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
```

```
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
```

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"))
```

```r
d2[UserId == 65,]$Q10 <- "In person"
d2[UserId == 13,]$Q6 <- "Through digital means"
d2$`Living Situation`[is.na(d2$`Living Situation`)] <- "Other"
d2$Age[is.na(d2$Age)] <- "Other"
d2$Q17[is.na(d2$Q17)] <- "Other"
# stringsAsFactors = F)
names(d2) <- str_replace_all(names(d2), c(" " = "." , "," = "" ))
# subset d2 for those who responded (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 = factor(Treatment.Seq),
             day1_treatment = factor(Q6, levels = c('Not applicable', 'Through digital means', 'In perso
                                                    labels = c(0, 1, 2)),
             day2_treatment = factor(Q10, levels = c('Not applicable', 'Through digital means', 'In pers
                                                    labels = c(0, 1, 2)),
             day3_treatment = factor(Q14, levels = c('Not applicable', 'Through digital means', 'In pers
                                                    labels = c(0, 1, 2)),
             day1_steps = as.numeric(gsub("\\,", "", Q7)),
             day2_steps = as.numeric(gsub("\\,", "", Q11)),
             day3_steps = as.numeric(gsub("\\,", "", Q15)),
             age_range = factor(Age, levels = c('18 - 24',
                                                "25 - 34",
                                                "35 - 44",
                                                "45 - 54",
                                                "55 - 64",
                                                "65+", "Other"),
                                labels = c(0, 1, 2, 3, 4, 5, 6)),
             # gender = factor(Gender),
             gender = factor(Gender, levels = c('Male', 'Female', 'Gender non-conforming'),
                                                    labels = c(0, 1, 2)),
             lives_with_others = factor(Living.Situation, levels = c('Alone', 'With others', "Other"),
                                                            labels = c(0, 1, 2)),
             # know_us = factor(Q17),
             know_us = factor(Q17, levels = c('No', 'Yes', "Other"),
                                                     labels = c(0, 1, 2)),
             location_lat = as.double(LocationLatitude),
             location_long = as.double(LocationLongitude),
             submitted_data = Submitted.Data
)]
```

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

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```

```r
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 submitted_data
## 1:       1     41.89250      -87.7895              1
## 2:       1     37.75101      -97.8220              1
## 3:       1     37.97240     -122.3369              0
## 4:       1     40.37070      -74.0084              1
## 5:       1     42.41730      -71.1087              1
```

```
#Covariate Balance Check 1
bal.tab(as.numeric(treatment_seq) ~ gender + age_range + lives_with_others + know_us + location_lat + lo
        data = d2)
```

```
## Balance Measures
##                        Type Corr.Un
## gender_0             Binary  0.0420
## gender_1             Binary -0.0182
## gender_2             Binary -0.1035
## age_range_0          Binary  0.0345
## age_range_1          Binary -0.0282
## age_range_2          Binary  0.0465
## age_range_3          Binary -0.0404
## age_range_4          Binary  0.0327
## age_range_5          Binary -0.1473
## age_range_6          Binary  0.1688
## lives_with_others_0  Binary  0.0253
## lives_with_others_1  Binary -0.0365
## lives_with_others_2  Binary  0.0327
## know_us_0            Binary  0.0588
## know_us_1            Binary -0.1192
## know_us_2            Binary  0.0945
## location_lat        Contin.  0.0157
## location_long       Contin. -0.0480
##
## Sample sizes
##     Total
## All    75
```

```
cov_check <- glm(treatment_seq ~ gender + age_range + lives_with_others + know_us + location_lat + locat
                 data = d2, family = "binomial")
summary(cov_check)
```

```
##
```

```
## Call:
## glm(formula = treatment_seq ~ gender + age_range + lives_with_others +
##     know_us + location_lat + location_long, family = "binomial",
##     data = d2)
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -2.38912   0.00013   0.44181   0.67023   1.06273
##
## Coefficients:
##                       Estimate Std. Error z value Pr(>|z|)
## (Intercept)          29.09470 2542.97303   0.011    0.991
## gender1               0.49426    0.72044   0.686    0.493
## gender2              17.75319 6522.63873   0.003    0.998
## age_range1           -1.10826    1.14725  -0.966    0.334
## age_range2           -0.94866    1.60418  -0.591    0.554
## age_range3           -0.67654    1.56728  -0.432    0.666
## age_range4           15.75157 6522.63872   0.002    0.998
## age_range5           16.20801 4588.30570   0.004    0.997
## age_range6           15.72524 6522.63877   0.002    0.998
## lives_with_others1  -16.68741 2542.95681  -0.007    0.995
## lives_with_others2   -0.89821 7000.81744   0.000    1.000
## know_us1             -0.82234    1.21485  -0.677    0.498
## know_us2              0.67090    1.62619   0.413    0.680
## location_lat         -0.19082    0.18154  -1.051    0.293
## location_long         0.02415    0.02545   0.949    0.343
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 65.950  on 74  degrees of freedom
## Residual deviance: 56.106  on 60  degrees of freedom
## AIC: 86.106
##
## Number of Fisher Scoring iterations: 17
```

```
stargazer(cov_check,
          dep.var.labels=c("Treatment sequence"),
          covariate.labels=c("Female", "Gender non-conforming",
                             "Ages 25-34",
                             "Ages 35-44",
                             "Ages 45-54",
                             "Ages 55-64",
                             "Ages 65+", "Agest other",
                             "Has housemates", "Housemates unknown",
                             "Knows authors", "Knows authors unkonwn",
                             "Latitude", "Longitutde"),
          omit.stat=c("all"),
          single.row = TRUE)
```

