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

```r
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 ~ gender + age_range + lives_with_others + know_us + location_lat + location_long
        data = d2)
```

```
## Balance Measures
##                      Type Corr.Un
## gender            Contin.  0.0455
## age_range         Contin. -0.0513
## lives_with_others Contin.  0.0586
## know_us            Binary  0.0426
## location_lat      Contin.  0.1095
## location_long     Contin.  0.0512
##
## Sample sizes
##     Total
## All    51
```

```
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
## -2.45660 -1.40345 -0.07703  1.42896  2.76916
##
## Coefficients:
##                    Estimate Std. Error t value Pr(>|t|)
## (Intercept)       -0.949777   5.637226  -0.168    0.867
## gender             0.222693   0.501518   0.444    0.659
## age_range         -0.037168   0.226080  -0.164    0.870
## lives_with_others  0.220037   0.932261   0.236    0.815
## know_us            0.316655   0.926045   0.342    0.734
## location_lat       0.074428   0.102173   0.728    0.470
## location_long     -0.007474   0.017363  -0.430    0.669
##
## Residual standard error: 1.789 on 44 degrees of freedom
## Multiple R-squared:  0.02282,    Adjusted R-squared:  -0.1104
## F-statistic: 0.1713 on 6 and 44 DF,  p-value: 0.9832
```

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?

```r
'%!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$day
                                  d_not_followed_treatment_sequence$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
## 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$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)
```

```r
# 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
```

```r
# 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)"
```

```r
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)"
```

```r
# 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
```

```r
# 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)"
```

```r
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)"
```

```r
# 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
```

```r
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)"
```

```r
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 - 23:55:32

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	

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)
```

