Final Study Data Analysis

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```r
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
```

```r
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
```

```r
library(stargazer)
```

```
## 
## Please cite as:
```

```
##  Hlavac, Marek (2018). stargazer: Well-Formatted Regression and Summary Statistics Tables.
```

```
##  R package version 5.2.2. https://CRAN.R-project.org/package=stargazer
```

```r
library(pander)
```

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(" " = "." , "," = "" ))
# subset d2 for those who responded (Submitted.Data = 1)
d2 <- d2[Submitted.Data == 1]

# 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 person
                                                                            'Through digital means'),
                                                             labels = c(0, 2, 1)))),
             day2_treatment = as.integer(as.character(factor(Q10, levels = c('Not applicable', 'In perso
                                                                             '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 perso
                                                                             '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
## Warning in eval(jsub, SDenv, parent.frame()): NAs introduced by coercion

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

```
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:     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
```

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

```
## Balance Measures
##                                Type Corr.Un
## factor(gender)_0             Binary -0.0770
## factor(gender)_1             Binary  0.1053
## factor(gender)_2             Binary -0.1007
## factor(age_range)_0          Binary  0.0138
## factor(age_range)_1          Binary -0.0633
## factor(age_range)_2          Binary  0.2684
## factor(age_range)_3          Binary -0.0503
## factor(age_range)_4          Binary  0.0677
## factor(age_range)_5          Binary -0.1438
## factor(lives_with_others)_0  Binary -0.0292
## factor(lives_with_others)_1  Binary -0.0094
## factor(lives_with_others)_2  Binary  0.0677
## factor(know_us)_1            Binary  0.0426
## location_lat                Contin.  0.1095
## location_long               Contin.  0.0512
##
```

```
## Sample sizes
##     Total
## All    51
```

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

```
##
## Call:
## lm(formula = treatment_seq ~ factor(gender) + factor(age_range) +
##     factor(lives_with_others) + factor(know_us) + location_lat +
##     location_long, data = d2)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -2.6981 -0.9913  0.0000  0.9265  2.9062
##
## Coefficients:
##                            Estimate Std. Error t value Pr(>|t|)
## (Intercept)                -6.17461    6.18816  -0.998   0.3247
## factor(gender)1             0.37850    0.57242   0.661   0.5125
## factor(gender)2            -1.89910    2.02685  -0.937   0.3547
## factor(age_range)1         -0.19090    0.77885  -0.245   0.8077
## factor(age_range)2          2.25170    1.29109   1.744   0.0892 .
## factor(age_range)3          0.41468    1.07541   0.386   0.7019
## factor(age_range)4          0.77973    1.96081   0.398   0.6931
## factor(age_range)5         -1.18844    1.44306  -0.824   0.4153
## factor(lives_with_others)1  0.52266    1.15299   0.453   0.6529
## factor(lives_with_others)2  1.27148    2.20112   0.578   0.5669
## factor(know_us)1            0.98364    1.00578   0.978   0.3343
## location_lat                0.15597    0.11227   1.389   0.1729
## location_long              -0.01893    0.01889  -1.002   0.3225
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.768 on 38 degrees of freedom
## Multiple R-squared:  0.1755, Adjusted R-squared:  -0.08485
## F-statistic: 0.6741 on 12 and 38 DF,  p-value: 0.7647
```

Checking for ordering/priming effect AND adding non-compliant but okay users

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

```
'%!in%' <- function(x,y)!('%in%'(x,y))
# n = 51
df1 <- d2

# remove subjects/rows who were non-compliant (n = 2)
# n = 49
df1 <- df1[rowSums(is.na(df1[,c(6:8)])) != ncol(df1[,c(6:8)]), ]
```

```
head(df1, 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
```

```
# n = 30
d_followed_treatment_sequence <- rbindlist(list(subset(df1, treatment_seq == 1 & df1$day1_treatment == a
                                                       & df1$day2_treatment == assigned_treatment_seq[1
                                                       & df1$day3_treatment == assigned_treatment_seq[1
                                                subset(df1, treatment_seq == 2 & df1$day1_treatment == a
                                                       & df1$day2_treatment == assigned_treatment_seq[2
                                                       & df1$day3_treatment == assigned_treatment_seq[2
                                                subset(df1, treatment_seq == 3 & df1$day1_treatment == a
                                                       & df1$day2_treatment == assigned_treatment_seq[3
                                                       & df1$day3_treatment == assigned_treatment_seq[3
                                                subset(df1, treatment_seq == 4 & df1$day1_treatment == a
                                                       & df1$day2_treatment == assigned_treatment_seq[4
                                                       & df1$day3_treatment == assigned_treatment_seq[4
                                                subset(df1, treatment_seq == 5 & df1$day1_treatment == a
                                                       & df1$day2_treatment == assigned_treatment_seq[5
                                                       & df1$day3_treatment == assigned_treatment_seq[5
                                                subset(df1, treatment_seq == 6 & df1$day1_treatment == a
                                                       & df1$day2_treatment == assigned_treatment_seq[6
                                                       & df1$day3_treatment == assigned_treatment_seq[6
))

