Pilot Data Cleaner

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Loading in data

I will start by creating a function to automatically set up the data.

All of this is a work in progress bla bla bla bla

```
# Creating a function to load datasets

data_cleaner <- function(d){

  df <- read_csv(d) %>% #reading in the data
  slice(c(-1, -2)) #qualtrics adds 2 rows of unnecessary headers. This removes them.

# Cleaning up the conjoint data.
# Note, this is not very efficient memory wise
# and may need to be tuned up for larger datasets

names <- colnames(df)

new_names <- paste0(1:243, "_conjoint_friend1")
new_names2 <- paste0(1:243, "_conjoint_friend2")

df2 <- df %>%
  setnames(old = names[246:488], new = new_names) %>%
  setnames(old = names[489:731], new = new_names2)


test2 <- df2 %>%
    pivot_longer(
          cols = ends_with("friend1"),
          names_to = "Conjoint_first_permutation",
          values_to = "Conjoint_first_permutation_answer") %>%
  filter(!is.na(Conjoint_first_permutation_answer)) %>%
    pivot_longer(
          cols = ends_with("_friend2"),
          names_to = "Conjoint_second_permutation",
          values_to = "Conjoint_second_permutation_answer") %>%
    filter(!is.na(Conjoint_second_permutation_answer)) %>%
   pivot_longer(
          cols = starts_with("ptt"),
          names_to = "Petition_Experiment_Treatment",
          values_to = "Petition_Experiment_Treatment_Answer") %>%
  filter(!is.na(Petition_Experiment_Treatment_Answer))
```

```
}
```

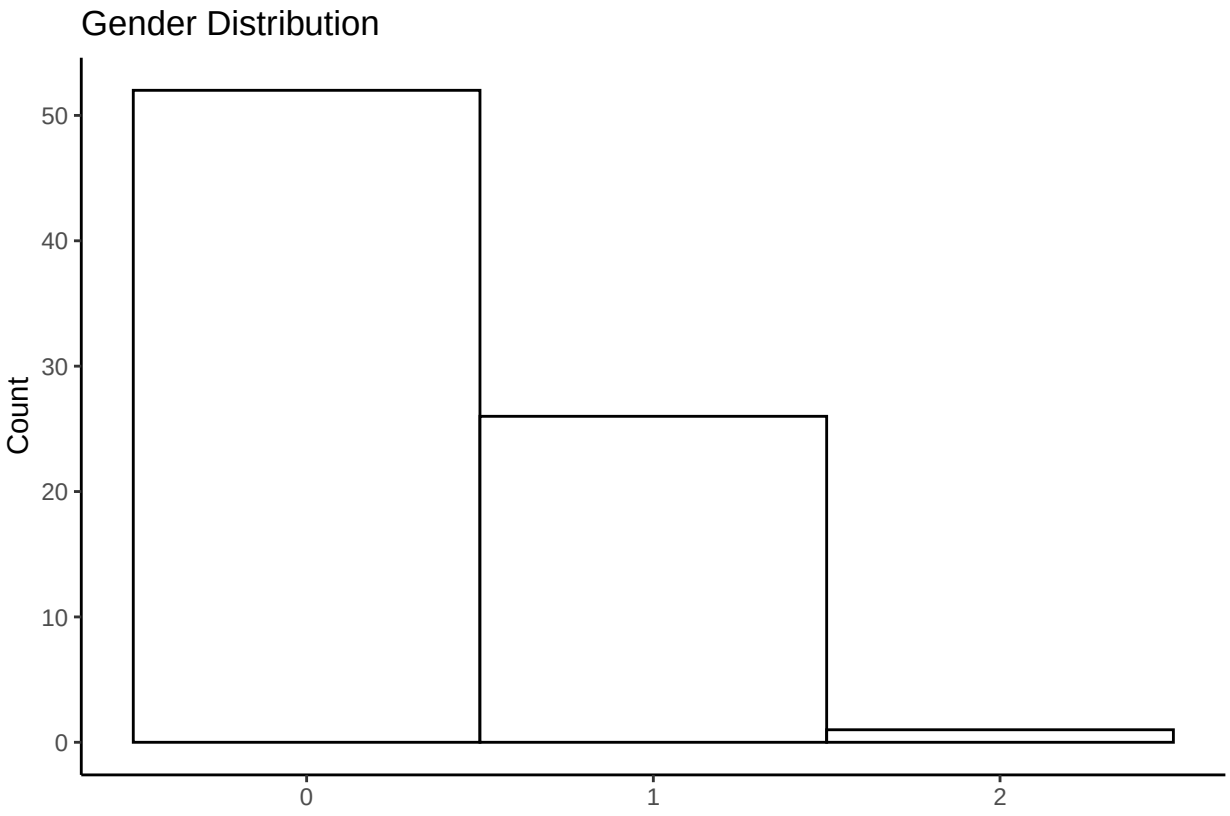
Now that the function is created, we can use it to make our data. There will be a warning, but it is totally ok for now.

```
csv <- c("D:/Lebanon_data/LEB Youth Civic Engagement ENG - postcut_December 11, 2020_21.29.csv",
         "D:/Lebanon_data/LEB Youth Civic Engagement ARA - postcut_December 11, 2020_22.09.csv")

ENG <- data_cleaner(csv[1])
ARA <- data_cleaner(csv[2])

# For now I will remove the Q_RecaptchaScore

ARA$Q_RecaptchaScore <- NULL
ENG$Q_RecaptchaScore <- NULL

# There is an extra att_women in English "att_women_4"

ENG$att_women_4 <- NULL


# For now I am just going to force the two datasets to have the same variable names

ARA <- ARA %>%
  setnames(old = colnames(ARA), new = colnames(ENG))

df <- rbind(ENG, ARA)
```

