# PK11195

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## Aims

The aim of this assignment is to analyze the PK11195 data in kinfitr

## Libraries

### CRAN libraries

First, the libraries for the analysis and plotting are loaded.

```r
library(tidyverse)
library(stringr)
library(corrplot)
library(grid)
library(gridExtra)
library(RColorBrewer)
library(psych)
library(readxl)
library(pracma)
library(lme4)
library(rjags)
library(knitr)
library(cowplot)
library(corrplot)
library(ggplotify)
```

### Non-CRAN libraries

The libraries above can be installed from CRAN. Those which cannot are installed as follows:

```r
install.packages("devtools")  # If you do not already have devtools
devtools::install_github("mathesong/kinfitr")
devtools::install_github("mathesong/granviller")
devtools::install_github("mvuorre/vmisc")
devtools::install_github("mathesong/kipettools")
devtools::install_github("mathesong/relfeas")
```

**Loading Non_CRAN libraries and setting theme**

```r
library(kinfitr)
library(vmisc)
library(kipettools)
library(granviller)
library(relfeas)
theme_set(theme_light())
```

## Creating folders using "initProjectFolder()"

```r
initProjectFolder()
```

# Extracting roistats and Tidying data.

```r
#Extracting tac data
tacs <- tibble(Filename = list.files(path = "../RawData/",
                                      pattern = "roistats.mat")) %>%
  group_by(Filename) %>%
  mutate(tacdata = map(Filename, ~kipettools::roistats_getData(
    paste0("../RawData/", .x))))
tacs <- tacs %>%
  ungroup() %>%
  mutate(Subjname = map_chr(tacdata, "Subjname"),
         PETNo = map_dbl(tacdata, "PETNo"),
         tacdata = map(tacdata, "tacdata")) %>%
  select(-Filename) %>%
  mutate(PET = paste(Subjname, PETNo, sep='_'))
#loading weights and blood data
oldwd <- getwd()
setwd("../RawData/")
blood <- list()
bloodfiles <- list.files(pattern='blood_processed_pfhill')
for(i in 1:length(bloodfiles)) {
blood[[bloodfiles[i]]] <- read_tsv(bloodfiles[i])
  print(paste0('Progress: ', i, ' / ', length(bloodfiles)))
 }
blood <- tibble(blood)
Weights_list <- list()
weightfiles <- list.files(pattern='_weights2009')
for(i in 1:length(weightfiles)) {
Weights_list[[weightfiles[i]]] <- read_csv(weightfiles[i], col_names = FALSE)
  print(paste0('Progress: ', i, ' / ', length(weightfiles)))
 }
setwd(oldwd)
Weights_list <- tibble(Weights_list)
Weights_list$PET <- weightfiles %>%
str_replace("_weights2009.txt", " ")
Weights_list <- Weights_list %>%
group_by(PET) %>%
unnest() %>%
rename(weights = X1) %>%
ungroup()

#Note: new weights added

tacs <- tacs %>%
unnest() %>%
rename(Times = times) %>%
select(Subjname:PET, Times, durations, WM, GM, WB, FC, OC, THA, STR, TC, ACC, CBL = CER, INS) %>%
add_column(weights = Weights_list$weights) %>%
select(-weights) %>%
```

```
mutate("start" = Times - (durations/2)) %>%
mutate("end" = Times + (durations/2))

tacs$weights <- weights_create(t_start = tacs$start, t_end = tacs$end,
                               tac = tacs$WB, radioisotope = "C11")

tacs <- tacs %>%
group_by(PET, Subjname, PETNo) %>%
nest(.key = tacdata) %>%
ungroup()

blood$PET. <- bloodfiles %>%
str_replace("_blood_processed_pfhill.txt", " ")
blood  <- blood %>%
  unnest() %>%
 rename(Cbl.disp.corr = "Cbl disp corr", Cpl = "Cpl (nCi/cc)", ABSS.sec = "ABSS sec" ) %>%
  mutate(Cbl.disp.corr = ifelse(Cbl.disp.corr < 0, 0, Cbl.disp.corr)) %>%
  group_by(PET.) %>%
  nest(.key='blooddata') %>%
  ungroup() %>%
   mutate(input = map(blooddata, ~blood_interp(
            t_blood = .x$ABSS.sec/60, blood =.x$Cbl.disp.corr,
            t_plasma=.x$ABSS.sec/60, plasma =.x$Cpl,
            t_parentfrac = .x$ABSS.sec/60 , parentfrac= .x$parent_fract ) ))

tacs <- tacs %>%
  arrange(PET, Subjname, PETNo) %>%
  bind_cols(blood)%>%
  select(-PET.)
saveRDS(tacs, '../DerivedData/tacs.rds')
```

