Final Study Data Analysis

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```
library(ggplot2)
library(data.table)
library(lmtest)
```

```
## Loading required package: zoo
```

```
##
## Attaching package: 'zoo'
```

```
## The following objects are masked from 'package:base':
##
##     as.Date, as.Date.numeric
```

```
library(pwr)
library(lsr)
library(cobalt)
library(stringr)
library(AER)
```

```
## Loading required package: car
```

```
## Loading required package: carData
```

```
## Loading required package: sandwich
```

```
## Loading required package: survival
```

Read in data and reformat

```
assigned_treatment_seq <- data.frame(seq_id = c(1,2,3,4,5,6),
                                     day1 = c(0,0,1,1,2,2),
                                     day2 = c(1,2,0,2,0,1),
                                     day3 = c(2,1,2,0,1,0))
d2 <- fread("241 Participant List - Final Study Results - 20181215.csv", na.strings=c("","NA"))
d2[UserId == 65,]$Q10 <- "In person"
d2[UserId == 13,]$Q6 <- "Through digital means"
# stringsAsFactors = F)
names(d2) <- str_replace_all(names(d2), c(" " = "." , "," = "" ))

# Not applicable = 0
# Through digital means = 1
# In person = 2
# Both in person and through digital means = 3
```

```
d2 <- d2[, .(userId = UserId,
             treatment_seq = as.integer(Treatment.Seq),
             day1_treatment = as.integer(as.character(factor(Q6, levels = c('Not applicable', 'In perso
                                                                            'Through digital means'),
                                                             labels = c(0, 2, 1)))),
             day2_treatment = as.integer(as.character(factor(Q10, levels = c('Not applicable', 'In pers
                                                                             'Through digital means',
                                                                             'Both in person and throug
                                                             labels = c(0, 2, 1, 3)))),
             day3_treatment = as.integer(as.character(factor(Q14, levels = c('Not applicable', 'In pers
                                                                             'Through digital means',
                                                                             'Both in person and throug
                                                             labels = c(0, 2, 1, 3)))),
             day1_steps = as.numeric(gsub("\\,", "", Q7)),
             day2_steps = as.numeric(gsub("\\,", "", Q11)),
             day3_steps = as.numeric(gsub("\\,", "", Q15)),
             age_range = as.integer(as.character(factor(Age, levels = c('18 - 24',
                                                                        "25 - 34",
                                                                        "35 - 44",
                                                                        "45 - 54",
                                                                        "55 - 64",
                                                                        "65+"),
                                                         labels = c(0, 1, 2, 3, 4, 5)))),
             # gender = factor(Gender),
             gender = as.integer(as.character(factor(Gender, levels = c('Male', 'Female', 'Gender non-c
                                                     labels = c(0, 1, 2)))),
             lives_with_others = as.integer(as.character(factor(Living.Situation, levels = c('Alone', '
                                                                labels = c(0, 1)))),
             # know_us = factor(Q17),
             know_us = as.integer(as.character(factor(Q17, levels = c('No', 'Yes'),
                                                      labels = c(0, 1)))),
             location_lat = as.double(LocationLatitude),
             location_long = as.double(LocationLongitude)
)]
```

