Replication Files for "Getting the Message? Choice, Self-Selection, and the Efficacy of Social Movement Arguments"

Overview

This document provides the code necessary to replicate the results of "Getting the Message? Choice, Self-Selection, and the Efficacy of Social Movement Arguments" It consist of the following sections

- **Setup** Sets up R environment:
  - Sets working directory and `knitr` options for display
  - Loads libraries (`tidyverse` packages, `car`, `Hmisc`, `kableExtra`)
  - Loads data (`df_mtg.rda`, `df_qg.rda`, `power_simulations.rda`)
- **Functions** Defines a set of custom functions to:
  - Calculate treatment effects (`diff_fn()`, `acte_fn()`, `cacte_fn()`)
  - Display treatment effects (`balance_fn()`, `plot_balance_fn()`, `effects_fn()`, `plot_effects_fn()`, `format_ci_fn()`, `table_fn()`,`table_app_fn()`)
  - Conduct power simulations (`data_fn()`, `power_fn()`, `sim_power_fn()`, `display_power_fn()`)
- **Main Figures** Produces Figures 1-6 as seen in text using functions defined above
- **Main Table** Produces Tables 1-2 as seen in text using functions defined above
- **Online Appendix** Produces tables and figures from Online Appendices C-F using functions defined above

Note: Each power simulations displayed in Figure 2 and Appendix C takes approximately 30-40 minutes to complete. The replication file loads the cached results of a round of power simulations. To conduct simulations, uncomment code.

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Setup

```
## - Session info ---------------------------------------------------------------
##  setting  value
##  version  R version 4.0.0 (2020-04-24)
##  os       macOS Catalina 10.15.5
##  system   x86_64, darwin17.0
##  ui       X11
##  language (EN)
##  collate  en_US.UTF-8
##  ctype    en_US.UTF-8
##  tz       America/New_York
##  date     2020-06-23
##
## - Packages -------------------------------------------------------------------
##  package      * version date       lib source
##  abind          1.4-5   2016-07-21 [1] CRAN (R 4.0.0)
##  acepack        1.4.1   2016-10-29 [1] CRAN (R 4.0.0)
##  assertthat     0.2.1   2019-03-21 [1] CRAN (R 4.0.0)
##  backports      1.1.8   2020-06-17 [1] CRAN (R 4.0.0)
##  base64enc      0.1-3   2015-07-28 [1] CRAN (R 4.0.0)
##  blob           1.2.1   2020-01-20 [1] CRAN (R 4.0.0)
##  broom          0.5.6   2020-04-20 [1] CRAN (R 4.0.0)
##  car          * 3.0-8   2020-05-21 [1] CRAN (R 4.0.0)
##  carData      * 3.0-4   2020-05-22 [1] CRAN (R 4.0.0)
##  cellranger     1.1.0   2016-07-27 [1] CRAN (R 4.0.0)
##  checkmate      2.0.0   2020-02-06 [1] CRAN (R 4.0.0)
##  cli            2.0.2   2020-02-28 [1] CRAN (R 4.0.0)
##  cluster        2.1.0   2019-06-19 [1] CRAN (R 4.0.0)
##  colorspace     1.4-1   2019-03-18 [1] CRAN (R 4.0.0)
##  crayon         1.3.4   2017-09-16 [1] CRAN (R 4.0.0)
##  curl           4.3     2019-12-02 [1] CRAN (R 4.0.0)
##  data.table     1.12.8  2019-12-09 [1] CRAN (R 4.0.0)
##  DBI            1.1.0   2019-12-15 [1] CRAN (R 4.0.0)
##  dbplyr         1.4.4   2020-05-27 [1] CRAN (R 4.0.0)
##  digest         0.6.25  2020-02-23 [1] CRAN (R 4.0.0)
##  dplyr        * 1.0.0   2020-05-29 [1] CRAN (R 4.0.0)
##  ellipsis       0.3.1   2020-05-15 [1] CRAN (R 4.0.0)
##  evaluate       0.14    2019-05-28 [1] CRAN (R 4.0.0)
##  fansi          0.4.1   2020-01-08 [1] CRAN (R 4.0.0)
##  forcats      * 0.5.0   2020-03-01 [1] CRAN (R 4.0.0)
##  foreign        0.8-80  2020-05-24 [1] CRAN (R 4.0.0)
##  Formula      * 1.2-3   2018-05-03 [1] CRAN (R 4.0.0)
##  fs             1.4.1   2020-04-04 [1] CRAN (R 4.0.0)
##  generics       0.0.2   2018-11-29 [1] CRAN (R 4.0.0)
##  ggplot2      * 3.3.1   2020-05-28 [1] CRAN (R 4.0.0)
##  glue           1.4.1   2020-05-13 [1] CRAN (R 4.0.0)
##  gridExtra      2.3     2017-09-09 [1] CRAN (R 4.0.0)
##  gtable         0.3.0   2019-03-25 [1] CRAN (R 4.0.0)
##  haven          2.3.1   2020-06-01 [1] CRAN (R 4.0.0)
##  Hmisc        * 4.4-0   2020-03-23 [1] CRAN (R 4.0.0)
##  hms            0.5.3   2020-01-08 [1] CRAN (R 4.0.0)
##  htmlTable      1.13.3  2019-12-04 [1] CRAN (R 4.0.0)
##  htmltools      0.5.0   2020-06-16 [1] CRAN (R 4.0.0)
```

```
##  htmlwidgets    1.5.1   2019-10-08 [1] CRAN (R 4.0.0)
##  httr           1.4.1   2019-08-05 [1] CRAN (R 4.0.0)
##  jpeg           0.1-8.1 2019-10-24 [1] CRAN (R 4.0.0)
##  jsonlite       1.6.1   2020-02-02 [1] CRAN (R 4.0.0)
##  kableExtra   * 1.1.0   2019-03-16 [1] CRAN (R 4.0.0)
##  knitr          1.28    2020-02-06 [1] CRAN (R 4.0.0)
##  lattice      * 0.20-41 2020-04-02 [1] CRAN (R 4.0.0)
##  latticeExtra   0.6-29  2019-12-19 [1] CRAN (R 4.0.0)
##  lifecycle      0.2.0   2020-03-06 [1] CRAN (R 4.0.0)
##  lubridate      1.7.9   2020-06-08 [1] CRAN (R 4.0.0)
##  magrittr       1.5     2014-11-22 [1] CRAN (R 4.0.0)
##  Matrix         1.2-18  2019-11-27 [1] CRAN (R 4.0.0)
##  modelr         0.1.8   2020-05-19 [1] CRAN (R 4.0.0)
##  munsell        0.5.0   2018-06-12 [1] CRAN (R 4.0.0)
##  nlme           3.1-148 2020-05-24 [1] CRAN (R 4.0.0)
##  nnet           7.3-14  2020-04-26 [1] CRAN (R 4.0.0)
##  openxlsx       4.1.5   2020-05-06 [1] CRAN (R 4.0.0)
##  pillar         1.4.4   2020-05-05 [1] CRAN (R 4.0.0)
##  pkgconfig      2.0.3   2019-09-22 [1] CRAN (R 4.0.0)
##  png            0.1-7   2013-12-03 [1] CRAN (R 4.0.0)
##  purrr        * 0.3.4   2020-04-17 [1] CRAN (R 4.0.0)
##  R6             2.4.1   2019-11-12 [1] CRAN (R 4.0.0)
##  RColorBrewer   1.1-2   2014-12-07 [1] CRAN (R 4.0.0)
##  Rcpp           1.0.4.6 2020-04-09 [1] CRAN (R 4.0.0)
##  readr        * 1.3.1   2018-12-21 [1] CRAN (R 4.0.0)
##  readxl         1.3.1   2019-03-13 [1] CRAN (R 4.0.0)
##  reprex         0.3.0   2019-05-16 [1] CRAN (R 4.0.0)
##  rio            0.5.16  2018-11-26 [1] CRAN (R 4.0.0)
##  rlang          0.4.6   2020-05-02 [1] CRAN (R 4.0.0)
##  rmarkdown      2.3     2020-06-18 [1] CRAN (R 4.0.0)
##  rpart          4.1-15  2019-04-12 [1] CRAN (R 4.0.0)
##  rstudioapi     0.11    2020-02-07 [1] CRAN (R 4.0.0)
##  rvest          0.3.5   2019-11-08 [1] CRAN (R 4.0.0)
##  scales         1.1.1   2020-05-11 [1] CRAN (R 4.0.0)
##  sessioninfo  * 1.1.1   2018-11-05 [1] CRAN (R 4.0.0)
##  stringi        1.4.6   2020-02-17 [1] CRAN (R 4.0.0)
##  stringr      * 1.4.0   2019-02-10 [1] CRAN (R 4.0.0)
##  survival     * 3.2-3   2020-06-13 [1] CRAN (R 4.0.0)
##  tibble       * 3.0.1   2020-04-20 [1] CRAN (R 4.0.0)
##  tidyr        * 1.1.0   2020-05-20 [1] CRAN (R 4.0.0)
##  tidyselect     1.1.0   2020-05-11 [1] CRAN (R 4.0.0)
##  tidyverse    * 1.3.0   2019-11-21 [1] CRAN (R 4.0.0)
##  vctrs          0.3.1   2020-06-05 [1] CRAN (R 4.0.0)
##  viridisLite    0.3.0   2018-02-01 [1] CRAN (R 4.0.0)
##  webshot        0.5.2   2019-11-22 [1] CRAN (R 4.0.0)
##  withr          2.2.0   2020-04-20 [1] CRAN (R 4.0.0)
##  xfun           0.14    2020-05-20 [1] CRAN (R 4.0.0)
##  xml2           1.3.2   2020-04-23 [1] CRAN (R 4.0.0)
##  yaml           2.2.1   2020-02-01 [1] CRAN (R 4.0.0)
##  zip            2.0.4   2019-09-01 [1] CRAN (R 4.0.0)
##
## [1] /Library/Frameworks/R.framework/Versions/4.0/Resources/library
```

