

STOPPD mean diffusivity analysis

left SLF

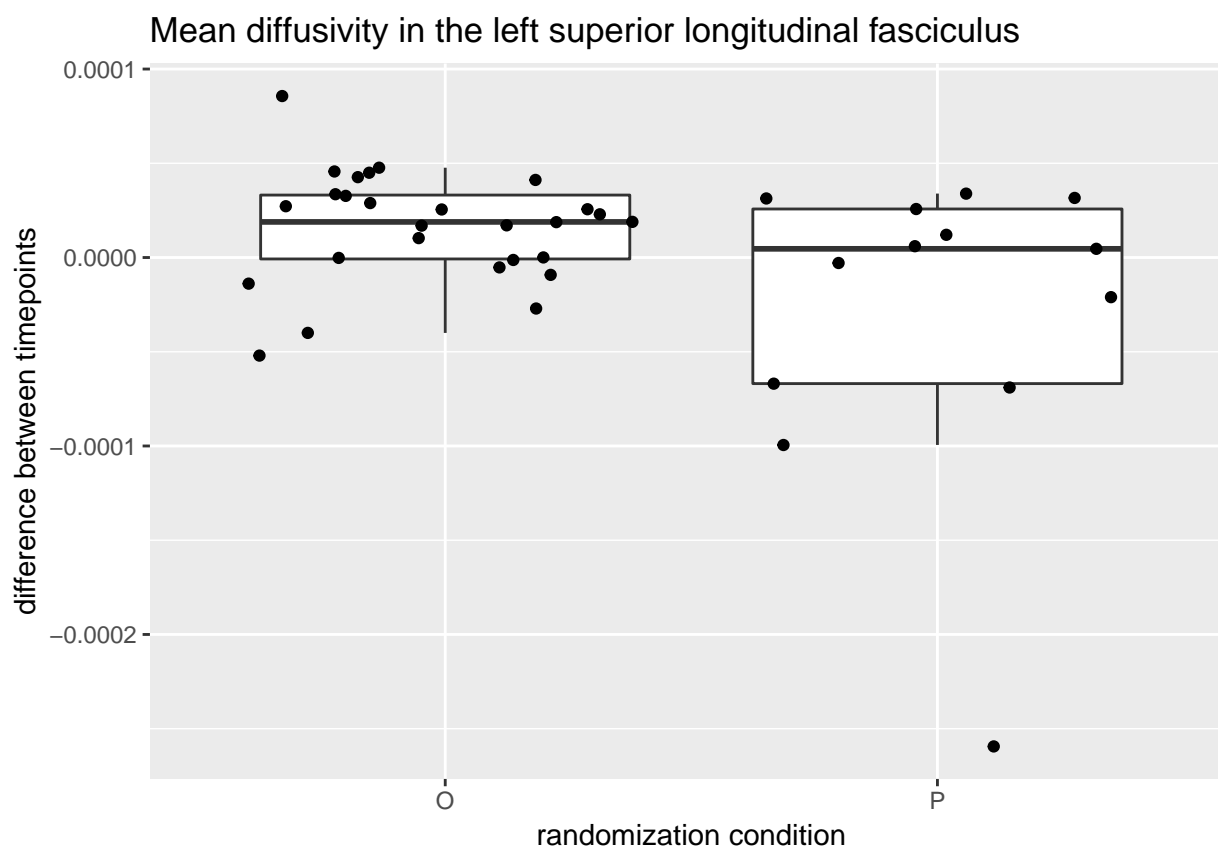
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This script analyses mean diffusivity in the left superior longitudinal fasciculus.

