Data and materials: Rapid recovery of peripheral oxygen saturation in hypoxic COVID-19 patients with ivermectin/doxycycline/zinc multidrug therapy

The following computer code has been used to generate automatically the tables of the article from the available data.

1. process.r

This file generates all tables of the paper except for the comorbidities table.

```
#############
# process.r
#############

library (dplyr)
library (magrittr)
source ("tables.r")

###########################################
# Calculate number of days between two dates
date_format <- "%m/%d/%Y"
not_a_date_p <- function (s) s == "NA" | s == "Declined" | s == "Death"
countdays <- function (from, to) ifelse (not_a_date_p (from) | not_a_date_p (to), NA, as.Date (to,
    date_format)-as.Date (from, date_format))

###########################################
# Load data
A <- read.csv ("hazan-case-series.csv") %>%
  mutate (temp = as.numeric (temp),
          basespo2 = as.numeric (basespo2),
          nextdayspo2 = ifelse (is.na (nextdayspo2), NA, as.numeric (nextdayspo2))) %>%
  mutate (rxstartdays = countdays (pospcr, rxstart),
          symptomdays = countdays (rxstart, symptomend),
          negpcrdays = countdays (rxstart, negpcr)) %>%
  mutate (o2delta = nextdayspo2 - basespo2,
          o2stabledelta = nextdayspo2 - 90,
          o2recoverdelta = nextdayspo2 - 95)

# Remove patients that did not adhere to treatment for per-protocol analysis
B <- A %>% filter (!grepl ("Declined", rxstart))

###########################################
# Median and IQR for SpO2 deltas

# report median and IQR
string_median_iqr <- function (x) paste ("median", median (x, na.rm=TRUE), "with IQR", quantile
    (x, 1/4, na.rm=TRUE), "to", quantile (x, 3/4, na.rm=TRUE), sep=" ")

# Report on SpO2 deltas
sink ("spo2-delta-median-iqr.txt")
cat (paste ("SpO2 delta day 1 to day 2:", string_median_iqr (A$o2delta), sep=" "), "\n")
cat (paste ("SpO2 delta for stabilization over 90% on day 2:", string_median_iqr
    (A$o2stabledelta), sep=" "), "\n")
cat (paste ("SpO2 delta for recovery over 95% on day 2:", string_median_iqr (A$o2recoverdelta),
    sep=" "), "\n")
sink ()

###########################################
# Create case series characteristics table
###########################################

###########################################
# Table configuration

table_format_case_series <- "cccclcccccccc"
```

```
table_header_case_series <- function () list (sprintf ("%s \\\\", paste (textbf ("ID"), textbf
    ("Age"), textbf ("Race"), textbf ("Sex"), textbf ("Symptoms"), textbf ("Temp"), multicol (2,
    paste (textbf ("SpO"),"$\\bm{_2}$",sep="")), multicol (2, textbf ("Rx start")), multicol (2,
    textbf ("Resolved")), multicol (2, textbf ("PCR")), sep=" & ")),
  paste (cline (7, 8), cline (9, 10), cline (11, 12), cline (13, 14), sep=""),
  sprintf ("&&&&&& %s \\\\", paste (textbf ("base"), textbf ("+24 h"), textbf ("days"), textbf
      ("date"), textbf ("days"), textbf ("date"), textbf ("positive"), textbf ("negative"), sep="
      & ")))
table_caption_case_series <- "Case series subjects, COVID-associated symptoms on presentation and
    other characteristics"
table_bottomcaption_case_series <- "\\textbf{NA:} not available; \\textbf{SOB:} shortness of
    breath; \\textbf{PE:} pulmonary embolism; \\textbf{ID:} identification number; \\textbf{Age:}
    patient age in years; \\textbf{Symptoms:} Patient symptoms upon presentation other than
    hypoxia; \\textbf{Temp:} Patient temperature in Fahrenheit upon first presentation;
    \\textbf{SpO}$\\bm{_2}$\\textbf{:} Room air peripheral oxygen saturation at baseline (base)
    and after 24 hours (+24 h); \\textbf{Rx start:} Onset of IDZCT treatment since positive PCR
    test (days) and date of beginning of IDZCT treatment administration (date);
    \\textbf{Resolved:} Days to symptom resolution since initiating treatment (days) and date of
    symptom resolution (date); \\textbf{PCR:} Date of first positive PCR test (positive) and date
    of first negative PCR test (negative)."