```
## Warning in eval(jsub, SDenv, parent.frame()): NAs introduced by coercion

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```

```
d2$gender[is.na(d2$gender)] <- 2
d2$age_range[is.na(d2$age_range)] <- 6
d2$lives_with_others[is.na(d2$lives_with_others)] <- 2
d2$know_us[is.na(d2$know_us)] <- 2

head(d2, 5)
```

```
##    userId treatment_seq day1_treatment day2_treatment day3_treatment
## 1:     82             6              0              1              0
## 2:     57             3              1              0              2
## 3:     89             4             NA             NA             NA
## 4:     69             3              1              0              2
```

```
## 5:     85             3              1              0              2
##    day1_steps day2_steps day3_steps age_range gender lives_with_others
## 1:         NA       5040       3788         1      0                 1
## 2:      21290      13959      13717         0      0                 1
## 3:         NA         NA         NA         1      0                 1
## 4:       6343       3247      10198         1      0                 1
## 5:      13624       5406       7851         1      1                 1
##    know_us location_lat location_long
## 1:       1     41.89250      -87.7895
## 2:       1     37.75101      -97.8220
## 3:       1     37.97240     -122.3369
## 4:       1     40.37070      -74.0084
## 5:       1     42.41730      -71.1087
```

```
#Covariate Balance Check
bal.tab(treatment_seq ~ gender + age_range + lives_with_others + know_us + location_lat + location_long
        data = d2)
```

```
## Balance Measures
##                      Type Corr.Un
## gender            Contin. -0.0625
## age_range         Contin. -0.0099
## lives_with_others Contin. -0.0105
## know_us           Contin.  0.0214
## location_lat      Contin.  0.0157
## location_long     Contin. -0.0480
##
## Sample sizes
##     Total
## All    75
```

```
cov_check <- lm(treatment_seq ~ gender + age_range + lives_with_others + know_us + location_lat + locati
                data = d2)
summary(cov_check)
```

```
##
## Call:
## lm(formula = treatment_seq ~ gender + age_range + lives_with_others +
##     know_us + location_lat + location_long, data = d2)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -2.7912 -1.4863  0.1883  1.4598  2.6363
##
## Coefficients:
##                    Estimate Std. Error t value Pr(>|t|)
## (Intercept)       1.1350717  4.1690323   0.272    0.786
## gender           -0.1639576  0.3999806  -0.410    0.683
## age_range        -0.0003737  0.1750913  -0.002    0.998
## lives_with_others -0.1171429  0.7099934  -0.165    0.869
## know_us           0.0212714  0.3840969   0.055    0.956
## location_lat      0.0465410  0.0841290   0.553    0.582
## location_long    -0.0082195  0.0124256  -0.661    0.511
```

```
##
## Residual standard error: 1.784 on 68 degrees of freedom
## Multiple R-squared:  0.01086,    Adjusted R-squared:  -0.07641
## F-statistic: 0.1245 on 6 and 68 DF,  p-value: 0.993
```

Checking for ordering/priming effect

Is previous day's treatment highly predictive of how many steps are taken today?

```
# n = 75
df <- d2

# remove subjects/rows who were non-compliant
# n = 24
df <- df[rowSums(is.na(df[,c(3:8)])) != ncol(df[,c(3:8)]), ]

head(df, 5)
```

```
