

STOPPD mean diffusivity analysis whole skeleton FA (not lateralized)

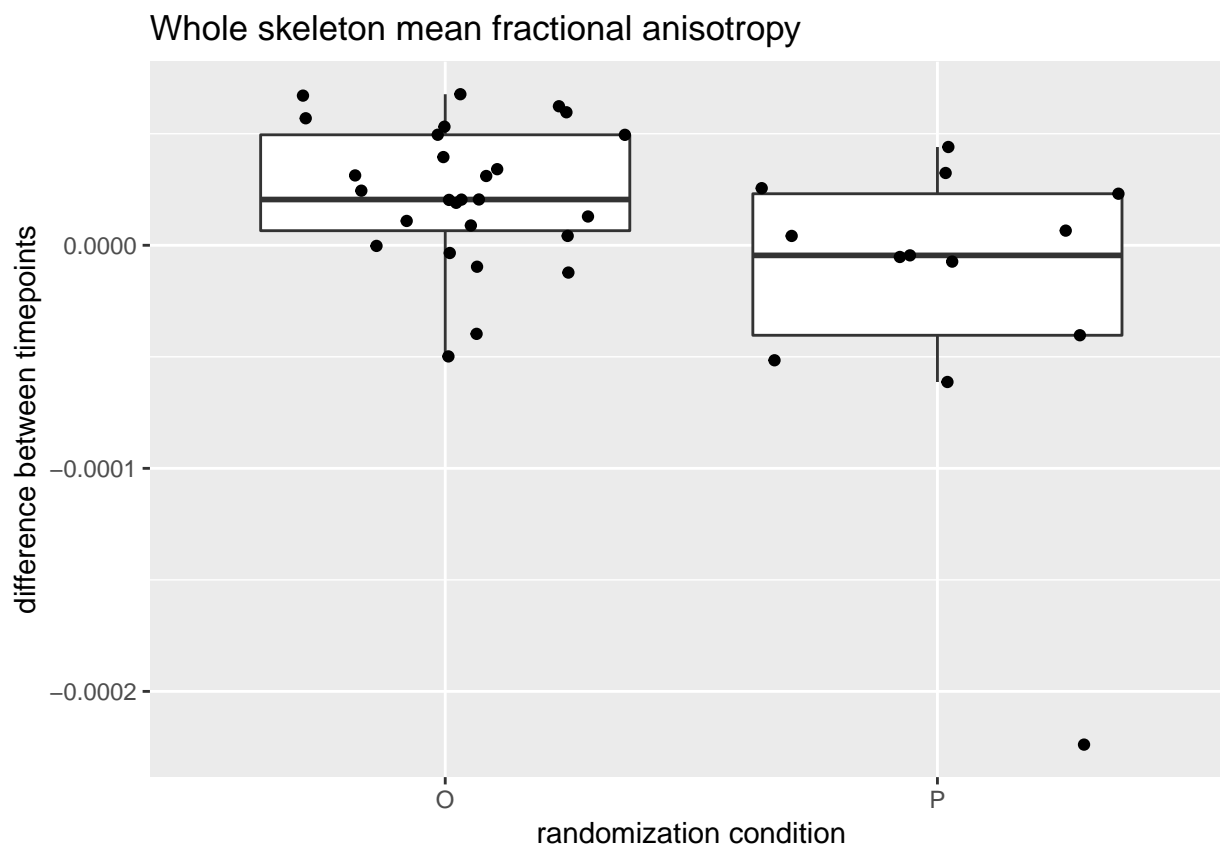
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This script analyses mean fractional anisotropy.

