Intro

The dataset is from a prospective population-based surveillance study. The observational study was conducted over 3 different South America cities across 3 different countries over a 3-year period to investigate the incidence rate of Community Acquired Pneumonia (CAP). The dataset has a wealth of variables which can be used for predictive modelling, there is no known predictive analysis published using this dataset. The aim of this project is to classify if patients with CAP became better after seeing a doctor or became worse despite seeing a doctor.

```
library(tidyverse)
theme_set(theme_light())

raw<- readxl::read_excel("Incidence rate of community-acquired pneumonia in
adults a population-based prospective active surveillance study in three cities
in South America.xls")
```

```
## Warning in read_fun(path = enc2native(normalizePath(path)), sheet_i = sheet,
:
## Expecting logical in EL1372 / R1372C142: got '2014-09-02'
```

```
## Warning in read_fun(path = enc2native(normalizePath(path)), sheet_i = sheet,
:
## Expecting logical in EM1372 / R1372C143: got '2014-09-08'
```

The dataset consists of 2302 rows and 176 columns.

```
dim(raw)
```

```
## [1] 2302  176
```

The original column names were the description of the variables (e.g. `Received flu shot in the last 12 months`). Based on these descriptions/column names, the columns can be classified into 13 categories (see table below). Most of the categories ae clinically related variables.

```
categories13<- readxl::read_excel("Incidence rate of community-acquired
pneumonia in adults a population-based prospective active surveillance study in
three cities in South America.xls", sheet=3)

categories13 %>%  DT::datatable(rownames = F, options = list(searchHighlight =
TRUE, paging= T))
```

Data dictionary

The column names are renamed to shorter column names (e.g. `Received flu shot in the last 12 months`-> `flu`) with prefixes to identify which of the above 13 categories they belong to (e.g. `flu`-> `V_flu`. Prefix `V_` stands for vaccine against the flu.).

```
metadata<- readxl::read_excel("Incidence rate of community-acquired pneumonia in
adults a population-based prospective active surveillance study in three cities
in South America.xls", sheet=2)

# metadata
metadata %>%  DT::datatable(rownames = F, options = list(searchHighlight = TRUE,
paging= T))
```

```
# rename col names
colnames(raw)<- metadata$`New column name` %>% t()
```

EDA blueprint

EDA will be iterated for each of the 13 categories as there are too many columns to do the EDA at once. Also, there may be some association among the variables for each category. EDA includes exploring (i) the types of variables for each category (ii) the number of missing values (iii) the number of outliers (iv) and data cleaning if needed. Customized functions were created to facilitate EDA:

1. `dtype` provides the number of columns beginning with the prefix (e.g. `dtype(dataframe, “Pt”)` will list all the columns related to patient (`pt`). The types of variables are also provided.
2. `eda_c` breaks down the labels for columns beginning with the prefix. Used mostly for categorical variables.
3. `eda_n_NAplt` plots the percentage of `NA`/missing values for each column beginning with the prefix. Used mostly for numeric variables.
4. `eda_n_NAcutoff` provides a vector of variable names with acceptable `NA` values. Used mostly for numeric variables. The ball park maximum amount of missing values is 20% though higher proportion of missing values may be included after inspecting the plot generated by `eda_n_NAplt`
5. `eda_n_outlier` plots boxplots for numeric variables beginning with the prefix. Variables with large number of outliers can be isolated for further investigation.

```
dtype<- function(datafr, x){
datafr %>% select(starts_with(x, ignore.case = F)) %>% str()
}

eda_c<- function(datafr,x){
  datafr %>% select(starts_with(x, ignore.case = F)) %>%  map(~ table(.x, useNA
= "always"))
}

eda_n_NAplt<- function (datafr, x){
  datafr %>% select(starts_with(x, ignore.case = F)) %>%
summarise(across(starts_with(x), ~mean(is.na(.)))) %>% pivot_longer(cols =
everything(), names_to= "Variables" , values_to="pct_na") %>% mutate(Variables=
fct_reorder(Variables, pct_na)) %>% ggplot(aes(x=Variables, y=pct_na, fill=
pct_na))+ geom_col() + coord_flip() + scale_y_continuous(labels=
scales::percent_format()) + scale_fill_viridis_c(option = "plasma")}

eda_n_NAcutoff<- function(datafr, x, low, high){
  datafr%>% select(starts_with(x, ignore.case = F)) %>%
summarise(across(starts_with(x), ~mean(is.na(.)))) %>% pivot_longer(cols =
everything(), names_to="Variables", values_to="pct_na") %>% filter((pct_na>low &
pct_na% pull(Variables)}

eda_n_outlier<-function(datafr, x_selected){
# nested df with plots
  plt<-datafr %>% select(all_of(x_selected)) %>% pivot_longer(cols=everything()
,names_to="Variables", values_to="values") %>% nest(-Variables) %>% mutate(plot=
map2(.x= data, .y= Variables,
~ggplot(data=.x, aes(x= values)) + geom_boxplot() + labs(title = .y)
))
# print the plots
  for (i in 1:length(x_selected)){
    p<-plt[[3]][[i]]
    print(p)}
  }
```

Outcome

The outcome will be `Other_Outcome`. As the prediction is whether the patient was `better` or `worse` after seeking medical treatment, a binary classification is warranted here. However the `Other_Outcome` has 4 values, namely `cure`, `improvement`, `unfavourable` and `death`.

```
eda_c(raw, "Other_Outcome")
```

```
## $Other_Outcome
## .x
##        Cure       death  Improvement unfavorable
##         799          277         1179           26           21
```

`cure` and `improvement` will be collapsed as `better` and `unfavourable` and `death` will be collapsed as `worse`. 6 times as many patients became better after seeking medical help. While encouraging from the doctor's and patient's perspective, it results in an imbalanced dataset for prediction. The imbalanced dataset will be addressed much later.

After removing 21 `NA` outcomes, there are 2281 observations remaining.

```
# collapse 4 categories into 2
raw$Other_Outcome<-fct_collapse(raw$Other_Outcome, better=c("Cure",
"Improvement"))
raw$Other_Outcome<-fct_collapse(raw$Other_Outcome, worse=c("unfavorable",
"death"))

# remove na
df<-raw %>%  filter(!is.na(Other_Outcome))
eda_c(df, "Other_Outcome")
```

```
## $Other_Outcome
## .x
## better  worse
##   1978    303      0
```