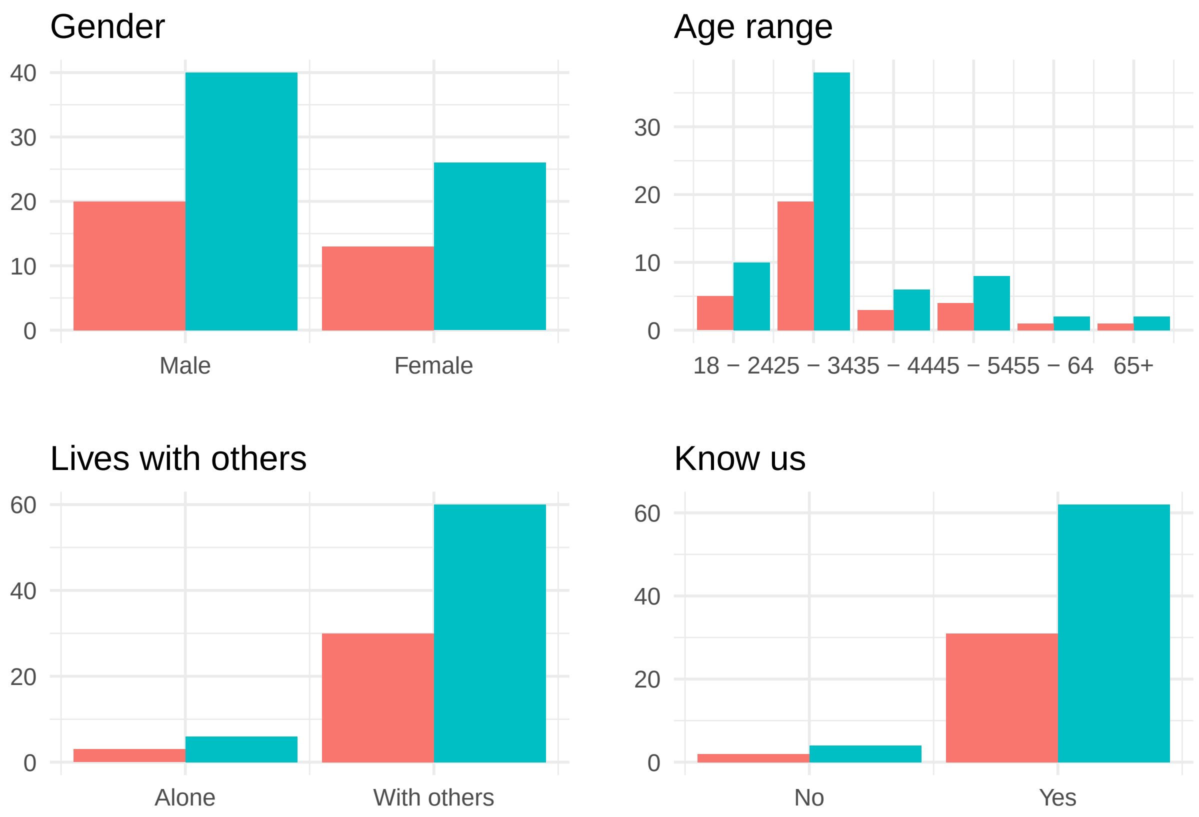
```
##    userId treatment_seq treatment steps age_range gender lives_with_others
## 1:     28             1         0 13929         0      0                 1
## 2:     56             1         0  5368         1      1                 1
## 3:     25             1         0  5802         1      0                 1
## 4:     22             1         0  5689         3      0                 1
## 5:     86             1         0  5868         1      0                 1
##    know_us location_lat location_long 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.

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

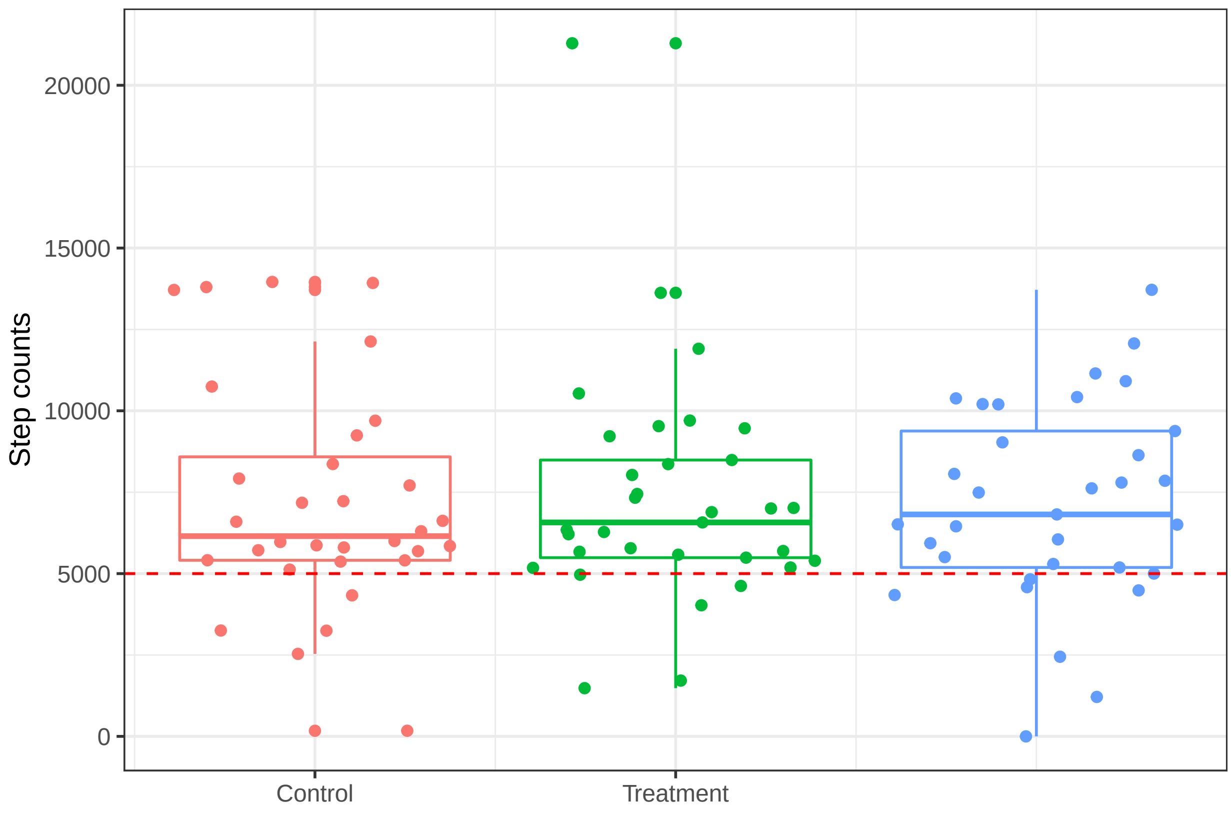
```
## Loading required package: gridExtra
```