Demographic distribution

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##  0.0000  0.0000  0.0000  0.3544  1.0000  2.0000
```

```
ggplot(df, aes(x = gender))+
  geom_histogram(bins = 3, fill="white", color="black")+
  labs(title="Gender Distribution",x="", y = "Count")+
  theme_classic()
```

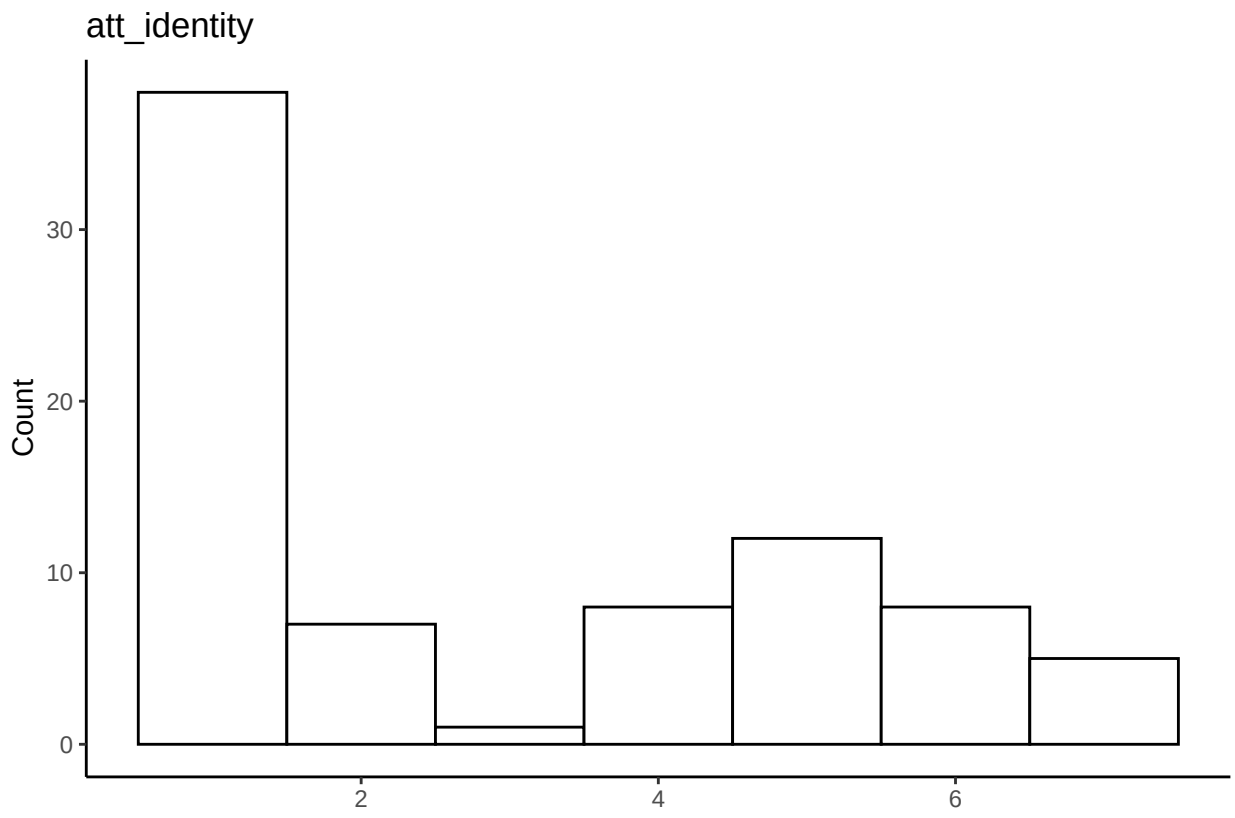


Religious demographics