## Fitting of the Delay and Blood Volume Fraction

```
tacs <- readRDS('../DerivedData/tacs.rds')
tacs <- tacs %>%
  group_by(PET, Subjname, PETNo) %>%
  mutate(delayFit = map2(tacdata,input,
                         ~twotcm(t_tac = .x$Times, tac = .x$WB, input = .y,
  mutate(inpshift = map_dbl(delayFit, c("par", "inpshift"))) %>%
  ungroup()
```

## creating logan_tstar

```
logantstar <- function(tacdata, input, inpshift) {
  Logan_tstar(t_tac = tacdata$Times, input = input, lowroi = tacdata$FC, medroi =    tacdata$CBL, highro
}
tacs <-  tacs %>%
  group_by(Subjname, PETNo) %>%
  mutate(logan_tstar = pmap(list(tacdata, input, inpshift), logantstar))
```

#Rearrangement of the Data into Long Format

```r
tacs_long <- tacs %>%
  select(PET, Subjname, PETNo, tacdata, logan_tstar, inpshift) %>%
  unnest(tacdata, .drop = FALSE) %>%
  gather(Region, TAC, -(PET:durations) , -(start:weights)) %>%
  group_by(PET, Subjname, PETNo, Region) %>%
  nest(.key = 'tacdata')


tacs_long <- tacs %>%
  select(PET, Subjname, PETNo, input, delayFit) %>%
  inner_join(tacs_long, by = c("PET", "Subjname", "PETNo"))
```

## Plotting logan_tstar

```r
set.seed(123)
tstar_fits <- tacs_long %>%
  ungroup() %>%
  select(tacdata, PET) %>%
  unnest() %>%
  select(PET, logan_tstar) %>%
  sample_n(size =  4, replace = F)
walk2(list(tstar_fits$logan_tstar), tstar_fits$PET,
    ~print(plot_grid(plotlist = .x, ncol = 1, nrow = 1, labels = paste('PET:',.y), label_x = 0.5, label
```

## All 4 tstar plots on a single page

```r
plot_grid(plotlist = tstar_fits$logan_tstar, ncol = 2, nrow = 1, labels = paste('PET:',tstar_fits$PET),
  draw_figure_label("t*", position = "top", fontface = "bold", size = 32, colour = "red")
```

# Define functions for fitting the models

Comment: when the argumant "multstart_iter" is equal to 1 for 2TCM, the estimated microparameters of a number of study participants have a tendency of approaching or even exceeding their default limits.

```r
# MA1 using the fitted delay and vB from delayFit
fitma1 <- function(tacdata, input, delayFit) {
  ma1(t_tac = tacdata$Times, tac = tacdata$TAC, input = input, tstarIncludedFrames = 6,
      inpshift = delayFit$par$inpshift, weights=tacdata$weights, vB= 0)
}
# 2TCM using the fitted delay and vB from delayFit
fit2tcm <- function(tacdata, input, delayFit) {
  twotcm(t_tac = tacdata$Times, tac = tacdata$TAC, input = input,
        inpshift = delayFit$par$inpshift, vB= 0.05, multstart_iter = 100, weights=tacdata$weights)
}
#Loganplot
fit_Logan <- function(tacdata, input, delayFit) {
  Loganplot(t_tac = tacdata$Times, tac = tacdata$TAC,
        input = input,
        inpshift = delayFit$par$inpshift, tstarIncludedFrames = 10, vB= 0)
}
```

# Fit kinetic models

```r
set.seed(123)

tacs_long <- tacs_long %>%

  # 2TCM using fitted vB and delay
  mutate(fit_2tcm= pmap(list(tacdata, input, delayFit), fit2tcm)) %>%
  mutate(Vt_2tcm = map_dbl(fit_2tcm, c('par', 'Vt'))) %>%

  # MA1
  mutate(fit_ma1 = pmap(list(tacdata, input, delayFit), fitma1))  %>%
  mutate(Vt_ma1 = map_dbl(fit_ma1, c('par', 'Vt'))) %>%

  #Loganplot
  mutate(Loganfit = pmap(list(tacdata, input, delayFit),
                         fit_Logan)) %>%
  mutate(Vt_Logan = map_dbl(Loganfit, c("par", "Vt")))
```

