

pbr28 test-retest

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16 February 2019

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Aims

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

Libraries

CRAN libraries

installing packages

```
install.packages("stringr")
install.packages("corrplot")
```

```
install.packages("grid")
install.packages("gridExtra")
install.packages("RColorBrewer")
install.packages("psych")
install.packages("readxl")
install.packages("pracma")
install.packages("lme4")
install.packages("rjags")
install.packages("knitr")
install.packages("cowplot")
install.packages("corrplot")
install.packages("kableExtra")
install.packages("tidyverse")
```

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

```
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(kableExtra)
library(tidyverse)
```

Non-CRAN libraries

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

```
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

```
library(kinfitr)
library(vmisc)
library(kipettools)
library(granviller)
library(relfeas)
library(pander)

theme_set(theme_light())
```

Creating folders using “initProjectFolder()”

```
initProjectFolder()
```

Demographic Data

Here, the demographic data is loaded in.

```
demog <- read_excel('DerivedData/TrT_chemistry_demograph.xlsx')
```

tidying the demographic data

```
demog <- demog %>%
  select(Subjname=Akronym, Gender=Sex, Age, Genotype,
         PET_same_day, `MBq PET1`, `MBq PET2`, bodyMass=Weight_kg) %>%
  gather(key = PETNo, value = injRad, contains('MBq')) %>%
  mutate(PETNo = as.numeric(str_match(PETNo, '\\d')) %>%
  mutate(PET = paste(Subjname, PETNo, sep='_'))
```

TACs and Blood Data

First, we must read in the TAC and blood data. It should be noted that the blood data is already dispersion corrected, and the plasma data is already metabolite corrected, thus the plasma fraction is set to 100% in the input data frame. It should also be noted that we set all negative values of both blood and plasma radioactivity concentrations to zero.

```
tacdata <- read_csv("DerivedData/tacdata.csv") %>%
  group_by(PET) %>%
  nest(.key = 'tacdata')
blooddata <- read_csv("DerivedData/blooddata.csv") %>%
  mutate(Cbl.disp.corr = ifelse(Cbl.disp.corr < 0, 0, Cbl.disp.corr),
  Cpl..metabcorr. = ifelse(Cpl..metabcorr. < 0, 0, Cpl..metabcorr.)) %>%
  group_by(PET) %>%
  nest(.key='blooddata') %>%
  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..metabcorr.,
    t_parentfrac = 1, parentfrac=1 ) ))
tacs <- inner_join(tacdata, blooddata) %>%
separate(PET, c("Subjname", "PETNo"), sep='_', remove = F, convert=T)

tacs <- tacs %>%
  inner_join(demog) %>%
  arrange(PET)

saveRDS(tacs, 'DerivedData/tacs.rds')
```

#Read tacs.rds and create delay fit and inputshift

Here, the delay and blood volume fraction are fitted using the whole brain ROI using 2TCM.

```
tacs <- readRDS('DerivedData/tacs.rds')
```

```
tacs <- tacs %>%
```

```

ungroup() %>%
arrange(PET) %>%
group_by(PET, Subjname, PETNo) %>%
mutate(delayFit = map2(tacdata, input,
                        ~twotcm(t_tac = .x$Times/60, tac = .x$WB, input = .y,
                                frameStartEnd = c(1,33)))) %>%
mutate(inpshift = map_dbl(delayFit, c("par", "inpshift"))) %>%
ungroup()

```

New weights with kinfitr::weights_create

```

#Creating start and end times and
#removing the old weights, so that there is no mix-up later on

```

```

# tacdata <- names(tacs$tacdata[[1]])

```

```

tacs <- tacs %>%
  unnest(tacdata, .drop = F) %>%
  select(-Weights)

```

```

# New weights

```

```

tacs$Weights <- weights_create(t_start = tacs$StartTime/60, t_end = (tacs$StartTime + tacs$Duration)/60)
#Nest

```

```

tacs <- tacs %>%
  nest(-(PET:Times), .key = 'tacdata')

```

Summary Statistics again

Below are presented some summary statistics of the demographic data. What's up with kurtosis?

```

tacs %>%
  select(Age, InjectedRadioactivity = injRad) %>%
  describe() %>%
  pandoc.table(digits=3, caption = "Summary Statistics", split.tables=Inf)

```

creating logan_tstar

```

logan_tstar <- function(tacdata, input, inpshift) {
  Logan_tstar(t_tac = tacdata$Times/60, input = input, lowroi = tacdata$FC, medroi = tacdata$CBL, highroi = tacdata$HBL)
}

```

```

tacs <- tacs %>%
  group_by(Subjname, PETNo) %>%
  mutate(logan_tstar = pmap(list(tacdata, input, inpshift), logan_tstar))

```

#Rearrangement of the Data into Long Format

```

tacs_long <- tacs %>%
  unnest(tacdata, .drop = FALSE) %>%
  select(-Weights)

```

```
tacs_long$weights = weights_create(t_start = tacs_long$StartTime/60, t_end = (tacs_long$StartTime + tacs_long$StartTime)/60)

tacs_long <- tacs_long %>%
gather(Region, TAC, -(PET:Times), -(StartTime:weights)) %>%
group_by(PET, Subjname, PETNo, Region) %>%
nest(-(blooddata:logan_tstar), .key = 'tacdata')

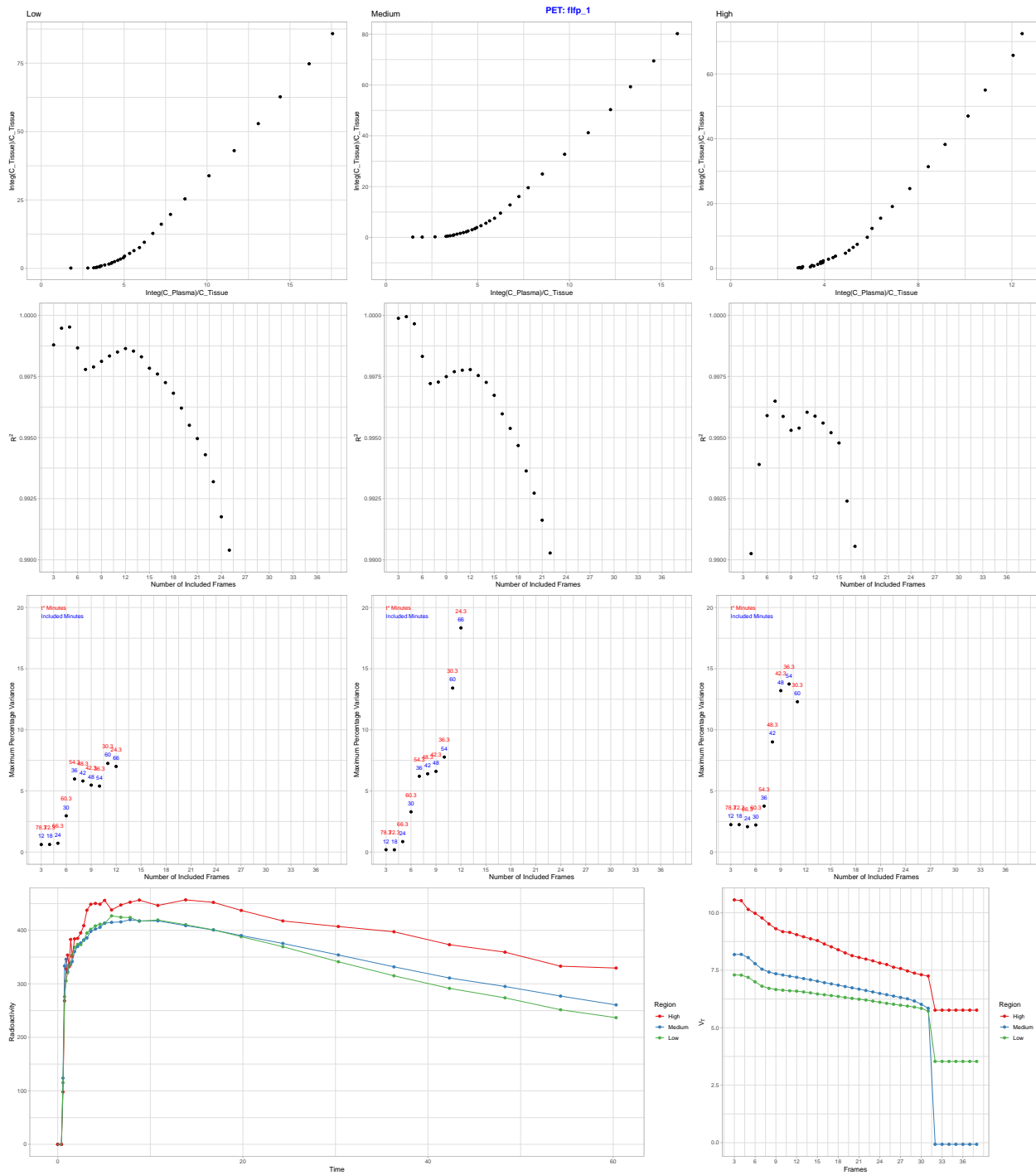
tacs_long <- tacs_long %>%
  select(PET, Subjname, PETNo, blooddata:logan_tstar) %>%
  inner_join(tacs_long, by = c("PET", "Subjname", "PETNo"))
```

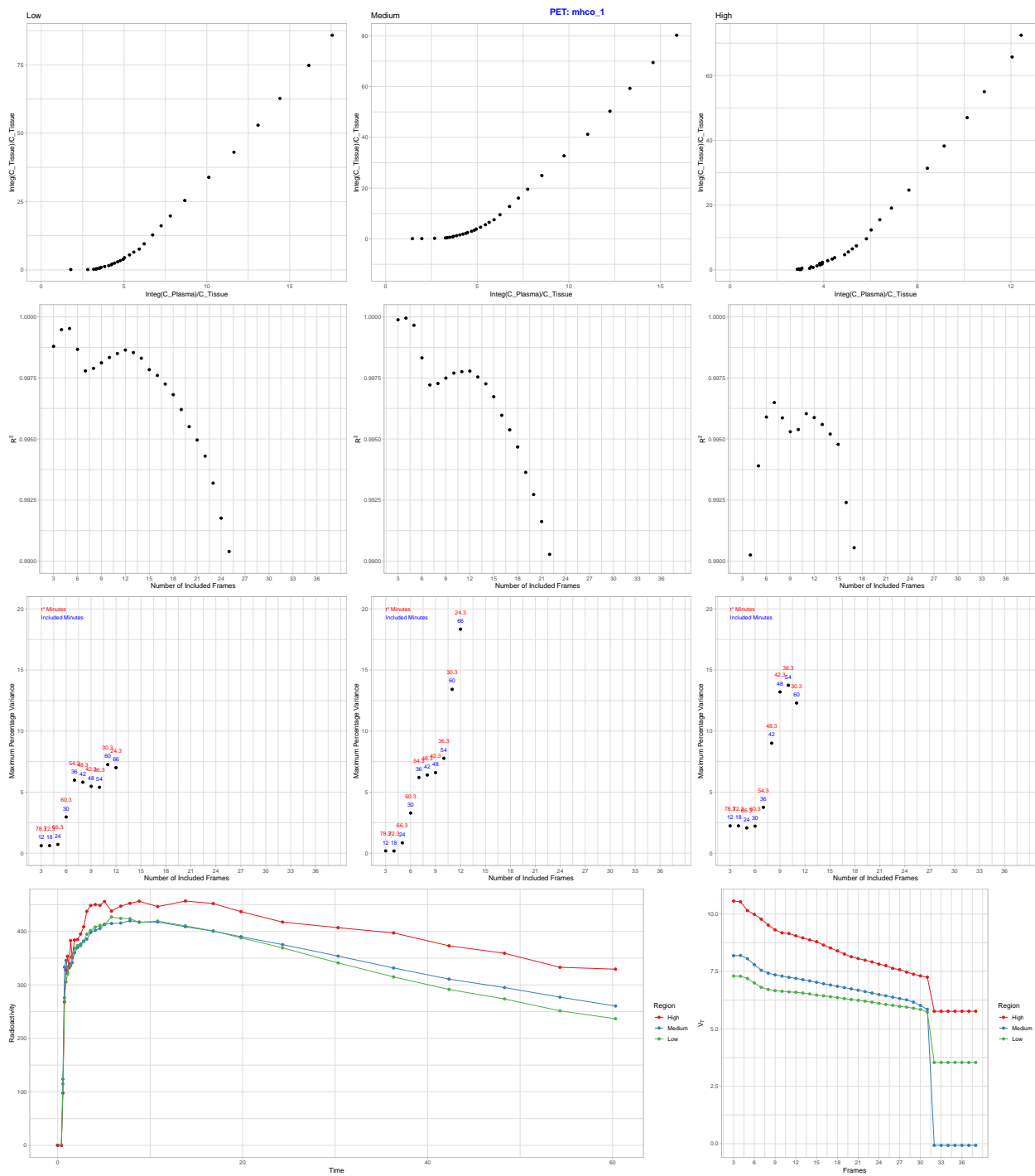
Plotting logan_tstar

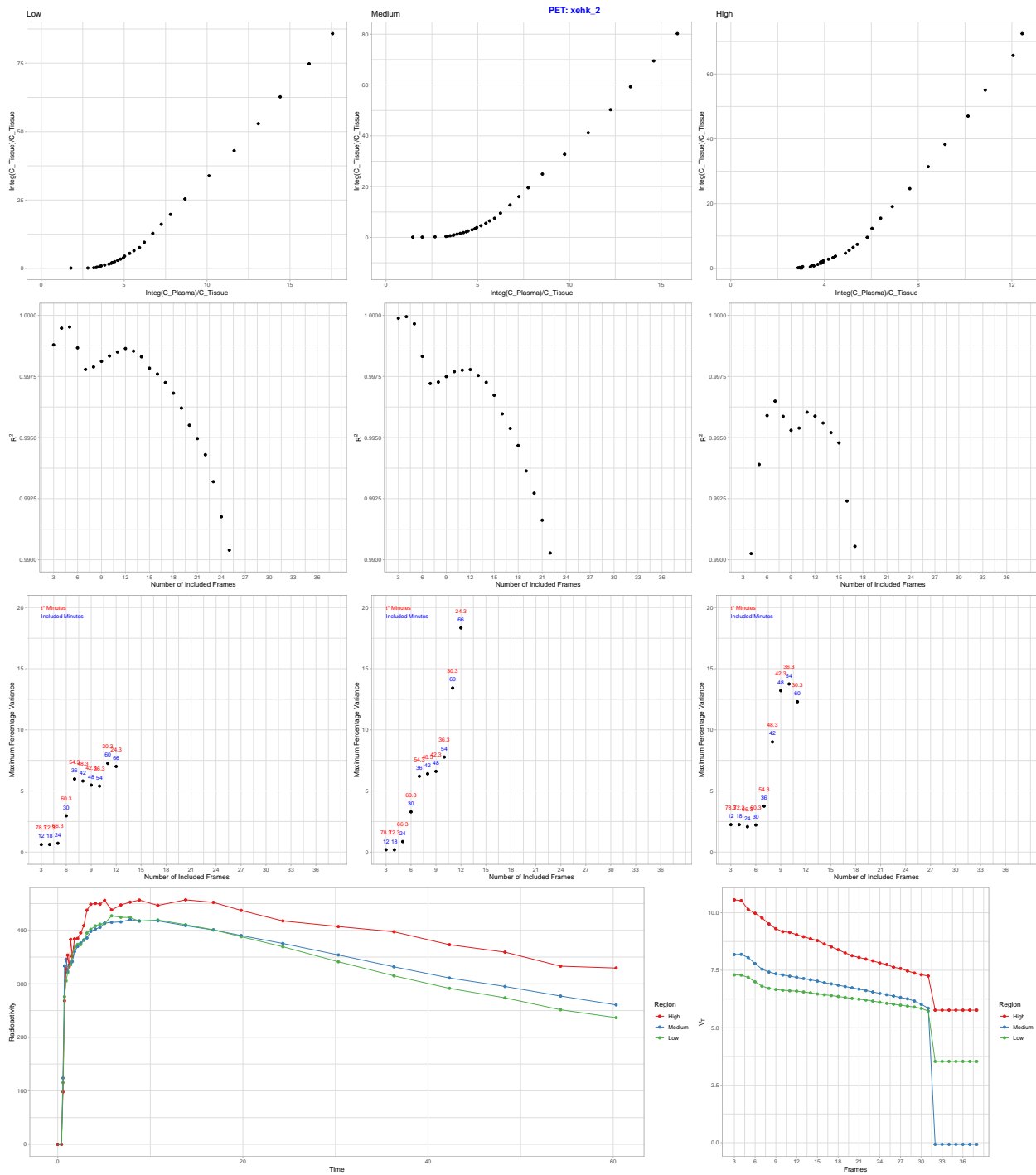
```
set.seed(123)