Functions

Functions to Calculate Treatment effects

- `diff_fn()`: Estimate differences in means

```
# Difference in Means Function
diff_fn <- function(the_data, dv1="Y",c,weights=F,...){
  # REQUIRES
    require(Hmisc)
  # INPUTS:
    # the_data: data frame
    # dv1: outcome
    # c: object containing names of treatment conditions
    # weights: boolean indicating whether to calculated weighted ATE
  # OUTPUTS:
    # result: vector containing Difference in Means, SE, 95% ci, 90%ci, and p-value

  tmp <- as.data.frame(the_data[the_data$treatment%in%c, ])

  if(weights==F){
    mu1 <- with(tmp, mean(tmp[treatment==c[1], dv1],na.rm=T))
    mu2 <- with(tmp, mean(tmp[treatment==c[2], dv1],na.rm=T))
    sd1 <- with(tmp, sd(tmp[treatment==c[1], dv1],na.rm=T))
    sd2 <- with(tmp, sd(tmp[treatment==c[2], dv1],na.rm=T))
  }
  if(weights==T){
    mu1 <- with(tmp, Hmisc::wtd.mean(
      tmp[treatment==c[1], dv1],na.rm=T,weights=tmp[treatment==c[1],"weights"])
      )
    mu2 <- with(tmp, Hmisc::wtd.mean(
      tmp[treatment==c[2], dv1],na.rm=T,weights=tmp[treatment==c[2],"weights"])
      )
    sd1 <- sqrt(with(tmp, Hmisc::wtd.var(
      tmp[treatment==c[1], dv1],na.rm=T,weights = tmp[treatment==c[1],"weights"])
      ))
    sd2 <- sqrt(with(tmp, Hmisc::wtd.var(
      tmp[treatment==c[2], dv1],na.rm=T,weights = tmp[treatment==c[2],"weights"])
      ))
  }
  # Calculate Difference
  diff <- mu2-mu1

  # Calculate N
  n1 <- with(tmp, sum(!is.na(tmp[treatment==c[1], dv1])*tmp[treatment==c[1],"weights"]))
  n2 <- with(tmp, sum(!is.na(tmp[treatment==c[2], dv1])*tmp[treatment==c[2],"weights"]))

   # SE of Difference
  se <- sqrt( sd1^2/n1 + sd2^2/n2)

  # Degrees of Freedom
  the_df <- (sd1^2/n1+sd2^2/n2)^2/((sd1^4)/(n1^2*(n1-1))+ (sd2^4)/(n2^2*(n2-1)))

  # 95% CI
  ll <- diff - qt(.975,the_df)*se
```

```
  ul <- diff + qt(.975,the_df)*se
  # 90% CI
  ll90 <- diff - qt(.95,the_df)*se
  ul90 <- diff + qt(.95,the_df)*se
  # t-stat
  stat <- diff/se
  # p-value
  pval = 2 * pt(-abs(stat),the_df)
  # Combine results
  results <- c(Difference = diff, SE = se, ll = ll, ul = ul,
               ll90=ll90,ul90=ul90, pval = pval)
  return(results)
}
```

