## alternative hypothesis: true odds ratio is not equal to 1
## 95 percent confidence interval:
##  0.9148775 4.8799321
## sample estimates:
## odds ratio
##   2.219605
```

Pneumologic

```
ctable(data$CVD, data$pneumologic, chisq=TRUE, prop="r", OR=TRUE, useNA = "no")
```

```
## Cross-Tabulation, Row Proportions
## CVD * pneumologic
## Data Frame: data
##
##
## ------- ------------- -------------- ----------- ---------------
##           pneumologic             no         yes           Total
##     CVD
```

```
##      no                2905 (98.9%)   31 (1.1%)   2936 (100.0%)
##     yes                 424 (97.0%)   13 (3.0%)    437 (100.0%)
##   Total                3329 (98.7%)   44 (1.3%)   3373 (100.0%)
## ------- ------------- -------------- ----------- ---------------
##
## ----------------------------
##  Chi.squared   df   p.value
## ------------- ---- ---------
##    9.4404      1    0.0021
## ----------------------------
##
## ---------------------------------
##  Odds Ratio   Lo - 95%   Hi - 95%
## ------------ ---------- ----------
##     2.87        1.49       5.53
## ---------------------------------
##
## -------------------------------
##  Risk Ratio   Lo - 0%   Hi - 0%
## ------------ --------- ---------
##     1.02        1.02      1.02
## -------------------------------
```

Immunodepression

```
ctable(data$CVD, data$imunodepre, chisq=TRUE, prop="r", OR=TRUE, useNA = "no")
```

```
## Cross-Tabulation, Row Proportions
## CVD * imunodepre
## Data Frame: data
##
##
## ------- ------------ -------------- ----------- ---------------
##           imunodepre              no         yes           Total
##     CVD
##      no                2874 (98.0%)   58 (2.0%)   2932 (100.0%)
##     yes                 418 (96.5%)   15 (3.5%)    433 (100.0%)
##   Total                3292 (97.8%)   73 (2.2%)   3365 (100.0%)
## ------- ------------ -------------- ----------- ---------------
##
## ----------------------------
##  Chi.squared   df   p.value
## ------------- ---- ---------
##    3.2567      1    0.0711
## ----------------------------
##
## ---------------------------------
##  Odds Ratio   Lo - 95%   Hi - 95%
## ------------ ---------- ----------
##     1.78        1.00       3.17
## ---------------------------------
##
```

```
## --------------------------------
##  Risk Ratio   Lo - 0%   Hi - 0%
## ------------ --------- ---------
##     1.02       1.02      1.02
## --------------------------------
```

Renal

```
ctable(data$CVD, data$renal, chisq=TRUE, prop="r", OR=TRUE, useNA = "no")
```

```
## Cross-Tabulation, Row Proportions
## CVD * renal
## Data Frame: data
##
##
## ------- ------- -------------- ----------- ---------------
##           renal              no         yes           Total
##     CVD
##      no            2890 (98.8%)   36 (1.2%)   2926 (100.0%)
##     yes             414 (95.6%)   19 (4.4%)    433 (100.0%)
##   Total            3304 (98.4%)   55 (1.6%)   3359 (100.0%)
## ------- ------- -------------- ----------- ---------------
##
## ----------------------------
##  Chi.squared   df   p.value
## ------------- ---- ---------
##    21.431      1       0
## ----------------------------
##
## ----------------------------------
##  Odds Ratio   Lo - 95%   Hi - 95%
## ------------ ---------- ----------
##     3.68        2.09       6.48
## ----------------------------------
##
## --------------------------------
##  Risk Ratio   Lo - 0%   Hi - 0%
## ------------ --------- ---------
##     1.03       1.03      1.03
## --------------------------------
```

The variable `comorb_group` indicates the number o comorbidities of each notification.

Any comorbidity

```
df <- select(data,obesity,hematologic,hepatic,asthma,diabetes,neurologic,pneumologic,imunodepre,renal)
soma <- function(x){
  if (sum(is.na(x))==9)
    return(NA_character_)
```

```
  else
   return(sum(!is.na(x) & x=="yes"))
}
data$qt_comorb_aux <- apply(df,1,soma)

data <-  data %>%
  mutate(qt_comorb = case_when(qt_comorb_aux== 9  ~ "9 comorbidities",
                               qt_comorb_aux == 7  ~ "7 comorbidities",
                               qt_comorb_aux== 6  ~ "6 comorbidities",
                               qt_comorb_aux == 5  ~ "5 comorbidities",
                               qt_comorb_aux== 4  ~ "4 comorbidities",
                               qt_comorb_aux == 3  ~ "3 comorbidities",
                               qt_comorb_aux == 2  ~ "2 comorbidities",
                               qt_comorb_aux == 1  ~ "1 comorbidity",
                               qt_comorb_aux == 0  ~ "No comorbidity",
                             TRUE ~ NA_character_))

data <-  data %>%
  mutate(comorb_group = case_when(qt_comorb_aux == 0 ~ "No comorbidity",
                               qt_comorb_aux == 1 ~ "1 comorbidity",
                               qt_comorb_aux == 2 ~ "2 comorbidities",
                               qt_comorb_aux > 2 ~ ">2 comorbidities",
                               TRUE ~ NA_character_))

data$comorb_group <-
  factor(data$comorb_group, levels = c("No comorbidity", "1 comorbidity", "2 comorbidities", ">2 comorbi
```

```
with(data, ctable(comorb_group, CVD, prop="c", useNA = "no", chisq = TRUE, OR = TRUE))
```

```
## Cross-Tabulation, Column Proportions
## comorb_group * CVD
## Data Frame: data
##
##
## ------------------ ----- --------------- -------------- ---------------
##                       CVD              no            yes           Total
##       comorb_group
##     No comorbidity         2126 ( 71.8%)   234 ( 46.8%)   2360 ( 68.2%)
##      1 comorbidity          701 ( 23.7%)   186 ( 37.2%)    887 ( 25.6%)
##    2 comorbidities          116 (  3.9%)    64 ( 12.8%)    180 (  5.2%)
##   >2 comorbidities           17 (  0.6%)    16 (  3.2%)     33 (  1.0%)
##              Total         2960 (100.0%)   500 (100.0%)   3460 (100.0%)
## ------------------ ----- --------------- -------------- ---------------
##
## ----------------------------
##  Chi.squared   df   p.value
## ------------- ---- ---------
##   165.5306     3       0
## ----------------------------
```

Outcome

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

# Ventilatory support
data <-  data %>%
  mutate(ven_support = case_when(SUPORT_VEN == 1 ~ "yes, invasive",
                                 SUPORT_VEN == 2 ~ "yes, noninvasive",
                                 SUPORT_VEN == 3 ~ "No",
                                TRUE ~ NA_character_))
```

ICU

```
#tabela cruzada de uti
with(data, ctable(CVD, icu, prop="r", OR=TRUE, useNA = "no", chisq = TRUE))
```

```
## Cross-Tabulation, Row Proportions
## CVD * icu
## Data Frame: data
##
##
## ------- ----- -------------- -------------- ---------------
##           icu             no            yes           Total
##     CVD
##      no         2043 (71.8%)    802 (28.2%)   2845 (100.0%)
##     yes          356 (63.0%)    209 (37.0%)    565 (100.0%)
##   Total         2399 (70.4%)   1011 (29.6%)   3410 (100.0%)
## ------- ----- -------------- -------------- ---------------
##
## ----------------------------
##  Chi.squared   df   p.value
## ------------- ---- ---------
##    17.0872     1       0
## ----------------------------
##
## ---------------------------------
##  Odds Ratio   Lo - 95%   Hi - 95%
## ------------ ---------- ----------
##     1.50        1.24       1.81
## ---------------------------------
##
## -------------------------------
##  Risk Ratio   Lo - 0%   Hi - 0%
## ------------ --------- ---------
##     1.14       1.14      1.14
## -------------------------------
```

1st trimester

```
df4 <- data %>%
  filter(classi_gesta_puerp == "1tri")

with(df4, ctable(CVD, icu, prop="r", OR=TRUE, useNA = "no", chisq = TRUE))
```

```
## Cross-Tabulation, Row Proportions
## CVD * icu
## Data Frame: df4
##
##
## ------- ----- ------------- ------------ --------------
##           icu             no          yes           Total
##     CVD
##      no          121 (77.1%)   36 (22.9%)   157 (100.0%)
##     yes           18 (58.1%)   13 (41.9%)    31 (100.0%)
##   Total          139 (73.9%)   49 (26.1%)   188 (100.0%)
## ------- ----- ------------- ------------ --------------
##
## ----------------------------
##  Chi.squared   df   p.value
## ------------- ---- ---------
##    3.9164      1    0.0478
## ----------------------------
##
## ----------------------------------
##  Odds Ratio   Lo - 95%   Hi - 95%
## ------------ ---------- ----------
##     2.43        1.09       5.43
## ----------------------------------
##
## --------------------------------
##  Risk Ratio   Lo - 0%   Hi - 0%
## ------------ --------- ---------
##     1.33        1.33      1.33
## --------------------------------
```

2nd trimester

```
df4 <- data %>%
  filter(classi_gesta_puerp == "2tri")

with(df4, ctable(CVD, icu, prop="r", OR=TRUE, useNA = "no", chisq = TRUE))
```

```
## Cross-Tabulation, Row Proportions
## CVD * icu
## Data Frame: df4
##
##
```

```
## ------- ----- ------------- ------------- --------------
##           icu            no           yes           Total
##     CVD
##      no          315 (68.8%)   143 (31.2%)   458 (100.0%)
##     yes           66 (58.4%)    47 (41.6%)   113 (100.0%)
##   Total          381 (66.7%)   190 (33.3%)   571 (100.0%)
## ------- ----- ------------- ------------- --------------
##
## ----------------------------
##  Chi.squared   df   p.value
## ------------- ---- ---------
##    3.9355      1    0.0473
## ----------------------------
##
## ---------------------------------
##  Odds Ratio   Lo - 95%   Hi - 95%
## ------------ ---------- ----------
##     1.57        1.03       2.39
## ---------------------------------
##
## --------------------------------
##  Risk Ratio   Lo - 0%   Hi - 0%
## ------------ --------- ---------
##     1.18       1.18      1.18
## --------------------------------
```

3rd trimester

```
df4 <- data %>%
  filter(classi_gesta_puerp == "3tri")

with(df4, ctable(CVD, icu, prop="r", OR=TRUE, useNA = "no", chisq = TRUE))
```

```
## Cross-Tabulation, Row Proportions
## CVD * icu
## Data Frame: df4
##
##
## ------- ----- -------------- ------------- ---------------
##           icu              no           yes            Total
##     CVD
##      no           883 (76.6%)   270 (23.4%)   1153 (100.0%)
##     yes           159 (68.2%)    74 (31.8%)    233 (100.0%)
##   Total          1042 (75.2%)   344 (24.8%)   1386 (100.0%)
## ------- ----- -------------- ------------- ---------------
##
## ----------------------------
##  Chi.squared   df   p.value
## ------------- ---- ---------
##    6.7894      1    0.0092
## ----------------------------
##
```

```
## ---------------------------------
##  Odds Ratio   Lo - 95%   Hi - 95%
## ------------ ---------- ----------
##     1.52        1.12       2.07
## ---------------------------------
##
## --------------------------------
##  Risk Ratio   Lo - 0%   Hi - 0%
## ------------ --------- ---------
##     1.12       1.12      1.12
## --------------------------------
```

