STOPPD cortical thickness analysis
(left hemisphere only)

Contents

This script analyses cortical thickness in the left hemisphere.

RCT only

```
#boxplot of difference in thickness (y axis) by randomization group (x axis)
  (plot <- ggplot(RCT_CT, aes(x= randomization, y = LDifference)) +
    geom_boxplot(outlier.shape = NA) + geom_jitter() +
    ggtitle("Cortical thickness (left hemisphere)") +
    xlab("randomization condition") +
    ylab("difference between timepoints"))
```


Cortical thickness (left hemisphere)
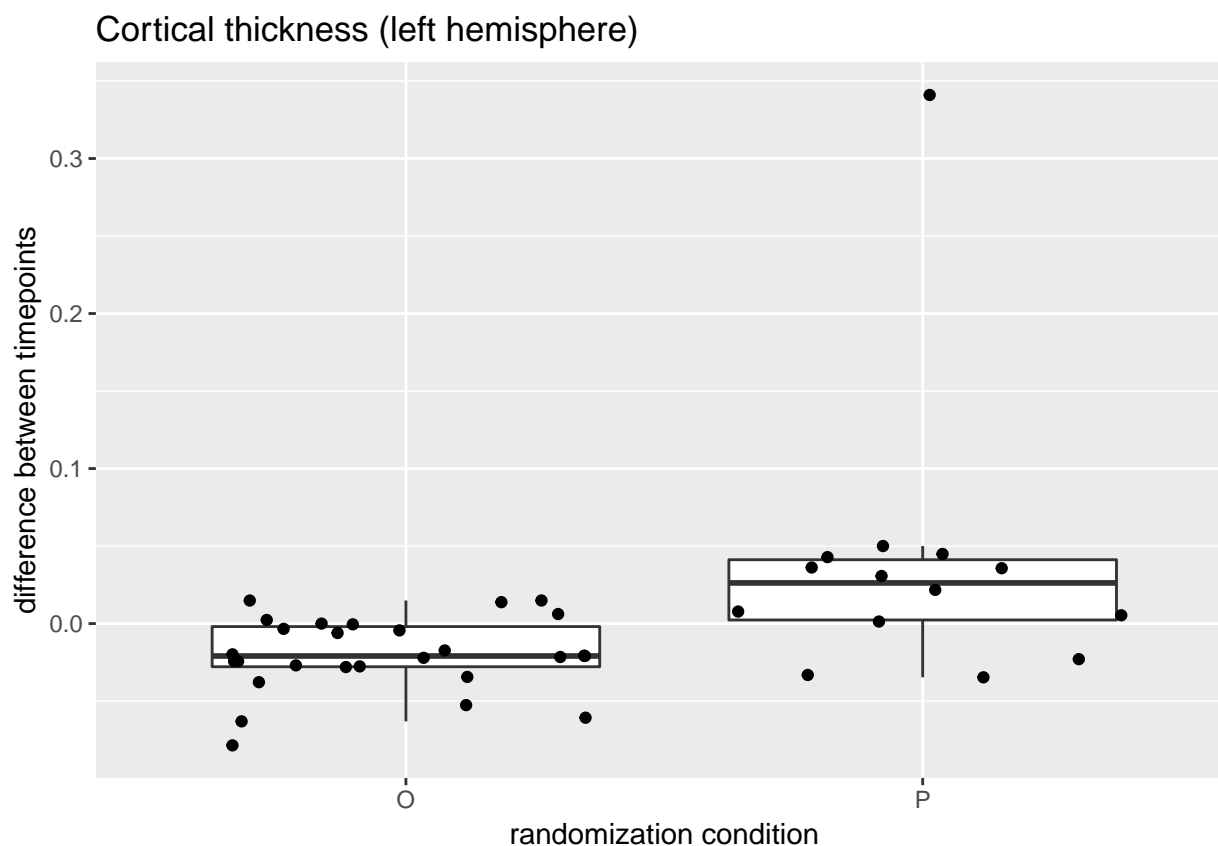
```
#run linear model without covariates
  fit_rct <- lm(LDifference ~ randomization + (1|STUDYID), data= RCT_CT)
  print(fit_rct)
```

```
##
## Call:
## lm(formula = LDifference ~ randomization + (1 | STUDYID), data = RCT_CT)
##
## Coefficients:
##     (Intercept)   randomizationP  1 | STUDYIDTRUE
##        -0.02010          0.05774               NA
```

```
  summary(fit_rct)
```

```
##
## Call:
## lm(formula = LDifference ~ randomization + (1 | STUDYID), data = RCT_CT)
##
## Residuals:
##       Min        1Q    Median        3Q       Max
## -0.072292 -0.017706 -0.001912  0.014044  0.303338
##
## Coefficients: (1 not defined because of singularities)
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -0.02010    0.01088  -1.847  0.07229 .
## randomizationP  0.05774    0.01862   3.100  0.00358 **
## 1 | STUDYIDTRUE      NA         NA      NA       NA
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.05655 on 39 degrees of freedom
