

CF Modulator Analysis

Dinh Tuan Phan, Ph.D.

5/16/2021

Load the required packages for analysis in this study

```
library(readxl)
library(tidyverse)
library(cowplot)
```

Load data

Function to read all the data in excel sheets

```
readExcel <- function(filename, tibble = FALSE) {
  sheets <- readxl::excel_sheets(filename)
  x <-
    lapply(sheets, function(X)
      readxl::read_excel(filename, sheet = X))
  x <- lapply(x, function(x)
    x[,!apply(is.na(x), 2, all)])
  if (!tibble)
    x <- lapply(x, as.data.frame)
  names(x) <- sheets
  x
}
```

Read data in all sheets

```
cf <- readExcel("20210514_updated_CF_subjects_iontophoresis.xlsx")
cf <- cf[-c(3, 40)]
names(cf)
```

```
## [1] "KF17_K1" "KF17_K2" "AM18_T1" "AM18_T2" "AM18_T3" "CM02_S1" "CM02_S2"
## [8] "CM02_S3" "CM02_S4" "CM02_S5" "CM02_T1" "JF06_S1" "JF06_S2" "JF06_S3"
## [15] "JF06_T1" "EM12_S1" "EM12_S2" "EM12_S3" "EM12_S4" "EM12_T1" "EM12_T2"
## [22] "JM07_01" "JM07_02" "JM07_03" "LF03_K1" "LF03_S1" "AF08_S1" "AF08_S2"
## [29] "AF08_S3" "JM11_1" "JM11_2" "JF19_1" "JF19_2" "JF19_T1" "CF22_T1"
## [36] "SF14_S1" "LF04_S1" "KF13_K1"
```

Basic exploratory data analysis (EDA) and data visualization

Plotting function

```
myplot <- function(i) {
  tryCatch(
    expr = {
```

```
p <-
  ggplot(cf[[i]],
    aes(x = `SR...28`, y = `C_postdose_smooth_2min`)) +
  geom_point() +
  geom_smooth(method = "lm",
    formula = "y~x",
    se = TRUE) +
  xlim(0, 1) +
  ylim(0, 120) +
  # labs (x = expression(Sweat~rate~(mu*"L"~min^-1~cm^-2)), y = "C (mM)")
  # xlab("Time (min)") +
  # ylab("C (mM)")
  xlab(expression(Sweat ~ rate ~ (mu * "L" ~ min ^ -1 ~ cm ^ -2))) +
  ylab("C (mM)")
p + ggtitle(sheets[i]) + theme(plot.title = element_text(hjust = 0.5))
},
error = function(e) {
  message('Caught an error!')
  print(e)
  return(NULL)
},
warning = function(w) {
  message('Caught a warning!')
  print(w)
  return(NULL)
}
)
}
```

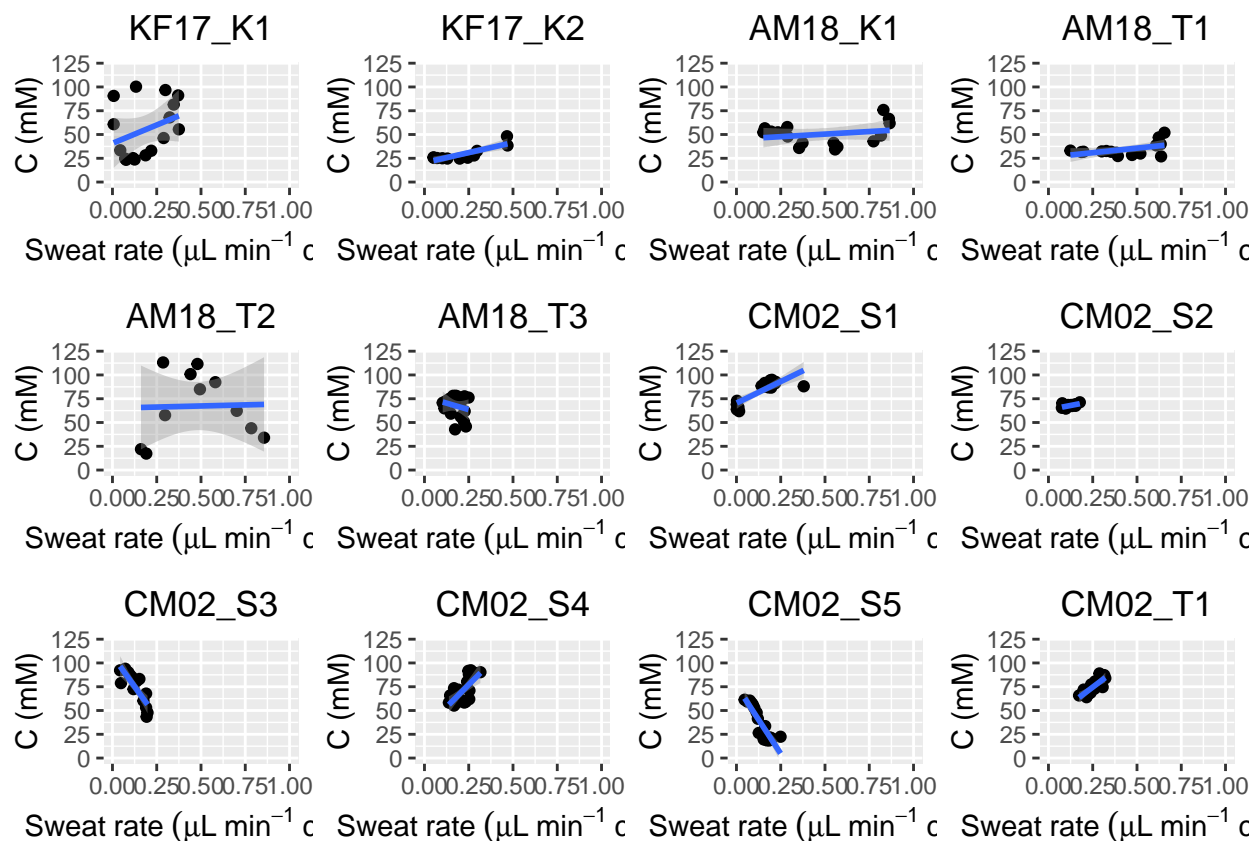
Create list of plots

```
plist <- lapply(1:12, myplot)
```

```
# Open an image file
png(
  file = "saving_plot.png",
  width = 17,
  height = 11,
  units = 'in',
  res = 600
)
```

Plot all together with cowplot

```
cowplot::plot_grid(plotlist = plist,
  align = "hv")
```



```
# Close the image file
dev.off()
```

Subsetting data into two groups for further analysis

```
# homogeneous F508del/F508del
homo <- subset(cf, sapply(cf, function(x) x$Genotype[1] == 'F508del/F508del'))

# heterogeneous F508del/G551D
hete <- subset(cf, sapply(cf, function(x) x$Genotype[1] == 'F508del/G551D'))
names(homo)

## [1] "CM02_S1" "CM02_S2" "CM02_S3" "CM02_S4" "CM02_S5" "CM02_T1" "JF06_S1"
## [8] "JF06_S2" "JF06_S3" "JF06_T1" "EM12_S1" "EM12_S2" "EM12_S3" "EM12_S4"
## [15] "EM12_T1" "EM12_T2" "JM07_01" "JM07_02" "JM07_03" "CF22_T1" "SF14_S1"
## [22] "LF04_S1"

names(hete)

## [1] "KF17_K1" "KF17_K2" "AM18_T1" "AM18_T2" "AM18_T3" "KF13_K1"
```