- `acte_fn()`: Estimate ACTEs using delta method

```
# ACTE function
acte_fn <- function(dat,dv2="Y",z,w,...){
  # REQUIRES
    require(car)
    require(Hmisc)

  # INPUTS:
    # dat: data frame
    # dv2: outcome
    # z: object containing treatment groups to calculate ACTE-Select or ACTE-Avoid
    # w: weight argument passed to diff_fn
  # OUTPUTS:
  # result: vector containing ATE, SE, 95% ci, 90%ci, and p-value

  df <- dat
  N <- dim(df)[1]
  # N assigned to random assignment
  n_exp <- sum(df$C=="Experiment")
  # N assigned to choice
  n_choice <- sum(df$C == "Choice")
  # N avoiding treatment
  n_ch_a <- sum(df$C=="Choice" & df$avoid01==1)
  # N selecting treatment
  n_select <- sum(df$C=="Choice" & df$avoid01==0, na.rm=T)
  # N avoiding treatment
  n_avoid <- sum(df$C=="Choice" & df$avoid01==1,na.rm = T)
  # N avoiding treatment who receive no treatment
  n_control <- sum(df$D_ch == "Control",na.rm = T)

  # Weights to reflect fact
  df$weights <- rep(1,N)
  df$weights[df$C=="Choice" & df$avoid01==0 & df$D_ch == "Control"] <-1/(n_select/n_choice)
  df$weights[df$C=="Choice" & df$avoid01==1 & df$D_ch == "Control"] <-1/(n_control/n_avoid)


  # Calculate ACTE using Delta Method
    # ACTE-Select: c = c_acte_s = c("Control","Selection")
    # ACTE-Avoid:  c = c_acte_a = c("Selection","Treatment")
```

```
  tmp <- diff_fn(the_data=df, dv1=dv2,c=z, weights=w)
  x <- as.numeric(tmp["Difference"])
  se_x <- as.numeric(tmp["SE"])
  # ACTE-Select
  if(z[1]=="Control"){
    y <- summary(lm(select01~1,df[df$C=="Choice",]))$coef[1,1]
    se_y <- summary(lm(select01~1,df[df$C=="Choice",]))$coef[1,2]}
  # ACTE-Avoid
  if(z[2]=="Treatment"){
    y <- summary(lm(avoid01~1,df[df$C=="Choice",]))$coef[1,1]
    se_y <- summary(lm(avoid01~1,df[df$C=="Choice",]))$coef[1,2]}
  mvec <- c(x=x, y= y)
  V <- diag(c(se_x,se_y)^2)
  est <- car::deltaMethod(mvec,"x/y",V,level=.95)
  est90 <- car::deltaMethod(mvec,"x/y",V,level=.90)
  stat <- as.numeric(est[1])/as.numeric(est[2])

  # Return results
  results <- c(Difference = as.numeric(est[1]),
               SE = as.numeric(est[2]),
               ll = as.numeric(est[3]), ul = as.numeric(est[4]),
               ll90 = as.numeric(est90[3]), ul90 = as.numeric(est90[4]),
               pval = 2 * pnorm(-abs(stat)))
  return(results)
}
```

- `cacte_fn()`: Estimate CACTEs

```
# CACTE function
cacte_fn <- function(d, dv3="Y", z, w2=F){
  # INPUTS:
    # d: data frame
    # dv3: outcome
    # z: object containing treatment groups to calculate ACTE-Select or ACTE-Avoid
    # w2: weight argument passed to diff_fn
  # OUTPUTS:
    # result: Matrix containing Female and Male CACTE, SE, 95% ci, 90%ci, and p-value

  tmp <- as.data.frame(d[d$avoid01 == 1, ])
  tmp$treatment <- tmp$D_ch

  # CACTE- Female
  cacte_female <- diff_fn(tmp, dv1=dv3,c=c("Control","Female"),weights=w2)

  # CACTE Male
  cacte_male <- diff_fn(tmp, dv1=dv3, c=c("Control","Male"),weights=w2)
  results <- rbind(cacte_female,cacte_male)
  return(results)

}
```

