# BA 830 Project

Team 10

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```
## -- Attaching packages --------------------------------------- tidyverse 1.3.0 --
## v ggplot2 3.3.3     v purrr   0.3.4
## v tibble  3.0.5     v dplyr   1.0.4
## v tidyr   1.1.2     v stringr 1.4.0
## v readr   1.4.0     v forcats 0.5.1
## -- Conflicts ------------------------------------------ tidyverse_conflicts() --
## x dplyr::between()   masks data.table::between()
## x dplyr::filter()    masks stats::filter()
## x dplyr::first()     masks data.table::first()
## x dplyr::lag()       masks stats::lag()
## x dplyr::last()      masks data.table::last()
## x purrr::transpose() masks data.table::transpose()
## Loading required package: Matrix
##
## Attaching package: 'Matrix'
## The following objects are masked from 'package:tidyr':
##
##     expand, pack, unpack
##
## Attaching package: 'lubridate'
## The following objects are masked from 'package:data.table':
##
##     hour, isoweek, mday, minute, month, quarter, second, wday, week,
##     yday, year
## The following objects are masked from 'package:base':
##
##     date, intersect, setdiff, union
##
## 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
```

```
#import the file
food <- fread('BA830-Project.csv')
```

```
food %>% mutate (outcome_plate = recode (outcome_plate, '0' = 1, '1' = 0))
```

```
##       Person_id   Age              Currently living Gender outcome_plate
##    1:         1 46-55                        Europe  Woman             0
##    2:         1 46-55                        Europe  Woman             0
##    3:         1 46-55                        Europe  Woman             0
##    4:         1 46-55                        Europe  Woman             1
##    5:         1 46-55                        Europe  Woman             0
##   ---
## 1766:       178 16-25 North America/Central America    Man             0
## 1767:       178 16-25 North America/Central America    Man             0
## 1768:       178 16-25 North America/Central America    Man             1
## 1769:       178 16-25 North America/Central America    Man             1
## 1770:       178 16-25 North America/Central America    Man             1
##       outcome_food outcome_question     food_name Treatment
##    1:            1                1        Burger         0
##    2:            1                1          Taco         0
##    3:            0                0 Fried Chicken         0
##    4:            0                0        Salmon         0
##    5:            1                1         Pasta         0
##   ---
## 1766:            1                1         Steak         1
## 1767:            1                1      Dumpling         1
## 1768:            1                1         Sushi         1
## 1769:            1                1    Fried Rice         1
## 1770:            0                0         Salad         1
```

```
#proportion test
prop.test(nrow(food[Treatment ==  1]), nrow(food), 0.5)
```

```
##
##  1-sample proportions test with continuity correction
##
## data:  nrow(food[Treatment == 1]) out of nrow(food), null probability 0.5
## X-squared = 13, df = 1, p-value = 0.0004
## alternative hypothesis: true p is not equal to 0.5
## 95 percent confidence interval:
##  0.434 0.481
## sample estimates:
##     p
## 0.458
```

The p value here is lower than 0.05, so we reject the null hypothesis which the randomization was not property done, so it may cause some problem with the experiment result.

```
reg.plate <- lm(outcome_plate ~ Treatment, data = food)
summary(reg.plate)
```

```
##
## Call:
## lm(formula = outcome_plate ~ Treatment, data = food)
##
## Residuals:
##    Min     1Q Median     3Q    Max
## -0.705 -0.531  0.295  0.469  0.469
##
```

```
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)   0.5313     0.0155   34.28  < 2e-16 ***
## Treatment     0.1737     0.0229    7.58  5.4e-14 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.48 on 1768 degrees of freedom
## Multiple R-squared:  0.0315, Adjusted R-squared:  0.0309
## F-statistic: 57.5 on 1 and 1768 DF,  p-value: 5.44e-14
```

```
reg.question <- lm(outcome_question ~ Treatment, data = food)
summary(reg.question)
```

```
##
## Call:
## lm(formula = outcome_question ~ Treatment, data = food)
##
## Residuals:
##    Min     1Q Median     3Q    Max
## -0.486 -0.486 -0.404  0.513  0.596
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)   0.4865     0.0160    30.4  < 2e-16 ***
## Treatment    -0.0828     0.0237    -3.5  0.00048 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.496 on 1768 degrees of freedom
## Multiple R-squared:  0.00687,    Adjusted R-squared:  0.00631
## F-statistic: 12.2 on 1 and 1768 DF,  p-value: 0.000481
```

# Regression

```
together <- feols(c(outcome_plate, outcome_food) ~ Treatment,
                  data = food, se = 'white')
etable(together)
```

