

mixmodel.R

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LINEAR MIXED MODELS FOR DIFFERENCES FROM BASE-LINE AFTER PRONE POSITIONING

Libraries

```
list.of.packages <- c(
  "rmarkdown", "tidyverse", "Rcpp", "knitr", "readxl", "xlsx"
)
new.packages <- list.of.packages[!(list.of.packages %in% installed.packages()[,"Package"])]
if(length(new.packages)) install.packages(new.packages, repos='https://cran.rstudio.com/')
library(tidyverse)

## Registered S3 methods overwritten by 'ggplot2':
##   method      from
##   [.quosures  rlang
##   c.quosures  rlang
##   print.quosures rlang

## Registered S3 method overwritten by 'rvest':
##   method      from
##   read_xml.response xml2

## -- Attaching packages -----

## v ggplot2 3.1.1    v purrr  0.3.3
## v tibble  2.1.1    v dplyr  0.8.5
## v tidyr   1.1.0    v stringr 1.4.0
## v readr   1.3.1    v forcats 0.4.0

## -- Conflicts -----
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()

library(lme4)

## Loading required package: Matrix

##
## Attaching package: 'Matrix'

## The following objects are masked from 'package:tidyr':
##
##   expand, pack, unpack
```

Scripts

```
source("./rscripts/kabler_tabler.R", echo=FALSE)
```

```
## Loading required package: magrittr

##
## Attaching package: 'magrittr'

## The following object is masked from 'package:purrr':
##
##     set_names

## The following object is masked from 'package:tidyr':
##
##     extract

source("./data_import.R", echo=FALSE)

## Parsed with column specification:
## cols(
##   .default = col_double(),
##   cama_paciente = col_character(),
##   horas = col_time(format = "")
## )

## See spec(...) for full column specifications.
```

OUTCOME 1: difference between PaO2/FiO2 mmHg in pre-prone versus prone positioning

Set covariables of interest

```
covars0 <- c(
  "cama_paciente",
  ""
)
covars <- covars0[-length(covars0)]
new_vars <- c("pafi_status", "pafi")
```

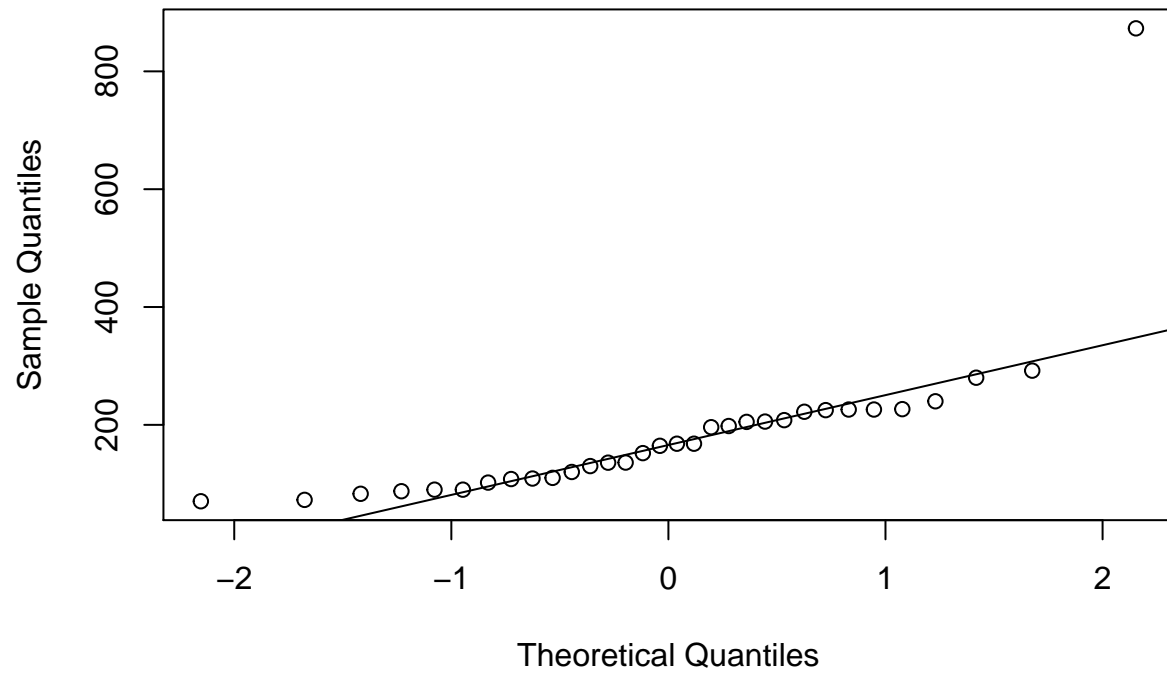
Data in long format

```
data_gathered <- mydata %>%
  select(
    !!covars,
    "po2_fio2_pre",
    "po2_fio2_prono"
  ) %>%
  gather(
    key = pafi_status,
    value = pafi,
    -!!covars
  )
```