##    userId treatment_seq day1_treatment day2_treatment day3_treatment
## 1:     82             6              0              1              0
## 2:     57             3              1              0              2
## 3:     69             3              1              0              2
## 4:     85             3              1              0              2
## 5:     66             4              1              2              0
##    day1_steps day2_steps day3_steps age_range gender lives_with_others
## 1:         NA       5040       3788         1      0                 1
## 2:      21290      13959      13717         0      0                 1
## 3:       6343       3247      10198         1      0                 1
## 4:      13624       5406       7851         1      1                 1
## 5:       7016       1211       5717         0      0                 1
##    know_us location_lat location_long
## 1:       1     41.89250      -87.7895
## 2:       1     37.75101      -97.8220
## 3:       1     40.37070      -74.0084
## 4:       1     42.41730      -71.1087
## 5:       1     42.35760      -71.0514
```

```
# day 3 steps using day 1 and 2 treatment
m1 <- lm(day3_steps ~ day1_treatment + day2_treatment, df)
summary(m1)
```

```
##
## Call:
## lm(formula = day3_steps ~ day1_treatment + day2_treatment, data = df)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -7119.9 -2316.1  -462.4  1377.2  8580.4
##
## Coefficients:
##                Estimate Std. Error t value Pr(>|t|)
```

```
## (Intercept)      7505.7      921.5   8.145 2.12e-10 ***
## day1_treatment   -385.7      672.7  -0.573    0.569
## day2_treatment   -365.5      600.8  -0.608    0.546
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3440 on 45 degrees of freedom
##   (3 observations deleted due to missingness)
## Multiple R-squared:  0.0142, Adjusted R-squared:  -0.02961
## F-statistic: 0.3241 on 2 and 45 DF,  p-value: 0.7248
```

```
# ATE (standard error)
print(paste0("Estimated effect of day1 treatment: ", signif(m1$coefficients[2], 3),
" (", signif(coef(summary(m1))[2,2], 3), ")"))
```

```
## [1] "Estimated effect of day1 treatment: -386 (673)"
```

```
print(paste0("Estimated effect of day2 treatment: ", signif(m1$coefficients[3], 3),
" (", signif(coef(summary(m1))[3,2], 3), ")"))
```

```
## [1] "Estimated effect of day2 treatment: -366 (601)"
```

```
# include days1,2 steps as covariates to uhderstand
# subjects' step counts hange as a function of
# treatment against waht they would typically do
m2 <- lm(day3_steps ~ day1_treatment + day2_treatment + day1_steps + day2_steps, df)
summary(m2)
```

```
##
## Call:
## lm(formula = day3_steps ~ day1_treatment + day2_treatment + day1_steps +
##     day2_steps, data = df)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -8183.6 -1375.5    61.2  1536.6  5057.0
##
## Coefficients:
##                 Estimate Std. Error t value Pr(>|t|)
## (Intercept)    2602.4071  1128.7513   2.306  0.02614 *
## day1_treatment -484.8396   517.7869  -0.936  0.35444
## day2_treatment -296.7856   460.9784  -0.644  0.52319
## day1_steps        0.2442     0.1230   1.985  0.05373 .
## day2_steps        0.4542     0.1341   3.386  0.00155 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2623 on 42 degrees of freedom
##   (4 observations deleted due to missingness)
## Multiple R-squared:  0.455,  Adjusted R-squared:  0.4031
## F-statistic: 8.766 on 4 and 42 DF,  p-value: 3.076e-05
```

```
print(paste0("Estimated effect of day1 treatment: ", signif(m2$coefficients[2], 3),
             " (", signif(coef(summary(m2))[2,2], 3), ")"))
```

```
## [1] "Estimated effect of day1 treatment: -485 (518)"
```

```
print(paste0("Estimated effect of day2 treatment: ", signif(m2$coefficients[3], 3),
             " (", signif(coef(summary(m2))[3,2], 3), ")"))
```

```
## [1] "Estimated effect of day2 treatment: -297 (461)"
```

