

Code ▼

W241 Class Project - Analysis

1. Load libraries, data

Load up the data and do simple analysis. This version uses the complete dataset.

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```
# Libraries
library(lmtest)
library(sandwich)
library(ggplot2)
library(data.table)
library(stargazer)
library(ri)
library(multiwayvcov)
library(AER)
rm(list=ls())
d <- read.csv('Analysis/Combined Log.csv')
#d <- read.csv("C:/Users/Chris/OneDrive/Documents/MIDS/WS241/final/mids-w241-final/Analysis/Combined Log.csv")
d <- data.table(d)
# d <- d[complete.cases(d),] drops any row that is incomplete - too stringent since we
  have some cols which are not essential
d <- d[!is.na(no)] # Just drop row with missing values
# d <- d[complete.cases(d),] drops any row that is too incomplete - too stringent since
  we have some cols which are not essential
#d <- d[!is.na(no)] # Just drop row with missing values
# Base data
head(d)
```

n	city	title
<int>	<fctr>	<fctr>
6	seattle	Top Floor 2x2 Park & Lake Side/Corner Home!! USB Plugins!!
87	chicago	836 S Bishop St #G
62	houston	Sophisticated Living 2 BR APT with Excellent Amenities-Receive Up To \$
89	chicago	ALL BRAND NEW OUTSTANDING EAST LAKEVIEW LOCATION
96	chicago	Upgrade your lifestyle. Inexpensive with great character!
26	seattle	LUXURY 2 BEDROOM ***2 Master Suites*Coming Soon! Call for Availability

6 rows | 1-4 of 17 columns

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```

# Convert, transform data for analysis
# Drop some cols
d[,c('title','full_URL', 'reply_email_TO_BE_FILLED_IN_standard','posting_ID','notes')
:=NULL]
# Set gender = 1 for Jane
d[treatment_assignment=='Jane_Control' | treatment_assignment=='Jane_Treat_High' | treat
ment_assignment=='Jane_Treat_Low',gender:=1]
d[treatment_assignment=='John_Control' | treatment_assignment=='John_Treat_High' | trea
tment_assignment=='John_Treat_Low',gender:=0]
# Set treatment variable = 0 for control, 1 for low, 2 for high (treatment here is cont
inuous)
d[treatment_assignment=='Jane_Control' | treatment_assignment=='John_Control', treatmen
t:=0]
d[treatment_assignment=='Jane_Treat_Low' | treatment_assignment=='John_Treat_Low', trea
tment:=1]
d[treatment_assignment=='Jane_Treat_High' | treatment_assignment=='John_Treat_High', tr
eatment:=2]
# Alternatively, treat treatment types as categorical variables instead of continuous
d[treatment_assignment=='Jane_Treat_Low' | treatment_assignment=='John_Treat_Low', low_
treatment:=1]
d[treatment_assignment=='Jane_Treat_High' | treatment_assignment=='John_Treat_High', hi
gh_treatment:=1]
d$low_treatment[is.na(d$low_treatment)] <- 0
d$high_treatment[is.na(d$high_treatment)] <- 0
d[low_treatment==1 | high_treatment==0, assigned:=1]
d$assigned[is.na(d$assigned)] <- 0
# Capture complier
#d[sent!='', compliers:=1]
#d$compliers[is.na(d$compliers)] <- 0
# Labeling data
d$gender <- factor(d$gender,labels = c("Male", "Female"))
d$outcome_f <- factor(d$outcome, labels = c("No Response", "Response"))
d$bedrooms <- factor(d$bedrooms, labels = c("1-bedroom", "2-bedroom"))
d$professional <- factor(d$professional, labels = c("Non-professional",
"Professional"))
d$treatment_f <- factor(d$treatment, labels = c("Control","Low","High"))
head(d)

```

n	city	posting_date	bedrooms	sqft	price	treatment_assignment	professional
<int>	<fctr>	<fctr>	<fctr>	<int>	<int>	<fctr>	<fctr>
6	seattle	3/17/2017 13:32	2-bedroom	974	1791	Jane_Treat_High	Professional
87	chicago	3/17/2017 15:22	2-bedroom	NA	2050	Jane_Treat_Low	Non-professional
62	houston	3/17/2017 15:24	2-bedroom	1141	1598	Jane_Treat_High	Professional
89	chicago	3/17/2017 15:27	1-bedroom	1100	1995	Jane_Treat_Low	Professional
96	chicago	3/17/2017 15:26	1-bedroom	NA	1650	Jane_Control	Non-professional
26	seattle	3/17/2017 13:11	2-bedroom	1234	1655	John_Treat_Low	Professional

6 rows | 1-8 of 19 columns

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NA

2. Check data, do simple tables to check for balance

Recode missing sqft values. It's not necessary but we use this in some of our model specifications.

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```
# Recode missing sqft with mean of cluster (city)
d[, Mean:=mean(sqft, na.rm=TRUE), by=city]
d[is.na(sqft)]$sqft <- d[is.na(sqft)]$Mean
```

Coerced 'double' RHS to 'integer' to match the column's type; may have truncated precision. Either change the target column to 'double' first (by creating a new 'double' vector length 483 (nrows of entire table) and assign that; i.e. 'replace' column), or coerce RHS to 'integer' (e.g. 1L, NA_[real|integer]_, as.*, etc) to make your intent clear and for speed. Or, set the column type correctly up front when you create the table and stick to it, please.

Hide

```
d[,c('Mean') :=NULL]
```

Remove duplicate emails

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```
# If duplicate, only retain first email sent, sets up for exploration later; in our base exploration we did not exclude duplicate emails
#d <- d[duplicate_email == 0]
```

For the most part it looks like we have a balanced dataset.

Hide

```
cat('Table of Outcomes:')
```

```
Table of Outcomes:
```

Hide

```
table(d$outcome_f)
```

No Response	Response
264	219

[Hide](#)

```
cat('\nTable of Outcomes (By Gender):')
```

Table of Outcomes (By Gender):

[Hide](#)

```
table(d$outcome_f, d$gender)
```

	Male	Female
No Response	135	129
Response	104	115

[Hide](#)

```
cat('\nTable of Outcomes (By Treatment):')
```

Table of Outcomes (By Treatment):

[Hide](#)

```
table(d$outcome_f, d$treatment_f)
```

	Control	Low	High
No Response	88	89	87
Response	72	72	75

[Hide](#)

```
cat('\nTable of Outcomes (By Treatment and Gender):')
```

Table of Outcomes (By Treatment and Gender):

[Hide](#)

```
table(d$outcome_f, factor(d$treatment_assignment))
```

	Jane_Control	Jane_Treat_High	Jane_Treat_Low	John_Control	John_Treat_High
John_Treat_Low					
No Response	39	41	49	49	46
Response	39	40	36	33	35

Hide

```
cat('\nTable of Outcomes (By City):')
```

Table of Outcomes (By City):