Puerperium

```
df4 <- data %>%
  filter(classi_gesta_puerp == "puerp")

with(df4, ctable(CVD, icu, prop="r", OR=TRUE, useNA = "no", chisq = TRUE))
```

```
## Cross-Tabulation, Row Proportions
## CVD * icu
## Data Frame: df4
##
##
## ------- ----- ------------ ------------ ---------------
##           icu            no           yes           Total
##     CVD
##      no         678 (66.9%)   335 (33.1%)   1013 (100.0%)
##     yes          94 (58.4%)    67 (41.6%)    161 (100.0%)
##   Total         772 (65.8%)   402 (34.2%)   1174 (100.0%)
## ------- ----- ------------ ------------ ---------------
##
## ----------------------------
##  Chi.squared   df   p.value
## ------------- ---- ---------
##    4.1332      1     0.042
## ----------------------------
##
## ---------------------------------
##  Odds Ratio   Lo - 95%   Hi - 95%
## ------------ ---------- ----------
##     1.44        1.03       2.03
## ---------------------------------
##
## --------------------------------
##  Risk Ratio   Lo - 0%   Hi - 0%
## ------------ --------- ---------
##     1.15       1.15      1.15
## --------------------------------
```

Duration of hospitalization in ICU

```
data <- data %>%
   dplyr::mutate(
    dt_entuti = as.Date(DT_ENTUTI, format = "%d/%m/%Y"),
    dt_saiduti = as.Date(DT_SAIDUTI, format = "%d/%m/%Y"),
    icu_days = as.numeric(dt_saiduti-dt_entuti)
)
```

```
df <- data[data$icu== "yes" & !is.na(data$icu) & !is.na(data$icu_days),]

datasummary((CVD) ~ icu_days*(n+media+DP+mediana+minimo+maximo+q25+q75+IQR),
            data = df, output = 'markdown')
```

	n	media	DP	mediana	minimo	maximo	q25	q75	IQR
no	514.00	10.53	10.73	7.00	0.00	94.00	3.00	15.00	12.00
yes	114.00	13.46	14.49	10.50	0.00	105.00	4.00	17.00	13.00

```
wilcox.test(icu_days ~ CVD, data = df)
```

```
##
##  Wilcoxon rank sum test with continuity correction
##
## data:  icu_days by CVD
## W = 25486, p-value = 0.02941
## alternative hypothesis: true location shift is not equal to 0
```

Ventilatory support

```
with(data, ctable(CVD, ven_support, prop="r", useNA = "no", chisq = TRUE))
```

```
## Cross-Tabulation, Row Proportions
## CVD * ven_support
## Data Frame: data
##
##
## ------- ------------- -------------- --------------- ------------------ ---------------
##           ven_support             No   yes, invasive   yes, noninvasive           Total
##     CVD
##      no                 1470 (52.7%)     443 (15.9%)        877 (31.4%)   2790 (100.0%)
##     yes                  226 (40.7%)     110 (19.8%)        219 (39.5%)    555 (100.0%)
##   Total                 1696 (50.7%)     553 (16.5%)       1096 (32.8%)   3345 (100.0%)
## ------- ------------- -------------- --------------- ------------------ ---------------
##
## ----------------------------
##  Chi.squared   df   p.value
## ------------- ---- ---------
##    26.5268     2       0
## ----------------------------
```

Intubation

```
data <- data %>%
  mutate(intubation = case_when(SUPORT_VEN == 1 ~ "yes",
                                SUPORT_VEN == 2 ~ "no",
                                SUPORT_VEN == 3 ~ "no",
                               TRUE ~ NA_character_)
         )
```

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

```
## Cross-Tabulation, Row Proportions
## CVD * intubation
## Data Frame: data
##
##
## ------- ------------ -------------- ------------- ---------------
##           intubation             no           yes           Total
##     CVD
##      no                2347 (84.1%)   443 (15.9%)   2790 (100.0%)
##     yes                 445 (80.2%)   110 (19.8%)    555 (100.0%)
##   Total                2792 (83.5%)   553 (16.5%)   3345 (100.0%)
## ------- ------------ -------------- ------------- ---------------
##
## ----------------------------
##  Chi.squared   df   p.value
## ------------ ---- ---------
##    4.9304      1    0.0264
## ----------------------------
##
## ---------------------------------
##  Odds Ratio   Lo - 95%   Hi - 95%
## ------------ ---------- ----------
##     1.31        1.04       1.65
## ---------------------------------
##
## -------------------------------
##  Risk Ratio   Lo - 0%   Hi - 0%
## ------------ --------- ---------
##     1.05       1.05      1.05
## -------------------------------
```

1st trimester

```
df4 <- data %>%
  filter(classi_gesta_puerp == "1tri")

with(df4, ctable(CVD, intubation, prop="r", OR=TRUE, useNA = "no", chisq = FALSE))
```

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

```
## CVD * intubation
## Data Frame: df4
##
##
## ------- ------------ ------------- ------------ --------------
##           intubation            no          yes          Total
##     CVD
##      no                135 (88.8%)   17 (11.2%)   152 (100.0%)
##     yes                 23 (79.3%)    6 (20.7%)    29 (100.0%)
##   Total                158 (87.3%)   23 (12.7%)   181 (100.0%)
## ------- ------------ ------------- ------------ --------------
##
## ----------------------------------
##  Odds Ratio   Lo - 95%   Hi - 95%
## ------------ ---------- ----------
##     2.07        0.74       5.80
## ----------------------------------
##
## --------------------------------
##  Risk Ratio   Lo - 0%   Hi - 0%
## ------------ --------- ---------
##     1.12       1.12      1.12
## --------------------------------
```

```
fisher.test(df4$CVD, df4$intubation)
```

```
##
##  Fisher's Exact Test for Count Data
##
## data:  df4$CVD and df4$intubation
## p-value = 0.2182
## alternative hypothesis: true odds ratio is not equal to 1
## 95 percent confidence interval:
##  0.601484 6.248095
## sample estimates:
## odds ratio
##   2.061721
```

2nd trimester

```
df4 <- data %>%
  filter(classi_gesta_puerp == "2tri")

with(df4, ctable(CVD, intubation, prop="r", OR=TRUE, useNA = "no", chisq = TRUE))
```

```
## Cross-Tabulation, Row Proportions
## CVD * intubation
## Data Frame: df4
##
##
## ------- ------------ ------------- ------------ --------------
```

```
##           intubation            no          yes          Total
##     CVD
##      no                373 (85.0%)   66 (15.0%)   439 (100.0%)
##     yes                 88 (79.3%)   23 (20.7%)   111 (100.0%)
##   Total                461 (83.8%)   89 (16.2%)   550 (100.0%)
## ------- ------------ ------------- ------------ --------------
##
## ----------------------------
##  Chi.squared   df   p.value
## ------------- ---- ---------
##    1.7139      1    0.1905
## ----------------------------
##
## ---------------------------------
##  Odds Ratio   Lo - 95%   Hi - 95%
## ------------ ---------- ----------
##     1.48        0.87       2.51
## ---------------------------------
##
## --------------------------------
##  Risk Ratio   Lo - 0%   Hi - 0%
## ------------ --------- ---------
##     1.07        1.07      1.07
## --------------------------------
```

3rd trimester

```
df4 <- data %>%
  filter(classi_gesta_puerp == "3tri")

with(df4, ctable(CVD, intubation, prop="r", OR=TRUE, useNA = "no", chisq = TRUE))
```

```
## Cross-Tabulation, Row Proportions
## CVD * intubation
## Data Frame: df4
##
##
## ------- ------------ -------------- ------------- ---------------
##           intubation             no           yes           Total
##     CVD
##      no                1007 (89.0%)   125 (11.0%)   1132 (100.0%)
##     yes                 195 (84.4%)    36 (15.6%)    231 (100.0%)
##   Total                1202 (88.2%)   161 (11.8%)   1363 (100.0%)
## ------- ------------ -------------- ------------- ---------------
##
## ----------------------------
##  Chi.squared   df   p.value
## ------------- ---- ---------
##    3.3759      1    0.0662
## ----------------------------
##
## ---------------------------------
```

```
##  Odds Ratio   Lo - 95%   Hi - 95%
## ------------ ---------- ----------
##     1.49        1.00       2.22
## ----------------------------------
##
## --------------------------------
##  Risk Ratio   Lo - 0%   Hi - 0%
## ------------ --------- ---------
##     1.05       1.05      1.05
## --------------------------------
```

Puerperium

```
df4 <- data %>%
  filter(classi_gesta_puerp == "puerp")

with(df4, ctable(CVD, intubation, prop="r", OR=TRUE, useNA = "no", chisq = TRUE))
```

```
## Cross-Tabulation, Row Proportions
## CVD * intubation
## Data Frame: df4
##
##
## ------- ------------ ------------- ------------- ---------------
##           intubation            no           yes           Total
##     CVD
##      no                778 (77.6%)   224 (22.4%)   1002 (100.0%)
##     yes                118 (75.2%)    39 (24.8%)    157 (100.0%)
##   Total                896 (77.3%)   263 (22.7%)   1159 (100.0%)
## ------- ------------ ------------- ------------- ---------------
##
## ----------------------------
##  Chi.squared   df   p.value
## ------------- ---- ---------
##    0.3468      1    0.5559
## ----------------------------
##
## ----------------------------------
##  Odds Ratio   Lo - 95%   Hi - 95%
## ------------ ---------- ----------
##     1.15        0.78       1.70
## ----------------------------------
##
## --------------------------------
##  Risk Ratio   Lo - 0%   Hi - 0%
## ------------ --------- ---------
##     1.03       1.03      1.03
## --------------------------------
```

Outcome - cure x death

```
with(data, ctable(CVD, evolution, prop="r", OR=TRUE, useNA = "no", chisq = TRUE))
```

```
## Cross-Tabulation, Row Proportions
## CVD * evolution
## Data Frame: data
##
##
## ------- ----------- -------------- ------------- ---------------
##           evolution            cure          death            Total
##     CVD
##      no                2559 (86.5%)   401 (13.5%)   2960 (100.0%)
##     yes                 488 (81.1%)   114 (18.9%)    602 (100.0%)
##   Total                3047 (85.5%)   515 (14.5%)   3562 (100.0%)
## ------- ----------- -------------- ------------- ---------------
##
## ----------------------------
##  Chi.squared   df   p.value
## ------------- ---- ---------
##    11.3176     1     8e-04
## ----------------------------
##
## ---------------------------------
##  Odds Ratio   Lo - 95%   Hi - 95%
## ------------ ---------- ----------
##     1.49        1.19       1.88
## ---------------------------------
##
## -------------------------------
##  Risk Ratio   Lo - 0%   Hi - 0%
## ------------ --------- ---------
##     1.07       1.07      1.07
## -------------------------------
```

1st trimester

```
df4 <- data %>%
  filter(classi_gesta_puerp == "1tri")

with(df4, ctable(CVD, evolution, prop="r", OR=TRUE, useNA = "no", chisq = FALSE))
```

```
## Cross-Tabulation, Row Proportions
## CVD * evolution
## Data Frame: df4
##
##
## ------- ----------- ------------- ------------ ---------------
##           evolution           cure        death           Total
##     CVD
```

```
##      no               146 (90.7%)   15 ( 9.3%)   161 (100.0%)
##     yes                30 (88.2%)    4 (11.8%)    34 (100.0%)
##   Total               176 (90.3%)   19 ( 9.7%)   195 (100.0%)
## ------- ----------- ------------- ------------ --------------
##
## ----------------------------------
##  Odds Ratio   Lo - 95%   Hi - 95%
## ------------ ---------- ----------
##     1.30        0.40       4.18
## ----------------------------------
##
## --------------------------------
##  Risk Ratio   Lo - 0%   Hi - 0%
## ------------ --------- ---------
##     1.03       1.03      1.03
## --------------------------------
```

```
fisher.test(df4$CVD, df4$evolution)
```

```
##
##  Fisher's Exact Test for Count Data
##
## data:  df4$CVD and df4$evolution
## p-value = 0.7494
## alternative hypothesis: true odds ratio is not equal to 1
## 95 percent confidence interval:
##  0.2926084 4.4639958
## sample estimates:
## odds ratio
##   1.295924
```