We do not see that the previous days' treatment assignments to predict the last day's step count is highgly predicitive and significant, which is super for us!

Condense treatment sequence to 1 treatment

```
df1 <- df[,-c(4,5,7,8)]
df2 <- df[,-c(3,5,6,8)]
df3 <- df[,-c(3,4,6,7)]
names(df1)[names(df1) == "day1_treatment"] = "treatment"
names(df1)[names(df1) == "day1_steps"] = "steps"
names(df2)[names(df2) == "day2_treatment"] = "treatment"
names(df2)[names(df2) == "day2_steps"] = "steps"
names(df3)[names(df3) == "day3_treatment"] = "treatment"
names(df3)[names(df3) == "day3_steps"] = "steps"
d <- rbind(df1, df2, df3)
# combine digital and in person treatment as one
d$treatment2 <- ifelse(d$treatment == 0, 0, 1)
d$outcome <- ifelse(d$steps > 5000, 1, 0)

head(d, 5)
```

```
##    userId treatment_seq treatment steps age_range gender lives_with_others
## 1:     82             6         0    NA         1      0                 1
## 2:     57             3         1 21290         0      0                 1
## 3:     69             3         1  6343         1      0                 1
## 4:     85             3         1 13624         1      1                 1
## 5:     66             4         1  7016         0      0                 1
##    know_us location_lat location_long treatment2 outcome
## 1:       1     41.89250      -87.7895          0      NA
## 2:       1     37.75101      -97.8220          1       1
## 3:       1     40.37070      -74.0084          1       1
## 4:       1     42.41730      -71.1087          1       1
## 5:       1     42.35760      -71.0514          1       1
```

Check covariates again after transforming and create plots (Maybe we can just check covariates here?)

```r
#Covariate Balance Check
bal.tab(treatment2 ~ gender + age_range + lives_with_others + know_us + location_lat + location_long,
        data = d)
```

```
## Note: estimand and s.d.denom not specified; assuming ATE and pooled.

## Balance Measures
##                       Type Diff.Un
## gender            Contin. -0.0582
## age_range         Contin.  0.2103
## lives_with_others Contin. -0.1690
## know_us            Binary -0.0093
## location_lat      Contin.  0.0444
## location_long     Contin.  0.0661
##
## Sample sizes
##     Control Treated
## All      71      82
```

```r
cov_check1 <- lm(treatment_seq ~ gender + age_range + lives_with_others + know_us + location_lat + loca
                 data = d)
summary(cov_check1)
```

```
##
## Call:
## lm(formula = treatment_seq ~ gender + age_range + lives_with_others +
##     know_us + location_lat + location_long, data = d)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.45660 -1.45557 -0.07703  1.47990  2.76916
##
## Coefficients:
##                    Estimate Std. Error t value Pr(>|t|)
## (Intercept)       -0.949777   3.094677  -0.307    0.759
## gender             0.222693   0.275319   0.809    0.420
## age_range         -0.037168   0.124112  -0.299    0.765
## lives_with_others  0.220037   0.511785   0.430    0.668
## know_us            0.316655   0.508372   0.623    0.534
## location_lat       0.074428   0.056090   1.327    0.187
## location_long     -0.007474   0.009532  -0.784    0.434
##
## Residual standard error: 1.701 on 146 degrees of freedom
## Multiple R-squared:  0.02282,    Adjusted R-squared:  -0.01733
## F-statistic: 0.5683 on 6 and 146 DF,  p-value: 0.755
```

```r
require(gridExtra)
```

```
## Loading required package: gridExtra
```