#Plot kinetic models

## Plot 2tcm

```r
delayFits <- map(tacs_long$delayFit[tacs_long$Region=='WB'],
                 ~plot_inptac_fit(.x) + ggtitle('Delay'))

delayFits  <- data.frame(PET = unique(tacs_long$PET)) %>%
              mutate(fit = delayFits)

plot_2tcm <- tacs_long %>%
 group_by(PET, Region) %>%
  mutate(fit = map2(fit_2tcm, Region,
      ~ plot_kinfit(.x, roiname = .y))) %>%
  ungroup() %>%
  filter(Region %in% c('FC', 'WB', 'ACC', 'CBL', 'THA')) %>%
  select(PET, fit) %>%
  group_by(PET) %>%
  arrange(PET) %>%
  bind_rows(delayFits)


walk2(list(plot_2tcm$fit), unique(plot_2tcm$PET),
    ~print(plot_grid( plotlist = .x, ncol = 2, nrow = 3, align = 'hv') +
  draw_plot_label( label = .y , y = 1, x = 0.5, fontface = "bold", size = 20, colour = "red", hjust = 1
```

###subplot version

```r
plot.TAC <- plot_kinfit(tacs_long$fit_2tcm[[4]], roiname = tacs_long$Region[4])

plot.AIF <- plot_kinfit(tacs_long$fit_2tcm[[4]], roiname = tacs_long$Region[4]) +
coord_cartesian(ylim=c(0,3000))

p <- ggdraw() +
  draw_plot(plot.TAC + theme(legend.position = "none"), 0, 0, 1, 1) +
```

```
    draw_plot(plot.AIF  +
              theme(legend.position = "none"), 0.5, 0.52, 0.5, 0.4) +
    draw_plot_label(c("A", "B"), c(0, 0.5), c(1, 0.92), size = 15)

legend <- get_legend(plot.TAC)

q <- plot_grid( legend, p , rel_widths = c(.35, 2))

ggsave(filename = "subplot.twotcm.2.pdf", plot = q, path = '../DerivedData/')
```

## new plot 2tcm

```
k <- tacs_long %>%
  group_by(PET, Region) %>%
  mutate(twotcm = map(fit_2tcm, c("tacs"))) %>%
   select(PET, Region, twotcm) %>%
  filter(Region %in% c('FC', 'WB', 'ACC', 'CBL')) %>%
  unnest()


ggplot(k, aes(x=Time, y=Target, color = Region)) +
  geom_point() + geom_line(aes(y=Target_fitted, color = Region)) +
  facet_wrap(~ PET , ncol=2)
```

## Plot ma1

```
plot_MA1 <- tacs_long %>%
 group_by(PET, Region) %>%
  mutate(fit = map2(fit_ma1, Region,
      ~ plot_kinfit(.x, roiname = .y))) %>%
  ungroup() %>%
  filter(Region %in% c('FC', 'WB', 'ACC', 'CBL', 'THA')) %>%
  select(PET, fit) %>%
  group_by(PET) %>%
  arrange(PET) %>%
  bind_rows(delayFits)


walk2(list(plot_MA1$fit), unique(plot_MA1$PET),
    ~print(plot_grid( plotlist = .x, ncol = 2, nrow = 3, align = 'hv') +
  draw_plot_label( label = .y , y = 1, x = 0.5, fontface = "bold", size = 20, colour = "red", hjust = 1
```

## Plot Loganplot

```
plot_Logan <- tacs_long %>%
 group_by(PET, Region) %>%
  mutate(fit = map2(Loganfit, Region,
      ~ plot(.x, roiname = .y))) %>%
  ungroup() %>%
  filter(Region %in% c('FC', 'WB', 'CBL', 'THA')) %>%
  select(PET, fit) %>%
```

```
  group_by(PET) %>%
  arrange(PET)



walk2(list(plot_Logan$fit), unique(plot_Logan$PET),
    ~print(plot_grid( plotlist = .x, ncol = 2, nrow = 2, align = 'hv') +
  draw_plot_label( label = .y , y = 1, x = 0.5, fontface = "bold", size = 20, colour = "red", hjust = 1
```

## Test-retest

### trt preparation

```
trt_check <- tacs_long %>%
  select(Subjname, PETNo, Region, Vt_ma1, Vt_2tcm, Vt_Logan) %>%
  gather(Measure, Value, -Subjname, -PETNo, -Region) %>%
  group_by(Region, Measure) %>%
  nest(.key = "data")

# saveRDS(tacs_long,'../DerivedData/raw_kinfit_pk11195.rds')
```

