Contents

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Aims

The aim of this assignment is to analyze the AZ10419369 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(viridis)
library(kableExtra)
```

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 kinfitresults

```r
tactibble <- tibble(Filename = list.files(path = "../RawData/",
                                          pattern = "kinfitresults.mat")) %>%
  group_by(Filename) %>%
```

```
  mutate(tacdata = map(Filename, ~kipettools::kfresults_getData(
    paste0("../RawData/", .x))))

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

Tidying data.

```
#loading data

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

tacs <- tacs %>%
  ungroup() %>%
  mutate(Subjname = map_chr(tacdata, "Subjname"),
         PETNo = map_dbl(tacdata, "PETNo"),
         tacdata = map(tacdata, "tacdata")) %>%
  select(-Filename)
```

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

tacs <- tacs %>%
  unnest() %>%
  mutate("start" = times - (durations/2)) %>%
  mutate("end" = times + (durations/2)) %>%
  select(-weights)

# New weights

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

tacs <- tacs %>%
  nest(-Subjname, -PETNo, .key = 'tacdata')
```

Fitting and plotting MRTM1 multiple times for regions FC and WB

```
#K2 prime for striatum to be used to MRTM2 later on

 tacs <- tacs %>%
  group_by(Subjname, PETNo) %>%
  mutate(MRTM1fit = map(tacdata, ~mrtm1(t_tac = .x$times, reftac = .x$gmRefCBL,
                               roitac = .x$gmfslSTR,
                                  weights = .x$weights))) %>%
  ungroup() %>%
```

```
    mutate(bp_MRTM1 = map_dbl(MRTM1fit, c("par", "bp")),
           k2prime_MRTM1 = map_dbl(MRTM1fit, c("par", "k2prime"))) %>%
    group_by(Subjname, PETNo) %>%
    mutate(logan_tstar = map2(tacdata, k2prime_MRTM1,
                  ~refLogan_tstar(t_tac = .x$times,
                     reftac = .x$gmRefCBL, lowroi = .x$gmL_fslThalamus,
                     medroi = .x$gmfslFrontal_Lobe, highroi = .x$gmfslOccipital_Lobe,
                   k2prime = .y)))
```

Fitting MRTM2 to each region of each individual

First, let's select some specific regions. Note: I duplicated the CBL region column into "CBL" and "Ref".
One of them is used to make the reference tissue models when nested in tacdata whereas the other is used for
plotting in the new "all regions per PET +facet wrap by PET" - plot. However, the srtm fitting gave me an
error when I did this

```
regions <- c("STR" = "gmfslSTR", "FC" = "gmfslFrontal_Lobe", "WB", "WM", "GM", "OC" = "gmfslOccipital_L
               "gmfslTemporal_Lobe")

tacs <- tacs %>%
  select(tacdata, Subjname, PETNo, k2prime_MRTM1, logan_tstar) %>%
  mutate(tacdata = map(tacdata, ~select(.x, regions, times, weights)))


#Long data. By gathering the regions into a single region collumn we can group_by region and then itera

tacs_long <- tacs %>%
  unnest(tacdata, .drop = FALSE) %>%
  gather(key = Region, value = TAC, -times, -weights,
         -Subjname, -PETNo, -k2prime_MRTM1, -CBL, -logan_tstar) %>%
  group_by(Subjname, PETNo, Region, k2prime_MRTM1) %>%
  nest(.key = "tacdata") %>%
  mutate(PET = paste(Subjname, PETNo, sep='_'))

#Fitting MRTM2 using the K2_prime values obtained for the striatum through the MRTM1 fitting earlier. n

tacs_long <- tacs_long %>%
  group_by(Subjname, PETNo, Region) %>%
  mutate(MRTM2fit = map2(tacdata, k2prime_MRTM1,
                    ~mrtm2(t_tac=.x$times, reftac = .x$CBL,
                          roitac = .x$TAC, k2prime = .y,
                          weights = .x$weights,tstarIncludedFrames = 20)),
         bp_MRTM2 = map_dbl(MRTM2fit, c("par", "bp")))
```

Plotting fitted MRTM2 model

And now, let's take a look at the BP_{ND} values. We'll want to divide them by ROI I think.

```
ggplot(tacs_long, aes(x=bp_MRTM2, fill=Region)) +
  geom_histogram(colour="black") +
  facet_wrap(~Region, scales="free") +
  guides(fill=FALSE)
```

Plot MRTM2 tacs

Labels for regions are wrong. My intention is to have one plot per region for each PET in the same grid.
Currently, all labels for the regions are the same for each individual.

```
mrtm2_fits = map2(tacs_long$MRTM2fit, tacs_long$Region,
                  ~plot_kinfit(.x, roiname=.y))


PETs <- unique(tacs_long$PET)

allFits <- data.frame(PET = rep(PETs, each= 9)) %>%
 mutate(Fit = mrtm2_fits,
          Plot = 'Fit',
          PET = as.character(PET)) %>%
   arrange(PET, Plot)

 marrangeGrob(allFits$Fit, nrow=3, ncol=3, top=quote(paste('PET: ', PETs[g])))
```
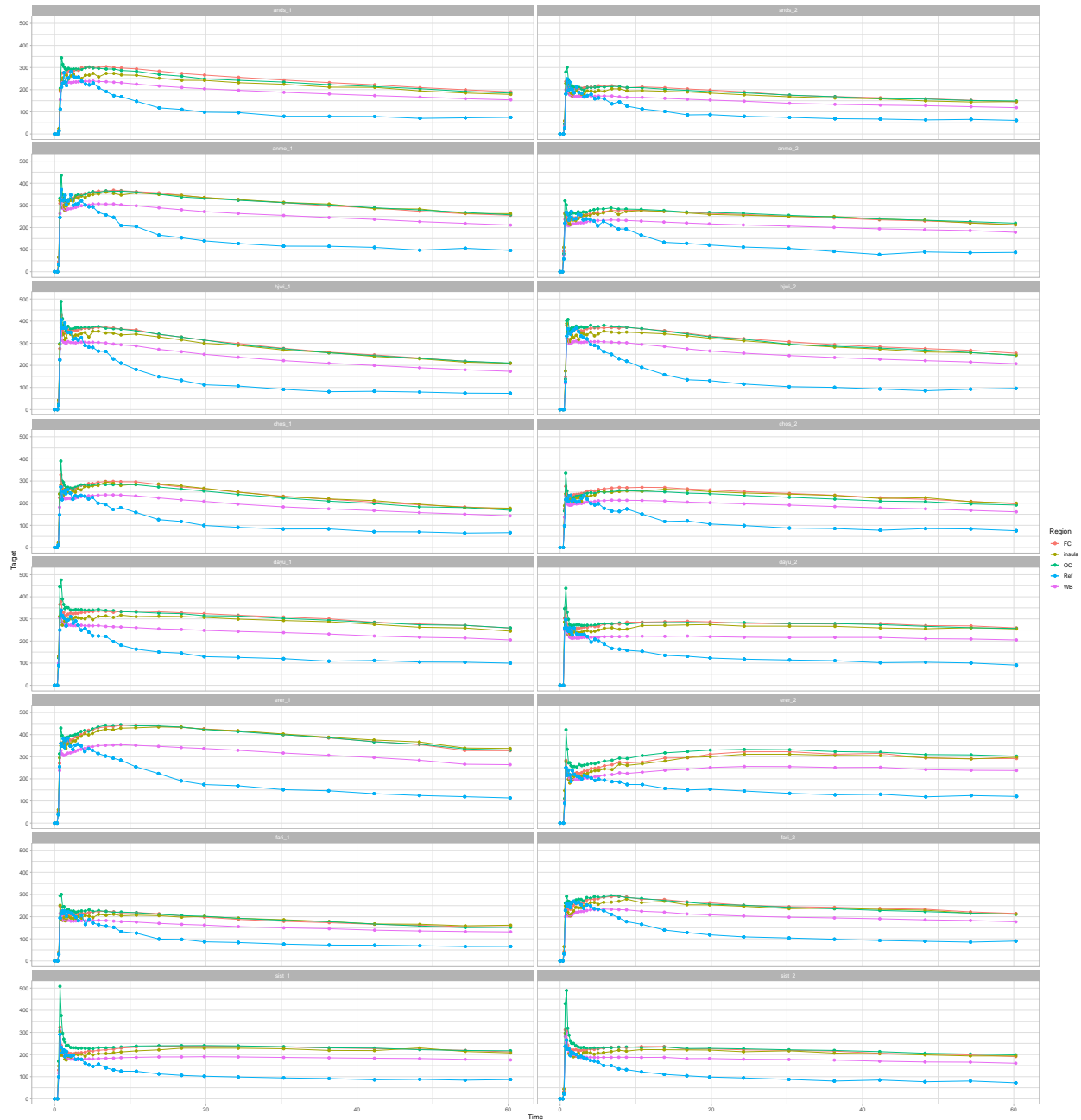
new plot MRTM2

```
MRTM2 <- tacs_long %>%
  group_by(PET, Region) %>%
  mutate(mrtm2fits = map(MRTM2fit, c("tacs"))) %>%
   select(PET, Region, mrtm2fits) %>%
  filter(Region %in% c('FC', 'WB', 'insula', 'OC')) %>%
  unnest()


ggplot() +
  geom_point(data = MRTM2, aes(x=Time, y=Target, color = Region)) + geom_line(data = MRTM2, aes(x = Time
  facet_wrap(~ PET , ncol=2)
```

Fitting kintetic model srtm

```r
tacs_long <- tacs_long %>%
  group_by(Subjname, PETNo, Region) %>%
  mutate(srtmfit = map(tacdata, ~srtm(t_tac = .x$times, reftac = .x$CBL,
                                      roitac = .x$TAC, weights = .x$weights))) %>%
  mutate(bp_srtm = map_dbl(srtmfit, c('par', 'bp')))

## Registered S3 methods overwritten by 'car':
##   method                from
##   influence.merMod      lme4
```

```
##    cooks.distance.influence.merMod lme4
##    dfbeta.influence.merMod         lme4
##    dfbetas.influence.merMod        lme4
```
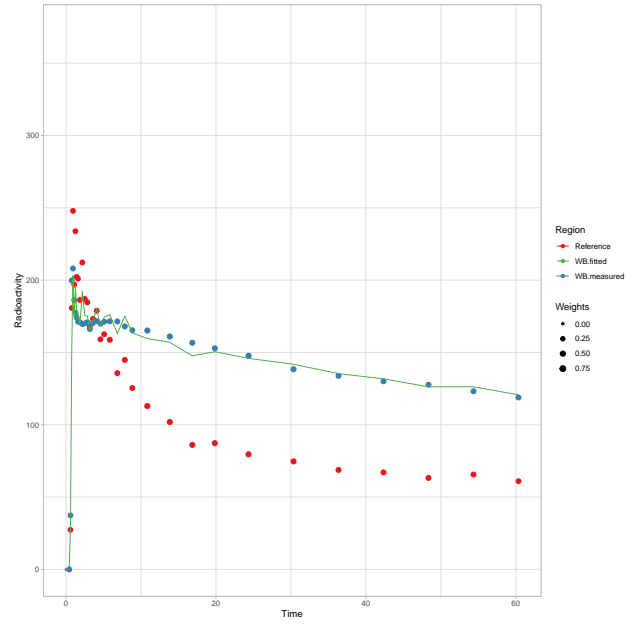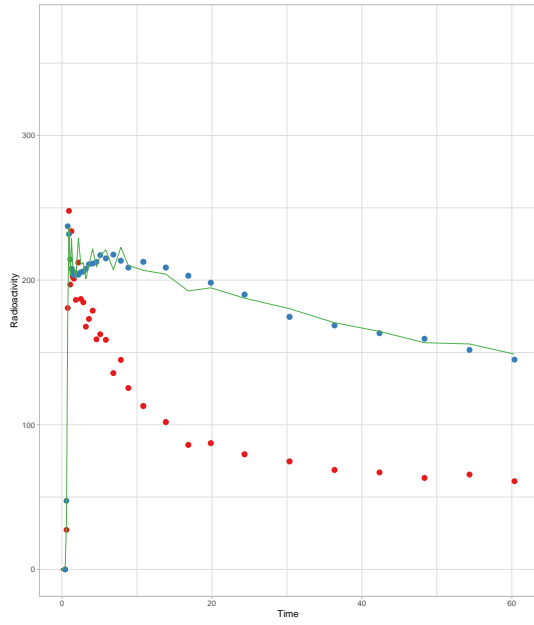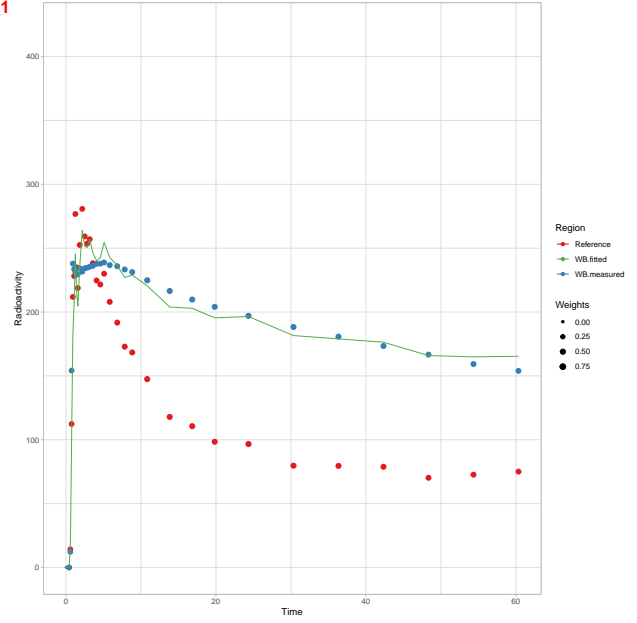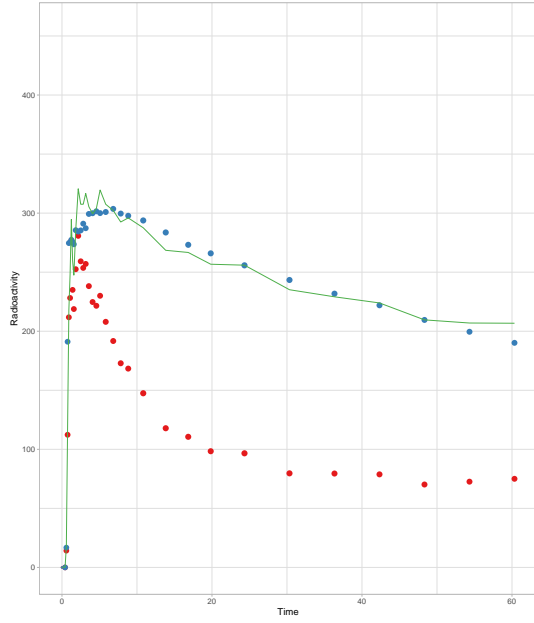
Plotting Kinetic Model srtm

Note: Labels are not quite at the same location for each PET, still unsolved.

```
srtm_plot <-tacs_long %>%
 group_by(PET, Region) %>%
  mutate(srtm_graph = map2(srtmfit, Region,
        ~ plot_kinfit(.x, roiname = .y))) %>%
  ungroup() %>%
  filter(Region %in% c('FC', 'WB', 'ACC', 'CBL')) %>%
  select(PET, srtm_graph) %>%
  group_by(PET) %>%
  arrange(PET)