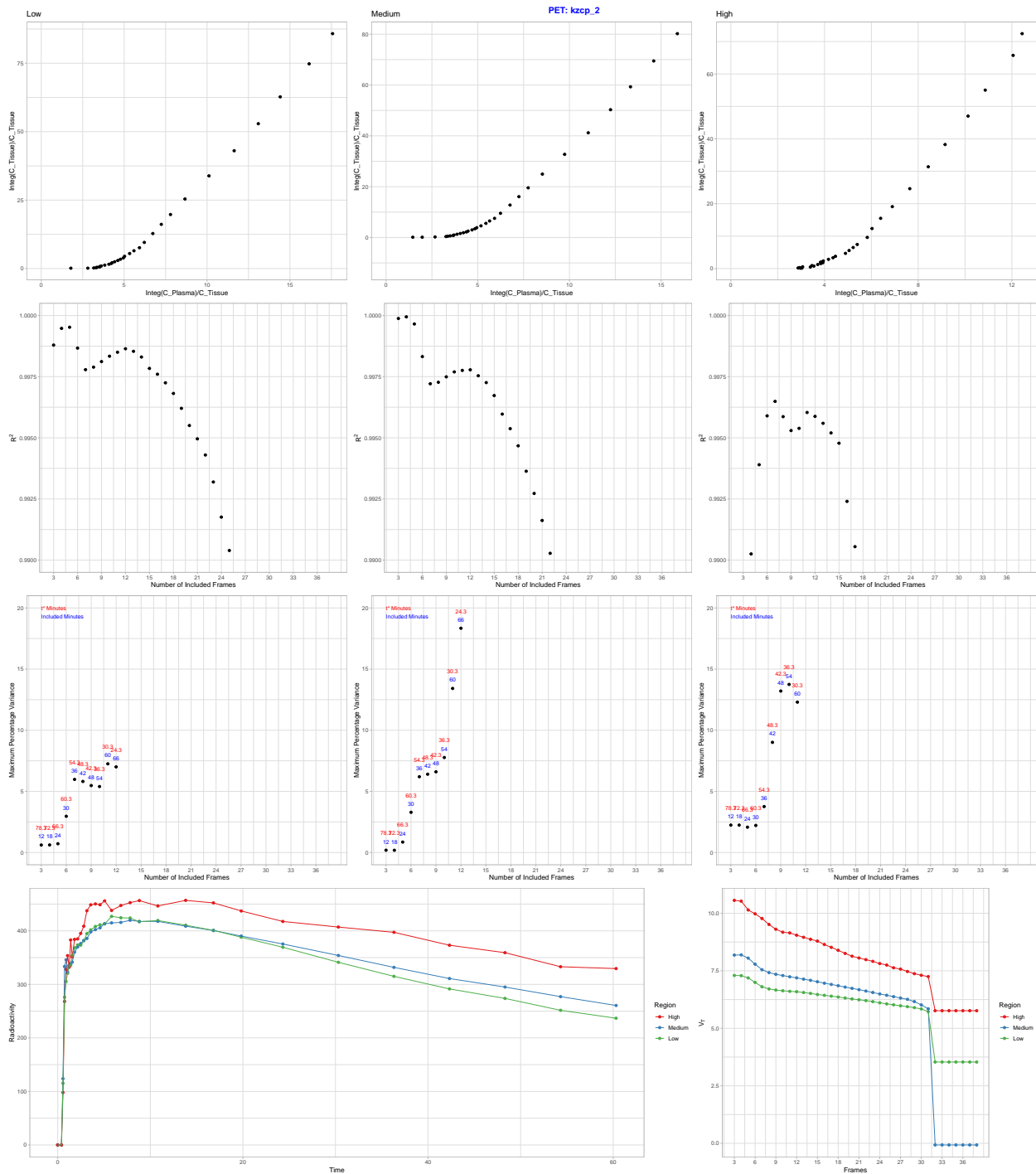
tstar_fits <- tacs_long %>%
  ungroup() %>%
  select(logan_tstar, PET) %>%
  select(PET, logan_tstar) %>%
  sample_n(size = 4, replace = F)

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_y = 0.5)))
```









All 4 tstar plots on a single page

Note: I would like to have the “draw_figure_label” be drawn a bit above the first PET, but that does not seem to be happening. Should I just skip it? I Placed the plots in a single column because it was a little hard distinguishing where one ands and another begins in a 2 x 2 format. Perhaps one could put borders and then the 2 x 2 would work better?

```
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

```
# MA1 using the fitted delay and vB from delayFit
fitma1 <- function(tacdata, input, delayFit) {
  ma1(t_tac = tacdata$Times/60, tac = tacdata$TAC, input = input, tstarIncludedFrames = 6,
      inpshift = delayFit$par$inpshift, weights=tacdata$weights, vB= 0, frameStartEnd = c(1,33))
}

# 2TCM using the fitted delay and vB from delayFit
fit2tcm <- function(tacdata, input, delayFit) {
  twotcm(t_tac = tacdata$Times/60, tac = tacdata$TAC, input = input,
      inpshift = delayFit$par$inpshift, vB= 0.05, weights=tacdata$weights, frameStartEnd = c(1,33),
  )
}

#Loganplot
fit_Logan <- function(tacdata, input, delayFit) {
  Loganplot(t_tac = tacdata$Times/60, tac = tacdata$TAC,
      input = input, inpshift = delayFit$par$inpshift, tstarIncludedFrames = 10, vB= 0, frameStartEnd = c(1,33))
}
```

Fit kinetic models

```
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

```
PETs <- unique(tacs_long$PET)

