Preoperative Atelectasis

Part 1: Overview, selection criteria, and missing data

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Setup

Packages used

```r
if (!require("pacman", quietly = TRUE)) {
  install.packages("pacman")
}

pacman::p_load(
  tidyverse, # Used for basic data handling and visualization.
  dataverse, # Retrieve dataset from the Harvard dataverse.
  overviewR, # Used to assess missing data.
  table1 #Used to add labels to variables.
)
```

Session and package dependencies

```
R version 4.3.2 (2023-10-31 ucrt)
Platform: x86_64-w64-mingw32/x64 (64-bit)
Running under: Windows 11 x64 (build 22621)

Matrix products: default


locale:
[1] LC_COLLATE=Spanish_Mexico.utf8  LC_CTYPE=Spanish_Mexico.utf8
[3] LC_MONETARY=Spanish_Mexico.utf8 LC_NUMERIC=C
[5] LC_TIME=Spanish_Mexico.utf8
```

```
time zone: Europe/Berlin
tzcode source: internal

attached base packages:
[1] stats     graphics  grDevices utils     datasets  methods   base

other attached packages:
 [1] table1_1.4.3     overviewR_0.0.13 dataverse_0.3.13 lubridate_1.9.3
 [5] forcats_1.0.0    stringr_1.5.0    dplyr_1.1.3      purrr_1.0.2
 [9] readr_2.1.4      tidyr_1.3.0      tibble_3.2.1     ggplot2_3.4.4
[13] tidyverse_2.0.0  pacman_0.5.1
```

