STOPPD mean diffusivity analysis
(left entorhinal cortex)

Contents

This script analyses mean diffusivity in the left entorhinal cortex.

RCT only

```r
#boxplot of difference in MD in EC (y axis) by randomization group (x axis)
(plot <- ggplot(RCT_MD_EC, aes(x= randomization, y = diffEC.L_MD)) +
    geom_boxplot(outlier.shape = NA) + geom_jitter() +
    ggtitle("Mean diffusivity in left entorhinal cortex") +
    xlab("randomization condition") +
    ylab("difference between timepoints"))
```
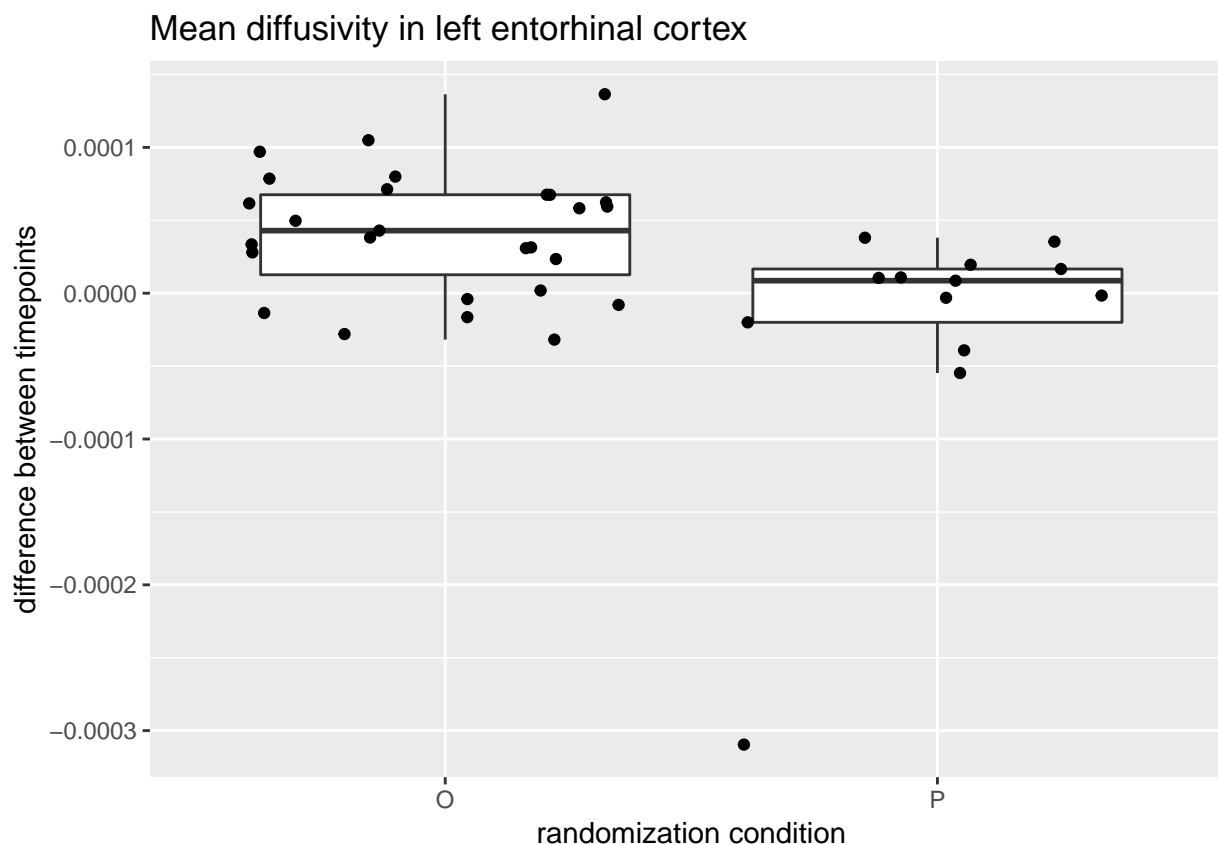


```r
#Note: the outlying participant is again 210030; this participant has NOT been excluded from subsequent
```

```
#run linear model without covariates
fit_rct <- lm(diffEC.L_MD ~ randomization + (1|id), data= RCT_MD_EC)
print(fit_rct)
```

```
##
## Call:
## lm(formula = diffEC.L_MD ~ randomization + (1 | id), data = RCT_MD_EC)
##
## Coefficients:
##    (Intercept)   randomizationP        1 | idTRUE
##     0.00004159      -0.00006380              NA
```

```
summary(fit_rct)
```

```
##
## Call:
## lm(formula = diffEC.L_MD ~ randomization + (1 | id), data = RCT_MD_EC)
##
## Residuals:
##          Min          1Q      Median          3Q         Max
## -0.00028737 -0.00001726  0.00001726  0.00003277  0.00009488
##
## Coefficients: (1 not defined because of singularities)
##                  Estimate  Std. Error  t value  Pr(>|t|)
## (Intercept)    0.00004159  0.00001186    3.507   0.00118 **
## randomizationP -0.00006380  0.00002080   -3.067   0.00397 **
## 1 | idTRUE             NA          NA       NA        NA
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.00006161 on 38 degrees of freedom