RCT only; left SLF

```
#boxplot of difference in MD in left SLF (y axis) by randomization group (x axis)
(plot <- ggplot(RCT_MD_SLF, aes(x = randomization, y = diffSLF.L_MD)) +
  geom_boxplot(outlier.shape = NA) + geom_jitter() +
  ggtitle("Mean diffusivity in the left superior longitudinal fasciculus") +
  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(diffSLF.L_MD ~ randomization + (1|id), data= RCT_MD_SLF)
print(fit_rct)
```

```
##
## Call:
## lm(formula = diffSLF.L_MD ~ randomization + (1 | id), data = RCT_MD_SLF)
##
## Coefficients:
##      (Intercept)  randomizationP      1 | idTRUE
##      0.00001619    -0.00004491                NA
```

```
summary(fit_rct)
```

```
##
## Call:
## lm(formula = diffSLF.L_MD ~ randomization + (1 | id), data = RCT_MD_SLF)
##
## Residuals:
##      Min          1Q      Median          3Q      Max
## -0.000230653 -0.000018476  0.000008481  0.000028982  0.000069479
##
## Coefficients: (1 not defined because of singularities)
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   0.00001619  0.00001000   1.619   0.1137
## randomizationP -0.00004491  0.00001754  -2.560   0.0146 *
## 1 | idTRUE           NA           NA      NA      NA
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.00005196 on 38 degrees of freedom
## (1 observation deleted due to missingness)
## Multiple R-squared:  0.1471, Adjusted R-squared:  0.1247
## F-statistic: 6.554 on 1 and 38 DF, p-value: 0.01456
```

#run linear model with covariates of sex and age

```
fit_rct <- lm(diffSLF.L_MD ~ randomization + sex + age + (1|id), data= RCT_MD_SLF)
print(fit_rct)
```

```
##
## Call:
## lm(formula = diffSLF.L_MD ~ randomization + sex + age + (1 |
##      id), data = RCT_MD_SLF)
##
## Coefficients:
##      (Intercept)  randomizationP          sexM          age
##      0.0000119667  -0.0000459426  -0.0000045746   0.0000001223
##      1 | idTRUE
##              NA
```

```
summary(fit_rct)
```

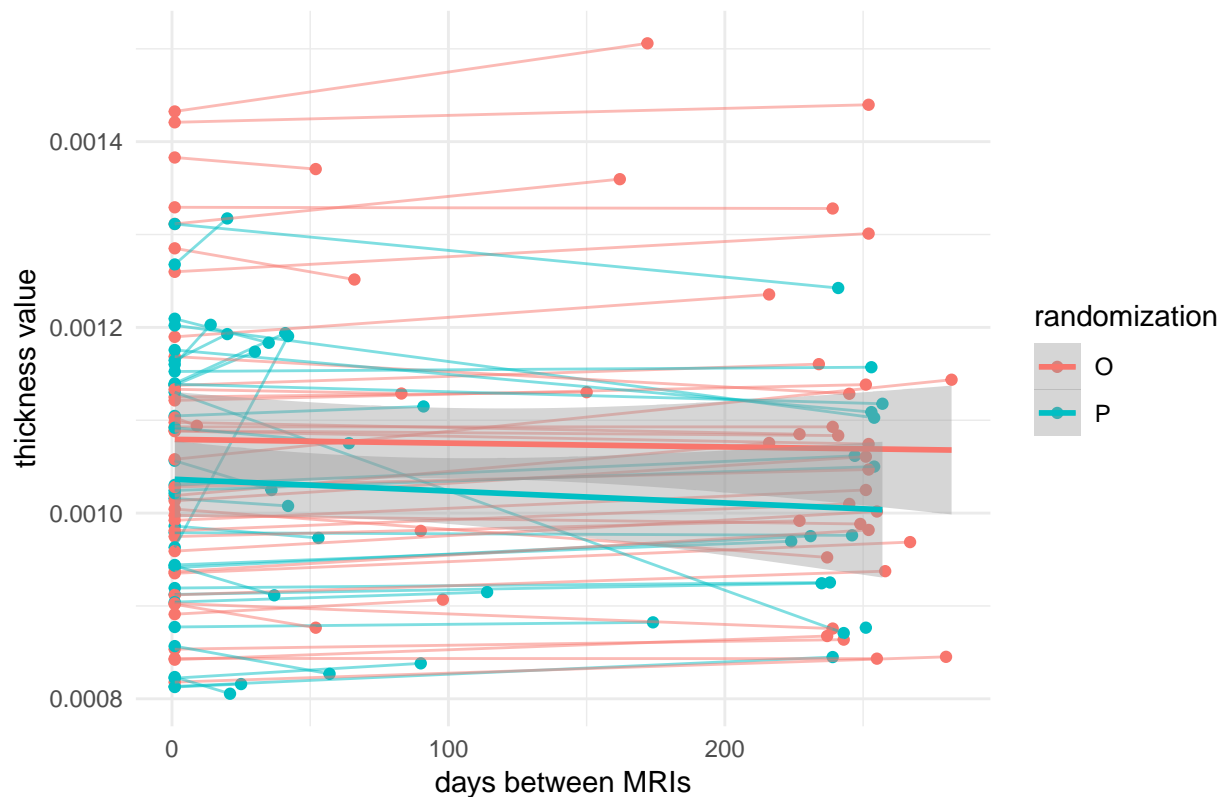
```
##
## Call:
```

```
## lm(formula = diffSLF.L_MD ~ randomization + sex + age + (1 |
##     id), data = RCT_MD_SLF)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.00022657 -0.00001903  0.00001066  0.00002896  0.00006979
##
## Coefficients: (1 not defined because of singularities)
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.0000119667  0.0000334444   0.358   0.7226
## randomizationP -0.0000459426  0.0000183868  -2.499   0.0172 *
## sexM          -0.0000045746  0.0000174467  -0.262   0.7947
## age           0.0000001223  0.0000006205   0.197   0.8449
## 1 | idTRUE      NA              NA      NA      NA
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.00005332 on 36 degrees of freedom
## (1 observation deleted due to missingness)
## Multiple R-squared:  0.1492, Adjusted R-squared:  0.07831
## F-statistic: 2.105 on 3 and 36 DF,  p-value: 0.1168
```