# n = 19
d_not_followed_treatment_sequence <- subset(df1, userId %!in% d_followed_treatment_sequence$userId)

d_not_followed_but_ok <- subset(d_not_followed_treatment_sequence, d_not_followed_treatment_sequence$da
                                  d_not_followed_treatment_sequence$day1_treatment != d_not_followed_tr
                                  d_not_followed_treatment_sequence$day2_treatment != d_not_followed_tr

na.omit(d_not_followed_but_ok)
```

```
##    userId treatment_seq day1_treatment day2_treatment day3_treatment
## 1:      3             3              1              2              0
## 2:     73             5              2              1              0
## 3:     75             5              2              1              0
##    day1_steps day2_steps day3_steps age_range gender lives_with_others
## 1:       7000       5000       6000         1      1                 1
## 2:       6050       5671       3251         1      0                 1
## 3:      10422       5187       9696         2      0                 1
##    know_us location_lat location_long
## 1:       1      48.2804       11.5768
## 2:       1      42.3576      -71.0514
## 3:       1      42.3576      -71.0514
```

```
d_not_followed_no_NA <- subset(d_not_followed_treatment_sequence, userId %!in% d_not_followed_but_ok$us
# n = 15
d_not_followed_no_NA <- na.omit(d_not_followed_no_NA)

# n = 33
df <- rbind(d_followed_treatment_sequence, d_not_followed_but_ok)
# n = 48
df2 <- rbind(d_followed_treatment_sequence, d_not_followed_but_ok, d_not_followed_no_NA)

# day 3 steps using day 1 and 2 treatment on complied + people who followed within subject design
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
## -7878.7 -1605.2   -79.7  1887.3  6165.3
##
## Coefficients:
##                Estimate Std. Error t value Pr(>|t|)
## (Intercept)      8615.6     1381.1   6.238  8.3e-07 ***
## day1_treatment   -736.9      804.1  -0.916    0.367
## day2_treatment   -957.0      804.1  -1.190    0.244
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3296 on 29 degrees of freedom
##   (1 observation deleted due to missingness)
## Multiple R-squared:  0.06136,    Adjusted R-squared:  -0.003372
## F-statistic: 0.9479 on 2 and 29 DF,  p-value: 0.3992
```

```
# 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: -737 (804)"
```

```
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: -957 (804)"
```

```
# include days1,2 steps as covariates to understand
# subjects' step counts have 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
## -8317.4  -898.4    88.7  1156.5  5167.1
##
## Coefficients:
##                 Estimate Std. Error t value Pr(>|t|)
## (Intercept)    2534.3724  2161.0040   1.173   0.2511
## day1_treatment -392.4212   702.2724  -0.559   0.5809
## day2_treatment   -8.3389   746.4587  -0.011   0.9912
## day1_steps        0.3441     0.1553   2.216   0.0353 *
## day2_steps        0.2922     0.2029   1.440   0.1614
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2845 on 27 degrees of freedom
##   (1 observation deleted due to missingness)
## Multiple R-squared:  0.3489, Adjusted R-squared:  0.2524
## F-statistic: 3.617 on 4 and 27 DF,  p-value: 0.01741
```

```
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: -392 (702)"
```

```
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: -8.34 (746)"
```

```
# day 3 steps using day 1 and 2 treatment on complied + people who followed within subject design + res
m1 <- lm(day3_steps ~ day1_treatment + day2_treatment, df2)
summary(m1)
```