```
summary(as.double(df$att_identity))
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   1.000   1.000   2.000   2.911   5.000   7.000
```

```
ggplot(df, aes(x = as.double(att_identity)))+
  geom_histogram(bins = 7, fill="white", color="black")+
  labs(title="att_identity",x="", y = "Count")+
  theme_classic()
```



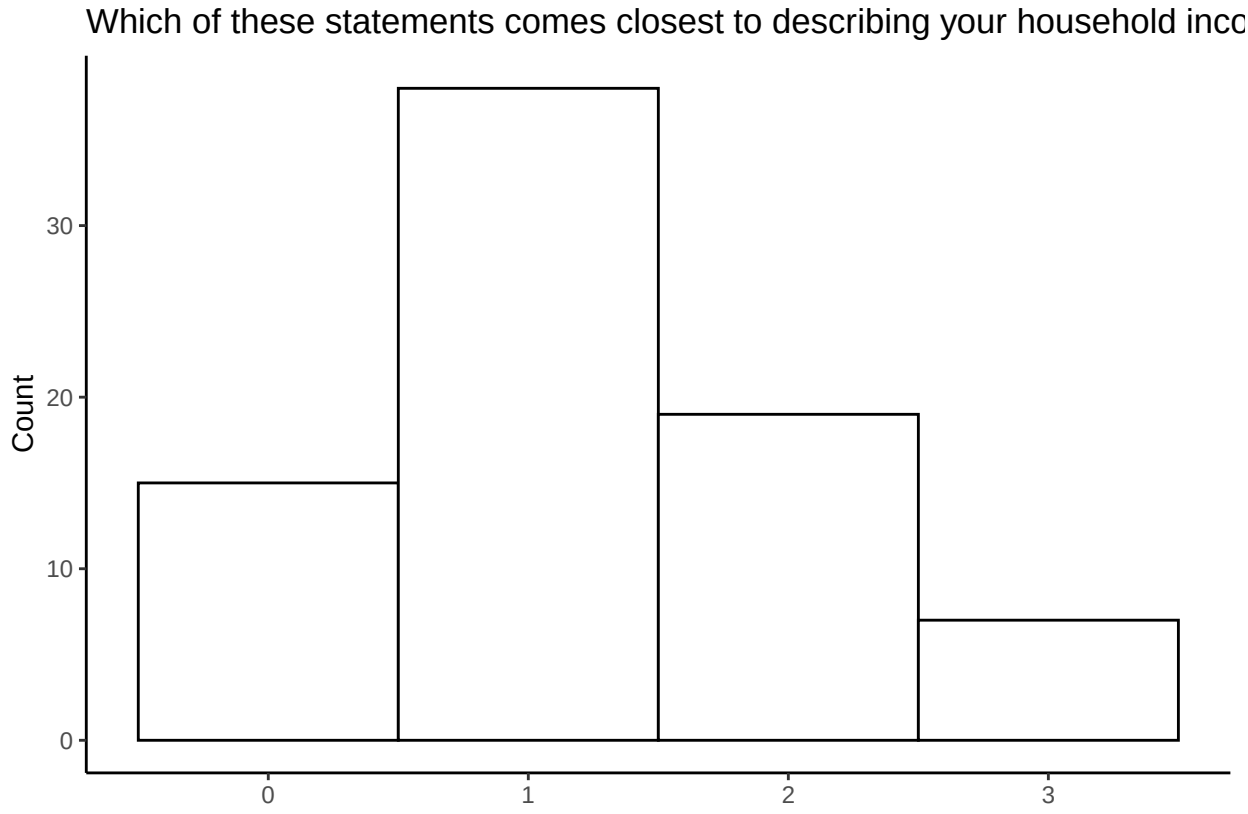
Income distribution

Below are some statements related to your household income. Which of these statements comes closest to describing your household income?