Discard the noise

There are column names with the prefix `rm_` in front of the category prefix (e.g. `rm_Other_`). These columns are removed for numerous reasons.

```
dtype(df,"rm")
```

```
## tibble [2,281 x 36] (S3: tbl_df/tbl/data.frame)
##  $ rm_R_CXR             : chr [1:2281] "Yes" "Yes" "Yes" "Yes" ...
##  $ rm_R_CT              : chr [1:2281] "No" "No" "No" "No" ...
##  $ rm_R_CT_date         : chr [1:2281] NA NA NA NA ...
##  $ rm_SS                : logi  [1:2281] NA NA NA NA NA NA ...
##  $ rm_SS_infilterate    : chr [1:2281] "Yes" "Yes" "Yes" "Yes" ...
##  $ rm_SS_WBC            : chr [1:2281] "Yes" "Yes" "No" "No" ...
##  $ rm_HCAP              : chr [1:2281] "No" "No" "No" "No" ...
##  $ rm_PE                : logi  [1:2281] NA NA NA NA NA NA ...
##  $ rm_PE_O2             : chr [1:2281] "Yes" "Yes" "Yes" "Yes" ...
##  $ rm_Lab               : logi  [1:2281] NA NA NA NA NA NA ...
##  $ rm_Lab_RBC           : chr [1:2281] "Yes" "Yes" "Yes" "Yes" ...
##  $ rm_Lab_Hb            : chr [1:2281] "Yes" "Yes" "Yes" "Yes" ...
##  $ rm_Lab_WBC           : chr [1:2281] "Yes" "Yes" "Yes" "Yes" ...
##  $ rm_Lab_NeuImu        : chr [1:2281] "No" "No" "No" "No" ...
##  $ rm_Lab_NeuImuDate    : chr [1:2281] NA NA NA NA ...
##  $ rm_Lab_Neu           : chr [1:2281] "Yes" "Yes" "Yes" "Yes" ...
##  $ rm_Lab_plt           : chr [1:2281] "Yes" "Yes" "Yes" "Yes" ...
##  $ rm_Lab_Na            : chr [1:2281] "No" "No" "No" "No" ...
##  $ rm_Lab_NaDate        : chr [1:2281] NA NA NA NA ...
##  $ rm_Lab_urea         : chr [1:2281] "Yes" "No" "Yes" "Yes" ...
##  $ rm_Lab_Cr           : chr [1:2281] "Yes" "No" "Yes" "Yes" ...
##  $ rm_Lab_Bicarb       : chr [1:2281] "No" "No" "No" "No" ...
##  $ rm_Lab_BicarbDate   : chr [1:2281] NA NA NA NA ...
##  $ rm_Lab_Sugar        : chr [1:2281] "Yes" "No" "Yes" "Yes" ...
##  $ rm_Lab_Alb          : chr [1:2281] "No" "No" "No" "No" ...
##  $ rm_Lab_AlbDate      : chr [1:2281] NA NA NA NA ...
##  $ rm_Lab_lactate      : chr [1:2281] "No" "No" "No" "No" ...
##  $ rm_Lab_lactateDate  : chr [1:2281] NA NA NA NA ...
##  $ rm_Lab_CRP          : chr [1:2281] "Yes" "Yes" "No" "Yes" ...
##  $ rm_Lab_ABG          : chr [1:2281] "No" "No" "No" "No" ...
##  $ rm_Lab_ABGDate      : chr [1:2281] NA NA NA NA ...
##  $ rm_Abx              : logi [1:2281] NA NA NA NA NA NA ...
##  $ rm_Care_ICUdate     : chr [1:2281] NA NA NA NA ...
##  $ rm_Other_phone      : chr [1:2281] "Yes" "Yes" "Yes" "Yes" ...
##  $ rm_Other_1yearstatus: chr [1:2281] "dead after 1 year" NA "dead after 1
year" "dead after 1 year" ...
##  $ rm_Abx_AbxDuration  : chr [1:2281] "Yes" "Yes" "Yes" "Yes" ...
```

For instance, `1 year status` contains information about the patient's status one year post CAP which is a data leakage as it reveals the patient's outcome from the CAP.

```
df %>% select(rm_Other_1yearstatus) %>% tail()
```

```
## # A tibble: 6 x 1
##   rm_Other_1yearstatus
##
## 1 alive
## 2 dead after 1 year
## 3 alive
## 4 alive
## 5 alive
## 6 alive
```

Other columns contained duplicated information. For lab results, there is a column, which indicates if the specific biochemical was tested (eg `rm_Lab_urea`), and another column of the result (eg `Lab_urea`). If the biochemical was not tested, the column will indicate `No` test being done and the result column will be blank. Keeping only the results column will suffice. The reasons for removing specific `rm_` columns is described in the above data dictionary.

```
df %>% select(rm_Lab_urea, Lab_urea) %>% head()
```

```
## # A tibble: 6 x 2
##   rm_Lab_urea Lab_urea
##
## 1 Yes             60
## 2 No              NA
## 3 Yes             99
## 4 Yes             56
## 5 Yes            143
## 6 Yes             56.3
```

The dataframe of 176 columns ends up with 140 columns after discarding `rm_` columns.

```
df<-df %>% select(-starts_with("rm"))
```

```
ncol(df)
```

```
## [1] 140
```

1 `Other_` related category

After removing redundant `Other_` variables, only `Other_Outcome` remains. Rename it to just `Outcome` for readability.

```
dtype(df, "Other")
```

```
## tibble [2,281 x 1] (S3: tbl_df/tbl/data.frame)
##  $ Other_Outcome: Factor w/ 2 levels "better","worse": 1 1 2 1 2 1 1 1 1 2
...
```

```
df<-df %>% rename(Outcome=Other_Outcome)
```

2 `Pt_` Patient related category

```
dtype(df, "Pt")
```

```
## tibble [2,281 x 5] (S3: tbl_df/tbl/data.frame)
##  $ Pt_Site      : chr [1:2281] "Location A" "Location A" "Location A"
"Location A" ...
##  $ Pt_CaseNumber: num [1:2281] 1 2 3 4 5 6 7 9 10 11 ...
##  $ Pt_Age       : num [1:2281] 95 79 89 93 81 83 88 65 27 37 ...
##  $ Pt_incorrect : logi [1:2281] NA NA NA NA NA NA ...
##  $ Pt_correct   : chr [1:2281] "Yes" "Yes" "Yes" "Yes" ...
```

Appropriate patients

`Pt_incorrect` and `Pt_correct` are columns to indicate if the patients enrolled met the criteria for the study. All the subjects met the criteria for the study. `Pt_incorrect` and `Pt_correct` can be dropped.

```
(df %>% count(Pt_incorrect))
```

```
## # A tibble: 1 x 2
##   Pt_incorrect     n
##
## 1 NA            2281
```

```
(df %>% count(Pt_correct))
```

```
## # A tibble: 1 x 2
##   Pt_correct     n
##
## 1 Yes         2281
```

```
df<-df %>% select(- c(Pt_correct, Pt_incorrect))
```