############################################
# Create table

sink ("table-case-series.tex")
use_latex_table (14)
begin_latex_table ("case-series", table_caption_case_series, table_format_case_series,
    table_header_case_series ())
for (i in 1:nrow (A)) {
  cat (sprintf ("%s \\\\", paste (A$id[i], A$age[i], A$race[i], A$sex[i], A$symptoms[i],
      A$temp[i], A$basespo2[i], A$nextdayspo2[i], A$rxstartdays[i], A$rxstart[i],
      A$symptomdays[i], A$symptomend[i], A$pospcr[i], A$negpcr[i], sep=" & ")), "\n")
  if (i<nrow (A)) hline()
}
end_latex_table_with_caption (table_bottomcaption_case_series)
sink ()

############################################
# Utilities for counting stuff
############################################

#######################################################
# Return percent in string form (n out of N)

percentage_without_the_symbol <- function (n, N) ifelse (n == 0, paste ("$", "0.0", "$", sep=""),
    ifelse (100*(n/N) >= 0.1, paste ("$", sprintf ("%s", round (100*(n/N), digits=1)), "$",
    sep=""), "$< 0.1$"))

#######################################################
# Percent string

percent_string <- function (a) paste (a, "\\", "%", sep="")

#######################################################
# LaTeX code for producing able entries for N and %

# Count yes and calculate percentage; save results in dataframe
# data = complete dataset
# filtered_data = filtered dataset for which N and % are needed
count_rows <- function (filtered_data, data) data.frame (all = data %>% nrow (), N = filtered_data
    %>% nrow ()) %>% mutate (percent = percentage_without_the_symbol (N, all))

# Convert the count dataframe to LaTeX code
write_latex <- function (result) sprintf (" $%s$ & %s ", as.character (result$N), as.character
    (result$percent))
```

```
######################################################
# Counters -- return LaTeX code for table entry

# Count male vs female
# Note: no missing data for intention-to-treat case series
count_male <- function (data) data %>% filter (grepl ("M", sex)) %>% count_rows (data) %>%
    write_latex ()
count_female <- function (data) data %>% filter (grepl ("F", sex)) %>% count_rows (data) %>%
    write_latex ()

# Count an age bracket
# count condition: a <= age <= b
# Note: no missing data for intention-to-treat case series
count_age_bracket <- function (data, a, b) data %>% filter (a <= age, age <= b) %>% count_rows
    (data) %>% write_latex ()

# Count race category
# Note: no missing data for intention-to-treat case series
count_race <- function (data, desc) data %>% filter (grepl (desc, race)) %>% count_rows (data) %>%
    write_latex ()

# Count temperature: a <= temp < b
# Note: no missing data for intention-to-treat case series
count_temp <- function (data, a, b) data %>% filter (a <= temp, temp < b) %>% count_rows (data)
    %>% write_latex ()

# Count days for treatment onset: a <= rxstartdays <= b
# Note no missing data for per-protocol subgroup
count_treatment_onset <- function (data, a, b) data %>% filter (a <= rxstartdays, rxstartdays <=
    b) %>% count_rows (data) %>% write_latex ()

# Count days for symptom resolution: a <= symptomdays <= b
# Note no missing data for per-protocol subgroup
count_symptom_resolution <- function (data, a, b) data %>% filter (a <= symptomdays, symptomdays
    <= b) %>% count_rows (data) %>% write_latex ()

# count entries with a < SpO2 <= b
# note: (0,0) counts missing values
count_spo2_baseline <- function (data, a, b) if (a > 0 & b > 0) data %>% filter (a < basespo2,
    basespo2 <= b) %>% count_rows (data) %>% write_latex () else data %>% filter (is.na
    (basespo2)) %>% count_rows (data) %>% write_latex ()
count_spo2_nextday <- function (data, a, b) if (a > 0 & b > 0) data %>% filter (a < nextdayspo2,
    nextdayspo2 <= b) %>% count_rows (data) %>% write_latex () else data %>% filter (is.na