% Table created by stargazer v.5.2.2 by Marek Hlavac, Harvard University. E-mail: hlavac at fas.harvard.edu
% Date and time: Sat, Dec 22, 2018 - 02:40:21

Table 1:

	Dependent variable:
	Treatment sequence
Female	0.494 (0.720)
Gender non-conforming	17.753 (6,522.639)
Ages 25-34	−1.108 (1.147)
Ages 35-44	−0.949 (1.604)
Ages 45-54	−0.677 (1.567)
Ages 55-64	15.752 (6,522.639)
Ages 65+	16.208 (4,588.306)
Agest other	15.725 (6,522.639)
Has housemates	−16.687 (2,542.957)
Housemates unknown	−0.898 (7,000.817)
Knows authors	−0.822 (1.215)
Knows authors unkonwn	0.671 (1.626)
Latitude	−0.191 (0.182)
Longitutde	0.024 (0.025)
Constant	29.095 (2,542.973)
Note:	*p<0.1; **p<0.05; ***p<0.01

attrition check

```
lm_attrit <- lm(submitted_data ~ treatment_seq + age_range + gender + lives_with_others + know_us + loca
summary(lm_attrit)
```

```
##
## Call:
## lm(formula = submitted_data ~ treatment_seq + age_range + gender +
##     lives_with_others + know_us + location_lat + location_long,
##     data = d2)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.00766 -0.08803  0.02795  0.20232  0.66351
##
## Coefficients:
##                    Estimate Std. Error t value Pr(>|t|)
## (Intercept)       -1.603817   0.994669  -1.612 0.112596
## treatment_seq2    -0.046842   0.155938  -0.300 0.765014
## treatment_seq3    -0.013064   0.149640  -0.087 0.930750
## treatment_seq4    -0.053922   0.149343  -0.361 0.719436
## treatment_seq5    -0.239999   0.149378  -1.607 0.113855
## treatment_seq6    -0.239732   0.142557  -1.682 0.098306 .
## age_range1         0.153469   0.116962   1.312 0.194928
## age_range2         0.168041   0.170424   0.986 0.328441
## age_range3         0.405011   0.176223   2.298 0.025371 *
## age_range4         0.327384   0.372228   0.880 0.382943
## age_range5         0.265268   0.280916   0.944 0.349148
## age_range6        -0.277031   0.391906  -0.707 0.482625
```

```
## gender1            -0.022546   0.087380  -0.258 0.797350
## gender2            -0.243760   0.399468  -0.610 0.544234
## lives_with_others1  0.153391   0.157930   0.971 0.335670
## lives_with_others2  0.472487   0.395141   1.196 0.236927
## know_us1            0.277886   0.134986   2.059 0.044279 *
## know_us2           -0.615430   0.162941  -3.777 0.000392 ***
## location_lat        0.041077   0.018501   2.220 0.030541 *
## location_long      -0.004258   0.003073  -1.386 0.171432
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.3418 on 55 degrees of freedom
## Multiple R-squared:  0.6063, Adjusted R-squared:  0.4703
## F-statistic: 4.458 on 19 and 55 DF,  p-value: 7.006e-06
```

```
# know_us is highly predictive of whether or not people attrited. This makes sense.
```

```
stargazer(lm_attrit,
          dep.var.labels=c("Final survey submitted"),
          covariate.labels=c("Treatment Seq 2", "Treatment Seq 3", "Treatment Seq 4", "Treatment Seq 5"
                             "Ages 25-34",
                             "Ages 35-44",
                             "Ages 45-54",
                             "Ages 55-64",
                             "Ages 65+", "Agest other",
                             "Female", "Gender non-conforming",
                             "Has housemates", "Housemates unknown",
                             "Knows authors", "Knows authors unkonwn",
                             "Latitude", "Longitutde"),
          omit.stat=c("all"),
          single.row = TRUE)
```

% Table created by stargazer v.5.2.2 by Marek Hlavac, Harvard University. E-mail: hlavac at fas.harvard.edu
% Date and time: Sat, Dec 22, 2018 - 02:40:21

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))

d2 <- d2[submitted_data == 1]

# 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)
```

Table 2:

	Dependent variable:
	Final survey submitted
Treatment Seq 2	−0.047 (0.156)
Treatment Seq 3	−0.013 (0.150)
Treatment Seq 4	−0.054 (0.149)
Treatment Seq 5	−0.240 (0.149)
Treatment Seq 6	−0.240* (0.143)
Ages 25-34	0.153 (0.117)
Ages 35-44	0.168 (0.170)
Ages 45-54	0.405** (0.176)
Ages 55-64	0.327 (0.372)
Ages 65+	0.265 (0.281)
Agest other	−0.277 (0.392)
Female	−0.023 (0.087)
Gender non-conforming	−0.244 (0.399)
Has housemates	0.153 (0.158)
Housemates unknown	0.472 (0.395)
Knows authors	0.278** (0.135)
Knows authors unkonwn	−0.615*** (0.163)
Latitude	0.041** (0.019)
Longitutde	−0.004 (0.003)
Constant	−1.604 (0.995)
Note:	*p<0.1; **p<0.05; ***p<0.01