## Multiple R-squared:  0.1977, Adjusted R-squared:  0.1771
## F-statistic: 9.611 on 1 and 39 DF,  p-value: 0.003583
```

```
#run linear model with covariates of sex and age
  fit_rct <- lm(LDifference ~ randomization + sex + age + (1|STUDYID), data= RCT_CT)
  print(fit_rct)
```

```
##
## Call:
## lm(formula = LDifference ~ randomization + sex + age + (1 | STUDYID),
##     data = RCT_CT)
##
## Coefficients:
##     (Intercept)   randomizationP             sexM              age
##       -0.009273         0.061106         0.024877        -0.000434
## 1 | STUDYIDTRUE
##              NA
```

```
  summary(fit_rct)
```

```
##
## Call:
## lm(formula = LDifference ~ randomization + sex + age + (1 | STUDYID),
##     data = RCT_CT)
##
```

```
## Residuals:
##       Min        1Q    Median        3Q       Max
## -0.080120 -0.023468  0.001322  0.018192  0.284658
##
## Coefficients: (1 not defined because of singularities)
##                 Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -0.0092726  0.0354584  -0.262  0.79515
## randomizationP  0.0611058  0.0189343   3.227  0.00262 **
## sexM            0.0248771  0.0181475   1.371  0.17869
## age            -0.0004340  0.0006568  -0.661  0.51284
## 1 | STUDYIDTRUE         NA         NA      NA       NA
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.05653 on 37 degrees of freedom
## Multiple R-squared:  0.2393, Adjusted R-squared:  0.1776
## F-statistic: 3.879 on 3 and 37 DF,  p-value: 0.01655
```