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) %>%
  filter(PET == PETs[5:8])
```

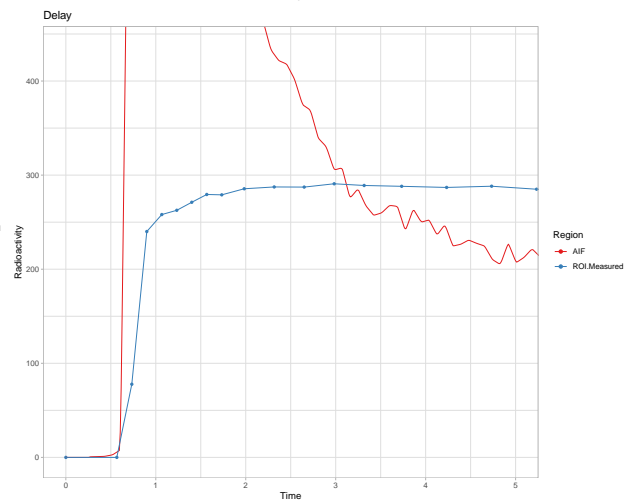
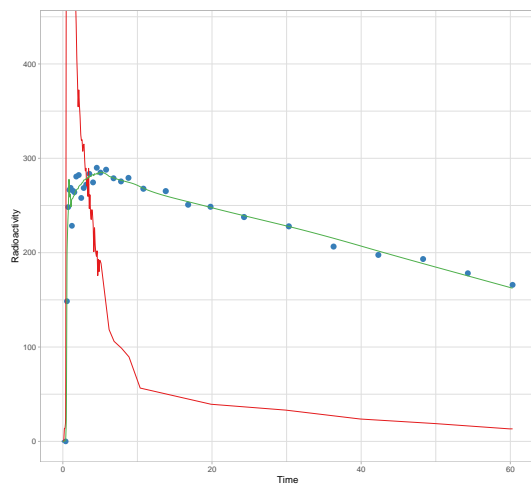
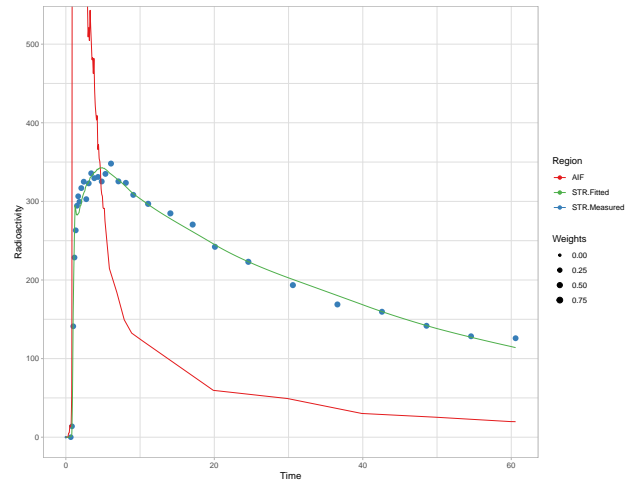
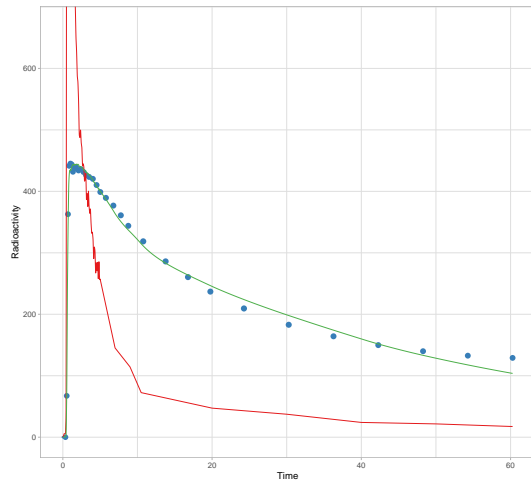
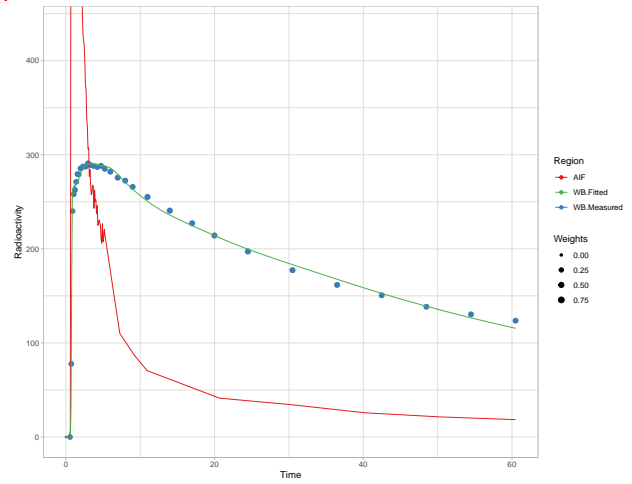
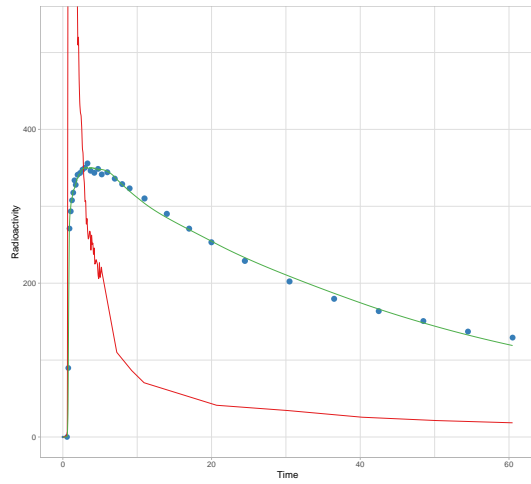
```

plot_2tcm <- tacs_long %>%
  filter(PET == PETs[5:8]) %>%
  group_by(PET, Region) %>%
  mutate(fit = map2(fit_2tcm, Region,
    ~ plot_kinf_fit(.x, roiname = .y))) %>%
  ungroup() %>%
  filter(Region %in% c('FC', 'WB', 'STR', 'CBL', 'THA')) %>%
  select(PET, fit) %>%
  group_by(PET) %>%
  arrange(PET) %>%
  bind_rows(delayFits)