```
##    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 submitted_data
## 1:       1     41.89250      -87.7895              1
## 2:       1     37.75101      -97.8220              1
## 3:       1     40.37070      -74.0084              1
## 4:       1     42.41730      -71.1087              1
## 5:       1     42.35760      -71.0514              1
```

```
# 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$day
                                d_not_followed_treatment_sequence$day1_treatment != d_not_followed_tre
                                d_not_followed_treatment_sequence$day2_treatment != d_not_followed_tre

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 submitted_data
## 1:       1      48.2804       11.5768              1
## 2:       1      42.3576      -71.0514              1
## 3:       1      42.3576      -71.0514              1
```

```
d_not_followed_no_NA <- subset(d_not_followed_treatment_sequence, userId %!in% d_not_followed_but_ok$use
# 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
## -8011.1 -2215.5  -140.7  1981.6  6162.7
##
## Coefficients:
##                 Estimate Std. Error t value Pr(>|t|)
## (Intercept)         9223       2210   4.173  0.00028 ***
## day1_treatment1    -1212       2011  -0.603  0.55174
## day1_treatment2    -1422       1694  -0.839  0.40862
## day2_treatment1    -1795       2301  -0.780  0.44220
## day2_treatment2    -2044       1694  -1.207  0.23799
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3406 on 27 degrees of freedom
##   (1 observation deleted due to missingness)
## Multiple R-squared:  0.06684,    Adjusted R-squared:  -0.0714
## F-statistic: 0.4835 on 4 and 27 DF,  p-value: 0.7476
```

```
# 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: -1210 (2010)"
```

```
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: -1420 (1690)"
```

```
# 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
## -8433.3 -1006.2   120.8  1148.3  5072.7
##
## Coefficients:
##                  Estimate Std. Error t value Pr(>|t|)
## (Intercept)     2967.7308  2745.2966   1.081   0.2900
## day1_treatment1 -592.3631  1756.6233  -0.337   0.7388
## day1_treatment2 -784.1472  1480.5725  -0.530   0.6010
```

```
## day2_treatment1 -703.6553  2026.6544  -0.347   0.7313
## day2_treatment2 -134.8561  1571.7867  -0.086   0.9323
## day1_steps         0.3476     0.1611   2.158   0.0408 *
## day2_steps         0.2882     0.2121   1.359   0.1863
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2944 on 25 degrees of freedom
##   (1 observation deleted due to missingness)
## Multiple R-squared:  0.3545, Adjusted R-squared:  0.1996
## F-statistic: 2.288 on 6 and 25 DF,  p-value: 0.06743
```

```
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: -592 (1760)"
```

```
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: -784 (1480)"
```

```
# 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
## -7337.2 -2223.0  -254.6  1440.9  8568.5
##
## Coefficients:
##                 Estimate Std. Error t value Pr(>|t|)
## (Intercept)       7565.3     1065.7   7.099 1.05e-08 ***
## day1_treatment1   -228.2     1243.9  -0.183    0.855
## day1_treatment2  -1104.7     1560.4  -0.708    0.483
## day2_treatment1   -272.7     1452.1  -0.188    0.852
## day2_treatment2   -778.9     1242.1  -0.627    0.534
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3519 on 42 degrees of freedom
##   (1 observation deleted due to missingness)
## Multiple R-squared:  0.01946,    Adjusted R-squared:  -0.07393
## F-statistic: 0.2084 on 4 and 42 DF,  p-value: 0.9324
```

```
# 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: -228 (1240)"
```

```
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: -1100 (1560)"
```

```
# 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
## -8371.9 -1147.5    -9.2  1643.8  4932.4
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)     2681.3421  1180.5601   2.271  0.02859 *
## day1_treatment1 -495.0087   948.4029  -0.522  0.60459
## day1_treatment2 -841.6432  1188.4174  -0.708  0.48292
## day2_treatment1 -857.1243  1110.6529  -0.772  0.44481
## day2_treatment2 -560.6809   951.8148  -0.589  0.55913
## day1_steps         0.2537     0.1268   2.001  0.05223 .
## day2_steps         0.4527     0.1368   3.308  0.00199 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2675 on 40 degrees of freedom
##   (1 observation deleted due to missingness)
## Multiple R-squared:  0.4601, Adjusted R-squared:  0.3792
## F-statistic: 5.682 on 6 and 40 DF,  p-value: 0.0002417
```

```
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: -495 (948)"
```

```
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: -842 (1190)"
```

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"),
          column.labels=c("Short", "Long"),
          covariate.labels=c("Digital - Day 1", "In person - Day 1", "Digital - Day 2", "In person - Day
          omit.stat=c("all"),
          single.row = TRUE)
```

% Table created by stargazer v.5.2.2 by Marek Hlavac, Harvard University. E-mail: hlavac at fas.harvard.edu
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Table 3:

	Dependent variable:	
	Steps - Day 3	
	Short	Long
	(1)	(2)
Digital - Day 1	−228.177 (1,243.893)	−495.009 (948.403)
In person - Day 1	−1,104.705 (1,560.442)	−841.643 (1,188.417)
Digital - Day 2	−272.684 (1,452.143)	−857.124 (1,110.653)
In person - Day 2	−778.868 (1,242.131)	−560.681 (951.815)
Steps - Day 1		0.254* (0.127)
Steps - Day 2		0.453*** (0.137)
Constant	7,565.343*** (1,065.706)	2,681.342** (1,180.560)
Note:		*p<0.1; **p<0.05; ***p<0.01

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)
```

```
##    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 submitted_data treatment2 outcome
## 1:       1     36.05251      -79.1077              1          0       1
## 2:       1     42.35760      -71.0514              1          0       1
## 3:       1     42.37700      -71.1256              1          0       1
## 4:       1     42.35760      -71.0514              1          0       1
## 5:       1     42.61240      -83.0345              1          0       1
```

```
#Covariate Balance Check on treatment = 0,1,2
bal.tab(as.numeric(treatment) ~ gender + age_range + lives_with_others + know_us + location_lat + locati
       data = d)
```

```
## Balance Measures
##                        Type Corr.Un
## gender_1             Binary       0
## age_range_0          Binary       0
## age_range_1          Binary       0
## age_range_2          Binary       0
## age_range_3          Binary       0
## age_range_4          Binary       0
## age_range_5          Binary       0
## lives_with_others_1  Binary       0
## know_us_1            Binary       0
## location_lat        Contin.       0
## location_long       Contin.       0
##
## Sample sizes
##     Total
## All    99
```

```
cov_check1 <- glm(treatment ~ gender + age_range + lives_with_others + know_us + location_lat + locatio
               data = d, family = "binomial")
summary(cov_check1)
```

```
##
## Call:
## glm(formula = treatment ~ gender + age_range + lives_with_others +
##     know_us + location_lat + location_long, family = "binomial",
##     data = d)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.4823  -1.4823   0.9005   0.9005   0.9005
##
## Coefficients:
##                      Estimate Std. Error z value Pr(>|z|)
## (Intercept)         6.931e-01  5.308e+00   0.131    0.896
## gender1             2.732e-15  4.935e-01   0.000    1.000
## age_range1         -3.597e-17  6.602e-01   0.000    1.000
## age_range2          4.724e-15  9.772e-01   0.000    1.000
## age_range3          5.482e-15  8.759e-01   0.000    1.000
## age_range4          5.798e-15  1.406e+00   0.000    1.000
## age_range5          9.445e-17  1.402e+00   0.000    1.000
```

```
## lives_with_others1  1.785e-15  8.347e-01   0.000    1.000
## know_us1            7.432e-15  1.054e+00   0.000    1.000
## location_lat        2.312e-15  1.020e-01   0.000    1.000
## location_long      -3.429e-16  1.617e-02   0.000    1.000
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 126.03  on 98  degrees of freedom
## Residual deviance: 126.03  on 88  degrees of freedom
## AIC: 148.03
##
## Number of Fisher Scoring iterations: 4
```

```
#Covariate Balance Check on treatment = 0,1
bal.tab(as.numeric(treatment2) ~ gender + age_range + lives_with_others + know_us + location_lat + loca
       data = d)
```

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

```
## Balance Measures
##                         Type Diff.Un
## gender_1              Binary       0
## age_range_0           Binary       0
## age_range_1           Binary       0
## age_range_2           Binary       0
## age_range_3           Binary       0
## age_range_4           Binary       0
## age_range_5           Binary       0
## lives_with_others_1   Binary       0
## know_us_1             Binary       0
## location_lat         Contin.       0
## location_long        Contin.       0
##
## Sample sizes
##     Control Treated
## All      33      66
```

```
cov_check2 <- glm(treatment2 ~ gender + age_range + lives_with_others + know_us + location_lat + locati
               data = d, family = "binomial")
summary(cov_check2)
```

```
##
## Call:
## glm(formula = treatment2 ~ gender + age_range + lives_with_others +
##     know_us + location_lat + location_long, family = "binomial",
##     data = d)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.4823  -1.4823   0.9005   0.9005   0.9005
##
## Coefficients:
```

```
##                      Estimate Std. Error z value Pr(>|z|)
## (Intercept)         6.931e-01  5.308e+00   0.131    0.896
## gender1             2.732e-15  4.935e-01   0.000    1.000
## age_range1         -3.597e-17  6.602e-01   0.000    1.000
## age_range2          4.724e-15  9.772e-01   0.000    1.000
## age_range3          5.482e-15  8.759e-01   0.000    1.000
## age_range4          5.798e-15  1.406e+00   0.000    1.000
## age_range5          9.445e-17  1.402e+00   0.000    1.000
## lives_with_others1  1.785e-15  8.347e-01   0.000    1.000
## know_us1            7.432e-15  1.054e+00   0.000    1.000
## location_lat        2.312e-15  1.020e-01   0.000    1.000
## location_long      -3.429e-16  1.617e-02   0.000    1.000
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 126.03  on 98  degrees of freedom
## Residual deviance: 126.03  on 88  degrees of freedom
## AIC: 148.03
##
## Number of Fisher Scoring iterations: 4
```