```
##
## Call:
## lm(formula = day3_steps ~ day1_treatment + day2_treatment, data = df2)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -7168.1 -2208.5  -428.6  1439.1  8449.1
##
## Coefficients:
##                 Estimate Std. Error t value Pr(>|t|)
## (Intercept)       7645.4      932.3   8.200 2.08e-10 ***
## day1_treatment    -477.2      679.0  -0.703    0.486
## day2_treatment    -369.8      600.9  -0.615    0.542
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3440 on 44 degrees of freedom
##   (1 observation deleted due to missingness)
## Multiple R-squared:  0.01807,    Adjusted R-squared:  -0.02657
## F-statistic: 0.4047 on 2 and 44 DF,  p-value: 0.6696
```

```
# 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: -477 (679)"
```

```
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: -370 (601)"
```

```
# include days1,2 steps as covariates to understand
# subjects' step counts have as a function of
# treatment against waht they would typically do
m2 <- lm(day3_steps ~ day1_treatment + day2_treatment + day1_steps + day2_steps, df2)
summary(m2)
```

```
##
## Call:
## lm(formula = day3_steps ~ day1_treatment + day2_treatment + day1_steps +
##     day2_steps, data = df2)
##
## 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
##   (1 observation 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!

```
stargazer(m1, m2,
          dep.var.labels=c("Steps - Day 3"),
          covariate.labels=c("Treatment - Day 1", "Treatment - Day 2", "Steps - Day 1", "Steps - Day 2"
          omit.stat=c("all"))
```

% Table created by stargazer v.5.2.2 by Marek Hlavac, Harvard University. E-mail: hlavac at fas.harvard.edu
% Date and time: Thu, Dec 20, 2018 - 23:45:11

Condense treatment sequence to 1 treatment

```
df1.1 <- df[,-c(4,5,7,8)]
df2.1 <- df[,-c(3,5,6,8)]
df3.1 <- df[,-c(3,4,6,7)]
names(df1.1)[names(df1.1) == "day1_treatment"] = "treatment"
names(df1.1)[names(df1.1) == "day1_steps"] = "steps"
names(df2.1)[names(df2.1) == "day2_treatment"] = "treatment"
names(df2.1)[names(df2.1) == "day2_steps"] = "steps"
names(df3.1)[names(df3.1) == "day3_treatment"] = "treatment"
names(df3.1)[names(df3.1) == "day3_steps"] = "steps"
d <- rbind(df1.1, df2.1, df3.1)
# 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)
```

Table 1:

	Dependent variable:	
	Steps - Day 3	
	(1)	(2)
Treatment - Day 1	−477.240	−484.840
	(679.024)	(517.787)
Treatment - Day 2	−369.761	−296.786
	(600.936)	(460.978)
Steps - Day 1		0.244*
		(0.123)
Steps - Day 2		0.454***
		(0.134)
Constant	7,645.381***	2,602.407**
	(932.308)	(1,128.751)
Note:	*p<0.1; **p<0.05; ***p<0.01	