General overview

```
summary(data)
```

```
      ID                 age             sex          weight          height
 Length:243         Min.   :20.00   Woman:221   Min.   : 73.8   Min.   :1.480
 Class :character   1st Qu.:33.00   Man  : 22   1st Qu.: 97.6   1st Qu.:1.620
 Mode  :character   Median :40.00               Median :111.2   Median :1.660
                    Mean   :40.37               Mean   :115.9   Mean   :1.670
                    3rd Qu.:49.00               3rd Qu.:129.7   3rd Qu.:1.715
                    Max.   :65.00               Max.   :264.6   Max.   :1.910

      BMI              type_obesity      ARISCAT              ARISCAT_group
 Min.   :30.00   Class 1 Obesity: 62   Min.   :23.0   Low Risk          :178
 1st Qu.:34.81   Class 2 Obesity: 55   1st Qu.:23.0   Intermediate Risk: 65
 Median :40.31   Class 3 Obesity:126   Median :23.0   High Risk        :  0
 Mean   :41.51                         Mean   :24.6
 3rd Qu.:46.15                         3rd Qu.:26.0
 Max.   :77.31                         Max.   :42.0

    ASA          spo2_VPO      surgical_procedure      CORADS     atelectasis
 ASA 1: 52   Min.   :88.00   SG  :192             CO-RADS 1:233   Yes: 81
 ASA 2:149   1st Qu.:93.00   RYGB:  7             CO-RADS 2:  6   No :162
 ASA 3: 33   Median :96.00   OAGB:  5             CO-RADS 3:  2
 NA's :  9   Mean   :94.93   LBGS: 31             CO-RADS 4:  2
             3rd Qu.:97.00   NA's:  8
             Max.   :99.00
```

```
atelectasis_location atelectasis_percent        hb              hct
Unilateral: 55       Min.   : 0.000     Min.   : 9.90   Min.   :30.30
Bilateral : 26       1st Qu.: 0.000     1st Qu.:13.90   1st Qu.:40.52
NA's       :162      Median : 0.000     Median :14.45   Median :42.60
                     Mean   : 2.778     Mean   :14.52   Mean   :42.68
                     3rd Qu.: 5.000     3rd Qu.:15.20   3rd Qu.:44.67
                     Max.   :27.500     Max.   :18.50   Max.   :52.90
                                        NA's   :5       NA's   :5
     leu             neu_percent       neu_absolute      linf_percent
Min.   : 3.100   Min.   :32.00     Min.   : 1.600    Min.   :14.00
1st Qu.: 6.600   1st Qu.:59.00     1st Qu.: 3.969    1st Qu.:30.00
Median : 7.700   Median :63.00     Median : 4.883    Median :35.00
Mean   : 7.826   Mean   :62.94     Mean   : 4.956    Mean   :34.87
3rd Qu.: 8.900   3rd Qu.:68.00     3rd Qu.: 5.894    3rd Qu.:39.00
Max.   :13.300   Max.   :84.00     Max.   :10.773    Max.   :66.00
NA's   :5        NA's   :5         NA's   :5         NA's   :5
linf_absolute    mon_percent       mon_absolute      platelets
Min.   :0.616    Min.   :0.000     Min.   :0.616     Min.   :154.0
1st Qu.:2.244    1st Qu.:1.000     1st Qu.:2.244     1st Qu.:272.2
Median :2.587    Median :2.000     Median :2.587     Median :316.0
Mean   :2.703    Mean   :1.626     Mean   :2.703     Mean   :317.2
3rd Qu.:3.095    3rd Qu.:2.000     3rd Qu.:3.095     3rd Qu.:354.8
Max.   :5.676    Max.   :4.000     Max.   :5.676     Max.   :495.0
NA's   :5        NA's   :5         NA's   :5         NA's   :5
   glucose            urea           creatinine      rapid_covid_test
Min.   : 59.00   Min.   :10.0    Min.   :0.5000    negative:243
1st Qu.: 74.00   1st Qu.:17.0    1st Qu.:0.6600
Median : 83.00   Median :20.5    Median :0.7500
Mean   : 85.61   Mean   :21.4    Mean   :0.7577
3rd Qu.: 92.00   3rd Qu.:26.0    3rd Qu.:0.8400
Max.   :200.00   Max.   :49.0    Max.   :1.5900
NA's   :5        NA's   :5       NA's   :5
   PCR_covid    surgery_performed   state_residence     altitude
negative: 3     No : 10            Texas     :87    Min.   :  31.0
NA's    :240    Yes:233           Washington:39    1st Qu.: 519.0
                                  Utah      :27    Median : 519.0
                                  Alberta   :22    Mean   : 650.1
                                  Florida   :20    3rd Qu.: 806.0
                                  California:16    Max.   :1861.0
                                  (Other)   :32
hypertension diabetes  sleep_apnea hypothyroidism dyslipidemia
No :179      No :218   No :224     No :219        No :224
```

3

```
Yes: 64       Yes: 25    Yes: 19      Yes: 24        Yes: 19
```

```
antidepressant_use prior_covid19 other_comorb
No :146            No :239        No :143
Yes: 97            Yes:  4        Yes:100
```

Exclude participants with CO-RADS 3:

Participants with higher probability of having a current diagnosis of COVID-19 are expected to have chest CT alterations due to COVID-19 pneumonia. Thus, will be excluded.

Number of patients according to CO-RADS:

```
summary(data$CORADS)
```

```
CO-RADS 1 CO-RADS 2 CO-RADS 3 CO-RADS 4
      233         6         2         2
```

```
count(data)
```

```
# A tibble: 1 x 1
      n
  <int>
1   243
```

```
data <- data %>%
  filter(as.numeric(CORADS) < 3) %>%
  droplevels(data$CORADS)
```

```
count(data)
```

```
# A tibble: 1 x 1
      n
  <int>
1   239
```

Exclude participants with prior COVID-19:

Since prior COVID-19 is considered a confounder and since there are only 3 participants with prior COVID-19 which would provide difficult to assess the role of prior COVID-19 in analyses, participants with prior COVID-19 were excluded from the analysis.

```
count(data)
```

```
# A tibble: 1 x 1
      n
  <int>
1   239
```

```
data <- data %>%
  filter(prior_covid19 == "No") %>%
  droplevels(data$prior_covid19)

count(data)
```

```
# A tibble: 1 x 1
      n
  <int>
1   236
```