```
stargazer(cov_check2, cov_check1,
          dep.var.labels=c("2 levels treatment", "3 levels treatment"),
          covariate.labels=c("Female",
                             "Ages 25-34",
                             "Ages 35-44",
                             "Ages 45-54",
                             "Ages 55-64",
                             "Ages 65+",
                             "Has housemate", "Knows us","Latitute", "Longitude", "Constant"),
          omit.stat=c("all"),
          single.row = TRUE)
```

% Table created by stargazer v.5.2.2 by Marek Hlavac, Harvard University. E-mail: hlavac at fas.harvard.edu
% Date and time: Sat, Dec 22, 2018 - 02:40:21

Make some pretty plots to show distribution, populatin etc.

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

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

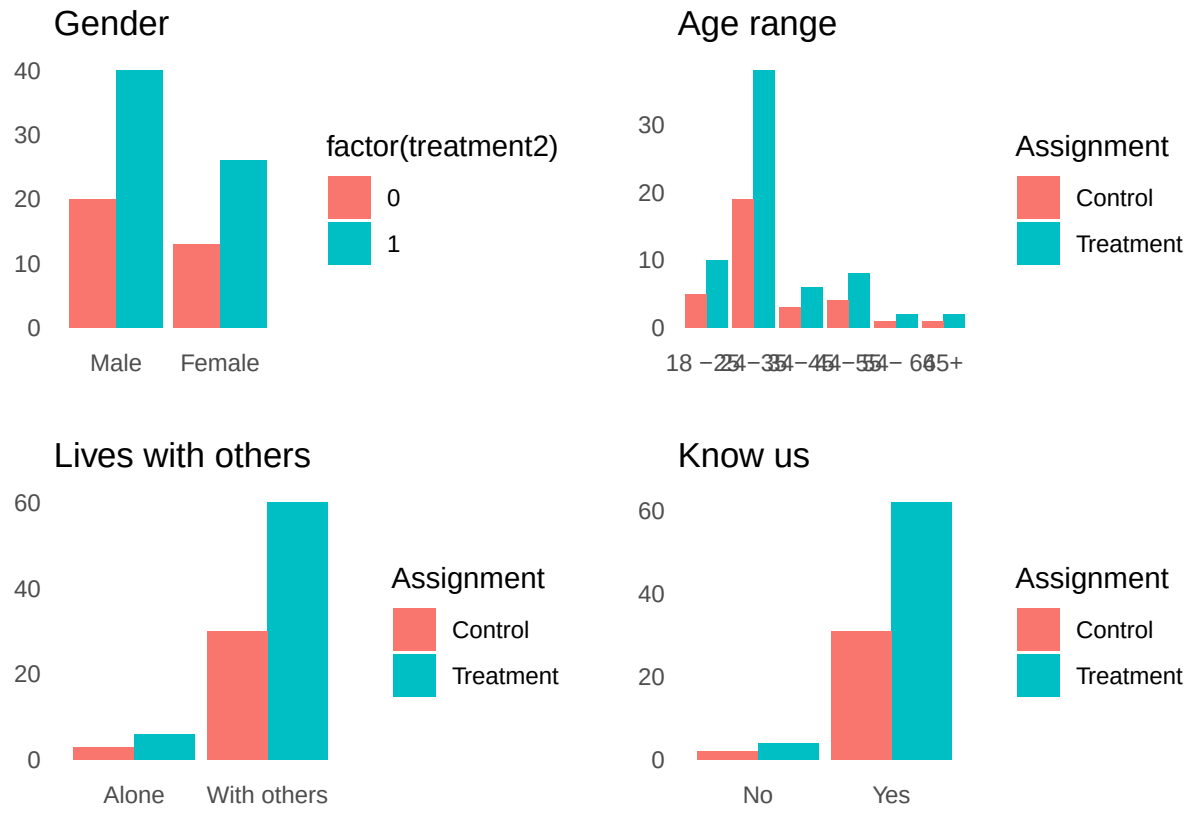
```
d.gender <- d[, c("gender", "treatment2")]
p_gender <- ggplot(d.gender, aes(x=gender, fill = factor(treatment2))) +
  geom_bar(stat="count", position=position_dodge()) +
  theme_minimal() + theme(legend.position="right",
                          panel.border = element_blank(),
          panel.grid.major = element_blank(),
          panel.grid.minor = element_blank()) +
  xlab("") + ylab("") + ggtitle("Gender") +
```

Table 4:

	Dependent variable:	
	2 levels treatment	3 levels treatment
	(1)	(2)
Female	0.000 (0.494)	0.000 (0.494)
Ages 25-34	−0.000 (0.660)	−0.000 (0.660)
Ages 35-44	0.000 (0.977)	0.000 (0.977)
Ages 45-54	0.000 (0.876)	0.000 (0.876)
Ages 55-64	0.000 (1.406)	0.000 (1.406)
Ages 65+	0.000 (1.402)	0.000 (1.402)
Has housemate	0.000 (0.835)	0.000 (0.835)
Knows us	0.000 (1.054)	0.000 (1.054)
Latitute	0.000 (0.102)	0.000 (0.102)
Longitude	−0.000 (0.016)	−0.000 (0.016)
Constant	0.693 (5.308)	0.693 (5.308)
Note:		*p<0.1; **p<0.05; ***p<0.01

```
  guides(fill = guide_legend(title = "Assignment")) +
  scale_fill_discrete(labels = c("Control", "Treatment")) +
  scale_x_discrete(breaks = c(0, 1, 2),
                   labels = c('Male', 'Female', 'Gender\n non-conforming'))
# ggsave("gender.png", width = 5, height = 3.5, units = "in",dpi = 300)