Case_number

Case numbers, `Pt_CaseNumber` are not distinct to the entire dataset. they are only distinct to the research site. Assign new unique case number for entire dataset.

```
# are case number distinct
(df %>% pull(Pt_CaseNumber) %>%  n_distinct())
```

```
## [1] 1231
```

```
# explore why case numbers are not distinct
(df %>% filter(Pt_CaseNumber==1))
```

```
## # A tibble: 3 x 138
##   Pt_Site Pt_CaseNumber Pt_Age R_CXR_infiltrate R_CXR_cavitation
```

```
R_CXR_effusion
##
## 1 Locati~             1     95 Yes              No               No
## 2 Locati~             1     26 Yes              No               No
## 3 Locati~             1     32 Yes              No               No
## # ... with 132 more variables: R_CXR_effusionSite , R_CT_inflitrate ,
## #   R_CT_cavitation , R_CT_effusion , R_CT_effusionSite ,
## #   SS_cough , SS_phlegm , SS_lungSounds , SS_temp ,
## #   SS_breathing , SS_daysOfRespSymp , Hx_mass , Hx_heart ,
## #   Hx_stroke , Hx_kidney , Hx_liver , Hx_brainMental ,
## #   Hx_diabetes , Hx_pastCAP , Hx_asp , Hx_alcohol ,
## #   Hx_immune , Hx_COPD , Social_drugs ,
## #   Social_overcrowded , Hx_heart_type , Social_smoke ,
## #   Social_smoke_duration , Hx_HIV , Hx_HIV_CD4 ,
## #   Hx_HIV_viralLoad , Hx_HIV_Medicine , HCAP_hospStay ,
## #   HCAP_IVAbx , HCAP_Chemo , HCAP_diaylsis , HCAP_injury ,
## #   PE_AMS , PE_HR , PE_RR , PE_BP_S , PE_BP_D ,
## #   PE_temp , PE_O2 , Lab_RBC , Lab_Hb , Lab_WBC ,
## #   Lab_NeuImu , Lab_Neu , Lab_plt , Lab_Na ,
## #   Lab_urea , Lab_Cr , Lab_Bicarb , Lab_Sugar ,
## #   Lab_Alb , Lab_lactate , Lab_lactateHigh , Lab_CRP ,
## #   Lab_CRPHigh , Lab_pH , Lab_CO2 , Lab_O2 ,
## #   Lab_FiO2 , CS_Resp , CS_Blood , CS_Urine ,
## #   CS_screen , CS_agent , CS_Organism1 ,
## #   CS_Organism1Blood , CS_Organism1Sputum ,
## #   CS_Organism1Tracheal , CS_Organism1BAL , CS_Organism1Urine ,
## #   CS_Organism1Sero , CS_Organism1Other ,
## #   CS_Organism1Comments , CS_Organism2 , CS_Orgainsim2Blood ,
## #   CS_Organism2Sputum , CS_Organism2Tracheal ,
## #   CS_Organism2BAL , CS_Organism2Urine , CS_OrganismSero ,
## #   CS_OrganismOther , CS_OrganismComments ,
## #   Abx_AmoxicillinSulbactam , Abx_AmoxicillinSulbactamOral ,
## #   Abx_AmoxicillinSulbactamNonoral ,
## #   Abx_AmoxicillinSulbactamNonoralStart ,
## #   Abx_AmoxicillinSulbactamNonoralEnd , Abx_Ampicillin ,
## #   Abx_AmpicillinStart , Abx_AmpicillinEnd ,
## #   Abx_AmpicillinSulbactam , Abx_Azithromycin ,
## #   Abx_Ceftriaxone , Abx_Cefotaxime , Abx_ClarithromycinOral ,
## #   ...
```

```
(df %>% filter(Pt_CaseNumber==11))
```

```
## # A tibble: 3 x 138
##   Pt_Site Pt_CaseNumber Pt_Age R_CXR_infiltrate R_CXR_cavitation
R_CXR_effusion
##
## 1 Locati~            11     37 Yes              No               Yes
## 2 Locati~            11     37 Yes              No               No
## 3 Locati~            11     76 Yes              Unavailable      Unavailable
## # ... with 132 more variables: R_CXR_effusionSite , R_CT_inflitrate ,
## #   R_CT_cavitation , R_CT_effusion , R_CT_effusionSite ,
## #   SS_cough , SS_phlegm , SS_lungSounds , SS_temp ,
## #   SS_breathing , SS_daysOfRespSymp , Hx_mass , Hx_heart ,
## #   Hx_stroke , Hx_kidney , Hx_liver , Hx_brainMental ,
## #   Hx_diabetes , Hx_pastCAP , Hx_asp , Hx_alcohol ,
## #   Hx_immune , Hx_COPD , Social_drugs ,
## #   Social_overcrowded , Hx_heart_type , Social_smoke ,
## #   Social_smoke_duration , Hx_HIV , Hx_HIV_CD4 ,
## #   Hx_HIV_viralLoad , Hx_HIV_Medicine , HCAP_hospStay ,
## #   HCAP_IVAbx , HCAP_Chemo , HCAP_diaylsis , HCAP_injury ,
## #   PE_AMS , PE_HR , PE_RR , PE_BP_S , PE_BP_D ,
## #   PE_temp , PE_O2 , Lab_RBC , Lab_Hb , Lab_WBC ,
## #   Lab_NeuImu , Lab_Neu , Lab_plt , Lab_Na ,
## #   Lab_urea , Lab_Cr , Lab_Bicarb , Lab_Sugar ,
## #   Lab_Alb , Lab_lactate , Lab_lactateHigh , Lab_CRP ,
## #   Lab_CRPHigh , Lab_pH , Lab_CO2 , Lab_O2 ,
## #   Lab_FiO2 , CS_Resp , CS_Blood , CS_Urine ,
## #   CS_screen , CS_agent , CS_Organism1 ,
## #   CS_Organism1Blood , CS_Organism1Sputum ,
## #   CS_Organism1Tracheal , CS_Organism1BAL , CS_Organism1Urine ,
## #   CS_Organism1Sero , CS_Organism1Other ,
## #   CS_Organism1Comments , CS_Organism2 , CS_Orgainsim2Blood ,
## #   CS_Organism2Sputum , CS_Organism2Tracheal ,
## #   CS_Organism2BAL , CS_Organism2Urine , CS_OrganismSero ,
## #   CS_OrganismOther , CS_OrganismComments ,
## #   Abx_AmoxicillinSulbactam , Abx_AmoxicillinSulbactamOral ,
## #   Abx_AmoxicillinSulbactamNonoral ,
## #   Abx_AmoxicillinSulbactamNonoralStart ,
## #   Abx_AmoxicillinSulbactamNonoralEnd , Abx_Ampicillin ,
## #   Abx_AmpicillinStart , Abx_AmpicillinEnd ,
## #   Abx_AmpicillinSulbactam , Abx_Azithromycin ,
## #   Abx_Ceftriaxone , Abx_Cefotaxime , Abx_ClarithromycinOral ,
## #   ...
```

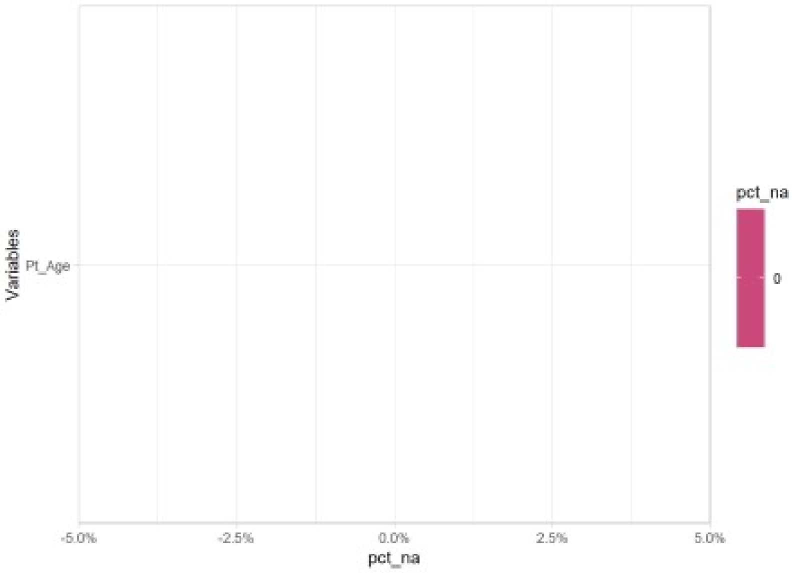
```
#assign unique case numbers
df<-df %>% mutate(Pt_CaseNumber=1:nrow(df))
(df %>% pull(Pt_CaseNumber) %>%  n_distinct())
```

```
## [1] 2281
```