Functions to display results

- `balance_function()`: Function to calculate covariate differences in respondents selecting and avoiding treatment

```
balance_fn <- function(the_data, dv1="Y",c,weights=F,...){
  # INPUTS
    # the_data: data frame
    # dv1: Variable to calculate difference in means
    # c: which group to compare
    # weights: Calcultate weighted differences (T/F)
  # OUTPUTS
  # result: summary stats of difference in means

  tmp <- as.data.frame(the_data[the_data$balance%in%c, ])
  if(weights==F){
    mu1 <- with(tmp, mean(tmp[balance==c[1], dv1],na.rm=T))
    mu2 <- with(tmp, mean(tmp[balance==c[2], dv1],na.rm=T))
  }
  if(weights==T){
    mu1 <- with(tmp, Hmisc::wtd.mean(
      tmp[balance==c[1], dv1],na.rm=T,weights=tmp[balance==c[1],"weights"])
      )
    mu2 <- with(tmp, Hmisc::wtd.mean(
      tmp[balance==c[2], dv1],na.rm=T,weights=tmp[balance==c[2],"weights"])
      )
  }
  diff <- mu1-mu2
  if(weights==F){
    sd1 <- with(tmp, sd(tmp[balance==c[1], dv1],na.rm=T))
    sd2 <- with(tmp, sd(tmp[balance==c[2], dv1],na.rm=T))
  }
  if(weights==T){
    sd1 <- sqrt(with(tmp, Hmisc::wtd.var(
      tmp[balance==c[1], dv1],na.rm=T,weights = tmp[balance==c[1],"weights"])
      ))
    sd2 <- sqrt(with(tmp, Hmisc::wtd.var(
      tmp[balance==c[2], dv1],na.rm=T,weights = tmp[balance==c[2],"weights"])
      ))
  }
  n1 <- with(tmp, sum(!is.na(tmp[balance==c[1], dv1])*tmp[balance==c[1],"weights"]))
  n2 <- with(tmp, sum(!is.na(tmp[balance==c[2], dv1])*tmp[balance==c[2],"weights"]))
  se <- sqrt( sd1^2/n1 + sd2^2/n2)
  the_df <- (sd1^2/n1+sd2^2/n2)^2/((sd1^4)/(n1^2*(n1-1))+ (sd2^4)/(n2^2*(n2-1)))
  ll <- diff - qt(.975,the_df)*se
  ul <- diff + qt(.975,the_df)*se
  ll90 <- diff - qt(.95,the_df)*se
  ul90 <- diff + qt(.95,the_df)*se
  stat <- diff/se
  pval = 2 * pt(-abs(stat),the_df)
  result <- c(Mu1= mu1, Mu2 = mu2, Difference = diff, SE = se, ll = ll, ul = ul,
              ll90 = ll90, ul90 = ul90, pval = pval, N1=n1,N2=n2)
  return(result)
}
```