### trt results

```
trt_check <- trt_check %>%
  group_by(Region, Measure) %>%
  mutate(trt = map(data, ~relfeas::trt(.x,
                                       values = "Value",
                                       cases = "Subjname")),
         trt_tidy = map(trt, c("tidy")))

trt_table <- select(trt_check, trt_tidy) %>%
  unnest()

kable(trt_table, digits=3)
```

| Region | Measure | mean | sd | cov | skew | kurtosis | icc | icc_l | icc_u | wscv | sdd | absvar | signva |
|--------|---------|------|------|------|------|----------|------|-------|-------|------|------|--------|--------|
| WM | Vt_ma1 | 0.850 | 0.213 | 0.251 | 0.121 | -1.703 | 0.708 | 0.031 | 0.951 | 0.142 | 0.335 | 0.129 | -0.10 |
| GM | Vt_ma1 | 0.794 | 0.178 | 0.224 | 0.170 | -1.546 | 0.675 | -0.078 | 0.946 | 0.132 | 0.291 | 0.150 | -0.04 |
| WB | Vt_ma1 | 0.802 | 0.185 | 0.231 | 0.175 | -1.557 | 0.666 | -0.095 | 0.944 | 0.137 | 0.306 | 0.156 | -0.04 |
| FC | Vt_ma1 | 0.785 | 0.162 | 0.206 | 0.176 | -1.560 | 0.652 | -0.120 | 0.941 | 0.125 | 0.273 | 0.148 | -0.04 |
| OC | Vt_ma1 | 0.849 | 0.200 | 0.236 | 0.069 | -1.596 | 0.683 | -0.063 | 0.947 | 0.137 | 0.323 | 0.153 | -0.04 |
| THA | Vt_ma1 | 0.836 | 0.220 | 0.264 | 0.405 | -1.180 | 0.731 | 0.034 | 0.956 | 0.141 | 0.328 | 0.179 | -0.04 |
| STR | Vt_ma1 | 0.793 | 0.167 | 0.211 | 0.281 | -0.736 | 0.584 | -0.228 | 0.928 | 0.140 | 0.308 | 0.154 | 0.07 |
| TC | Vt_ma1 | 0.784 | 0.179 | 0.229 | 0.061 | -1.643 | 0.660 | -0.105 | 0.943 | 0.138 | 0.299 | 0.156 | -0.04 |
| ACC | Vt_ma1 | 0.760 | 0.180 | 0.236 | 0.436 | -1.122 | 0.569 | -0.250 | 0.924 | 0.160 | 0.337 | 0.212 | -0.09 |
| CBL | Vt_ma1 | 0.797 | 0.199 | 0.250 | 0.095 | -1.602 | 0.696 | -0.038 | 0.950 | 0.142 | 0.314 | 0.151 | -0.05 |
| INS | Vt_ma1 | 0.776 | 0.193 | 0.249 | 0.217 | -1.647 | 0.621 | -0.171 | 0.935 | 0.158 | 0.340 | 0.169 | -0.07 |
| WM | Vt_2tcm | 14.879 | 23.778 | 1.598 | 1.013 | -1.024 | 0.637 | -0.146 | 0.938 | 0.993 | 40.932 | 0.445 | -0.33 |
| GM | Vt_2tcm | 0.683 | 0.156 | 0.228 | 0.472 | -0.799 | 0.749 | 0.075 | 0.960 | 0.118 | 0.224 | 0.156 | 0.00 |
| WB | Vt_2tcm | 0.725 | 0.155 | 0.214 | 0.231 | -1.333 | 0.734 | 0.039 | 0.957 | 0.115 | 0.230 | 0.145 | -0.02 |
| FC | Vt_2tcm | 0.689 | 0.141 | 0.205 | 0.369 | -1.072 | 0.711 | -0.007 | 0.953 | 0.115 | 0.220 | 0.152 | -0.00 |
| OC | Vt_2tcm | 0.728 | 0.168 | 0.230 | 0.308 | -1.002 | 0.731 | 0.033 | 0.956 | 0.124 | 0.249 | 0.168 | 0.01 |