walk2(list(srtm_plot$srtm_graph), unique(srtm_plot$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
```
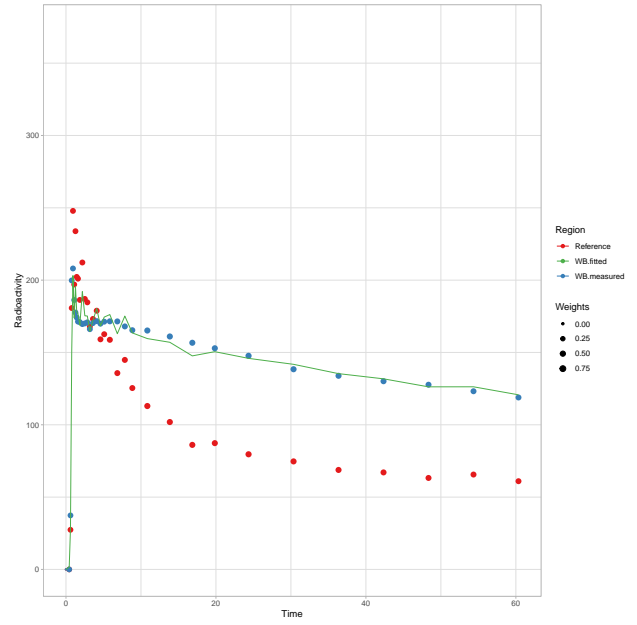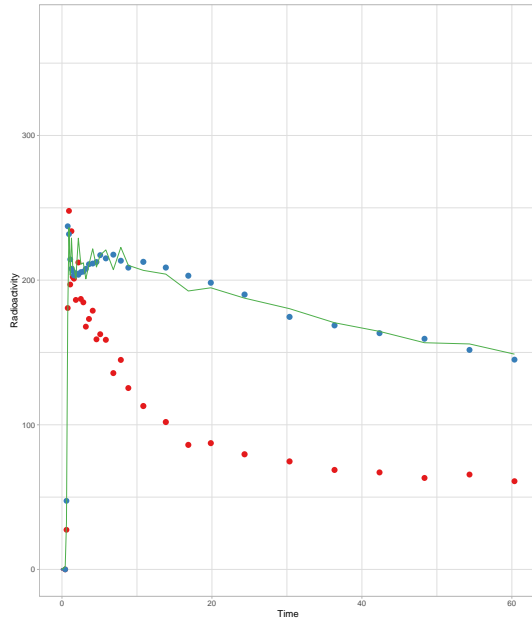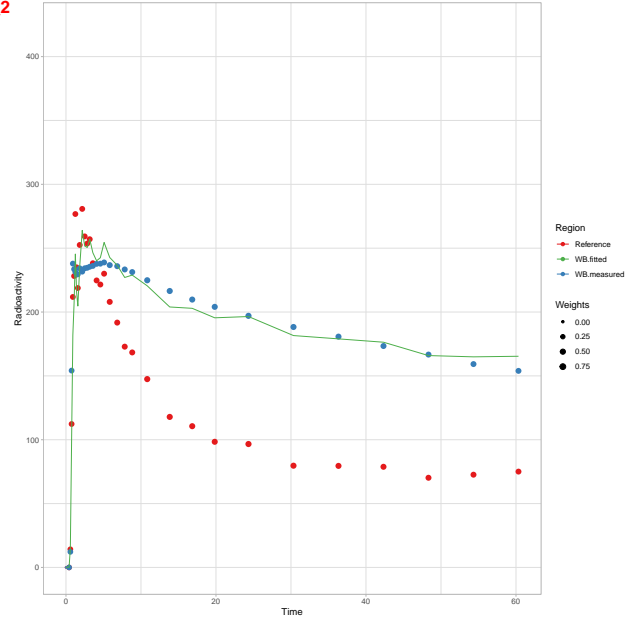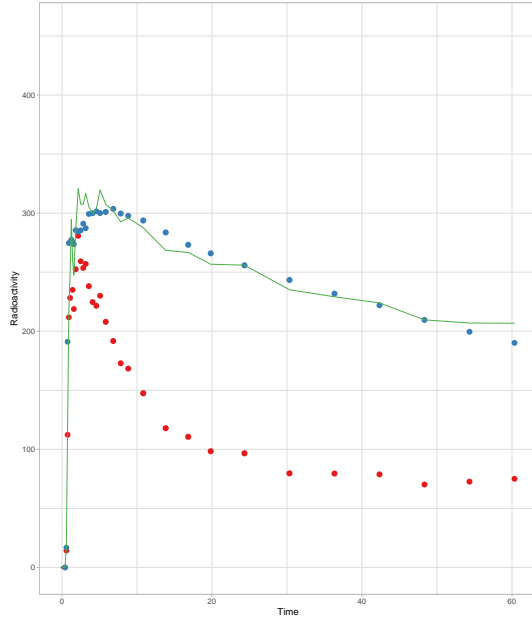
ands_1

8

anmo_2

11
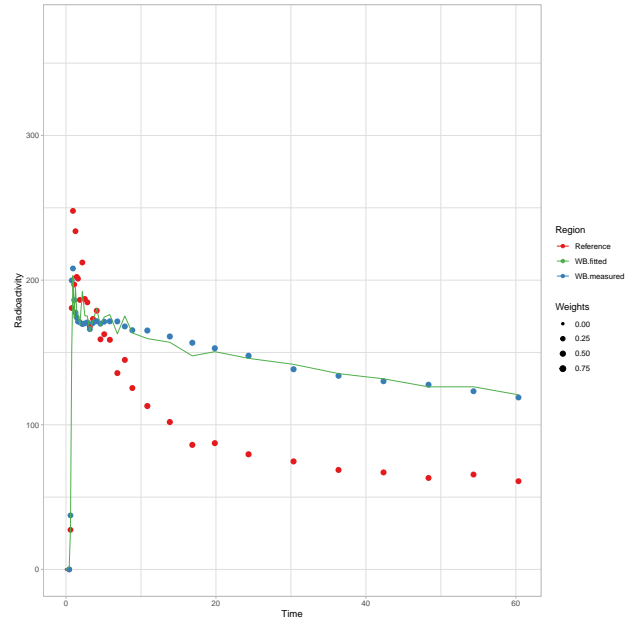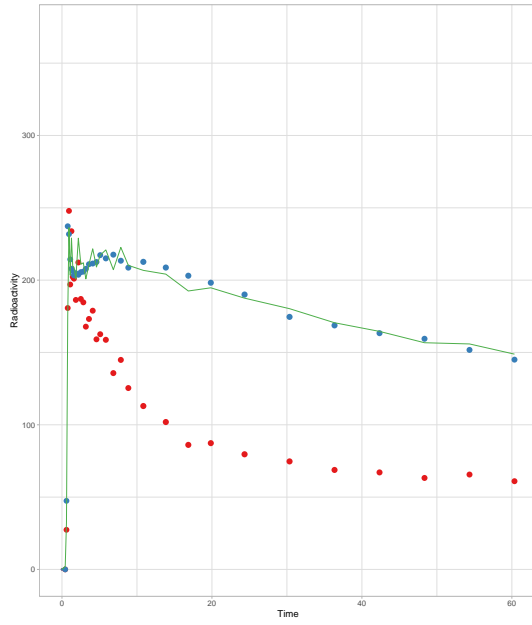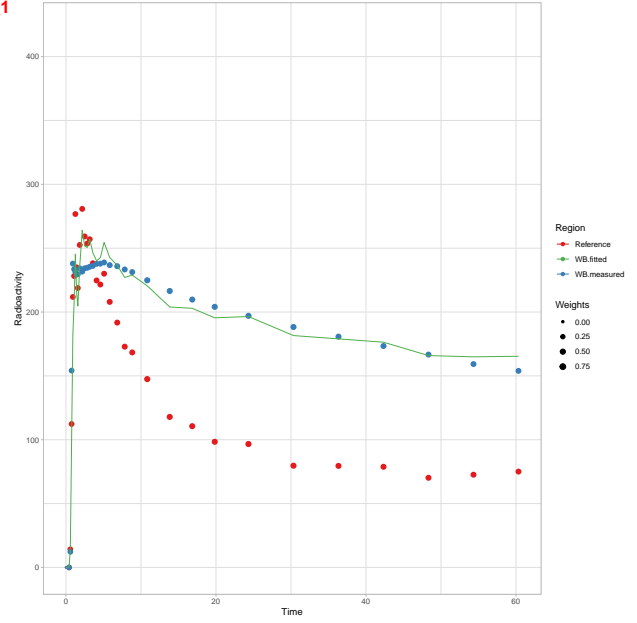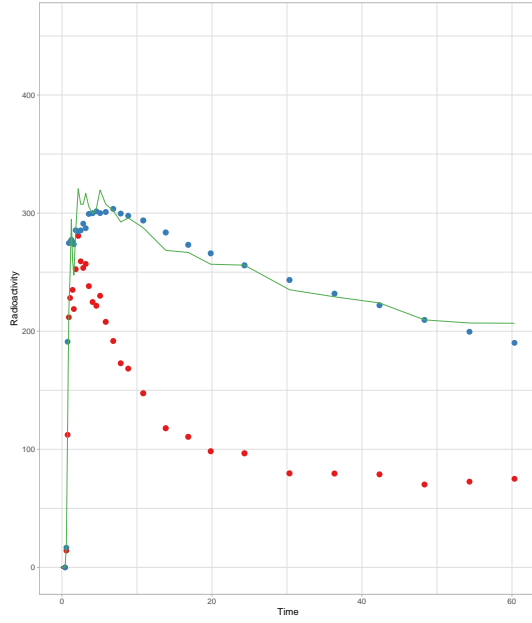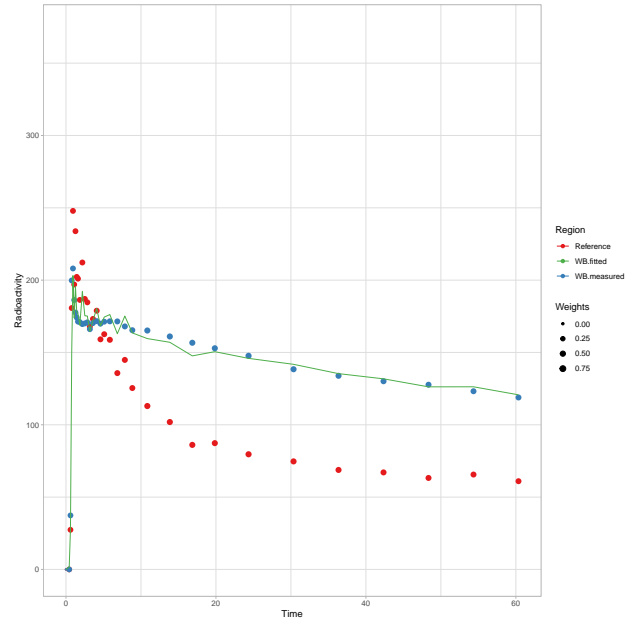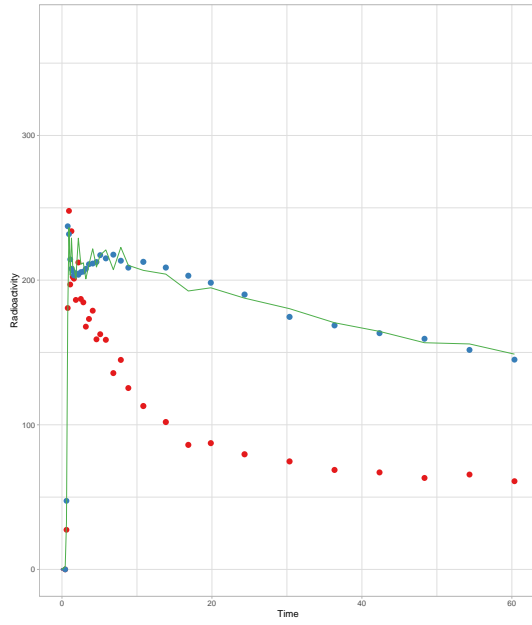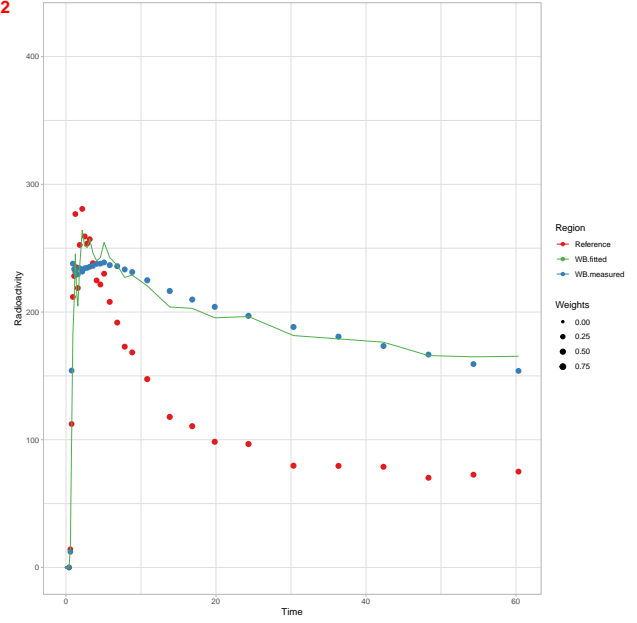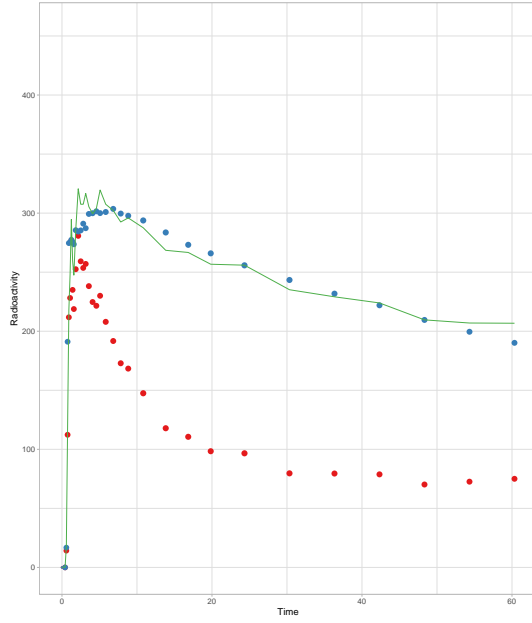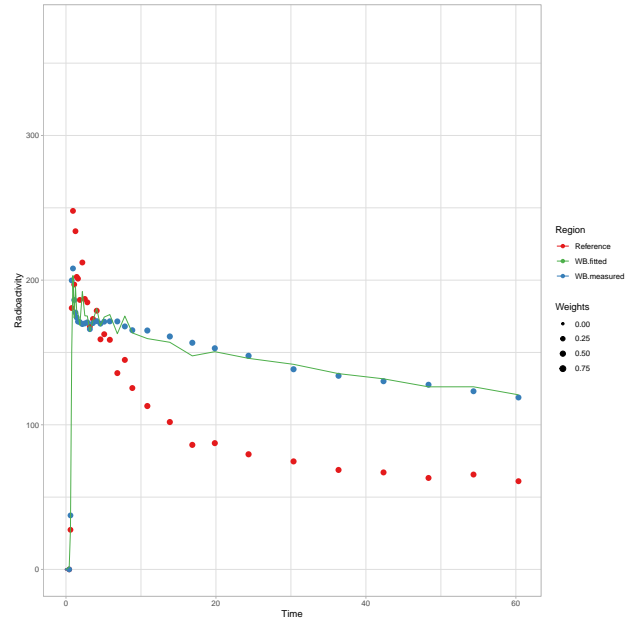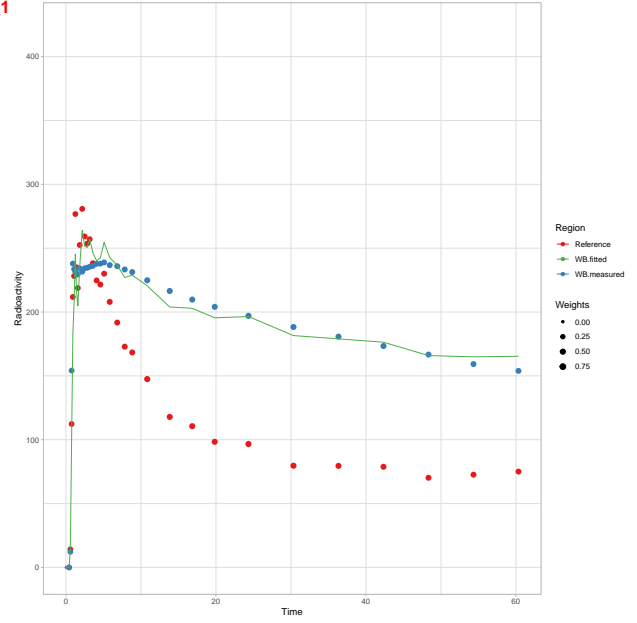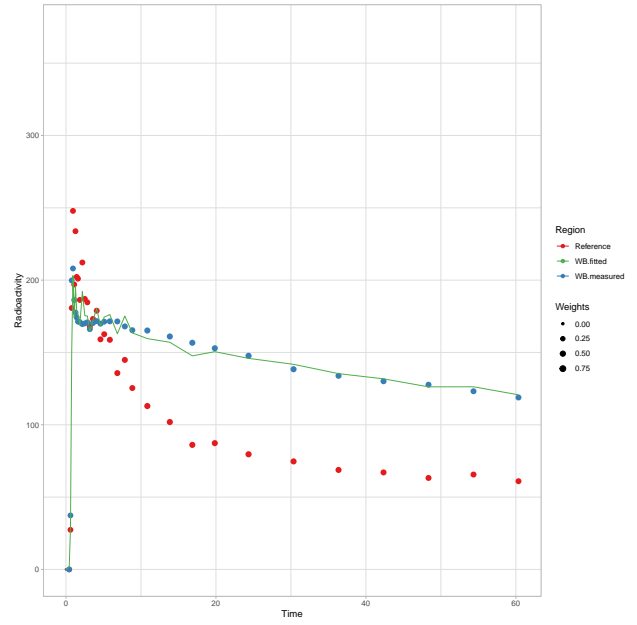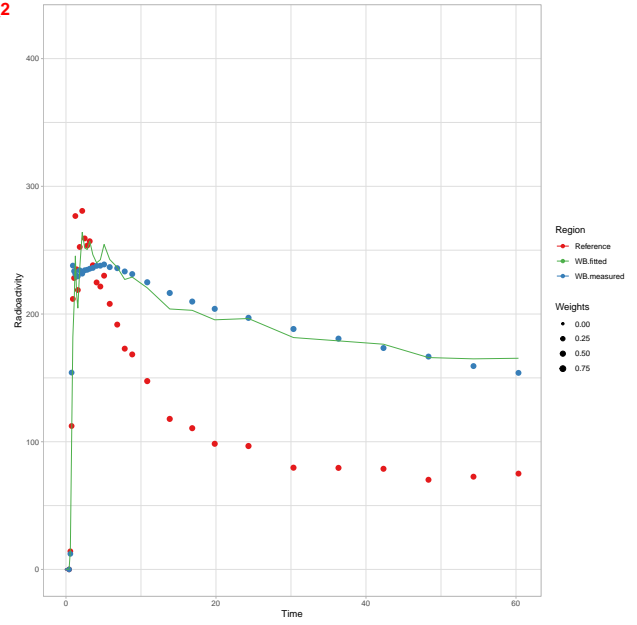
bjwi_1
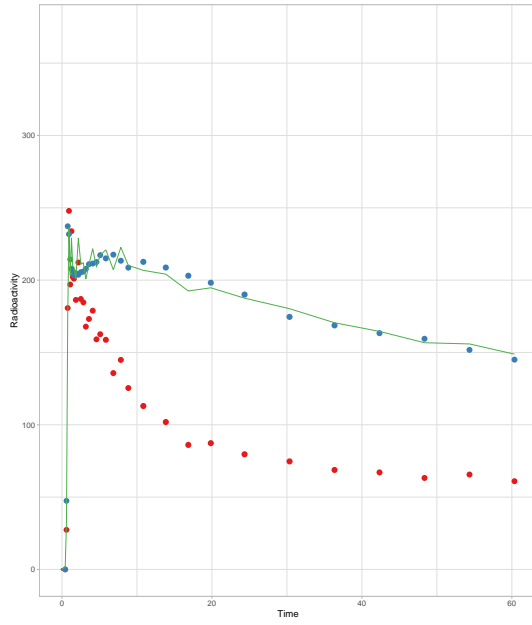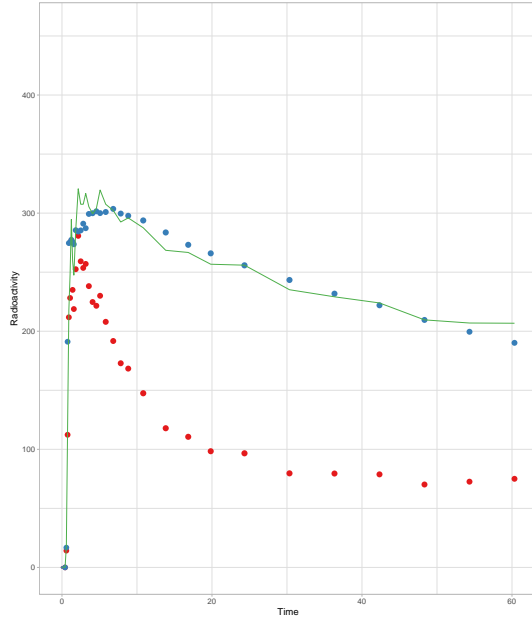
bjwi_2
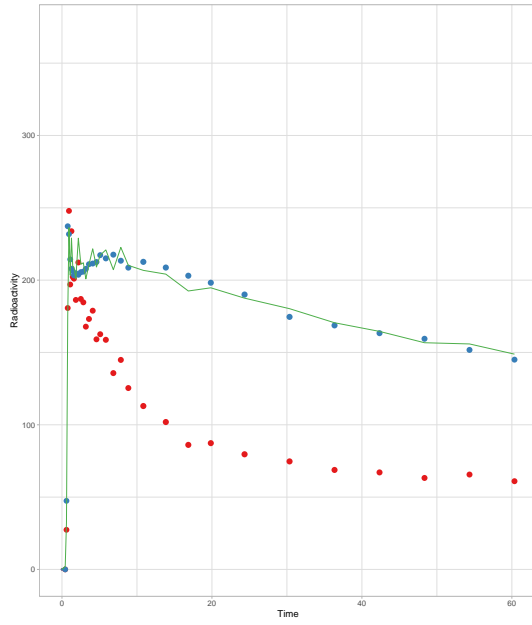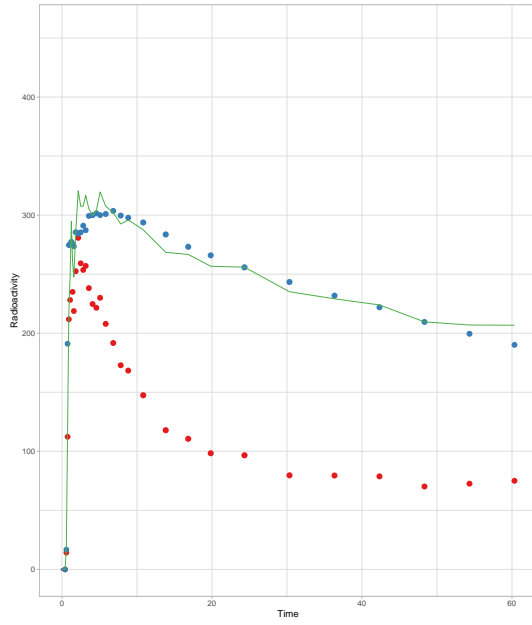