2nd trimester

```
df4 <- data %>%
  filter(classi_gesta_puerp == "2tri")

with(df4, ctable(CVD, evolution, prop="r", OR=TRUE, useNA = "no", chisq = TRUE))
```

```
## Cross-Tabulation, Row Proportions
## CVD * evolution
## Data Frame: df4
##
##
## ------- ----------- ------------- ------------ --------------
##           evolution          cure        death          Total
##     CVD
##      no               410 (87.0%)   61 (13.0%)   471 (100.0%)
##     yes                90 (75.0%)   30 (25.0%)   120 (100.0%)
##   Total               500 (84.6%)   91 (15.4%)   591 (100.0%)
## ------- ----------- ------------- ------------ --------------
##
```

```
## ----------------------------
##  Chi.squared   df   p.value
## ------------- ---- ---------
##     9.753      1    0.0018
## ----------------------------
##
## ----------------------------------
##  Odds Ratio   Lo - 95%   Hi - 95%
## ------------ ---------- ----------
##     2.24        1.37       3.67
## ----------------------------------
##
## --------------------------------
##  Risk Ratio   Lo - 0%   Hi - 0%
## ------------ --------- ---------
##     1.16        1.16      1.16
## --------------------------------
```

3rd trimester

```
df4 <- data %>%
  filter(classi_gesta_puerp == "3tri")

with(df4, ctable(CVD, evolution, prop="r", OR=TRUE, useNA = "no", chisq = TRUE))
```

```
## Cross-Tabulation, Row Proportions
## CVD * evolution
## Data Frame: df4
##
##
## ------- ----------- -------------- ------------- ----------------
##           evolution            cure          death            Total
##     CVD
##      no                1071 (89.3%)   128 (10.7%)   1199 (100.0%)
##     yes                 212 (85.5%)    36 (14.5%)    248 (100.0%)
##   Total                1283 (88.7%)   164 (11.3%)   1447 (100.0%)
## ------- ----------- -------------- ------------- ----------------
##
## ----------------------------
##  Chi.squared   df   p.value
## ------------- ---- ---------
##    2.6461      1    0.1038
## ----------------------------
##
## ----------------------------------
##  Odds Ratio   Lo - 95%   Hi - 95%
## ------------ ---------- ----------
##     1.42        0.95       2.12
## ----------------------------------
##
## --------------------------------
##  Risk Ratio   Lo - 0%   Hi - 0%
```

```
## ------------ --------- ---------
##     1.04       1.04      1.04
## --------------------------------
```

Puerperium

```
df4 <- data %>%
  filter(classi_gesta_puerp == "puerp")

with(df4, ctable(CVD, evolution, prop="r", OR=TRUE, useNA = "no", chisq = TRUE))
```

```
## Cross-Tabulation, Row Proportions
## CVD * evolution
## Data Frame: df4
##
##
## ------- ----------- ------------- ------------- ---------------
##           evolution          cure         death           Total
##     CVD
##      no                856 (81.9%)   189 (18.1%)   1045 (100.0%)
##     yes                133 (78.2%)    37 (21.8%)    170 (100.0%)
##   Total                989 (81.4%)   226 (18.6%)   1215 (100.0%)
## ------- ----------- ------------- ------------- ---------------
##
## ----------------------------
##  Chi.squared   df   p.value
## ------------- ---- ---------
##    1.0751      1    0.2998
## ----------------------------
##
## ----------------------------------
##  Odds Ratio   Lo - 95%   Hi - 95%
## ------------ ---------- ----------
##     1.26        0.85       1.87
## ----------------------------------
##
## --------------------------------
##  Risk Ratio   Lo - 0%   Hi - 0%
## ------------ --------- ---------
##     1.05       1.05      1.05
## --------------------------------
```

Time elapsed between the start of symptoms and the outcome (days)

```
data <- data %>%
   dplyr::mutate(
    dt_sin_pri = as.Date(DT_SIN_PRI, format = "%d/%m/%Y"),
    dt_evoluca = as.Date(DT_EVOLUCA, format = "%d/%m/%Y"),
    days_symp_evol = as.numeric(dt_evoluca-dt_sin_pri)
)
```

```r
df <- data[!is.na(data$days_symp_evol) & !is.na(data$CVD),]

datasummary((CVD) ~ days_symp_evol*(n+media+DP+mediana+minimo+maximo+q25+q75+IQR),
            data = df, output = 'markdown')
```

	n	media	DP	mediana	minimo	maximo	q25	q75	IQR
no	2863.00	16.00	15.80	13.00	0.00	244.00	8.00	19.00	11.00
yes	586.00	17.10	12.80	14.00	0.00	113.00	9.00	20.75	11.75

```r
wilcox.test(days_symp_evol ~ CVD, data = df)
```

```
##
##  Wilcoxon rank sum test with continuity correction
##
## data:  days_symp_evol by CVD
## W = 751451, p-value = 6.809e-05
## alternative hypothesis: true location shift is not equal to 0
```

Considering only death cases

```r
df <- data[!is.na(data$days_symp_evol) & !is.na(data$CVD),]

df <- df %>%
  filter(evolution == "death")

datasummary((CVD) ~ days_symp_evol*(n+media+DP+mediana+minimo+maximo+q25+q75+IQR),
            data = df, output = 'markdown')
```

	n	media	DP	mediana	minimo	maximo	q25	q75	IQR
no	399.00	20.34	13.86	18.00	0.00	158.00	12.00	27.00	15.00
yes	114.00	20.04	14.11	17.00	0.00	113.00	11.00	26.75	15.75

```r
wilcox.test(days_symp_evol ~ CVD, data = df)
```

```
##
##  Wilcoxon rank sum test with continuity correction
##
## data:  days_symp_evol by CVD
## W = 23410, p-value = 0.6331
## alternative hypothesis: true location shift is not equal to 0
```

Considering only cure cases

```r
df <- data[!is.na(data$days_symp_evol) & !is.na(data$CVD),]

df <- df %>%
  filter(evolution == "cure")

datasummary((CVD) ~ days_symp_evol*(n+media+DP+mediana+minimo+maximo+q25+q75+IQR),
            data = df, output = 'markdown')
```

	n	media	DP	mediana	minimo	maximo	q25	q75	IQR
no	2464.00	15.30	15.99	12.00	0.00	244.00	7.00	18.00	11.00
yes	472.00	16.39	12.37	13.00	0.00	93.00	9.00	19.00	10.00

```r
wilcox.test(days_symp_evol ~ CVD, data = df)
```

```
##
##  Wilcoxon rank sum test with continuity correction
##
## data:  days_symp_evol by CVD
## W = 513735, p-value = 5.814e-05
## alternative hypothesis: true location shift is not equal to 0
```

Distribution of number of hospitalizations due to COVID-19 infection by month of first symptoms, stratified by groups with and without CVD

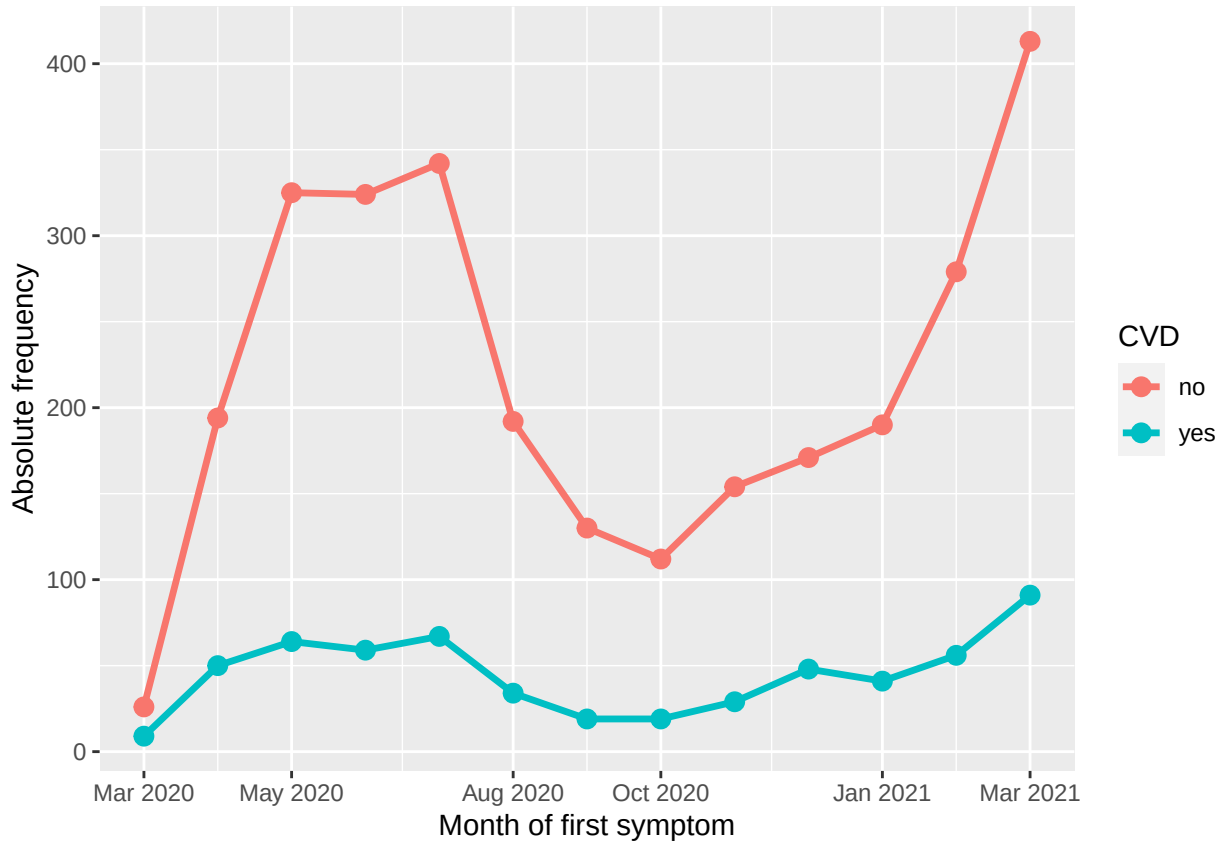
```r
# Date of the first symptoms
data <- data %>%
mutate(dt_first_symp = as.Date(DT_SIN_PRI, format = "%d/%m/%Y")
)
```

The next graph presents the temporal evolution of hospitalizations by month of first symptoms, stratified by groups with and without cardiovascular disease.

```r
## Creating the variable month_year
d1 <- data[data$dt_first_symp < as.Date("01/04/2021",format="%d/%m/%Y"),]
d1 <- d1 %>%
mutate(month_year = paste(formatC(month(dt_first_symp), width=2, format="d", flag="0"),year(dt_first_sy

d<- table(factor(d1$month_year, levels = c("03/2020", "04/2020", "05/2020", "06/2020", "07/2020", "08/2
G <- data.table(d)
Sys.setlocale("LC_TIME","C")
```

```
## [1] "C"
```

```r
G$V1 <- as.yearmon(G$V1, format = "%m/%Y")
ggplot(G, aes(x=V1, y=N, colour=factor(V2), group=V2)) +
geom_line(size=1.2) + geom_point(size=3) +
labs( x="Month of first symptom", y="Absolute frequency", color = "CVD")
```



Frequency table of number of hospitalizations due to COVID-19 infection by month of first symptoms, stratified by groups with and without CVD.