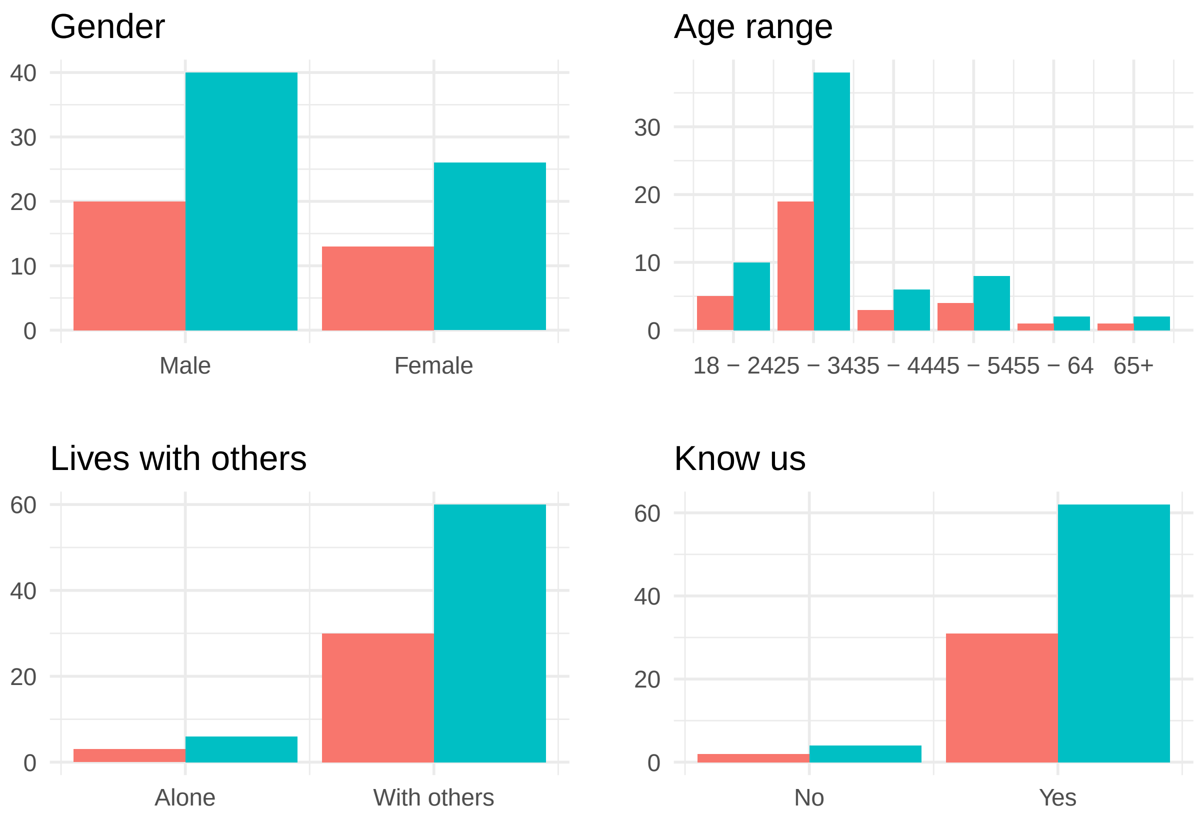
```
##    userId treatment_seq treatment steps age_range gender lives_with_others
## 1:     28             1         0 13929         0      0                 1
## 2:     56             1         0  5368         1      1                 1
## 3:     25             1         0  5802         1      0                 1
## 4:     22             1         0  5689         3      0                 1
## 5:     86             1         0  5868         1      0                 1
##    know_us location_lat location_long treatment2 outcome
## 1:       1     36.05251      -79.1077          0       1
## 2:       1     42.35760      -71.0514          0       1
## 3:       1     42.37700      -71.1256          0       1
## 4:       1     42.35760      -71.0514          0       1
## 5:       1     42.61240      -83.0345          0       1
```

Make some pretty plots to show distribution, populatin etc.

```r
# population that actually responded to data collection survey
require(gridExtra)
```

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

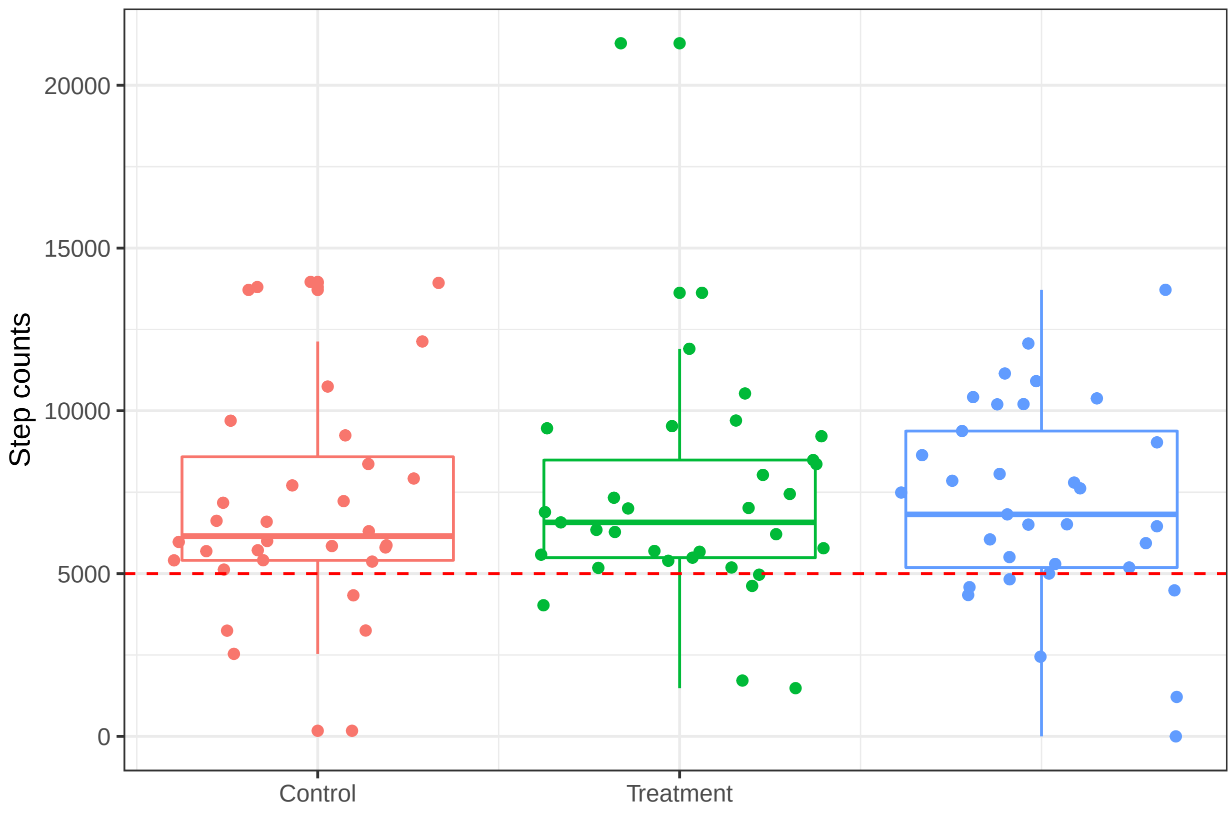
```r
d.gender <- d[, c("gender", "treatment2")]
p_gender <- ggplot(d.gender, aes(x=gender, fill = factor(treatment2))) +
  geom_bar(stat="count", position=position_dodge()) +
  theme_minimal() + theme(legend.position="right") +
  xlab("") + ylab("") + ggtitle("Gender") +
  guides(fill = guide_legend(title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

p_gender_no_legend <- ggplot(d.gender, aes(x=gender, fill = factor(treatment2))) +
  geom_bar(stat="count", position=position_dodge()) +
  theme_minimal() + theme(legend.position="none") +
  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\n 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'))

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