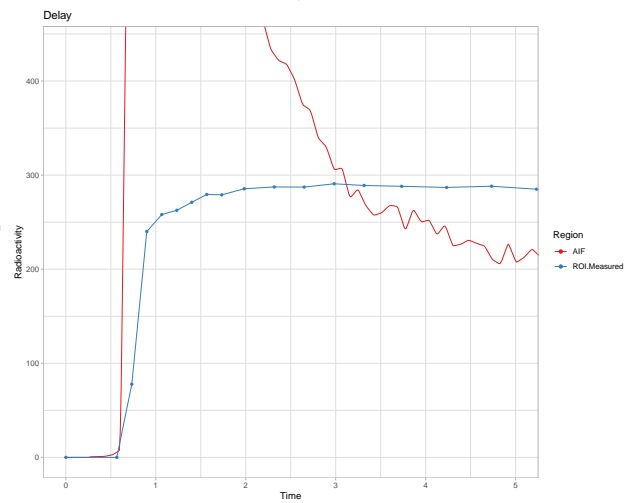
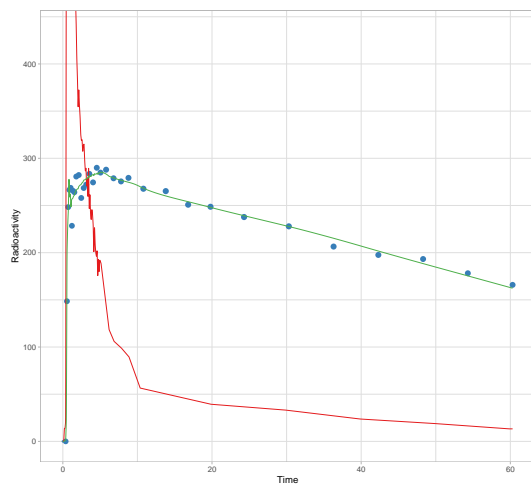
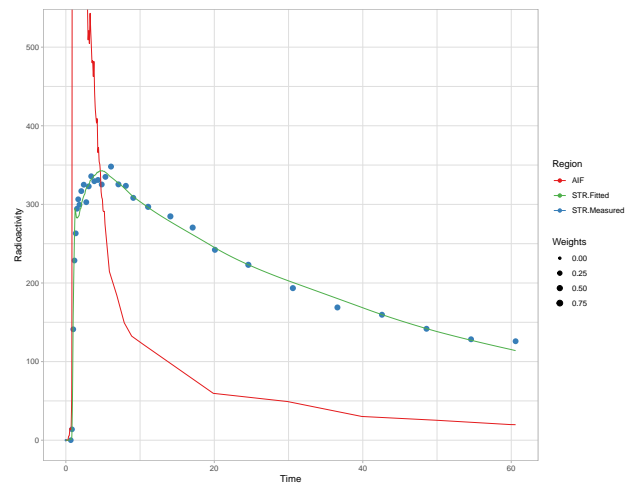
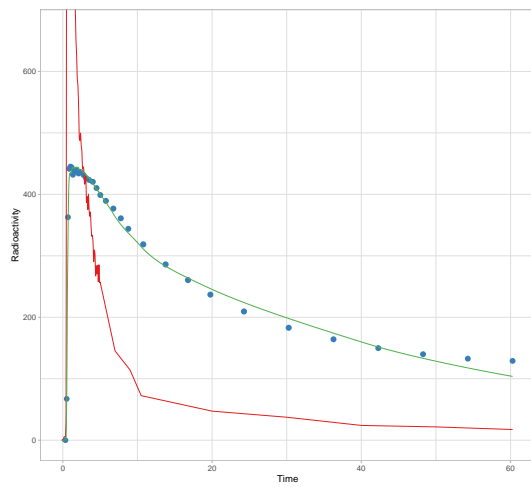
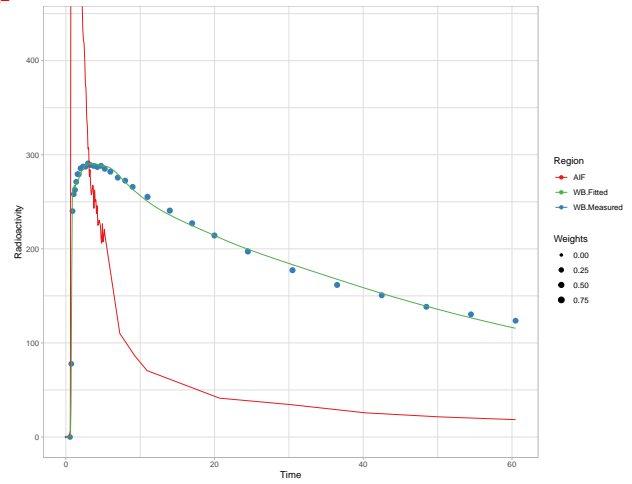
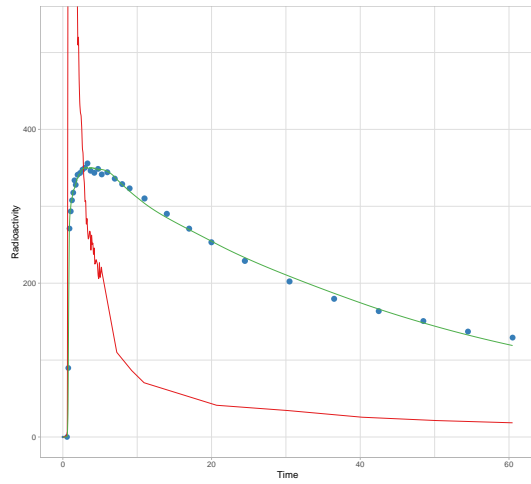
walk2(list(plot_2tcm$fit), unique(plot_2tcm$PET),
  ~print(plot_grid( plotlist = .x, ncol = 2, nrow = 3, align = 'hv') +
    draw_plot_label( label = .y , y = 1, x = 0.5, fontface = "bold", size = 20, colour = "red", hjust = 1

```

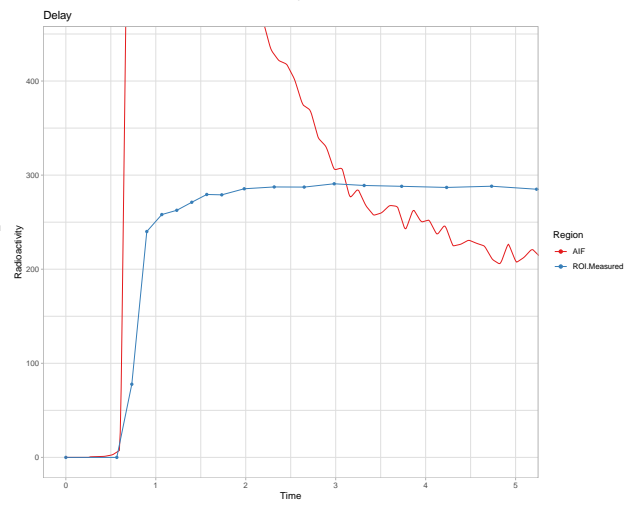
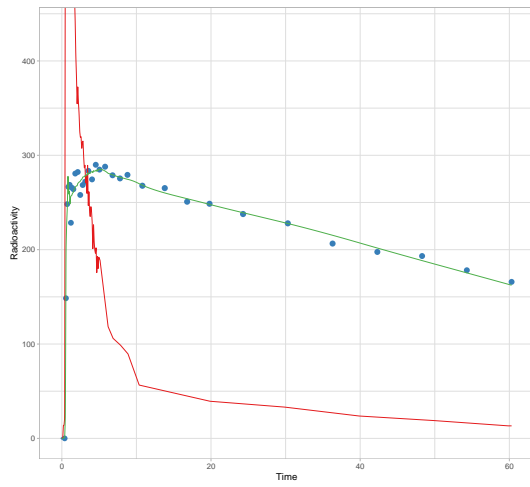
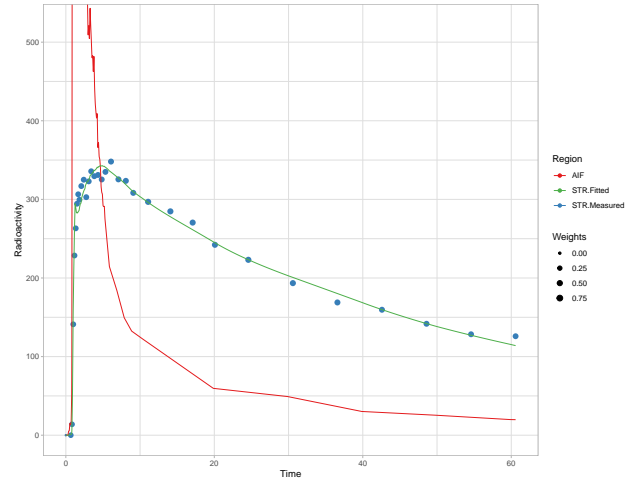
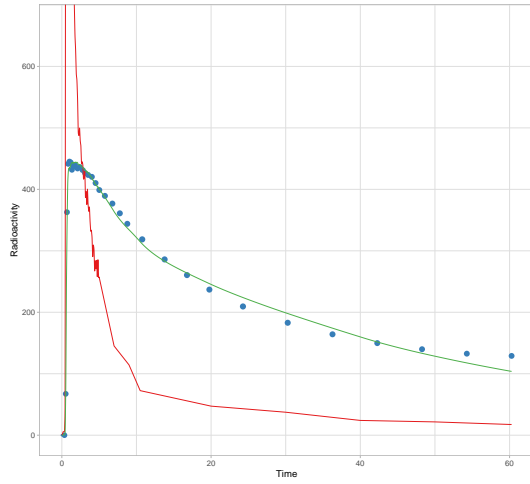
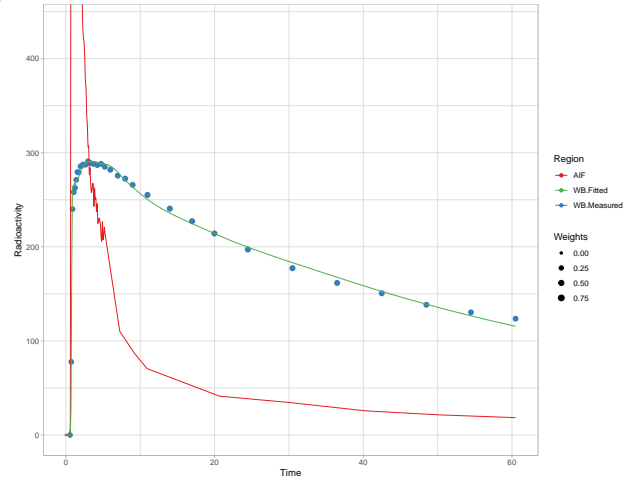
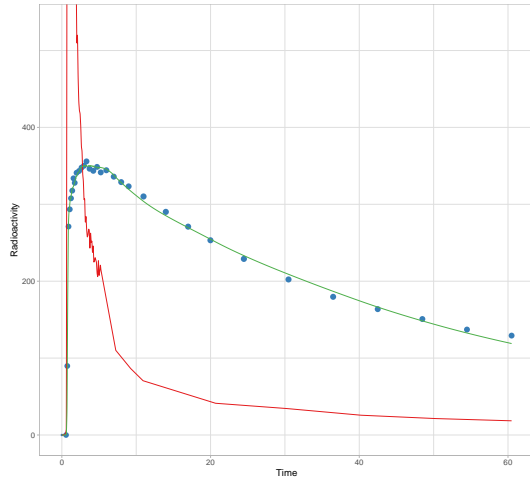
jdcs_1



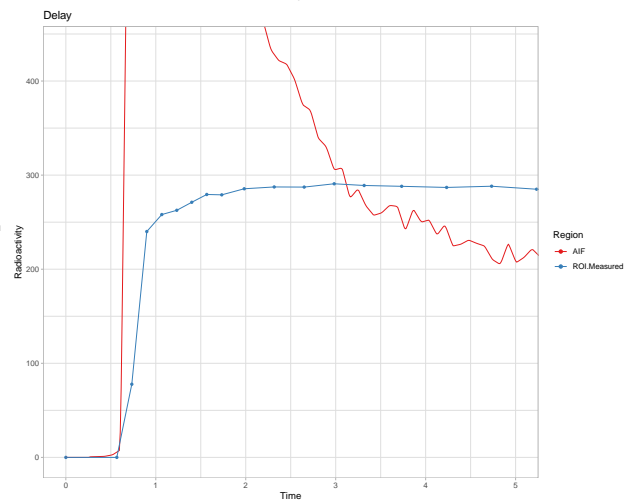
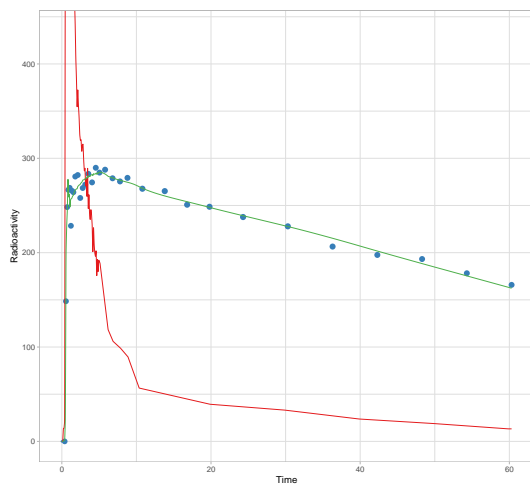
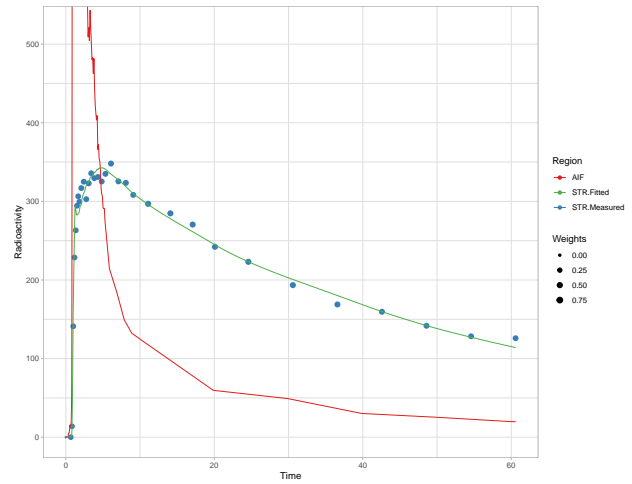
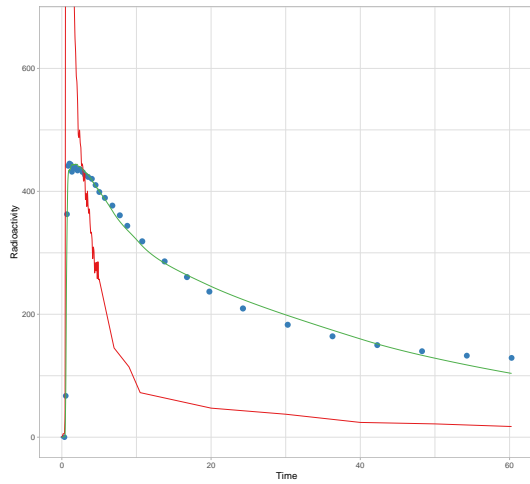
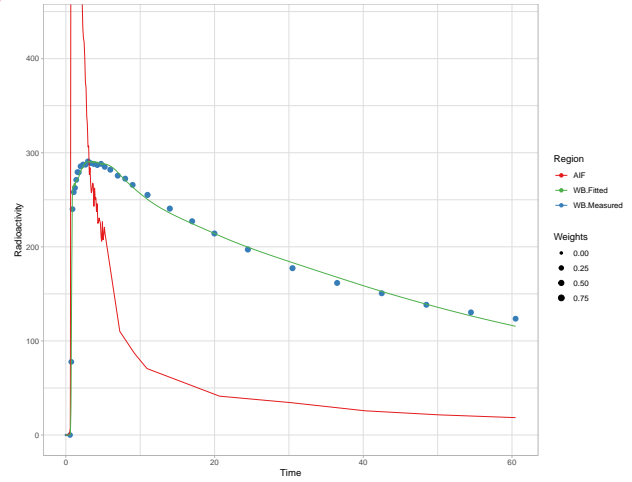
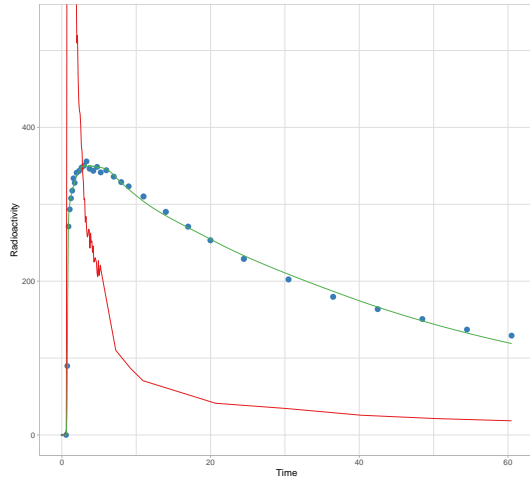
jdcs_2



kzcp_1



kzcp_2



###subplot version

```
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",
          panel.grid = element_blank(),
          axis.title = element_blank(),
          axis.text = element_blank(),
          axis.ticks = element_blank()), 0.5, 0.6, 0.5, 0.4)

legend <- get_legend(plot.TAC)