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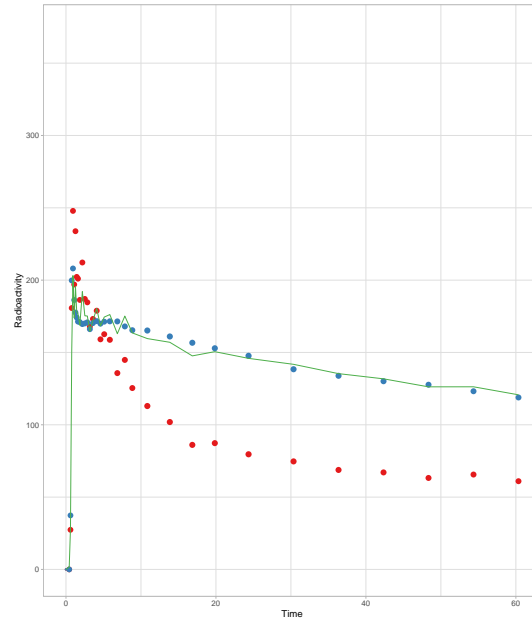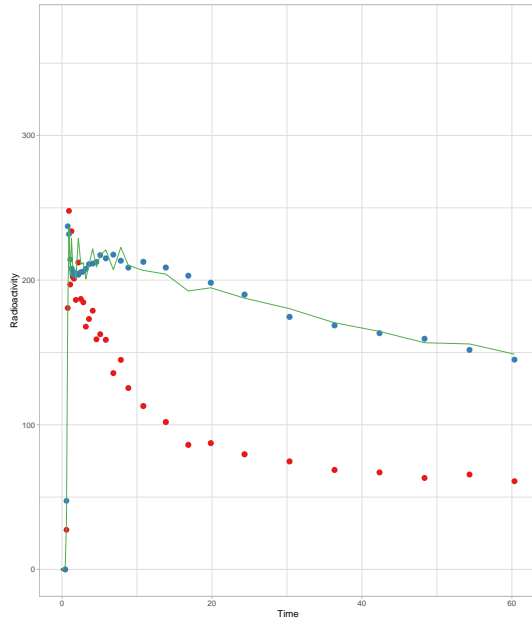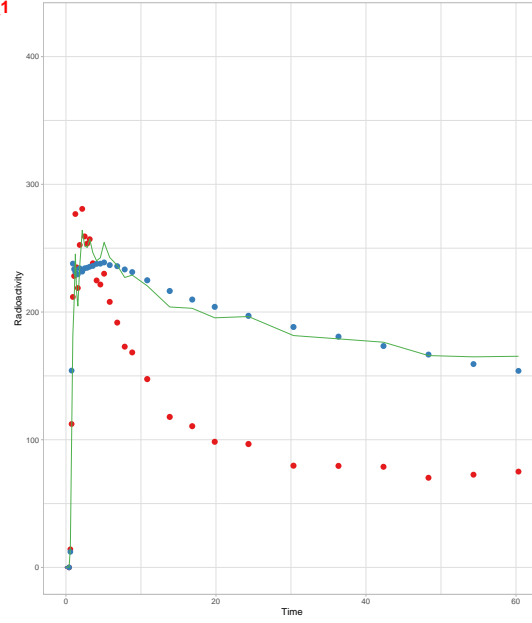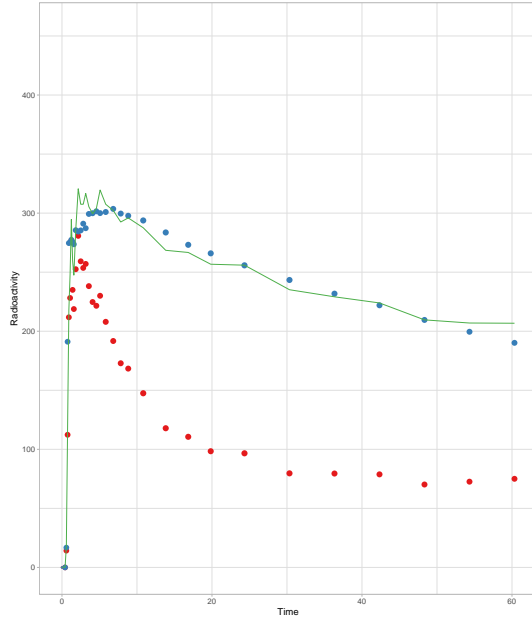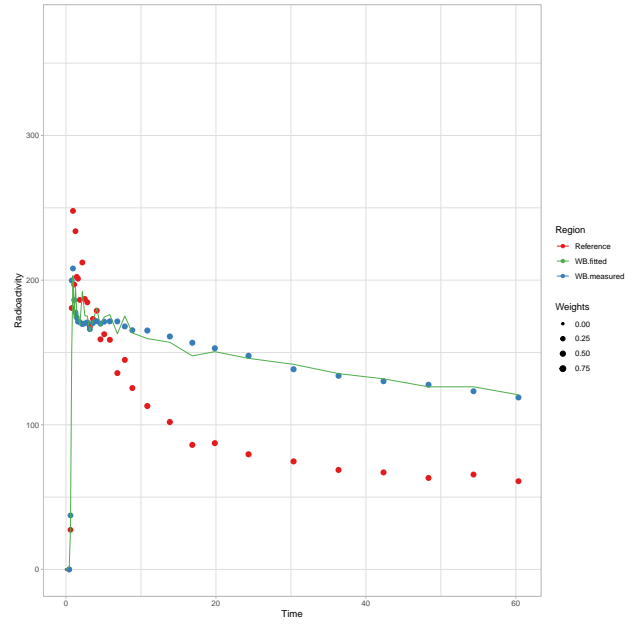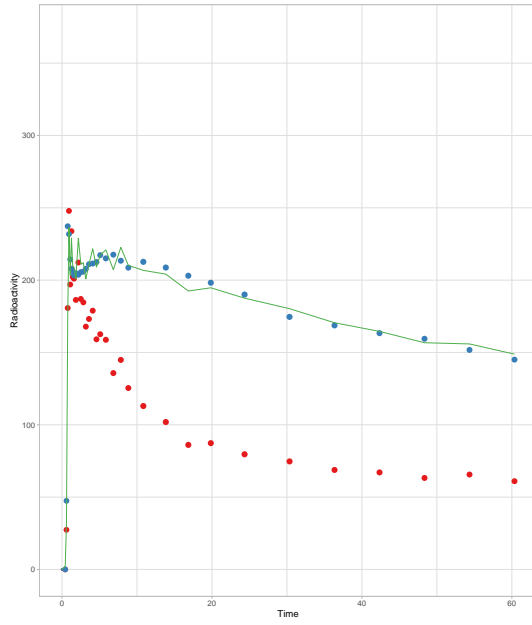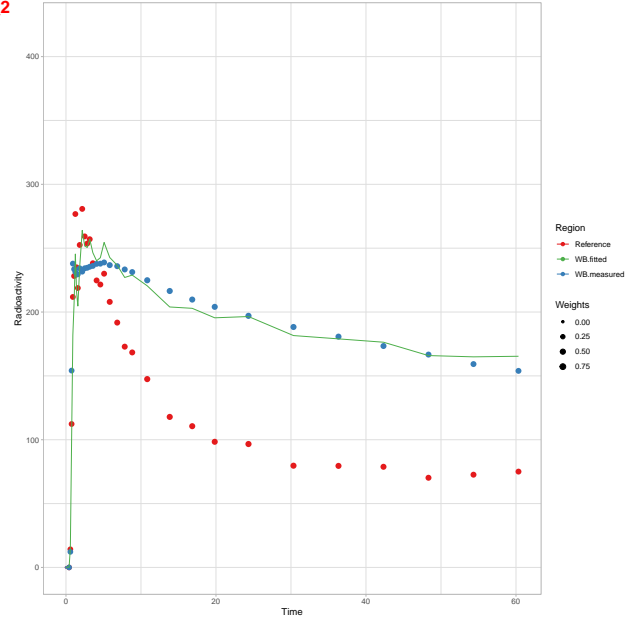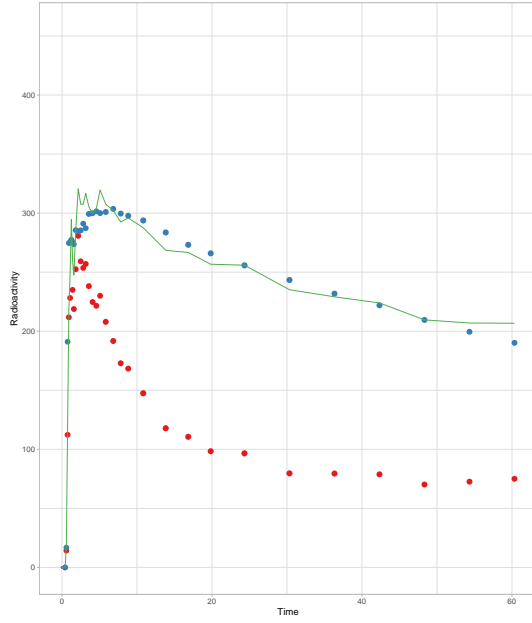
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dayu_2
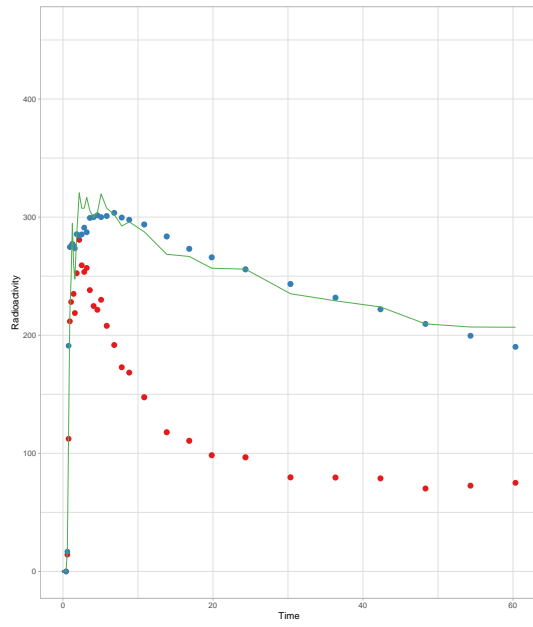
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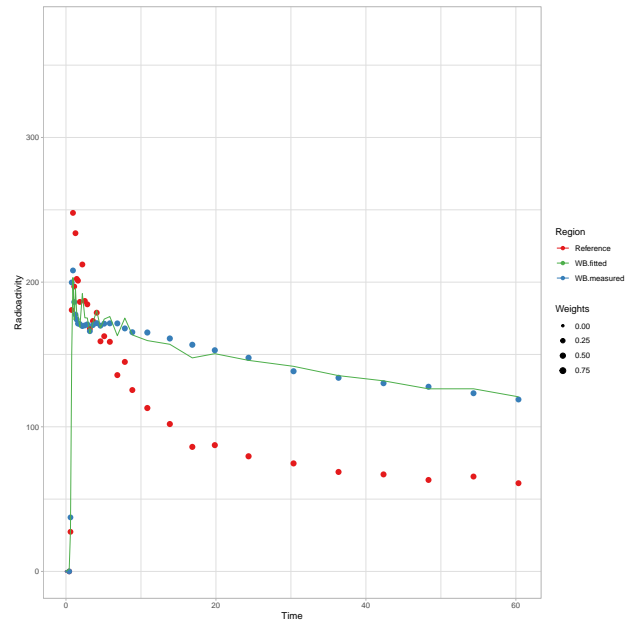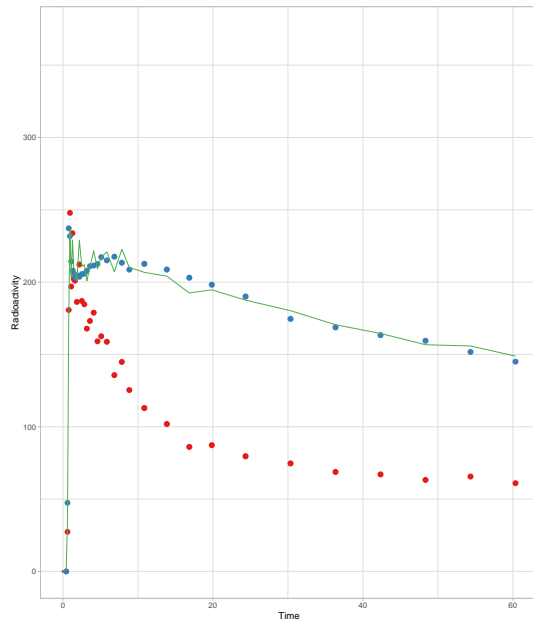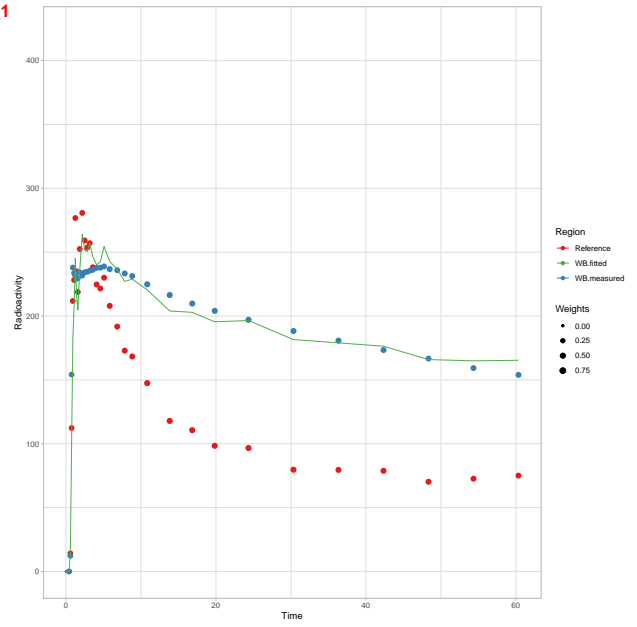
erer_2

fari_1

fari_2

sist_1

sist_2
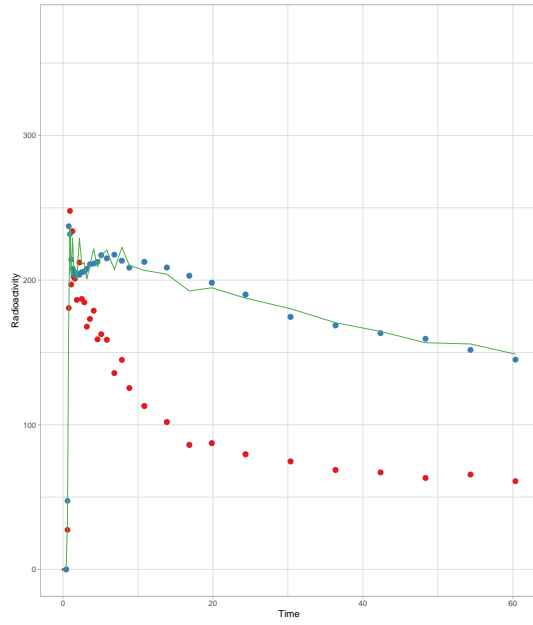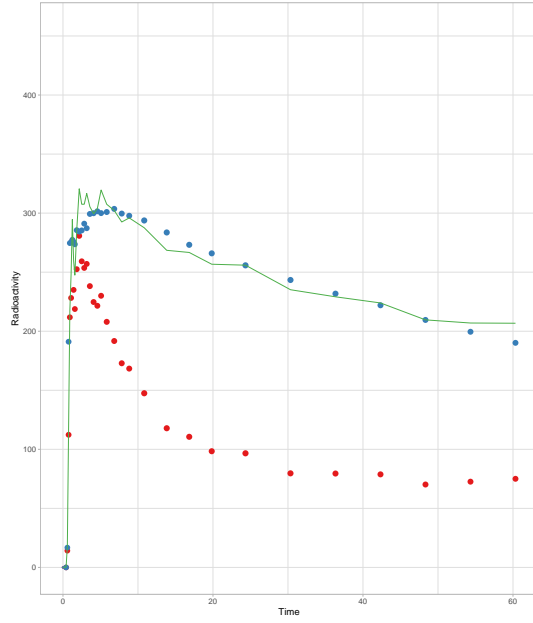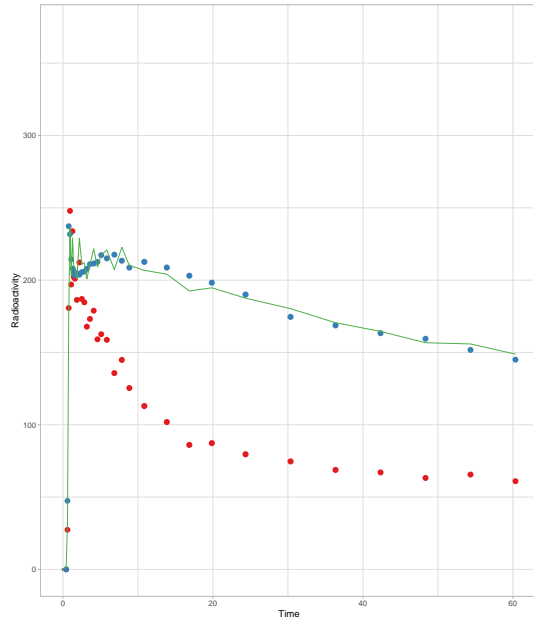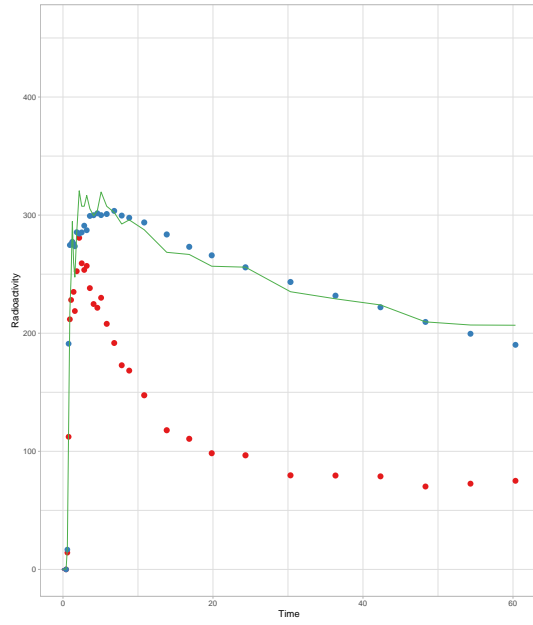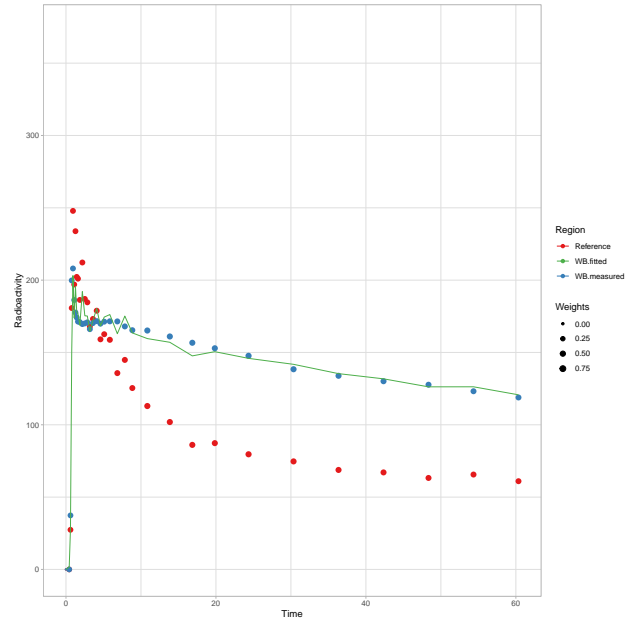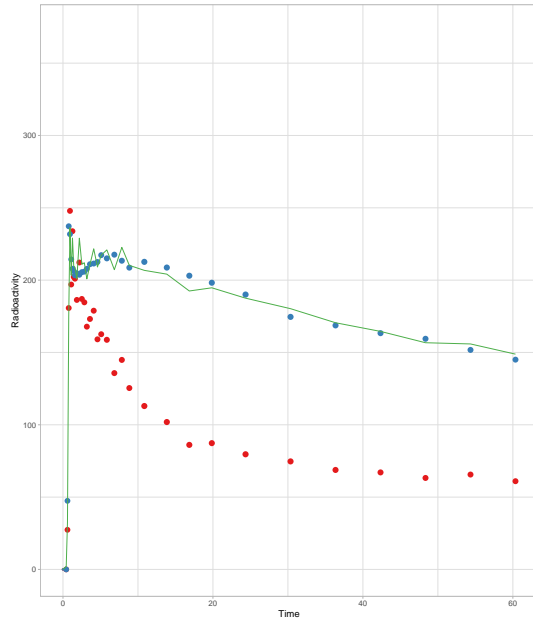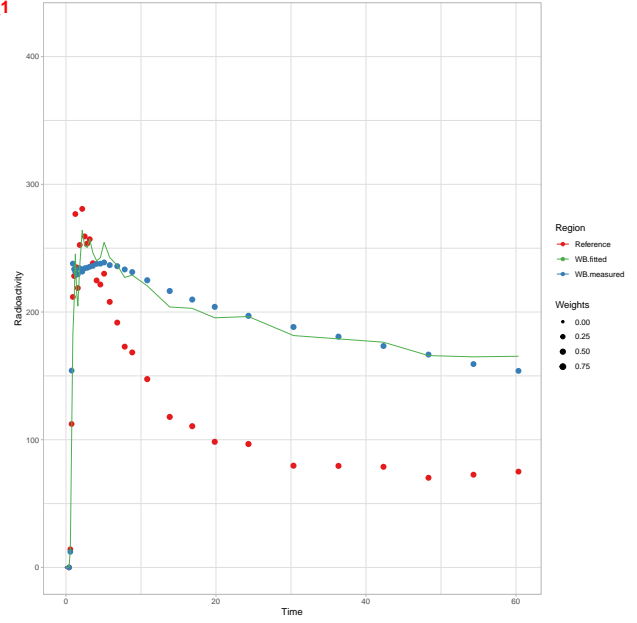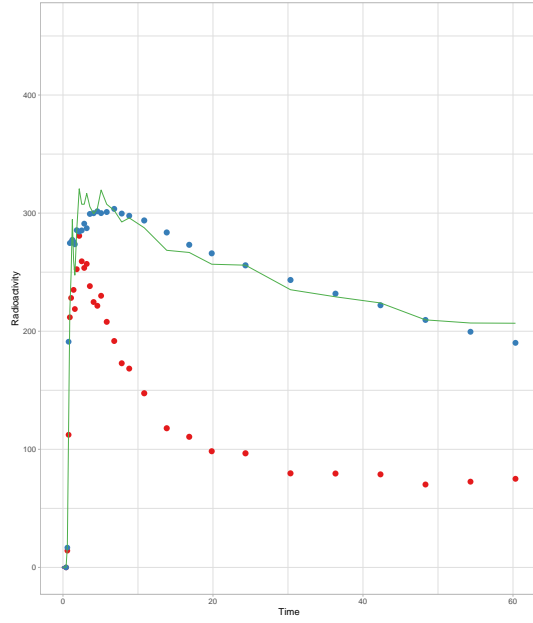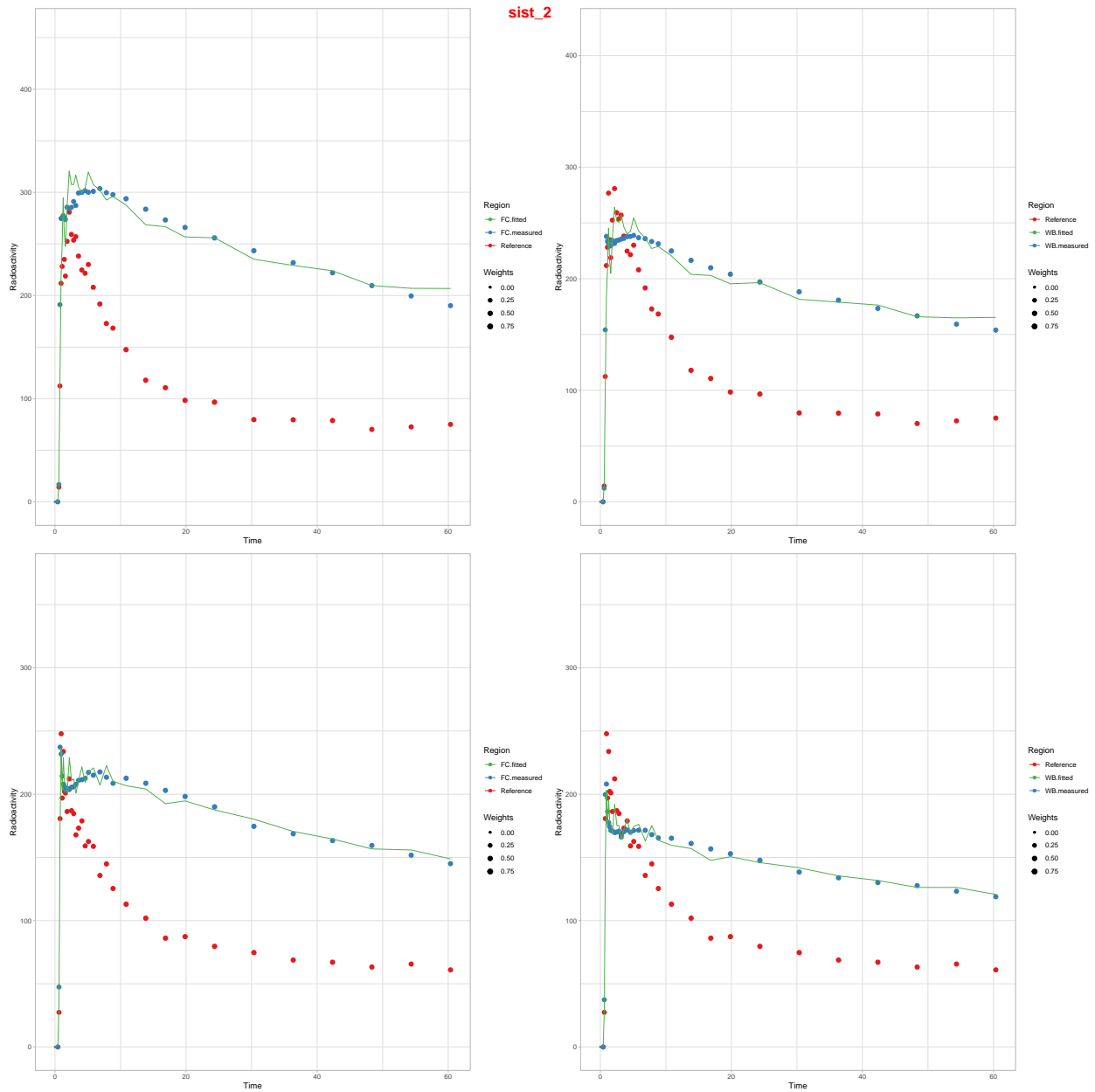
new plot srtm