##    (1 observation deleted due to missingness)
## Multiple R-squared:  0.1985, Adjusted R-squared:  0.1774
## F-statistic: 9.408 on 1 and 38 DF,  p-value: 0.003969
```

```
#run linear model with covariates of sex and age
fit_rct <- lm(diffEC.L_MD ~ randomization + sex + age + (1|id), data= RCT_MD_EC)
print(fit_rct)
```

```
##
## Call:
## lm(formula = diffEC.L_MD ~ randomization + sex + age + (1 | id),
##     data = RCT_MD_EC)
##
## Coefficients:
##    (Intercept)   randomizationP             sexM             age
##    -0.000027848     -0.000071170     -0.000007033     0.000001386
##       1 | idTRUE
##             NA
```

```
summary(fit_rct)
```

```
##
## Call:
## lm(formula = diffEC.L_MD ~ randomization + sex + age + (1 | id),
##     data = RCT_MD_EC)
```

```
## 
## Residuals:
##          Min          1Q      Median          3Q         Max
## -0.00026865 -0.00001959  0.00001092  0.00003146  0.00007775
## 
## Coefficients: (1 not defined because of singularities)
##                    Estimate    Std. Error t value Pr(>|t|)
## (Intercept)    -0.0000278479  0.0000376993  -0.739  0.46489
## randomizationP -0.0000711702  0.0000207260  -3.434  0.00151 **
## sexM           -0.0000070333  0.0000196664  -0.358  0.72271
## age             0.0000013856  0.0000006994   1.981  0.05526 .
## 1 | idTRUE               NA            NA      NA       NA
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 0.0000601 on 36 degrees of freedom
##   (1 observation deleted due to missingness)
## Multiple R-squared:  0.2774, Adjusted R-squared:  0.2171
## F-statistic: 4.606 on 3 and 36 DF,  p-value: 0.007912
```