Hide

```
table(d$outcome_f,factor(d$city))
```

	chicago	houston	sandiego	seattle
No Response	63	79	65	57
Response	61	40	52	66

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```
cat('\nTable of Outcomes (By Rooms):')
```

Table of Outcomes (By Rooms):

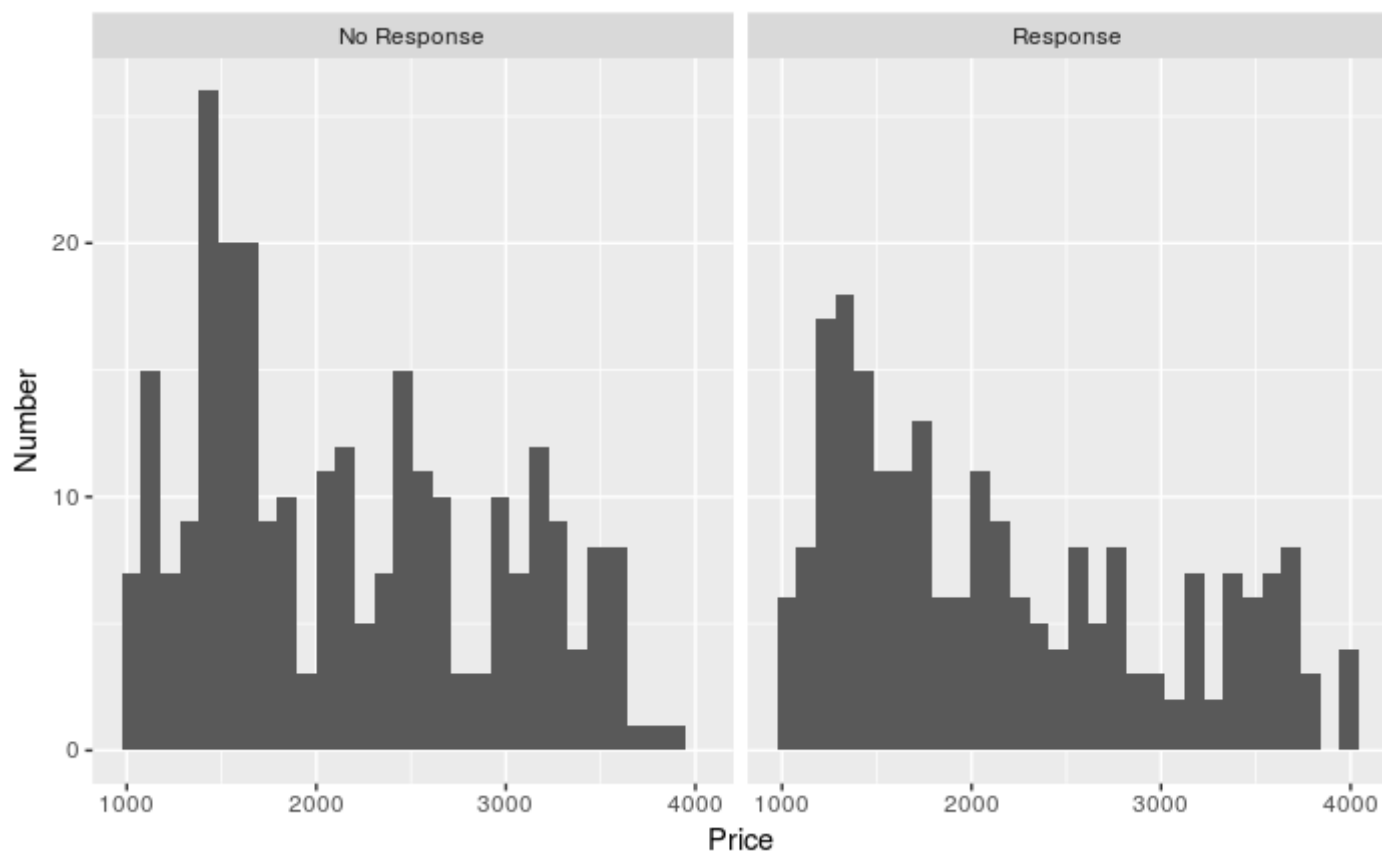
Hide

```
table(d$outcome_f,factor(d$bedrooms))
```

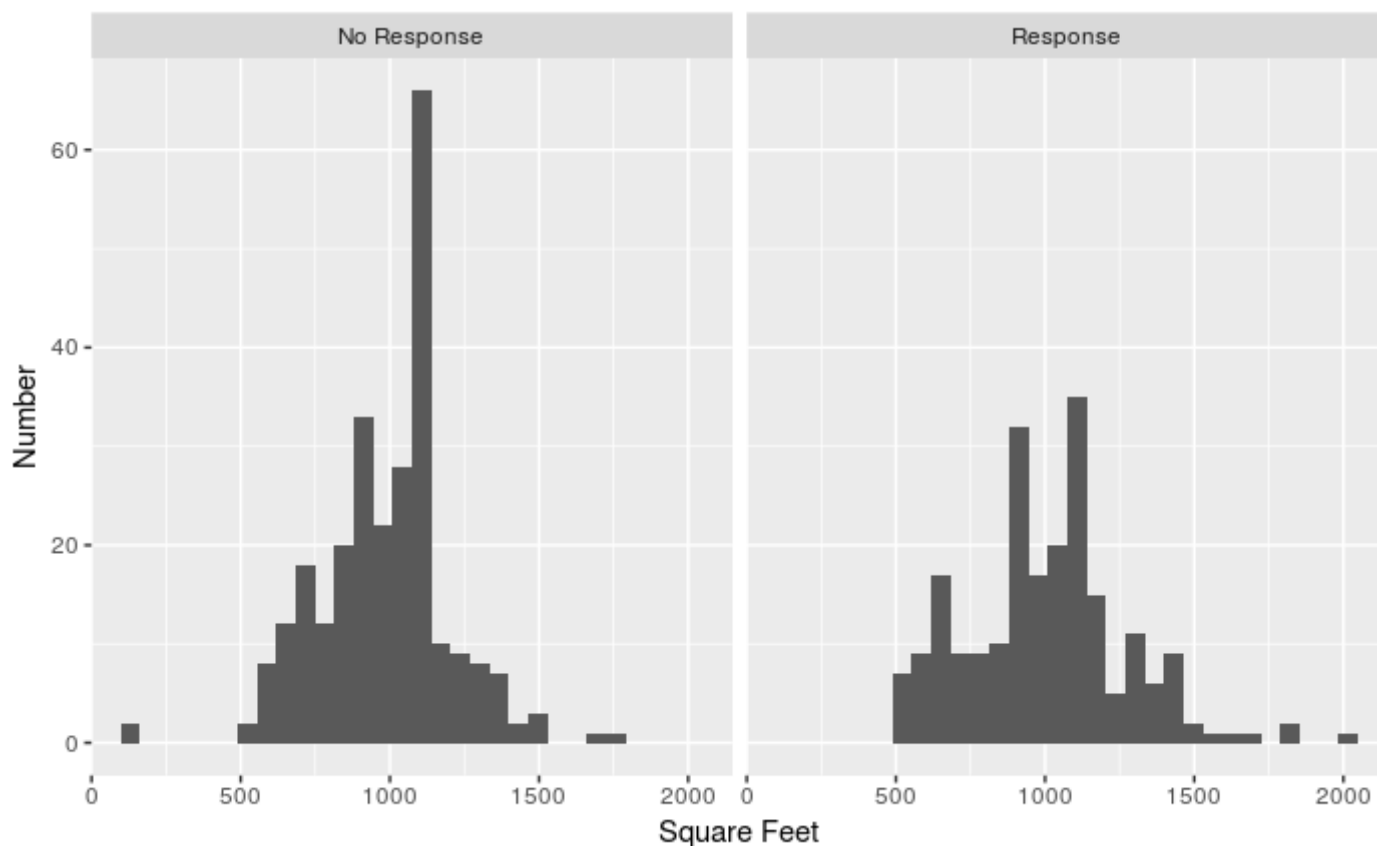
	1-bedroom	2-bedroom
No Response	130	134
Response	103	116

Hide