RCT only

```
#boxplot of difference in MD in whole skeleton (y axis) by randomization group (x axis)  
plot <- ggplot(RCT_FA, aes(x= randomization, y = diffAverageFA_MD)) +  
  geom_boxplot(outlier.shape = NA) + geom_jitter() +  
  ggtitle("Whole skeleton mean fractional anisotropy") +  
  xlab("randomization condition") +  
  ylab("difference between timepoints")
```



#Note: the outlying participant is again 210030; this participant has NOT been excluded from subsequent

```
#run linear model without covariates
```

```
fit_rct <- lm(diffAverageFA_MD ~ randomization + (1|id), data= RCT_FA)
print(fit_rct)
```

```
##
## Call:
## lm(formula = diffAverageFA_MD ~ randomization + (1 | id), data = RCT_FA)
##
## Coefficients:
## (Intercept) randomizationP      1 | idTRUE
## 0.00002328   -0.00004315                NA
```

```
summary(fit_rct)
```

```
##
## Call:
## lm(formula = diffAverageFA_MD ~ randomization + (1 | id), data = RCT_FA)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.00020397 -0.00001941  0.00000791  0.00002729  0.00006391
##
## Coefficients: (1 not defined because of singularities)
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.000023280  0.000008929   2.607  0.01297 *
## randomizationP -0.000043150  0.000015663  -2.755  0.00896 **
## 1 | idTRUE      NA              NA      NA      NA
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.0000464 on 38 degrees of freedom
## (1 observation deleted due to missingness)
## Multiple R-squared:  0.1665, Adjusted R-squared:  0.1445
## F-statistic:  7.59 on 1 and 38 DF,  p-value: 0.008962
```

```
#run linear model with covariates of sex and age
```

```
fit_rct <- lm(diffAverageFA_MD ~ randomization + sex + age + (1|id), data= RCT_FA)
print(fit_rct)
```

```
##
## Call:
## lm(formula = diffAverageFA_MD ~ randomization + sex + age + (1 |
##      id), data = RCT_FA)
##
## Coefficients:
## (Intercept) randomizationP      sexM      age
## -0.0000057068 -0.0000474955 -0.0000119230  0.0000006608
##      1 | idTRUE
##              NA
```

```
summary(fit_rct)
```

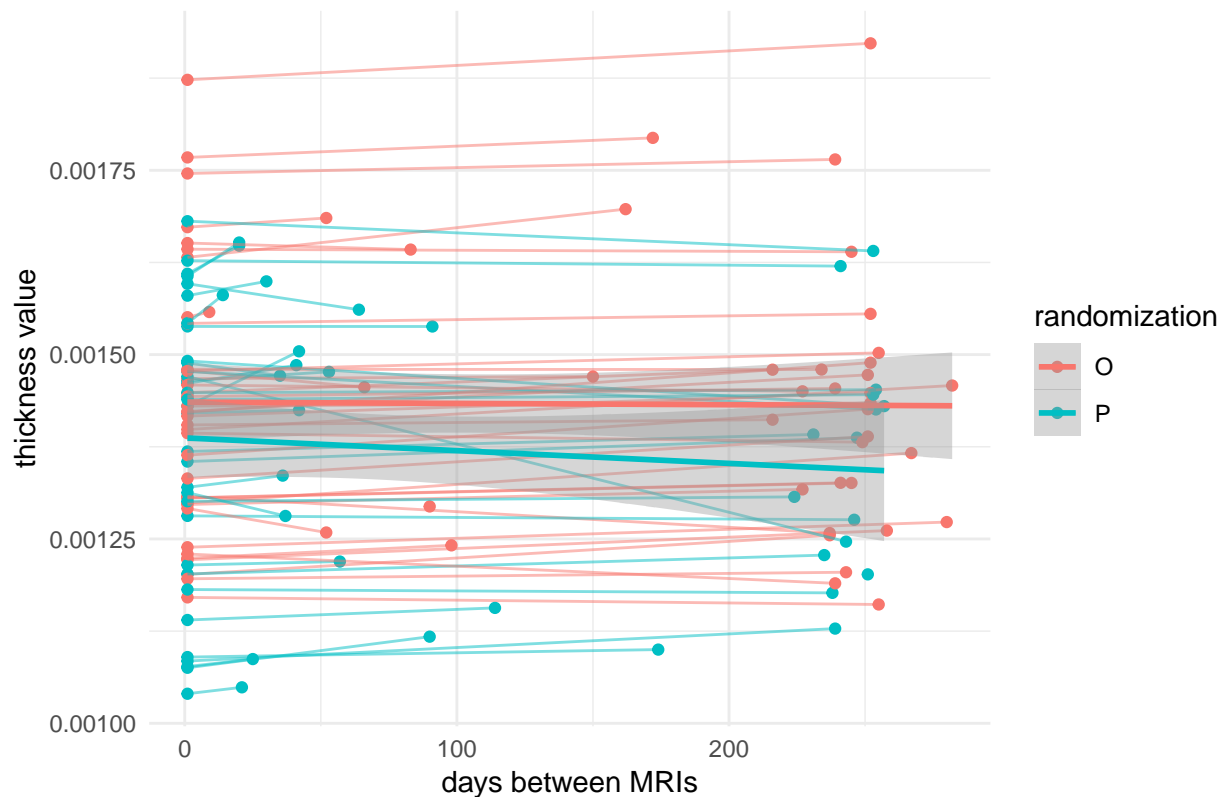
```
##
## Call:
## lm(formula = diffAverageFA_MD ~ randomization + sex + age + (1 |
##      id), data = RCT_FA)
```

```
##
## Residuals:
##      Min        1Q      Median        3Q      Max
## -0.000189771 -0.000017147  0.000007741  0.000027600  0.000073455
##
## Coefficients: (1 not defined because of singularities)
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  -0.0000057068  0.0000291916  -0.195  0.84611
## randomizationP -0.0000474955  0.0000160487  -2.959  0.00542 **
## sexM          -0.0000119230  0.0000152282  -0.783  0.43877
## age           0.0000006608  0.0000005416   1.220  0.23038
## 1 | idTRUE      NA            NA        NA      NA
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.00004654 on 36 degrees of freedom
## (1 observation deleted due to missingness)
## Multiple R-squared:  0.2055, Adjusted R-squared:  0.1392
## F-statistic: 3.103 on 3 and 36 DF,  p-value: 0.03858
```