```
summary(as.double(df$dem_income1))
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   0.000   1.000   1.000   1.228   2.000   3.000
```

```
ggplot(df, aes(x = as.double(dem_income1)))+
  geom_histogram(bins = 4, fill="white", color="black")+
  labs(title="Which of these statements comes closest to describing your household income?",x="", y = "
  theme_classic()
```



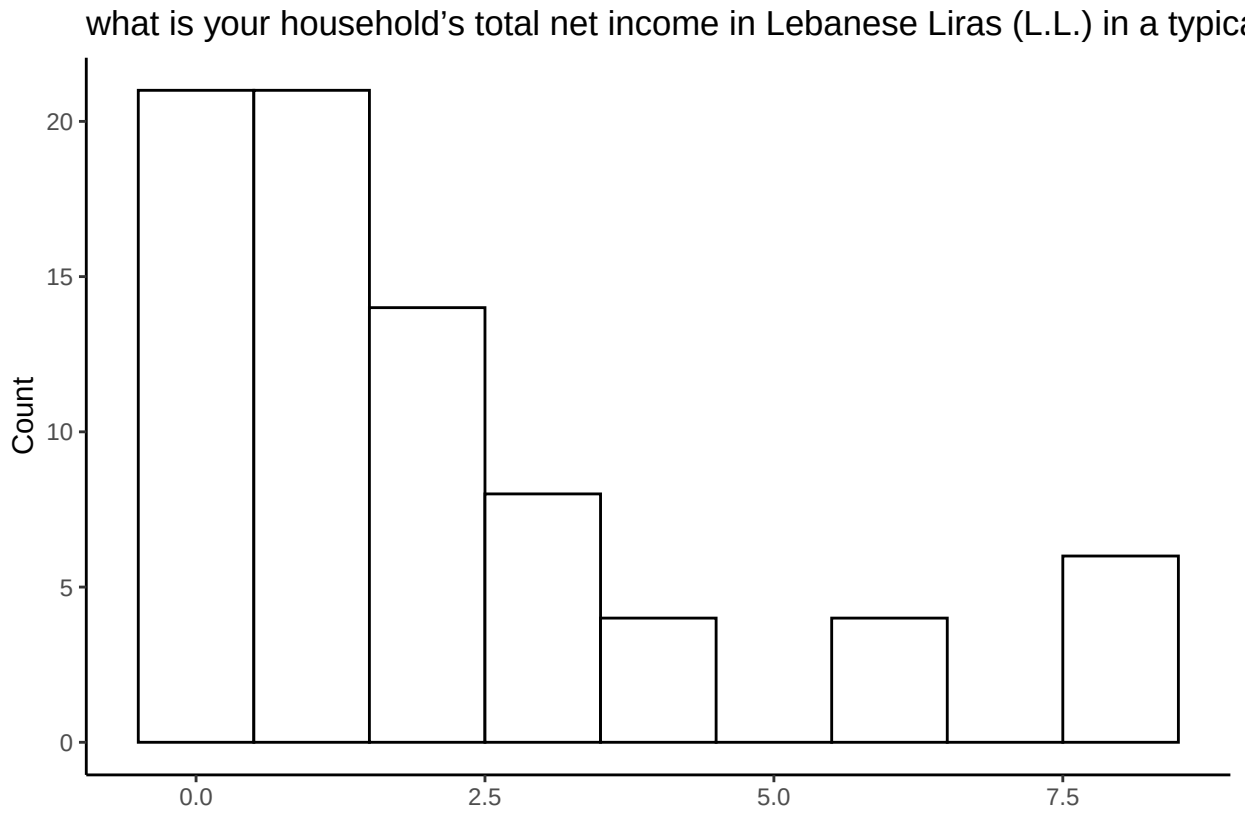
To the best of your knowledge, what is your household's total net income in Lebanese Liras (L.L.) in a typical month?

```
summary(as.double(df$dem_income2))
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
##   0.000   0.000   1.000   2.064   3.000   8.000       1
```