```r
Srtm <- tacs_long %>%
  group_by(PET, Region) %>%
  mutate(srtmtacs = map(srtmfit, c("tacs"))) %>%
   select(PET, Region, srtmtacs) %>%
  filter(Region %in% c('FC', 'WB', 'insula', 'OC')) %>%
  unnest()

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

plot logan_tstar

Trouble with label, it is at the same level as the medium, high and low ROI labels. Tried moving label with vjust = 0.5. It works, sort of. the label moves up, half of it dissapears and part of the plots at the bottom dissapear. Solution?? Addition: in the end I did manage to get the label up a bit without harming the graph, vjust = 0.97 was the lowest vjust value I could make. I temporarilly changed the color of the label to distinguish easier. Looks a little unprofessional, though. I tried with draw_labels or draw-figure_labels and didn't see any improvement. Also, I tried getting all the subjects into the same pane by making ncol = 2 and nrow = 3 or making sample_n(size = 4) and ncol and nrow = 2. It just got really messy. Also, initially I thought I could skip "print", but that is not possible. you get no error without print, but no graphs either. I thought I got no graph because of eval = FALSE, but that was an incorrect assumption.

```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_
```

PET: erer_1

PET: anmo_2
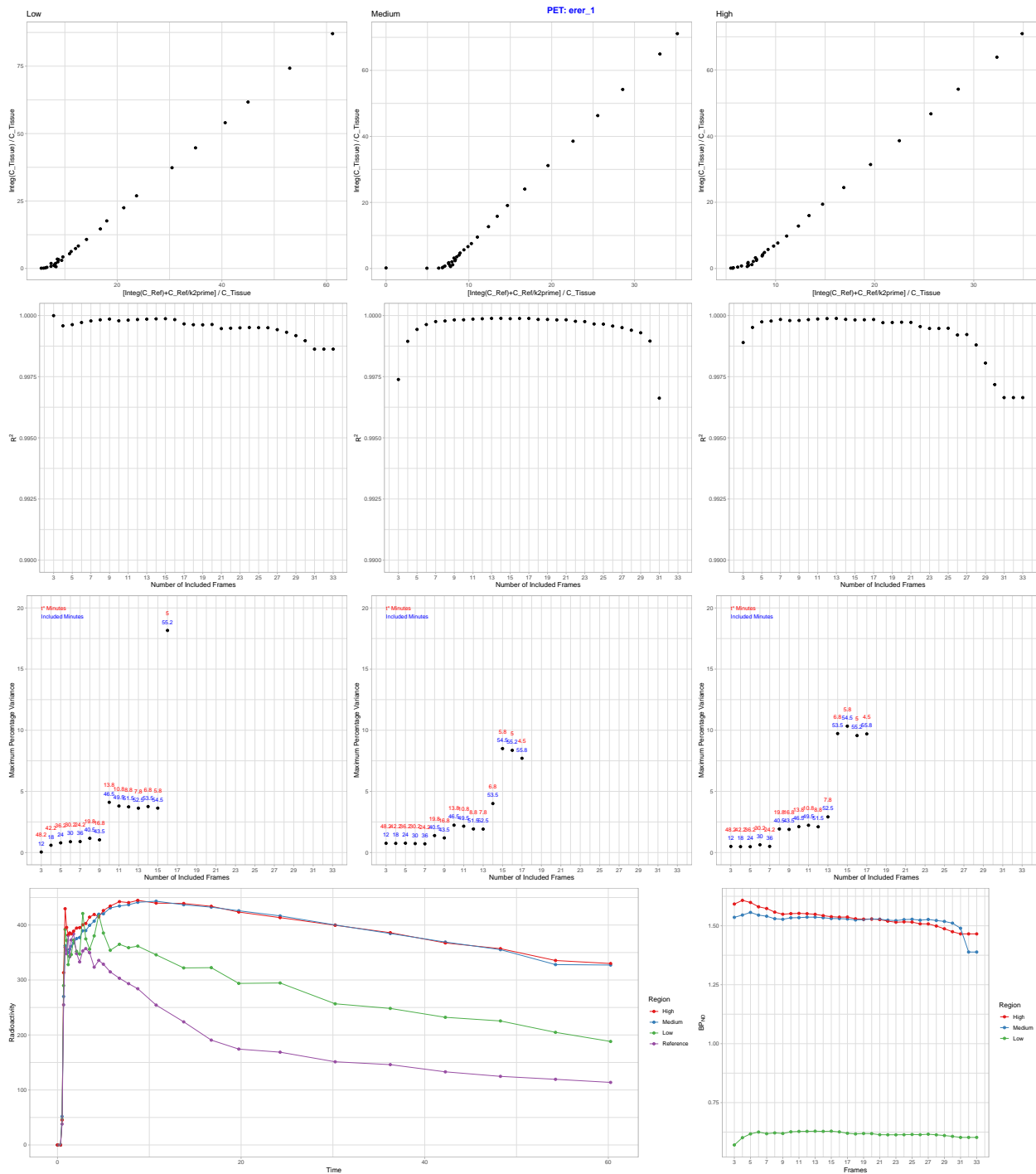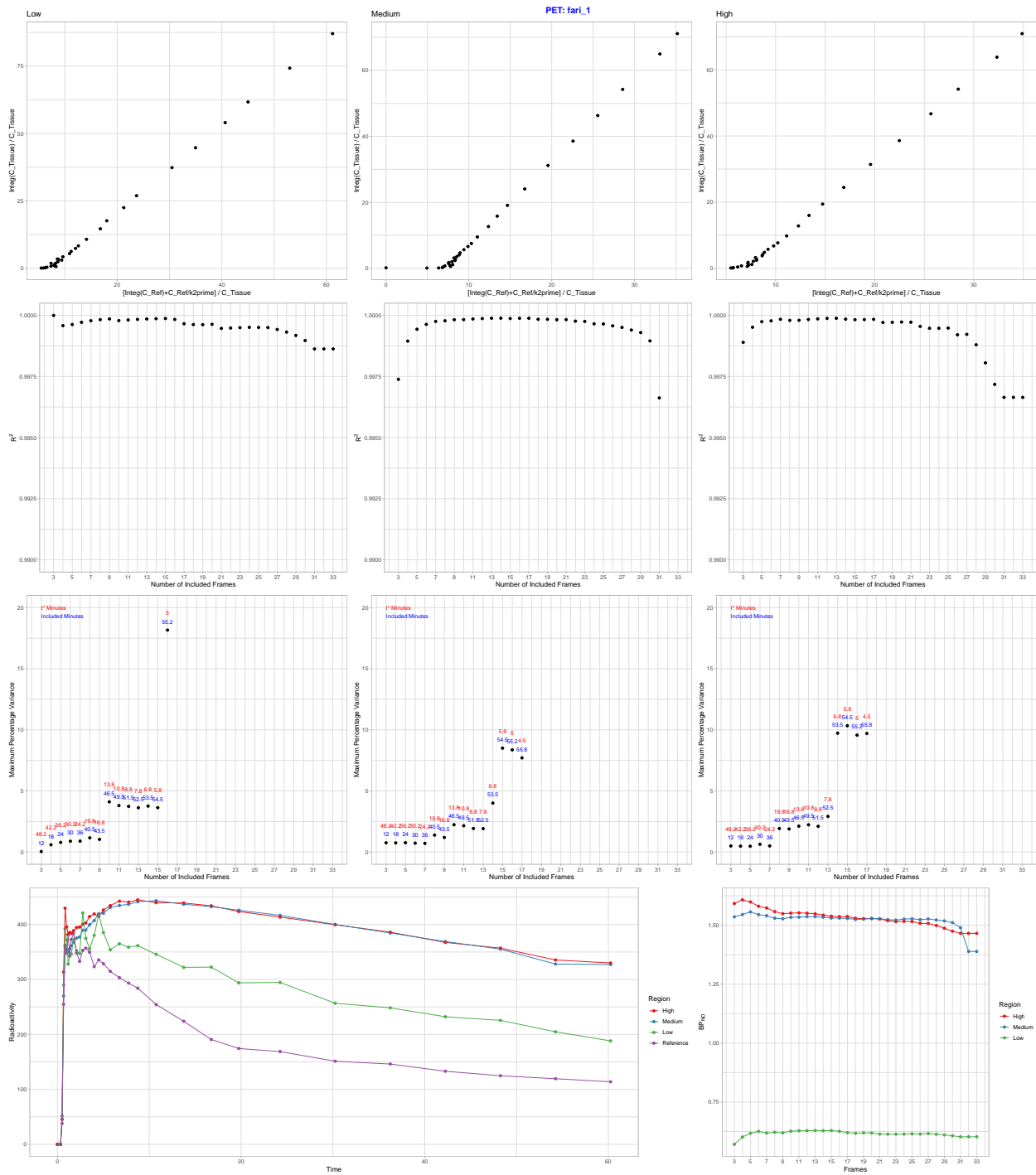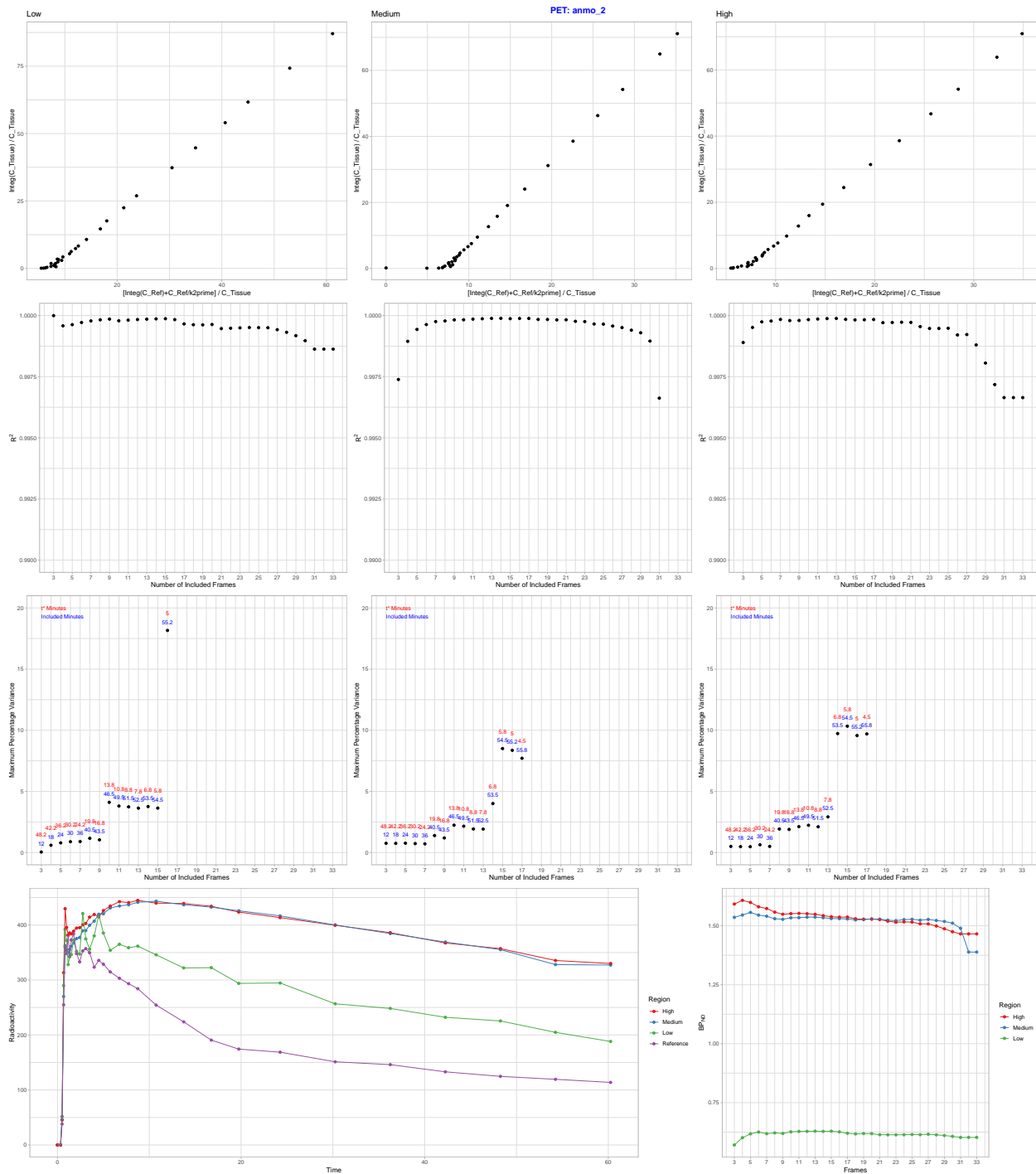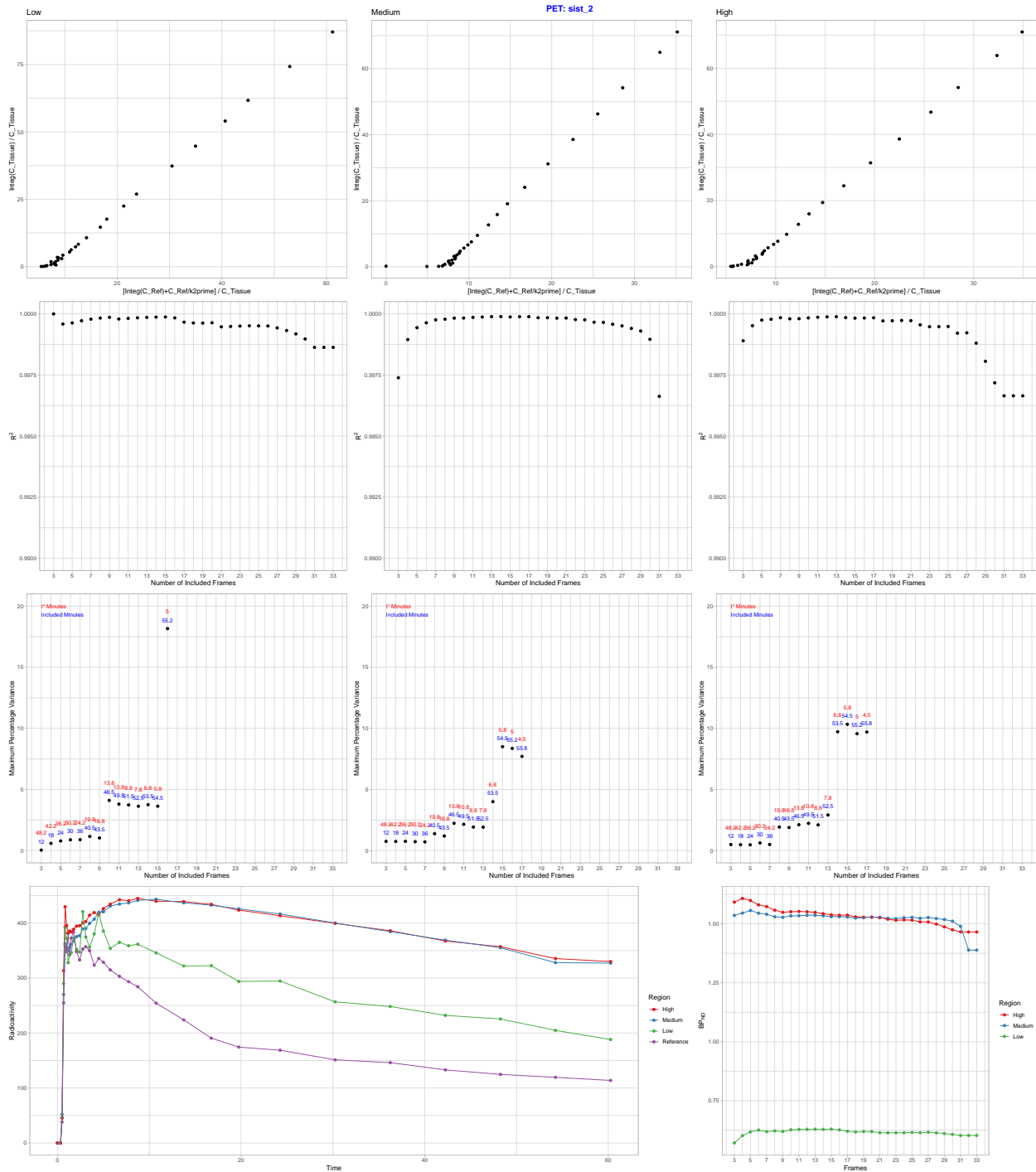
All 4 tstar plots on a single page

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$logan_tstar, ncol = 1, nrow = 4, labels = paste('PET:',tstar_fits$PET),
  #draw_figure_label("t*", position = "top", fontface = "bold", size = 32, colour = "red")
```

#Fitting and plotting Kinetic Model refLogan

Note: no weights are used here!

```
tacs_long <- tacs_long %>%
   group_by(PET, Subjname, PETNo, Region) %>%
  mutate(loganfit = map2(tacdata, k2prime_MRTM1,
          ~refLogan(t_tac = .x$times , reftac = .x$CBL, roitac = .x$TAC, tstarIncludedFrames = 10, k2pri
      mutate(bp_refLogan = map_dbl(loganfit, c("par", "bp"))) %>%
  ungroup()
```

Plot refLogan

```
logan_plot <-tacs_long %>%
 group_by(PET, Region) %>%
  mutate(logan_graph = map2(loganfit, Region,
      ~ plot(.x, roiname = .y))) %>%
  ungroup() %>%
  filter(Region %in% c('FC', 'WB', 'STR', 'OC')) %>%
  select(PET, logan_graph) %>%
  group_by(PET) %>%
  arrange(PET)