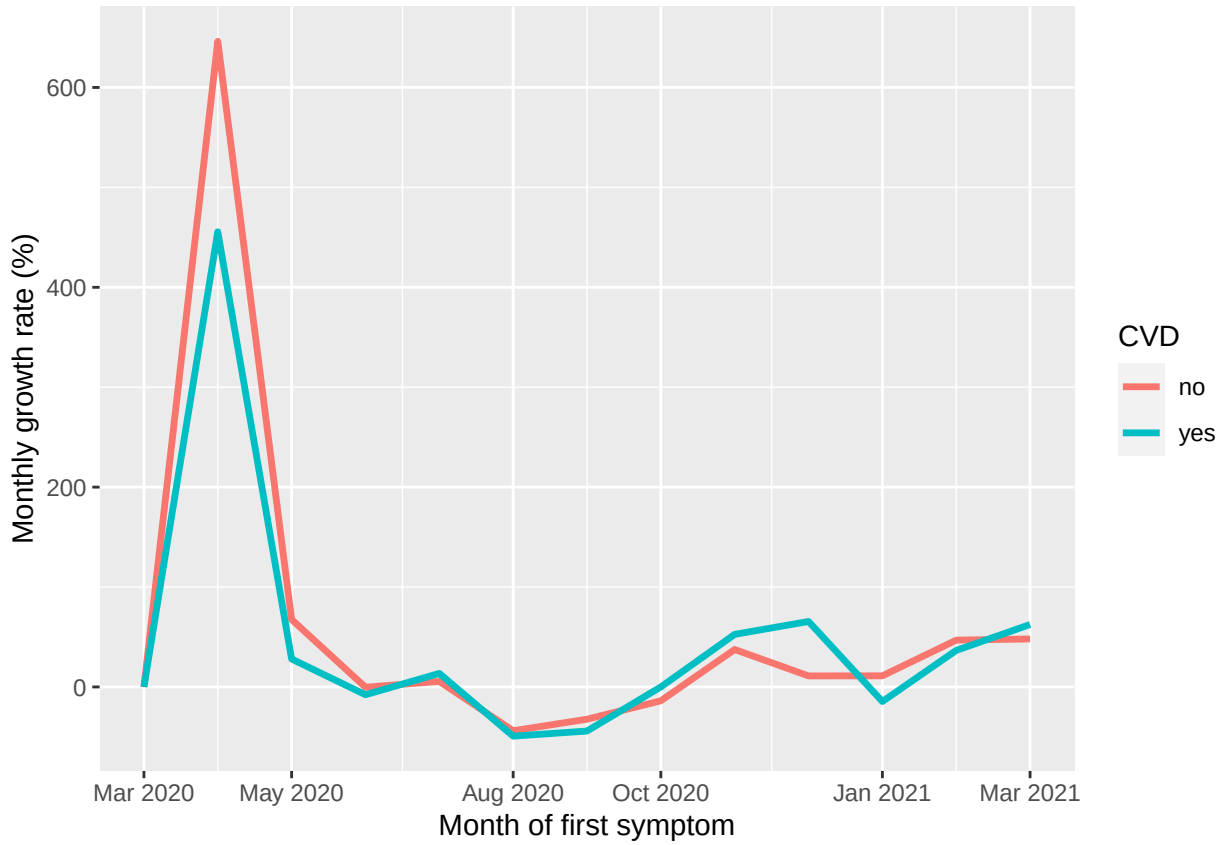
```
d1$mes_ano <- factor(d1$month_year, levels = c("03/2020", "04/2020", "05/2020", "06/2020", "07/2020", "
ctable(d1$month_year, d1$CVD, prop="c", useNA = "no")
```

```
## Cross-Tabulation, Column Proportions
## month_year * CVD
## Data Frame: d1
##
## ------------ ----- --------------- -------------- ---------------
##                CVD              no            yes           Total
##   month_year
##      01/2021          190 (  6.7%)    41 (  7.0%)    231 (  6.7%)
##      02/2021          279 (  9.8%)    56 (  9.6%)    335 (  9.7%)
##      03/2020           26 (  0.9%)     9 (  1.5%)     35 (  1.0%)
##      03/2021          413 ( 14.5%)    91 ( 15.5%)    504 ( 14.7%)
##      04/2020          194 (  6.8%)    50 (  8.5%)    244 (  7.1%)
##      05/2020          325 ( 11.4%)    64 ( 10.9%)    389 ( 11.3%)
##      06/2020          324 ( 11.4%)    59 ( 10.1%)    383 ( 11.1%)
##      07/2020          342 ( 12.0%)    67 ( 11.4%)    409 ( 11.9%)
##      08/2020          192 (  6.7%)    34 (  5.8%)    226 (  6.6%)
##      09/2020          130 (  4.6%)    19 (  3.2%)    149 (  4.3%)
##      10/2020          112 (  3.9%)    19 (  3.2%)    131 (  3.8%)
##      11/2020          154 (  5.4%)    29 (  4.9%)    183 (  5.3%)
##      12/2020          171 (  6.0%)    48 (  8.2%)    219 (  6.4%)
```

```
##        Total         2852 (100.0%)   586 (100.0%)   3438 (100.0%)
## ------------ ----- --------------- -------------- ---------------
```

Now, to understand better the monthly growth rate of hospitalized cases by COVID-19, we present the following graph:

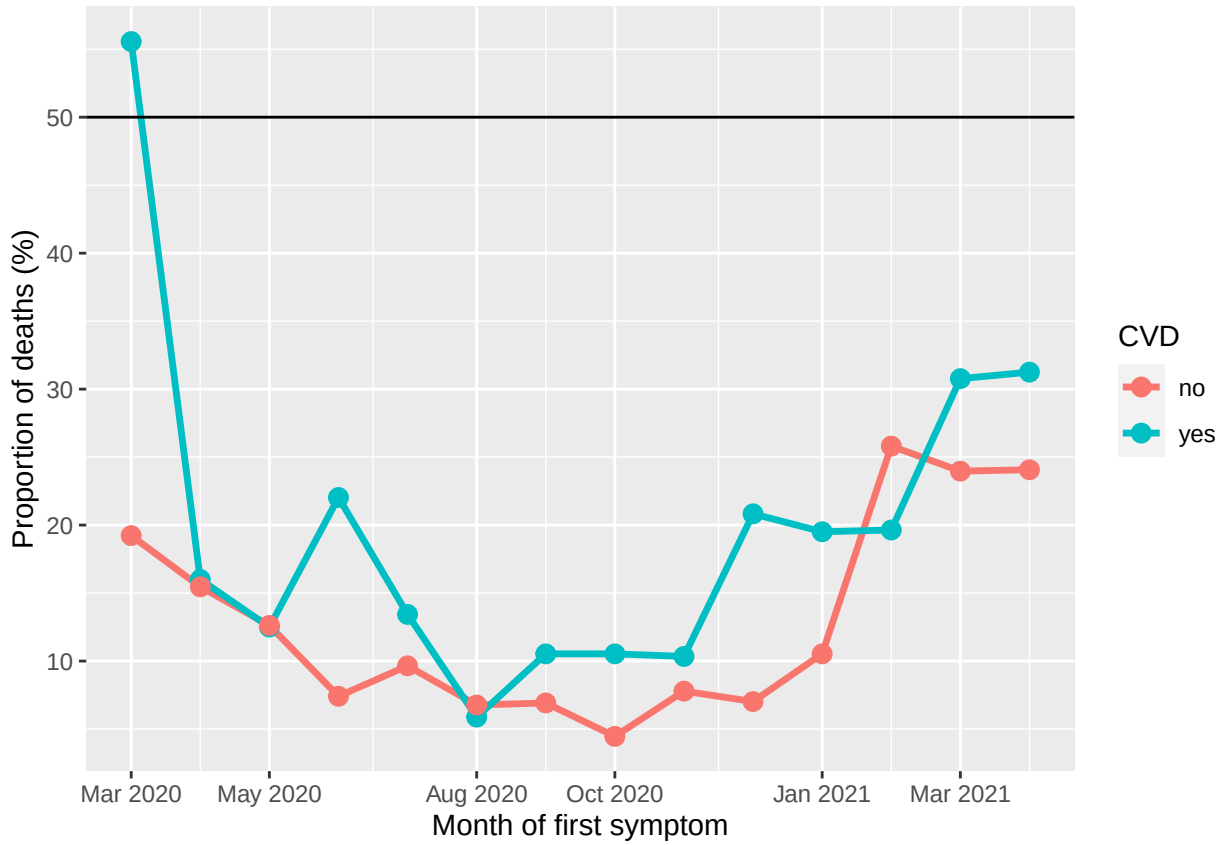
```
D1<- table(d1$month_year, d1$CVD) %>%
      data.table()
D1$V1 <- as.yearmon(D1$V1, format = "%m/%Y")

# Calculating the monthly growth rate
D1 <- D1 %>%
  arrange(D1)

dif<-c()
dif[1:2]<-0
for(i in 1:nrow(D1)){
  if( i %% 2 == 0){
    dif[i]<-D1$N[i+2]-D1$N[i]
  }
  else{
    dif[i]<-D1$N[i+2]-D1$N[i]
  }
}
D1$dif<-dif

taxa_cresc<-c()
taxa_cresc[1:2]<-0
for(i in 1:(nrow(D1)-2)){
  if( i %% 2 == 0){
    taxa_cresc[i+2]<-(dif[i])/(D1$N[i])
  }
  else{
    taxa_cresc[i+2]<-(dif[i])/(D1$N[i])
  }
}

D1$growth_rate <-taxa_cresc*100

ggplot(D1) + geom_line(aes(x=V1, y = growth_rate, color = V2), size=1.2) + labs( x="Month of first symp
```



Proportion of deaths in the CVD and non-CVD groups, fixed the month of the first symptom.

```
# Proportion of deaths in the group with presence of CVD
d1 <- data
d1 <- d1 %>%
  filter(CVD == 'yes')
d1 <-  d1 %>%
  mutate(month_year = paste(formatC(month(dt_first_symp), width=2, format="d", flag="0"),year(dt_first_s

d<- prop.table(table(d1$month_year, d1$evolution),1)
G3 <- as.data.frame(d)
G3 <- G3[G3$Var2 == "death",]
G3$Freq <- round((G3$Freq)*100, 2)
G3$Var1 <- as.yearmon(G3$Var1, format = "%m/%Y")

# Proportion of deaths in the group with absence of CVD
d2 <- data
d2 <- d2 %>%
  filter(CVD == 'no')
d2 <-  d2 %>%
  mutate(month_year = paste(formatC(month(dt_first_symp), width=2, format="d", flag="0"),year(dt_first_s

d2<- prop.table(table(d2$month_year, d2$evolution),1)
G32 <- as.data.frame(d2)
```

```r
G32 <- G32[G32$Var2 == "death",]
G32$Freq <- round((G32$Freq)*100, 2)
G32$Var1 <- as.yearmon(G32$Var1, format = "%m/%Y")

# Concatening the proportion of deaths in both groups, with and without CVD
G33 <- rbind(G3, G32)
cardio <- c(rep("yes", nrow(G3)), rep("no", nrow(G32)))
G33 <- cbind(G33, cardio)

ggplot(data=G33,aes(x = Var1, y=Freq, color = cardio)) + geom_line(size=1.2) +
geom_point(size=3) +
geom_hline(yintercept = 50) +
labs( x="Month of first symptom", y="Proportion of deaths (%)", color = "CVD")
```



Propensity Score Matching (PSM):

The analysis that will be made in this section aims to understand the effect of having cardiovascular disease or not on some variables of interest such as symptoms and outcome. In order to make the CVD and non-CVD groups similar with respect to the distribution of some variables that may bring confusion to the study, we will make use of the Propensity Score Matching (PSM) technique. The variables we will control in the analysis are: age, race, diabetes and obesity.