Age

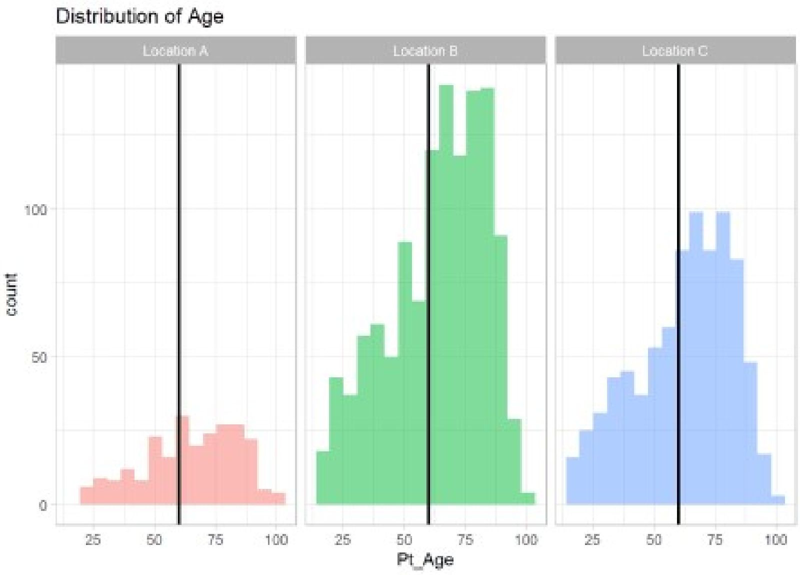
There is no missing age and mostly elderly >60 across all three sites

```
# any m/s age
(eda_n_NAplt(df, "Pt_Age"))
```



```
# distribution of age
(ggplot(df, aes(Pt_Age)) + geom_histogram(aes(fill=Pt_Site),alpha=.5,bins=round(
sqrt(nrow(df)))/3)) +labs(title = "Distribution of Age") + facet_wrap(.~Pt_Site)
```

```
+theme(legend.position="none") + geom_vline(xintercept = 60, size=1)
```



3 `R_` Radiology related category

```
dtype(df, "R")
```

```
## tibble [2,281 x 8] (S3: tbl_df/tbl/data.frame)
##  $ R_CXR_infiltrate  : chr [1:2281] "Yes" "Yes" "Yes" "Yes" ...
##  $ R_CXR_cavitation  : chr [1:2281] "No" "No" "Yes" "No" ...
##  $ R_CXR_effusion    : chr [1:2281] "No" "No" "No" "No" ...
##  $ R_CXR_effusionSite: chr [1:2281] NA NA NA NA ...
##  $ R_CT_inflitrate   : chr [1:2281] "Unavailable" "Unavailable" "Unavailable"
"Unavailable" ...
##  $ R_CT_cavitation   : chr [1:2281] "Unavailable" "Unavailable" "Unavailable"
"Unavailable" ...
##  $ R_CT_effusion     : chr [1:2281] "Unavailable" "Unavailable" "Unavailable"
"Unavailable" ...
##  $ R_CT_effusionSite : chr [1:2281] NA NA NA NA ...
```

Effusion and effusion site

`R_CXR_effusion` and `R_CT_effusion` indicates if effusion was seen on the radiological imaging while `R_CXR_effusionSite` and `R_CT_effusionSite` records the location of the effusion site. These columns contain different facets of the same information; the values of these columns can be integrated into single columns.

On chest x-ray (`R_CXR_effusion`, `R_CXR_effusionSite`)

2080 effusion sites on chest x-rays , `R_CXR_effusionSite`, were recorded as `NA` not because they are truly missing but because these x-rays have no effusion sites in the begin with. They will be relabelled as `nil` effusion sites. 43 effusions sites were recorded as `NA` and whether effusion sites were found the x-rays are unknown. These observations will retain their `NA` values. 9 effusion sites were recorded as `NA` but effusions were detected on x-rays. They will be relabelled as `effusion but ? site`.

After relabelling `R_CXR_effusionSite` using information from `R_CXR_effusion`, the latter column will be removed.

```
(table(df$R_CXR_effusion, df$R_CXR_effusionSite, useNA = "always"))
```

```
##
##                Bilateral Left Right
##   No                  0    0     0 2080
##   Unavailable         0    0     0   43
##   Yes                27   52    70    9
##                   0    0     0    0
```

```
# relabel effusion sites
df<-df %>% mutate(R_CXR_effusionSite=case_when(
   R_CXR_effusion=='No' & is.na(R_CXR_effusionSite)~ "Nil",
    R_CXR_effusion=='Unavailable' & is.na(R_CXR_effusionSite) ~ "Unavailable",
    R_CXR_effusion=="Yes" & is.na(R_CXR_effusionSite) ~"Effusion but ?site",
    T~as.character(R_CXR_effusionSite)
  ))

(table(df$R_CXR_effusion, df$R_CXR_effusionSite, useNA = "always"))
```

```
##
##               Bilateral Effusion but ?site Left  Nil Right Unavailable
##   No                  0                  0    0 2080     0           0    0
##   Unavailable         0                  0    0    0     0          43    0
##   Yes                27                  9   52    0    70           0    0
##                   0                  0    0    0     0           0    0
```

```
# remove R_CXR_effusion
df<-df %>% select(- R_CXR_effusion)
```

On CT chest (`R_CT_effusion`, `R_CT_effusionSite`)

Repeat the same for effusion related variables on CT chest.

```
(table(df$R_CT_effusion, df$R_CT_effusionSite, useNA = "always"))
```

```
##
##               Bilateral Left Right
##   No                  0    0     0   45
##   Unavailable         0    0     0 2205
##   Yes                15    6    10    0
##                   0    0     0    0
```

```
# relabel effusion site
df<-df %>% mutate(R_CT_effusionSite=case_when(
    R_CT_effusion=='No' & is.na(R_CT_effusionSite)~ "Nil",
    R_CT_effusion=='Unavailable' & is.na(R_CT_effusionSite) ~ "Unavailable",
    T~as.character(R_CT_effusionSite)
  ))

(table(df$R_CT_effusion, df$R_CT_effusionSite, useNA = "always"))
```

```
##
##               Bilateral Left  Nil Right Unavailable
##   No                  0    0   45     0           0    0
##   Unavailable         0    0    0     0        2205    0
##   Yes                15    6    0    10           0    0
##                   0    0    0     0           0    0
```

```
#remove CT_effusion
df<-df %>% select(-R_CT_effusion)
```

4 `SS_` Category related to signs and symptoms of CAP

`99` days of respiratory symptoms `SS_daysOfRespSymp` are outliers and likely represents missing values Relabel `99` as `NA`. The usage of `99` occurs frequently for numeric variables in this dataset, more examples to follow in later sections.

```
(dtype(df, "SS"))
```

```
## tibble [2,281 x 6] (S3: tbl_df/tbl/data.frame)
##  $ SS_cough         : chr [1:2281] "Yes" "Yes" "Yes" "Yes" ...
##  $ SS_phlegm        : chr [1:2281] "No" "Yes" "Yes" "Yes" ...
##  $ SS_lungSounds    : chr [1:2281] "Yes" "Yes" "Yes" "Yes" ...
##  $ SS_temp          : chr [1:2281] "Yes" "Yes" "No" "Yes" ...
##  $ SS_breathing     : chr [1:2281] "Yes" "Yes" "Yes" "Yes" ...
##  $ SS_daysOfRespSymp: num [1:2281] 1 2 5 3 3 4 3 4 NA NA ...
```

```
## NULL
```

```
(eda_c(df, "SS"))
```

```
## $SS_cough
## .x
##   No  Yes      
##  145 2136    0 
## 
## $SS_phlegm
## .x
##   No  Yes      
##  536 1745    0 
## 
## $SS_lungSounds
## .x
##   No  Yes      
##  267 2014    0 
## 
## $SS_temp
## .x
##   No  Yes      
##  798 1483    0 
## 
## $SS_breathing
## .x
##   No  Yes      
##  532 1749    0 
## 
## $SS_daysOfRespSymp
## .x
##    0    1    2    3    4    5    6    7    8    9   10   12   13   14   15 
20 
##    2  203  414  397  224  267   69  357   43    1   69    2    1    3   55 
12 
##   21   22   23   30   99      
##    1    1    1    6    4  149
```

```
df<-df %>% mutate(SS_daysOfRespSymp=na_if(SS_daysOfRespSymp, 99))
```