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

anmo_1

anmo_2

33

erer_2

41

sist_1

sist_2
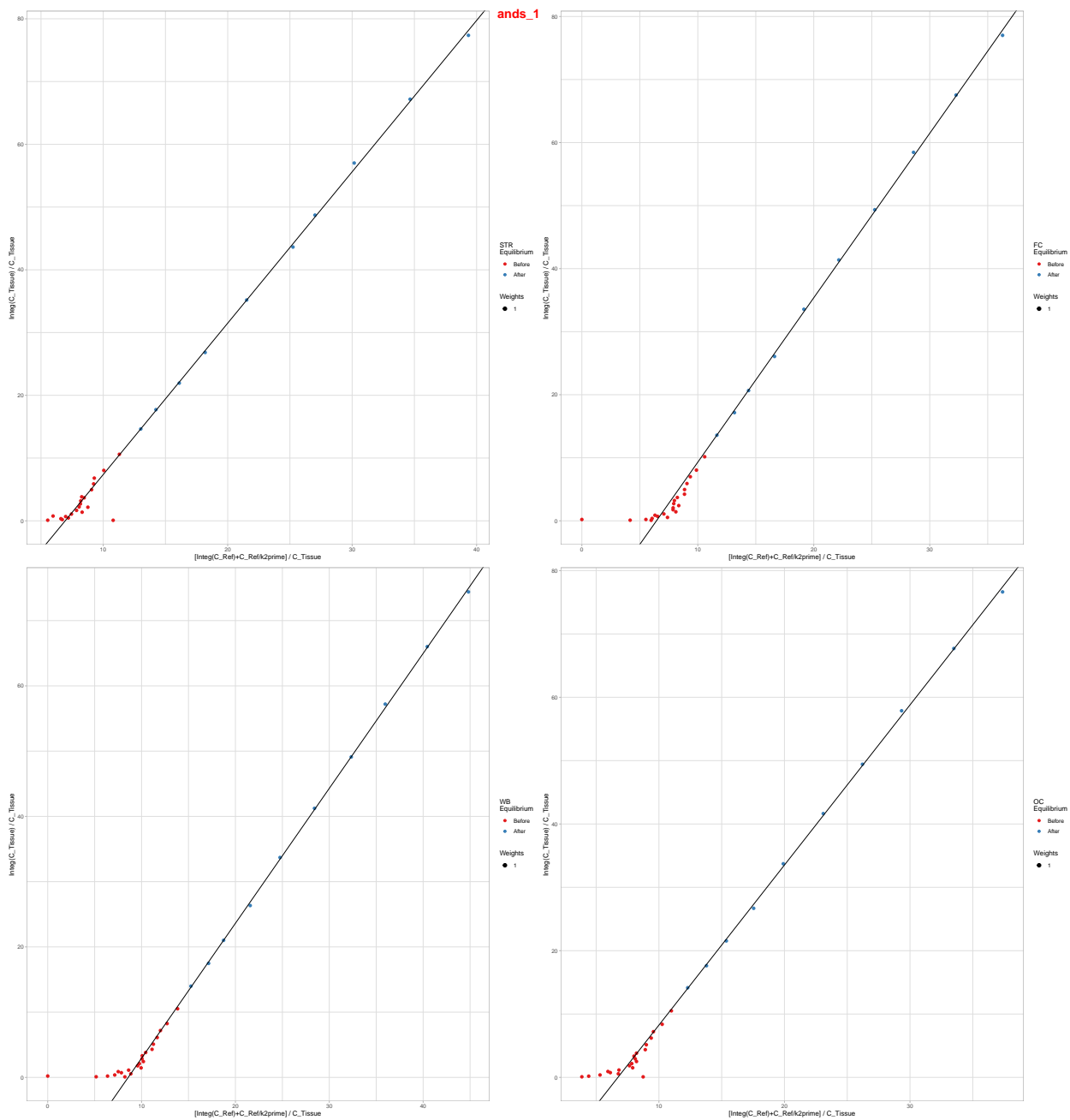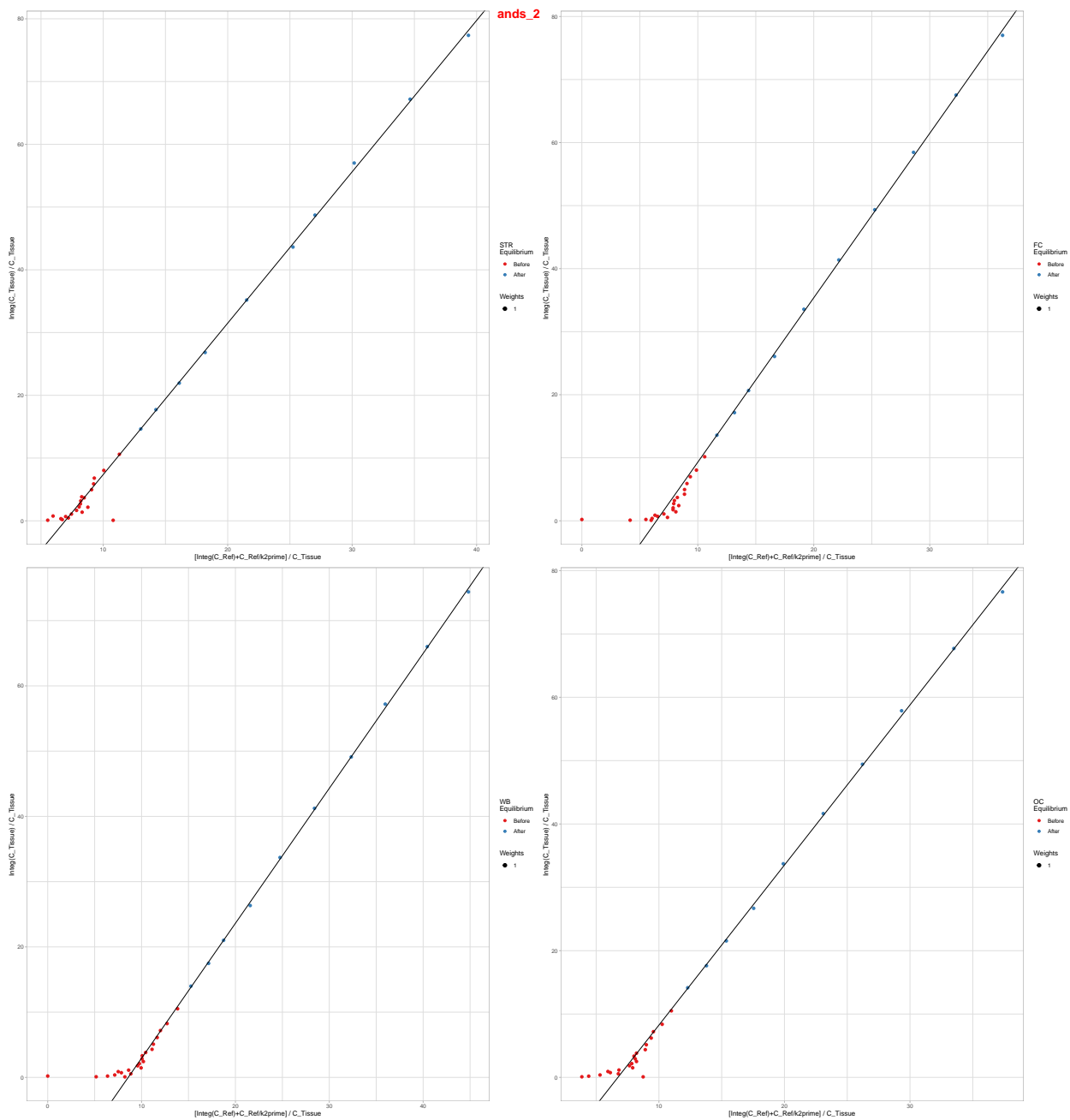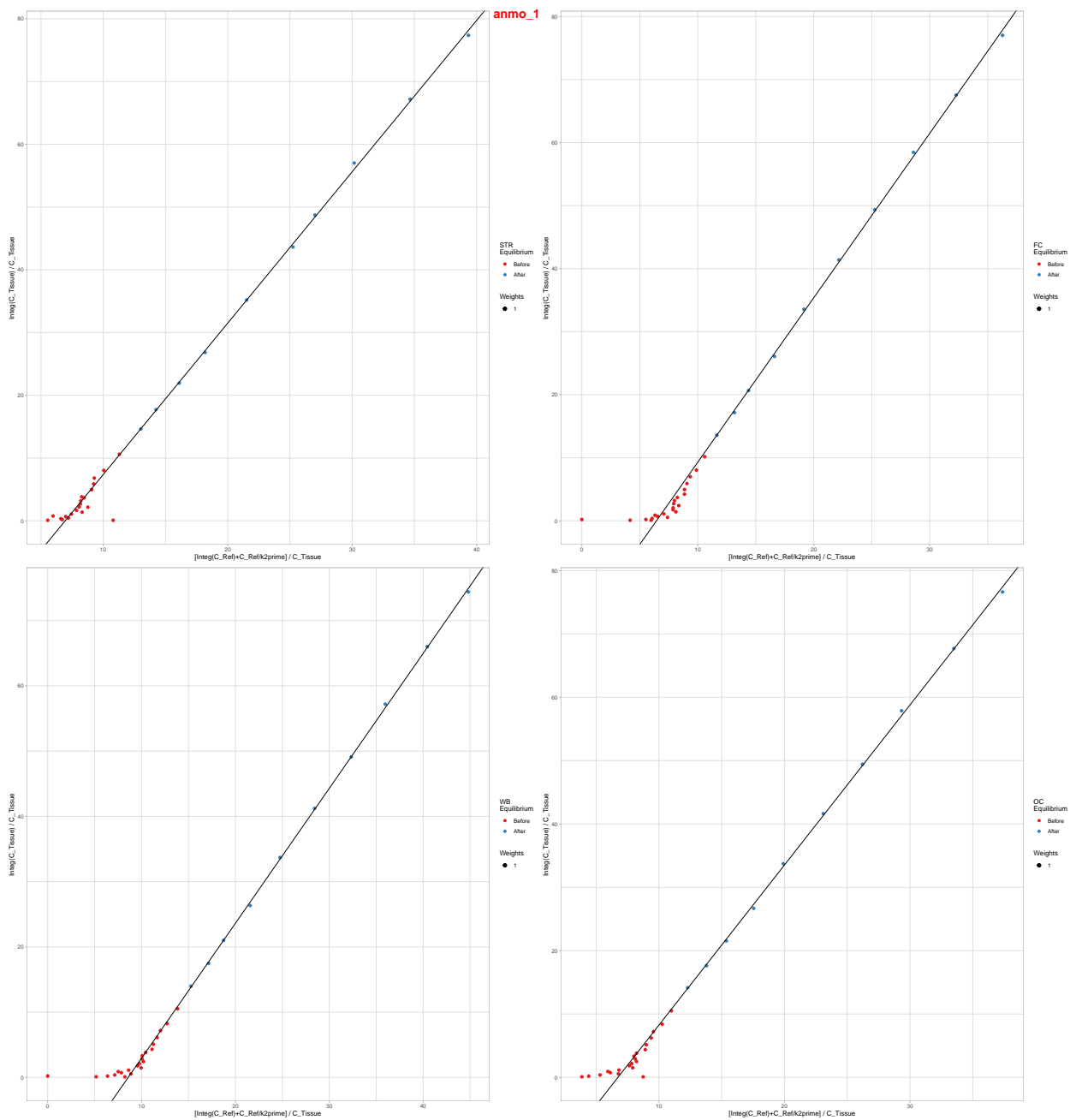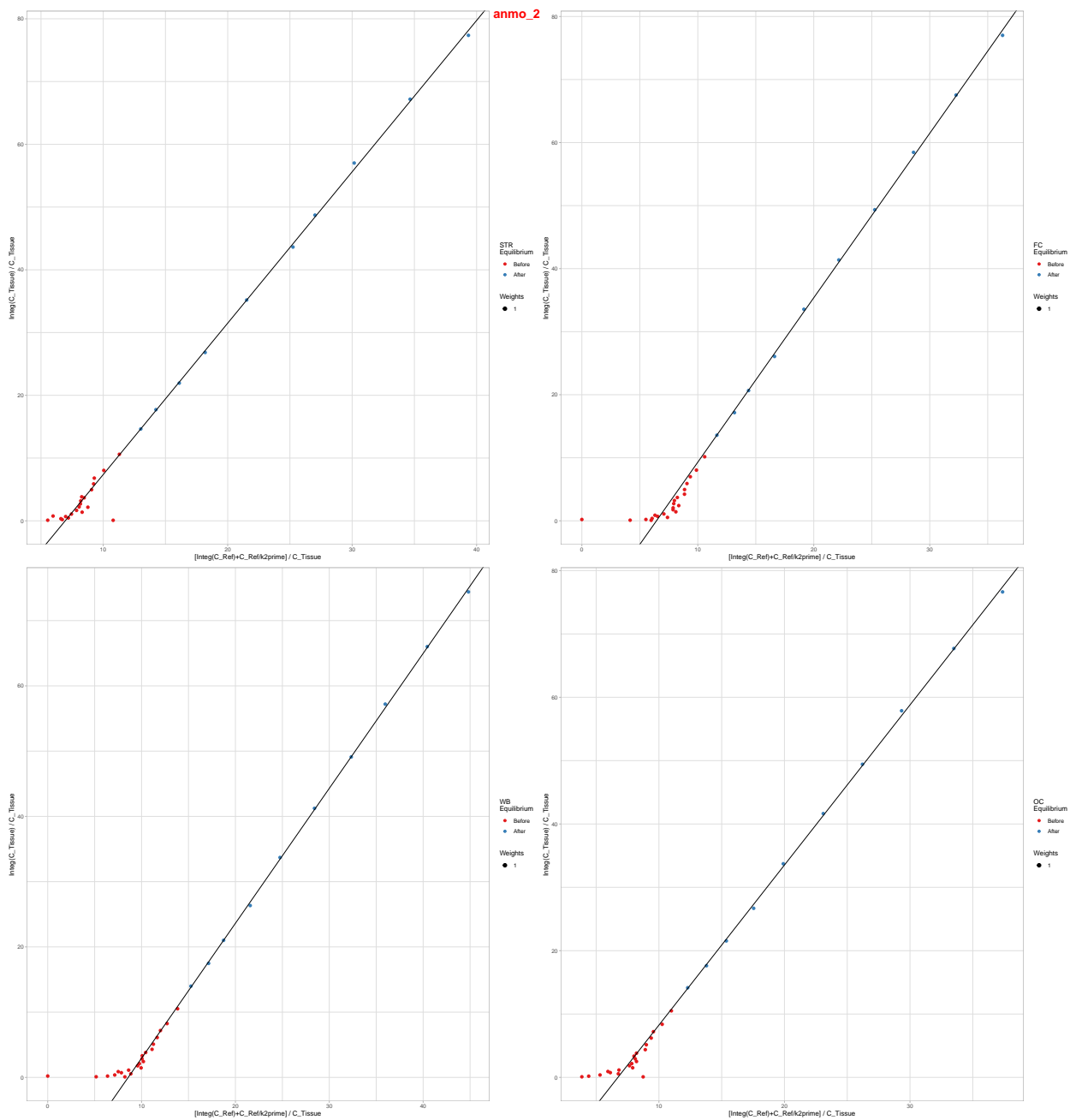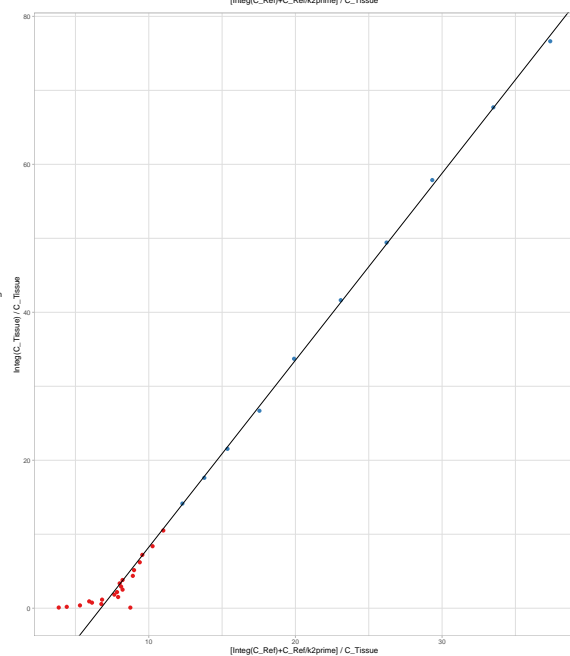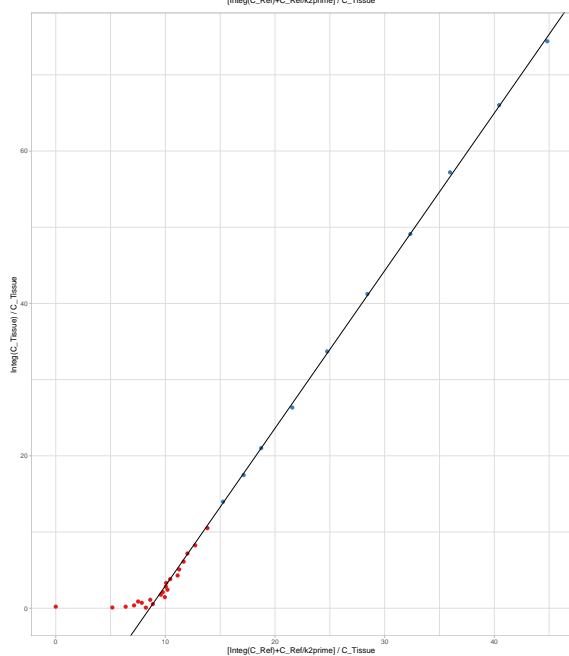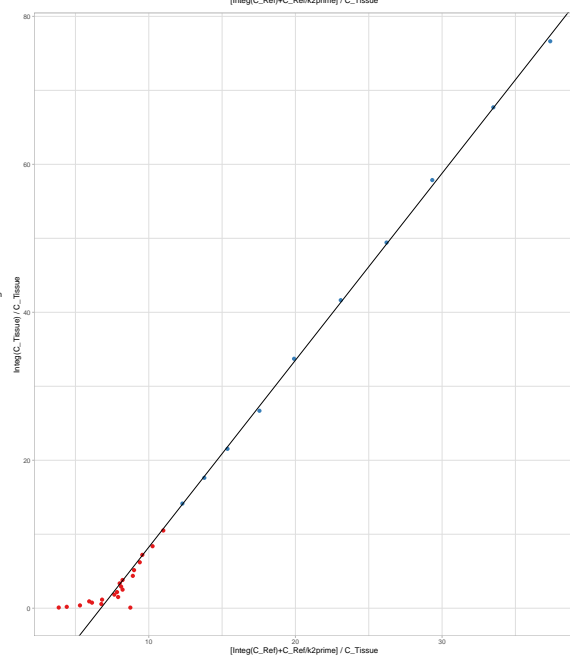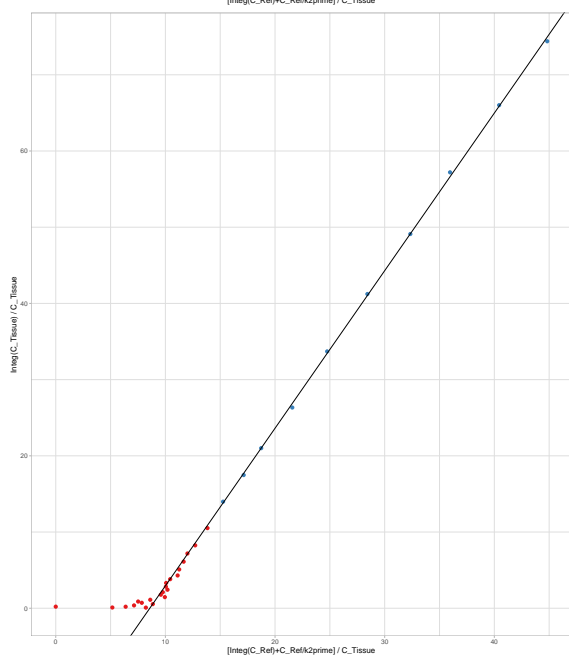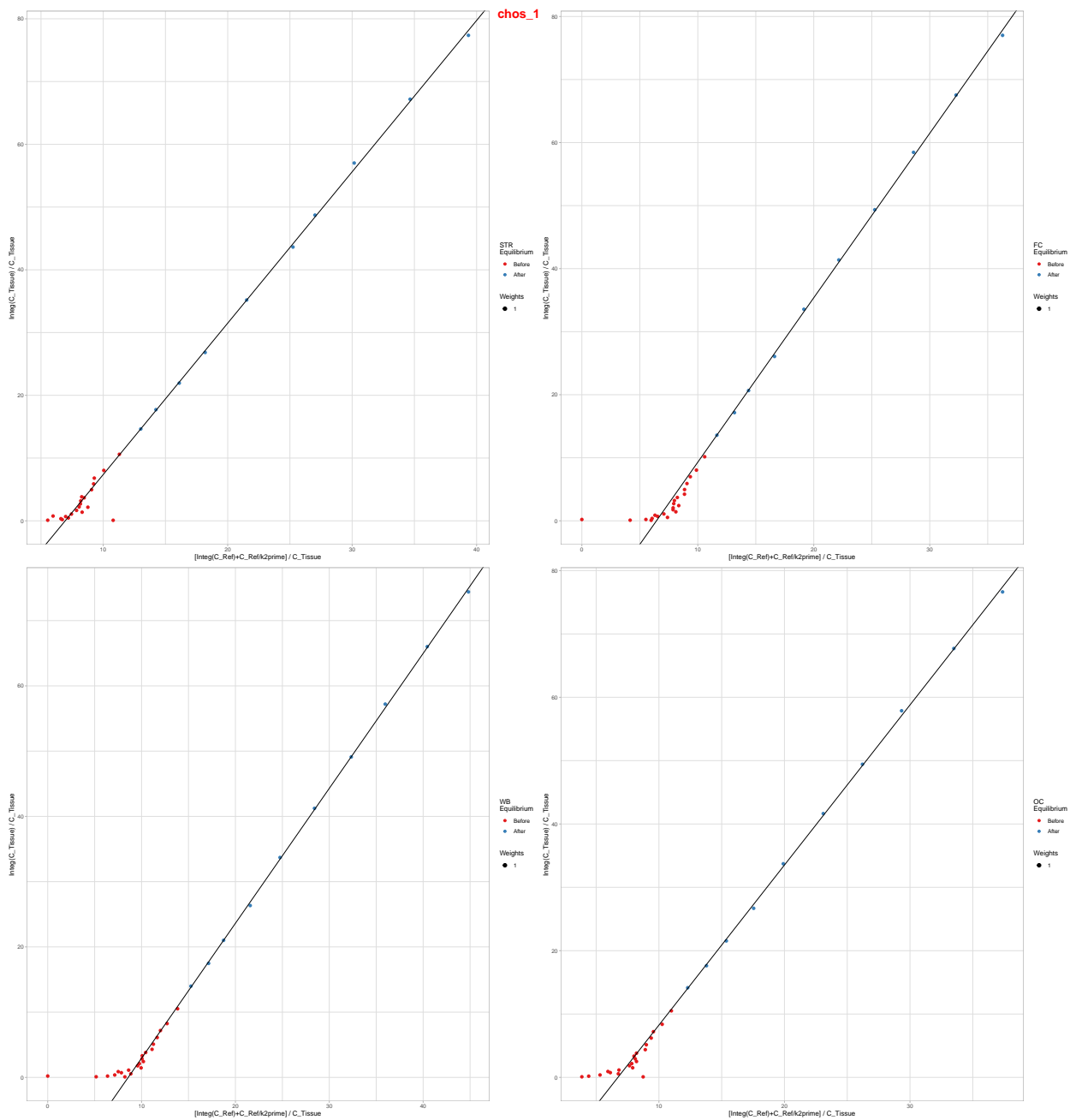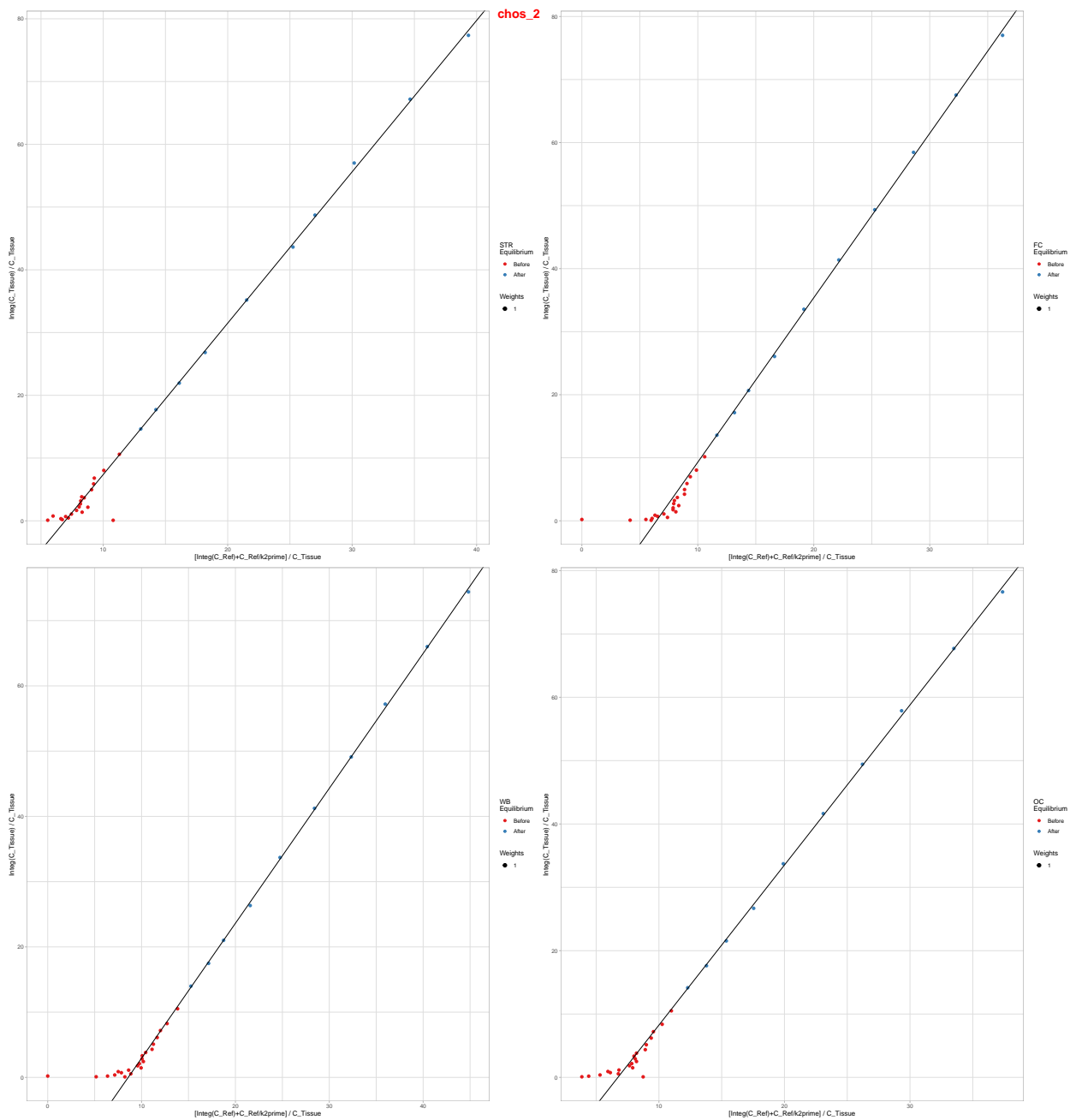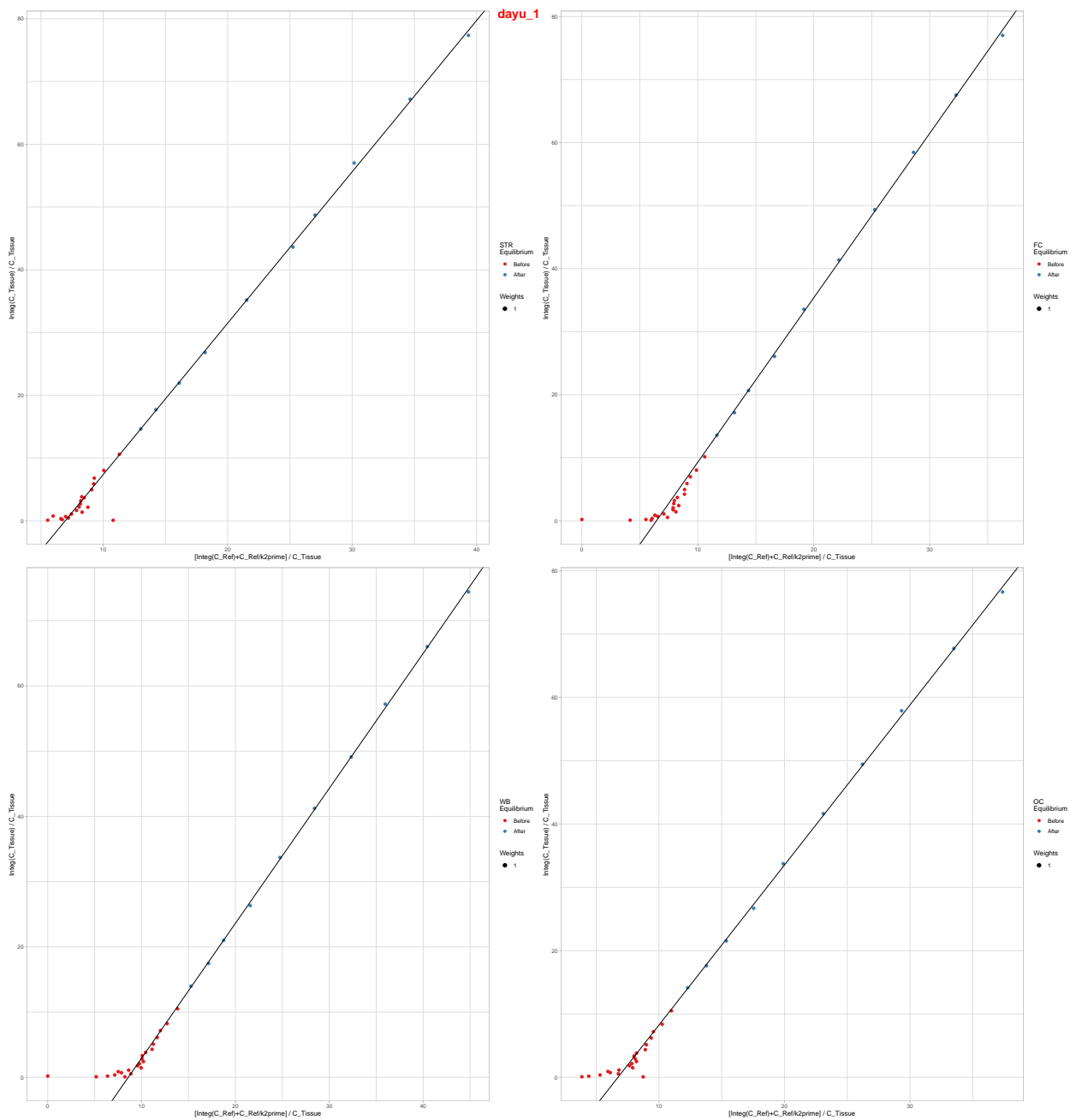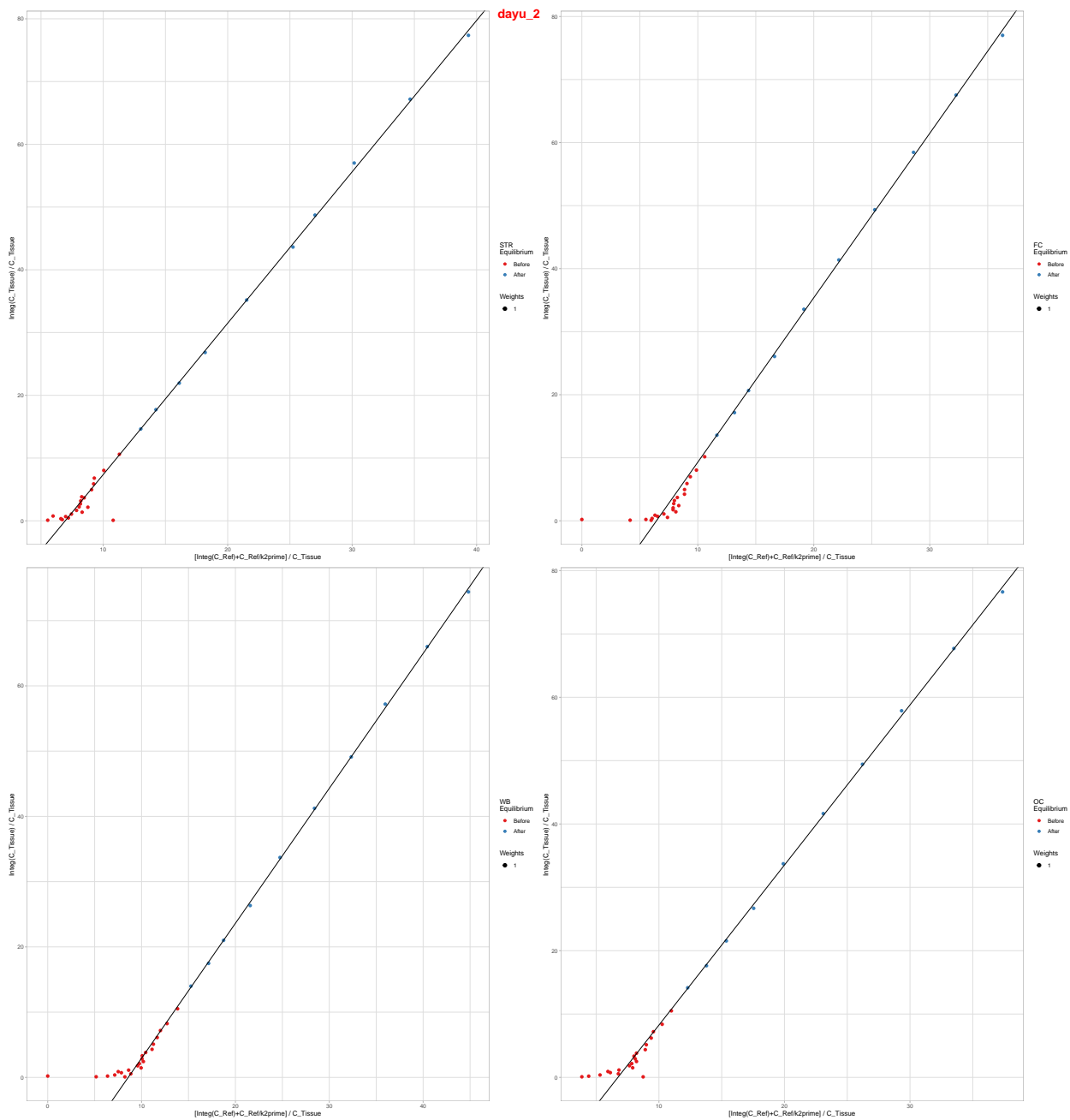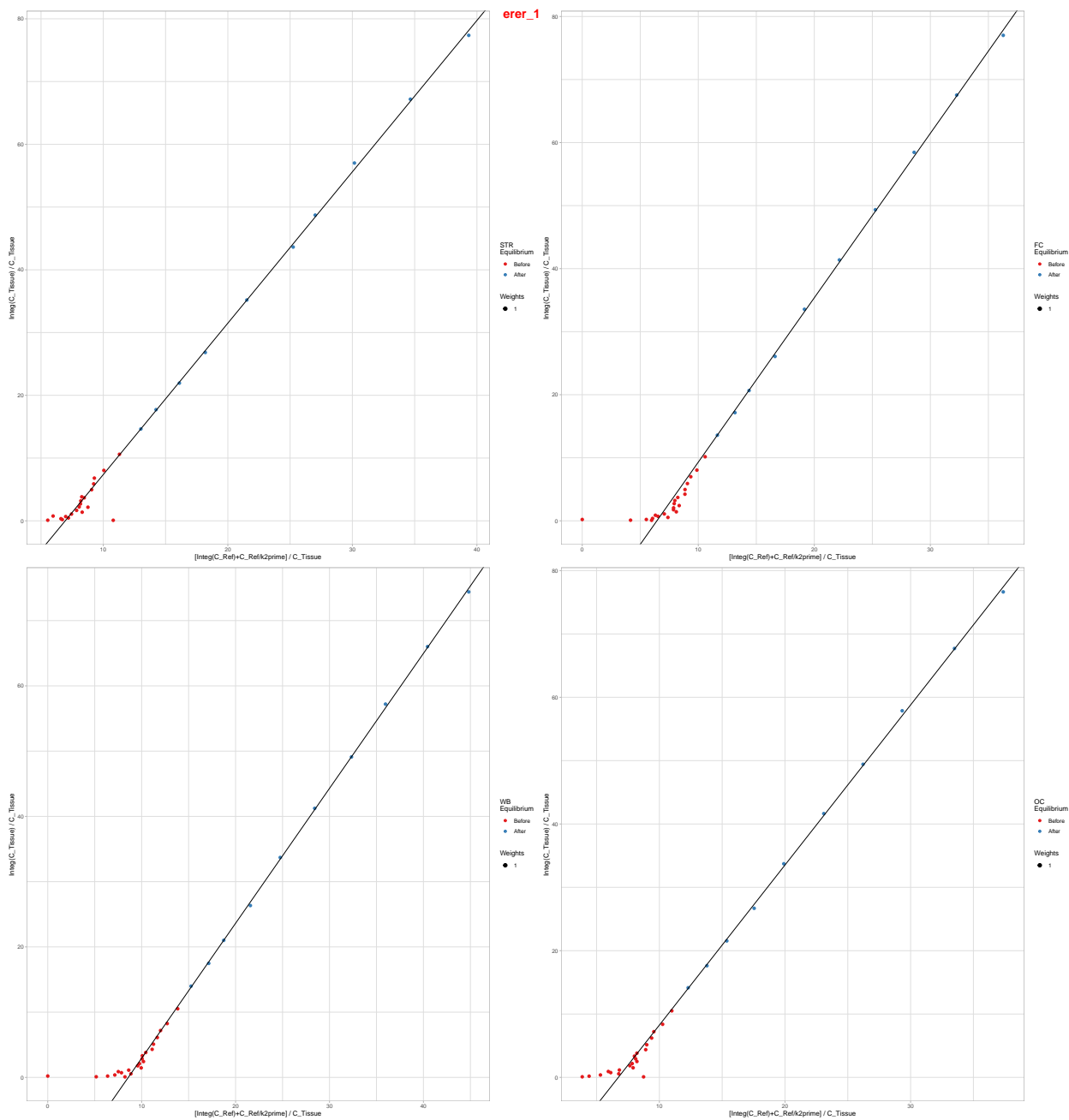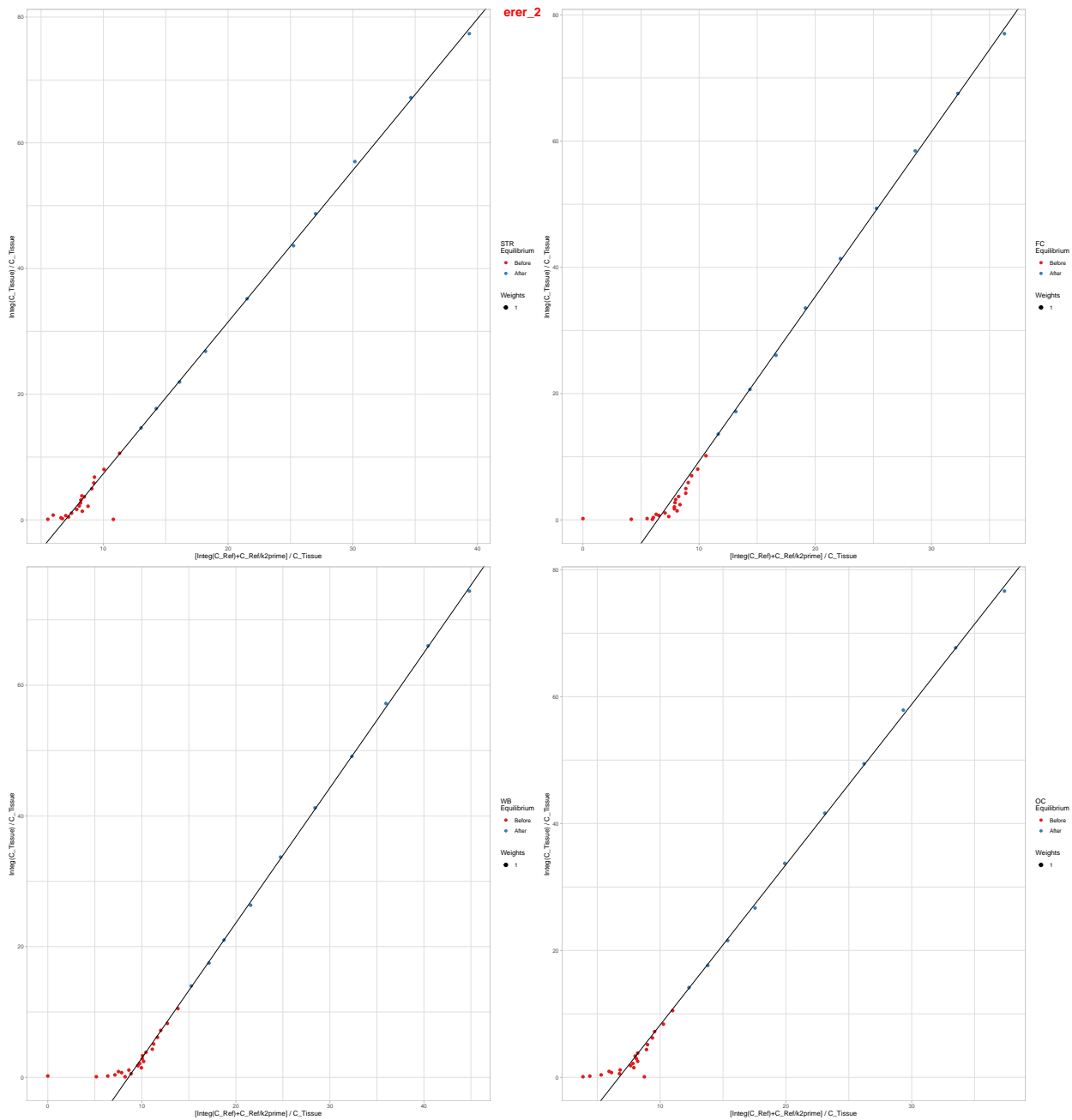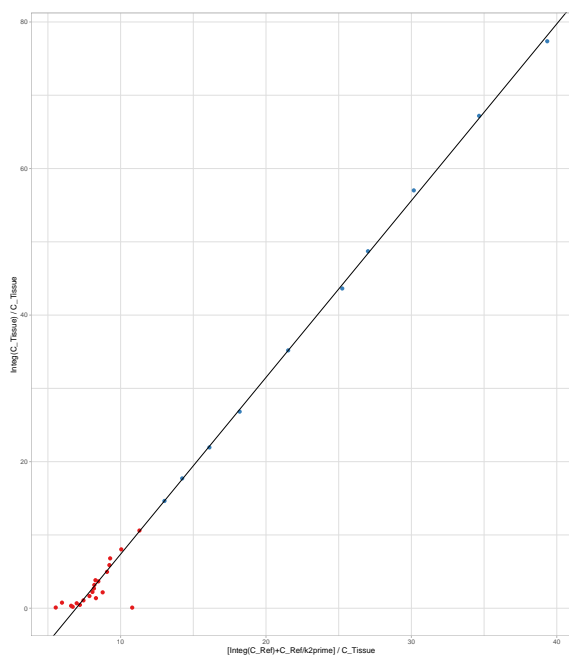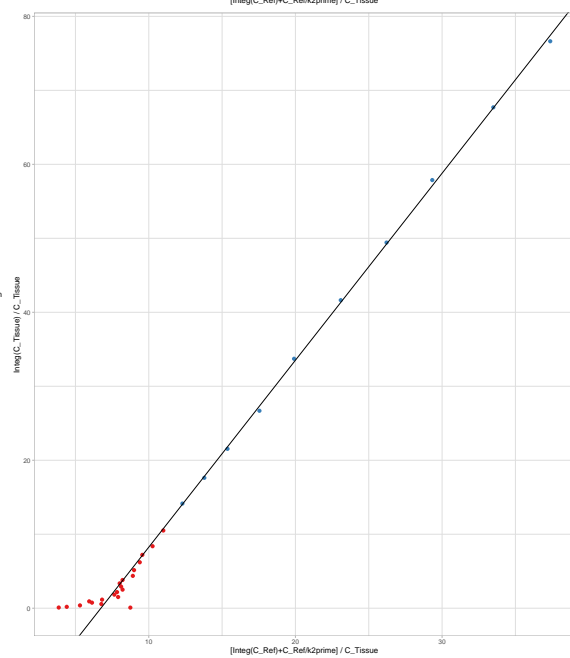