Will remove prior_covid19 column as it no longer provides information of a varying characteristic. Similarly, rapid_covid_test does not provide additional information.
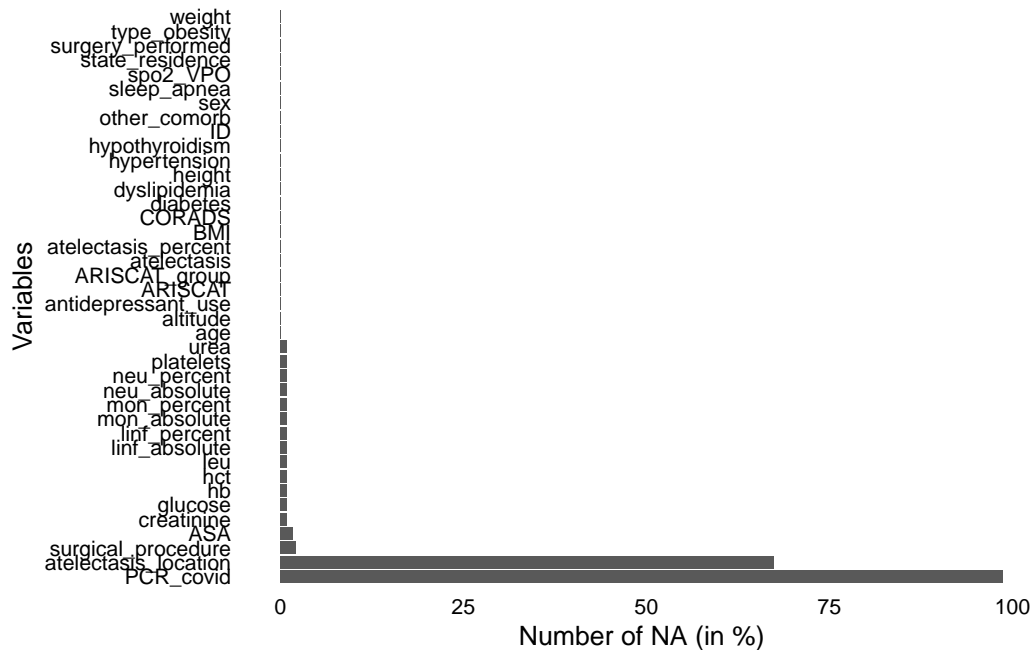
```
length(data)
```

```
[1] 42
```

```
data <- data %>% select(-c(prior_covid19, rapid_covid_test))
```

```
length(data)
```

[1] 40

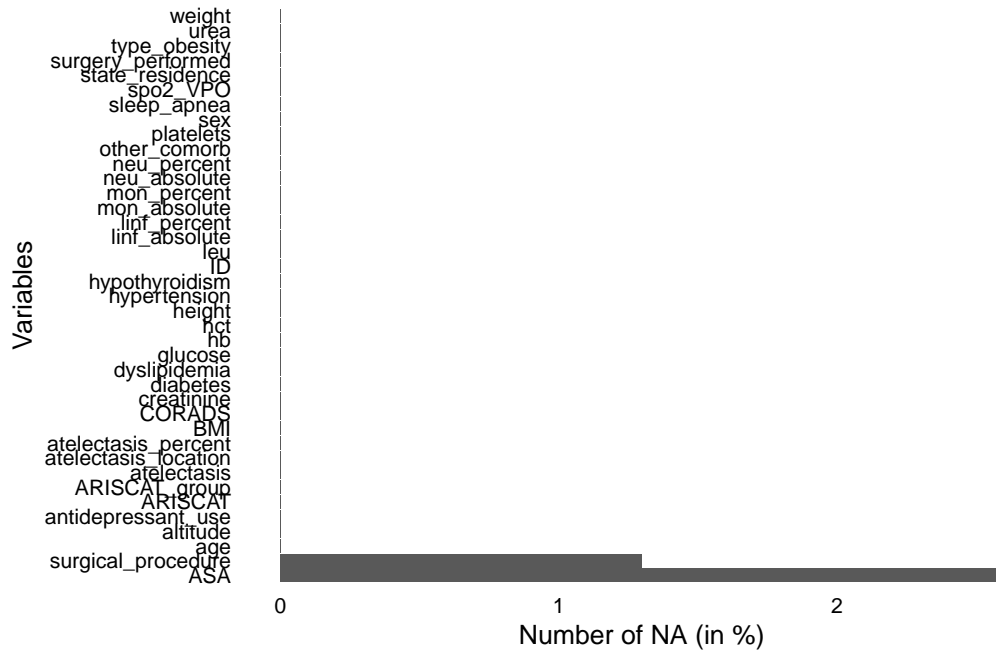## Missing data per variable

```
overview_na(data)
```