5 `Hx_` medical history category

```
(dtype(df, "Hx"))
```

```
## tibble [2,281 x 17] (S3: tbl_df/tbl/data.frame)
##  $ Hx_mass         : chr [1:2281] "No" "No" "No" "No" ...
##  $ Hx_heart        : chr [1:2281] "No" "No" "Yes" "Yes" ...
##  $ Hx_stroke       : chr [1:2281] "No" "No" "No" "No" ...
##  $ Hx_kidney       : chr [1:2281] "No" "No" "No" "No" ...
##  $ Hx_liver        : chr [1:2281] "No" "No" "No" "No" ...
##  $ Hx_brainMental  : chr [1:2281] "No" "No" "No" "No" ...
##  $ Hx_diabetes     : chr [1:2281] "No" "No" "No" "No" ...
##  $ Hx_pastCAP      : chr [1:2281] "No" "No" "No" "No" ...
##  $ Hx_asp          : chr [1:2281] "Yes" "No" "No" "No" ...
##  $ Hx_alcohol      : chr [1:2281] "No" "No" "No" "No" ...
##  $ Hx_immune       : chr [1:2281] "No" "No" "No" "No" ...
##  $ Hx_COPD         : chr [1:2281] "No" "Yes" "No" "No" ...
##  $ Hx_heart_type   : chr [1:2281] NA NA NA NA ...
##  $ Hx_HIV          : chr [1:2281] "No" "No" "No" "No" ...
##  $ Hx_HIV_CD4      : num [1:2281] NA NA NA NA NA NA NA NA NA NA ...
##  $ Hx_HIV_viralLoad: chr [1:2281] NA NA NA NA ...
##  $ Hx_HIV_Medicine : chr [1:2281] "Unavailable" "Unavailable" "Unavailable"
"Unavailable" ...
```

```
## NULL
```

```
(eda_c(df,"Hx"))
```

```
## $Hx_mass
## .x
##        No Uncertain       Yes
##      2152         9       117         3
##
## $Hx_heart
## .x
##        No Uncertain       Yes
##      1273        19       983         6
##
## $Hx_stroke
## .x
##        No Uncertain       Yes
##      2105        11       161         4
##
## $Hx_kidney
## .x
##        No Uncertain       Yes
##      2110         7       156         8
##
## $Hx_liver
## .x
##        No Uncertain       Yes
##      2214         4        58         5
##
## $Hx_brainMental
## .x
##        No Uncertain       Yes
##      1907        28       341         5
##
## $Hx_diabetes
## .x
##        No Uncertain       Yes
##      1907        13       358         3
##
```

```
## $Hx_pastCAP
## .x
##        No Uncertain       Yes           
##      1985         5       287         4 
## 
## $Hx_asp
## .x
##        No Uncertain       Yes           
##      2202        15        59         5 
## 
## $Hx_alcohol
## .x
##        No Uncertain       Yes           
##      2117        18       135        11 
## 
## $Hx_immune
## .x
##        No Uncertain       Yes           
##      2130         4       139         8 
## 
## $Hx_COPD
## .x
##        No Uncertain       Yes           
##      1879        50       343         9 
## 
## $Hx_heart_type
## .x
##              Arrhythmia                     CHF            Hypertension 
##                      23                      43                     220 
## Isquemic cardiomyopathy                   Other                         
##                      20                       1                    1974 
## 
## $Hx_HIV
## .x
##          No Unavailable         Yes             
##        2134         105          42           0 
## 
## $Hx_HIV_CD4
## .x
##   14   41   74   99  127  175  245  291  324  349  485  493  844 1104      
##    1    1    1    3    1    1    1    1    1    1    1    1    1    1 2265 
## 
## $Hx_HIV_viralLoad
## .x
## < Detection limit > Detection limit             Value                   
##                 5                 3                 4              2269 
## 
## $Hx_HIV_Medicine
## .x
##          No Unavailable         Yes             
##         596        1671          14           0
```

HIV details

Remove `Hx_HIV_CD4` & `Hx_HIV_viralLoad` as there are too many `NA`. Remove `Hx_HIV_Medicine` as there are too many `Unavailable`.

```
df<-df %>% select(-contains("Hx_HIV_"))
```

Heart disease

`Hx_heart` indicates whether the patient has heart disease or not. `Hx_heart_type` provides details on the type of heart disease. Both the variables can be integrated into a variable.

1273 observations for heart disease details, `Hx_heart_type` were labelled as `NA` not because they are truly missing but because these patients have `No` heart disease. These values will be labelled as `None`. 19 observations for heart disease details were labelled as `NA` when the heart disease status is `Uncertain`. These values will be labelled as `Query heart disease`. 676 observations for heart disease details were labelled as `NA` but were classified to have a heart disease. As these patients have heart diseases but no details can be obtained, the `NA` values will be treated as `Other` types of heart disease.

After using `Hx_heart` to expand `Hx_heart_type`, `Hx_heart` will be dropped.

```
(table(df$Hx_heart, df$Hx_heart_type, useNA="always"))
```

```
##
##             Arrhythmia  CHF Hypertension Isquemic cardiomyopathy Other
##   No                 0    0            0                       0     0 1273
##   Uncertain          0    0            0                       0     0   19
##   Yes               23   43          220                      20     1  676
##                  0    0            0                       0     0    6
```

```
# relabel
df<- df %>% mutate(Hx_heart_type=case_when(
  Hx_heart== "No" & is.na(Hx_heart_type) ~ "None",
  Hx_heart=="Uncertain" & is.na(Hx_heart_type) ~ "Query heart disease",
  Hx_heart=="Yes" & is.na(Hx_heart_type) ~ "Other",
  T~ Hx_heart_type))
```

```
(table(df$Hx_heart, df$Hx_heart_type, useNA="always"))
```

```
##
##             Arrhythmia  CHF Hypertension Isquemic cardiomyopathy None Other
##   No                 0    0            0                       0 1273     0
##   Uncertain          0    0            0                       0    0     0
##   Yes               23   43          220                      20    0   677
##                  0    0            0                       0    0     0
##
##             Query heart disease
##   No                          0    0
##   Uncertain                  19    0
##   Yes                         0    0
##                           0    6
```

```
# remove `hx_heart`
df <- df %>% select (-Hx_heart)
```

6 `Social_` social history category

```
(dtype(df, "Social"))
```

```
## tibble [2,281 x 4] (S3: tbl_df/tbl/data.frame)
##  $ Social_drugs         : chr [1:2281] "No" "No" "No" "No" ...
##  $ Social_overcrowded   : chr [1:2281] "No" "No" "No" "No" ...
##  $ Social_smoke         : chr [1:2281] "No" "Yes" "No" "No" ...
##  $ Social_smoke_duration: chr [1:2281] NA "Previous to the last 5 years" NA
NA ...
```

```
## NULL
```

```
(eda_c(df, "Social"))
```

```
## $Social_drugs
## .x
##        No Uncertain       Yes
##      2263         3        10         5
##
## $Social_overcrowded
## .x
##        No Uncertain       Yes
##      2193         7        51        30
##
## $Social_smoke
## .x
##          No Unavailable         Yes
##        1276         175         830           0
##
## $Social_smoke_duration
## .x
##                       current          In the last 5 years
##                           394                          200
## Previous to the last 5 years
##                           236                         1451
```

smoking

`Social_smoke` indicates if the patient smokes or not. `Social_smoke_duration` records how long the patients was smoking. These variables contain different facets of the same information; the values can be integrated into a single column.