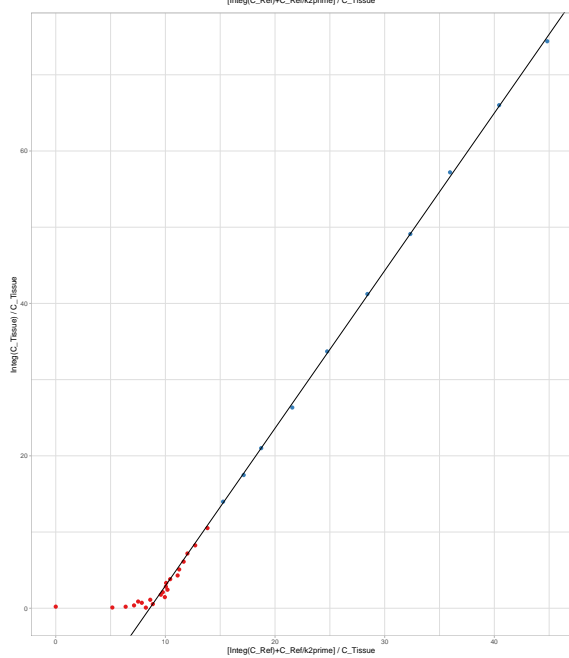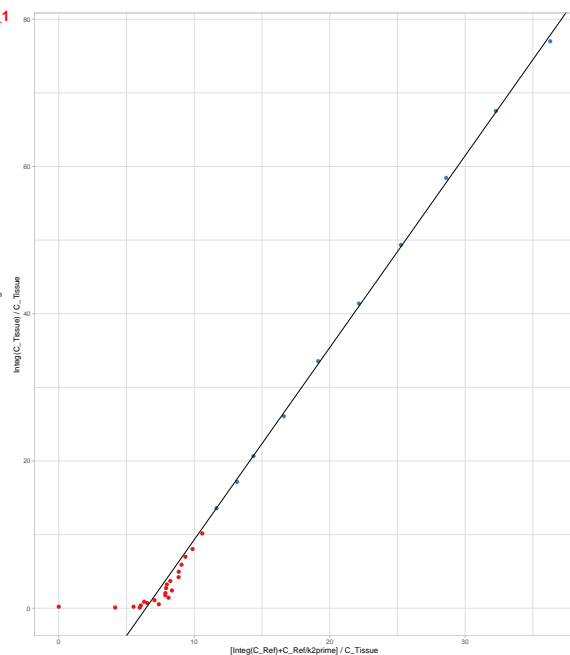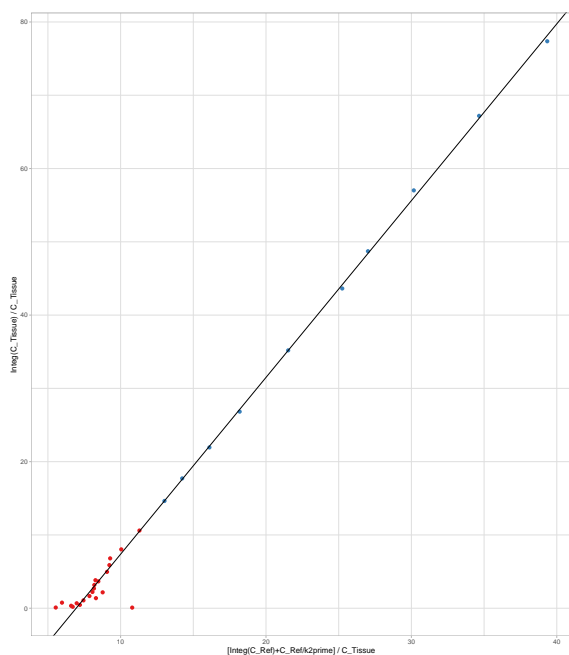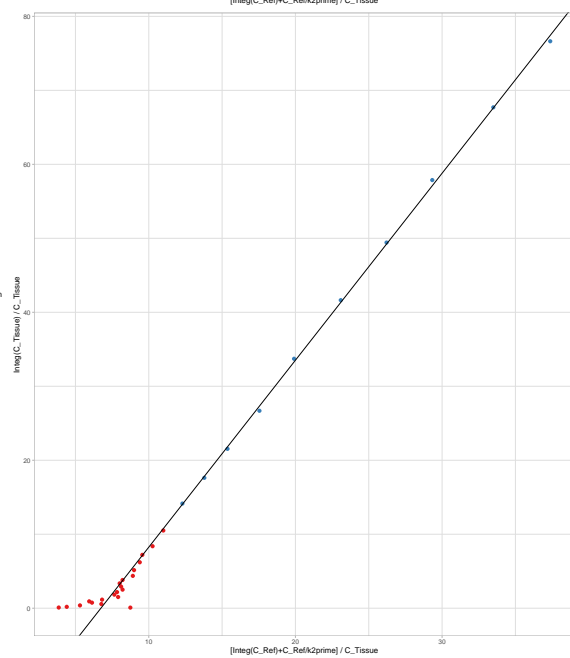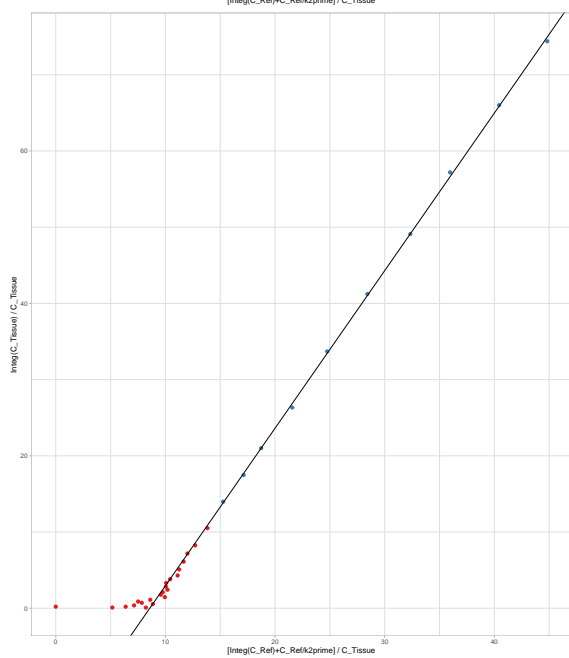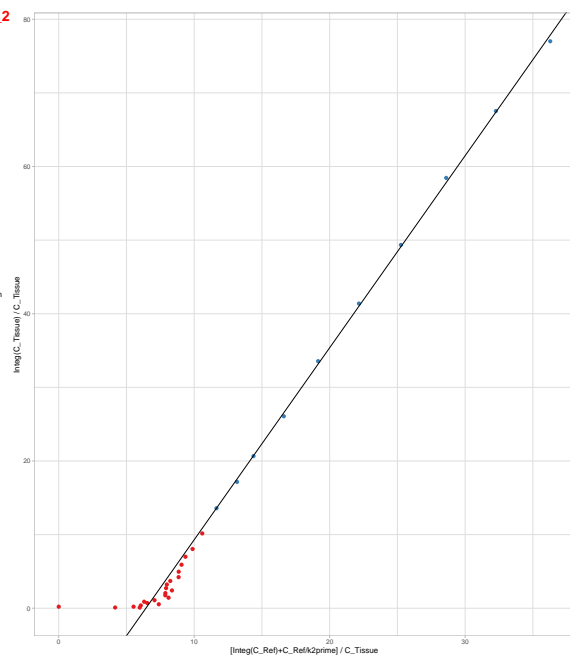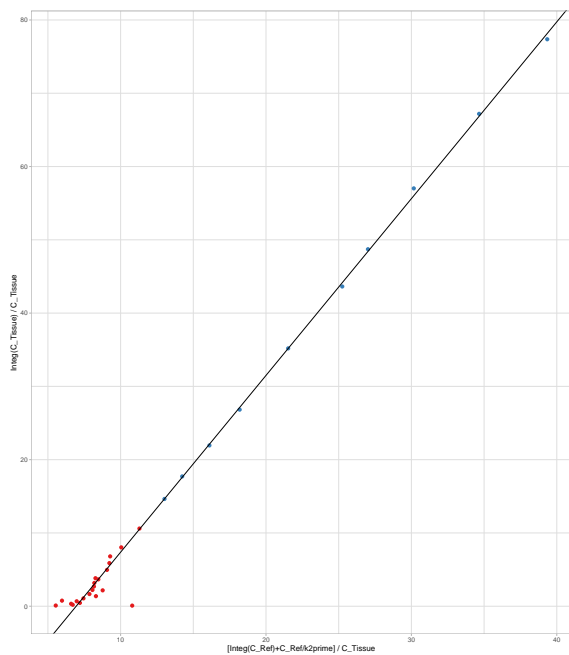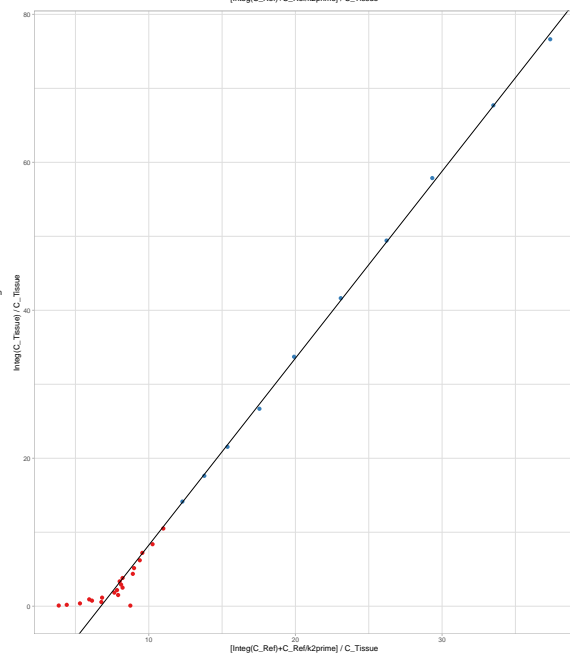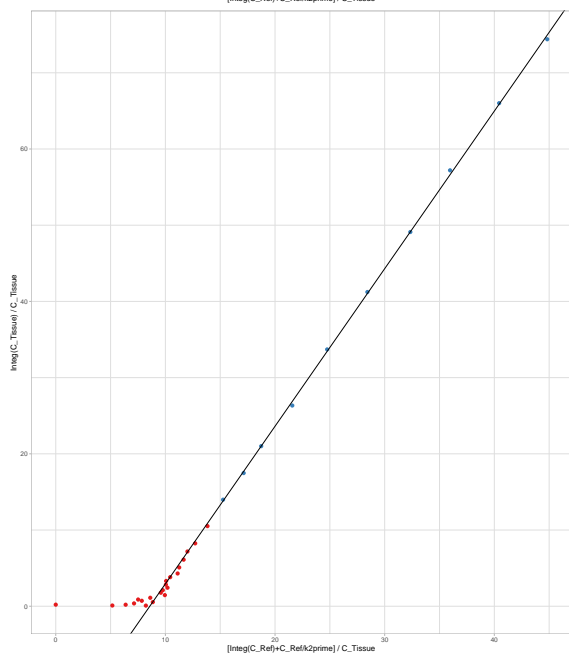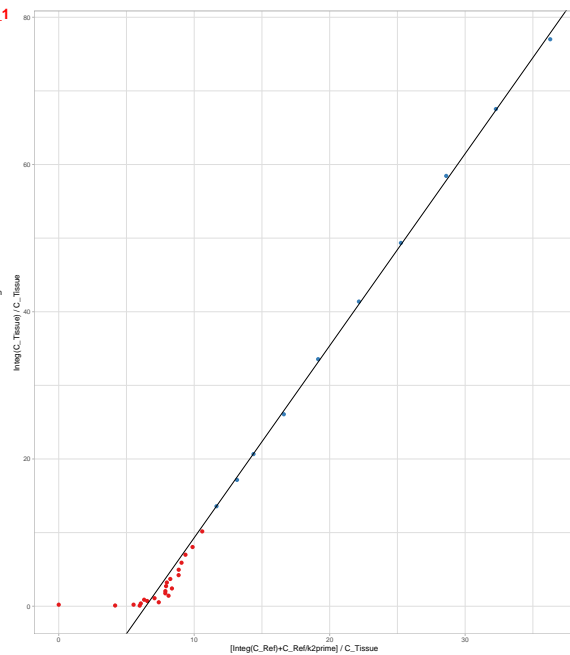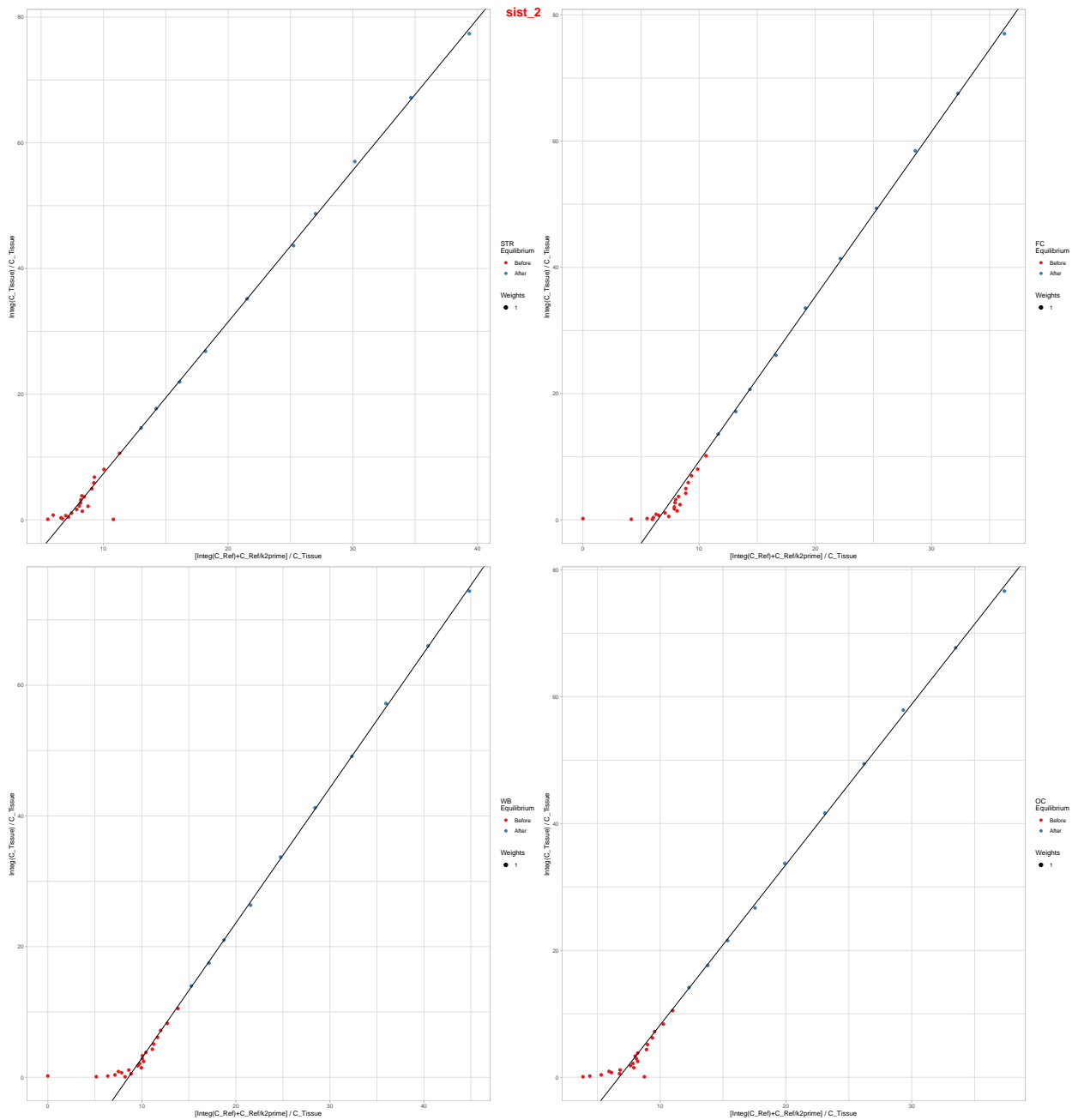
Test-retest

```r
trt_check <- tacs_long %>%
  select(Subjname, PETNo, Region, bp_MRTM2, bp_srtm, bp_refLogan) %>%
  gather(Measure, Value, -Subjname, -PETNo, -Region) %>%
  group_by(Region, Measure) %>%
  nest(.key = "data")

# saveRDS(tacs_long,'../DerivedData/raw_kinfit_AZ10419369.rds')
```