RCT & Relapse (with time as factor)

```
#plot
RCTRelapse_FA %>%
  ggplot(aes(x=model_days, y=metric_t, colour=randomization)) +
  geom_point() +
  geom_line(aes(group=id), alpha = 0.5) +
  geom_smooth(method="lm", formula=y~poly(x,1)) +
  ggtitle("Whole skeleton mean fractional anisotropy over time") +
  xlab("days between MRIs") +
  ylab("thickness value") +
  theme_minimal()
```

Whole skeleton mean fractional anisotropy over time



```
#run mixed linear model, with covariates
fit_all <- lmer(metric_t ~ randomization*model_days + sex + age + (1|id), data= RCTRelapse_FA)
summary(fit_all)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: metric_t ~ randomization * model_days + sex + age + (1 | id)
## Data: RCTRelapse_FA
##
## REML criterion at convergence: -2212
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.7218 -0.3729  0.0105  0.4067  3.7866
##
## Random effects:
## Groups   Name                Variance  Std.Dev.
## id      (Intercept)  0.0000000160257  0.00012659
## Residual                    0.000000007732  0.00002781
## Number of obs: 145, groups: id, 74
##
## Fixed effects:
##              Estimate      Std. Error      df
## (Intercept)    0.00097464533  0.00005864533  70.19033165120
## randomizationP -0.00005038338  0.00003021245  72.57742540601
## model_days      0.00000009182  0.00000002884  69.19236215567
## sexM            0.00003475045  0.00003008178  69.82520592848
```

```

## age 0.00000784383 0.00000098752 69.74162385679
## randomizationP:model_days -0.00000015405 0.00000005015 70.08773056884
## t value Pr(>|t|)
## (Intercept) 16.619 < 0.0000000000000002 ***
## randomizationP -1.668 0.09970 .
## model_days 3.184 0.00218 **
## sexM 1.155 0.25195
## age 7.943 0.00000000000238 ***
## randomizationP:model_days -3.072 0.00303 **
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
## (Intr) rndmzP mdl_dy sexM age
## randomiztnP -0.223
## model_days -0.057 0.100
## sexM -0.163 0.062 0.001
## age -0.902 -0.039 0.005 -0.094
## rndmztnP:m_ 0.033 -0.136 -0.575 -0.003 -0.003

#cleanup
rm('df', 'fit_all', 'fit_rct', 'MD', 'plot', 'RCT_FA', 'RCTRelapse_FA')

```