```
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") +
  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)
```



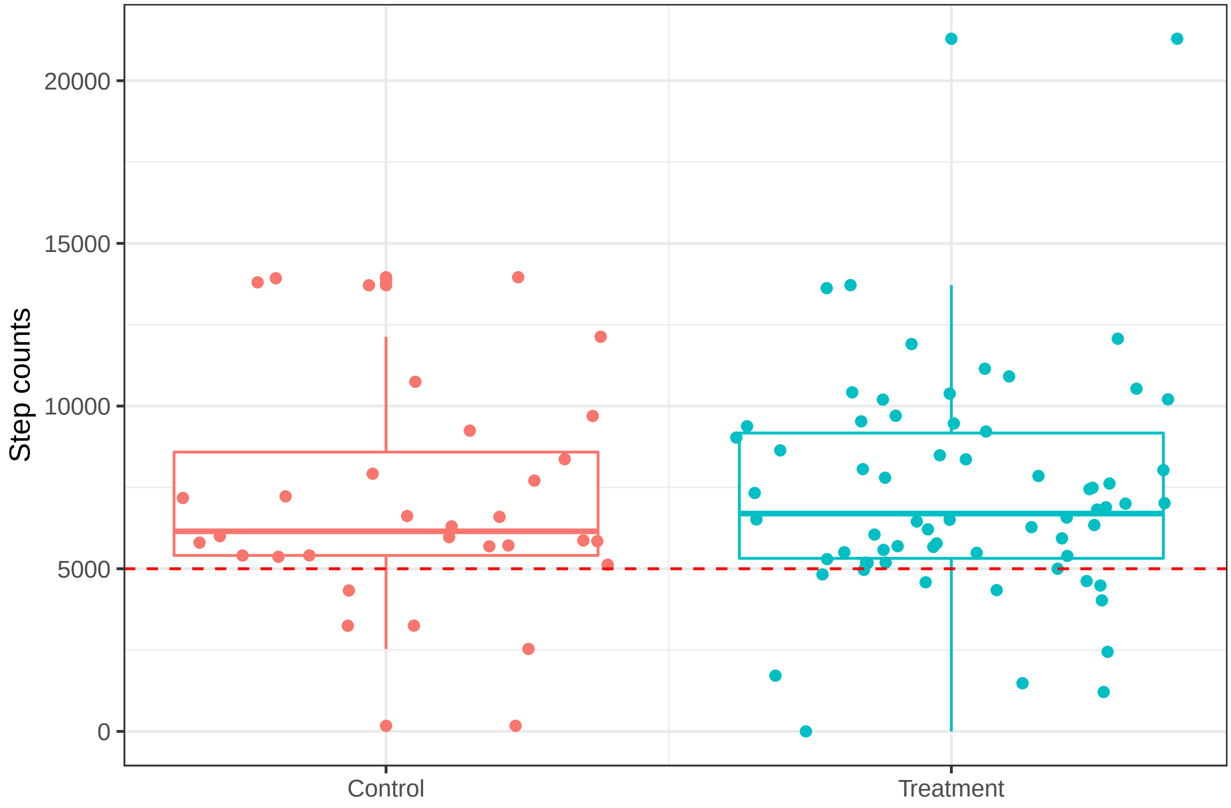
```
# control and digital and in person distribution
ggplot(d, aes(x=treatment, y=steps, colour = factor(treatment))) +
geom_boxplot() + geom_jitter() +
geom_hline(yintercept=5000, linetype="dashed", color = "red") +
xlab("") + ylab("Step counts") + theme_bw() +
    scale_x_continuous(breaks = c(0, 1),
                     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[,2]),
          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 - 23:55:34

```
stargazer(fit_3, fit_3_covariates,
          se=list(se_3[,2], 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 - 23:55:34

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_covariate
" (", 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[,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
	(0.038)
userId2	0.333
	(0.254)
userId3	0.667***
	(0.254)
userId6	1.000***
	(0.031)
userId13	1.000***
	(0.031)
userId14	0.333
	(0.254)
userId17	0.333
	(0.254)
userId19	1.000***
	(0.031)
userId22	0.667***
	(0.254)
userId25	1.000***
	(0.031)
userId26	1.000***
	(0.031)
userId28	1.000***
	(0.031)
userId33	1.000***
	(0.031)
userId39	1.000***
	(0.031)
userId45	1.000***
	(0.031)
userId47	0.333
	(0.292)
userId54	1.000***
	(0.031)
userId56	1.000***
	(0.031)
userId57	1.000***

Table 3:

	Dependent variable:	
	Steps > 5000	
	User ID	Covariates
	(1)	(2)
treatment	−0.047	−0.045
	(0.038)	(0.046)
userId2	0.333	
	(0.254)	
userId3	0.667***	
	(0.254)	
userId6	1.000***	
	(0.031)	
userId13	1.000***	
	(0.031)	
userId14	0.333	
	(0.254)	
userId17	0.333	
	(0.254)	
userId19	1.000***	
	(0.031)	
userId22	0.667***	
	(0.254)	
userId25	1.000***	
	(0.031)	
userId26	1.000***	
	(0.031)	
userId28	1.000***	
	(0.031)	
userId33	1.000***	
	(0.031)	
userId39	1.000***	
	(0.031)	
userId45	1.000***	
	(0.031)	
userId47	0.333	
	(0.292)	
userId54	1.000***	
	(0.031)	
userId56	1.000***	
	(0.031)	

Table 4:

	Dependent variable:
	Steps > 5000
treatment2	−0.047
	(0.064)
userId2	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***

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```
stargazer(fit_2, fit_2_covariates,
          se=list(se_2[,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 - 23:55:34

power calculations

```
###  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
```

```
# 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
```

```
#
#
#
#
```

Table 5:

	Dependent variable:	
	Steps > 5000	
	User ID	Covariates
	(1)	(2)
treatment2	−0.047	−0.045
	(0.064)	(0.073)
userId2	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)	

```
###  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")
```