```
ggplot(df, aes(x = as.double(dem_income2)))+
  geom_histogram(bins = 9, fill="white", color="black")+
  labs(title="what is your household's total net income in Lebanese Liras (L.L.) in a typical month?",x=
  theme_classic()
```

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

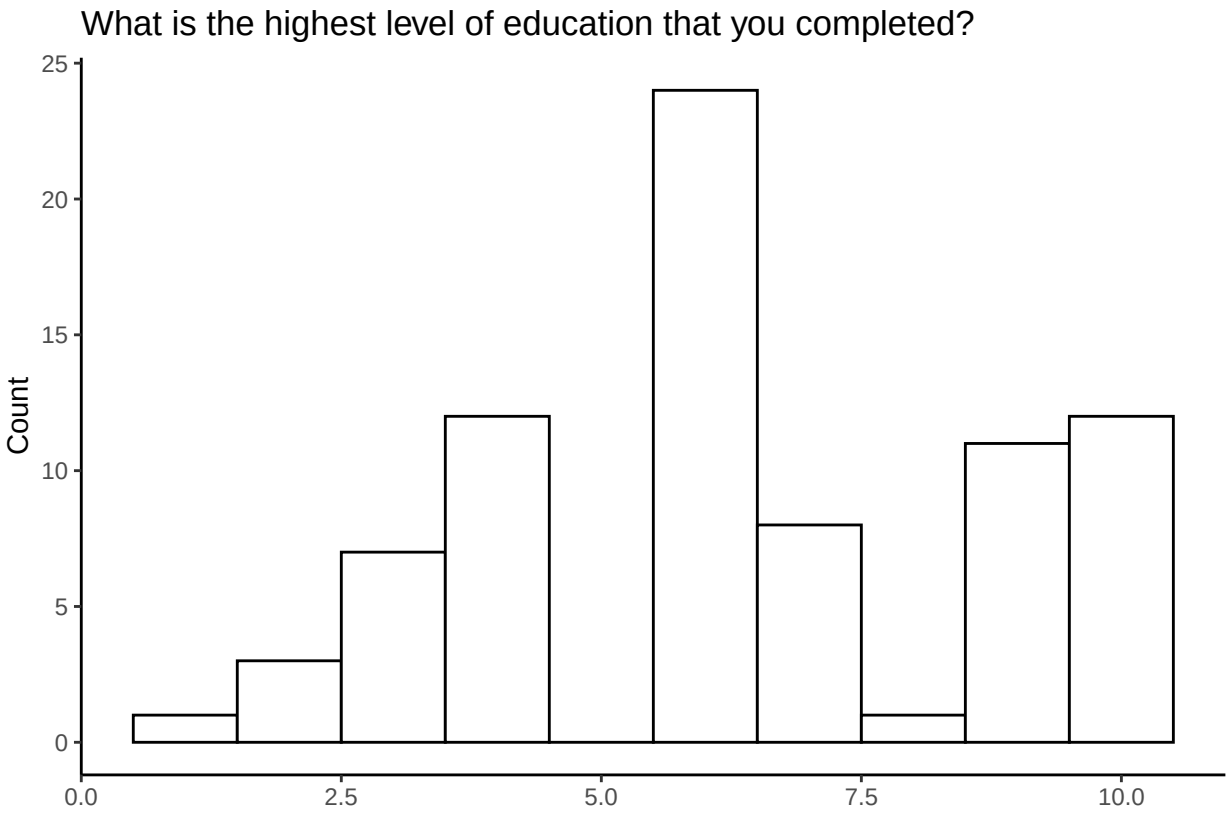


What is the highest level of education that you completed?

```
summary(as.double(df$dem_edu))
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   1.000   4.000   6.000   6.367   9.000  10.000
```