    (nextdayspo2)) %>% count_rows (data) %>% write_latex ()

###########################################
# Make demographic table
###########################################

###########################################
# Functions for writing table rows

add_male <- function (desc) cat (sprintf ("%s \\\\", paste (desc, A %>% count_male (), B %>%
    count_male () , sep=" & ")), "\n")
add_female <- function (desc) cat (sprintf ("%s \\\\", paste (desc, A %>% count_female (), B %>%
    count_female () , sep=" & ")), "\n")
add_age <- function (desc, a, b) cat (sprintf ("%s \\\\", paste (desc, A %>% count_age_bracket (a,
    b), B %>% count_age_bracket (a, b), sep=" & ")), "\n")
add_race <- function (desc) cat (sprintf ("%s \\\\", paste (desc, A %>% count_race (desc), B %>%
    count_race (desc) , sep=" & ")), "\n")
add_temp <- function (desc, a, b) cat (sprintf ("%s \\\\", paste (desc, A %>% count_temp (a, b), B
    %>% count_temp (a, b), sep=" & ")), "\n")

spo2_describe <- function (a, b) if (a > 0 & b > 0) paste ("$", percent_string (a), " <
```

```
    \\text{SpO}_2 \\leq ", percent_string (b), "$", sep="") else paste ("Missing $\\text{SpO}_2$",
    sep="")
add_spo2 <- function (a, b) cat (sprintf ("%s \\\\", paste (spo2_describe (a, b), A %>%
    count_spo2_baseline (a, b), B %>% count_spo2_baseline (a, b), sep=" & ")), "\n")

############################################
# Configure demographic table

table_demographic_caption <- "Demographic and clinical characteristics of patients upon
    presentation"
table_demographic_format <- "lcccc"
table_demographic_header <- function () list (sprintf ("%s \\\\", paste (textbf
    ("Characteristic"), multicol (2, textbf ("Intention-to-treat")), multicol (2, textbf
    ("Per-protocol")), sep=" & ")),
  paste (cline (2, 3), cline (4, 5), sep=""),
  sprintf ("& %s \\\\", paste ("N", "\\%", "N", "\\%", sep=" & ")))

table_demographic_bottomcaption <- "\\emph{Intention-to-treat:} Reports on all 26 patients;
\\emph{Per-protocol:} Reports on 24 patients that adhered to 10-day treatment;
\\emph{Low-grade fever:} \\ctemp{37.0} $\\leq T < $ \\ctemp{38.0} (\\ftemp{98.6} $\\leq T < $
    \\ftemp{100.4});
\\emph{Moderate-grade fever:} \\ctemp{38.0} $\\leq T < $ \\ctemp{39.0} (\\ftemp{100.4} $\\leq T <
    $ \\ftemp{102.2});
\\emph{High-grade fever:} \\ctemp{39.0} $\\leq T < $ \\ctemp{41.0} (\\ftemp{102.2} $\\leq T < $
    \\ftemp{105.8})"

############################################
# Create demographic table

sink ("table-demographic.tex")
use_latex_table (5)
begin_latex_table ("demographic", table_demographic_caption, table_demographic_format,
    table_demographic_header ())
category ("Sex")
add_male ("Male")
add_female ("Female")
hline ()
category ("Age")
add_age ("41 to 50 years", 41, 50)
add_age ("51 to 60 years", 51, 60)
add_age ("61 to 70 years", 61, 70)
add_age ("71 to 80 years", 71, 80)
add_age ("81 to 90 years", 81, 90)
add_age ("91 years or older", 91, 100)
hline ()
category ("Race")
add_race ("Caucasian")
add_race ("Hispanic")
add_race ("Other")
hline ()
category ("Baseline temperature")
add_temp ("No fever", 0, 98.6)
add_temp ("Low-grade fever", 98.6, 100.4)
add_temp ("Moderate-grade fever", 100.4, 102.2)
add_temp ("High-grade fever", 102.2, 105.8)
hline ()
category ("Baseline \\bfspotwo\\ on room air")
add_spo2 (90, 95)
add_spo2 (85, 90)
add_spo2 (80, 85)
add_spo2 (75, 80)
add_spo2 (70, 75)
end_latex_table_with_caption (table_demographic_bottomcaption)
sink ()
```

```
####################################################
# Make trearment onset and symptom resolution table
####################################################

####################################################
# Write rows for timing table

add_timing <- function (desc, a, b) cat (sprintf ("%s \\\\", paste (desc, B %>%
    count_treatment_onset (a, b), B %>% count_symptom_resolution (a, b), sep=" & ")), "\n")