RCT & Relapse (with time as factor)

```r
#plot
RCTRelapse_MD_EC %>%
  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 left entorhinal cortex over time") +
      xlab("days between MRIs") +
      ylab("thickness value") +
  theme_minimal()
```

Mean diffusivity in left entorhinal cortex over time
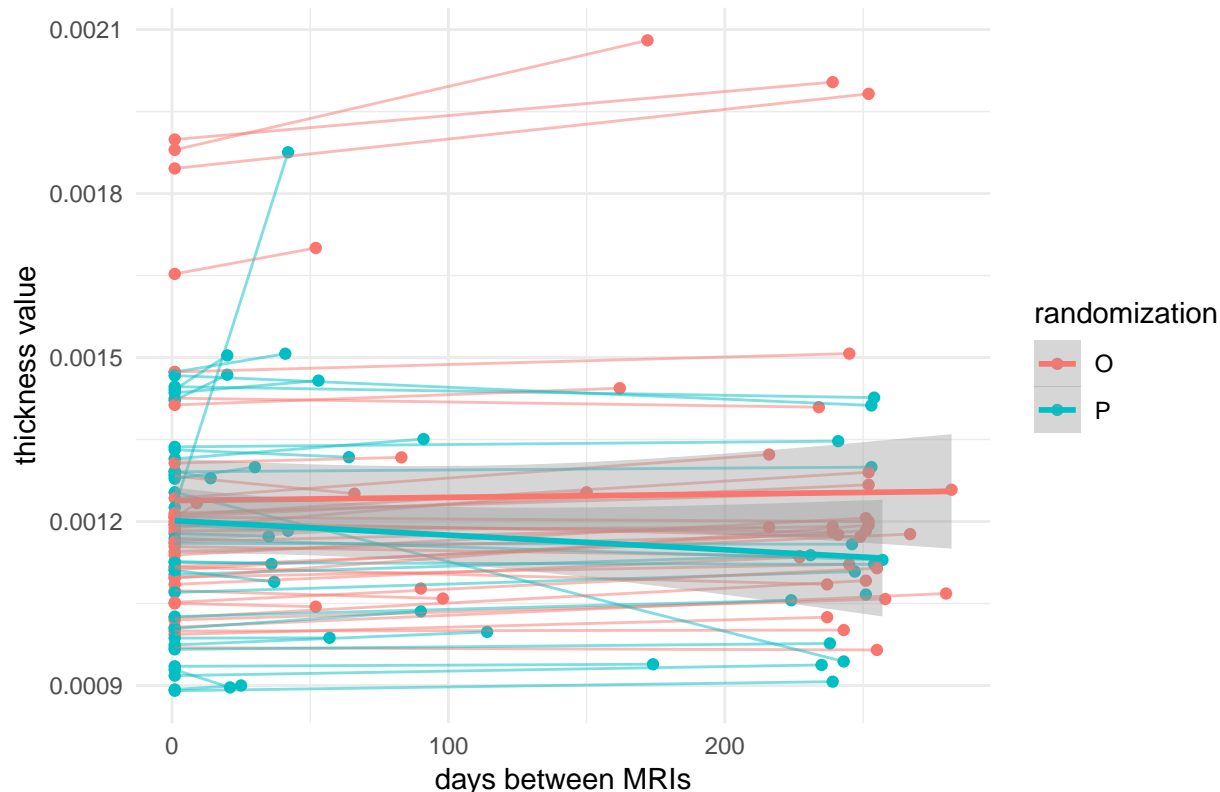
```
#run mixed linear model, with covariates
fit_all <- lmer(metric_t ~ randomization*model_days + sex + age + (1|id), data= RCTRelapse_MD_EC)
summary(fit_all)
```

```
## 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_EC
##
## REML criterion at convergence: -2047.5
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -4.6057 -0.2380 -0.0556  0.1704  5.0738
##
## Random effects:
##  Groups   Name        Variance       Std.Dev.
##  id       (Intercept) 0.000000027731 0.00016653
##  Residual             0.000000004538 0.00006736
## Number of obs: 145, groups:  id, 74
##
## Fixed effects:
##                                Estimate     Std. Error           df
## (Intercept)                0.00069690121  0.00007959345 70.90555071633
## randomizationP            -0.00004668352  0.00004173267 78.20715931040
## model_days                 0.00000017088  0.00000006967 69.92199936771
## sexM                       0.00001292656  0.00004070983 69.72529056632
```

```
## age                        0.00000949733  0.00000133558 69.48416020572
## randomizationP:model_days -0.00000022928  0.00000012035 72.66074479641
##                              t value         Pr(>|t|)
## (Intercept)                    8.756 0.000000000000671 ***
## randomizationP                -1.119            0.2667
## model_days                     2.453            0.0167 *
## sexM                           0.318            0.7518
## age                            7.111 0.000000000810388 ***
## randomizationP:model_days     -1.905            0.0607 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##            (Intr) rndmzP mdl_dy sexM   age
## randomiztnP -0.229
## model_days  -0.101  0.176
## sexM        -0.164  0.063  0.002
## age         -0.899 -0.038  0.009 -0.094
## rndmztnP:m_  0.059 -0.237 -0.579 -0.005 -0.005
```

```r
#cleanup
rm(df, fit_all, fit_rct, MD, MD_wide, plot, RCT_MD_EC, RCTRelapse_MD_EC, completers)
```