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

print(q)

```

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', 'STR', '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

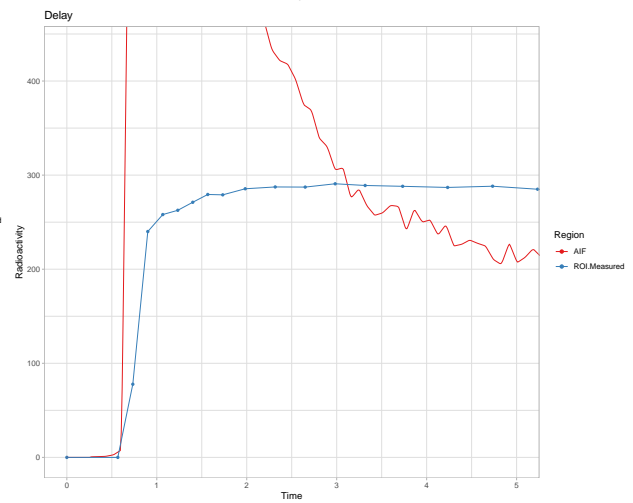
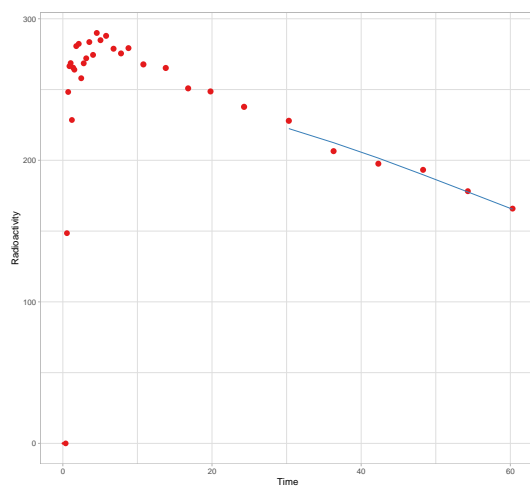
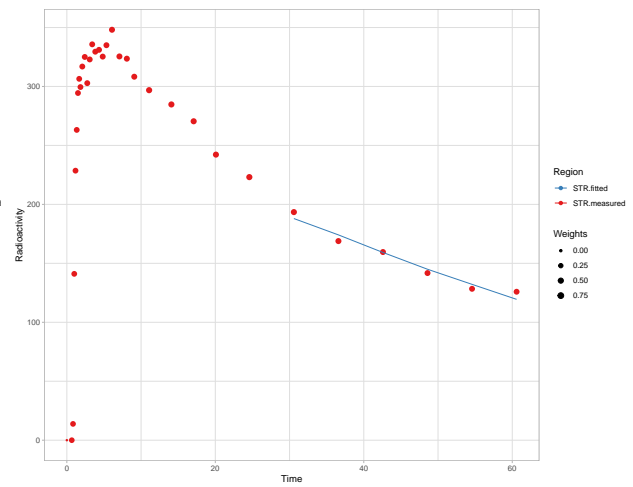
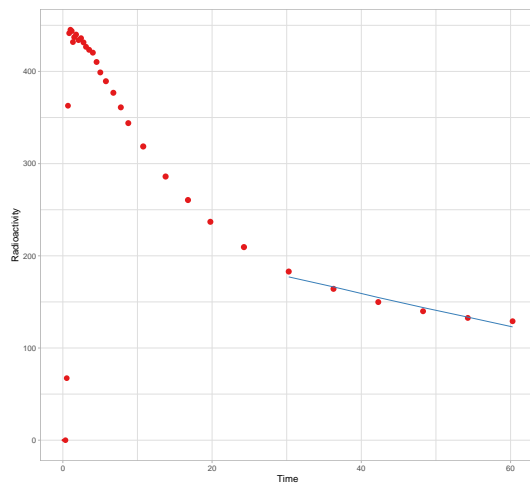
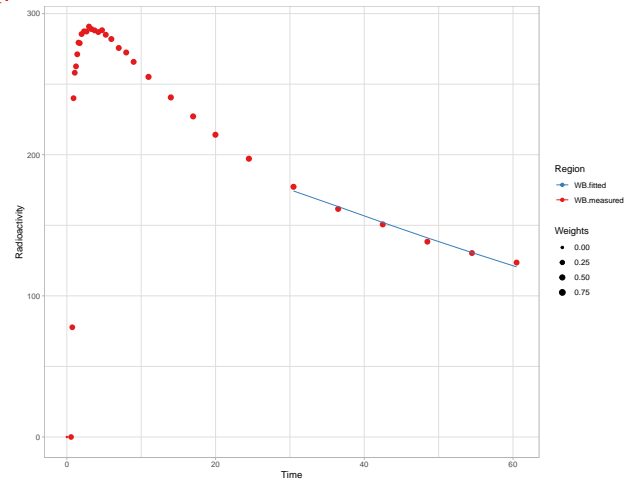
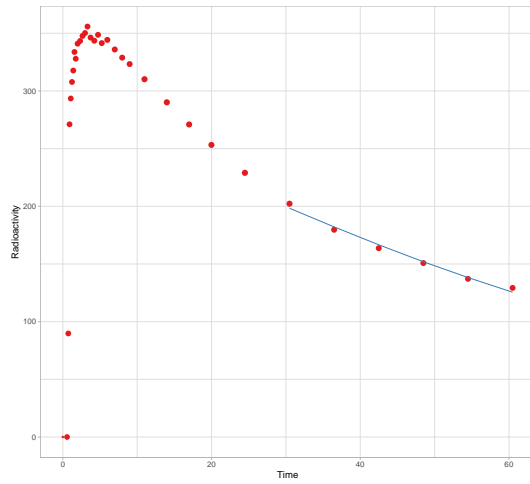
```

plot_MA1 <- tacs_long %>%
  filter(PET == PETs[5:8]) %>%
  group_by(PET, Region) %>%
  mutate(fit = map2(fit_ma1, Region,
    ~ plot_kinfir(.x, roiname = .y))) %>%
  ungroup() %>%
  filter(Region %in% c('FC', 'WB', 'STR', 'CBL', 'THA')) %>%
  select(PET, fit) %>%
  group_by(PET) %>%
  arrange(PET) %>%
  bind_rows(delayFits)