Making the `trt_table`

```
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
STR	bp_MRTM2	1.304	0.158	0.121	0.258	-1.383	0.659	0.066	0.918	0.073	0.264	0.078
FC	bp_MRTM2	1.453	0.133	0.091	-0.087	-0.887	0.237	-0.485	0.777	0.080	0.324	0.075
WB	bp_MRTM2	0.957	0.094	0.098	-0.086	-1.014	0.281	-0.389	0.789	0.085	0.224	0.071
WM	bp_MRTM2	0.164	0.131	0.802	0.034	-1.222	0.526	-0.130	0.878	0.567	0.257	0.509
GM	bp_MRTM2	1.122	0.096	0.085	0.219	-0.909	0.300	-0.384	0.799	0.073	0.226	0.058
OC	bp_MRTM2	1.423	0.117	0.082	-0.476	-0.955	0.520	-0.137	0.877	0.059	0.231	0.047
insula	bp_MRTM2	1.416	0.123	0.087	-0.395	-1.033	0.307	-0.304	0.793	0.075	0.295	0.074
Putamen	bp_MRTM2	1.407	0.138	0.098	-0.059	-1.245	0.504	-0.148	0.871	0.071	0.277	0.073
Caudate	bp_MRTM2	0.866	0.145	0.167	0.262	-1.429	0.632	0.021	0.911	0.106	0.254	0.118
THA	bp_MRTM2	0.551	0.071	0.129	0.219	-1.728	0.453	-0.133	0.852	0.106	0.161	0.122
TC	bp_MRTM2	1.107	0.094	0.085	-0.210	-0.883	0.171	-0.499	0.744	0.078	0.240	0.060
STR	bp_srtm	1.306	0.159	0.122	0.239	-1.455	0.666	0.078	0.920	0.073	0.263	0.078
FC	bp_srtm	1.513	0.132	0.087	-0.284	-0.608	0.345	-0.386	0.820	0.071	0.299	0.069
WB	bp_srtm	1.065	0.094	0.088	-0.390	-0.559	0.339	-0.392	0.818	0.073	0.214	0.069
WM	bp_srtm	0.394	0.182	0.462	-0.279	-1.344	0.430	-0.294	0.850	0.354	0.387	0.425
GM	bp_srtm	1.227	0.098	0.080	-0.268	-0.831	0.373	-0.357	0.830	0.064	0.217	0.057
OC	bp_srtm	1.595	0.171	0.107	0.414	0.254	0.666	0.046	0.921	0.063	0.281	0.059
insula	bp_srtm	1.484	0.120	0.081	-0.493	-0.543	0.439	-0.267	0.852	0.062	0.253	0.057
Putamen	bp_srtm	1.437	0.137	0.095	-0.106	-1.321	0.457	-0.227	0.857	0.072	0.286	0.069
Caudate	bp_srtm	0.876	0.149	0.170	0.093	-1.486	0.598	-0.015	0.900	0.113	0.274	0.126
THA	bp_srtm	0.611	0.084	0.138	0.632	-0.916	0.294	-0.182	0.765	0.127	0.214	0.131
TC	bp_srtm	1.215	0.108	0.089	-0.410	-0.437	0.414	-0.312	0.845	0.069	0.232	0.066
STR	bp_refLogan	1.317	0.152	0.115	0.236	-1.494	0.656	0.063	0.917	0.070	0.255	0.078
FC	bp_refLogan	1.462	0.127	0.087	-0.203	-0.579	0.334	-0.397	0.816	0.072	0.291	0.074
WB	bp_refLogan	0.995	0.091	0.091	-0.021	-0.443	0.392	-0.336	0.837	0.072	0.199	0.064
WM	bp_refLogan	0.230	0.137	0.597	0.102	-1.039	0.631	-0.015	0.912	0.370	0.236	0.518
GM	bp_refLogan	1.151	0.094	0.082	0.136	-0.557	0.382	-0.347	0.833	0.065	0.207	0.058
OC	bp_refLogan	1.450	0.117	0.081	-0.549	-0.787	0.607	-0.054	0.905	0.052	0.208	0.048
insula	bp_refLogan	1.424	0.116	0.081	-0.360	-0.597	0.410	-0.270	0.840	0.064	0.252	0.062
Putamen	bp_refLogan	1.442	0.129	0.089	-0.180	-1.307	0.483	-0.172	0.864	0.066	0.264	0.067
Caudate	bp_refLogan	0.869	0.147	0.169	0.126	-1.507	0.640	0.037	0.913	0.105	0.254	0.120
THA	bp_refLogan	0.568	0.077	0.136	0.376	-1.435	0.375	-0.149	0.811	0.119	0.187	0.133
TC	bp_refLogan	1.124	0.095	0.084	-0.521	-0.361	0.299	-0.431	0.802	0.071	0.222	0.065

Interregional Correlation

Here the interregional correlations for BP values

```r
bp_srtm <- tacs_long %>%
  select(PET, Region, bp_srtm) %>%
  spread(Region, bp_srtm)

bp_mrtm2 <- tacs_long %>%
  select(PET, Region, bp_MRTM2) %>%
  spread(Region, bp_MRTM2)

bp_logan <- tacs_long %>%
  select(PET, Region, bp_refLogan) %>%
  spread(Region, bp_refLogan)

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

par(mfrow=c(2,2))