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="right",
                          panel.border = element_blank(),
          panel.grid.major = element_blank(),
          panel.grid.minor = element_blank()) +
  xlab("") + ylab("") + ggtitle("Gender") +
  # guides(fill = guide_legend(title = "Assignment")) +
  # scale_fill_discrete(labels = c("Control", "Treatment")) +
  scale_x_discrete(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="right",
                          panel.border = element_blank(),
          panel.grid.major = element_blank(),
          panel.grid.minor = element_blank()) +
  xlab("") + ylab("") + ggtitle("Age range") +
  guides(fill = guide_legend(title = "Assignment")) +
  scale_fill_discrete(labels = c("Control", "Treatment")) +
  scale_x_discrete(breaks = c(0, 1, 2, 3, 4, 5, 6 ),
                   labels = c('18 - 24',
                              "25 - 34",
```

```
                              "35 - 44",
                              "45 - 54",
                              "55 - 64",
                              "65+", "NA"))

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="right",
                          panel.border = element_blank(),
          panel.grid.major = element_blank(),
          panel.grid.minor = element_blank()) +
  xlab("") + ylab("") + ggtitle("Lives with others") +
  guides(fill = guide_legend(title = "Assignment")) +
  scale_fill_discrete(labels = c("Control", "Treatment")) +
  scale_x_discrete(breaks = c(0, 1, 2),
                   labels = c('Alone', 'With others', "NA"))
ggsave("other.png", width = 5, height = 3.5, units = "in",dpi = 300)


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="right",
                          panel.border = element_blank(),
          panel.grid.major = element_blank(),
          panel.grid.minor = element_blank()) +
  xlab("") + ylab("") + ggtitle("Know us") +
  guides(fill = guide_legend(title = "Assignment")) +
  scale_fill_discrete(labels = c("Control", "Treatment")) +
  scale_x_discrete(breaks = c(0, 1),
                   labels = c('No', 'Yes'))
ggsave("know.png", width = 5, height = 3.5, units = "in",dpi = 300)


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



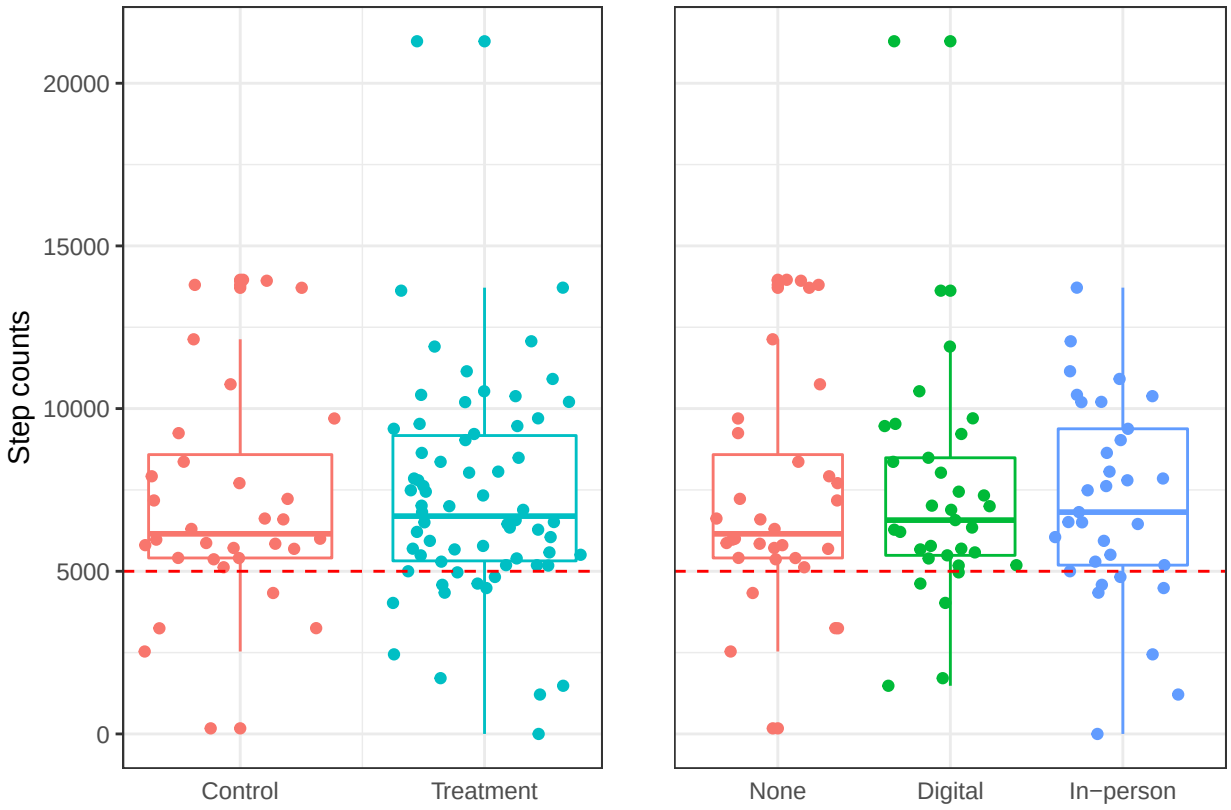

```
# control and digital and in person distribution
dist3 <- ggplot(d, aes(x=treatment, y=steps, colour = factor(treatment))) +
geom_boxplot() + geom_jitter() +
geom_hline(yintercept=5000, linetype="dashed", color = "red") +
xlab("") + ylab("") + theme_bw() +
   theme(axis.text.y = element_blank(), axis.ticks = element_blank()) +
    scale_x_discrete(breaks = c(0, 1, 2),
                     labels = c('None', 'Digital', "In-person")) +
  theme(legend.position="none")

# control and treatment (digital+in person) when time component removed
dist2 <- 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() + theme(axis.ticks.x = element_blank()) +
    scale_x_continuous(breaks = c(0, 1),
                     labels = c('Control', 'Treatment')) +
  theme(legend.position="none")

grid.arrange(dist2, dist3,
             ncol = 2)
```