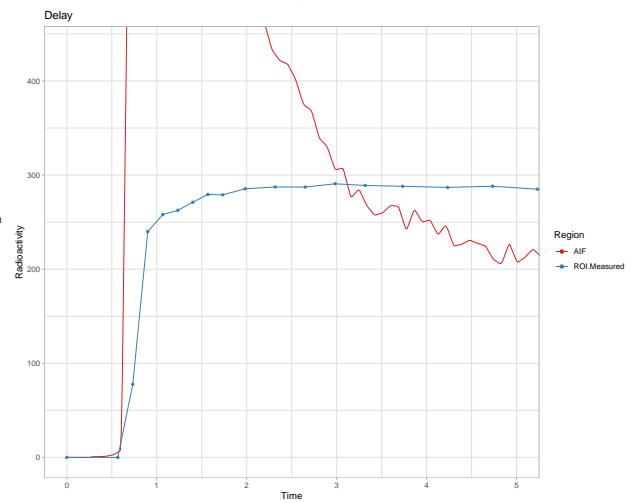
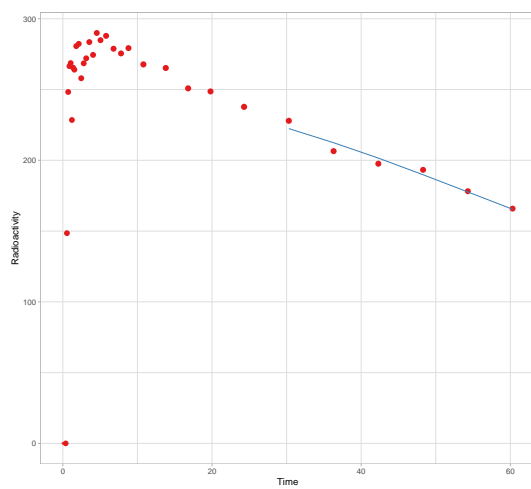
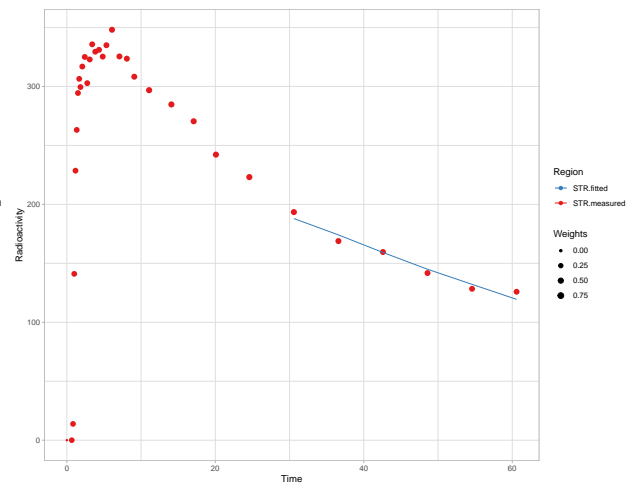
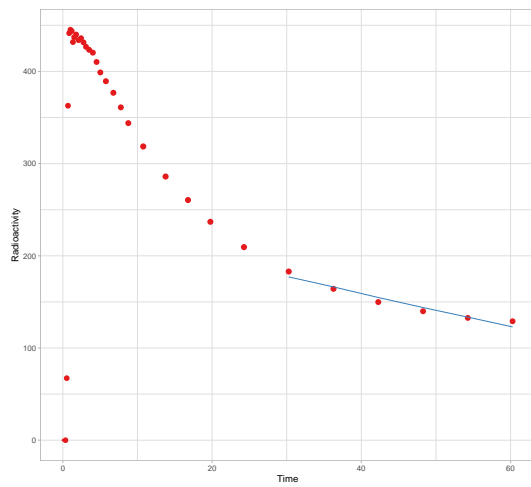
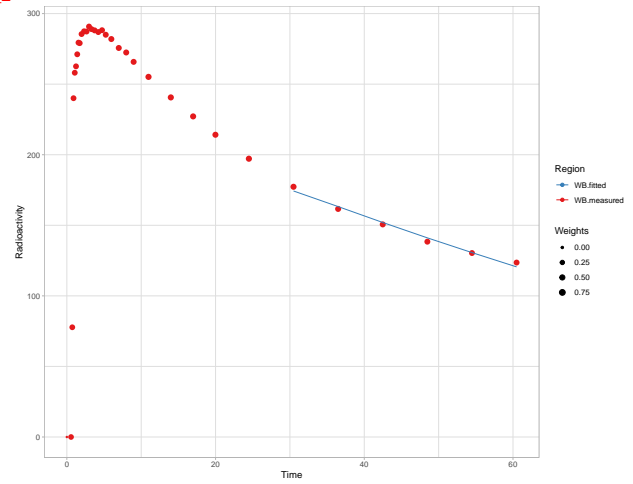
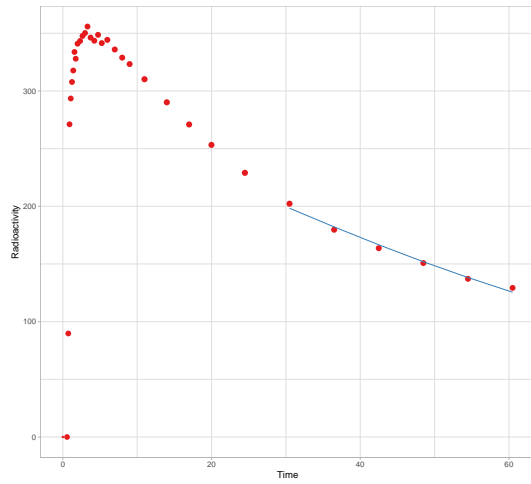
walk2(list(plot_MA1$fit), unique(plot_MA1$PET),
  ~print(plot_grid( plotlist = .x, ncol = 2, nrow = 3, align = 'hv') +
    draw_plot_label( label = .y , y = 1, x = 0.5, fontface = "bold", size = 20, colour = "red", hjust = 1

```

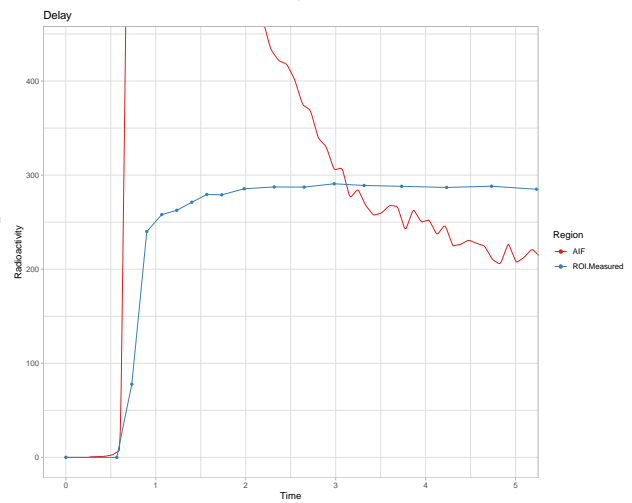
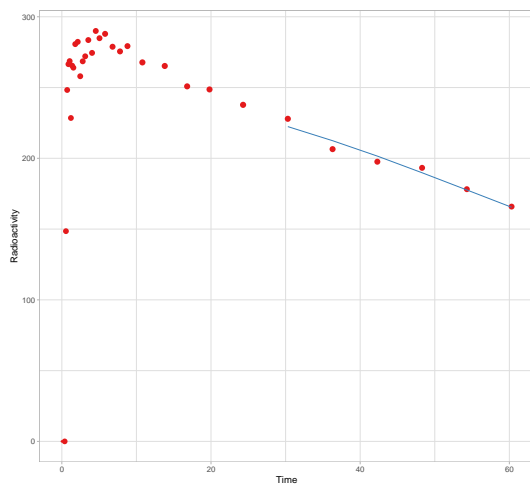
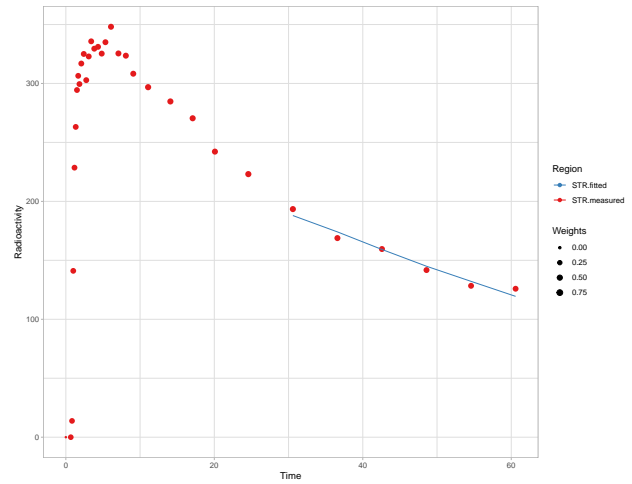
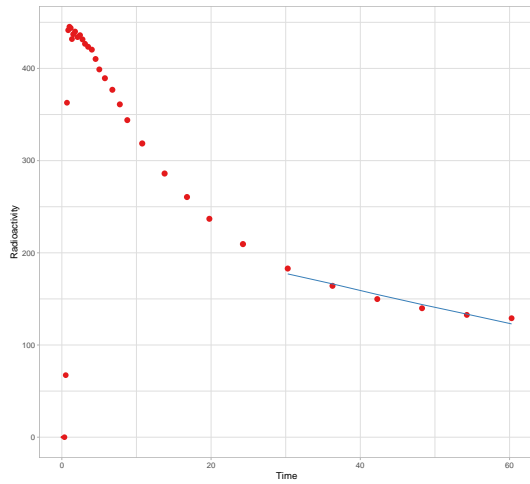
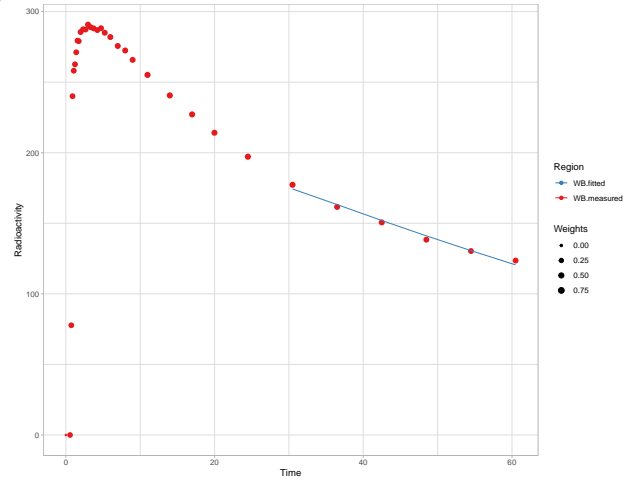
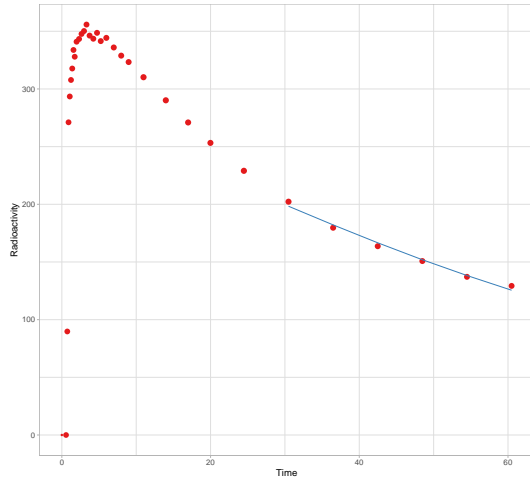

jdcs_1

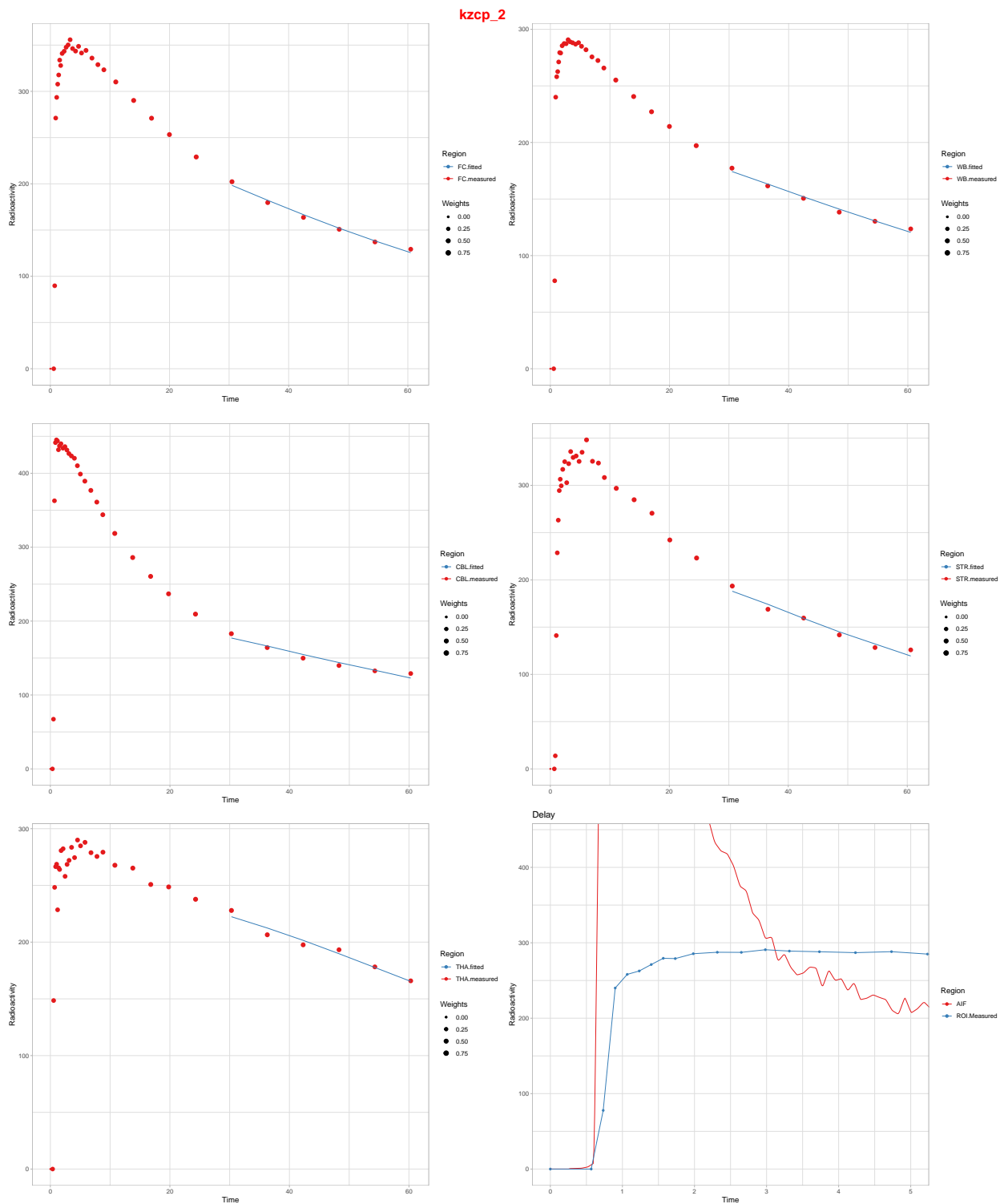


jdcs_2



kzcp_1





Plot Loganplot

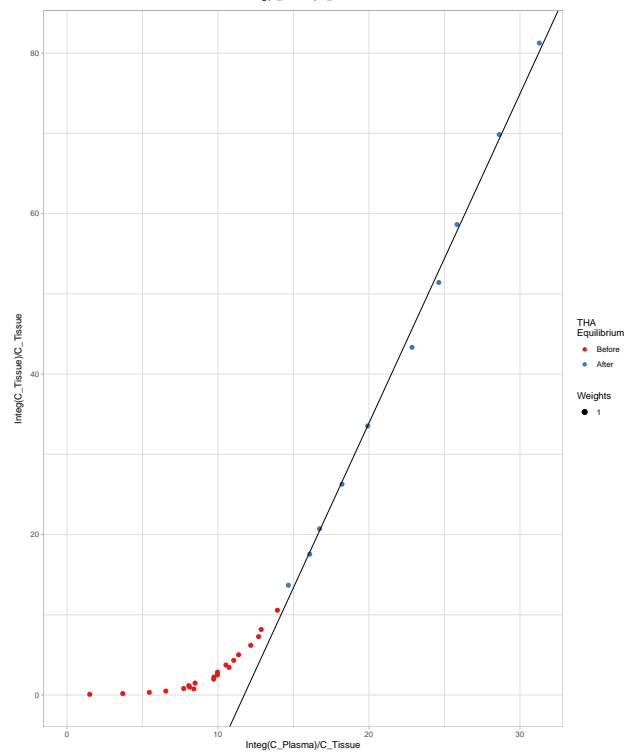
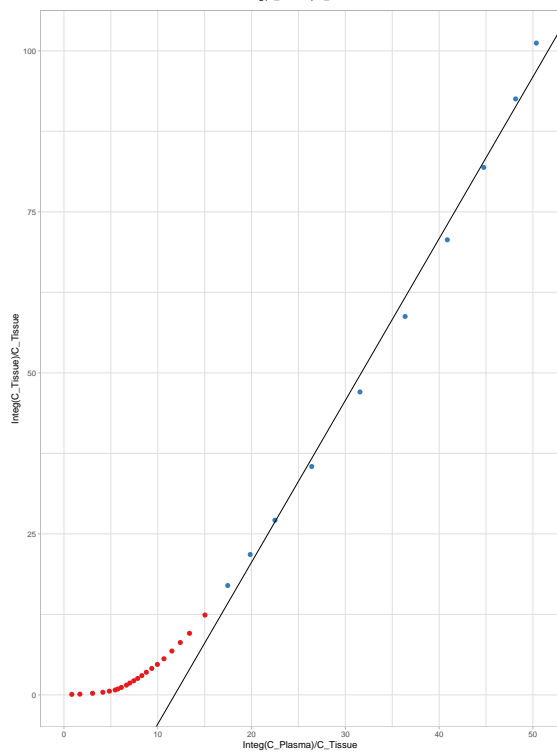
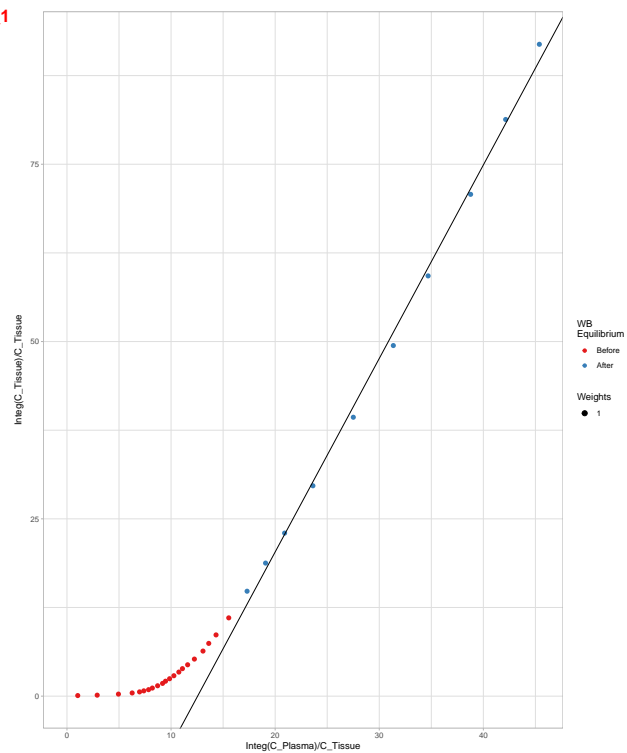
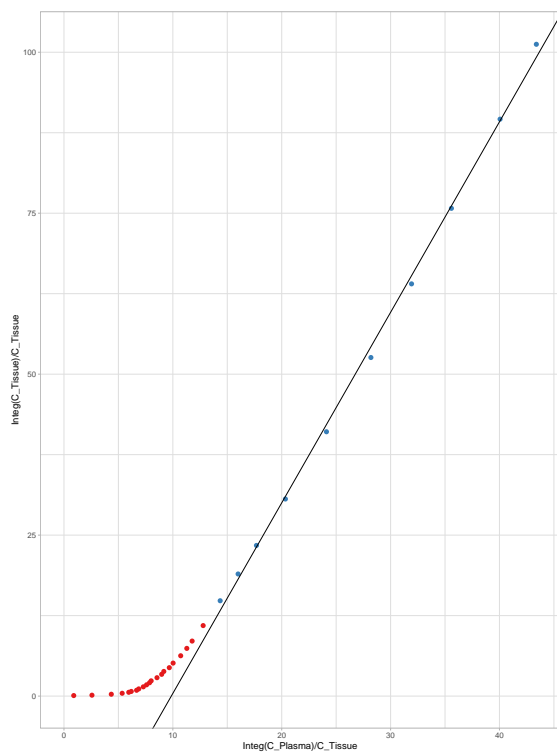
```
plot_Logan <- tacs_long %>%
  filter(PET == PETs[5:8]) %>%
  group_by(PET, Region) %>%
```

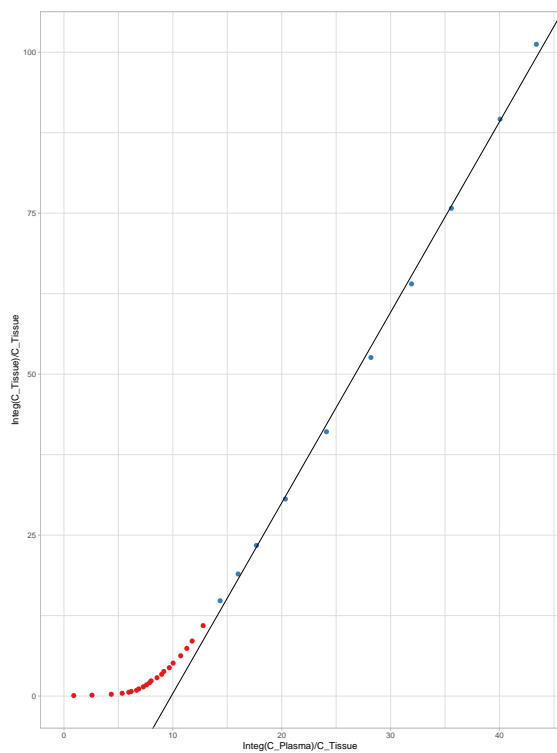
```