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

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

bp_mrtm2 %>%
  select(FC:WM, - Putamen) %>%
  cor() %>%
  corrplot.mixed(lower='ellipse', upper='number',
                 lower.col = col2(200), upper.col = col2(200),  diag='n',
                 number.digits = 2, title=expression(bp_MRTM2 ~ Correlations),
                 mar=c(0,0,1,0))
```

bp_srtm Correlations

bp_logan Correlations

bp_MRTM2 Correlations
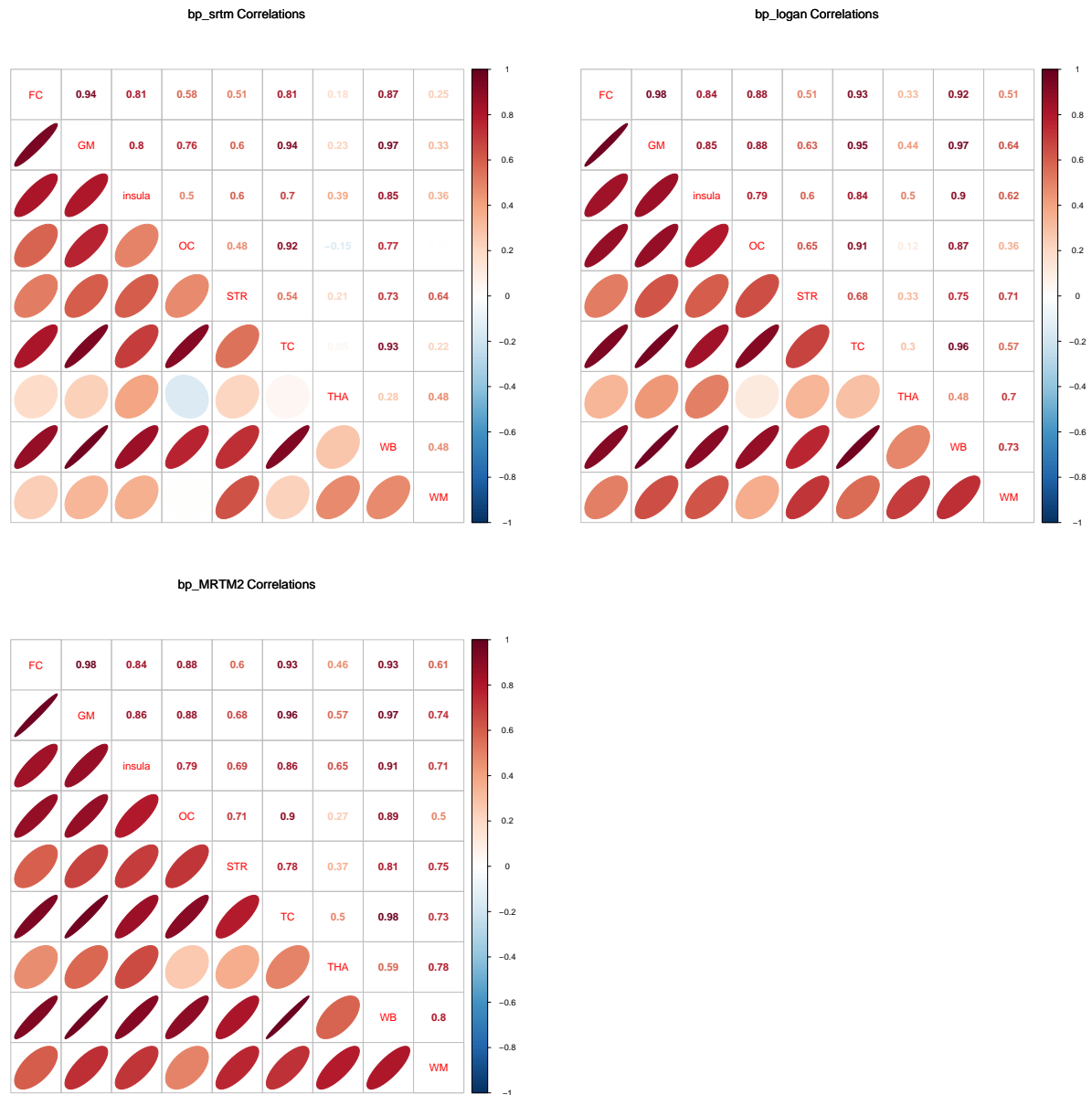
#Corrplot between measures for a single region

```
compare <- tacs_long %>%
  select(PET, Region, bp_srtm, bp_refLogan ,bp_MRTM2 ) %>%
  filter(Region %in% c('FC', 'WB', 'insula', 'OC'))

par(mfrow=c(2,2))

compare %>%
  filter(Region == "FC") %>%
  select(bp_srtm:bp_MRTM2) %>%
  cor() %>%
  corrplot.mixed(lower='ellipse', upper='number',
                 lower.col = col2(200), upper.col = col2(200),  diag='n',
```

```r
                  number.digits = 2, title=expression(Model ~ Correlations ~ Region: FC),
                  mar=c(0,0,1,0))

compare %>%
  filter(Region == "OC") %>%
  select(bp_srtm:bp_MRTM2) %>%
  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 == "insula") %>%
  select(bp_srtm:bp_MRTM2) %>%
  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: insula),
                  mar=c(0,0,1,0))

compare %>%
  filter(Region == "WB") %>%
  select(bp_srtm:bp_MRTM2) %>%
  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
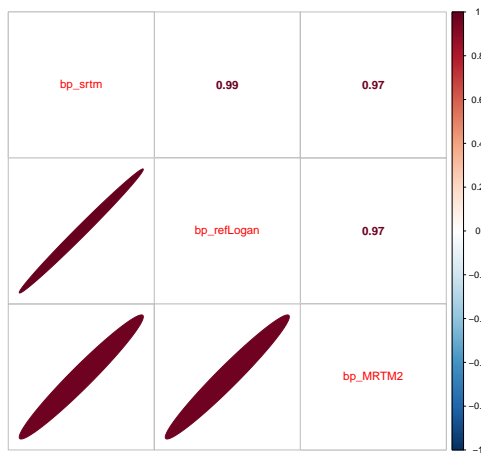
Model Correlations Region : OC
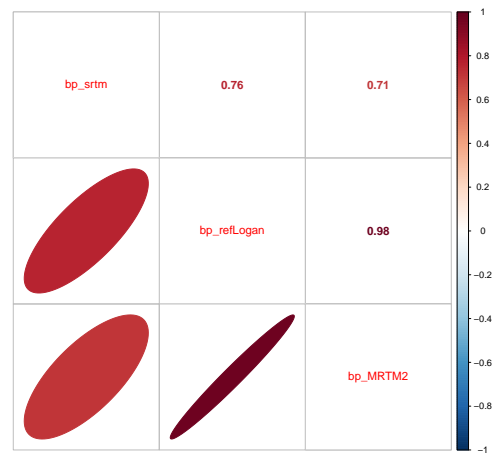
Model Correlations Region : insula
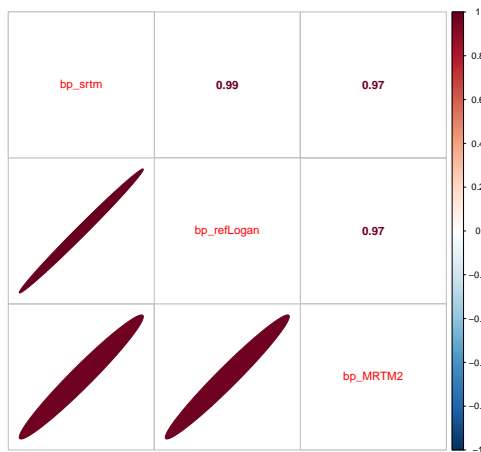
Model Correlations Region : WB
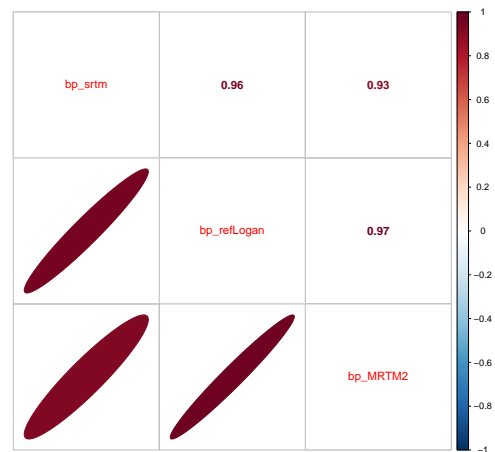
bp corellation

R-squared

```
trtdata <- tacs_long %>%
  select(PET, Subjname, PETNo, Region, bp_refLogan, bp_srtm, bp_MRTM2) %>%
  gather(Measure, Value, -(PET:Region)) %>%
  spread(Region, Value)

trtdata <- trtdata %>%
  select( -(c(Caudate, Putamen, insula))) %>%
  gather(Region, Value, -(PET:Measure)) %>%
  unite(Outcome, Measure, Region) %>%
```

```
  spread(Outcome, Value)

corout <- trtdata %>%
  gather(Measure, Binding, -(PET:PETNo), -bp_srtm_WB) %>%
  group_by(Measure) %>%
  summarise('R^2^'=cor(Binding, bp_srtm_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='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$_{\mathrm{WB}}$}

Measure	R^2^
bp~MRTM2_FC~	0.70
bp~MRTM2_GM~	0.77
bp~MRTM2_OC~	0.75
bp~MRTM2_STR~	0.54
bp~MRTM2_TC	0.90
bp~MRTM2_THA	0.17
bp~MRTM2_WB~	0.86
bp~MRTM2_WM~	0.43
bp~refLogan_FC~	0.74
bp~refLogan_GM~	0.84
bp~refLogan_OC~	0.77
bp~refLogan_STR~	0.52
bp~refLogan_TC	0.92
bp~refLogan_THA	0.13
bp~refLogan_WB~	0.91
bp~refLogan_WM~	0.39
bp~srtm_FC~	0.76
bp~srtm_GM~	0.93
bp~srtm_OC~	0.59
bp~srtm_STR~	0.54
bp~srtm_TC	0.86
bp~srtm_THA	0.08
bp~srtm_WM~	0.23

\end{table}

#Plot of the change between PETNo = 1 and PETNo = 2. error bars for the wscv probably mean nothing as there is just a single value, but looks nice?

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

```
  unite(outcome, outcome, Measure, sep = '_') %>%
  ungroup()

trtsrtm <- trtdata %>%
  filter(outcome == 'bp_srtm')

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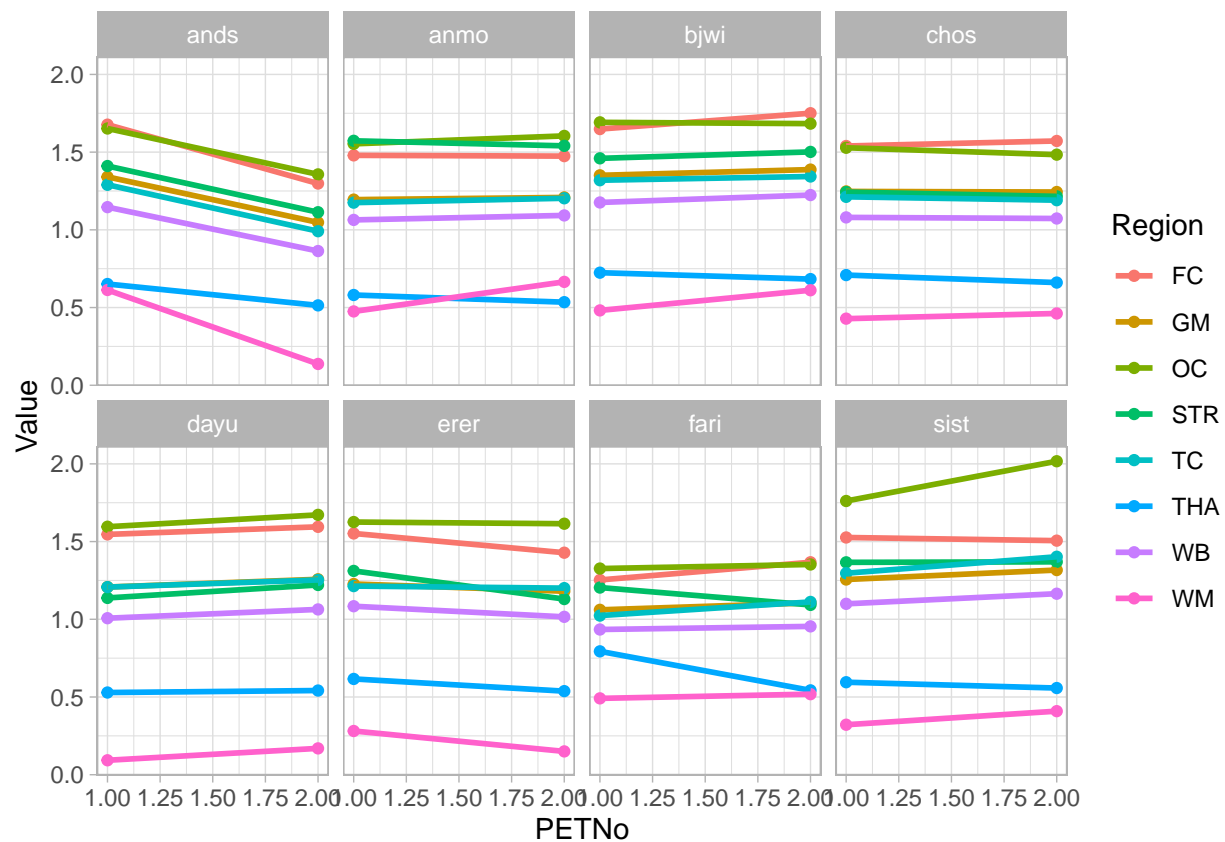


```
#same as above, just made into a variable for plot.grid

q <- ggplot(trtsrtm, aes(x = PETNo, y = Value,
                     group = Region, colour=Region)) +
  geom_point() +
  geom_smooth(method = 'lm', se = FALSE) +
  facet_wrap( ~ Subjname, ncol = 4)

#plot wscv by model

ggplot(trt_table, aes(y = wscv, x = Measure, colour = Region ))+
  geom_point()+
  geom_errorbar(aes(ymin=wscv, ymax=wscv)) +
  facet_grid(Measure~.) + coord_flip()
```
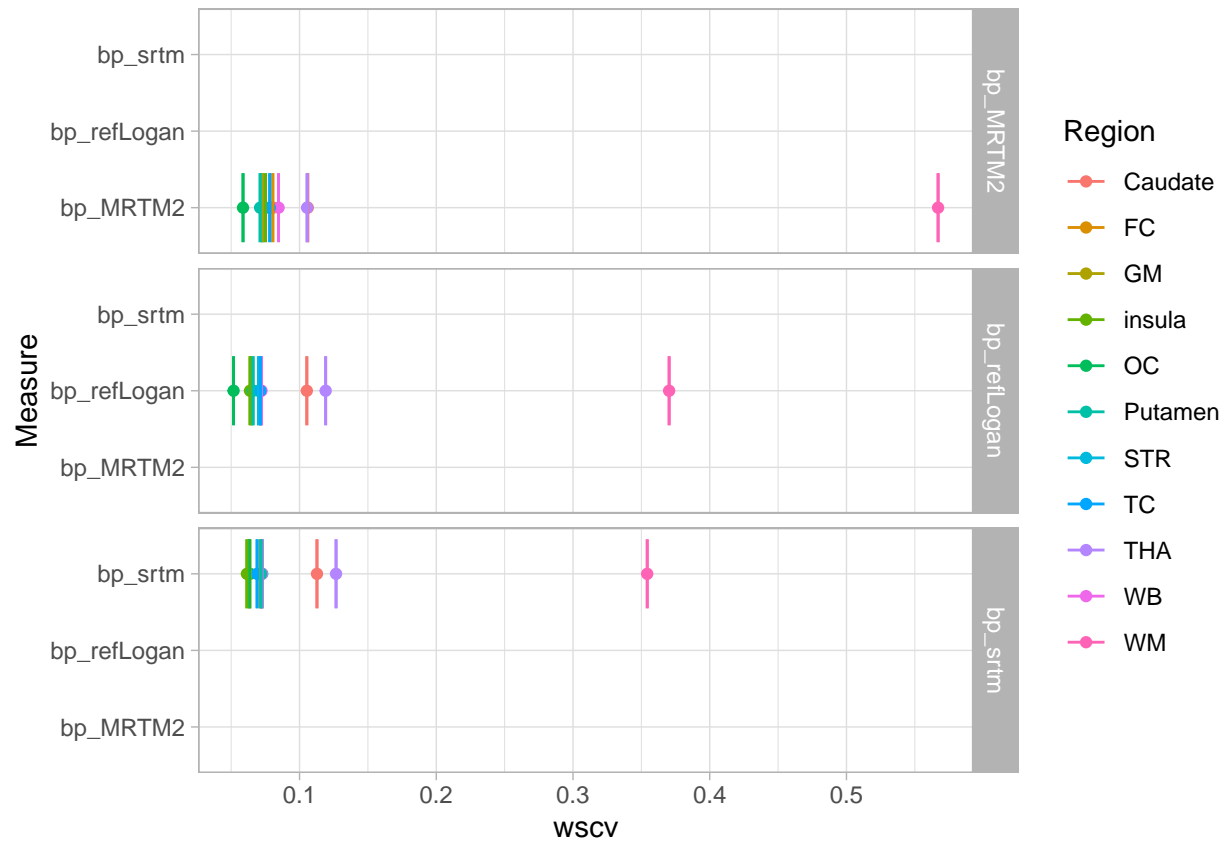
```
srtm_trt_table <-  trt_table %>%
  filter(Measure == "bp_srtm") %>%
  rename(bp_srtm = Measure)


p <- ggplot(srtm_trt_table, aes(y = wscv, x = bp_srtm, colour = Region ))+
  geom_point()+
  geom_errorbar(aes(ymin=wscv, ymax=wscv))+
  coord_flip()

#plot_grid of change between PETNo 1 and 2 (plot q) and wscv.
#note: Regions coloured differently. This is what I try to do with ggdraw() below, I just want the wscv

plot_grid(q,p, rel_widths = c(1.5,1), rel_heights = c(1.5,1))
```
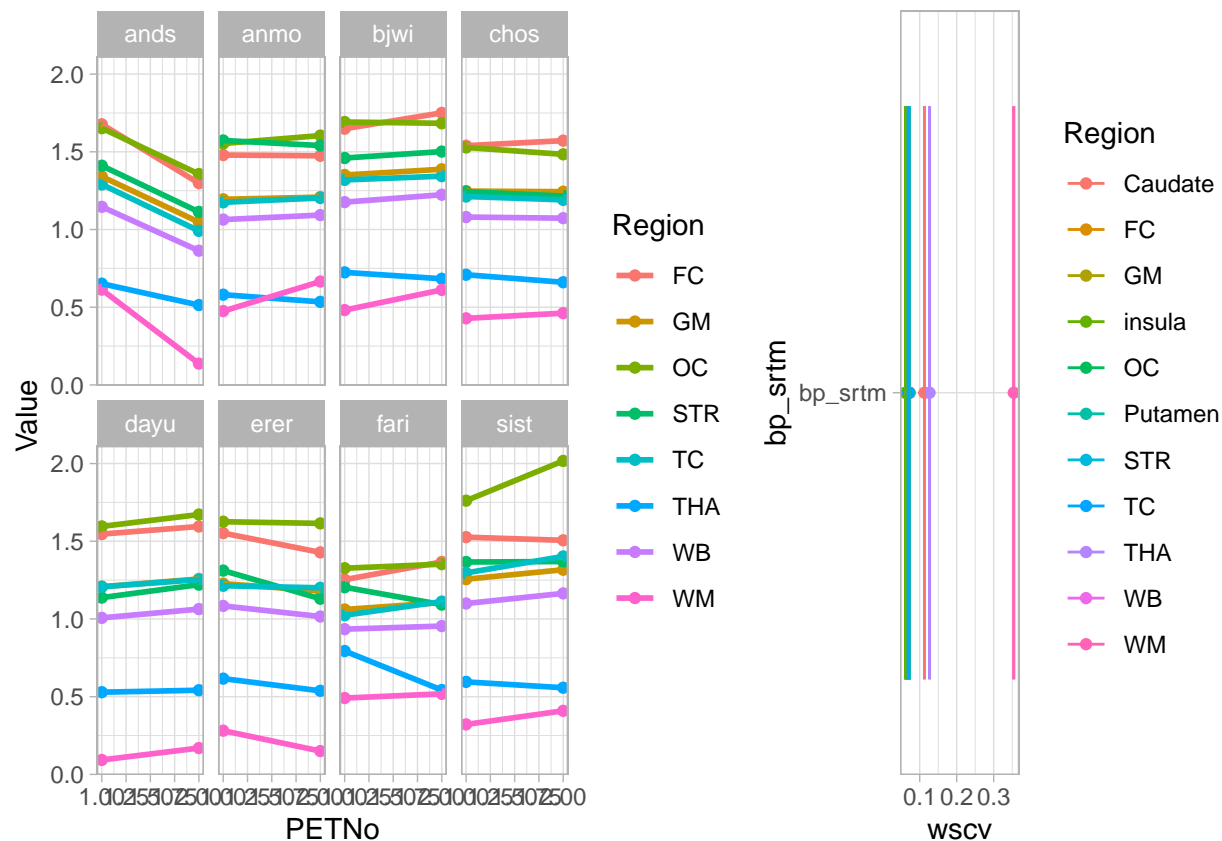
##draw_plot-related failures. attempt to create a subplot in the top right corner as shown in the cowplot tutorial

```
q <- ggplot(trtsrtm, aes(x = PETNo, y = Value,
                         group = Region, colour=Region)) +
  geom_point() +
  geom_smooth(method = 'lm', se = FALSE) +
  facet_wrap( ~ Subjname, ncol = 4)

p <- ggplot(srtm_trt_table, aes(y = wscv, x = bp_srtm, colour = region ))+
  geom_point()+
  geom_errorbar(aes(ymin=wscv, ymax=wscv))+
  coord_flip()


ggdraw() +
  draw_plot(q + theme(legend.justification = "bottom"), 0, 0, 1, 1 +
             scale_color_viridis(discrete = TRUE)) +
  draw_plot(p + scale_color_viridis(discrete = TRUE) +
             theme(legend.justification = "top"), .6, .6, .4, .4) +
  draw_plot_label(c("A", "B"), c(0, 0.5), c(1, 0.92), size = 15)
```

#all estimates in all models using facet_grid.

Idea: scale the estimates to the same scale and have them all in the same facet as the Y- axis and remove the current faceting by estimate on the x-axis

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


#This one needs work

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