####################################################
# Configure the timing table

table_timing_caption <- "Number of days for onset of treatment and symptom resolution for
    per-protocol subgroup"
table_timing_format <- "ccccc"
table_timing_header <- function () list (sprintf ("%s \\\\", paste (textbf ("Duration"), multicol
    (2, textbf ("Treatment onset")), multicol (2, textbf ("Symptom resolution")), sep=" & ")),
  paste (cline (2, 3), cline (4, 5), sep=""),
  sprintf ("& %s \\\\", paste ("N", "\\%", "N", "\\%", sep=" & ")))

table_timing_bottomcaption <- "\\emph{Treatment onset:} Number of days from date of positive PCR
    test to date of start of IDZCT protocol \\par\\emph{Symptom resolution:} Number of days from
    date of start of IDZCT protocol to date of symptom resolution"

####################################################
# Create the timing table

sink ("table-timing.tex")
use_latex_table (5)
begin_latex_table ("timing", table_timing_caption, table_timing_format, table_timing_header ())
add_timing ("0 days", 0, 0)
add_timing ("1 to 5 days", 1, 5)
add_timing ("6 to 10 days", 6, 10)
add_timing ("11 to 20 days", 11, 20)
add_timing ("21 to 30 days", 21, 30)
add_timing ("31 to 40 days", 31, 40)
end_latex_table_with_caption (table_timing_bottomcaption)
sink ()

####################################################
# Create an SpO2 double-column table including delta
####################################################

####################################################
# SpO2 table configuration

# LaTeX code for boldfont SpO2
spo2_bf_string <- paste (textbf ("SpO"), "$\\bm{_2}$", sep="")

# Repeat LaTeX code for portion of a row twice
repeat_twice <- function (s) paste (s, s, sep=" & ")

# Table parameters
table_format_spo2 <- strrep ("c", 12)
table_header_spo2 <- function () list (sprintf ("%s \\\\", repeat_twice (paste (textbf ("ID"),
    multicol (5, spo2_bf_string), sep=" & "))),
   paste (cline (2, 6), cline (8, 12), sep=""),
   sprintf ("%s \\\\", repeat_twice (paste ("", textbf ("day 1"), textbf ("day 2"),
       "$\\bm{\\Delta}$", "$\\bm{\\Delta_{90}}$", "$\\bm{\\Delta_{95}}$", sep=" & "))))
table_caption_spo2 <- "Baseline \\spotwo vs \\spotwo on day 2 at room air for all
    intention-to-treat patients"
table_bottomcaption_spo2 <- "\\textbf{day 1:} Baseline \\spotwo on room air prior to commencing
    IDZCT treatment. \\par\\textbf{day 2:} Peak \\spotwo on room air by the end of day 2. \\par
    $\\bm{\\Delta} = $ Change of \\spotwo on room air from day 1 to day 2. \\par
```

```
    $\\bm{\\Delta_{90}} = $ Difference between peak \\spotwo on day 2 and the 90\\% \\spotwo
    stabilization threshold. \\par $\\bm{\\Delta_{95}} = $ Difference between peak \\spotwo on day
    2 and the 95\\% \\spotwo curative threshold.\\par\\textbf{NA:} Not available; \\textbf{ID:}
    identification number."

####################################################
# Create the SpO2 table

# For deltas, add a plus sign when positive and return as string
add_plus_sign <- function (n) ifelse (n>0, paste ("+", as.character (n), sep=""), as.character (n))

# Make string with table entries for a specific patient
patient_spo2_before_after <- function (n) paste (A$id[n], A$basespo2[n], A$nextdayspo2[n],
  add_plus_sign (A$o2delta[n]), add_plus_sign (A$o2stabledelta[n]), add_plus_sign
      (A$o2recoverdelta[n]), sep=" & ")

# Create table
sink ("table-spo2-day1-vs-day2.tex")
use_latex_table (12)
begin_latex_table ("spo2-before-after", table_caption_spo2, table_format_spo2, table_header_spo2
    ())
for (i in 1:13) cat (sprintf ("%s & %s \\\\", patient_spo2_before_after (i),
    patient_spo2_before_after (i+13)), "\n")
end_latex_table_with_caption (table_bottomcaption_spo2)
sink ()
```

2. comorbidities.r

This file defines the comorbidity data and generates the comorbidities table.