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)

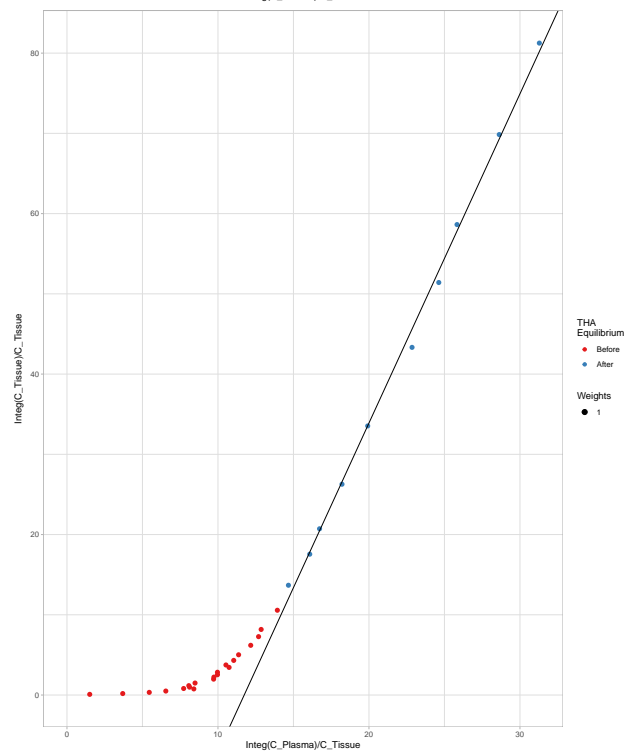
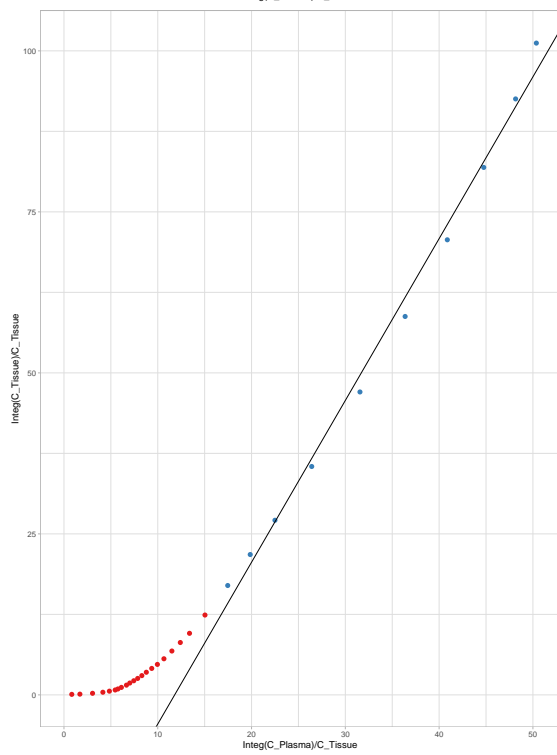
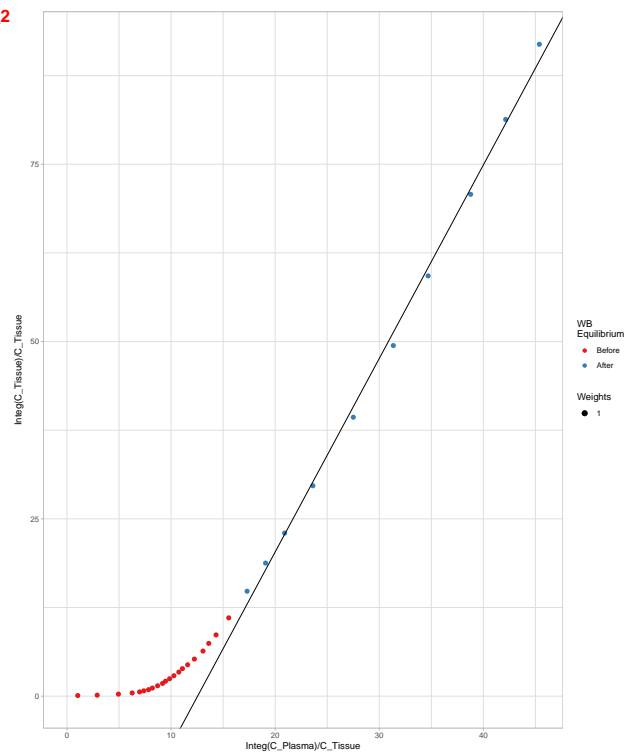
walk2(list(plot_Logan$fit), unique(plot_Logan$PET),
  ~print(plot_grid( plotlist = .x, ncol = 2, nrow = 2, align = 'hv') +
    draw_plot_label( label = .y , y = 1, x = 0.5, fontface = "bold", size = 20, colour = "red", hjust = 1

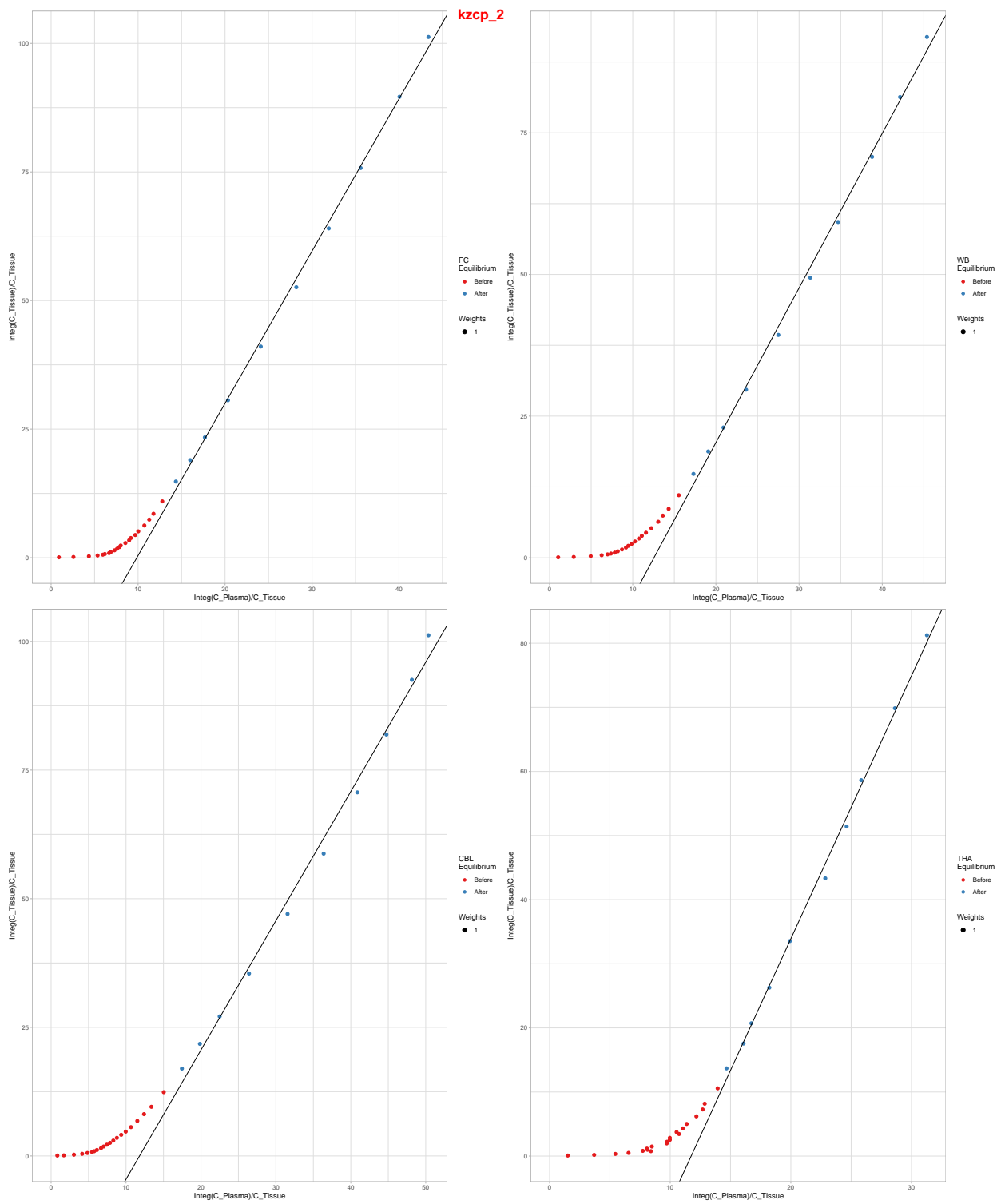
```





jdc2_2





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_pbr28.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() %>%
  ungroup() %>%
  select(Region:wscv)

measure <- unique(trt_table$Measure)

trt_table %>%
  select(-Measure) %>%
  kable(digits=3)
```