PaO2/FiO2 qqplot (acceptable except in extremes)

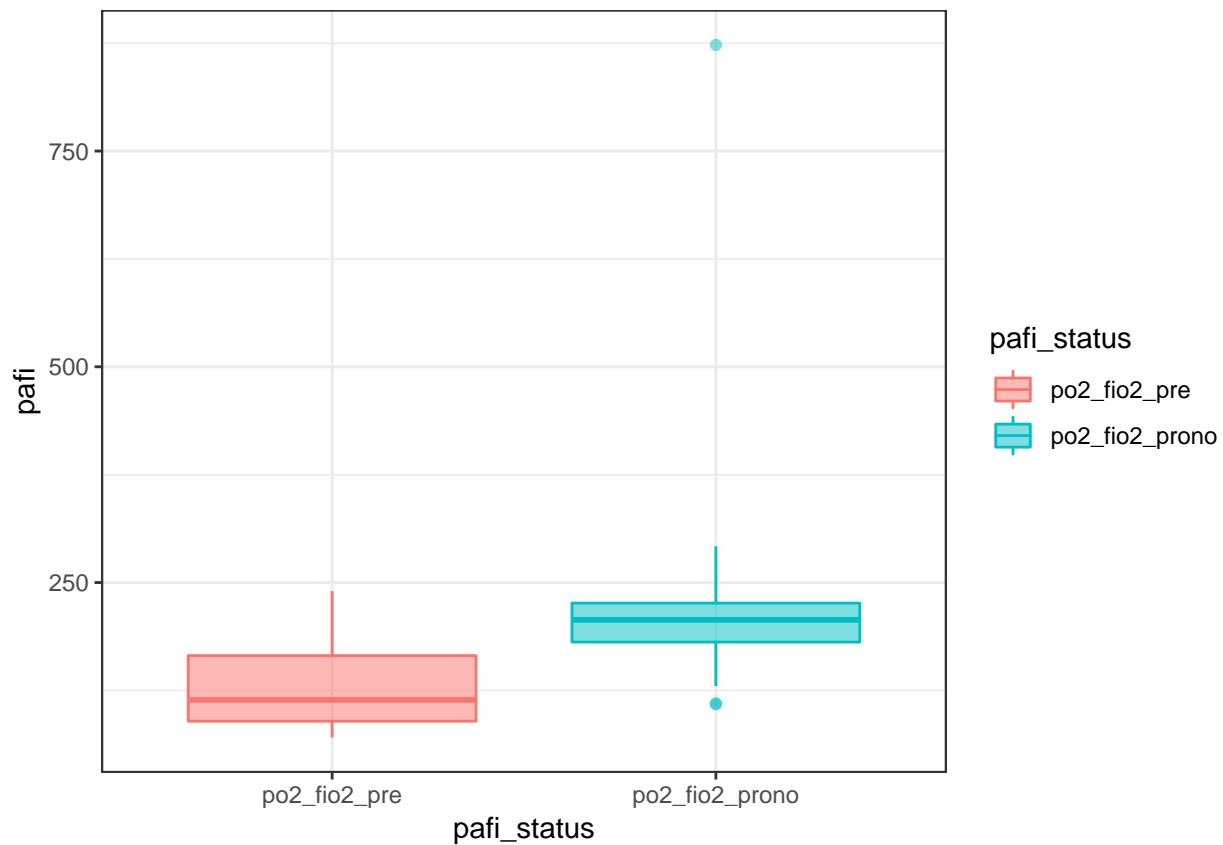
```
qqnorm(data_gathered$pafi)
qqline(data_gathered$pafi)
```