```
ggplot(d,aes(x=price))+geom_histogram()+facet_grid(~outcome_f)+labs(x="Price",y="Number")
```

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```
# Sqft info has missing values => we can drop all cases (see above) but for now leave this alone or we use the clustering estimate
# Similar but somewhat worse issue for professional, same.email info
ggplot(d,aes(x=sqft))+geom_histogram()+facet_grid(~outcome_f)+labs(x="Square Feet",y="Number")
```



Hide

```
cat('\nTable of Outcomes (By Professional):')
```

Table of Outcomes (By Professional):

Hide

```
table(d$outcome_f, factor(d$professional))
```

	Non-professional	Professional
No Response	55	209
Response	35	184

3. Analysis

Simple Analysis

We do a chi-squared test of independence to see if the observations are independent. We cannot reject the hypothesis that the observations are independent. This is true for even the professional category.

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```
# For Outcome and Gender
tbl <- table(d$outcome_f,d$gender)
tbl
```

	Male	Female
No Response	135	129
Response	104	115

[Hide](#)

```
chisq.test(tbl)
```

Pearson's Chi-squared test with Yates' continuity correction

```
data:  tbl
X-squared = 0.49961, df = 1, p-value = 0.4797
```

[Hide](#)

```
# On Outcome and Treatment
tbl <- table(d$outcome_f,d$treatment)
tbl
```

	0	1	2
No Response	88	89	87
Response	72	72	75

[Hide](#)

```
chisq.test(tbl)
```

Pearson's Chi-squared test

```
data:  tbl
X-squared = 0.092173, df = 2, p-value = 0.955
```

[Hide](#)

```
# On Outcome and Treatment Assignment
tbl <- table(d$outcome_f,factor(d$treatment_assignment))
tbl
```


	Jane_Control	Jane_Treat_High	Jane_Treat_Low	John_Control	John_Treat_High
John_Treat_Low					
No Response	39	41	49	49	46
Response	39	40	36	33	35

Hide

```
chisq.test(tbl)
```

Pearson's Chi-squared test

data: tbl

X-squared = 2.6574, df = 5, p-value = 0.7526

Hide

```
# On Outcome and Professional
tbl <- table(d$outcome_f,d$professional)
tbl
```

	Non-professional	Professional
No Response	55	209
Response	35	184

Hide

```
chisq.test(tbl)
```

Pearson's Chi-squared test with Yates' continuity correction

data: tbl

X-squared = 1.5521, df = 1, p-value = 0.2128

Regression

We run regression on treatment as a factor (control, low, high) with and without gender as another factor. Other co-variates are added including city, price, bedrooms.

Basic model

```
Outcome variable = alpha + B_high + B_low + gender + covariates
```

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```
# First we treat treatment as a continous variable
# Model 1a - Basic model
m1 <- lm(outcome~treatment,data=d)
stargazer(m1,type='text')
```

```
=====
                        Dependent variable:
                        -----
                        outcome
-----
treatment                0.007
                        (0.028)

Constant                0.447***
                        (0.036)

-----
Observations                483
R2                        0.0001
Adjusted R2                -0.002
Residual Std. Error      0.499 (df = 481)
F Statistic              0.055 (df = 1; 481)
=====
Note:          *p<0.1; **p<0.05; ***p<0.01
```

Hide

```
coeftest(m1, vcovHC(m1)) # Robust se
```

```
t test of coefficients:
```

```
                Estimate Std. Error t value Pr(>|t|)
(Intercept) 0.4468885   0.0360544  12.395   <2e-16 ***
treatment    0.0065007   0.0279011   0.233   0.8159
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Hide

```
# Model 2a - Treatment & gender
m2 <- lm(outcome~treatment*gender,data=d)
stargazer(m2,type='text')
```

```

=====
                        Dependent variable:
                        -----
                                outcome
                        -----
treatment                0.015
                        (0.039)

genderFemale              0.054
                        (0.072)

treatment:genderFemale   -0.018
                        (0.056)

Constant                 0.420***
                        (0.051)

-----
Observations              483
R2                        0.002
Adjusted R2              -0.005
Residual Std. Error      0.499 (df = 479)
F Statistic              0.261 (df = 3; 479)
=====
Note:                    *p<0.1; **p<0.05; ***p<0.01

```

[Hide](#)

```
coeftest(m2, vcovHC(m2)) # Robust se
```

```
t test of coefficients:
```

```

                Estimate Std. Error t value Pr(>|t|)
(Intercept)    0.420269   0.050348  8.3472 7.548e-16 ***
treatment      0.014940   0.039035  0.3827  0.7021
genderFemale   0.053678   0.072275  0.7427  0.4580
treatment:genderFemale -0.017544  0.055980 -0.3134  0.7541
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

[Hide](#)

```

# Model 3a - Treatment & gender + covariates
m3 <- lm(outcome~treatment*gender+factor(city)+factor(bedrooms)+price,data=d)
stargazer(m3,type='text')

```

```

=====
                        Dependent variable:
                        -----
                                outcome
                        -----
treatment                0.015
                        (0.039)

genderFemale             0.052
                        (0.072)

factor(city)houston     -0.155**
                        (0.064)

factor(city)sandiego    -0.046
                        (0.064)

factor(city)seattle      0.048
                        (0.064)

factor(bedrooms)2-bedroom 0.031
                        (0.049)

price                   -0.00000
                        (0.00003)

treatment:genderFemale  -0.017
                        (0.055)

Constant                0.452***
                        (0.087)

-----
Observations              483
R2                        0.025
Adjusted R2              0.008
Residual Std. Error      0.496 (df = 474)
F Statistic              1.503 (df = 8; 474)
=====
Note:                    *p<0.1; **p<0.05; ***p<0.01

```

[Hide](#)

```
coeftest(m3, vcovHC(m3)) # Robust se
```

t test of coefficients:

	Estimate	Std. Error	t value	Pr(> t)	
(Intercept)	4.5237e-01	8.8895e-02	5.0887	5.205e-07	***
treatment	1.5360e-02	3.9044e-02	0.3934	0.69420	
genderFemale	5.1775e-02	7.2094e-02	0.7182	0.47301	
factor(city)houston	-1.5451e-01	6.3680e-02	-2.4263	0.01563	*
factor(city)sandiego	-4.5650e-02	6.5718e-02	-0.6946	0.48763	
factor(city)seattle	4.7687e-02	6.4965e-02	0.7340	0.46329	
factor(bedrooms)2-bedroom	3.0561e-02	4.8223e-02	0.6337	0.52655	
price	-4.8779e-06	3.0726e-05	-0.1588	0.87393	
treatment:genderFemale	-1.7236e-02	5.5989e-02	-0.3078	0.75834	