Region	mean	sd	cov	skew	kurtosis	icc	icc_l	icc_u	wscv
FC	3.131	1.499	0.479	1.243	0.977	0.913	0.736	0.974	0.145
TC	3.157	1.544	0.489	1.311	1.342	0.927	0.777	0.978	0.135
STR	3.026	1.465	0.484	1.220	0.982	0.906	0.720	0.972	0.151
THA	4.050	2.239	0.553	1.204	0.831	0.905	0.715	0.971	0.174
WB	3.050	1.469	0.481	1.301	1.192	0.905	0.715	0.971	0.152
CBL	3.355	1.680	0.501	1.352	1.367	0.922	0.759	0.977	0.143
FC	3.083	1.496	0.485	0.922	0.214	0.899	0.699	0.969	0.158
TC	3.028	1.517	0.501	1.053	0.659	0.917	0.750	0.975	0.147
STR	8.798	27.297	3.102	4.266	17.026	0.010	-0.545	0.560	3.087
THA	3.907	2.196	0.562	1.067	0.401	0.910	0.728	0.973	0.173
WB	2.919	1.437	0.492	1.031	0.455	0.902	0.707	0.970	0.158
CBL	3.054	1.631	0.534	1.227	0.926	0.909	0.716	0.973	0.165
FC	2.940	1.471	0.501	1.173	0.827	0.917	0.741	0.975	0.147
TC	2.933	1.480	0.505	1.259	1.198	0.922	0.756	0.977	0.144
STR	2.816	1.426	0.506	1.156	0.830	0.906	0.719	0.972	0.158
THA	3.794	2.062	0.544	1.182	0.781	0.907	0.722	0.972	0.169
WB	2.822	1.401	0.497	1.254	1.098	0.907	0.718	0.972	0.155
CBL	3.103	1.603	0.517	1.321	1.290	0.915	0.736	0.975	0.154

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"))))

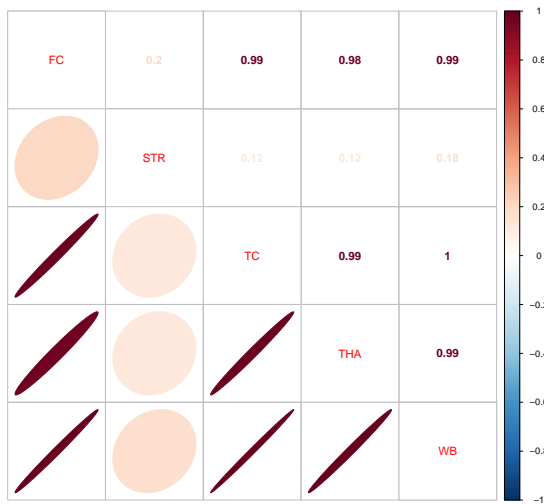
par(mfrow=c(2,2))

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))

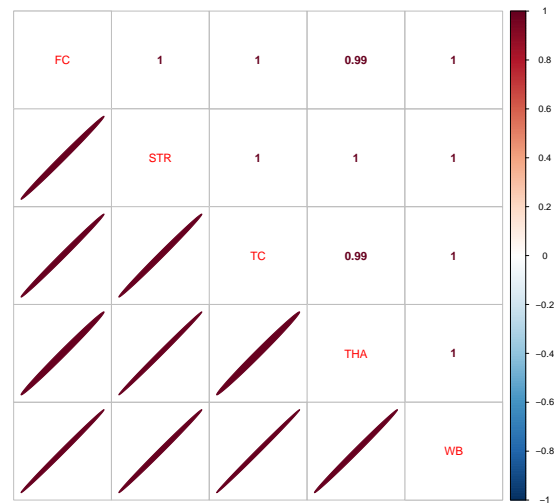
Vt_logan %>%
  select(FC:WB) %>%
  cor() %>%
  corrplot.mixed(lower='ellipse', upper='number',
                 lower.col = col2(200), upper.col = col2(200), diag='n',
                 number.digits = 2, title=expression(Vt_logan ~ Correlations),
                 mar=c(0,0,1,0))

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))
```

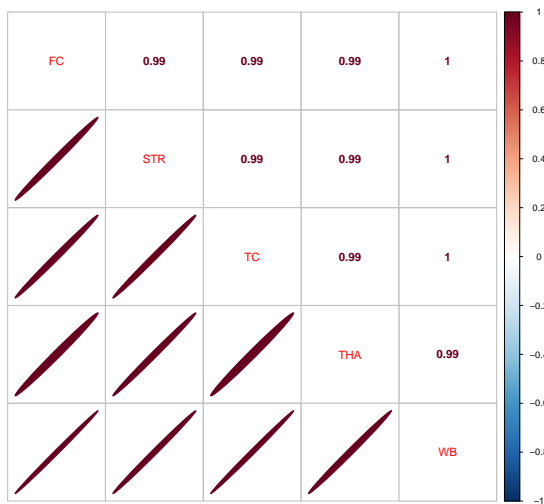
Vt_2TCM Correlations



Vt_logan Correlations



Vt_MA1 Correlations



#Corrplot between measures for a single region

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

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))

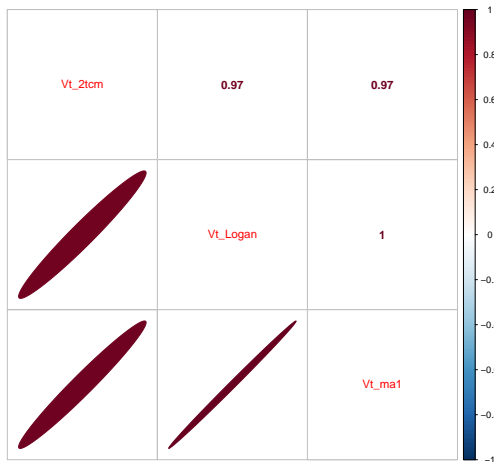
compare %>%
  filter(Region == "THA") %>%
  select(Vt_2tcm:Vt_ma1) %>%
  cor() %>%
  corrplot.mixed(lower='ellipse', upper='number',
                 lower.col = col2(200), upper.col = col2(200), diag='n',
                 number.digits = 2, title=expression(Model ~ Correlations ~ Region: OC), mar=c(0,0,1,0))

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))

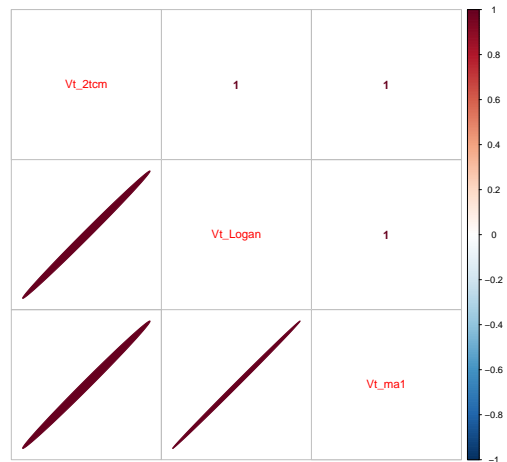
compare %>%
  filter(Region == "WB") %>%
  select(Vt_2tcm:Vt_ma1) %>%
  cor() %>%
  corrplot.mixed(lower='ellipse', upper='number',
                 lower.col = col2(200), upper.col = col2(200), diag='n',
                 number.digits = 2, title=expression(Model ~ Correlations ~ Region: WB),
      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

```

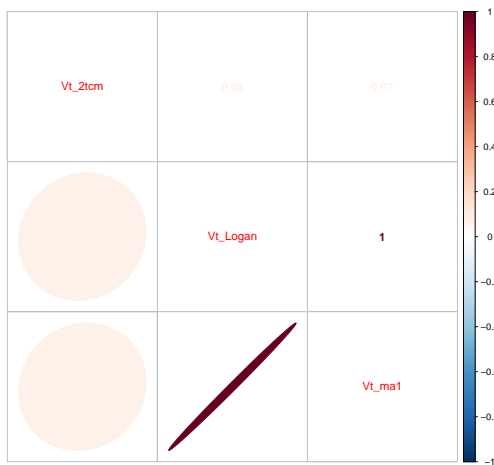
Model Correlations Region : FC



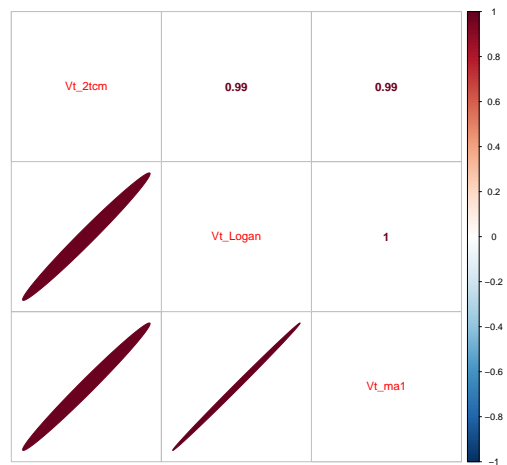
Model Correlations Region : OC



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~")

```

\begin{table}[t]

\caption{Correlations with BP_srtm_{WB}}

Measure	R ²
Vt~2tcm_CBL~	0.97
Vt~2tcm_FC~	0.98
Vt~2tcm_STR~	0.03
Vt~2tcm_TC	0.99
Vt~2tcm_THA~	0.98
Vt~Logan_CBL~	0.96
Vt~Logan_FC~	0.97
Vt~Logan_STR~	0.98
Vt~Logan_TC	0.97
Vt~Logan_THA~	0.98
Vt~Logan_WB~	0.97
Vt~ma1_CBL~	0.95
Vt~ma1_FC~	0.97
Vt~ma1_STR~	0.98
Vt~ma1_TC	0.97
Vt~ma1_THA~	0.97
Vt~ma1_WB~	0.98

\end{table}

#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)
  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)
```