- `plot_balance_function()`: Wrapper function to display results of `balance_function()`:

```
plot_balance_fn <- function(d,
                            bal_labs = c("Female", "Non-white", "Education",
                                         "Income", "PID", "Ideology",
                                         "MeToo Familiarity",
                                         "Specific Support", "General Support"),
                            comparison = c("Select Treatment", "Avoid Treatment")
                            ){
  # INPUTS
    # d: data frame
    # bal_labs: Covariate labels
    # comparison: which group to compare
  # OUTPUTS
    # fig: ggplot of comparisons


  # Descriptives Differences in Selecting Treatment - Overall
  bal_gen <- data.frame(
    rbind(
      balance_fn(the_data = d, "gender", comparison),
      balance_fn(the_data = d, "non_white", comparison),
      balance_fn(the_data = d, "education", comparison),
      balance_fn(the_data = d, "income", comparison),
      balance_fn(the_data = d, "pid", comparison),
      balance_fn(the_data = d, "ideo", comparison),
      balance_fn(the_data = d, "fam_movement", comparison),
      balance_fn(the_data = d, "dv_pca_metoo", comparison),
      balance_fn(the_data = d, "dv_pca_general", comparison)
    ))
  bal_gen$Covariate <- factor(bal_labs, levels=rev(bal_labs))
  rownames(bal_gen) <- bal_gen$Covariate

  # Descriptives Differences in Selecting Treatment - Men
  bal_gen_male <- data.frame(
    rbind(
      balance_fn(the_data = d[d$gender==0,],
                 "gender", comparison),
      balance_fn(the_data = d[d$gender==0,],
                 "non_white", comparison),
      balance_fn(the_data = d[d$gender==0,],
                 "education", comparison),
      balance_fn(the_data = d[d$gender==0,],
                 "income", comparison),
      balance_fn(the_data = d[d$gender==0,],
                 "pid", comparison),
      balance_fn(the_data = d[d$gender==0,],
                 "ideo", comparison),
      balance_fn(the_data = d[d$gender==0,],
                 "fam_movement", comparison),
      balance_fn(the_data = d[d$gender==0,],
                 "dv_pca_metoo", comparison),
      balance_fn(the_data = d[d$gender==0,],
                 "dv_pca_general", comparison)
```

```
  ))
bal_gen_male$Covariate <- factor(bal_labs, levels=rev(bal_labs))
rownames(bal_gen_male) <- bal_gen_male$Covariate
bal_gen_male[1,3] <-NA


# Descriptives Differences in Selecting Treatment - Women
bal_gen_female <- data.frame(
  rbind(
    balance_fn(the_data = d[d$gender==1,], "gender", comparison),
    balance_fn(the_data = d[d$gender==1,], "non_white", comparison),
    balance_fn(the_data = d[d$gender==1,], "education", comparison),
    balance_fn(the_data = d[d$gender==1,], "income", comparison),
    balance_fn(the_data = d[d$gender==1,], "pid", comparison),
    balance_fn(the_data = d[d$gender==1,], "ideo", comparison),
    balance_fn(the_data = d[d$gender==1,], "fam_movement", comparison),
    balance_fn(the_data = d[d$gender==1,], "dv_pca_metoo", comparison),
    balance_fn(the_data = d[d$gender==1,], "dv_pca_general", comparison)
  ))
bal_gen_female$Covariate <- factor(bal_labs, levels=rev(bal_labs))
rownames(bal_gen_female) <- bal_gen_female$Covariate
bal_gen_female[1,3] <-NA

# Descriptives Differences in Selecting Treatment - Democrats
bal_gen_dem <- data.frame(
  rbind(
    balance_fn(the_data = d[d$pid<4,], "gender", comparison),
    balance_fn(the_data = d[d$pid<4,], "non_white", comparison),
    balance_fn(the_data = d[d$pid<4,], "education", comparison),
    balance_fn(the_data = d[d$pid<4,], "income", comparison),
    balance_fn(the_data = d[d$pid<4,], "pid", comparison),
    balance_fn(the_data = d[d$pid<4,], "ideo", comparison),
    balance_fn(the_data = d[d$pid<4,], "fam_movement", comparison),
    balance_fn(the_data = d[d$pid<4,], "dv_pca_metoo", comparison),
    balance_fn(the_data = d[d$pid<4,], "dv_pca_general", comparison)
  ))
bal_gen_dem$Covariate <- factor(bal_labs, levels=rev(bal_labs))
rownames(bal_gen_dem) <- bal_gen_dem$Covariate

# Descriptives Differences in Selecting Treatment - Republicans
bal_gen_rep <- data.frame(
  rbind(
    balance_fn(the_data = d[d$pid>4,], "gender", comparison),
    balance_fn(the_data = d[d$pid>4,], "non_white", comparison),
    balance_fn(the_data = d[d$pid>4,], "education", comparison),
    balance_fn(the_data = d[d$pid>4,], "income", comparison),
    balance_fn(the_data = d[d$pid>4,], "pid", comparison),
    balance_fn(the_data = d[d$pid>4,], "ideo", comparison),
    balance_fn(the_data = d[d$pid>4,], "fam_movement", comparison),
    balance_fn(the_data = d[d$pid>4,], "dv_pca_metoo", comparison),
    balance_fn(the_data = d[d$pid>4,], "dv_pca_general", comparison)
  ))
bal_gen_rep$Covariate <- factor(bal_labs, levels=rev(bal_labs))
```

```r
rownames(bal_gen_rep) <- bal_gen_rep$Covariate

# Create data frame for plotting
fig_df <- rbind(
  data.frame(
    bal_gen,
    Group = "Overall",
    Type = "Overall"
  ),
  data.frame(
    bal_gen_male,
    Group = "Men",
    Type = "By Gender"
  ),
  data.frame(
    bal_gen_female,
    Group = "Women",
    Type = "By Gender"
  ),
  data.frame(
    bal_gen_rep,
    Group = "Republicans",
    Type = "By Partisanship"
  ),
  data.frame(
    bal_gen_female,
    Group = "Democrats",
    Type = "By Partisanship"
  )
)

# Set labels as factors for plotting
fig_df$Type <- factor(fig_df$Type, levels = unique(fig_df$Type))
fig_df$Group <- factor(fig_df$Group , levels = unique(fig_df$Group ))

# Create Figure
fig <- fig_df %>%
  ggplot(
    aes(Covariate, Difference, col = Group, shape = Group)
  )+
  geom_hline(
    yintercept = 0, linetype = "dashed",alpha = .5
  )+
  facet_wrap(
    ~Type, ncol = 3, drop = T)+
  geom_point(
    aes(shape=Group),
    position = position_dodge(width = .5), size=2
  )+
  geom_linerange(
    aes(ymin=ll,ymax=ul),
    size=.3,
    position = position_dodge(width = .5))+
```

```
    geom_linerange(
      aes(ymin=ll90,ymax=ul90),
      size=.6,
      position = position_dodge(width = .5))+
    theme(
      axis.text.x = element_text(angle = 0, hjust = 1)
    )+
    ylab("Difference\n(Treatment Selectors - Treatment Avoiders)")+
    coord_flip()+
    theme_bw()+
    scale_color_grey(start = 0, end = .75)+
    scale_shape_manual(values = c(16, 17, 15, 23, 4))+
    theme(
      panel.grid.minor = element_blank(),
      legend.position = "bottom"
    )

  # Display Figure
  fig

}
```

- `effects_fn()`: Wrapper function to calculated ATE, ACTEs, CACTEs, and CATEs

```
effects_fn <- function(the_dat,
                       the_dv,
                       the_lab = c("ATE",
                                   "ACTE:","Select Treatment","Avoid Treatment",
                                   "CACTE:","Female Treatment","Male Treatment",
                                   "CATE:",
                                   "White","Non-White",
                                   "Male","Female",
                                   "Democrat","Independent","Republican",
                                   "Liberal","Moderate","Conservative",
                                   "College Degree ","No Degree",
                                   "Familiar","Unfamiliar"
                       ),...){
  # INPUTS:
    # the_dat: data frame
    # dv1: outcome
    # the_lab: object containing row names
  # OUTPUTS:
    # result: dataframe containing ATE, ACTES, CACTEs, CATE


  # Calculate ATE, ACTE, CACTEs
  tmp <- rbind(
    diff_fn(the_dat, dv1=the_dv,c("Control","Treatment")),
    rep(NA,7),
    acte_fn(the_dat, dv2=the_dv,c("Control","Selection"),w = T),
    acte_fn(the_dat, dv2=the_dv,c("Selection","Treatment"),w = T),
    rep(NA,7),
    cacte_fn(the_dat, dv3=the_dv),
    rep(NA,7),
```

```
    diff_fn(the_data = the_dat[the_dat$non_white==0,],the_dv,c("Control","Treatment")),
    diff_fn(the_data = the_dat[the_dat$non_white==1,],the_dv,c("Control","Treatment")),
    diff_fn(the_data = the_dat[the_dat$gender==0,],the_dv,c("Control","Treatment")),
    diff_fn(the_data = the_dat[the_dat$gender==1,],the_dv,c("Control","Treatment")),
    diff_fn(the_data = the_dat[the_dat$pid<4,],the_dv,c("Control","Treatment")),
    diff_fn(the_data = the_dat[the_dat$pid==4,],the_dv,c("Control","Treatment")),
    diff_fn(the_data = the_dat[the_dat$pid>4,],the_dv,c("Control","Treatment")),
    diff_fn(the_data = the_dat[the_dat$ideo<4,],the_dv,c("Control","Treatment")),
    diff_fn(the_data = the_dat[the_dat$ideo==4,],the_dv,c("Control","Treatment")),
    diff_fn(the_data = the_dat[the_dat$ideo>4,],the_dv,c("Control","Treatment")),
    diff_fn(the_data = the_dat[the_dat$education>4,],the_dv,c("Control","Treatment")),
    diff_fn(the_data = the_dat[the_dat$education<5,],the_dv,c("Control","Treatment")),
    diff_fn(the_data = the_dat[the_dat$fam_movement>2,],the_dv,c("Control","Treatment")),
    diff_fn(the_data = the_dat[the_dat$fam_movement<3,],the_dv,c("Control","Treatment"))
    )

  results <- data.frame(tmp)

  # Format labels
  results$Estimate <- as.character(the_lab)
  results$Estimate <- factor(results$Estimate,levels=rev(the_lab))
  results$Estimand <- c("ATE",
                        rep("ACTE",3),
                        rep("CACTE",3),
                        rep("CATE",15)

  )
  results$Estimand <- factor(results$Estimand, levels =c("ATE","ACTE","CACTE","CATE"))

  return(results)
}
```