```
# control and digital and in person distribution
ggplot(d, aes(x=treatment, y=steps, colour = factor(treatment))) +
geom_boxplot() + geom_jitter() +
geom_hline(yintercept=5000, linetype="dashed", color = "red") +
xlab("") + ylab("Step counts") + theme_bw() +
    scale_x_continuous(breaks = c(0, 1),
                       labels = c('Control', 'Treatment')) +
  theme(legend.position="none")
```

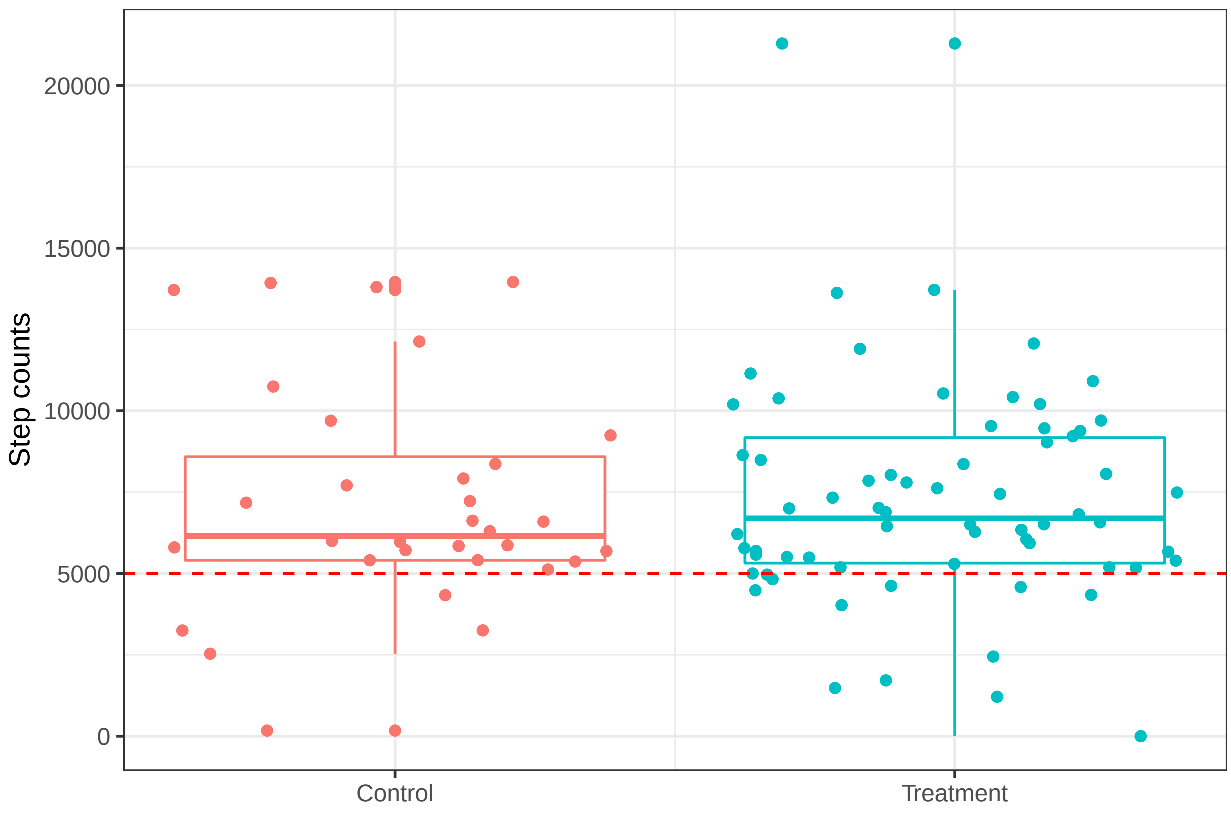
```
## Warning: Removed 1 rows containing non-finite values (stat_boxplot).
```