```
##                            model 1             model 2
## Dependent Var.:      outcome_plate        outcome_food
##
## (Intercept)     0.5312*** (0.0161)  0.4865*** (0.0161)
## Treatment       0.1737*** (0.0227) -0.0828*** (0.0236)
## _______________ __________________ __________________
## S.E. type       Heteroskedas.-rob. Heteroskedast.-rob.
## Observations                 1,770               1,770
## R2                         0.03150             0.00687
## Adj. R2                    0.03095             0.00631
```

In the regression of model 1 we looked at the outcome_plate as the outcome variable first. We get an intercept of 0.5312, which represents the mean of the outcome of our control group. The estimate for the treatment effect is 0.1737 and has a standard error of 0.0227. Therefore, we have a positive treatment effect which indicates a positive relationship between Treatment and outcome_plate.

We know from the stars that this result is statistically significant. This means that people in the treatment group are more likely to choose the red plate.

For model 2 we used outcome_food as our outcome variable. The intercept is 0.4865. Our estimated treatment effect is -0.0828 and has a standard error of 0.0236. This indicates that we have a negative relationship between Treatment and outcome_food. These results are also statistically significant. It still indicates that people in the treatment group are more likely to choose the food on the red plate. The negtaive treatment effect shows us that people in the treatment group are more likely to choose the plate that is positioned on the right.

```
fixed_effects <- feols(outcome_plate ~ Treatment
                  | outcome_food + food_name, data = food,
            se = 'white')
etable(fixed_effects)
```

```
##                       fixed_effects
## Dependent Var.:       outcome_plate
##
## Treatment       0.1788*** (0.0230)
## Fixed-Effects:  ------------------
## outcome_food                   Yes
## food_name                      Yes
## _______________ __________________
## S.E. type       Heteroskedas.-rob.
## Observations                1,770
## R2                        0.04394
## Within R2                 0.03349
```

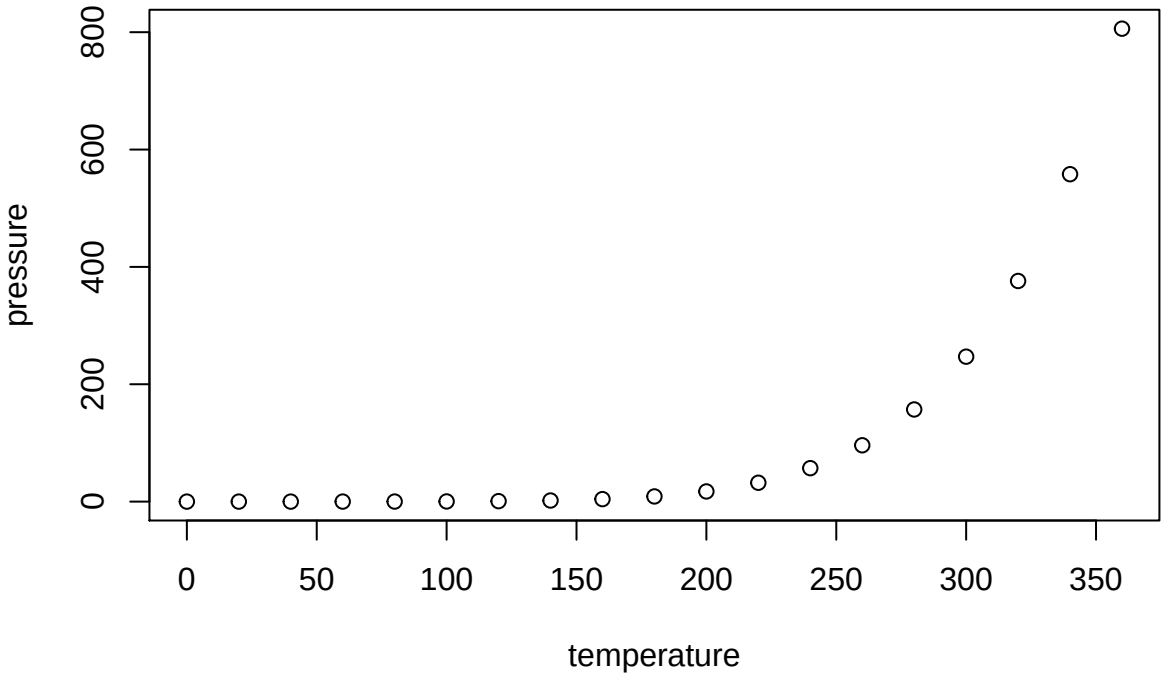
For the regression above we added two fixed effects: outcome_food and food_name to see if the food has an impact on the outcome. The outcome variable is outcome_plate and has an estimated treatment effect of 0.1788 with an standard error of 0.0230, which is really similar to the regression above without the fixed effects. The results of this regression are also statistically significant.

```
fixed_effects2 <- feols(outcome_plate ~ Treatment
                  | outcome_food + food_name + Gender + Age, data = food,
            se = 'white')
etable(fixed_effects)
```

```
##                       fixed_effects
## Dependent Var.:       outcome_plate
##
## Treatment       0.1788*** (0.0230)
## Fixed-Effects:  ------------------
## outcome_food                   Yes
## food_name                      Yes
## _______________ __________________
## S.E. type       Heteroskedas.-rob.
## Observations                1,770
## R2                        0.04394
## Within R2                 0.03349
```

## Including Plots

You can also embed plots, for example:




Note that the `echo = FALSE` parameter was added to the code chunk to prevent printing of the R code that generated the plot.