- `plot_effects_fn()`: Wrapper to plot results of `effects_fn()`

```
plot_effects_fn <- function(d, dv){
  # INPUTS:
    # d: data frame
    # dv: outcome
  # OUTPUTS:
    # fig: ggplot of results

  # Create dataframe of effects for plotting
  fig_df <- rbind(
    data.frame(
      effects_fn(d, dv),
      Group = "Overall",
      Type = "Overall"
    ),
    data.frame(
      effects_fn(d[d$gender==0,], dv),
      Group = "Men",
      Type = "By Gender"),
    data.frame(
      effects_fn(d[d$gender==1,], dv),
```

```
    Group = "Women",
    Type = "By Gender"),
  data.frame(
    effects_fn(d[d$pid > 4,], dv),
    Group = "Republicans",
    Type = "By Partisanship"),
  data.frame(
    effects_fn(d[d$pid < 4,], dv),
    Group = "Democrats",
    Type = "By Partisanship")
)

# Set labels as factors for plotting
fig_df$Type <- factor(fig_df$Type, levels = unique(fig_df$Type))
fig_df$Group <- factor(fig_df$Group , levels = unique(fig_df$Group ))


# Creat Figure
fig <- fig_df %>%
  filter(Estimand!="CATE") %>%
  ggplot(
    aes(Estimate, Difference,col=Group,shape=Group)
  )+
  geom_hline(yintercept = 0,linetype="dashed",alpha=.5)+
  facet_grid(~Type)+
  geom_point(
    aes(shape=Group),
    position = position_dodge(width = .5),size=2
  )+
  geom_linerange(
    aes(ymin=ll,ymax=ul),
    size=.3,
    position = position_dodge(width = .5)
  )+
  geom_linerange(
    aes(ymin=ll90,ymax=ul90),
    size=.6,
    position = position_dodge(width = .5)
  )+
  ylab("Difference\n(Treatment Selectors - Treatment Avoiders)")+
  coord_flip()+
  theme_bw()+
  theme(
    panel.grid.minor = element_blank(),
    legend.position = "bottom"
  )
# Format axis labels
fig <- fig +
  theme(
    axis.text.y = element_text(
      face = ifelse(rev(fig$data$Estimate) %in% c("ATE", "ACTE:", "CACTE:", "CATE:"),
                    "bold", "italic")
    )
```

```
    ) +
    scale_shape_manual(values = c(16, 17,15,23,4))

  return(fig)


}
```

- format_ci_fn(): Helper function to format CIs

```
format_ci_fn <- function(est){
  paste("[",sprintf("%.2f",est[,"ll"]),", ", sprintf("%.2f",est[,"ul"]),"]",sep="")
}
```

- `table_fn()`: Wrapper to format results of `plot_effects_fn()` as LaTeX table

```
table_fn <- function(d, the_cap=NULL){
  # INPUTS:
    # d: a dataframe of effects
  # OUTUTS
    # A LaTeX table
  tab_df <- d %>%filter(Estimand!="CATE") %>% na.omit()


  tab <- data.frame(matrix(NA,nrow=10,ncol=6))
  est_seq <- seq(1,dim(tab)[1], by=2)
  ci_seq <- seq(2,dim(tab)[1], by=2)
  tab[est_seq,1] <- as.character(tab_df[tab_df$Group == "Overall", "Estimate"])
  tab[ci_seq,1] <- ""

  tab[est_seq,2] <- sprintf("%.2f",tab_df[tab_df$Group == "Overall", "Difference"])
  tab[ci_seq,2] <- format_ci_fn(tab_df[tab_df$Group == "Overall",])

  tab[est_seq,3] <- sprintf("%.2f",tab_df[tab_df$Group == "Men", "Difference"])
  tab[ci_seq, 3] <- format_ci_fn(tab_df[tab_df$Group == "Men",])

  tab[est_seq,4] <- sprintf("%.2f",tab_df[tab_df$Group == "Women", "Difference"])
  tab[ci_seq, 4] <- format_ci_fn(tab_df[tab_df$Group == "Women",])

  tab[est_seq,5] <- sprintf("%.2f",tab_df[tab_df$Group == "Republicans", "Difference"])
  tab[ci_seq, 5] <- format_ci_fn(tab_df[tab_df$Group == "Republicans",])

  tab[est_seq,6] <- sprintf("%.2f",tab_df[tab_df$Group == "Democrats", "Difference"])
  tab[ci_seq, 6] <- format_ci_fn(tab_df[tab_df$Group == "Democrats",])

  colnames(tab) <- c("","Overall","Men","Women","Republicans","Democrats")

  kable(
    tab,
    booktabs = TRUE,
    caption = the_cap,
    digits=2,
    align = c("l",rep("c",3))
  ) %>%
    kable_styling(latex_options = c("HOLD_position",font_size=10)) %>%
```

```
    kableExtra::group_rows("ATE",1,2) %>%
    kableExtra::group_rows("ACTE",3,6) %>%
    kableExtra::group_rows("CACTE",7,10)%>%
    footnote(general = "The table provides point estimates and 95% confidence intervals for treatment e
             threeparttable = T,
             fixed_small_size = T)
}
```