1276 observations for smoking duration, `Social_smoke_duration` were labelled as `NA` but these values were not truly missing. These patients did not smoke. The values will be relabelled as `non-smoker`. 175 observations for smoking duration were labelled as `NA` but the information if they smoked was `Unavailable`. These values will be relabelled as `Unavailable`. All the patients who smoked had the duration of their smoking habit recorded. The bins of smoking duration were relabelled to terms that are more intuitive. `current` was relabelled as `still smokes`, `In the last 5 years` was relabelled as `smoked in the last 5y`, `Previous to the last 5 years` was relabelled as `smoked >5y ago`.

After using `Social_smoke` to expand `Social_smoke_duration`, `Social_smoke` is dropped.

```
(table(df$Social_smoke, df$Social_smoke_duration, useNA = "always"))
```

```
##
##               current In the last 5 years Previous to the last 5 years
##   No                0                   0                            0 1276
##   Unavailable       0                   0                            0  175
##   Yes             394                 200                          236    0
##                 0                   0                            0    0
```

```
# relabel
df<-df %>% mutate(Social_smoke=case_when(
  Social_smoke=="Yes" & Social_smoke_duration=="current"~ "still smokes",
  Social_smoke=="Yes" & Social_smoke_duration=="In the last 5 years"~ "smoked in
last 5y",
  Social_smoke=="Yes" & Social_smoke_duration=="Previous to the last 5 years"~
"smoked >5y ago",
  T~as.character(Social_smoke)
))
```

```
(df %>% count(Social_smoke))
```

```
## # A tibble: 5 x 2
##   Social_smoke          n
##                          
## 1 No                 1276
## 2 smoked >5y ago      236
## 3 smoked in last 5y   200
## 4 still smokes        394
## 5 Unavailable         175
```

```
# remove
df <- df %>% select(-Social_smoke_duration)
```

7 HCAP_ healthcare associated pneumonia category

No data cleaning is needed for this category.

```
(dtype(df,"HCAP"))
```

```
## tibble [2,281 x 5] (S3: tbl_df/tbl/data.frame)
##  $ HCAP_hospStay: chr [1:2281] "Yes" "No" "No" "No" ...
##  $ HCAP_IVAbx   : chr [1:2281] "No" "No" "No" "No" ...
##  $ HCAP_Chemo   : chr [1:2281] "No" "No" "No" "No" ...
##  $ HCAP_diaylsis: chr [1:2281] "No" "No" "No" "No" ...
##  $ HCAP_injury  : chr [1:2281] "No" "No" "No" "No" ...
```

```
## NULL
```

```
(eda_c(df, "HCAP"))
```

```
## $HCAP_hospStay
## .x
##        No Uncertain       Yes           
##      2039         3       236         3 
## 
## $HCAP_IVAbx
## .x
##        No Uncertain       Yes           
##      2074         1       203         3 
## 
## $HCAP_Chemo
## .x
##        No Uncertain       Yes           
##      2240         3        33         5 
## 
## $HCAP_diaylsis
## .x
##        No Uncertain       Yes           
##      2234         1        41         5 
## 
## $HCAP_injury
## .x
##        No Uncertain       Yes           
##      2206         3        63         9
```

8 `PE_` observations during physical examination category

```
(dtype(df, "PE"))
```

```
## tibble [2,281 x 7] (S3: tbl_df/tbl/data.frame)
##  $ PE_AMS : chr [1:2281] "No" "No" "No" "Unavailable" ...
##  $ PE_HR  : num [1:2281] 88 92 100 95 95 110 85 85 110 85 ...
##  $ PE_RR  : num [1:2281] 26 24 48 30 30 28 26 25 26 28 ...
##  $ PE_BP_S: num [1:2281] 100 110 140 140 120 140 100 120 120 100 ...
##  $ PE_BP_D: num [1:2281] 50 60 80 80 60 90 60 60 80 60 ...
##  $ PE_temp: num [1:2281] 38 38 36 37 36 39 37 37 40 37 ...
##  $ PE_O2  : chr [1:2281] NA NA NA NA ...
```

```
## NULL
```

```
# explore categorical
(eda_c(df, "PE_AMS"))
```

```
## $PE_AMS
## .x
##          No Unavailable         Yes
##        1832          29         420           0
```

Oxygen levels, `PE_O2` are calculated in the form of percentage. In this case, there is a mixture of pure numbers and numbers ending with `%` resulting in the variable to be treated as a character variable. `%` will be omitted and the variable will be converted to a numeric variable.

```
(eda_c(df, "PE_O2"))
```

```
## $PE_O2
## .x
##                100                 37                 55                 58
##                  3                  1                  1                  1
##                 60                 63                 65                 67
##                  3                  1                  3                  1
##                  7                 70                 73                 74
##                  1                  9                  3                  6
##                 75                 76                 77                 78
##                  3                  2                  3                 10
##                 79                 80 80.099999999999994                 82
##                  4                 23                  1                 18
##                 83                 84                 85               85 %
##                 12                 17                 23                  2
##                 86               86,7 86.599999999999994                 87
##                 21                  1                  1                 19
##                 88                88%               88,9 88.900000000000006
##                 55                  1                  1                  1
##                 89                 90                 91 91.299999999999997
##                 50                116                 62                  1
##                 92                92% 92.400000000000006                 93
##                124                  1                  1                107
##               93 % 93.400000000000006 93.599999999999994                 94
##                  1                  1                  1                153
##               94 % 94.299999999999997               94.5                 95
##                  1                  1                  1                153
##               95.5 95.609999999999999 95.900000000000006                 96
##                  1                  1                  1                191
##               96 %               96.5 96.700000000000003                 97
##                    1                    1                    1                  142
##                 97.5                   98                   99
##                    1                   97                   35                  784
```

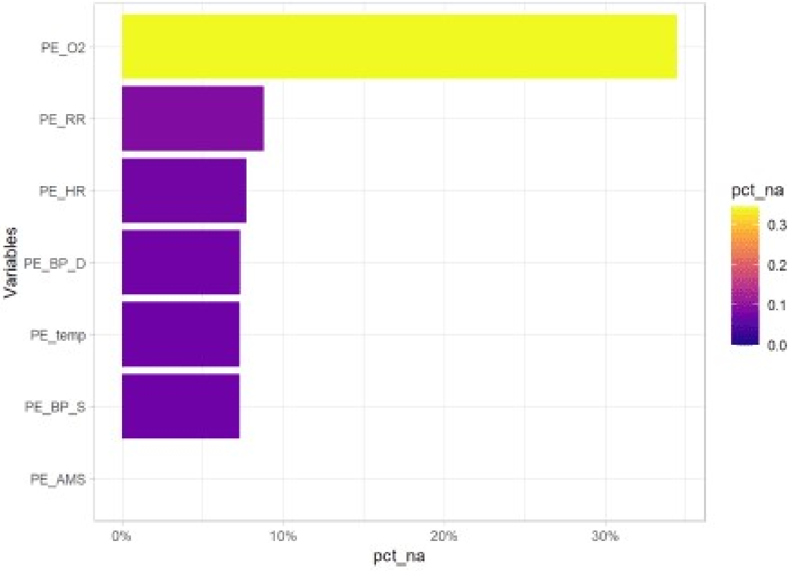
```
# clean  up `PE_O2`
df<-df %>% mutate(PE_O2= as.numeric(str_replace_all(PE_O2,pattern="%",
replacement = "")))
```

```
## Warning in mask$eval_all_mutate(dots[[i]]): NAs introduced by coercion
```