```
ggplot(df, aes(x = as.double(dem_edu)))+
  geom_histogram(bins = 10, fill="white", color="black")+
  labs(title="What is the highest level of education that you completed?",x="", y = "Count")+
  theme_classic()
```



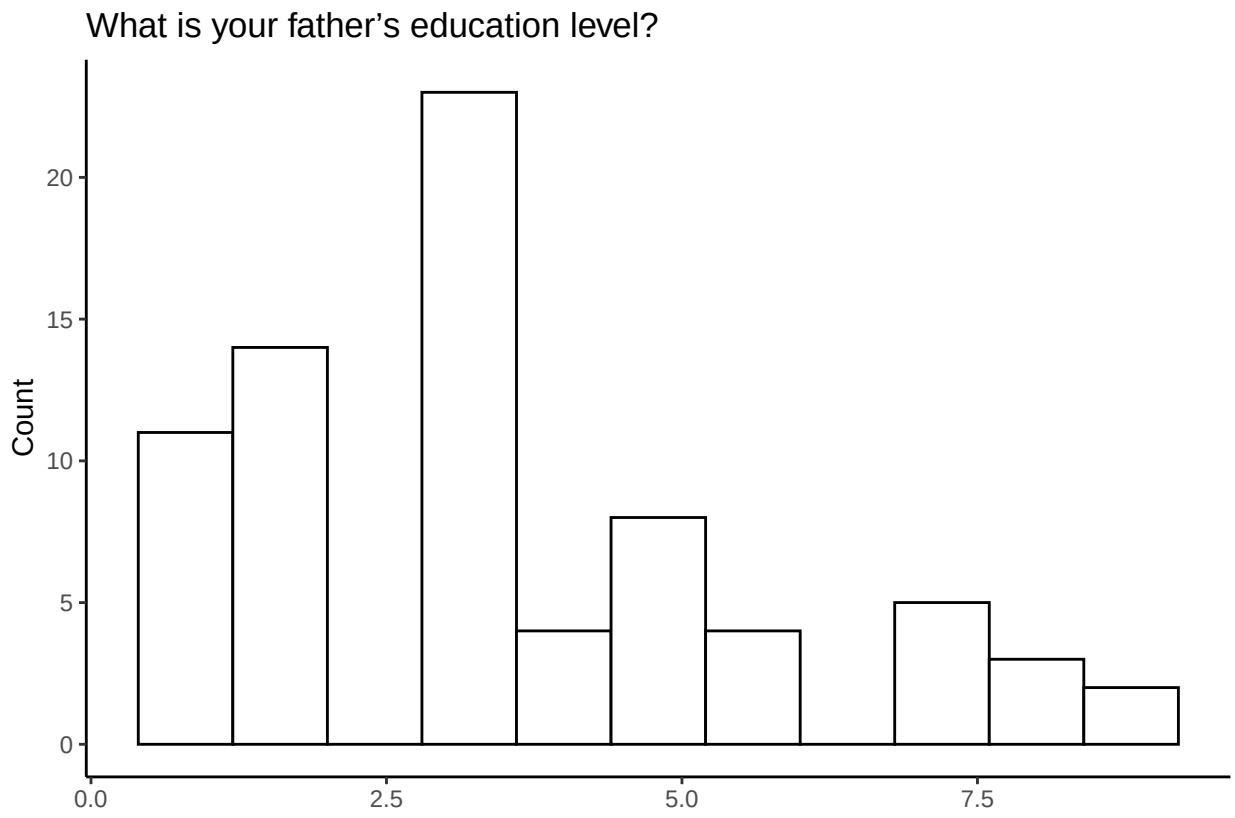
What is your father's education level?

```
summary(as.double(df$dem_fatheredu))
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
##   1.000   2.000   3.000   3.581   5.000   9.000       5
```

```
ggplot(df, aes(x = as.double(dem_fatheredu)))+
  geom_histogram(bins = 11, fill="white", color="black")+
  labs(title="What is your father's education level? ",x="", y = "Count")+
  theme_classic()
```

```
## Warning: Removed 5 rows containing non-finite values (stat_bin).
```

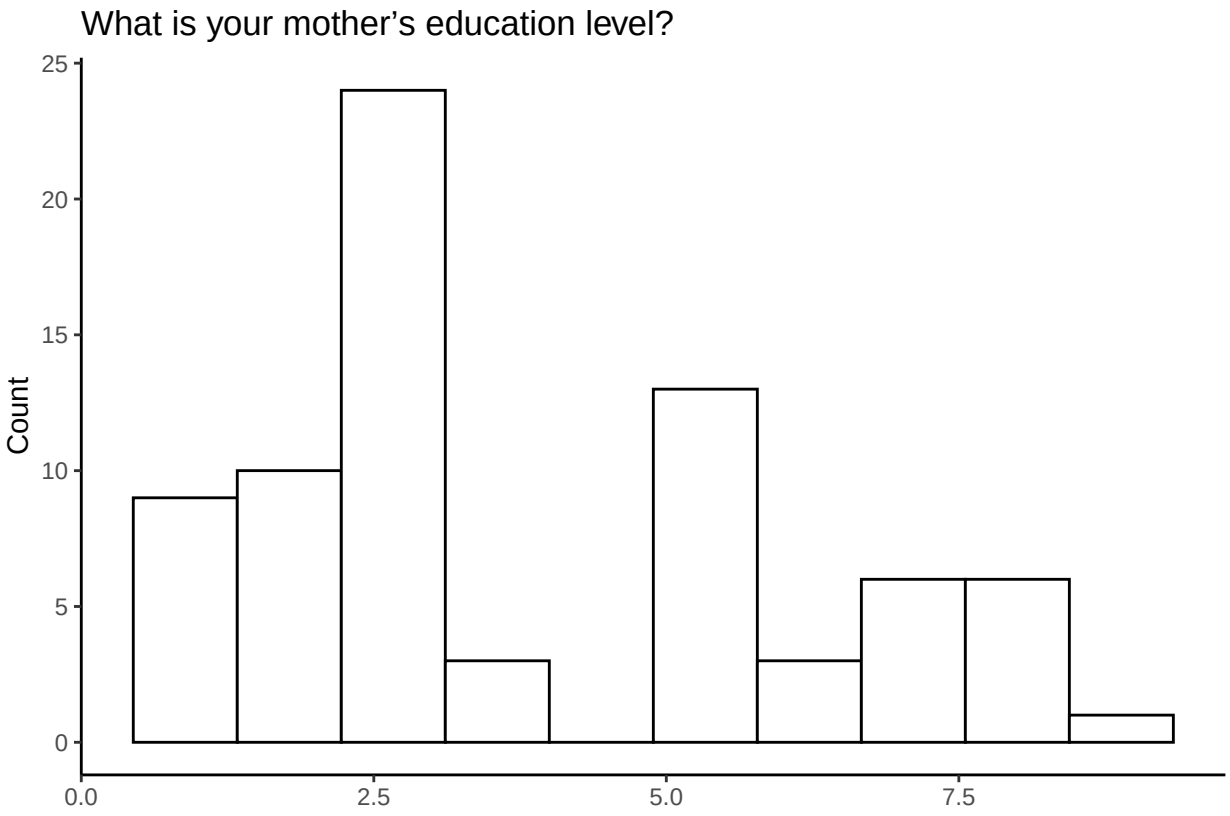