| Region | Measure | mean | sd | cov | skew | kurtosis | icc | icc_l | icc_u | wscv | sdd | absvar | signva |
|--------|---------|------|------|------|------|----------|------|--------|-------|------|------|--------|--------|
| THA | Vt_2tcm | 0.760 | 0.206 | 0.271 | 0.689 | -0.601 | 0.753 | 0.083 | 0.960 | 0.139 | 0.294 | 0.189 | -0.01 |
| STR | Vt_2tcm | 0.761 | 0.180 | 0.237 | 0.541 | -0.796 | 0.132 | -0.672 | 0.804 | 0.222 | 0.468 | 0.248 | 0.07 |
| TC | Vt_2tcm | 0.673 | 0.149 | 0.221 | 0.320 | -1.035 | 0.715 | 0.001 | 0.954 | 0.122 | 0.228 | 0.159 | 0.00 |
| ACC | Vt_2tcm | 0.670 | 0.162 | 0.242 | 0.812 | -0.320 | 0.643 | -0.135 | 0.940 | 0.149 | 0.277 | 0.175 | -0.03 |
| CBL | Vt_2tcm | 0.689 | 0.170 | 0.247 | 0.529 | -0.992 | 0.617 | -0.178 | 0.934 | 0.157 | 0.300 | 0.175 | -0.05 |
| INS | Vt_2tcm | 0.664 | 0.173 | 0.260 | 0.694 | -0.586 | 0.792 | 0.178 | 0.967 | 0.123 | 0.227 | 0.154 | 0.00 |
| WM | Vt_Logan | 0.720 | 0.191 | 0.265 | 0.097 | -1.620 | 0.659 | -0.089 | 0.943 | 0.160 | 0.319 | 0.174 | -0.08 |
| GM | Vt_Logan | 0.691 | 0.164 | 0.238 | 0.483 | -1.010 | 0.753 | 0.084 | 0.960 | 0.122 | 0.234 | 0.151 | -0.03 |
| WB | Vt_Logan | 0.688 | 0.168 | 0.245 | 0.407 | -1.104 | 0.730 | 0.032 | 0.956 | 0.131 | 0.251 | 0.163 | -0.04 |
| FC | Vt_Logan | 0.673 | 0.152 | 0.226 | 0.525 | -0.937 | 0.728 | 0.028 | 0.956 | 0.122 | 0.227 | 0.152 | -0.04 |
| OC | Vt_Logan | 0.730 | 0.177 | 0.242 | 0.341 | -1.155 | 0.752 | 0.080 | 0.960 | 0.125 | 0.253 | 0.153 | -0.03 |
| THA | Vt_Logan | 0.764 | 0.208 | 0.272 | 0.645 | -0.741 | 0.795 | 0.186 | 0.968 | 0.129 | 0.273 | 0.172 | -0.01 |
| STR | Vt_Logan | 0.674 | 0.160 | 0.238 | 0.674 | -0.299 | 0.683 | -0.062 | 0.948 | 0.138 | 0.258 | 0.149 | 0.00 |
| TC | Vt_Logan | 0.679 | 0.157 | 0.231 | 0.380 | -1.183 | 0.762 | 0.105 | 0.962 | 0.117 | 0.220 | 0.144 | -0.03 |
| ACC | Vt_Logan | 0.682 | 0.172 | 0.252 | 0.515 | -0.851 | 0.631 | -0.154 | 0.937 | 0.157 | 0.297 | 0.204 | -0.07 |
| CBL | Vt_Logan | 0.701 | 0.168 | 0.239 | 0.553 | -0.850 | 0.738 | 0.049 | 0.958 | 0.127 | 0.246 | 0.152 | -0.03 |
| INS | Vt_Logan | 0.690 | 0.179 | 0.259 | 0.489 | -1.032 | 0.781 | 0.151 | 0.965 | 0.126 | 0.241 | 0.154 | -0.03 |

## Interregional Correlation

Here the interregional correlations for $V_T$ are assessed

```
Vt_2TCM <- tacs_long %>%
  ungroup() %>%
  select(PET, Region, Vt_2tcm) %>%
  spread(Region, Vt_2tcm)

Vt_MA1 <- tacs_long %>%
  ungroup() %>%
  select(PET, Region, Vt_ma1) %>%
  spread(Region, Vt_ma1)

Vt_logan <- tacs_long %>%
  ungroup() %>%
  select(PET, Region, Vt_Logan) %>%
  spread(Region, Vt_Logan)

col2 <- colorRampPalette(rev(c("#67001F", "#B2182B", "#D6604D", "#F4A582", "#FDDBC7",
                        "#FFFFFF", "#D1E5F0", "#92C5DE", "#4393C3", "#2166AC", "#053061")))

par(mfrow=c(2,2))

Vt_2TCM %>%
  select(FC:WB) %>%
  cor() %>%
  corrplot.mixed(lower='ellipse', upper='number',
             lower.col = col2(200), upper.col = col2(200),  diag='n',
             number.digits = 2, title=expression(Vt_2TCM ~ Correlations),
             mar=c(0,0,1,0))

Vt_logan %>%
  select(FC:WB) %>%
```
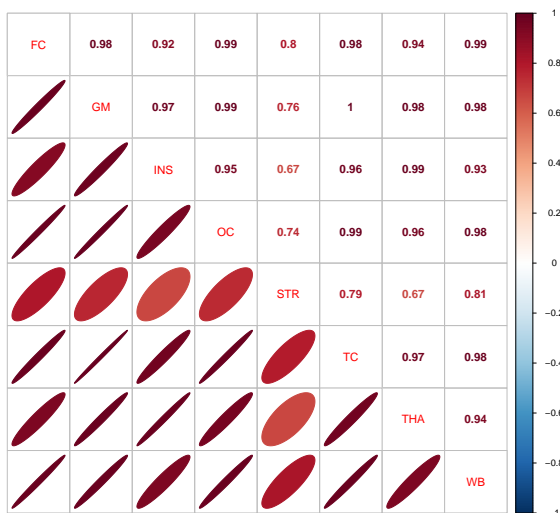
```
  cor() %>%
  corrplot.mixed(lower='ellipse', upper='number',
                  lower.col = col2(200), upper.col = col2(200),  diag='n',
                  number.digits = 2, title=expression(Vt_logan ~ Correlations),
                  mar=c(0,0,1,0))

Vt_MA1 %>%
  select(FC:WB) %>%
  cor() %>%
  corrplot.mixed(lower='ellipse', upper='number',
                  lower.col = col2(200), upper.col = col2(200),  diag='n',
                  number.digits = 2, title=expression(Vt_MA1 ~ Correlations),
                  mar=c(0,0,1,0))
```
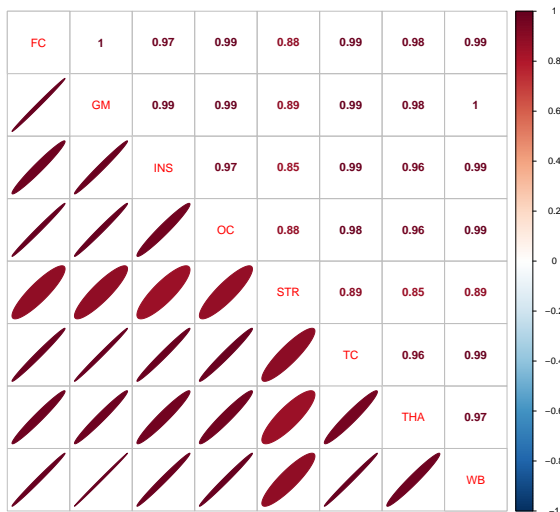
Vt_2TCM Correlations