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Hide

```
# Model 3a-1 - Treatment & gender + all covariates including less reliable sqft and professional
m3.1 <- lm(outcome~treatment*gender+factor(city)+factor(bedrooms)+price+sqft+professional,data=d)
stargazer(m3.1,type='text')
```

```

=====
                        Dependent variable:
                        -----
                        outcome
                        -----
treatment                0.014
                        (0.039)

genderFemale              0.058
                        (0.071)

factor(city)houston      -0.175***
                        (0.066)

factor(city)sandiego     -0.031
                        (0.068)

factor(city)seattle      0.050
                        (0.069)

factor(bedrooms)2-bedroom 0.0004
                        (0.054)

price                    -0.00003
                        (0.00003)

sqft                     0.0002
                        (0.0001)

professionalProfessional  0.128**
                        (0.063)

treatment:genderFemale   -0.017
                        (0.055)

Constant                 0.227
                        (0.143)

-----
Observations              483
R2                        0.036
Adjusted R2              0.016
Residual Std. Error      0.494 (df = 472)
F Statistic              1.783* (df = 10; 472)
=====
Note:                    *p<0.1; **p<0.05; ***p<0.01

```

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```
coeftest(m3.1, vcovHC(m3.1)) # Robust se
```

t test of coefficients:

	Estimate	Std. Error	t value	Pr(> t)	
(Intercept)	2.2731e-01	1.4428e-01	1.5755	0.115820	
treatment	1.3932e-02	3.9228e-02	0.3552	0.722631	
genderFemale	5.8443e-02	7.2131e-02	0.8102	0.418215	
factor(city)houston	-1.7503e-01	6.6137e-02	-2.6465	0.008405	**
factor(city)sandiego	-3.1060e-02	6.9732e-02	-0.4454	0.656226	
factor(city)seattle	4.9789e-02	7.0678e-02	0.7044	0.481500	
factor(bedrooms)2-bedroom	3.9049e-04	5.2663e-02	0.0074	0.994087	
price	-3.0782e-05	3.3423e-05	-0.9210	0.357527	
sqft	1.9279e-04	1.2237e-04	1.5754	0.115840	
professionalProfessional	1.2797e-01	6.3556e-02	2.0135	0.044634	*
treatment:genderFemale	-1.7051e-02	5.6090e-02	-0.3040	0.761264	

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

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```
# Next we treat treatment as a categorical variable (effect might not be linear)
# Model lb - Basic model
m4 <- lm(outcome~treatment_f,data=d)
stargazer(m4,type='text')
```

```
=====
Dependent variable:
-----
outcome
-----
treatment_fLow      -0.003
                    (0.056)

treatment_fHigh      0.013
                    (0.056)

Constant             0.450***
                    (0.039)

-----
Observations          483
R2                    0.0002
Adjusted R2           -0.004
Residual Std. Error   0.499 (df = 480)
F Statistic           0.046 (df = 2; 480)
=====
Note:                *p<0.1; **p<0.05; ***p<0.01
```

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```
coeftest(m4, vcovHC(m4)) # Robust se
```

t test of coefficients:

```

              Estimate Std. Error t value Pr(>|t|)
(Intercept)    0.450000   0.039578 11.3700  <2e-16 ***
treatment_fLow -0.002795   0.055867  -0.0500   0.9601
treatment_fHigh 0.012963   0.055859   0.2321   0.8166
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

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```

# Model 2b - Treatment & gender
m5 <- lm(outcome~treatment_f*gender,data=d)
stargazer(m5,type='text')

```

```

=====
                        Dependent variable:
                        -----
                        outcome
-----
treatment_fLow          0.071
                        (0.080)

treatment_fHigh         0.030
                        (0.078)

genderFemale            0.098
                        (0.079)

treatment_fLow:genderFemale -0.148
                        (0.112)

treatment_fHigh:genderFemale -0.036
                        (0.111)

Constant                0.402***
                        (0.055)

-----
Observations              483
R2                        0.006
Adjusted R2              -0.005
Residual Std. Error      0.500 (df = 477)
F Statistic              0.528 (df = 5; 477)
=====
Note:                    *p<0.1; **p<0.05; ***p<0.01

```

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```
coeftest(m5, vcovHC(m5)) # Robust se
```


t test of coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	0.402439	0.054823	7.3407	9.234e-13 ***
treatment_fLow	0.071245	0.079837	0.8924	0.3726
treatment_fHigh	0.029660	0.078175	0.3794	0.7046
genderFemale	0.097561	0.079338	1.2297	0.2194
treatment_fLow:genderFemale	-0.147716	0.112268	-1.3157	0.1889
treatment_fHigh:genderFemale	-0.035833	0.112088	-0.3197	0.7493

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Hide

```
# Model 3b - Treatment & gender + covariates
m6 <- lm(outcome~treatment_f*gender+factor(city)+factor(bedrooms)+price,data=d)
stargazer(m6,type='text')
```

```

=====
                        Dependent variable:
                        -----
                        outcome
                        -----
treatment_fLow           0.074
                        (0.079)

treatment_fHigh          0.031
                        (0.078)

genderFemale             0.097
                        (0.079)

factor(city)houston      -0.157**
                        (0.064)

factor(city)sandiego     -0.047
                        (0.064)

factor(city)seattle      0.044
                        (0.064)

factor(bedrooms)2-bedroom 0.032
                        (0.049)

price                   -0.00000
                        (0.00003)

treatment_fLow:genderFemale -0.151
                        (0.111)

treatment_fHigh:genderFemale -0.035
                        (0.111)

Constant                 0.433***
                        (0.091)

-----
Observations              483
R2                        0.029
Adjusted R2               0.008
Residual Std. Error       0.496 (df = 472)
F Statistic               1.399 (df = 10; 472)
=====
Note:                      *p<0.1; **p<0.05; ***p<0.01

```

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```
coeftest(m6, vcovHC(m6)) # Robust se
```

t test of coefficients:

	Estimate	Std. Error	t value	Pr(> t)	
(Intercept)	4.3327e-01	9.3187e-02	4.6495	4.325e-06	***
treatment_fLow	7.3544e-02	7.9784e-02	0.9218	0.3571	
treatment_fHigh	3.0518e-02	7.8207e-02	0.3902	0.6966	
genderFemale	9.6823e-02	7.9161e-02	1.2231	0.2219	
factor(city)houston	-1.5723e-01	6.3812e-02	-2.4639	0.0141	*
factor(city)sandiego	-4.6826e-02	6.5934e-02	-0.7102	0.4779	
factor(city)seattle	4.4475e-02	6.5228e-02	0.6818	0.4957	
factor(bedrooms)2-bedroom	3.2102e-02	4.8609e-02	0.6604	0.5093	
price	-4.1162e-06	3.0934e-05	-0.1331	0.8942	
treatment_fLow:genderFemale	-1.5084e-01	1.1212e-01	-1.3453	0.1792	
treatment_fHigh:genderFemale	-3.5359e-02	1.1210e-01	-0.3154	0.7526	

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

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```
# Model 3b-1 - Treatment & gender + all covariates including less reliable sqft and professional
m6.1 <- lm(outcome~treatment_f*gender+factor(city)+factor(bedrooms)+price+sqft+professional,data=d)
stargazer(m6.1,type='text')
```