```
summary(as.double(df$dem_motheredu))
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
##   1.000   2.500   3.000   3.933   5.000   9.000       4
```

```
ggplot(df, aes(x = as.double(dem_motheredu)))+
  geom_histogram(bins = 10, fill="white", color="black")+
  labs(title="What is your mother's education level?",x="", y = "Count")+
  theme_classic()
```

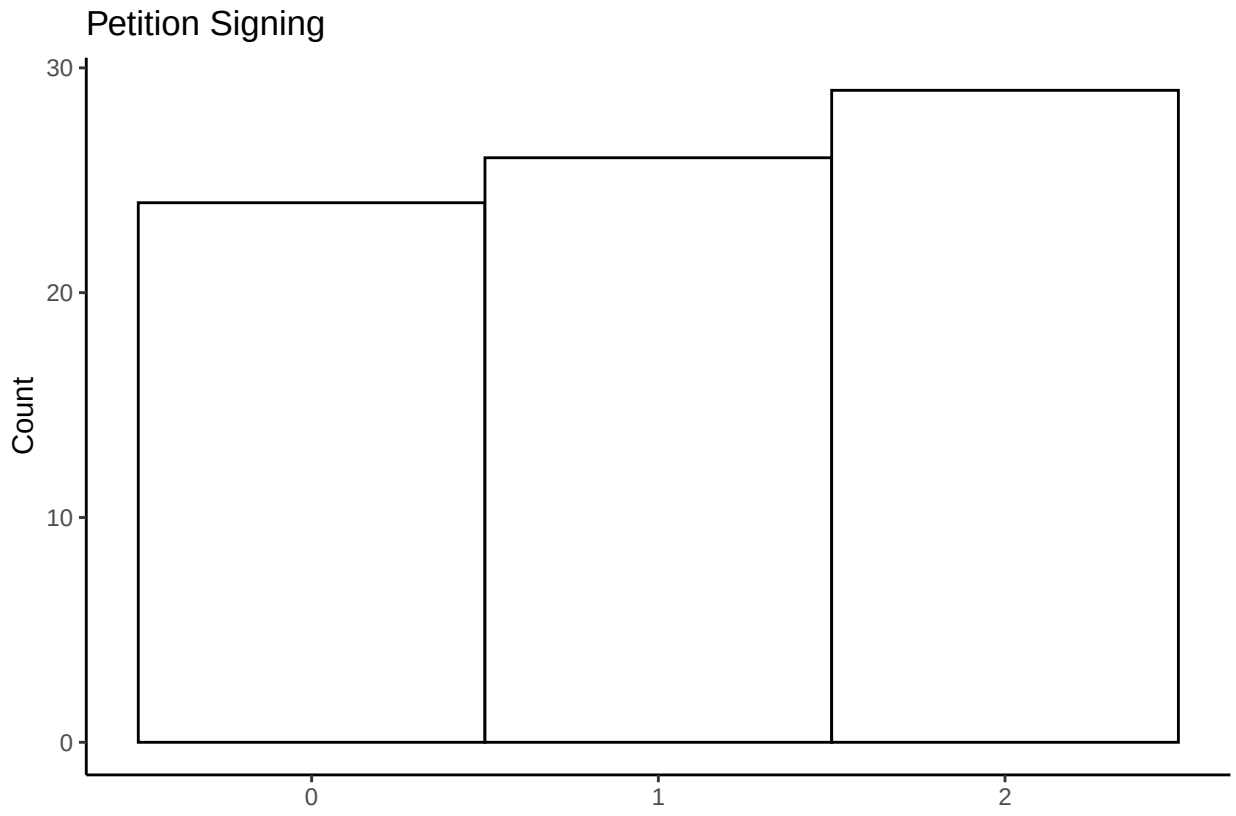
```
## Warning: Removed 4 rows containing non-finite values (stat_bin).
```



Mother's are better educated than fathers in this sample

Petition Signing distribution

How many people actually signed the petition? Lets find out.



Lets do some basic stats on the petition experiment. Here is a simple logistic regression to see if the control group is different from any of the treatments.