Vt_logan Correlations



Vt_MA1 Correlations

#Corrplot between measures for a single region

```r
compare <- tacs_long %>%
  ungroup() %>%
  select(PET, Region, Vt_2tcm, Vt_Logan ,Vt_ma1 ) %>%
  filter(Region %in% c('FC', 'WB', 'STR', 'OC'))

par(mfrow=c(2,2))

compare %>%
  filter(Region == "FC") %>%
  select(Vt_2tcm:Vt_ma1) %>%
  cor() %>%
  corrplot.mixed(lower='ellipse', upper='number',
                 lower.col = col2(200), upper.col = col2(200),  diag='n',
                 number.digits = 2, title=expression(Model ~ Correlations ~ Region: FC),
                 mar=c(0,0,1,0))

compare %>%
  filter(Region == "OC") %>%
  select(Vt_2tcm:Vt_ma1) %>%
  cor() %>%
  corrplot.mixed(lower='ellipse', upper='number',
                 lower.col = col2(200), upper.col = col2(200),  diag='n',
                 number.digits = 2, title=expression(Model ~ Correlations ~ Region: OC),
                 mar=c(0,0,1,0))

compare %>%
  filter(Region == "STR") %>%
  select(Vt_2tcm:Vt_ma1) %>%
  cor() %>%
  corrplot.mixed(lower='ellipse', upper='number',
                 lower.col = col2(200), upper.col = col2(200),  diag='n',
                 number.digits = 2, title=expression(Model ~ Correlations ~ Region: STR),
                 mar=c(0,0,1,0))

compare %>%
  filter(Region == "WB") %>%
  select(Vt_2tcm:Vt_ma1) %>%
  cor() %>%
  corrplot.mixed(lower='ellipse', upper='number',
                 lower.col = col2(200), upper.col = col2(200),  diag='n',
                 number.digits = 2, title=expression(Model ~ Correlations ~ Region: WB),
                 mar=c(0,0,1,0))
```
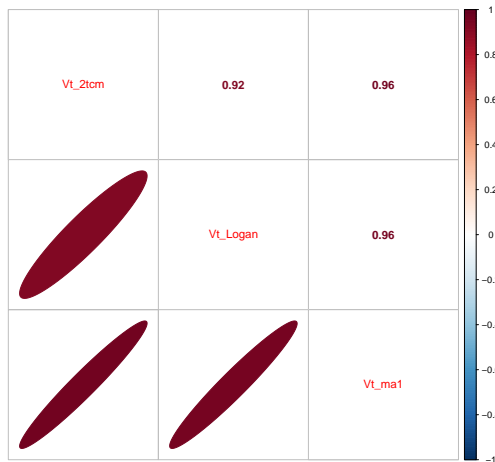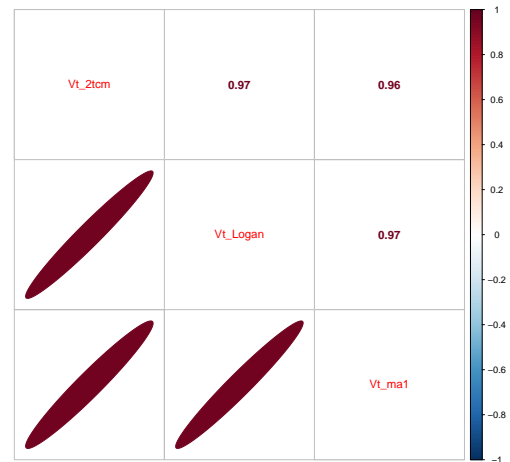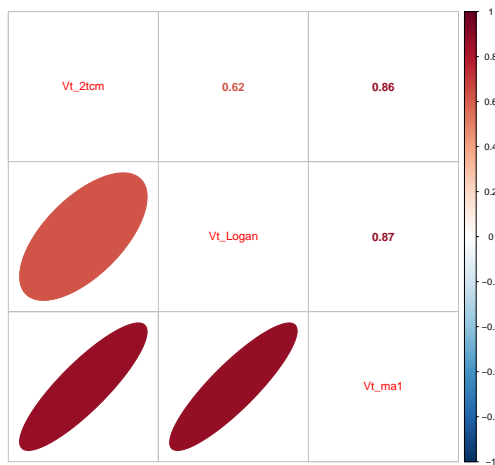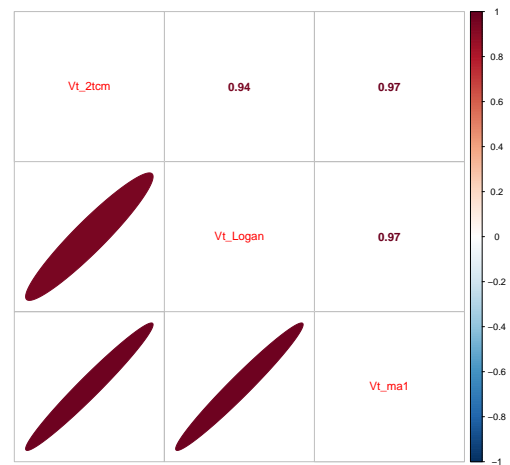
Model Correlations Region : FC