```
###################
# comorbidities.r
###################

library (dplyr)
library (magrittr)
source ("tables.r")

##############
# Load data
##############

# Make a vector of 26 patients and set the ones on the list L equal to 1, all others 0
mkitem <- function (L) {
  a <- rep (0, 26)
  a[L] <- 1
  a
}

# Comorbidity data for intention-to-treat group
A <- data.frame (id = 1:26, prediabetic = mkitem (c (1, 12, 13, 16, 22)),
  diabetes = mkitem (c (5, 9, 10, 11, 25, 26)),
  pulmembolism = mkitem (c (6)),
  cardiovascular = mkitem (c (1, 2, 10, 21, 22, 24, 25)),
  copd = mkitem (c (2, 9, 25)),
  kidney = mkitem (c (2, 10, 22)),
  immunocompromised = mkitem (c (20)),
  overweight = mkitem (c (4, 12, 14, 24)),
  obese = mkitem (c (1, 13)),
  veryobese = mkitem (c (5, 7, 17, 23)),
  hypertension = mkitem (c (2, 3, 4, 5, 8, 10, 11, 13, 16, 19, 25, 22)),
  apnea = mkitem (c (1, 7, 12, 13, 14, 15, 16, 17, 22, 23)),
  hyperlipidemia = mkitem (c (3, 9, 10, 11, 12, 16, 22, 23, 26)),
  asthma = mkitem (c (8, 14)),
  neurocognitive = mkitem (c (9, 18, 21)),
  thyroid = mkitem (c (5, 6)),
  psychological = mkitem (c (4, 11)),
  rheumatic = mkitem (c (6, 26)),
  gastrointestinal = mkitem (c (3, 4, 10)),
  musculoskeletal = mkitem (c (3, 9, 13)),
  liver = mkitem (c (4)),
  other = mkitem (c (5, 14)))

# Comorbidity data for per-protocol subgroup
B <- A %>% filter (!(id %in% c (10, 26)))

# Count the comorbidities
# cmbd = count of all comorbidities
# c19cmbd = count of c19 susceptible comorbidities
add_comorbidities <- function (data) data %>% mutate (cmbd = prediabetic + diabetes + pulmembolism
    + cardiovascular + copd + kidney + immunocompromised + overweight + obese + veryobese +
    hypertension + apnea + hyperlipidemia + asthma + neurocognitive + thyroid + psychological +
    rheumatic + gastrointestinal + musculoskeletal + liver + other) %>%
  mutate (c19cmbd = cmbd - prediabetic - hyperlipidemia - thyroid - rheumatic - gastrointestinal -
      musculoskeletal - other)


# Add cmbd and c19cmbd counts to A and B
A <- A %>% add_comorbidities ()
B <- B %>% add_comorbidities ()
```

```
############################################
# Utilities for counting stuff
############################################

#######################################################
# Return percent in string form (n out of N)
percentage_without_the_symbol <- function (n, N) ifelse (n == 0, paste ("$", "0.0", "$", sep=""),
    ifelse (100*(n/N) >= 0.1, paste ("$", sprintf ("%s", round (100*(n/N), digits=1)), "$",
    sep=""), "$< 0.1$"))

#######################################################
# Percent string
percent_string <- function (a) paste (a, "\\", "%", sep="")

#######################################################
# Count yes and calculate percentage; save results in dataframe
# data = complete dataset
# filtered_data = filtered dataset for which N and % are needed
count_rows <- function (filtered_data, data) data.frame (all = data %>% nrow (), N = filtered_data
    %>% nrow ()) %>% mutate (percent = percentage_without_the_symbol (N, all))

# Convert the count dataframe to LaTeX code
write_latex <- function (result) sprintf (" $%s$ & %s ", as.character (result$N), as.character
    (result$percent))

#######################################################
# Counters -- return LaTeX code for table entry

# Count some comorbidity
# e.g. A %>% count_it ("hyperlipidemia")
count_it <- function (data, something) data %>% filter (data[[something]] == 1) %>% count_rows
    (data) %>% write_latex ()

# Count patients with n comorbidities
count_cmbd <- function (data, n) data %>% filter (cmbd == n) %>% count_rows (data) %>% write_latex
    ()

# Count patients with n covid susceptible comorbidities
count_c19cmbd <- function (data, n) data %>% filter (c19cmbd == n) %>% count_rows (data) %>%
    write_latex ()

############################################
# Make comorbidities table
############################################

####################################
# Functions for writing table rows

# Add a comorbidity count row
# e.g. add ("Hyperlipidemia", hyperlipidemia)
add <- function (desc, what) {
  something <- deparse (substitute (what))
  cat (sprintf ("%s \\\\", paste (desc, A %>% count_it (something), B %>% count_it (something),
      sep=" & ")), "\n")
}

# Describe the number of concurrent comorbidites
describe_cmbd_count <- function (n) ifelse (n == 0, "No concurrent comorbidities", ifelse (n == 1,
    "One comorbidity", sprintf ("%s concurrent comorbidities", as.character (n))))

# Add count of patients with n comorbidities
add_cmbd <- function (n) cat (sprintf ("%s \\\\", paste (describe_cmbd_count (n), A %>% count_cmbd
    (n), B %>% count_cmbd (n), sep=" & ")), "\n")

# Add count of patients with n covid susceptible comorbidities
```

```
add_c19cmbd <- function (n) cat (sprintf ("%s \\\\", paste (describe_cmbd_count (n), A %>%
    count_c19cmbd (n), B %>% count_c19cmbd (n), sep=" & ")), "\n")

####################################
# Configure the comorbidities table

table_comorbidity_caption <- "Prevalence of comorbidities in patients"
table_comorbidity_format <- "lcccc"
table_comorbidity_header <- function () list (sprintf ("%s \\\\", paste (textbf ("Comorbidity"),
    multicol (2, textbf ("Intention-to-treat")), multicol (2, textbf ("Per-protocol")), sep=" &
    ")),
  paste (cline (2, 3), cline (4, 5), sep=""),
  sprintf ("& %s \\\\", paste ("N", "\\%", "N", "\\%", sep=" & ")))
table_comorbidity_bottomcaption <- "\\emph{Intention-to-treat:} Reports on all 26 patients;
\\emph{Per-protocol:} Reports on 24 patients that adhered to 10-day treatment;
\\emph{Other:} includes glaucoma, prostate disease, and essential tremors;
\\emph{BMI:} Body mass index;
\\emph{GERD:} Gastroesophageal reflux disease;
\\emph{HIV/AIDS:} Human immunodeficiency virus, acquired immunodeficiency syndrome."