```
## Warning: Removed 1 rows containing missing values (geom_point).
```



```
# control and treatment (digital+in person) when time component removed
ggplot(d, aes(x=treatment2, y=steps, colour = factor(treatment2))) +
geom_boxplot() + geom_jitter() +
geom_hline(yintercept=5000, linetype="dashed", color = "red") +
xlab("") + ylab("Step counts") + theme_bw() +
    scale_x_continuous(breaks = c(0, 1),
                       labels = c('Control', 'Treatment')) +
  theme(legend.position="none")
```

```
## Warning: Removed 1 rows containing non-finite values (stat_boxplot).

## Warning: Removed 1 rows containing missing values (geom_point).
```



For control vs digital and control vs in person

```
# d$treatment <- factor(d$treatment)
d$userId <- factor(d$userId)
fit_3 <- lm(outcome ~ treatment + userId , d)
# se clustered based on userID
se_3 <- coeftest(fit_3, vcovHC(fit_3, type = 'HC', cluster = "userID"))

fit_3_covariates <- lm(outcome ~ treatment + age_range + gender + lives_with_others + know_us + locatio
# robust se
se_3_covariates <- sqrt(diag(vcovHC(fit_3_covariates, type = 'HC')))

# ATE (standard error)
print(paste0("Estimated effect of treatment (control, in person, digital): ", signif(fit_3$coefficients
" (", signif(se_3[2,2], 3), ")"))
```

```
## [1] "Estimated effect of treatment (control, in person, digital): -0.0465 (0.0379)"
```

```
print(paste0("Estimated effect of treatment (control, in person, digital) + covariates: ", signif(fit_3
" (", signif(se_3_covariates[2], 3), ")"))
```

```
## [1] "Estimated effect of treatment (control, in person, digital) + covariates: 0.0468 (0.0465)"
```

```
stargazer(fit_3,
          se=list(se_3),
          omit = c("treatment0"),
          dep.var.labels=c("Steps > 5000"),
          # covariate.labels=c('Commit digitally', 'Commit in person', "User ID", "Constant"),
          omit.stat=c("all"))
```

% Table created by stargazer v.5.2.2 by Marek Hlavac, Harvard University. E-mail: hlavac at fas.harvard.edu
% Date and time: Thu, Dec 20, 2018 - 23:45:13

```
stargazer(fit_3, fit_3_covariates,
          se=list(se_3, se_3_covariates),
          dep.var.labels=c("Steps > 5000"),
          column.labels = c("User ID", "Covariates"),
          # covariate.labels=c('Commit digitally', 'Commit in person', "User ID", "Age range", "Gender"
          omit.stat=c("all"))
```

% Table created by stargazer v.5.2.2 by Marek Hlavac, Harvard University. E-mail: hlavac at fas.harvard.edu
% Date and time: Thu, Dec 20, 2018 - 23:45:13

test hypothesis that telling others make it more likely to take >5000 steps (control vs treatment)