Model Correlations Region : OC



Model Correlations Region : STR



Model Correlations Region : WB

# Vt corellation

## R-squared

```
trtdata <- tacs_long %>%
  select(PET, Subjname, PETNo, Region, Vt_2tcm, Vt_Logan ,Vt_ma1) %>%
  gather(Measure, Value, -(PET:Region)) %>%
  spread(Region, Value)

trtdata <- trtdata %>%
  gather(Region, Value, -(PET:Measure)) %>%
  unite(Outcome, Measure, Region) %>%
  spread(Outcome, Value)
```

```
corout <- trtdata %>%
  gather(Measure, Binding, -(PET:PETNo), -Vt_2tcm_WB) %>%
  group_by(Measure) %>%
  summarise('R^2^'=cor(Binding, Vt_2tcm_WB)^2) %>%
  arrange(Measure) %>%
  ungroup() %>%
  mutate(Measure = str_replace(string=Measure, pattern='_', replacement='~')) %>%
  mutate(Measure = str_replace(string=Measure, pattern='FC', replacement='FC~')) %>%
   mutate(Measure = str_replace(string=Measure, pattern='CBL', replacement='CBL~')) %>%
   mutate(Measure = str_replace(string=Measure, pattern='ACC', replacement='ACC~')) %>%
   mutate(Measure = str_replace(string=Measure, pattern='INS', replacement='INS~')) %>%
   mutate(Measure = str_replace(string=Measure, pattern='THA', replacement='THA~')) %>%
  mutate(Measure = str_replace(string=Measure, pattern='WB', replacement='WB~')) %>%
  mutate(Measure = str_replace(string=Measure, pattern='OC', replacement='OC~')) %>%
  mutate(Measure = str_replace(string=Measure, pattern='WM', replacement='WM~')) %>%
  mutate(Measure = str_replace(string=Measure, pattern='GM', replacement='GM~')) %>%
  mutate(Measure = str_replace(string=Measure, pattern='STR', replacement='STR~'))

kable(corout, digits=2, caption="Correlations with BP_srtm~WB~")
```