####################################
# Make the comorbidities table

sink ("table-comorbidities.tex")
use_latex_table (5)
begin_latex_table ("comorbidities", table_comorbidity_caption, table_comorbidity_format,
    table_comorbidity_header ())
category ("COVID-19 susceptible comorbidities")
add ("Type 1 or type 2 diabetes", diabetes)
add ("Heart or cardiovascular disease", cardiovascular)
add ("Chronic obstructive pulmonary disease", copd)
add ("Pulmonary embolism", pulmembolism)
add ("Kidney disease", kidney)
add ("Liver disease (primary biliary cirrhosis)", liver)
add ("Immunocompromised state (HIV/AIDS)", immunocompromised)
add ("Overweight (BMI: 25.0--29.9 $\\text{kg}/\\text{m}^2$)", overweight)
add ("Obese (BMI: 30.0--39.9$\\text{kg}/\\text{m}^2$)", obese)
add ("Morbidly obese (BMI: 40 $\\text{kg}/\\text{m}^2$ or more)", veryobese)
add ("Hypertension", hypertension)
add ("Sleep apnea", apnea)
add ("Asthma", asthma)
add ("Neurocognitive disorders (dementia or Alzheimer's)", neurocognitive)
add ("Psychological disorders (anxiety or depression)", psychological)
hline ()
category ("Other comorbidities")
add ("Prediabetic", prediabetic)
add ("Hyperlipidemia", hyperlipidemia)
add ("Thyroid", thyroid)
add ("Rheumatic diseases (gout or Sjorgren's)", rheumatic)
add ("Gastrointestinal disorders (GERD/gastritis)", gastrointestinal)
add ("Musculoskeletal disorders (osteoarthritis or osteopathy or osteoporosis)", musculoskeletal)
add ("Other", other)
hline ()
category ("Concurrent COVID-19 susceptible comorbidities in patients")
N <- max (A$c19cmbd)
for (n in 0:N) add_c19cmbd (n)
hline ()
category ("All concurrent comorbidities in patients")
N <- max (A$cmbd)
for (n in 0:N) add_cmbd (n)
end_latex_table_with_caption (table_comorbidity_bottomcaption)
sink ()
```

---

3. tables.r

Utility for generating LaTeX code for tables.