=====	
Dependent variable:	

	outcome

treatment_fLow	0.063 (0.079)
treatment_fHigh	0.028 (0.078)
genderFemale	0.102 (0.078)
factor(city)houston	-0.177*** (0.066)
factor(city)sandiego	-0.032 (0.068)
factor(city)seattle	0.047 (0.069)
factor(bedrooms)2-bedroom	0.002 (0.054)
price	-0.00003 (0.00003)
sqft	0.0002 (0.0001)
professionalProfessional	0.128** (0.063)
treatment_fLow:genderFemale	-0.147 (0.111)
treatment_fHigh:genderFemale	-0.035 (0.111)
Constant	0.212 (0.144)

Observations	483
R2	0.040
Adjusted R2	0.016
Residual Std. Error	0.494 (df = 470)
F Statistic	1.649* (df = 12; 470)
=====	
Note:	*p<0.1; **p<0.05; ***p<0.01

Hide

```
coeftest(m6.1, vcovHC(m6.1)) # Robust se
```

```
t test of coefficients:
```

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	2.1190e-01	1.4458e-01	1.4656	0.143427
treatment_fLow	6.2881e-02	8.0392e-02	0.7822	0.434503
treatment_fHigh	2.7746e-02	7.8568e-02	0.3531	0.724137
genderFemale	1.0238e-01	7.9039e-02	1.2953	0.195852
factor(city)houston	-1.7745e-01	6.6167e-02	-2.6819	0.007579 **
factor(city)sandiego	-3.2071e-02	6.9557e-02	-0.4611	0.644961
factor(city)seattle	4.6910e-02	7.0773e-02	0.6628	0.507773
factor(bedrooms)2-bedroom	2.2089e-03	5.2914e-02	0.0417	0.966719
price	-3.0535e-05	3.3802e-05	-0.9033	0.366804
sqft	1.9285e-04	1.2171e-04	1.5845	0.113755
professionalProfessional	1.2789e-01	6.3882e-02	2.0020	0.045859 *
treatment_fLow:genderFemale	-1.4664e-01	1.1200e-01	-1.3093	0.191081
treatment_fHigh:genderFemale	-3.5093e-02	1.1223e-01	-0.3127	0.754666

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

In all models, the coefficients on treatment, whether continuous or as a factor, are not statistically significant. If we add gender, there is also no evidence of a the interaction term being statistically significant. Thus, there is no evidence that exclamation points have influenced the likelihood of receiving a response.

Hide

```
# We try an alternative specification for treatment (as dummy variables)
# Model 1c - Basic model
m7 <- lm(outcome ~ low_treatment + high_treatment, data=d)

stargazer(m7, type='text')
```

```

=====
                        Dependent variable:
                        -----
                        outcome
                        -----
low_treatment           -0.003
                        (0.056)

high_treatment          0.013
                        (0.056)

Constant                0.450***
                        (0.039)

-----
Observations            483
R2                      0.0002
Adjusted R2             -0.004
Residual Std. Error     0.499 (df = 480)
F Statistic             0.046 (df = 2; 480)
=====
Note:                   *p<0.1; **p<0.05; ***p<0.01

```

Hide

```
coeftest(m7, vcovHC(m7)) # Robust se
```

t test of coefficients:

```

                Estimate Std. Error t value Pr(>|t|)
(Intercept)    0.450000    0.039578 11.3700  <2e-16 ***
low_treatment  -0.002795    0.055867 -0.0500  0.9601
high_treatment  0.012963    0.055859  0.2321  0.8166
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

Hide

```

# Model 2c - Treatment & gender
m8 <- lm(outcome ~ low_treatment + high_treatment*gender, data=d)
stargazer(m8, type='text')

```

```

=====
                        Dependent variable:
                        -----
                        outcome
                        -----
low_treatment           -0.004
                        (0.056)

high_treatment          -0.006
                        (0.073)

genderFemale            0.024
                        (0.056)

high_treatment:genderFemale 0.038
                        (0.096)

Constant                0.439***
                        (0.048)

-----
Observations            483
R2                      0.002
Adjusted R2             -0.007
Residual Std. Error     0.500 (df = 478)
F Statistic              0.222 (df = 4; 478)
=====
Note:                    *p<0.1; **p<0.05; ***p<0.01

```

[Hide](#)

```
coeftest(m8, vcovHC(m8)) # Robust se
```

```
t test of coefficients:
```

```

                        Estimate Std. Error t value Pr(>|t|)
(Intercept)           0.4385118  0.0478301  9.1681   <2e-16 ***
low_treatment         -0.0037483  0.0561084 -0.0668   0.9468
high_treatment        -0.0064131  0.0734399 -0.0873   0.9305
genderFemale           0.0235655  0.0561118  0.4200   0.6747
high_treatment:genderFemale 0.0381629  0.0970455  0.3932   0.6943
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

[Hide](#)

```

# Model 3c - Treatment & gender + covariates
m9 <- lm(outcome ~ low_treatment + high_treatment + gender + factor(city) + factor(bedrooms) + price, data=d)
stargazer(m9, type='text')

```

```

=====
                        Dependent variable:
                        -----
                                outcome
-----
low_treatment                -0.004
                              (0.056)

high_treatment                0.014
                              (0.055)

genderFemale                  0.035
                              (0.045)

factor(city)houston          -0.154**
                              (0.064)

factor(city)sandiego          -0.046
                              (0.064)

factor(city)seattle           0.048
                              (0.064)

factor(bedrooms)2-bedroom     0.031
                              (0.049)

price                        -0.00001
                              (0.00003)

Constant                      0.466***
                              (0.084)

-----
Observations                  483
R2                            0.025
Adjusted R2                   0.008
Residual Std. Error           0.496 (df = 474)
F Statistic                    1.497 (df = 8; 474)
=====
Note:                         *p<0.1; **p<0.05; ***p<0.01

```

[Hide](#)

```
coeftest(m9, vcovHC(m9)) # Robust se
```


t test of coefficients:

	Estimate	Std. Error	t value	Pr(> t)	
(Intercept)	4.6571e-01	8.6773e-02	5.3669	1.256e-07	***
low_treatment	-3.7784e-03	5.5953e-02	-0.0675	0.94619	
high_treatment	1.3738e-02	5.5896e-02	0.2458	0.80596	
genderFemale	3.4752e-02	4.5695e-02	0.7605	0.44732	
factor(city)houston	-1.5429e-01	6.3676e-02	-2.4230	0.01577	*
factor(city)sandiego	-4.5755e-02	6.5682e-02	-0.6966	0.48638	
factor(city)seattle	4.7974e-02	6.4963e-02	0.7385	0.46059	
factor(bedrooms)2-bedroom	3.0814e-02	4.8250e-02	0.6386	0.52337	
price	-5.6698e-06	3.0873e-05	-0.1836	0.85437	

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

The coefficients on treatment are also statistically insignificant. There is no evidence that exclamation points have an effect.

Randomization Inference

Next we use randomization inference (assuming a Sharp Null of No Effect) to understand if our observation is consistent with an empirical null distribution. For this, we combine low and high treatment into treatment (since we have not learned more complex fixes for heterogenous effects).

[Hide](#)

```
# Combining treatments
di <- d
di[treatment==2,treatment:=1]
# Define distributions
y <- di$outcome
Z <- di$treatment
blk1 <- as.numeric(di$gender) # We block by gender
blk2 <- as.numeric(di$city) # Block by city
blk3 <- as.numeric(di$bedrooms)
# By gender
perms <- genperms(Z, clustvar = NULL, blockvar = blk1)
```

Too many permutations to use exact method.
Defaulting to approximate method.
Increase maxiter to at least 4.19386819554668e+130 to perform exact estimation.