Table 2: Correlations with BP_srtm$_{\text{WB}}$

| Measure | $R^2$ |
| --- | --- |
| Vt$_{\text{2tcm\_ACC}}$ | 0.86 |
| Vt$_{\text{2tcm\_CBL}}$ | 0.94 |
| Vt$_{\text{2tcm\_FC}}$ | 0.98 |
| Vt$_{\text{2tcm\_GM}}$ | 0.96 |
| Vt$_{\text{2tcm\_INS}}$ | 0.87 |
| Vt$_{\text{2tcm\_OC}}$ | 0.96 |
| Vt$_{\text{2tcm\_STR}}$ | 0.66 |
| Vt~2tcm__TC | 0.97 |
| Vt$_{\text{2tcm\_THA}}$ | 0.88 |
| Vt$_{\text{2tcm\_WM}}$ | 0.52 |
| Vt$_{\text{Logan\_ACC}}$ | 0.81 |
| Vt$_{\text{Logan\_CBL}}$ | 0.87 |
| Vt$_{\text{Logan\_FC}}$ | 0.87 |
| Vt$_{\text{Logan\_GM}}$ | 0.87 |
| Vt$_{\text{Logan\_INS}}$ | 0.86 |
| Vt$_{\text{Logan\_OC}}$ | 0.91 |
| Vt$_{\text{Logan\_STR}}$ | 0.80 |
| Vt~Logan__TC | 0.88 |
| Vt$_{\text{Logan\_THA}}$ | 0.81 |
| Vt$_{\text{Logan\_WB}}$ | 0.89 |
| Vt$_{\text{Logan\_WM}}$ | 0.88 |
| Vt$_{\text{ma1\_ACC}}$ | 0.85 |
| Vt$_{\text{ma1\_CBL}}$ | 0.95 |
| Vt$_{\text{ma1\_FC}}$ | 0.96 |
| Vt$_{\text{ma1\_GM}}$ | 0.95 |
| Vt$_{\text{ma1\_INS}}$ | 0.89 |
| Vt$_{\text{ma1\_OC}}$ | 0.94 |
| Vt$_{\text{ma1\_STR}}$ | 0.84 |
| Vt~ma1__TC | 0.94 |
| Vt$_{\text{ma1\_THA}}$ | 0.90 |

| Measure | $R^2$ |
|---|---|
| $Vt_{ma1\_WB}$ | 0.95 |
| $Vt_{ma1\_WM}$ | 0.86 |

#Plot of the change between PETNo = 1 and PETNo = 2.

```
trtdata <- trtdata %>%
  gather(Region, Value, -(PET:PETNo)) %>%
  separate(col = "Region", into = c("outcome","Measure", "Region"), sep = '_') %>%
  unite(outcome, outcome, Measure, sep = '_') %>%
  ungroup()

trt_2tcm <- trtdata %>%
  filter(outcome == 'Vt_2tcm')

ggplot(trt_2tcm, aes(x = PETNo, y = Value,
                     group = Region, colour=Region)) +
  geom_point() +
  geom_smooth(method = 'lm', se = FALSE) +
  facet_wrap( ~ Subjname, ncol = 4) +
  ylim( 0,2)
```

#all estimates in all models using facet_grid.

```
trt_table_2tcm <-  trt_table %>%
  gather(estimate, Value, -(Region:Measure))


ggplot(trt_table_2tcm, aes(y = Region, x = Value, colour = Region ))+
  geom_point()+
  facet_grid(  Measure ~ estimate)+
  coord_flip()
```

###All estimates in all models using facet_wrap, improved version?

```
trt_table_2TCM <-  trt_table %>%
  gather(estimate, Value, -(Region:mean)) %>%
  filter(estimate %in% c('icc','wscv', 'sd', 'cov'))

ggplot(trt_table_2TCM, aes(y = estimate, x = Value, colour = Region ))+
  geom_point()+
  facet_wrap( ~ Measure)+
  coord_flip()+
  xlim( 0, 1.25)
```

#Old version ma1 plot

Kept in case we would require this code in the future

```
Fits_ma1 = map2(longdat_showFits$fit_ma1, longdat_showFits$Region,
                ~plot_kinfit(.x, roiname=.y))

allfits_ma1 <- data.frame(PET = rep(PETs, each=5)) %>%
  mutate(Fit = Fits_ma1,
         Plot = 'Fit',
         PET = as.character(PET)) %>%
```

```
  bind_rows(DelayFits) %>%
  arrange(PET, Plot)

allFits_ma1_excluded <- allfits_2tcm %>%
  filter(grepl(PET, pattern='uqis_2'))

allfits_ma1 <- allfits_ma1 %>%
  filter(!grepl(PET, pattern='uqis_2'))

fitLabels <- unique(allfits_ma1$PET)
marrangeGrob(allfits_ma1$Fit, nrow=2, ncol=3, top=quote(paste('PET: ', PETs[g])))
```