Missing `PE_` values

Now, all the `PE_` variables are in numeric form and the proportion of `NA` can be appropriately calculated. Oxygen levels `PE_O2` has the highest proportion of missing values, >30% values are missing. `PE_O2` will be dropped.

```
(eda_n_NAplt(df,"PE"))
```



```
df<-df %>% select(-PE_O2)
```

Outlier `PE_` values

The following variables have unrealistic outliers:

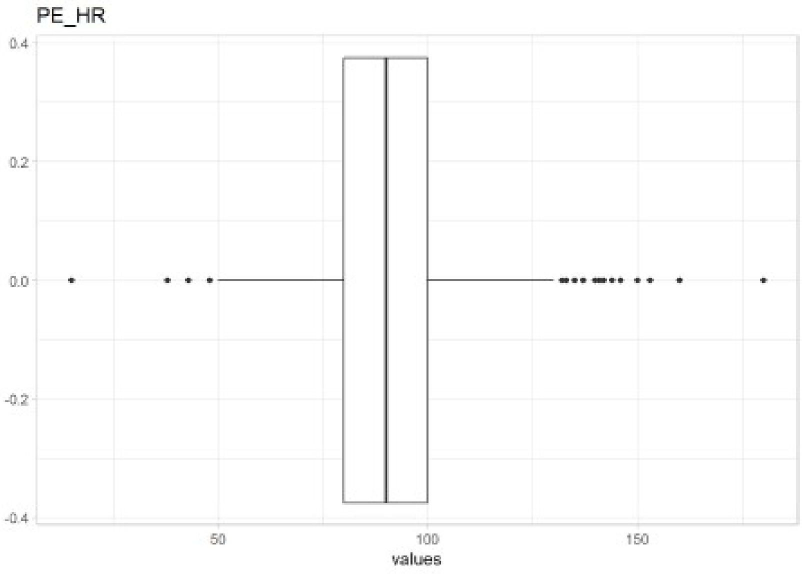
- Temperature, `PE_temp`. Outliers >50'C will be explored
- Breathing rate, `PE_RR`. Outliers of >50 breaths per minute will be explored
- Diastolic blood pressure, `PE_BP_D`. There is only one observation with a diastolic blood pressure >300, this observation will be removed.

```
pe_selected<-eda_n_NAcutoff(df, "PE", 0, 0.3)
```

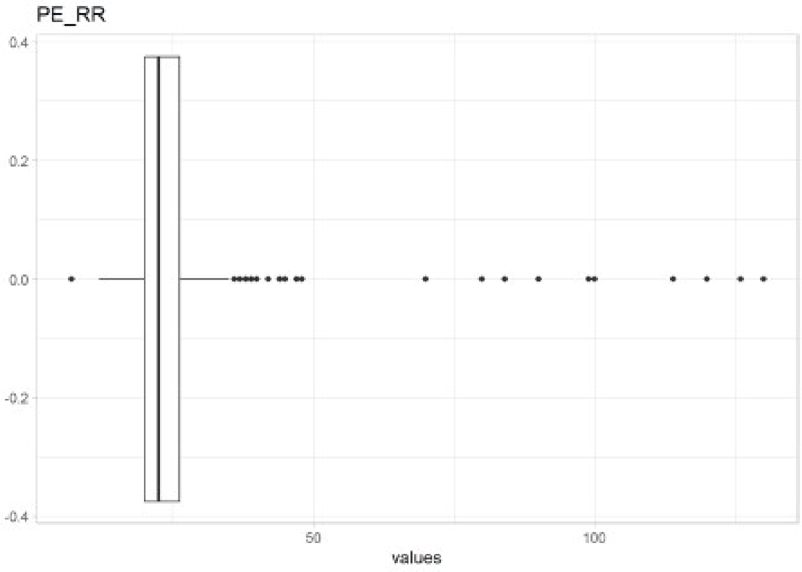
```
(eda_n_outlier(df,pe_selected))
```

```
## Warning: All elements of `...` must be named.
## Did you want `data = c(values)`?
```

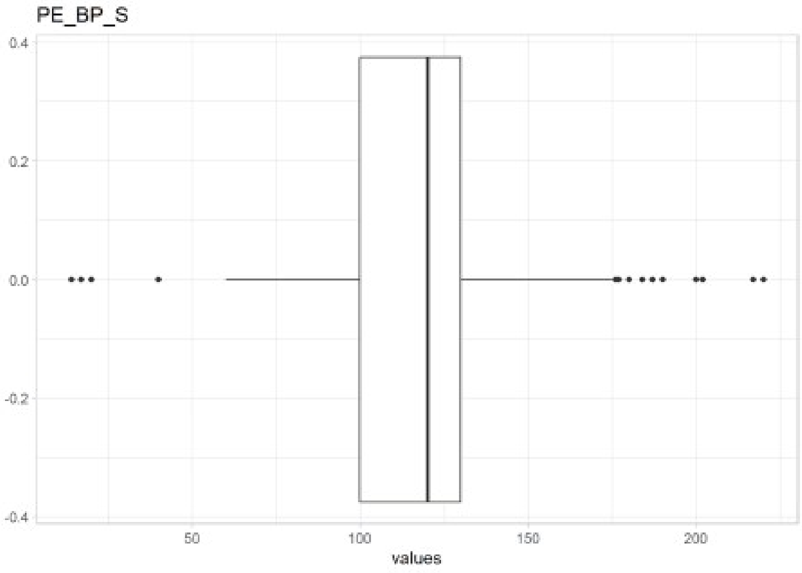
```
## Warning: Removed 176 rows containing non-finite values (stat_boxplot).
```



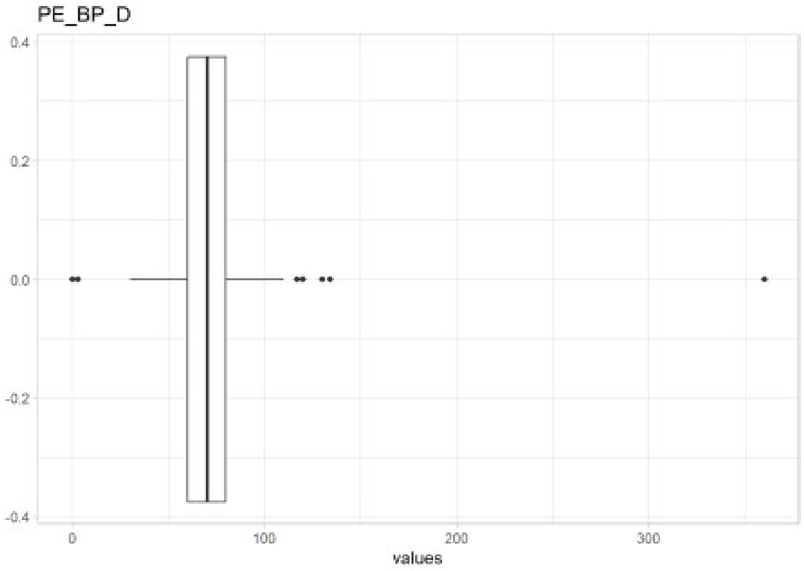
```
## Warning: Removed 201 rows containing non-finite values (stat_boxplot).
```