Missing data for PCR_covid and is explained since only patients who decided to have a test performed on their own will reported the result. The medical center did not require a negative PCR test at that time during the pandemic, reason why PCR tests were not systematically performed. As shown in earlier summary of variables, all available tests (n=3) were negative. This variable will not be analyzed further downstream:

```
data <- data %>% select(-PCR_covid)
```

The variable atelectasis_location has missing data since those patients who did not have atelectasis naturally do not have a location recorded. Will assess if data are missing for those who had atelectasis:
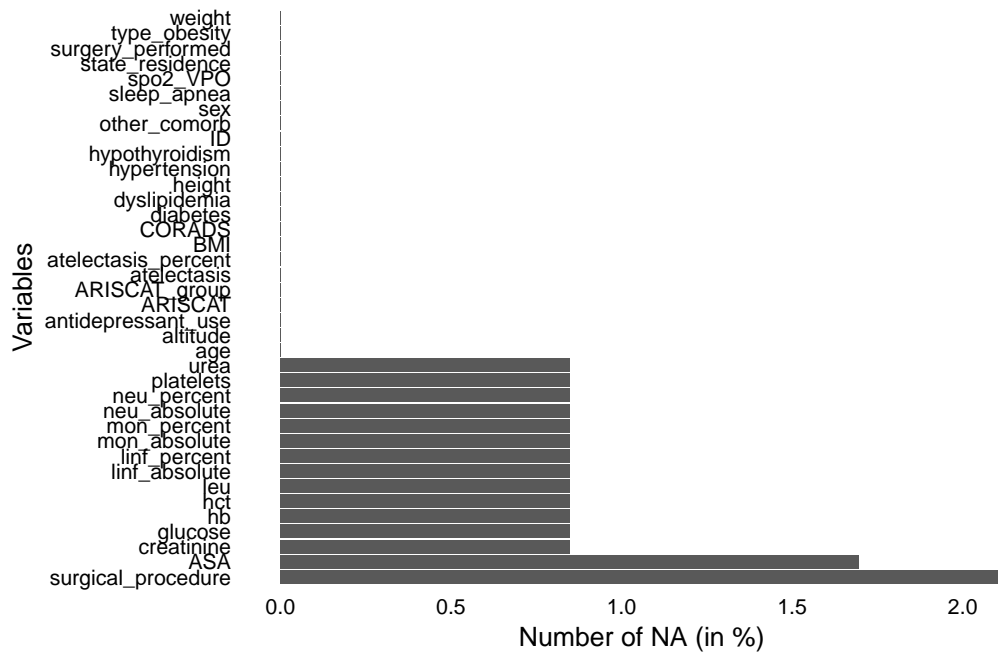
```
data %>%
  filter(atelectasis == "Yes") %>%
  group_by(atelectasis_location) %>%
  overview_na()
```


There is no missing data for ***atelectasis_location*** after sub-setting only those who had atelectasis.

Lastly, I will subset all participants without the prior variable to further assess the extent of missing data for other variables:

```
data %>%
  select(-c(atelectasis_location)) %>%
  overview_na()
```

Missing data constitutes **less than 5%** for all remaining variables. Thus, will proceed with **complete-case analysis** without performing any data imputation procedure.