First, we present the difference result between the groups regarding the control variables before the PSM. We consider as "balanced" the cases with mean difference greater than 0.05. As we can see, for most categories of control variables the groups are not balanced before the matching.

```r
data$cardio <- ifelse(data$CVD=="yes",1,0)

bal.tab(cardio ~ NU_IDADE_N + ethnicity + diabetes + obesity, data = data, estimand = "ATE", m.threshol
```

```
## Balance Measures
##                          Type Diff.Un      M.Threshold.Un
## NU_IDADE_N           Contin.  0.5949 Not Balanced, >0.05
## ethnicity_black       Binary  0.0258     Balanced, <0.05
## ethnicity_brown       Binary -0.0535 Not Balanced, >0.05
## ethnicity_indigenous  Binary -0.0097     Balanced, <0.05
## ethnicity_white       Binary  0.0429     Balanced, <0.05
## ethnicity_yellow      Binary -0.0054     Balanced, <0.05
## ethnicity:<NA>        Binary  0.0264     Balanced, <0.05
## diabetes_yes          Binary  0.2218 Not Balanced, >0.05
## diabetes:<NA>         Binary  0.2149 Not Balanced, >0.05
## obesity_yes           Binary  0.1461 Not Balanced, >0.05
## obesity:<NA>          Binary  0.2359 Not Balanced, >0.05
##
## Balance tally for mean differences
##                      count
## Balanced, <0.05          5
## Not Balanced, >0.05      6
##
## Variable with the greatest mean difference
##    Variable Diff.Un      M.Threshold.Un
##  NU_IDADE_N  0.5949 Not Balanced, >0.05
##
## Sample sizes
##     Control Treated
## All    2960     602
```

As one can see, all variables categories are balanced after PSM.

```r
## Estimating the weights of each sampling unit
fit <- weightit(cardio ~ NU_IDADE_N + ethnicity + diabetes + obesity, use.mlogit = FALSE, data = data,
                method = "ps", estimand = "ATE")

data$weight <- fit$weights

bal.tab(fit, m.threshold = 0.05, disp.v.ratio = TRUE)
```

```
## Call
##  weightit(formula = cardio ~ NU_IDADE_N + ethnicity + diabetes +
##     obesity, data = data, method = "ps", estimand = "ATE", use.mlogit = FALSE)
##
## Balance Measures
##                           Type Diff.Adj     M.Threshold V.Ratio.Adj
## prop.score            Distance   0.0394 Balanced, <0.05      1.3504
## NU_IDADE_N             Contin.   0.0041 Balanced, <0.05      0.9849
## ethnicity_black         Binary  -0.0003 Balanced, <0.05           .
## ethnicity_brown         Binary  -0.0088 Balanced, <0.05           .
## ethnicity_indigenous    Binary   0.0056 Balanced, <0.05           .
```

```
## ethnicity_white        Binary   0.0088 Balanced, <0.05           .
## ethnicity_yellow       Binary  -0.0052 Balanced, <0.05           .
## ethnicity:<NA>         Binary   0.0144 Balanced, <0.05           .
## diabetes_yes           Binary  -0.0036 Balanced, <0.05           .
## diabetes:<NA>          Binary   0.0117 Balanced, <0.05           .
## obesity_yes            Binary   0.0064 Balanced, <0.05           .
## obesity:<NA>           Binary   0.0133 Balanced, <0.05           .
##
## Balance tally for mean differences
##                      count
## Balanced, <0.05         12
## Not Balanced, >0.05      0
##
## Variable with the greatest mean difference
##         Variable Diff.Adj     M.Threshold
##  ethnicity:<NA>   0.0144 Balanced, <0.05
##
## Effective sample sizes
##            Control Treated
## Unadjusted  2960.   602.
## Adjusted    2332.6  331.15
```

Symptom analysis after PSM:

```
with(data, ctable(CVD, fever, prop="r", OR=TRUE, useNA = "no", chisq = TRUE, weights = weight))
```

Fever

```
## Cross-Tabulation, Row Proportions
## CVD * fever
## Data Frame: data
##
##
## ------- ------- ---------------- ---------------- ------------------
##           fever                no                yes              Total
##     CVD
##      no           1535.7 (44.5%)   1914.5 (55.5%)   3450.2 (100.0%)
##     yes           1510.0 (43.0%)   1997.8 (57.0%)   3507.8 (100.0%)
##   Total           3045.8 (43.8%)   3912.2 (56.2%)   6958.0 (100.0%)
## ------- ------- ---------------- ---------------- ------------------
##
## ----------------------------
##  Chi.squared   df   p.value
## ------------ ---- ---------
##    1.4563      1    0.2275
## ----------------------------
##
## ----------------------------------
##  Odds Ratio   Lo - 95%   Hi - 95%
## ------------ ---------- ----------
##     1.06        0.97       1.17
```

```
## ----------------------------------
##
## --------------------------------
##  Risk Ratio   Lo - 0%   Hi - 0%
## ------------ --------- ---------
##     1.03       1.03      1.03
## --------------------------------
```

```
with(data, ctable(CVD, cough, prop="r", OR=TRUE, useNA = "no", chisq = TRUE, weights = weight))
```

Cough

```
## Cross-Tabulation, Row Proportions
## CVD * cough
## Data Frame: data
##
##
## ------- ------- ---------------- ----------------- ------------------
##           cough                no                yes              Total
##     CVD
##      no            1161.8 (33.7%)   2290.8 (66.3%)   3452.6 (100.0%)
##     yes            1124.8 (32.0%)   2395.0 (68.0%)   3519.8 (100.0%)
##   Total            2286.6 (32.8%)   4685.8 (67.2%)   6972.4 (100.0%)
## ------- ------- ---------------- ----------------- ------------------
##
## ----------------------------
##  Chi.squared   df   p.value
## ------------ ---- ---------
##    2.1957      1    0.1384
## ----------------------------
##
## ----------------------------------
##  Odds Ratio   Lo - 95%   Hi - 95%
## ------------ ---------- ----------
##     1.08        0.98       1.19
## ----------------------------------
##
## --------------------------------
##  Risk Ratio   Lo - 0%   Hi - 0%
## ------------ --------- ---------
##     1.05       1.05      1.05
## --------------------------------
```

```
with(data, ctable(CVD, sore_throat, prop="r", OR=TRUE, useNA = "no", chisq = TRUE, weights = weight))
```

Sore throat

```
## Cross-Tabulation, Row Proportions
## CVD * sore_throat
## Data Frame: data
##
##
## ------- ------------- ---------------- ---------------- ------------------
##           sore_throat               no              yes              Total
##     CVD
##      no                 2651.6 (78.2%)    738.2 (21.8%)   3389.8 (100.0%)
##     yes                 2588.7 (76.6%)    790.8 (23.4%)   3379.6 (100.0%)
##   Total                 5240.3 (77.4%)   1529.0 (22.6%)   6769.3 (100.0%)
## ------- ------------- ---------------- ---------------- ------------------
##
## ----------------------------
##  Chi.squared   df   p.value
## ------------- ---- ---------
##    2.4586      1    0.1169
## ----------------------------
##
## ---------------------------------
##  Odds Ratio   Lo - 95%   Hi - 95%
## ------------ ---------- ----------
##     1.10        0.98       1.23
## ---------------------------------
##
## -------------------------------
##  Risk Ratio   Lo - 0%   Hi - 0%
## ------------ --------- ---------
##     1.02       1.02      1.02
## -------------------------------
```

```
with(data, ctable(CVD, dyspnea, prop="r", OR=TRUE, useNA = "no", chisq = TRUE, weights = weight))
```

Dyspnea

```
## Cross-Tabulation, Row Proportions
## CVD * dyspnea
## Data Frame: data
##
##
## ------- --------- ---------------- ---------------- ------------------
##           dyspnea               no              yes              Total
##     CVD
##      no              1574.0 (45.6%)   1876.2 (54.4%)   3450.2 (100.0%)
##     yes              1196.9 (33.9%)   2337.6 (66.1%)   3534.4 (100.0%)
##   Total              2770.8 (39.7%)   4213.8 (60.3%)   6984.6 (100.0%)
## ------- --------- ---------------- ---------------- ------------------
##
## ----------------------------
##  Chi.squared   df   p.value
## ------------- ---- ---------
```

```
##   100.3512     1       0
## ---------------------------
##
## ---------------------------------
##  Odds Ratio   Lo - 95%   Hi - 95%
## ------------ ---------- ----------
##     1.64        1.49       1.80
## ---------------------------------
##
## --------------------------------
##  Risk Ratio   Lo - 0%   Hi - 0%
## ------------ --------- ---------
##     1.35       1.35      1.35
## --------------------------------
```

```
with(data, ctable(CVD, resp_dist, prop="r", OR=TRUE, useNA = "no", chisq = TRUE, weights = weight))
```

Respiratory distress

```
## Cross-Tabulation, Row Proportions
## CVD * resp_dist
## Data Frame: data
##
##
## ------- ----------- ---------------- ---------------- ------------------
##           resp_dist                no              yes              Total
##     CVD
##      no               1789.1 (52.1%)   1645.7 (47.9%)   3434.8 (100.0%)
##     yes               1578.1 (45.4%)   1900.2 (54.6%)   3478.3 (100.0%)
##   Total               3367.2 (48.7%)   3545.9 (51.3%)   6913.1 (100.0%)
## ------- ----------- ---------------- ---------------- ------------------
##
## ----------------------------
##  Chi.squared   df   p.value
## ------------- ---- ---------
##    30.9549     1       0
## ----------------------------
##
## ---------------------------------
##  Odds Ratio   Lo - 95%   Hi - 95%
## ------------ ---------- ----------
##     1.31        1.19       1.44
## ---------------------------------
##
## --------------------------------
##  Risk Ratio   Lo - 0%   Hi - 0%
## ------------ --------- ---------
##     1.15       1.15      1.15
## --------------------------------
```

```r
with(data, ctable(CVD, saturation, prop="r", OR=TRUE, useNA = "no", chisq = TRUE, weights = weight))
```

Saturation

```
## Cross-Tabulation, Row Proportions
## CVD * saturation
## Data Frame: data
##
##
## ------- ------------ ---------------- ---------------- ------------------
##           saturation               no              yes              Total
##     CVD
##      no                2164.0 (63.5%)   1241.8 (36.5%)   3405.8 (100.0%)
##     yes                1810.9 (52.3%)   1654.5 (47.7%)   3465.4 (100.0%)
##   Total                3974.9 (57.8%)   2896.3 (42.2%)   6871.2 (100.0%)
## ------- ------------ ---------------- ---------------- ------------------
##
## ----------------------------
##  Chi.squared   df   p.value
## ------------- ---- ---------
##    89.2193     1       0
## ----------------------------
##
## ---------------------------------
##  Odds Ratio   Lo - 95%   Hi - 95%
## ------------ ---------- ----------
##     1.59        1.45       1.75
## ---------------------------------
##
## -------------------------------
##  Risk Ratio   Lo - 0%   Hi - 0%
## ------------ --------- ---------
##     1.22       1.22      1.22
## -------------------------------
```

```r
with(data, ctable(CVD, diarrhea, prop="r", OR=TRUE, useNA = "no", chisq = TRUE, weights = weight))
```