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

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

```
## 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 + location
# 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): -0.00142 (0.0652)"
```

```
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: -0.0884 (0.078)"
```

```
stargazer(fit_3,
          se=list(se_3[,2]),
          omit = "userId",
          omit.labels = "Subject IDs ommitted",
          dep.var.labels=c("Steps > 5000"),
          covariate.labels=c('Digital commitment', 'In person commitment',"Constant"),
          omit.stat=c("all"),
          single.row = TRUE)
```

% Table created by stargazer v.5.2.2 by Marek Hlavac, Harvard University. E-mail: hlavac at fas.harvard.edu
% Date and time: Sat, Dec 22, 2018 - 02:40:23

Table 5:

	Dependent variable:
	Steps > 5000
Digital commitment	−0.001 (0.065)
In person commitment	−0.092 (0.076)
Constant	0.031 (0.049)
Subject IDs ommitted	Yes
Note:	*p<0.1; **p<0.05; ***p<0.01

```
stargazer(fit_3,
          se=list(se_3[,2]),
          dep.var.labels=c("Steps > 5000"),
          covariate.labels=c('Digital commitment', 'In person commitment',"Constant"),
          omit.stat=c("all"),
          single.row = TRUE)
```

% Table created by stargazer v.5.2.2 by Marek Hlavac, Harvard University. E-mail: hlavac at fas.harvard.edu
% Date and time: Sat, Dec 22, 2018 - 02:40:23

```
stargazer(fit_3, fit_3_covariates,
          se=list(se_3[,2], se_3_covariates),
                    omit = "userId",
          omit.labels = "Subject IDs ommitted",
          dep.var.labels=c("Steps > 5000"),
          column.labels = c("User ID", "Covariates"),
          covariate.labels=c('Digital commitment',
                             'In person commitment',
                             "Ages 25-34",
                             "Ages 35-44",
                             "Ages 45-54",
                             "Ages 55-64",
```

Table 6:

	Dependent variable:
	Steps > 5000
Digital commitment	−0.001 (0.065)
In person commitment	−0.092 (0.076)
Constant	0.333 (0.261)
userId3	0.667*** (0.248)
userId6	1.000*** (0.035)
userId13	1.000*** (0.035)
userId14	0.333 (0.261)
userId17	0.333 (0.261)
userId19	1.000*** (0.035)
userId22	0.667*** (0.248)
userId25	1.000*** (0.035)
userId26	1.000*** (0.035)
userId28	1.000*** (0.035)
userId33	1.000*** (0.035)
userId39	1.000*** (0.035)
userId45	1.000*** (0.035)
userId47	0.333 (0.298)
userId54	1.000*** (0.035)
userId56	1.000*** (0.035)
userId57	1.000*** (0.035)
userId58	0.667** (0.287)
userId59	1.000*** (0.035)
userId65	1.016*** (0.046)
userId66	0.667*** (0.248)
userId68	1.000*** (0.035)
userId69	0.667** (0.287)
userId73	0.667** (0.287)
userId75	1.000*** (0.035)
userId77	1.000*** (0.035)
userId84	1.000*** (0.035)
userId85	1.000*** (0.035)
userId86	0.667*** (0.248)
userId88	1.000*** (0.035)
userId91	1.000*** (0.035)
Constant	0.031 (0.049)
Note:	*p<0.1; **p<0.05; ***p<0.01

```
                          "Ages 65+",
                          "Female","Has housemate",
                          "Knows us",
                          "Latitute",
                          "Longitude",
                          "Constant"),
          omit.stat=c("all"),
          single.row = TRUE)
```

% Table created by stargazer v.5.2.2 by Marek Hlavac, Harvard University. E-mail: hlavac at fas.harvard.edu
% Date and time: Sat, Dec 22, 2018 - 02:40:23

Table 7:

	Dependent variable:	
	Steps > 5000	
	User ID	Covariates
	(1)	(2)
Digital commitment	−0.001 (0.065)	0.003 (0.078)
In person commitment	−0.092 (0.076)	−0.088 (0.092)
Ages 25-34		0.157 (0.139)
Ages 35-44		0.156 (0.141)
Ages 45-54		0.086 (0.157)
Ages 55-64		0.369** (0.144)
Ages 65+		0.340** (0.145)
Female		−0.068 (0.076)
Has housemate		0.303* (0.160)
Knows us		0.237* (0.132)
Latitute		0.030 (0.019)
Longitude		−0.004 (0.003)
Constant	0.031 (0.049)	−1.315 (0.951)
Subject IDs ommitted	Yes	No
Note:		*p<0.1; **p<0.05; ***p<0.01