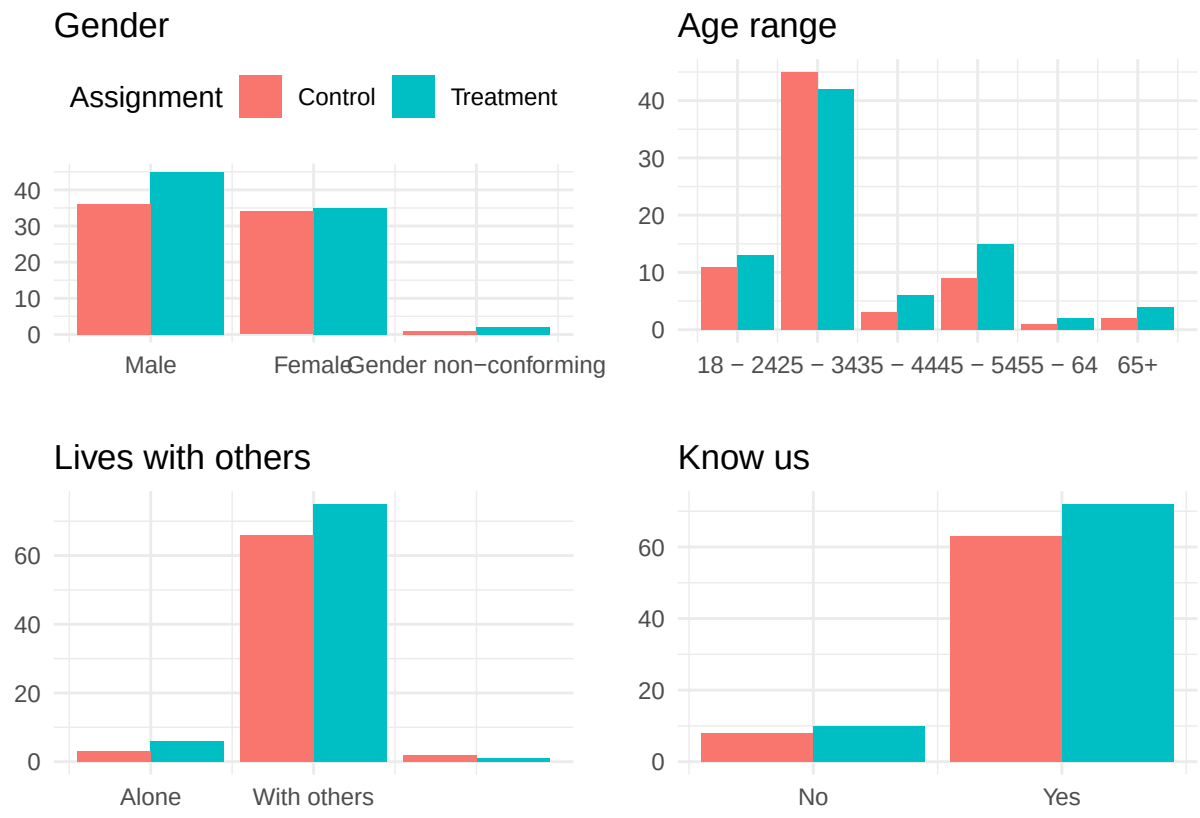
```r
d.gender <- d[, c("gender", "treatment2")]
p_gender <- ggplot(d.gender, aes(x=gender, fill = factor(treatment2))) +
  geom_bar(stat="count", position=position_dodge()) +
  theme_minimal() + theme(legend.position="top") +
  xlab("") + ylab("") + ggtitle("Gender") +
  guides(fill = guide_legend(title = "Assignment")) +
  scale_fill_discrete(labels = c("Control", "Treatment")) +
  scale_x_continuous(breaks = c(0, 1, 2),
                     labels = c('Male', 'Female', 'Gender non-conforming'))

d.age <- d[, c("age_range", "treatment2")]
p_age <- ggplot(d.age, aes(x=age_range, fill = factor(treatment2))) +
  geom_bar(stat="count", position=position_dodge()) +
  theme_minimal() + theme(legend.position="none") +
  xlab("") + ylab("") + ggtitle("Age range") +
  # guides(fill = guide_legend(title = "Assignment")) +
  # scale_fill_discrete(labels = c("Control", "Treatment")) +
  scale_x_continuous(breaks = c(0, 1, 2, 3, 4, 5),
                   labels = c('18 - 24',
                              "25 - 34",
                              "35 - 44",
                              "45 - 54",
                              "55 - 64",
                              "65+"))

d.others <- d[, c("lives_with_others", "treatment2")]
p_others <- ggplot(d.others, aes(x=lives_with_others, fill = factor(treatment2))) +
  geom_bar(stat="count", position=position_dodge()) +
  theme_minimal() + theme(legend.position="none") +
  xlab("") + ylab("") + ggtitle("Lives with others") +
  # guides(fill = guide_legend(title = "Assignment")) +
  # scale_fill_discrete(labels = c("Control", "Treatment")) +
  scale_x_continuous(breaks = c(0, 1),
                     labels = c('Alone', 'With others'))

d.know_us <- d[, c("know_us", "treatment2")]
p_know_us <- ggplot(d.know_us, aes(x=know_us, fill = factor(treatment2))) +
  geom_bar(stat="count", position=position_dodge()) +
  theme_minimal() + theme(legend.position="none") +
  xlab("") + ylab("") + ggtitle("Know us") +
  # guides(fill = guide_legend(title = "Assignment")) +
  # scale_fill_discrete(labels = c("Control", "Treatment")) +
  scale_x_continuous(breaks = c(0, 1),
                     labels = c('No', 'Yes'))

grid.arrange(p_gender, p_age, p_others, p_know_us,
             ncol = 2)
```



