CF Modulator Analysis

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Load the required packages for analysis in this study

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

Load data

Function to read all the data in excel sheets

```r
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

```r
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_O1" "JM07_O2" "JM07_O3" "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

```r
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
)
```
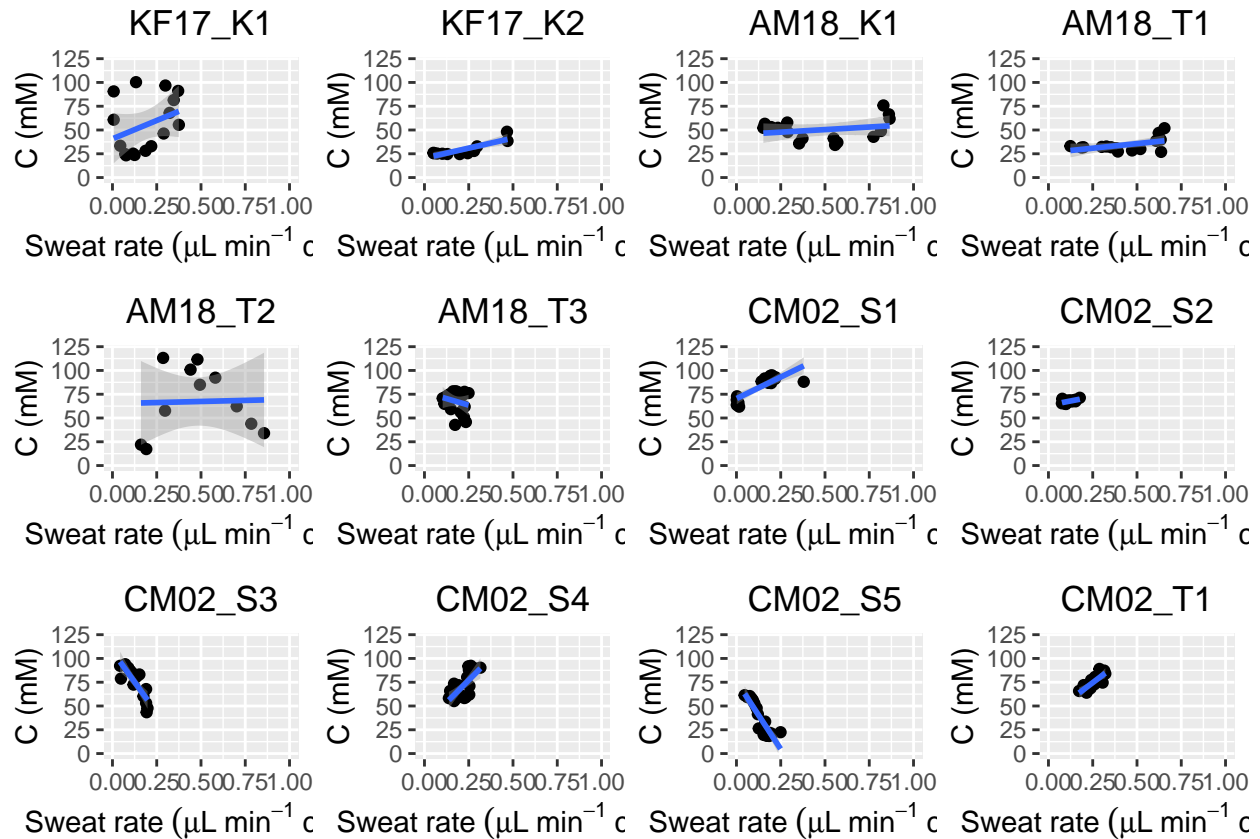
Plot all together with cowplot

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

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

Subsetting data into two groups for further analysis

```r
# 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_O1" "JM07_O2" "JM07_O3" "CF22_T1" "SF14_S1"
## [22] "LF04_S1"
```

```r
names(hete)
```

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