```
####################
# tables.r
####################

####################
# Make LaTeX tables
####################

# Boldfont used for table headers
textbf <- function (s) paste ("\\textbf{", s, "}", sep="")

# Multicolumn
multicol <- function (n, description) sprintf ("\\multicolumn{%s}{c}{%s} ", as.character (n),
    description)
multicol_left <- function (n, description) sprintf ("\\multicolumn{%s}{l}{%s} ", as.character (n),
    description)

# Multicolumn category entry
category <- function (s) cat (multicol_left (table_columns, textbf (s)), "\\\\ \n")

#######################################################
# Tabularx tables

# Define table lines for tabularx
# N is number of columns
use_latex_table <- function (N) {
  hline <<- function () cat ("\\midrule", "\n")
  bottomrule <<- function () cat ("\\bottomrule", "\n")
  toprule <<- function () cat ("\\toprule", "\n")
  cline <<- function (a, b) sprintf ("\\cmidrule(lr){%s-%s}", as.character (a), as.character (b))
  table_columns <<- N
}

# The length \tablewidth is used to control horizontal size of table
# Add \newlength{\tablewidth} to preamble of your document
# To load table, one can use a macro like:
# \newcommand{\loadtable}[2]{\setlength{\tablewidth}{#1\textwidth}\input{#1}}

# Open table. Arguments: table label, table caption, table format, table header
begin_latex_table <- function (tablelabel, tablecaption, tableformat, tableheader) {
  cat ("\\begin{table}[htb!]\\begin{center}", "\n")
  cat (sprintf ("\\caption{\\label{fig:%s} %s}", tablelabel, tablecaption), "\n")
  cat ("{\\small", "\n")
  cat (sprintf ("\\begin{tabularx}{\\tablewidth}{%s}", tableformat), "\n")
  toprule ()
  for (i in tableheader) cat (i, "\n")
  hline ()
}

# Close table
end_latex_table <- function () {
  bottomrule ()
  cat ("\\end{tabularx}", "\n")
  cat ("\\end{center}\\end{table}", "\n")
}

# Close table with bottom caption
# Definition of bottom caption command
# \newcommand{\bottomcaption}[3]{\multicolumn{#1}{l}{\parbox{#2}{\vspace{6pt}\small #3}} \\}
end_latex_table_with_caption <- function (desc) {
  bottomrule ()
```

```
  cat (sprintf ("\\bottomcaption{%i}{\\tablewidth}{%s} \\\\", table_columns, desc), "\n")
  cat ("\\end{tabularx}", "\n")
  cat ("}", "\n")
  cat ("\\end{center}\\end{table}", "\n")
}


#######################################################
# longtable for doublespaced version of manuscript

# Define table lines for longtable
# N is number of columns
use_latex_longtable <- function (N) {
  hline <<- function () cat ("\\hline", "\n")
  bottomrule <<- hline
  toprule <<- hline
  cline <<- function (a, b) sprintf ("\\cline{%s-%s}", as.character (a), as.character (b))
  table_columns <<- N
}

# Open LaTeX longtable for doublespaced versions
begin_latex_longtable <- function (tablelabel, tablecaption, tableformat, tableheader) {
  cat ("\\begin{center}", "\n")
  cat ("{\\small", "\n")
  cat (sprintf ("\\begin{longtable}{%s}", tableformat), "\n")
  cat (sprintf ("\\caption{\\small %s}", tablecaption), "\n")
  cat (sprintf ("\\label{fig:%s} \\\\", tablelabel), "\n")
  toprule ()
  for (i in tableheader) cat (i, "\n")
  hline ()
}

# Close longtable
end_latex_longtable <- function () {
  bottomrule ()
  cat ("\\end{longtable}", "\n")
  cat ("\\end{center}", "\n")
}

# Close longtable with bottom caption
end_latex_longtable_with_caption <- function (desc) {
  bottomrule ()
  cat (sprintf ("\\bottomcaption{%i}{\\tablewidth}{%s} \\\\", table_columns, desc), "\n")
  cat ("\\end{longtable}", "\n")
  cat ("}", "\n")
  cat ("\\end{center}", "\n")
}
```

4. test-tables.tex

Wrapper LaTeX file to display the tables generated from the data.

```
\documentclass[11pt,reqno,fleqn]{article}

% Load packages
\usepackage{geometry}
\geometry{top=0.9in,left=1in, right=1in,bottom=0.9in}
\usepackage{times}
\usepackage{tabularx}
\usepackage{booktabs}
\usepackage{longtable}
\usepackage{lscape}
\usepackage{amsmath}
\usepackage{amssymb}
\usepackage{bm}

% Tack notes at the bottom of a table: \bottomcaption{number of columns{width}{text}
\newcommand{\bottomcaption}[3]{\multicolumn{#1}{l}{\parbox{#2}{\vspace{6pt}\small #3}} \\}

%=================================================================
% Commands for inserting tables

% This is used to control the width of tabularx tables
\newlength{\tablewidth}

% 8pt and 9pt font setting to use for tables when compiling in 12pt mode
\newcommand{\ninefont}{\fontsize{9}{11}\selectfont}
\newcommand{\eightfont}{\fontsize{8}{10}\selectfont}

% Display table
\newcommand{\loadtable}[2]{\setlength{\tablewidth}{#1\linewidth}\input{#2}}

%=================================================================
% Local macros

\newcommand{\ftemp}[1]{$#1\;^{\circ}\text{F}$}
\newcommand{\ctemp}[1]{$#1\;^{\circ}\text{C}$}
\newcommand{\oxygen}[1]{ $\text{SpO}_{2}#1$ }
\newcommand{\spotwo}{\oxygen{}}
\newcommand{\bfspotwo}{\textbf{SpO}$\bm{_2} $}

%=================================================================

\begin{document}

\begin{landscape}
{\let\small\eightfont
\loadtable{1}{table-case-series.tex}}
\end{landscape}

\loadtable{0.6}{table-demographic.tex}
\loadtable{0.55}{table-timing.tex}
\loadtable{0.77}{table-spo2-day1-vs-day2.tex}
\loadtable{1}{table-comorbidities.tex}

\clearpage
\end{document}
```

---

5. hazan-case-series.csv

Case series data file, not including comorbidities. This file is processed by process.r to generate tables.