Diarrhea

```
## Cross-Tabulation, Row Proportions
## CVD * diarrhea
## Data Frame: data
##
##
## ------- ---------- ---------------- --------------- ------------------
##           diarrhea               no             yes              Total
##     CVD
##      no               3021.0 (88.6%)   389.7 (11.4%)   3410.7 (100.0%)
```

```
##     yes              3002.5 (89.0%)   371.5 (11.0%)   3374.1 (100.0%)
##   Total              6023.5 (88.8%)   761.2 (11.2%)   6784.7 (100.0%)
## ------- ---------- ---------------- --------------- -----------------
##
## ----------------------------
##  Chi.squared   df   p.value
## ------------ ---- ---------
##    0.2517      1    0.6159
## ----------------------------
##
## ---------------------------------
##  Odds Ratio   Lo - 95%   Hi - 95%
## ------------ ---------- ----------
##     0.96        0.82       1.12
## ---------------------------------
##
## -------------------------------
##  Risk Ratio   Lo - 0%   Hi - 0%
## ------------ --------- ---------
##     1.00        1.00      1.00
## -------------------------------
```

```
with(data, ctable(CVD, vomit, prop="r", OR=TRUE, useNA = "no", chisq = TRUE, weights = weight))
```

Vomit

```
## Cross-Tabulation, Row Proportions
## CVD * vomit
## Data Frame: data
##
##
## ------- ------- ---------------- --------------- -----------------
##           vomit                no             yes              Total
##     CVD
##      no           3062.7 (90.1%)   337.3 ( 9.9%)   3400.1 (100.0%)
##     yes           2998.6 (89.3%)   359.5 (10.7%)   3358.1 (100.0%)
##   Total           6061.3 (89.7%)   696.8 (10.3%)   6758.1 (100.0%)
## ------- ------- ---------------- --------------- -----------------
##
## ----------------------------
##  Chi.squared   df   p.value
## ------------- ---- ---------
##    1.0397      1    0.3079
## ----------------------------
##
## ---------------------------------
##  Odds Ratio   Lo - 95%   Hi - 95%
## ------------ ---------- ----------
##     1.09        0.93       1.27
## ---------------------------------
##
```

```
## --------------------------------
##  Risk Ratio   Lo - 0%   Hi - 0%
## ------------ --------- ---------
##     1.01       1.01      1.01
## --------------------------------
```

```
with(data, ctable(CVD, fatigue, prop="r", OR=TRUE, useNA = "no", chisq = TRUE, weights = weight))
```

Fatigue

```
## Cross-Tabulation, Row Proportions
## CVD * fatigue
## Data Frame: data
##
##
## ------- --------- ---------------- ---------------- -----------------
##           fatigue                no              yes             Total
##     CVD
##      no             1892.0 (76.5%)    579.8 (23.5%)   2471.8 (100.0%)
##     yes             1733.2 (74.8%)    583.8 (25.2%)   2317.0 (100.0%)
##   Total             3625.2 (75.7%)   1163.6 (24.3%)   4788.8 (100.0%)
## ------- --------- ---------------- ---------------- -----------------
##
## ----------------------------
##  Chi.squared   df   p.value
## ------------- ---- ---------
##     1.871      1    0.1714
## ----------------------------
##
## ---------------------------------
##  Odds Ratio   Lo - 95%   Hi - 95%
## ------------ ---------- ----------
##     1.10        0.96       1.25
## ---------------------------------
##
## --------------------------------
##  Risk Ratio   Lo - 0%   Hi - 0%
## ------------ --------- ---------
##     1.02       1.02      1.02
## --------------------------------
```

```
with(data, ctable(CVD, loss_smell, prop="r", OR=TRUE, useNA = "no", chisq = TRUE, weights = weight))
```

Loss of smell

```
## Cross-Tabulation, Row Proportions
## CVD * loss_smell
```

```
## Data Frame: data
##
##
## ------- ------------ ---------------- --------------- -----------------
##           loss_smell               no             yes             Total
##     CVD
##      no                2002.3 (81.1%)   467.5 (18.9%)   2469.8 (100.0%)
##     yes                1787.6 (77.5%)   520.4 (22.5%)   2308.0 (100.0%)
##   Total                3789.9 (79.3%)   987.9 (20.7%)   4777.7 (100.0%)
## ------- ------------ ---------------- --------------- -----------------
##
## ----------------------------
##  Chi.squared   df   p.value
## ------------ ---- ---------
##    9.2983      1    0.0023
## ----------------------------
##
## ---------------------------------
##  Odds Ratio   Lo - 95%   Hi - 95%
## ------------ ---------- ----------
##     1.25        1.08       1.43
## ---------------------------------
##
## -------------------------------
##  Risk Ratio   Lo - 0%   Hi - 0%
## ------------ --------- ---------
##     1.05       1.05      1.05
## -------------------------------
```

```
with(data, ctable(CVD, loss_taste, prop="r", OR=TRUE, useNA = "no", chisq = TRUE, weights = weight))
```

Loss of taste

```
## Cross-Tabulation, Row Proportions
## CVD * loss_taste
## Data Frame: data
##
##
## ------- ------------ ---------------- --------------- -----------------
##           loss_taste               no             yes             Total
##     CVD
##      no                2008.7 (81.5%)   455.8 (18.5%)   2464.6 (100.0%)
##     yes                1792.7 (77.6%)   518.6 (22.4%)   2311.3 (100.0%)
##   Total                3801.4 (79.6%)   974.4 (20.4%)   4775.9 (100.0%)
## ------- ------------ ---------------- --------------- -----------------
##
## ----------------------------
##  Chi.squared   df   p.value
## ------------- ---- ---------
##    11.1723     1     8e-04
## ----------------------------
```

```
##
## ----------------------------------
##  Odds Ratio   Lo - 95%   Hi - 95%
## ------------ ---------- ----------
##     1.27        1.11       1.47
## ----------------------------------
##
## -------------------------------
##  Risk Ratio   Lo - 0%   Hi - 0%
## ------------ --------- ---------
##     1.05       1.05      1.05
## -------------------------------
```

```
with(data, ctable(CVD, abd_pain, prop="r", OR=TRUE, useNA = "no", chisq = TRUE, weights = weight))
```

Abdominal pain

```
## Cross-Tabulation, Row Proportions
## CVD * abd_pain
## Data Frame: data
##
##
## ------- ---------- ---------------- -------------- ------------------
##           abd_pain                no             yes              Total
##     CVD
##      no              2243.3 (91.3%)   214.6 (8.7%)   2457.9 (100.0%)
##     yes              2102.5 (92.1%)   180.7 (7.9%)   2283.2 (100.0%)
##   Total              4345.8 (91.7%)   395.3 (8.3%)   4741.2 (100.0%)
## ------- ---------- ---------------- -------------- ------------------
##
## ----------------------------
##  Chi.squared   df   p.value
## ------------- ---- ---------
##    0.9274      1    0.3355
## ----------------------------
##
## ----------------------------------
##  Odds Ratio   Lo - 95%   Hi - 95%
## ------------ ---------- ----------
##     0.90        0.73       1.10
## ----------------------------------
##
## -------------------------------
##  Risk Ratio   Lo - 0%   Hi - 0%
## ------------ --------- ---------
##     0.99       0.99      0.99
## -------------------------------
```

Any respiratory symptom Now we are going to create the variable `resp_symp` indicating the presence of at least one respiratory symptom (Dyspnea, Fadigue, Saturation, Respiratory distress). Empty cells are

considered missing data (<NA>). The variable qt_resp_symp indicates the number of respiratory symptoms of each case.

```
with(data, ctable(CVD, resp_symp, prop="r", OR=TRUE, useNA = "no", chisq = TRUE, weights = weight))
```

```
## Cross-Tabulation, Row Proportions
## CVD * resp_symp
## Data Frame: data
##
##
## ------- ----------- ---------------- ---------------- -----------------
##           resp_symp               no              yes             Total
##     CVD
##      no               1056.4 (30.5%)   2408.6 (69.5%)   3465.1 (100.0%)
##     yes                738.7 (20.7%)   2834.6 (79.3%)   3573.4 (100.0%)
##   Total               1795.2 (25.5%)   5243.3 (74.5%)   7038.5 (100.0%)
## ------- ----------- ---------------- ---------------- -----------------
##
## ----------------------------
##  Chi.squared   df   p.value
## ------------- ---- ---------
##    88.6786     1       0
## ----------------------------
##
## ---------------------------------
##  Odds Ratio   Lo - 95%   Hi - 95%
## ------------ ---------- ----------
##     1.68        1.51       1.88
## ---------------------------------
##
## --------------------------------
##  Risk Ratio   Lo - 0%   Hi - 0%
## ------------ --------- ---------
##     1.47       1.47      1.47
## --------------------------------
```

```
with(data, ctable(CVD, qt_resp_symp, prop="r", OR=TRUE, useNA = "no", chisq = TRUE, weights = weight))
```

```
## Cross-Tabulation, Row Proportions
## CVD * qt_resp_symp
## Data Frame: data
##
##
## ------- -------------- ---------------- ---------------- ---------------- -------------- ------------
##           qt_resp_symp        1 symptom       2 symptoms       3 symptoms     4 symptoms   No respira
##     CVD
##      no                    763.3 (22.0%)    616.1 (17.8%)    768.8 (22.2%)   260.4 (7.5%)           1
##     yes                    709.1 (19.8%)    892.6 (25.0%)    949.9 (26.6%)   283.0 (7.9%)
##   Total                   1472.4 (20.9%)   1508.7 (21.4%)   1718.8 (24.4%)   543.3 (7.7%)           1
## ------- -------------- ---------------- ---------------- ---------------- -------------- ------------
##
## ----------------------------
##  Chi.squared   df   p.value
```

```
## ------------- ---- ---------
##   127.2795     4       0
## ----------------------------
```

Any symptom Similar to the analysis of any respiratory symptom, we are going to create the variable `symp` indicating the presence of at least one symptom (Dyspnea, Fatigue, Saturation, Respiratory distress, Fever, Cough, Sore throat, Diarrhea, Vomit, Abdominal pain, Loss of smell, Loss of taste). Empty cells are considered missing data (`<NA>`).

```
with(data, ctable(CVD, symp, prop="r", OR=TRUE, useNA = "no", chisq = TRUE, weights = weight))
```

```
## Cross-Tabulation, Row Proportions
## CVD * symp
## Data Frame: data
##
##
## ------- ------ -------------- ---------------- ------------------
##           symp              no              yes              Total
##     CVD
##      no           285.8 (8.2%)   3197.3 (91.8%)   3483.1 (100.0%)
##     yes           135.9 (3.8%)   3458.6 (96.2%)   3594.5 (100.0%)
##   Total           421.7 (6.0%)   6655.9 (94.0%)   7077.6 (100.0%)
## ------- ------ -------------- ---------------- ------------------
##
## ----------------------------
##  Chi.squared   df   p.value
## ------------- ---- ---------
##    61.0734     1       0
## ----------------------------
##
## ---------------------------------
##  Odds Ratio   Lo - 95%   Hi - 95%
## ------------ ---------- ----------
##     2.28        1.85       2.81
## ---------------------------------
##
## --------------------------------
##  Risk Ratio   Lo - 0%   Hi - 0%
## ------------ --------- ---------
##     2.17       2.17      2.17
## --------------------------------
```

Outcome analysis after PSM:

ICU

```
with(data, ctable(CVD, icu, prop="r", OR=TRUE, useNA = "no", chisq = TRUE,  weights = weight))
```

```
## Cross-Tabulation, Row Proportions
## CVD * icu
```

```
## Data Frame: data
##
##
## ------- ----- ---------------- ---------------- ------------------
##           icu               no              yes              Total
##     CVD
##      no          2421.5 (71.6%)    959.7 (28.4%)   3381.2 (100.0%)
##     yes          2318.3 (67.5%)   1117.4 (32.5%)   3435.7 (100.0%)
##   Total          4739.9 (69.5%)   2077.1 (30.5%)   6817.0 (100.0%)
## ------- ----- ---------------- ---------------- ------------------
##
## ----------------------------
##  Chi.squared   df   p.value
## ------------ ---- ---------
##    13.5876     1     2e-04
## ----------------------------
##
## ---------------------------------
##  Odds Ratio   Lo - 95%   Hi - 95%
## ------------ ---------- ----------
##     1.22         1.10       1.35
## ---------------------------------
##
## -------------------------------
##  Risk Ratio   Lo - 0%   Hi - 0%
## ------------ --------- ---------
##     1.06        1.06      1.06
## -------------------------------
```

```
df43 <- data %>%
  filter(classi_gesta_puerp == "1tri")

with(df43, ctable(CVD, icu, prop="r", useNA = "no", OR=TRUE, chisq = TRUE, weights = weight))
```

1st trimester

```
## Cross-Tabulation, Row Proportions
## CVD * icu
## Data Frame: df43
##
##
## ------- ----- --------------- -------------- ----------------
##           icu               no             yes              Total
##     CVD
##      no          137.3 (76.8%)   41.4 (23.2%)   178.7 (100.0%)
##     yes           83.2 (63.3%)   48.2 (36.7%)   131.4 (100.0%)
##   Total          220.5 (71.1%)   89.6 (28.9%)   310.2 (100.0%)
## ------- ----- --------------- -------------- ----------------
##
## ----------------------------
##  Chi.squared   df   p.value
```

```
## ------------- ---- ---------
##    6.0614      1    0.0138
## ---------------------------
##
## ---------------------------------
##  Odds Ratio   Lo - 95%   Hi - 95%
## ------------ ---------- ----------
##     1.92        1.17       3.15
## ---------------------------------
##
## --------------------------------
##  Risk Ratio   Lo - 0%   Hi - 0%
## ------------ --------- ---------
##     1.21        1.21      1.21
## --------------------------------
```

```
df43 <- data %>%
  filter(classi_gesta_puerp == "2tri")

with(df43, ctable(CVD, icu, prop="r", OR=TRUE, useNA = "no", chisq = TRUE,  weights = weight))
```

2nd trimester

```
## Cross-Tabulation, Row Proportions
## CVD * icu
## Data Frame: df43
##
##
## ------- ----- --------------- --------------- -----------------
##           icu               no             yes             Total
##     CVD
##      no          362.9 (68.1%)   169.9 (31.9%)    532.9 (100.0%)
##     yes          377.5 (61.4%)   237.4 (38.6%)    614.9 (100.0%)
##   Total          740.4 (64.5%)   407.4 (35.5%)   1147.8 (100.0%)
## ------- ----- --------------- --------------- -----------------
##
## ----------------------------
##  Chi.squared   df   p.value
## ------------- ---- ---------
##    5.3395      1    0.0208
## ----------------------------
##
## ---------------------------------
##  Odds Ratio   Lo - 95%   Hi - 95%
## ------------ ---------- ----------
##     1.34        1.05       1.71
## ---------------------------------
##
## --------------------------------
##  Risk Ratio   Lo - 0%   Hi - 0%
## ------------ --------- ---------
```

```
##     1.11       1.11      1.11
## ---------------------------------
```

```
df43 <- data %>%
  filter(classi_gesta_puerp == "3tri")

with(df43, ctable(CVD, icu, prop="r", OR=TRUE, useNA = "no", chisq = TRUE,  weights = weight))
```

3rd trimester

```
## Cross-Tabulation, Row Proportions
## CVD * icu
## Data Frame: df43
##
##
## ------- ----- ---------------- --------------- -----------------
##           icu                no             yes             Total
##     CVD
##      no          1058.1 (76.8%)   318.8 (23.2%)   1376.8 (100.0%)
##     yes          1252.9 (74.1%)   437.2 (25.9%)   1690.1 (100.0%)
##   Total          2311.0 (75.4%)   755.9 (24.6%)   3066.9 (100.0%)
## ------- ----- ---------------- --------------- -----------------
##
## ----------------------------
##  Chi.squared   df   p.value
## ------------- ---- ---------
##    2.8646      1    0.0905
## ----------------------------
##
## ---------------------------------
##  Odds Ratio   Lo - 95%   Hi - 95%
## ------------ ---------- ----------
##     1.16        0.98       1.37
## ---------------------------------
##
## --------------------------------
##  Risk Ratio   Lo - 0%   Hi - 0%
## ------------ --------- ---------
##     1.04       1.04      1.04
## --------------------------------
```

```
df43 <- data %>%
  filter(classi_gesta_puerp == "puerp")

with(df43, ctable(CVD, icu, prop="r", OR=TRUE, useNA = "no", chisq = TRUE,  weights = weight))
```

Puerperium

```
## Cross-Tabulation, Row Proportions
## CVD * icu
## Data Frame: df43
##
##
## ------- ----- ---------------- --------------- -----------------
##           icu                no             yes             Total
##     CVD
##      no           802.7 (66.3%)   407.6 (33.7%)   1210.3 (100.0%)
##     yes           540.2 (60.3%)   355.7 (39.7%)    896.0 (100.0%)
##   Total          1342.9 (63.8%)   763.4 (36.2%)   2106.3 (100.0%)
## ------- ----- ---------------- --------------- -----------------
##
## ----------------------------
##  Chi.squared   df   p.value
## ------------- ---- ---------
##    7.8264      1    0.0051
## ----------------------------
##
## ---------------------------------
##  Odds Ratio   Lo - 95%   Hi - 95%
## ------------ ---------- ----------
##     1.30        1.08       1.55
## ---------------------------------
##
## -------------------------------
##  Risk Ratio   Lo - 0%   Hi - 0%
## ------------ --------- ---------
##     1.10        1.10      1.10
## -------------------------------
```

Days of hospitalization in ICU

```
d_yes <- data %>%
   filter(CVD == "yes" & !is.na(icu_days))
d_no <- data %>%
   filter(CVD == "no" & !is.na(icu_days))

wtd.t.test(d_yes$icu_days, d_no$icu_days, weight = d_yes$weight, weighty = d_no$weight)
```

```
## $test
## [1] "Two Sample Weighted T-Test (Welch)"
##
## $coefficients
##     t.value          df     p.value
##   1.2896729 164.5233473   0.1989742
##
## $additional
## Difference     Mean.x     Mean.y   Std. Err
##   1.437357  11.941962  10.504606   1.114513
```

Ventilatory support

```
with(data, ctable(CVD, ven_support, prop="r", OR=TRUE, useNA = "no", chisq = TRUE,  weights = weight))
```

```
## Cross-Tabulation, Row Proportions
## CVD * ven_support
## Data Frame: data
##
##
## ------- ------------- ---------------- ---------------- ------------------ -----------------
##           ven_support               No    yes, invasive   yes, noninvasive              Total
##     CVD
##      no                 1693.0 (51.3%)    540.7 (16.4%)     1068.2 (32.4%)   3301.9 (100.0%)
##     yes                 1611.5 (47.2%)    603.3 (17.7%)     1197.4 (35.1%)   3412.2 (100.0%)
##   Total                 3304.6 (49.2%)   1144.0 (17.0%)     2265.6 (33.7%)   6714.2 (100.0%)
## ------- ------------- ---------------- ---------------- ------------------ -----------------
##
## ----------------------------
##  Chi.squared   df   p.value
## ------------- ---- ---------
##    10.9876     2    0.0041
## ----------------------------
```

Intubation

```
with(data, ctable(CVD, intubation, prop="r", OR=TRUE, useNA = "no", chisq = TRUE,  weights = weight))
```

```
## Cross-Tabulation, Row Proportions
## CVD * intubation
## Data Frame: data
##
##
## ------- ------------ ---------------- ---------------- -----------------
##           intubation               no              yes             Total
##     CVD
##      no                2761.2 (83.6%)    540.7 (16.4%)   3301.9 (100.0%)
##     yes                2809.0 (82.3%)    603.3 (17.7%)   3412.2 (100.0%)
##   Total                5570.2 (83.0%)   1144.0 (17.0%)   6714.2 (100.0%)
## ------- ------------ ---------------- ---------------- -----------------
##
## ----------------------------
##  Chi.squared   df   p.value
## ------------- ---- ---------
##     1.927      1    0.1651
## ----------------------------
##
## ---------------------------------
##  Odds Ratio   Lo - 95%   Hi - 95%
## ------------ ---------- ----------
##     1.10         0.97       1.25
```

```
## ---------------------------------
##
## --------------------------------
##  Risk Ratio   Lo - 0%   Hi - 0%
## ------------ --------- ---------
##     1.02       1.02      1.02
## --------------------------------
```

1st trimester

```
df4 <- data %>%
  filter(classi_gesta_puerp == "1tri")

with(df4, ctable(CVD, intubation, prop="r", OR=TRUE, useNA = "no", chisq = TRUE, weights = weight))
```

```
## Cross-Tabulation, Row Proportions
## CVD * intubation
## Data Frame: df4
##
##
## ------- ------------ --------------- -------------- -----------------
##           intubation              no            yes             Total
##     CVD
##       no                153.4 (88.7%)   19.6 (11.3%)   173.0 (100.0%)
##      yes                 97.1 (80.6%)   23.4 (19.4%)   120.5 (100.0%)
##    Total                250.5 (85.3%)   43.0 (14.7%)   293.5 (100.0%)
## ------- ------------ --------------- -------------- -----------------
##
## ----------------------------
##  Chi.squared   df   p.value
## ------------ ---- ---------
##    3.1142      1    0.0776
## ----------------------------
##
## ---------------------------------
##  Odds Ratio   Lo - 95%   Hi - 95%
## ------------ ---------- ----------
##     1.89        0.98       3.62
## ---------------------------------
##
## --------------------------------
##  Risk Ratio   Lo - 0%   Hi - 0%
## ------------ --------- ---------
##     1.10       1.10      1.10
## --------------------------------
```

2nd trimester

```
df4 <- data %>%
  filter(classi_gesta_puerp == "2tri")
```

```r
with(df4, ctable(CVD, intubation, prop="r", OR=TRUE, useNA = "no", chisq = TRUE, weights = weight))
```

```
## Cross-Tabulation, Row Proportions
## CVD * intubation
## Data Frame: df4
##
##
## ------- ------------ --------------- --------------- ------------------
##           intubation              no             yes              Total
##     CVD
##      no                429.5 (84.4%)    79.6 (15.6%)    509.2 (100.0%)
##     yes                493.7 (81.6%)   111.4 (18.4%)    605.1 (100.0%)
##   Total                923.2 (82.9%)   191.1 (17.1%)   1114.3 (100.0%)
## ------- ------------ --------------- --------------- ------------------
##
## ----------------------------
##  Chi.squared   df   p.value
## ------------- ---- ---------
##     1.31       1    0.2524
## ----------------------------
##
## ---------------------------------
##  Odds Ratio   Lo - 95%   Hi - 95%
## ------------ ---------- ----------
##     1.22        0.89       1.67
## ---------------------------------
##
## --------------------------------
##  Risk Ratio   Lo - 0%   Hi - 0%
## ------------ --------- ---------
##     1.03       1.03      1.03
## --------------------------------
```