```
#suppress intercept term
fit_2 <- lm(outcome ~ treatment2 + userId, d)
#  se clustered based on userID
se_2 <- coeftest(fit_2, vcovHC(fit_2, type = 'HC', cluster = "userID"))

fit_2_covariates <- lm(outcome ~ treatment2 + age_range + gender + lives_with_others + know_us + locati
# robust se
se_2_covariates <- sqrt(diag(vcovHC(fit_2_covariates, type = 'HC')))

# ATE (standard error)
print(paste0("Estimated effect of treatment (control, treatment): ", signif(fit_2$coefficients[2], 3),
" (", signif(se_2[2], 3), ")"))
```

```
## [1] "Estimated effect of treatment (control, treatment): -0.0469 (-0.0469)"
```

```
print(paste0("Estimated effect of treatment (control, treatment) + covariates: ", signif(fit_2_covariat
" (", signif(se_2_covariates[2], 3), ")"))
```

```
## [1] "Estimated effect of treatment (control, treatment) + covariates: -0.0447 (0.073)"
```

```
stargazer(fit_2,
          se=list(se_2),
          dep.var.labels=c("Steps > 5000"),
          # covariate.labels=c("Social commitment", "User ID"),
          omit.stat=c("all"))
```

Table 2:

	Dependent variable:
	Steps > 5000
treatment	−0.047
	(−0.047)
userId2	0.333
	(0.333)
userId3	0.667
	(0.667)
userId6	1.000
	(1.000)
userId13	1.000
	(1.000)
userId14	0.333
	(0.333)
userId17	0.333
	(0.333)
userId19	1.000
	(1.000)
userId22	0.667
	(0.667)
userId25	1.000
	(1.000)
userId26	1.000
	(1.000)
userId28	1.000
	(1.000)
userId33	1.000
	(1.000)
userId39	1.000
	(1.000)
userId45	1.000
	(1.000)
userId47	0.333
	(0.333)
userId54	1.000
	(1.000)
userId56	1.000
	(1.000)
userId57	1.000

Table 3:

	Dependent variable:	
	Steps > 5000	
	User ID	Covariates
	(1)	(2)
treatment	−0.047	−0.045
	(−0.047)	(0.046)
userId2	0.333	
	(0.333)	
userId3	0.667	
	(0.667)	
userId6	1.000	
	(1.000)	
userId13	1.000	
	(1.000)	
userId14	0.333	
	(0.333)	
userId17	0.333	
	(0.333)	
userId19	1.000	
	(1.000)	
userId22	0.667	
	(0.667)	
userId25	1.000	
	(1.000)	
userId26	1.000	
	(1.000)	
userId28	1.000	
	(1.000)	
userId33	1.000	
	(1.000)	
userId39	1.000	
	(1.000)	
userId45	1.000	
	(1.000)	
userId47	0.333	
	(0.333)	
userId54	1.000	
	(1.000)	
userId56	1.000	
	(1.000)	

Table 4:

	Dependent variable:
	Steps > 5000
treatment2	−0.047 (−0.047)
userId2	0.333 (0.333)
userId3	0.667 (0.667)
userId6	1.000 (1.000)
userId13	1.000 (1.000)
userId14	0.333 (0.333)
userId17	0.333 (0.333)
userId19	1.000 (1.000)
userId22	0.667 (0.667)
userId25	1.000 (1.000)
userId26	1.000 (1.000)
userId28	1.000 (1.000)
userId33	1.000 (1.000)
userId39	1.000 (1.000)
userId45	1.000 (1.000)
userId47	0.333 (0.333)
userId54	1.000 (1.000)
userId56	1.000 (1.000)
userId57	1.000

% Table created by stargazer v.5.2.2 by Marek Hlavac, Harvard University. E-mail: hlavac at fas.harvard.edu
% Date and time: Thu, Dec 20, 2018 - 23:45:13

```r
stargazer(fit_2, fit_2_covariates,
          se=list(se_2, se_2_covariates),
          dep.var.labels=c("Steps > 5000"),
          column.labels = c("User ID", "Covariates"),
          # covariate.labels=c("Treatment", "User ID", "Age range", "Gender", "Has housemate", "Knows u
          omit.stat=c("all"))
```

% Table created by stargazer v.5.2.2 by Marek Hlavac, Harvard University. E-mail: hlavac at fas.harvard.edu
% Date and time: Thu, Dec 20, 2018 - 23:45:13

power calculations