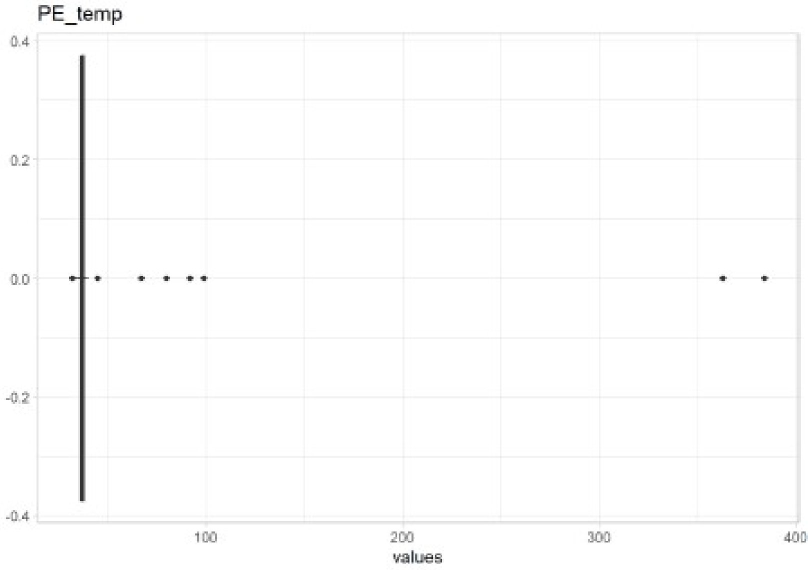
```
## Warning: Removed 167 rows containing non-finite values (stat_boxplot).
```



```
## Warning: Removed 168 rows containing non-finite values (stat_boxplot).
```



```
## Warning: Removed 167 rows containing non-finite values (stat_boxplot).
```



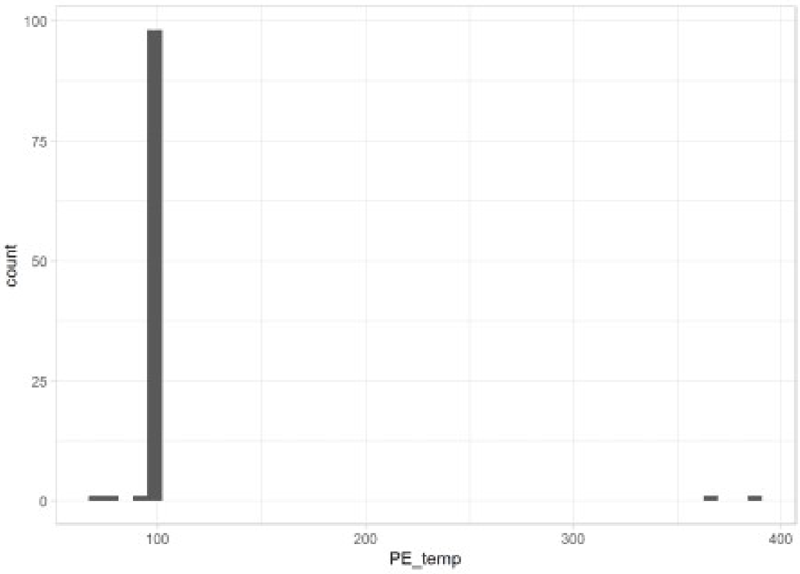
```
## NULL
```

```
df<-df %>% filter(PE_BP_D<300)
```

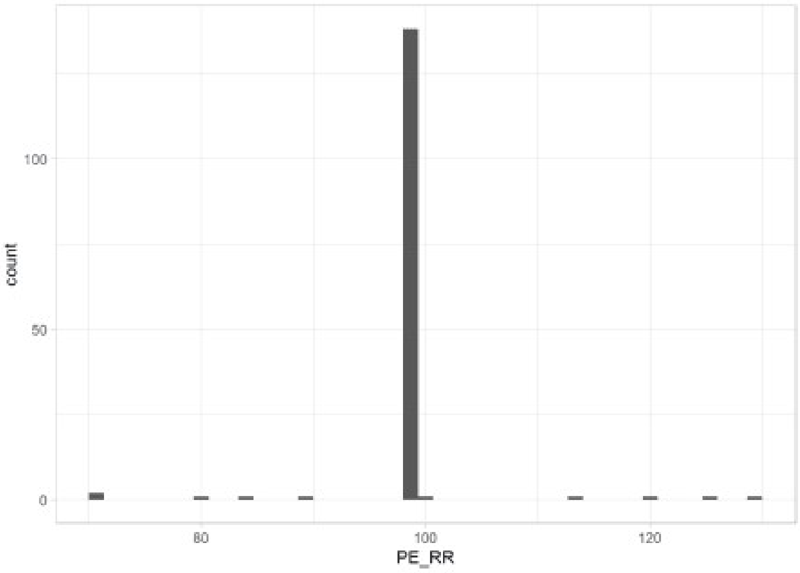
Further investigation of outliers

The 90-ish values stand out for both `PE_temp` and `PE_RR`. A frequency count will be done.

```
(df %>% filter(PE_temp>50) %>% ggplot(aes(PE_temp)) + geom_histogram(bins=round(
sqrt(nrow(df)))))
```



```
(df %>% filter(PE_RR>50) %>% ggplot(aes(PE_RR)) + geom_histogram(bins=round(
sqrt(nrow(df)))))
```



99 is the most common value. Similar to previous numeric variables where 99 is an outlier, it will be converted to NA. For PE_temp, the values 363 and 384, are likely missing a decimal point (It is more likely your body’s temperature is 36.3’C instead of 363’C) .

```
# PE_temp
(df %>% filter(PE_temp>50) %>% group_by(PE_temp) %>% summarise(n(),
.groups="drop"))
```

```
## # A tibble: 6 x 2
##   PE_temp `n()`
##     
## 1      67     1
## 2      80     1
## 3      92     1
## 4      99    98
## 5     363     1
## 6     384     1
```

```
# PE_RR
(df %>% filter(PE_RR>50) %>% group_by(PE_RR) %>% summarise(n(), .groups="drop"))
```

```
## # A tibble: 10 x 2
##    PE_RR `n()`
##
##  1    70     2
##  2    80     1
##  3    84     1
##  4    90     1
##  5    99   138
##  6   100     1
##  7   114     1
##  8   120     1
##  9   126     1
## 10   130     1
```

The rest of the outliers will take a plausible maximum value based on the 90th-95th percentile.

```
# 90-ish percentile
(quantile(df$PE_temp, probs = seq(0,1,.05), na.rm = T))
```

```
##   0%   5%  10%  15%  20%  25%  30%  35%  40%  45%  50%  55%  60%  65%  70%
75%
##   32   36   36   36   36   36   36   37   37   37   37   37   37   38   38
38
##  80%  85%  90%  95% 100%
##   38   38   39   40  384
```

```
(quantile(df$PE_RR, probs = seq(0,1,.05), na.rm = T))
```

```
##   0%   5%  10%  15%  20%  25%  30%  35%  40%  45%  50%  55%  60%  65%  70%
75%
##    7   16   16   18   18   20   20   20   21   22   23   24   24   24   26
27
##  80%  85%  90%  95% 100%
##   28   30   35   99  130
```

```
# clean up PE_temp and PE_RR
df<-df %>% mutate(PE_temp=na_if(PE_temp, 99), PE_RR=na_if(PE_RR, 99),
          PE_temp=if_else(PE_temp==363, 36.3, PE_temp),
PE_temp=if_else(PE_temp==384, 38.4, PE_temp),
          PE_temp=if_else(PE_temp>50, 40, PE_temp), PE_RR=if_else(PE_RR>50, 35,
PE_RR))
```