RCT only, exclude outlier

```r
#exclude outlier (participant 210030)
 RCT_CT_no210030 <- RCT_CT[!(RCT_CT$STUDYID == "210030"),]

#boxplot of difference in thickness (y axis) by randomization group (x axis)
  (plot <- ggplot(RCT_CT_no210030, aes(x= randomization, y = LDifference)) +
         geom_boxplot(outlier.shape = NA) + geom_jitter() +
         ggtitle("Cortical thickness (left hemisphere), outlier removed") +
         xlab("randomization condition") +
         ylab("difference between timepoints"))
```

Cortical thickness (left hemisphere), outlier removed
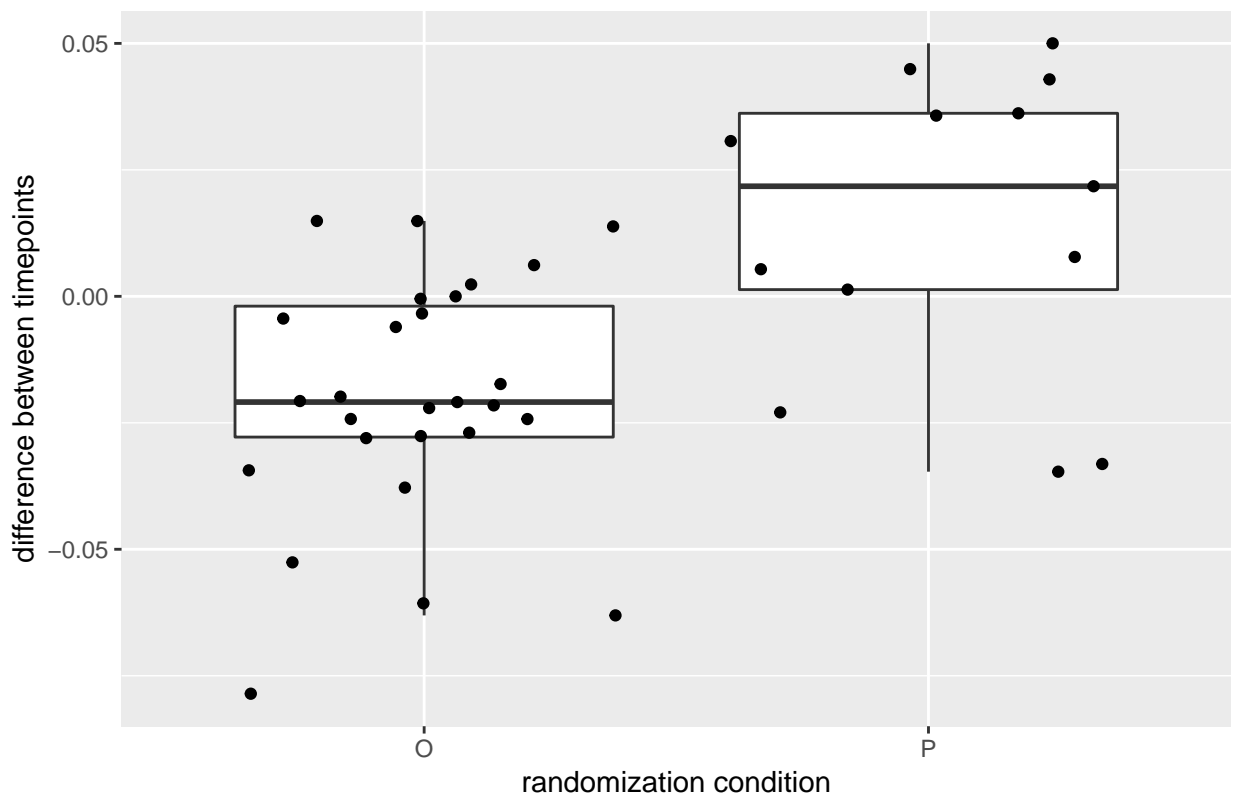
outlier-1.bb

```r
#run linear model without covariates
  fit_rct_no210030 <- lm(LDifference ~ randomization + (1|STUDYID), data= RCT_CT_no210030)
  print(fit_rct_no210030)
```

```
##
## Call:
## lm(formula = LDifference ~ randomization + (1 | STUDYID), data = RCT_CT_no210030)
##
## Coefficients:
##     (Intercept)   randomizationP  1 | STUDYIDTRUE
##         -0.0201           0.0344               NA
```

```r
  summary(fit_rct_no210030)
```

```
##
## Call:
## lm(formula = LDifference ~ randomization + (1 | STUDYID), data = RCT_CT_no210030)
##
## Residuals:
##       Min        1Q    Median        3Q       Max
## -0.058446 -0.009946 -0.000696  0.020434  0.035712
##
## Coefficients: (1 not defined because of singularities)
##                Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -0.020104   0.004997  -4.023 0.000264 ***
## randomizationP  0.034403   0.008766   3.925 0.000353 ***
## 1 | STUDYIDTRUE       NA         NA      NA       NA
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.02597 on 38 degrees of freedom