```
# colnames(df)
# unique(df$Petition_Experiment_Treatment)

df2 <- df %>%
  filter(Petition_Experiment_Treatment == "ptt_treat_control_fo" | Petition_Experiment_Treatment == "pt

df2$pt_econ_treatment <- 0
df2$pt_econ_treatment[which(df2$Petition_Experiment_Treatment == "ptt_treat_eco_foll")] <- 1
df2$signed <- 0
df2$signed[which(df2$Q144 > 0)] <- 1

test <- glm(signed ~ pt_econ_treatment, data = df2, family = binomial())

summary(test)
```

```
##
## Call:
## glm(formula = signed ~ pt_econ_treatment, family = binomial(),
##     data = df2)
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -1.84648   0.00008   0.00008   0.63352   0.63352
##
```

```
## Coefficients:
##                   Estimate Std. Error z value Pr(>|z|)
## (Intercept)          19.57    3584.67   0.005    0.996
## pt_econ_treatment   -18.06    3584.67  -0.005    0.996
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 13.003  on 19  degrees of freedom
## Residual deviance: 10.431  on 18  degrees of freedom
## AIC: 14.431
##
## Number of Fisher Scoring iterations: 18
```

```
## combined table
(ctable <- cbind(ctable, "p value" = p))
```

```
##                                                    Value Std. Error
## Petition_Experiment_Treatmentptt_treat_bft_foll   -0.1667512  0.7582067
## Petition_Experiment_Treatmentptt_treat_control_fo  2.0974644  0.9855129
## Petition_Experiment_Treatmentptt_treat_cor_foll   -0.1171191  0.7088077
## Petition_Experiment_Treatmentptt_treat_eco_foll    0.9024628  0.8248948
## Petition_Experiment_Treatmentptt_treat_sec_foll   -0.6321240  0.7543644
## 0|1                                               -0.7742921  0.5908313
## 1|2                                                0.7744112  0.5908326
##                                                      t value    p value
## Petition_Experiment_Treatmentptt_treat_bft_foll   -0.2199285 0.82592686
## Petition_Experiment_Treatmentptt_treat_control_fo  2.1282973 0.03331245
## Petition_Experiment_Treatmentptt_treat_cor_foll   -0.1652339 0.86875986
## Petition_Experiment_Treatmentptt_treat_eco_foll    1.0940338 0.27394015
## Petition_Experiment_Treatmentptt_treat_sec_foll   -0.8379557 0.40205559
## 0|1                                               -1.3105130 0.19002234
## 1|2                                                1.3107116 0.18995522
```

The Covid Treatment was the treatment left out for comparison by the model. Lets take a look at that.

```
signif((ctable <- cbind(ctable, "p value" = p)),3)
```

```
##                                                   Value Std. Error t value
## Petition_Experiment_Treatmentptt_treat_control_fo  2.040      1.010    2.03
## 0|1                                               -0.713      0.639   -1.12
## 1|2                                                0.714      0.639    1.12
##                                                   p value
## Petition_Experiment_Treatmentptt_treat_control_fo   0.042
## 0|1                                                 0.264
## 1|2                                                 0.264
```

Something appears to be going on here, but the N is so small that it could still be chance