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: -0.0429 (0.0737)"
```

```
stargazer(fit_2,
          se=list(se_2[,2]),
          omit = "userId",
          omit.labels = "Subject IDs ommitted",
          dep.var.labels=c("Steps > 5000"),
          covariate.labels=c('Social commitment', "Constant"),
          omit.stat=c("all"),
          single.row = TRUE)
```

% Table created by stargazer v.5.2.2 by Marek Hlavac, Harvard University. E-mail: hlavac at fas.harvard.edu
% Date and time: Sat, Dec 22, 2018 - 02:40:24

Table 8:

	Dependent variable:
	Steps > 5000
Social commitment	−0.047 (0.064)
Constant	0.031 (0.045)
Subject IDs ommitted	Yes
Note:	*p<0.1; **p<0.05; ***p<0.01

```
stargazer(fit_2,
          se=list(se_2[,2]),
          dep.var.labels=c("Steps > 5000"),
          covariate.labels=c('Social commitment', "Constant"),
          omit.stat=c("all"),
          single.row = TRUE)
```

% Table created by stargazer v.5.2.2 by Marek Hlavac, Harvard University. E-mail: hlavac at fas.harvard.edu
% Date and time: Sat, Dec 22, 2018 - 02:40:24

```
stargazer(fit_2, fit_2_covariates,
          se=list(se_2[,2], se_2_covariates),
          omit = "userId",
          omit.labels = "Subject IDs ommitted",
          dep.var.labels=c("Steps > 5000"),
          column.labels = c("User ID", "Covariates"),
          covariate.labels=c('Social commitment',
```

Table 9:

	Dependent variable:
	Steps > 5000
Social commitment	−0.047 (0.064)
Constant	0.333 (0.260)
userId3	0.667** (0.266)
userId6	1.000*** (0.018)
userId13	1.000*** (0.018)
userId14	0.333 (0.260)
userId17	0.333 (0.260)
userId19	1.000*** (0.018)
userId22	0.667** (0.266)
userId25	1.000*** (0.018)
userId26	1.000*** (0.018)
userId28	1.000*** (0.018)
userId33	1.000*** (0.018)
userId39	1.000*** (0.018)
userId45	1.000*** (0.018)
userId47	0.333 (0.279)
userId54	1.000*** (0.018)
userId56	1.000*** (0.018)
userId57	1.000*** (0.018)
userId58	0.667** (0.285)
userId59	1.000*** (0.018)
userId65	1.016*** (0.025)
userId66	0.667** (0.266)
userId68	1.000*** (0.018)
userId69	0.667** (0.285)
userId73	0.667** (0.285)
userId75	1.000*** (0.018)
userId77	1.000*** (0.018)
userId84	1.000*** (0.018)
userId85	1.000*** (0.018)
userId86	0.667** (0.266)
userId88	1.000*** (0.018)
userId91	1.000*** (0.018)
Constant	0.031 (0.045)
Note:	*p<0.1; **p<0.05; ***p<0.01

```
                          "Ages 25-34",
                          "Ages 35-44",
                          "Ages 45-54",
                          "Ages 55-64",
                          "Ages 65+",
                          "Female",
                          "Has housemate",
                          "Knows us",
                          "Latitute",
                          "Longitude",
                          "Constant"),
          omit.stat=c("all"),
          single.row = TRUE)
```

% Table created by stargazer v.5.2.2 by Marek Hlavac, Harvard University. E-mail: hlavac at fas.harvard.edu
% Date and time: Sat, Dec 22, 2018 - 02:40:24

Table 10:

	Dependent variable:	
	Steps > 5000	
	User ID	Covariates
	(1)	(2)
Social commitment	−0.047 (0.064)	−0.043 (0.074)
Ages 25-34		0.157 (0.140)
Ages 35-44		0.156 (0.140)
Ages 45-54		0.086 (0.160)
Ages 55-64		0.369*** (0.143)
Ages 65+		0.340** (0.144)
Female		−0.068 (0.076)
Has housemate		0.303* (0.155)
Knows us		0.237* (0.131)
Latitute		0.030 (0.019)
Longitude		−0.004 (0.003)
Constant	0.031 (0.045)	−1.315 (0.970)
Subject IDs ommitted	Yes	No
Note:		*p<0.1; **p<0.05; ***p<0.01

power calculations

.
.
.
.
.
.

```
### power analysis
###  Control vs treatment (digital + in person)
```

```r
effect_size <- cohensD(d[treatment2 == 0]$outcome, d[treatment2 == 1]$outcome)
#power we got from our experiment
pwr.t2n.test(n1 = nrow(d[treatment2 == 0,]), n2 = nrow(d[treatment2 == 1,]), d = effect_size, sig.level
```

```
##
##      t test power calculation
##
##              n1 = 33
##              n2 = 66
##               d = 0.1042079
##       sig.level = 0.05
##           power = 0.07723521
##     alternative = two.sided
```

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

```
##
##      Two-sample t test power calculation
##
##               n = 1446.518
##               d = 0.1042079
##       sig.level = 0.05
##           power = 0.8
##     alternative = two.sided
##
## NOTE: n is number in *each* group
```

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


### 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")
```

```r
# 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")
```