## Multiple R-squared:  0.2884, Adjusted R-squared:  0.2697
## F-statistic:  15.4 on 1 and 38 DF,  p-value: 0.0003527
```

```r
#run linear model with covariates of sex and age
  fit_rct_no210030 <- lm(LDifference ~ randomization + sex + age + (1|STUDYID), data= RCT_CT_no210030)
  print(fit_rct_no210030)
```

```
##
## Call:
## lm(formula = LDifference ~ randomization + sex + age + (1 | STUDYID),
##     data = RCT_CT_no210030)
##
## Coefficients:
##    (Intercept)   randomizationP            sexM              age
##     -0.0303806        0.0337598       0.0029604        0.0001684
## 1 | STUDYIDTRUE
##             NA
```

```r
  summary(fit_rct_no210030)
```

```
##
## Call:
## lm(formula = LDifference ~ randomization + sex + age + (1 | STUDYID),
##     data = RCT_CT_no210030)
##
## Residuals:
##       Min        1Q    Median        3Q       Max
## -0.056253 -0.010930  0.000732  0.021250  0.036791
##
## Coefficients: (1 not defined because of singularities)
##                  Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -0.0303806  0.0167121  -1.818 0.077413 .
## randomizationP  0.0337598  0.0091826   3.676 0.000766 ***
## sexM            0.0029604  0.0087121   0.340 0.735977
## age             0.0001684  0.0003121   0.540 0.592809
## 1 | STUDYIDTRUE        NA         NA      NA       NA
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.02648 on 36 degrees of freedom
## Multiple R-squared:  0.2987, Adjusted R-squared:  0.2403
## F-statistic: 5.111 on 3 and 36 DF,  p-value: 0.00476
```