T-test and power calculations

```
###  Control vs treatment (digital+in person)
t.test(d[treatment == 0]$outcome, d[treatment == 1]$outcome)
```

```
##
##  Welch Two Sample t-test
##
## data:  d[treatment == 0]$outcome and d[treatment == 1]$outcome
## t = -1.5548, df = 87.831, p-value = 0.1236
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -0.29649330  0.03620224
## sample estimates:
## mean of x mean of y
## 0.7076923 0.8378378
```

```
# since we fail to reject the null hypothesis,
# let's calculate number of subjects needed for 80% power
effect_size <- cohensD(d[treatment == 0]$outcome, d[treatment == 1]$outcome)
pwr.t.test(power = 0.8, d = effect_size, sig.level = 0.05, type = "two.sample")
```

```
##
```

```
##      Two-sample t test power calculation
##
##               n = 172.172
##               d = 0.3028018
##       sig.level = 0.05
##           power = 0.8
##     alternative = two.sided
##
## NOTE: n is number in *each* group
```

data manipulation for paired t test!

```
'%!in%' <- function(x,y)!('%in%'(x,y))
# limit to those who complied and
# get data frame in workable format
d_complied <- rbindlist(list(subset(df, treatment_seq == 1 & df$day1_treatment == assigned_treatment_seq
                                    & df$day2_treatment == assigned_treatment_seq[1,2]
                                    & df$day3_treatment == assigned_treatment_seq[1,3]),
                             subset(df, treatment_seq == 2 & df$day1_treatment == assigned_treatment_seq
                                    & df$day2_treatment == assigned_treatment_seq[2,2]
                                    & df$day3_treatment == assigned_treatment_seq[2,3]),
                             subset(df, treatment_seq == 3 & df$day1_treatment == assigned_treatment_seq
                                    & df$day2_treatment == assigned_treatment_seq[3,2]
                                    & df$day3_treatment == assigned_treatment_seq[3,3]),
                             subset(df, treatment_seq == 4 & df$day1_treatment == assigned_treatment_seq
                                    & df$day2_treatment == assigned_treatment_seq[4,2]
                                    & df$day3_treatment == assigned_treatment_seq[4,3]),
                             subset(df, treatment_seq == 5 & df$day1_treatment == assigned_treatment_seq
                                    & df$day2_treatment == assigned_treatment_seq[5,2]
                                    & df$day3_treatment == assigned_treatment_seq[5,3]),
                             subset(df, treatment_seq == 6 & df$day1_treatment == assigned_treatment_seq
                                    & df$day2_treatment == assigned_treatment_seq[6,2]
                                    & df$day3_treatment == assigned_treatment_seq[6,3])
))
d_not_complied <- subset(df, userId %!in% d_complied$userId)
d_not_complied_ok <- subset(d_not_complied, d_not_complied$day1_treatment != d_not_complied$day2_treatme
                            d_not_complied$day1_treatment != d_not_complied$day3_treatment &
                            d_not_complied$day2_treatment != d_not_complied$day3_treatment)

d_usable <- rbind(d_complied, d_not_complied_ok)
d <- rbindlist(list(d_usable[1:nrow(d_usable),c("day1_treatment","day1_steps")],
                    d_usable[1:nrow(d_usable),c("day2_treatment","day2_steps")],
                    d_usable[1:nrow(d_usable),c("day3_treatment","day3_steps")]))
names(d) <- c("treatment","steps")
# interpolate using median steps
d$steps[is.na(d$steps)] <- median(d[which(!is.na(d$steps))]$steps)
d$outcome <- ifelse(d$steps > 5000, 1, 0)

# CACE
ITT_lm <- lm(outcome ~ treatment, data = d)
summary(ITT_lm)$coefficients[2]
```

```
## [1] -0.04411765
```

```
# COMMENTED LINES BELOW HAS TO BE FIXED!
# SKIP DOWN TO T TEST IN LINE 290
# combine digital and in person as one treatment as
# "Both in person and through digital means"
# d1 <- d_usable
# d1a <- subset(d1, d1$day1_treatment == 1 & d1$day2_treatment == 2)
# d1a[, treatment_total_steps := day1_steps + day2_steps]
# d1b <- subset(d1, d1$day2_treatment == 1 & d1$day3_treatment == 2)
# d1b[, treatment_total_steps := day2_steps + day3_steps]
# d1c <- subset(d1, d1$day1_treatment == 1 & d1$day3_treatment == 2)
# d1c[, treatment_total_steps := day1_steps + day2_steps]
# d1d <- subset(d1, d1$day2_treatment == 2 & d1$day3_treatment == 1)
# d1d[, treatment_total_steps := day2_steps + day3_steps]
# d1e <- subset(d1, d1$day1_treatment == 2 & d1$day3_treatment == 1)
# d1e[, treatment_total_steps := day1_steps + day2_steps]
# d1f <- subset(d1, d1$day1_treatment == 2 & d1$day2_treatment == 1)
# d1f[, treatment_total_steps := day2_steps + day3_steps]
#
# d1_comb <- rbind(d1a, d1b, d1c, d1d, d1e, d1f)
#
# d1 <- rbindlist(list(d1_comb[1:nrow(d1_comb),c("day1_treatment","day1_steps")],
#                      d1_comb[1:nrow(d1_comb),c("day2_treatment","day2_steps")],
#                      d1_comb[1:nrow(d1_comb),c("day3_treatment","day3_steps")]))
# names(d1) <- c("treatment","steps")
# d1[d1$treatment == 1 | d1$treatment == 2, ]$treatment <- 3
# # linear interpolation
# # d1 <- na.approx(d1, maxgap=5)
# d1 <- data.table(d1)
# d1$steps[is.na(d1$steps)] <- median(d1[which(!is.na(d1$steps))]$steps)
# d1$outcome <- ifelse(d1$steps > 5000, 1, 0)

t.test(d[treatment == 0]$outcome, d[treatment == 1]$outcome, paired = T)
```

```
##
##  Paired t-test
##
## data:  d[treatment == 0]$outcome and d[treatment == 1]$outcome
## t = 0, df = 33, p-value = 1
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -0.1920722  0.1920722
## sample estimates:
## mean of the differences
##                       0
```

```
cohensD(d[treatment == 0]$outcome, d[treatment == 1]$outcome, method = "paired")
```

```
## [1] 0
```

```r
### Control vs in person
t.test(d[treatment == 0]$outcome, d[treatment == 2]$outcome, paired = T)
```

```
##
##  Paired t-test
##
## data:  d[treatment == 0]$outcome and d[treatment == 2]$outcome
## t = 0.90205, df = 33, p-value = 0.3736
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -0.1107732  0.2872437
## sample estimates:
## mean of the differences
##              0.08823529
```

```r
cohensD(d[treatment == 0]$outcome, d[treatment == 2]$outcome, method = "paired")
```

```
## [1] 0.1547007
```

```r
### Control vs in person + digital
# t.test(d1[treatment == 0]$outcome, d1[treatment == 3]$outcome)
```