[Hide](#)

```
probs <- genprobexact(Z, clustvar = NULL, blockvar = blk1) # probability of treatment
ate <- estate(y,Z,prob=probs) # estimate the ATE
Ys <- genouts(y,Z,ate=0) # generate potential outcomes under sharp null of no effect
distout <- gendist(Ys,perms, prob=probs) # generate sampling dist. under sharp null
dispdist(distout, ate, quantiles = c(0.025, 0.975), display.plot = TRUE) # display characteristics of sampling dist. for inference
```

```

$two.tailed.p.value
[1] 0.9952

$two.tailed.p.value.abs
[1] 0.9899

$greater.p.value
[1] 0.4976

$lesser.p.value
[1] 0.5102

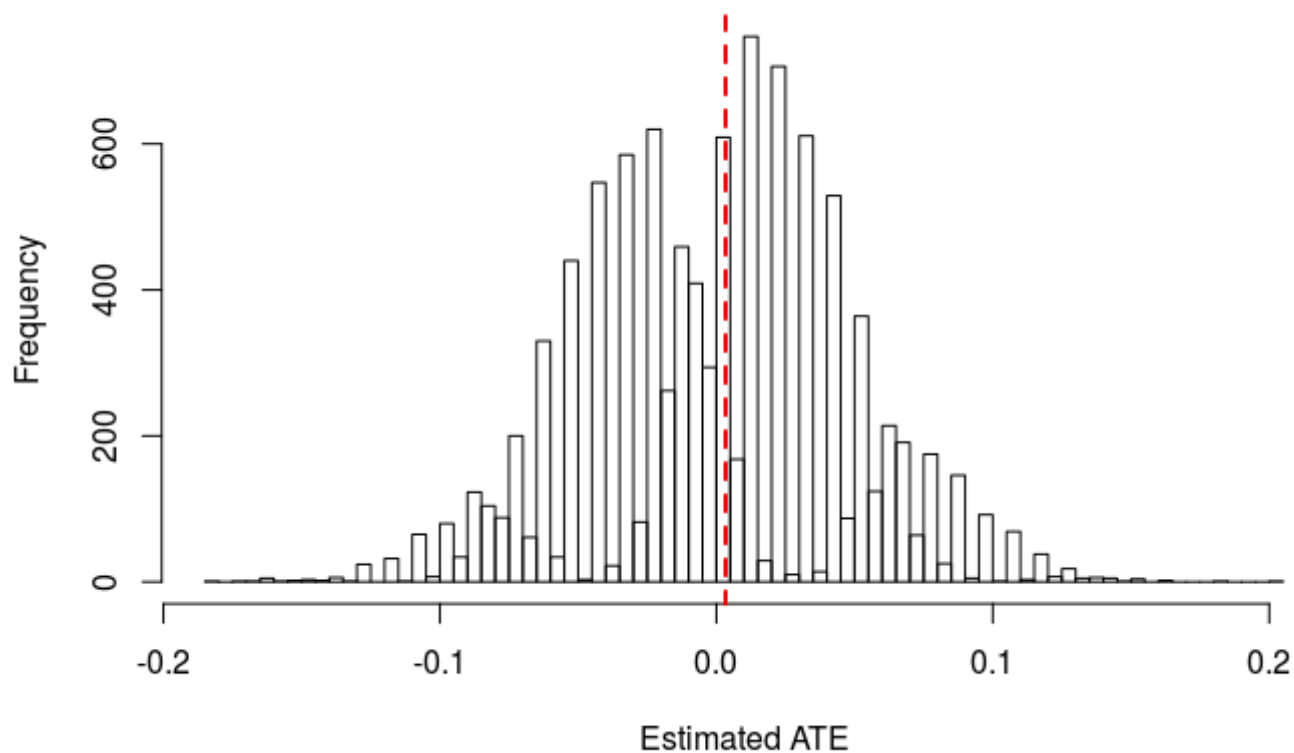
$quantile
      2.5%      97.5%
-0.09019532  0.09553867

$sd
[1] 0.04786495

$exp.val
[1] -0.0002936077

```

Distribution of the Estimated ATE


[Hide](#)

```

# By city
perms <- genperms(Z, clustvar = NULL, blockvar = blk2)

```

Too many permutations to use exact method.
Defaulting to approximate method.
Increase maxiter to at least 4.59676200506436e+128 to perform exact estimation.

[Hide](#)

```
probs <- genprobexact(Z, clustvar = NULL, blockvar = blk2) # probability of treatment
ate <- estate(y,Z,prob=probs) # estimate the ATE
Ys <- genouts(y,Z,ate=0) # generate potential outcomes under sharp null of no effect
distout <- gendist(Ys,perms, prob=probs) # generate sampling dist. under sharp null
dispdist(distout, ate, quantiles = c(0.025, 0.975), display.plot = TRUE) # display characteristics of sampling dist. for inference
```

```
$two.tailed.p.value
[1] 0.9044
```

```
$two.tailed.p.value.abs
[1] 0.8913
```

```
$greater.p.value
[1] 0.4522
```

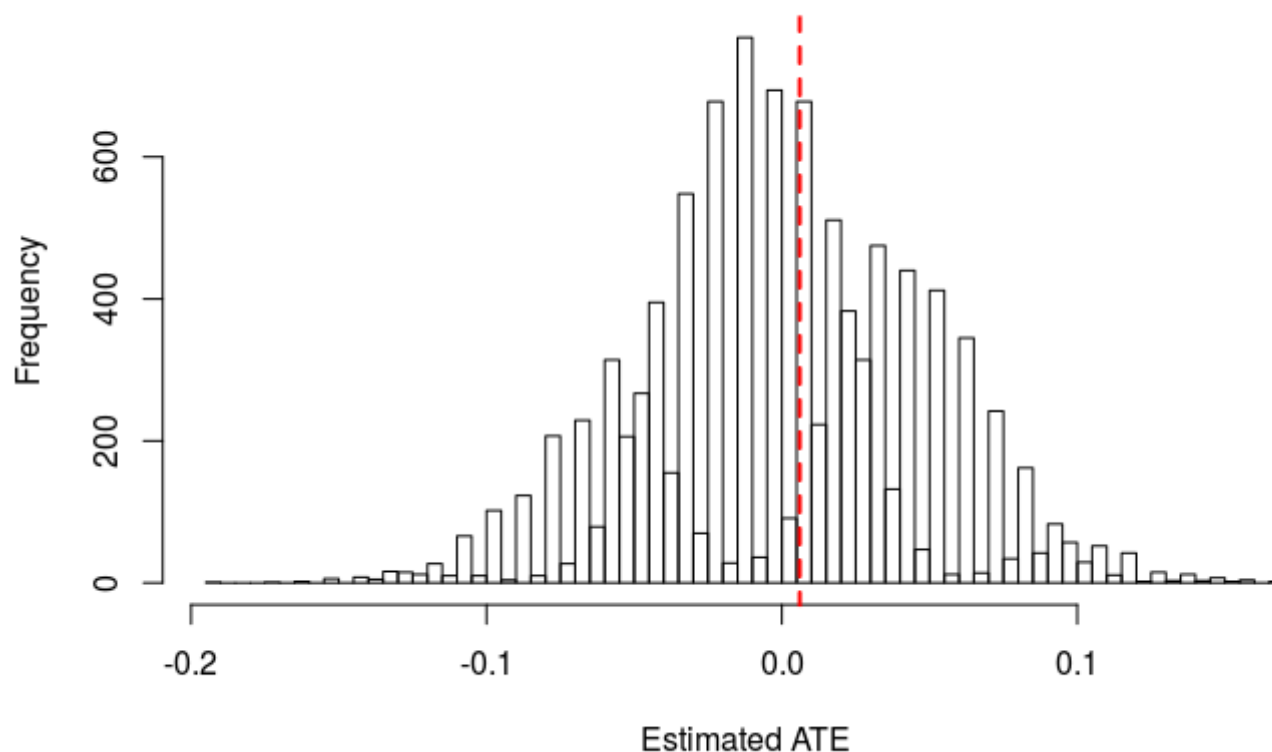
```
$lesser.p.value
[1] 0.5482
```

```
$quantile
      2.5%      97.5%
-0.09639898  0.09205564
```

```
$sd
[1] 0.04813268
```

```
$exp.val
[1] -1.890316e-05
```