- `table_app_fn()`: Wrapper to format results of `effects_fn()` as LaTeX tables for appendix

```
table_app_fn <- function(d, dv, g,eg,the_cap="Treatment Effects"){
  # INPUTS:
    # d: data frame
    # dv: outcome
    # g: variable to group by (Quotes)
    # eg: variable to group by (No quotes)
    # the_cap: caption for table
  # OUTPUTS:
    # tab: table of results
  tmp <- effects_fn(d,dv)%>%filter(Estimand!="CATE")
  tmp <- tmp[-c(2,5,8),-c(5:7,9)]




  the_vals <- na.omit(unlist(unique(d[,g])))

  enquo_g <- enquo(eg)
  quo_g <- quo_name(enquo(eg))

  tmp1 <- effects_fn(d[d[,quo_g]==the_vals[1],], dv)%>%filter(Estimand!="CATE")
  tmp1[,g] <- the_vals[1]
  tmp1 <- tmp1[-c(2,5,8),-c(5:7,9)]

  tmp2 <- effects_fn(d[d[,quo_g]==the_vals[2],], dv)%>%filter(Estimand!="CATE")
  tmp2[,g] <- the_vals[2]
  tmp2 <- tmp2[-c(2,5,8),-c(5:7,9)]



  d_m <- d %>%filter(gender==0)
  tmp1_m <- effects_fn(d_m[d_m[,quo_g]==the_vals[1],], dv)%>%filter(Estimand!="CATE")
  tmp1_m[,g] <- the_vals[1]
  tmp1_m <- tmp1_m[-c(2,5,8),-c(5:7,9)]

  tmp2_m <- effects_fn(d_m[d_m[,quo_g]==the_vals[2],], dv)%>%filter(Estimand!="CATE")
  tmp2_m[,g] <- the_vals[2]
  tmp2_m <- tmp2_m[-c(2,5,8),-c(5:7,9)]

  d_f <- d %>%filter(gender==1)
  tmp1_f <- effects_fn(d_f[d_f[,quo_g]==the_vals[1],], dv)%>%filter(Estimand!="CATE")
  tmp1_f[,g] <- the_vals[1]
  tmp1_f <- tmp1_f[-c(2,5,8),-c(5:7,9)]
```

```
  tmp2_f <- effects_fn(d_f[d_f[,quo_g]==the_vals[2],], dv)%>%filter(Estimand!="CATE")
  tmp2_f[,g] <- the_vals[2]
  tmp2_f <- tmp2_f[-c(2,5,8),-c(5:7,9)]


  tab <- data.frame(matrix(NA,nrow=dim(tmp)[1]*2,ncol=7))
  est_seq <- seq(1,dim(tab)[1], by=2)
  ci_seq <- seq(2,dim(tab)[1], by=2)

  tab[est_seq,1] <- as.character(tmp[,c("Estimate")])
  tab[ci_seq,1] <- ""

  tab[est_seq,2] <- sprintf("%.2f",tmp1[,c("Difference")])
  tab[ci_seq, 2] <- format_ci_fn(tmp1)
  tab[est_seq, 3] <- sprintf("%.2f",tmp2[,c("Difference")])
  tab[ci_seq, 3] <- format_ci_fn(tmp2)

  tab[est_seq,4] <- sprintf("%.2f",tmp1_m[,c("Difference")])
  tab[ci_seq, 4] <- format_ci_fn(tmp1_m)
  tab[est_seq, 5] <- sprintf("%.2f",tmp2_m[,c("Difference")])
  tab[ci_seq, 5] <- format_ci_fn(tmp2_m)


  tab[est_seq,6] <- sprintf("%.2f",tmp1_f[,c("Difference")])
  tab[ci_seq, 6] <- format_ci_fn(tmp1_f)
  tab[est_seq, 7] <- sprintf("%.2f",tmp2_f[,c("Difference")])
  tab[ci_seq, 7] <- format_ci_fn(tmp2_f)
  colnames(tab) <- c(" ",the_vals[1],the_vals[2],
                     the_vals[1],the_vals[2],
                     the_vals[1],the_vals[2])

  tab <- kable(tab,
               booktabs = TRUE,
               caption = the_cap,
               digits=2,
               align = c("l",rep("c",6))) %>%
    kable_styling(latex_options = c("HOLD_position",font_size=10)) %>%
    kableExtra::group_rows("ATE",1,2) %>%
    kableExtra::group_rows("ACTE",3,6) %>%
    kableExtra::group_rows("CACTE",7,10)%>%
    add_header_above(c(" " = 1, "Full Sample" = 2, "Men" = 2, "Women" = 2))
  return(tab)

}
```