RCT & Relapse (with time as factor)

```r
#plot all data, including outlier (participant 210030)
  RCTRelapse_CT %>%
  ggplot(aes(x=model_days, y=thickness, colour=randomization)) +
  geom_point() +
  geom_line(aes(group=STUDYID), alpha = 0.5) +
  geom_smooth(method="lm", formula=y~poly(x,1)) +
```

```
  ggtitle("Cortical thickness in left hemisphere over time") +
  xlab("days between MRIs") +
  ylab("thickness value") +
  theme_minimal()
```

Cortical thickness in left hemisphere over time
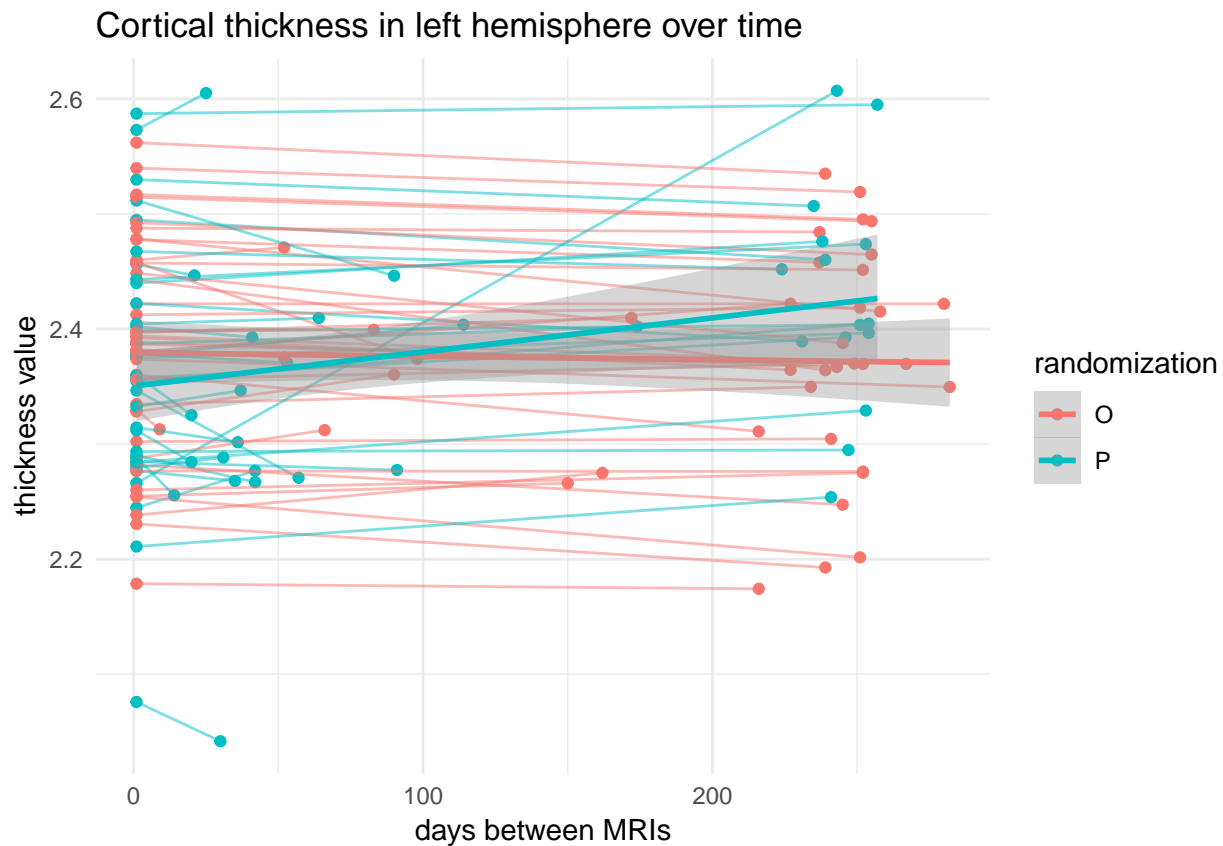
```
#run mixed linear model, with covariates
  fit_all <- lmer(thickness ~ randomization*model_days + sex + age + (1|STUDYID), data= RCTRelapse_CT)
  summary(fit_all)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula:
## thickness ~ randomization * model_days + sex + age + (1 | STUDYID)
##    Data: RCTRelapse_CT
##
## REML criterion at convergence: -338.3
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -4.4306 -0.3311  0.0568  0.2930  4.5992
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  STUDYID  (Intercept) 0.005958 0.07719
##  Residual             0.001152 0.03394
## Number of obs: 148, groups:  STUDYID, 74
##
```

```
## Fixed effects:
##                             Estimate Std. Error         df t value
## (Intercept)                2.584e+00  3.715e-02  7.130e+01  69.538
## randomizationP            -1.940e-02  1.949e-02  7.878e+01  -0.996
## model_days                -6.762e-05  3.500e-05  7.314e+01  -1.932
## sexM                      -1.040e-02  1.897e-02  6.968e+01  -0.548
## age                       -3.555e-03  6.230e-04  6.969e+01  -5.707
## randomizationP:model_days  2.101e-04  5.938e-05  7.519e+01   3.539
##                             Pr(>|t|)
## (Intercept)                  < 2e-16 ***
## randomizationP              0.322424
## model_days                  0.057240 .
## sexM                        0.585349
## age                         2.59e-07 ***
## randomizationP:model_days  0.000693 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##            (Intr) rndmzP mdl_dy sexM   age
## randomiztnP -0.231
## model_days  -0.108  0.187
## sexM        -0.162  0.059  0.000
## age         -0.899 -0.036  0.011 -0.094
## rndmztnP:m_  0.062 -0.244 -0.589  0.004 -0.006
```