```r
###  Control vs digital
# since we fail to reject the null hypothesis,
# let's calculate number of subjects needed for 80% power
effect_size_digital <- cohensD(d[treatment == 0]$steps, d[treatment == 1]$steps)
#power we got from our experiment
pwr.t2n.test(n1 = nrow(d[treatment == 0,]), n2 = nrow(d[treatment == 1,]), d = effect_size_digital, sig
```

```
##
##      t test power calculation
##
##              n1 = 33
##              n2 = 33
##               d = 0.03394626
##       sig.level = 0.05
##           power = 0.05211626
##     alternative = two.sided
```

```r
# 80% powered test
pwr.t.test(power = 0.8, d = effect_size_digital, sig.level = 0.05, type = "two.sample")
```

```
##
##      Two-sample t test power calculation
##
##               n = 13623.33
##               d = 0.03394626
##       sig.level = 0.05
##           power = 0.8
##     alternative = two.sided
##
## NOTE: n is number in *each* group
```

```r
#
#
#
#
```

Table 5:

	Dependent variable:	
	Steps > 5000	
	User ID	Covariates
	(1)	(2)
treatment2	−0.047	−0.045
	(−0.047)	(0.073)
userId2	0.333	
	(0.333)	
userId3	0.667	
	(0.667)	
userId6	1.000	
	(1.000)	
userId13	1.000	
	(1.000)	
userId14	0.333	
	(0.333)	
userId17	0.333	
	(0.333)	
userId19	1.000	
	(1.000)	
userId22	0.667	
	(0.667)	
userId25	1.000	
	(1.000)	
userId26	1.000	
	(1.000)	
userId28	1.000	
	(1.000)	
userId33	1.000	
	(1.000)	
userId39	1.000	
	(1.000)	
userId45	1.000	
	(1.000)	
userId47	0.333	
	(0.333)	
userId54	1.000	
	(1.000)	
userId56	1.000	
	(1.000)	

```
###  Control vs in person
# since we fail to reject the null hypothesis,
# let's calculate number of subjects needed for 80% power
effect_size_person <- cohensD(d[treatment == 0]$steps, d[treatment == 2]$steps)
#power we got from our experiment
pwr.t2n.test(n1 = nrow(d[treatment == 0,]), n2 = nrow(d[treatment == 2,]), d = effect_size_person, sig.l
```

```
##
##      t test power calculation
##
##              n1 = 33
##              n2 = 33
##               d = 0.01871318
##       sig.level = 0.05
##           power = 0.05064253
##     alternative = two.sided
```

```
# 80% powered test
pwr.t.test(power = 0.8, d = effect_size_person, sig.level = 0.05, type = "two.sample")
```

```
##
##      Two-sample t test power calculation
##
##               n = 44828.14
##               d = 0.01871318
##       sig.level = 0.05
##           power = 0.8
##     alternative = two.sided
##
## NOTE: n is number in *each* group
```

```
### extra plots
# day1
pd1 <- ggplot(df, aes(x=day1_treatment, y=day1_steps, colour = factor(day1_treatment))) +
  geom_boxplot() + geom_jitter() +
  geom_hline(yintercept=5000, linetype="dashed", color = "red") +
  xlab("") + ylab("Step counts") + theme_bw() +
  scale_x_continuous(breaks = c(0, 1, 2),
                     labels = c(0, 1, 2)) +
  # labels = c('Control', 'In person', 'Through digital means')) +
  theme(legend.position="none") + ggtitle("Step count - day 1")
# day2
pd2 <- ggplot(df, aes(x=day2_treatment, y=day2_steps, colour = factor(day2_treatment))) +
geom_boxplot() + geom_jitter() +
geom_hline(yintercept=5000, linetype="dashed", color = "red") +
xlab("") + ylab("Step counts") + theme_bw() +
    scale_x_continuous(breaks = c(0, 1, 2),
                       labels = c(0, 1, 2)) +
    #                  labels = c('Control', 'In person', 'Through digital means')) +
  theme(legend.position="none") + ggtitle("Step count - day 2")
# day3
pd3 <- ggplot(df, aes(x=day3_treatment, y=day3_steps, colour = factor(day3_treatment))) +
geom_boxplot() + geom_jitter() +
geom_hline(yintercept=5000, linetype="dashed", color = "red") +
xlab("") + ylab("Step counts") + theme_bw() +
    scale_x_continuous(breaks = c(0, 1, 2),
                       labels = c(0, 1, 2)) +
    #                  labels = c('Control', 'In person', 'Through digital means')) +
  theme(legend.position="none") + ggtitle("Step count - day 3")
```