Distribution of the Estimated ATE


[Hide](#)

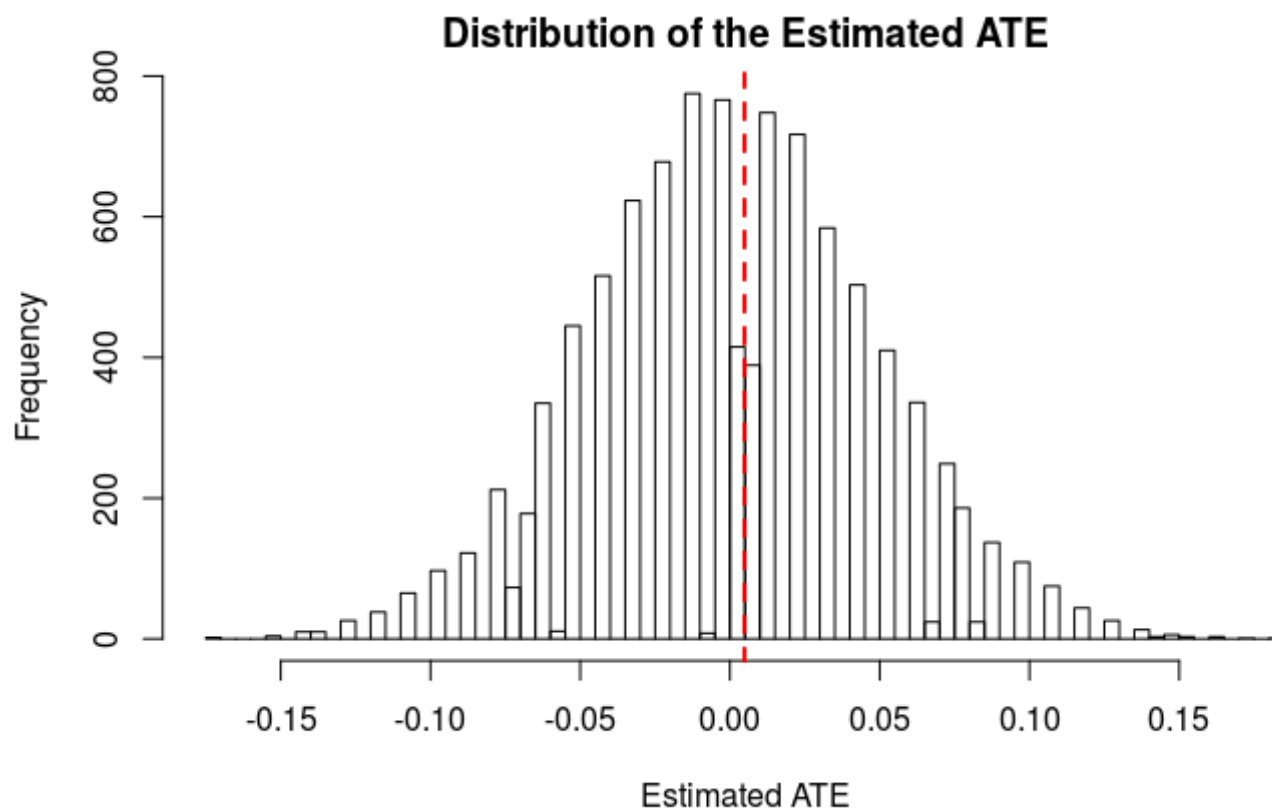
```
# By bedroom
perms <- genperms(Z, clustvar = NULL, blockvar = blk3)
```

```
Too many permutations to use exact method.
Defaulting to approximate method.
Increase maxiter to at least 4.80931839467142e+130 to perform exact estimation.
```

[Hide](#)

```
probs <- genprobexact(Z, clustvar = NULL, blockvar = blk3) # probability of treatment
ate <- estate(y,Z,prob=probs) # estimate the ATE
Ys <- genouts(y,Z,ate=0) # generate potential outcomes under sharp null of no effect
distout <- gendist(Ys,perms, prob=probs) # generate sampling dist. under sharp null
dispdist(distout, ate, quantiles = c(0.025, 0.975), display.plot = TRUE) # display characteristics of sampling dist. for inference
```

```
$two.tailed.p.value  
[1] 0.9636  
  
$two.tailed.p.value.abs  
[1] 0.9069  
  
$greater.p.value  
[1] 0.4818  
  
$lesser.p.value  
[1] 0.5299  
  
$quantile  
      2.5%      97.5%  
-0.09734619  0.09827367  
  
$sd  
[1] 0.04794351  
  
$exp.val  
[1] 0.0005390847
```

[Hide](#)

```
#P-value for actual data  
p.val.actual = sum(abs(distout) > ate) / length(distout)  
p.val.actual
```

```
[1] 0.8952
```

Hide

```
#get response rate by treatment or control
actual.response.rate.by.treatment <- di[, mean(outcome), by = c("treatment")]
actual.response.rate.by.treatment
```

treatment <dbl>	V1 <dbl>
1	0.4551084
0	0.4500000

2 rows

Hide

```
di[, sum(outcome > -100), by = c("treatment")]
```

treatment <dbl>	V1 <int>
1	323
0	160

2 rows

Once again, we cannot reject the null hypothesis of no effect.

Other Analysis

1. Although not a significant issue for this experiment we estimate the CACE. For this we define non-compliers as those for who we sent emails but did not receive them - and we know this because we received a "bounced" email message.