RCT & Relapse (with time as factor), exclude outlier

```r
#do same analysis as above with outlier removed (participant 210030)
  RCTRelapse_CT_no210030 <- RCTRelapse_CT[!(RCTRelapse_CT$STUDYID == "210030"),]

#plot data excluding outlier
  RCTRelapse_CT_no210030 %>%
    ggplot(aes(x=model_days, y=thickness, colour=randomization)) +
    geom_point() +
    geom_line(aes(group=STUDYID), alpha = 0.5) +
    geom_smooth(method="lm", formula=y~poly(x,1)) +
    ggtitle("Cortical thickness in left hemisphere over time, outlier removed") +
    xlab("days between MRIs") +
    ylab("thickness value") +
    theme_minimal()
```

Cortical thickness in left hemisphere over time, outlier removed
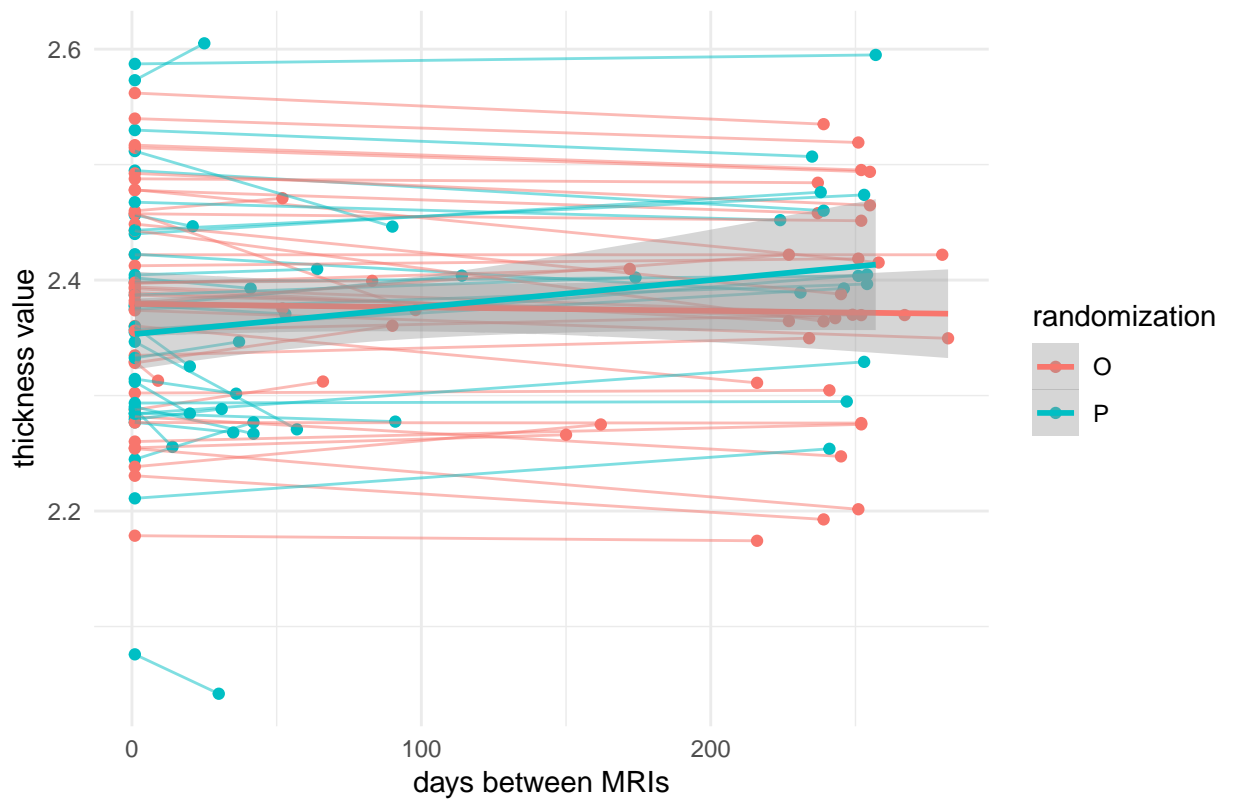
outlier-1.bb

```
#run mixed linear model, with covariates, as above
  fit_all_no210030 <- lmer(thickness ~ randomization*model_days + sex + age + (1|STUDYID), data= RCTRela
  summary(fit_all_no210030)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula:
## thickness ~ randomization * model_days + sex + age + (1 | STUDYID)
##    Data: RCTRelapse_CT_no210030
##
## REML criterion at convergence: -398.9
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.97106 -0.49857  0.05197  0.45132  1.90348
##
## Random effects:
##  Groups   Name        Variance  Std.Dev.
##  STUDYID  (Intercept) 0.0065441 0.08090
##  Residual             0.0004404 0.02099
## Number of obs: 146, groups:  STUDYID, 73
##
## Fixed effects:
##                       Estimate Std. Error         df t value
## (Intercept)          2.583e+00  3.770e-02  6.944e+01  68.523
## randomizationP      -1.441e-02  1.961e-02  7.220e+01  -0.735
## model_days          -6.865e-05  2.171e-05  7.138e+01  -3.163
```

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```
## sexM                     -1.189e-02  1.950e-02  6.885e+01  -0.610
## age                       -3.531e-03  6.361e-04  6.885e+01  -5.551
## randomizationP:model_days  1.174e-04  3.775e-05  7.218e+01   3.110
##                           Pr(>|t|)
## (Intercept)                < 2e-16 ***
## randomizationP             0.46476
## model_days                 0.00229 **
## sexM                       0.54401
## age                       4.95e-07 ***
## randomizationP:model_days  0.00268 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##            (Intr) rndmzP mdl_dy sexM   age
## randomiztnP -0.216
## model_days  -0.066  0.115
## sexM        -0.155  0.079  0.000
## age         -0.901 -0.049  0.006 -0.104
## rndmztnP:m_  0.038 -0.151 -0.575  0.005 -0.005
```

```r
#cleanup
  rm(df, fit_all, fit_all_no210030, fit_rct, fit_rct_no210030, plot, RCT_CT, RCT_CT_no210030, RCTRelaps
```