RCT & Relapse (with time as factor) - left SLF

```
#plot
RCTRelapse_MD_SLF %>%
  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("Mean diffusivity in the left superior longitudinal fasciculus over time") +
  xlab("days between MRIs") +
  ylab("thickness value") +
  theme_minimal()
```

Mean diffusivity in the left superior longitudinal fasciculus over time



```
#run mixed linear model, with covariates
fit_all <- lmer(metric_t ~ randomization*model_days + sex + age + (1|id), data=RCTRelapse_MD_SLF)
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_MD_SLF
##
## REML criterion at convergence: -2190.6
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.2487 -0.3571 -0.0561  0.3536  3.3023
##
## Random effects:
## Groups   Name                Variance  Std.Dev.
## id      (Intercept)  0.000000012359  0.00011117
## Residual                    0.00000001331  0.00003649
## Number of obs: 145, groups: id, 74
##
## Fixed effects:
##              Estimate      Std. Error      df
## (Intercept)    0.00069685393  0.00005235010  70.71029809443
## randomizationP -0.00004061074  0.00002722718  75.75865753200
## model_days      0.00000007090  0.00000003779  69.71829402560
## sexM            0.00001595658  0.00002681187  69.91490040142
```

```

## age 0.00000659042 0.00000087988 69.74366897813
## randomizationP:model_days -0.00000015925 0.00000006548 71.61107687865
## t value Pr(>|t|)
## (Intercept) 13.311 < 0.0000000000000002 ***
## randomizationP -1.492 0.1400
## model_days 1.876 0.0648 .
## sexM 0.595 0.5537
## age 7.490 0.000000000161 ***
## randomizationP:model_days -2.432 0.0175 *
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
## (Intr) rndmzP mdl_dy sexM age
## randomiztnP -0.226
## model_days -0.083 0.146
## sexM -0.164 0.062 0.002
## age -0.900 -0.038 0.007 -0.094
## rndmztnP:m_ 0.049 -0.198 -0.577 -0.004 -0.004
#cleanup
rm(df, fit_all, fit_rct, MD, plot, RCT_MD_SLF, RCTRelapse_MD_SLF)

```