Hide

```
# We calculate the CACE manually
# Manually compute CACE
itt <- mean(d$outcome[d$treatment != 0]) - mean(d$outcome[d$treatment == 0])
prop_treated <- 481/483
sprintf("\nThe estimated CACE is: %.5f", itt / prop_treated)
```

```
[1] "\nThe estimated CACE is: 0.00513"
```

Hide

```
# or 2SLS
#itt_fit <- ivreg(outcome ~treatment,~compliers,data=d)
#stargazer(itt_fit, type='text')
```

2. We also did some work Work to find treatment response rate required to reject null.

[Hide](#)

```
# First, we use RI. create a new temp column of outcomes where the share of responses i
s n%
#To see what treatment response rate is required for significant result, adjust this va
riable.
#Found that a treatment response rate of about 0.6 would be required to observe signifi
cant result
treatment.response.rate <- 0.6
di$hypothetical.outcomes.temp <- sample(c(0,1), size = nrow(d), replace = TRUE, prob =
c(1-treatment.response.rate, treatment.response.rate))
#create new outcome column that takes original outcomes for control group, but new hypo
thetical outcomes with adjusted response rate for treatment rows
di$hypothetical.outcomes = d$outcome
di[treatment==1, hypothetical.outcomes:=hypothetical.outcomes.temp]
```

Coerced 'double' RHS to 'integer' to match the column's type; may have truncated precis
ion. Either change the target column to 'double' first (by creating a new 'double' vect
or length 483 (nrows of entire table) and assign that; i.e. 'replace' column), or coerc
e RHS to 'integer' (e.g. 1L, NA_[real|integer]_, as.*, etc) to make your intent clear a
nd for speed. Or, set the column type correctly up front when you create the table and
stick to it, please.

[Hide](#)

```
fake.response.rate.by.treatment <- di[, mean(hypothetical.outcomes), by =
c("treatment")]
fake.response.rate.by.treatment
```

treatment	V1
<dbl>	<dbl>
1	0.5758514
0	0.4500000

2 rows

[Hide](#)

```
#run RI using the fake data
y.fake <- di$hypothetical.outcomes
Z.fake <- di$treatment
cls.fake <- di$gender
blk.fake <- di$city
perms.fake <- genperms(Z.fake, clustvar = NULL, blockvar = blk.fake)
```

Too many permutations to use exact method.
Defaulting to approximate method.
Increase maxiter to at least 4.59676200506436e+128 to perform exact estimation.

[Hide](#)

```
probs.fake <- genprobexact(Z.fake, clustvar = NULL, blockvar = blk.fake) # probability
  of treatment
ate.fake <- estate(y.fake,Z.fake,prob=probs.fake) # estimate the ATE
Ys.fake <- genouts(y.fake,Z.fake,ate=0) # generate potential outcomes under sharp null
  of no effect
distout.fake <- gendist(Ys.fake,perms.fake, prob=probs.fake) # generate sampling dist.
  under sharp null
dispdist(distout.fake, ate.fake, quantiles = c(0.025, 0.975), display.plot = TRUE) # di
  splay characteristics of sampling dist. for inference
```

```
$two.tailed.p.value
[1] 0.0084

$two.tailed.p.value.abs
[1] 0.0095

$greater.p.value
[1] 0.0042

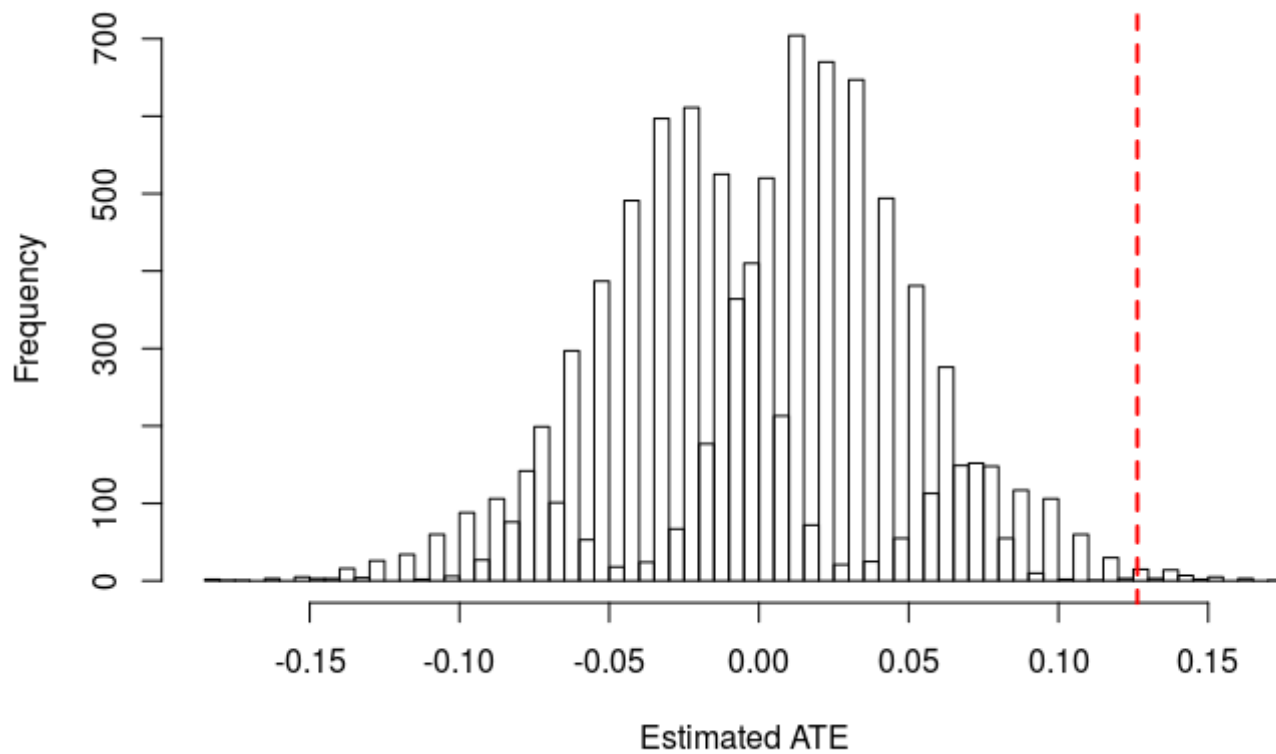
$lesser.p.value
[1] 0.9958

$quantile
      2.5%      97.5%
-0.09647689  0.09624912

$sd
[1] 0.04834024

$exp.val
[1] 0.0002227324
```


Distribution of the Estimated ATE


[Hide](#)

```
#P-value for actual data
p.val.fake = sum(abs(distout.fake) > ate.fake) / length(distout.fake)
p.val.fake
```

```
[1] 0.0095
```

[Hide](#)

```
# We can also do this using the regression estimate. For this we use the more general m
odel, m1. Given this model, if we would want to see treatment be statistically signific
ant we either have a larger coefficient or a lower standard error. Choosing a larger n
might be one way to reduce the standard error.
z <- coeftest(m1, vcovHC(m1)) # Robust se
# We want Est/Stderr > 2
t.stderr <- z[2]/2
std <- z[4]*sqrt(483)
newn <- (std/t.stderr)^2
sprintf("To attain enough power, i.e. to drive the standard error small enough (all thi
ngs unchanged), we would need a sample size of %.0f", newn)
```

```
[1] "To attain enough power, i.e. to drive the standard error small enough (all things
unchanged), we would need a sample size of 35590"
```

[Hide](#)

```
# Conversely we can also estimate the required difference in coefficient:  
newest <- 2*z[4]  
sprintf("We need to see an effect of greater than: %.3f", newest)
```

```
[1] "We need to see an effect of greater than: 0.056"
```

[Hide](#)

```
sprintf("Which is about %0.f times more than what we see currently", 2/z[6])
```

```
[1] "Which is about 9 times more than what we see currently"
```

4. Conclusion

Despite running a few different models, we find no evidence that the number of exclamation points affected response rates to our email.