Normal Q-Q Plot



PaO2/FiO2 boxplot

```
data_gathered %>%  
  ggplot(  
    aes(  
      x=pafi_status,  
      y=pafi,  
      colour=pafi_status, fill=pafi_status  
    )  
  ) + geom_boxplot(alpha=0.5) + theme_bw()
```



Fit LMM

```
lmm1 <- lmer(pafi ~ pafi_status + (1 | cama_paciente), data_gathered) # cama_paciente is the patient ID
lmm1
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: pafi ~ pafi_status + (1 | cama_paciente)
## Data: data_gathered
## REML criterion at convergence: 380.8378
## Random effects:
## Groups      Name      Std.Dev.
## cama_paciente (Intercept) 93.49
## Residual      109.35
## Number of obs: 32, groups: cama_paciente, 7
## Fixed Effects:
##              (Intercept) pafi_statuspo2_fio2_prono
##                   149.9                110.4
```

Tidy LMM

```
new_vars_status <- new_vars[1]
new_vars_value <- new_vars[2]
new_vars_status_q <- rlang::sym(new_vars_status)
new_vars_status_num <- paste0(new_vars_status, "_num")
```

```

model_name <- "Changes in PaO2/FiO2 pre - prone"

data_gathered0 <- data_gathered %>%
  mutate(
    !!new_vars_status_num := case_when(
      str_locate(tolower(!!new_vars_status_q), "pre")[,1] >= 1 ~ 0,
      str_locate(tolower(!!new_vars_status_q), "prone")[,1] >= 1 ~ 1,
      str_locate(tolower(!!new_vars_status_q), "post")[,1] >= 1 ~ 1,
      TRUE ~ 1
    )
  )

# Write formula
my_formula <- as.formula(
  paste0(
    new_vars_value, " ~ ", new_vars_status_num, " + (1 | cama_paciente)"
  )
)

# Fit LMM
lmm1 <- lmer(my_formula, data=data_gathered0) # rowid is the patient ID, set as random effect # lmm1; s
sumlmm1 <- lmm1 %>% broom::tidy()

## Warning in bind_rows(x, .id): binding factor and character vector, coercing
## into character vector

## Warning in bind_rows(x, .id): binding character and factor vector, coercing
## into character vector

confints0 <- confint(lmm1) %>% broom::tidy() %>%
  rename(
    term = .rownames,
  ) %>%
  mutate(
    `95% CI` = paste0(
      "[", round(X2.5..., 3), "; ", round(X97.5..., 2), "]"
    )
  ) %>%
  select(term, `95% CI`)

## Computing profile confidence intervals ...

## Warning: 'tidy.matrix' is deprecated.
## See help("Deprecated")

# Tidy results
sumlmm1_estimate <- sumlmm1 %>%
  mutate(
    group = case_when(
      group != "fixed" ~ "random effect",
      TRUE ~ "fixed effect"
    )
  ) %>%
  mutate(
    terms = c(
      "Intercept",
      model_name,
      "Intercept SD (random effect)",

```

```

    "Residual SD (random effect)"
  ),
  name = case_when(
    terms == "Intercept" ~ model_name,
    TRUE ~ ""
  )
) %>%
left_join(
  confints0
) %>%
select(
  name, terms, everything(), -term
) %>%
mutate_at(
  vars(estimate:statistic),
  list(~round(., 2))
)

```

Joining, by = "term"

LMM Table

```
sumlmm1_estimate %>% pander::pander()
```

Table 1: Table continues below

name	terms	estimate
Changes in PaO2/FiO2 pre - prone	Intercept	149.9
	Changes in PaO2/FiO2 pre - prone	110.4
	Intercept SD (random effect)	93.49
	Residual SD (random effect)	109.3

std.error	statistic	group	95% CI
45.17	3.32	fixed effect	[59.958; 247.07]
38.66	2.86	fixed effect	[31.756; 189.09]
NA	NA	random effect	NA
NA	NA	random effect	NA