```
id, age, race, sex, symptoms, temp, basespo2, nextdayspo2, rxstart, symptomend, pospcr, negpcr
1,66, Caucasian, M, "Runny nose, sore throat, dizzy, low energy",99.3,90,94, 12/14/2020,
    12/21/2020, 11/6/2020, 1/17/2021
2,62, Caucasian, M, "SOB, chest congestion, productive cough, nausea, vomiting",105,77,87,
    12/8/2020, 12/18/2020, 11/30/2020, 12/18/2020
3,75, Caucasian, M, "Low energy",101,88,96, 10/26/2020, 11/1/2020, 10/15/2020, 10/30/2020
4,66, Caucasian, F, "Loss of appetite, cough, chills, SOB",101,97,96, 10/26/2020, 10/29/2020,
    10/15/2020, 10/30/2020
5,66, Caucasian, F, "Vomiting, weak, body aches, anosmia",101,89,95, 12/18/2020, 12/22/2020,
    12/18/2020, NA
6,43, Caucasian, F, "PE, headache, body ache, cough",101,88,94, 1/26/2021, 2/12/2021, 1/26/2021,
    2/9/2021
7,62, Caucasian, M, "Productive cough, headache",102,86.5,91, 11/24/2020, 12/8/2020, 11/13/2020,
    12/8/2020
8,57, Caucasian, M, "Cough, nasal congestion, SOB, body aches",102,88,96, 10/27/2020, 11/10/2020,
    10/26/2020, 11/15/2020
9,94, Hispanic, F, "Low energy, SOB, confusion, loss of appetite, shaking",102,88,94, 1/10/2021,
    1/20/2021, 12/22/2020, NA
10,66, Hispanic, M, "Cough, SOB, respiratory failure",100.6,72,87, "Declined", "Death",
    12/22/2020, NA
11,63, Hispanic, F, "Cough, SOB",102,90,96, 1/10/2021, 1/20/2021, 12/22/2020, NA
12,47, Hispanic, M, "SOB",104,84,91, 12/19/2020, 12/25/2020, 12/16/2020, NA
13,69, Caucasian, F, "Cough, congestion, rash",102,88,91, 11/17/2020, 12/3/2020, 11/13/2020, NA
14,69, Caucasian, M, "Post-nasal drip, cough, sinus pain",98,88,91, 11/17/2020, 12/3/2020,
    11/13/2020, NA
15,71, Hispanic, M, "Low energy, productive cough, anosmia",101,88,NA, 12/17/2020, 1/5/2021,
    12/13/2020, NA
16,67, Hispanic, F, "Dry cough, body aches, low energy, anosmia",100,88,NA, 12/17/2020,
    1/5/2021,12/13/2020, NA
17,46, Caucasian, F, "Diarrhea, rash, renal pain",102,87,94, 8/8/2020, 8/19/2020, 7/2/2020, NA
18,86, Caucasian, M, "Cough, fever, low energy",102,88,95, 1/9/2021, 1/19/2021, 1/8/2021, 1/19/2021
19,59, Caucasian, F, "Stomach pain, diarrhea, cough, rash",102,90,95, 9/16/2020, 9/25/2020,
    8/19/2020, NA
20,54, Other, M, "Cough, fever, loss of appetite, chills",101.2,88,NA, 10/16/2020, 10/28/2020,
    10/15/2020, 10/28/2020
21,92, Caucasian, M, "Low energy",102,85,91, 2/5/2021, 2/11/2021, 2/2/2021, 2/15/2021
22,63, Hispanic, M, "Cough, low energy, loss of appetite",101.3,90,96, 2/2/2021, 2/12/2021,
    2/2/2021, NA
23,57, Hispanic, M, "Cough, SOB",98,73,90, 1/6/2021, 2/8/2021, 12/30/2020, 1/24/2021
24,46, Hispanic, F, "Chest pain, SOB",98.6,90,NA, 2/18/2021, 2/24/2021, 2/17/2021, NA
25,87, Hispanic, M, "Severe SOB, low energy, trouble walking",101.6,90,95, 2/27/2021, 3/5/2021,
    2/17/2021, NA
26,86, Caucasian, M, "SOB",102,88,NA, "Declined", "Death", 10/6/2020, NA
```