3rd trimester

```r
df4 <- data %>%
  filter(classi_gesta_puerp == "3tri")

with(df4, ctable(CVD, intubation, prop="r", OR=TRUE, useNA = "no", chisq = TRUE, weights = weight))
```

```
## Cross-Tabulation, Row Proportions
## CVD * intubation
## Data Frame: df4
##
##
## ------- ------------ --------------- --------------- ------------------
##           intubation              no             yes              Total
##     CVD
##      no                1205.3 (89.1%)   147.2 (10.9%)   1352.5 (100.0%)
##     yes                1479.2 (86.3%)   234.6 (13.7%)   1713.7 (100.0%)
```

```
##   Total                2684.5 (87.5%)   381.8 (12.5%)   3066.3 (100.0%)
## ------- ------------ ---------------- --------------- -----------------
##
## ----------------------------
##  Chi.squared   df   p.value
## ------------- ---- ---------
##    5.1945      1    0.0227
## ----------------------------
##
## ---------------------------------
##  Odds Ratio   Lo - 95%   Hi - 95%
## ------------ ---------- ----------
##     1.30        1.04       1.62
## ---------------------------------
##
## -------------------------------
##  Risk Ratio   Lo - 0%   Hi - 0%
## ------------ --------- ---------
##     1.03       1.03      1.03
## -------------------------------
```

Puerperium

```
df4 <- data %>%
  filter(classi_gesta_puerp == "puerp")

with(df4, ctable(CVD, intubation, prop="r", OR=TRUE, useNA = "no", chisq = TRUE, weights = weight))
```

```
## Cross-Tabulation, Row Proportions
## CVD * intubation
## Data Frame: df4
##
##
## ------- ------------ ---------------- --------------- -----------------
##           intubation               no             yes             Total
##     CVD
##      no                 903.0 (76.3%)   280.6 (23.7%)   1183.6 (100.0%)
##     yes                 654.0 (75.2%)   215.5 (24.8%)    869.5 (100.0%)
##   Total                1557.0 (75.8%)   496.2 (24.2%)   2053.1 (100.0%)
## ------- ------------ ---------------- --------------- -----------------
##
## ----------------------------
##  Chi.squared   df   p.value
## ------------- ---- ---------
##    0.2619      1    0.6088
## ----------------------------
##
## ---------------------------------
##  Odds Ratio   Lo - 95%   Hi - 95%
## ------------ ---------- ----------
##     1.06        0.86       1.30
## ---------------------------------
```

```
##
## -------------------------------
##  Risk Ratio   Lo - 0%   Hi - 0%
## ------------ --------- ---------
##     1.01       1.01      1.01
## -------------------------------
```

Outcome - cure x death

```
with(data, ctable(CVD, evolution, prop="r", OR=TRUE, useNA = "no", chisq = TRUE, weights = weight))
```

```
## Cross-Tabulation, Row Proportions
## CVD * evolution
## Data Frame: data
##
##
## ------- ----------- ---------------- ---------------- ------------------
##           evolution              cure            death              Total
##     CVD
##      no                3020.3 (86.0%)    491.3 (14.0%)   3511.6 (100.0%)
##     yes                2974.7 (82.4%)    636.8 (17.6%)   3611.5 (100.0%)
##   Total                5995.0 (84.2%)   1128.1 (15.8%)   7123.1 (100.0%)
## ------- ----------- ---------------- ---------------- ------------------
##
## ----------------------------
##  Chi.squared   df   p.value
## ------------- ---- ---------
##    17.433      1       0
## ----------------------------
##
## ---------------------------------
##  Odds Ratio   Lo - 95%   Hi - 95%
## ------------ ---------- ----------
##     1.32        1.16       1.50
## ---------------------------------
##
## -------------------------------
##  Risk Ratio   Lo - 0%   Hi - 0%
## ------------ --------- ---------
##     1.04       1.04      1.04
## -------------------------------
```

1st trimester

```
df4 <- data %>%
  filter(classi_gesta_puerp == "1tri")

with(df4, ctable(CVD, evolution, prop="r", OR=TRUE, useNA = "no", chisq = TRUE, weights = weight))
```

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

```
## CVD * evolution
## Data Frame: df4
##
##
## ------- ----------- --------------- -------------- ----------------
##           evolution             cure          death             Total
##     CVD
##      no                165.5 (90.4%)   17.5 ( 9.6%)   183.1 (100.0%)
##     yes                121.1 (88.1%)   16.4 (11.9%)   137.4 (100.0%)
##   Total                286.6 (89.4%)   33.9 (10.6%)   320.5 (100.0%)
## ------- ----------- --------------- -------------- ----------------
##
## ----------------------------
##  Chi.squared   df   p.value
## ------------ ---- ---------
##    0.2366      1    0.6267
## ----------------------------
##
## ---------------------------------
##  Odds Ratio   Lo - 95%   Hi - 95%
## ------------ ---------- ----------
##     1.28        0.62       2.60
## ---------------------------------
##
## --------------------------------
##  Risk Ratio   Lo - 0%   Hi - 0%
## ------------ --------- ---------
##     1.03       1.03      1.03
## --------------------------------
```

2nd trimester

```
df4 <- data %>%
  filter(classi_gesta_puerp == "2tri")

with(df4, ctable(CVD, evolution, prop="r", OR=TRUE, useNA = "no", chisq = TRUE, weights = weight))
```

```
## Cross-Tabulation, Row Proportions
## CVD * evolution
## Data Frame: df4
##
##
## ------- ----------- --------------- --------------- -----------------
##           evolution             cure           death              Total
##     CVD
##      no                471.8 (86.2%)    75.7 (13.8%)    547.5 (100.0%)
##     yes                484.2 (76.2%)   151.0 (23.8%)    635.3 (100.0%)
##   Total                956.0 (80.8%)   226.7 (19.2%)   1182.7 (100.0%)
## ------- ----------- --------------- --------------- -----------------
##
## ----------------------------
##  Chi.squared   df   p.value
```

```
## ------------- ---- ---------
##    18.1283     1       0
## ------------------------------
##
## ---------------------------------
##  Odds Ratio   Lo - 95%   Hi - 95%
## ------------ ---------- ----------
##     1.94        1.43       2.63
## ---------------------------------
##
## --------------------------------
##  Risk Ratio   Lo - 0%   Hi - 0%
## ------------ --------- ---------
##     1.13       1.13      1.13
## --------------------------------
```

3rd trimester

```
df4 <- data %>%
  filter(classi_gesta_puerp == "3tri")

with(df4, ctable(CVD, evolution, prop="r", OR=TRUE, useNA = "no", chisq = TRUE, weights = weight))
```

```
## Cross-Tabulation, Row Proportions
## CVD * evolution
## Data Frame: df4
##
##
## ------- ----------- ---------------- --------------- -----------------
##           evolution             cure           death             Total
##     CVD
##      no               1279.2 (89.5%)   150.6 (10.5%)   1429.8 (100.0%)
##     yes               1565.4 (86.8%)   237.9 (13.2%)   1803.3 (100.0%)
##   Total               2844.6 (88.0%)   388.5 (12.0%)   3233.1 (100.0%)
## ------- ----------- ---------------- --------------- -----------------
##
## ----------------------------
##  Chi.squared   df   p.value
## ------------- ---- ---------
##    5.0783      1    0.0242
## ----------------------------
##
## ---------------------------------
##  Odds Ratio   Lo - 95%   Hi - 95%
## ------------ ---------- ----------
##     1.29        1.04       1.60
## ---------------------------------
##
## --------------------------------
##  Risk Ratio   Lo - 0%   Hi - 0%
## ------------ --------- ---------
##     1.03       1.03      1.03
```

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

Puerperium

```
df4 <- data %>%
  filter(classi_gesta_puerp == "puerp")

with(df4, ctable(CVD, evolution, prop="r", OR=TRUE, useNA = "no", chisq = TRUE, weights = weight))
```

```
## Cross-Tabulation, Row Proportions
## CVD * evolution
## Data Frame: df4
##
##
## ------- ----------- ---------------- --------------- ------------------
##           evolution              cure           death              Total
##     CVD
##      no                1009.5 (81.0%)   237.0 (19.0%)   1246.5 (100.0%)
##     yes                 709.0 (77.1%)   210.6 (22.9%)    919.6 (100.0%)
##   Total                1718.5 (79.3%)   447.5 (20.7%)   2166.1 (100.0%)
## ------- ----------- ---------------- --------------- ------------------
##
## ----------------------------
##  Chi.squared   df   p.value
## ------------- ---- ---------
##    4.6463      1    0.0311
## ----------------------------
##
## ---------------------------------
##  Odds Ratio   Lo - 95%   Hi - 95%
## ------------ ---------- ----------
##     1.27        1.03       1.56
## ---------------------------------
##
## --------------------------------
##  Risk Ratio   Lo - 0%   Hi - 0%
## ------------ --------- ---------
##     1.05       1.05      1.05
## --------------------------------
```

Time elapsed between the start of symptoms and the outcome (days) after PSM

```
d_yes <- data %>%
   filter(CVD == "yes" & !is.na(days_symp_evol))
d_no <- data %>%
   filter(CVD == "no" & !is.na(days_symp_evol))

# Performing weighted Student's t-tests to compare the CVD and non-CVD groups with respect to the time
wtd.t.test(d_yes$days_symp_evol, d_no$days_symp_evol, weight = d_yes$weight, weighty = d_no$weight)
```

```
## $test
## [1] "Two Sample Weighted T-Test (Welch)"
##
## $coefficients
##      t.value           df      p.value
##    0.1099695 1063.6837985    0.9124543
##
## $additional
##  Difference      Mean.x      Mean.y    Std. Err
##  0.06197113 16.09992557 16.03795444  0.56353001
```

Considering only death cases

```
df <- data[!is.na(data$days_symp_evol) & !is.na(data$CVD),]

df <- df %>%
  filter(evolution == "death")
```

```
d_yes <- df %>%
   filter(CVD == "yes" & !is.na(days_symp_evol))
d_no <- df %>%
   filter(CVD == "no" & !is.na(days_symp_evol))

# Fixed the death cases, we perform a weighted Student's t-tests to compare the CVD and non-CVD groups
wtd.t.test(d_yes$days_symp_evol, d_no$days_symp_evol, weight = d_yes$weight, weighty = d_no$weight)
```

```
## $test
## [1] "Two Sample Weighted T-Test (Welch)"
##
## $coefficients
##     t.value          df     p.value
##  -1.2611092 209.4593902   0.2086723
##
## $additional
## Difference     Mean.x     Mean.y   Std. Err
##  -1.603168  18.525606  20.128775   1.271237
```

Considering only cure cases

```
df <- data[!is.na(data$days_symp_evol) & !is.na(data$CVD),]

df <- df %>%
  filter(evolution == "cure")
```

```
d_yes <- df %>%
   filter(CVD == "yes" & !is.na(days_symp_evol))
d_no <- df %>%
   filter(CVD == "no" & !is.na(days_symp_evol))
```

```r
# Fixed the cure cases, we perform a weighted Student's t-tests to compare the CVD and non-CVD groups w
wtd.t.test(d_yes$days_symp_evol, d_no$days_symp_evol, weight = d_yes$weight, weighty = d_no$weight)
```

```
## $test
## [1] "Two Sample Weighted T-Test (Welch)"
##
## $coefficients
##     t.value          df     p.value
##   0.3550950 844.4701387   0.7226071
##
## $additional
## Difference     Mean.x     Mean.y   Std. Err
##  0.2215881 15.5695137 15.3479256  0.6240248
```