Functions to conduct power simulations

- data_fn(): Simulate data for power simulations

```
# Generate simulated data
data_fn <- function(N=1000,
                    sigma = 2,
                    p_treat=.5,
                    prop_select=.5,
```

```
                    p_treat_select = c(.25,.5,.25),
                    tau_st = .5,
                    tau_af = -.5,
                    tau_am = .5,
                    select_effect = 0,
                    ...
){
  # INPUTS:
    # N: sample size
    # sigma: SE of outcome
    # p_treat: Prob of treatment assignment in experiment condition
    # prop_select: Proportion selecting treatment in choice conditoin
    # p_treat_select: Prob of treatment assignment for CACTE
    # tau_st: effect among those selecting treatment
    # tau_af: effect among those avoiding treatment assigned to receive female treatment
    # tau_am: effect among those avoiding treatment assigned to receive mael treatment
    # select_effect: creates correlation between outcome and selecting treatment
  # OUTPUTS:
    # df: data frame of simualted responses

  select <- rbinom(n=N, size=1,prob = prop_select)
  avoid <- as.numeric(select!=1)

  # Baseline
  Y0 <- rnorm(n=N, mean = 0, sd = sigma) + select_effect * select

  # Condition
  C <- sample(c("Choice","Experiment"),size=N,
              prob = c(prop_select, 1- prop_select),replace = T)
  n_exp <- sum(C=="Experiment")
  n_ch_a <- sum(C=="Choice" & avoid==1)

  # Treatment status in experimental arm
  D_exp <- rep("Selection",N)
  D_exp[C=="Experiment"] <- sample(c("Treatment","Control"),size=n_exp,
                                   prob = c(p_treat,1-p_treat), replace = T)

  D_ch <- rep("Experiment",N)
  D_ch[C=="Choice" & avoid==1] <- sample(c("Treatment","Control", "Alternative"),
                                         size=n_ch_a,
                                         prob = p_treat_select,replace = T)
  n_choice <- sum(C == "Choice")
  n_select <- sum(C=="Choice" & avoid==0)
  n_avoid <- sum(C=="Choice" & avoid==1)
  n_control <- sum(D_ch == "Control")
  weights <- rep(1,N)
  weights[C=="Choice" & avoid==0 & D_ch == "Control"] <-1/(n_select/n_choice)
  weights[C=="Choice" & avoid==1 & D_ch == "Control"] <-1/(n_control/n_avoid)

  # Potential outcome is conditional on preferences
  Y1 <- Y0 + tau_st*(select == 1 & D_exp == "Treatment") + tau_af*(avoid == 1 & D_exp == "Treatment" ) +
    tau_st*(select == 1 & C == "Choice")+
    tau_af*(avoid == 1 & D_ch == "Treatment" ) + tau_am*(avoid == 1 & D_ch == "Alternative" )
```

```
  # Observed Outcome

  Y <- rep(NA,N)
  Y[C=="Experiment"] <- Y0[C=="Experiment"]*(D_exp[C=="Experiment"]=="Control") +
    Y1[C=="Experiment"]*(D_exp[C=="Experiment"]=="Treatment")
  Y[C=="Choice" & select == 1] <- Y1[C=="Choice" & select == 1]
  Y[C=="Choice" & select == 0 & D_ch == "Control"] <- Y0[C=="Choice" & select == 0 & D_ch == "Control"]
  Y[C=="Choice" & select == 0 & D_ch == "Treatment"] <- Y1[C=="Choice" & select == 0 & D_ch == "Treatmer
  Y[C=="Choice" & select == 0 & D_ch == "Alternative"] <- Y1[C=="Choice" & select == 0 & D_ch == "Alter


  treatment = rep(NA, N)
  treatment[C=="Experiment" & D_exp == "Treatment"] <- "Treatment"
  treatment[C=="Experiment" & D_exp == "Control"] <- "Control"
  treatment[C=="Choice"] <- "Selection"
  treatment[C=="Choice" & D_ch == "Treatment" ] <- NA
  treatment[C=="Choice" & D_ch == "Alternative" ] <- NA

  avoid01 <- NA
  avoid01[C == "Choice" & avoid == 1] <- 1
  avoid01[C == "Choice" & avoid == 0] <- 0

  select01 <- NA
  select01[C == "Choice" & avoid == 0] <- 1
  select01[C == "Choice" & avoid == 1] <- 0

  df <- data.frame(Y0,Y1,Y,true_diff = Y1-Y0,
                   C, treatment, select, avoid,
                   select01,avoid01,
                   D_exp, D_ch, weights)
  return(df)
}
```

- power_fn(): Calculate power for given treatment effects

```
# Calculate power for given parameters
power_fn <- function(sims,
                     p_N=1000,
                     p_sigma = 1,
                     p_p_treat=.5,
                     p_prop_select=.5,
                     p_p_treat_select = c(.25,.5,.25),
                     p_tau_st = .5,
                     p_tau_af = -.5,
                     p_tau_am = .5,
                     p_select_effect = 0,

                     ...){
  # INPUTS:
    # sims: number of simulations
    # p_*: arguments passed to data_fn()
  # OUTPUTS:
```

```
  # results: results of power simulation

ate <- rep(NA,sims)
acte_s <- rep(NA,sims)
acte_a <- rep(NA,sims)
cacte_female <- rep(NA,sims)
cacte_male <- rep(NA,sims)

sig_ate <- rep(NA,sims)
sig_acte_s <- rep(NA,sims)
sig_acte_a <- rep(NA,sims)
sig_cacte_female <- rep(NA,sims)
sig_cacte_male <- rep(NA,sims)
cor_select <- rep(NA,sims)


for(i in 1:sims){
  df <- data_fn(N=p_N,sigma= p_sigma ,
                p_treat=p_p_treat,
                prop_select = p_prop_select,
                p_treat_select = p_p_treat_select ,
                tau_st= p_tau_st ,
                tau_af= p_tau_af ,
                tau_am= p_tau_am ,
                select_effect= p_select_effect )
  sig_ate[i] <- diff_fn(df,dv1="Y",c=c("Control","Treatment"),weights = T)["pval"]
  sig_acte_s[i] <- acte_fn(df,z=c_acte_s, w=T)["pval"]
  sig_acte_a[i] <- acte_fn(df,z=c_acte_a, w=T)["pval"]
  sig_cacte_female[i] <- cacte_fn(df)[1,"pval"]
  sig_cacte_male[i] <- cacte_fn(df)[2,"pval"]
  cor_select[i] <- cor(df$Y,df$select)

  ate[i] <- diff_fn(df,dv1="Y",c=c("Control","Treatment"))["Difference"]
  acte_s[i] <- acte_fn(df,z=c_acte_s, w=T)["Difference"]
  acte_a[i] <- acte_fn(df,z=c_acte_a,w = T)["Difference"]
  cacte_female[i] <- cacte_fn(df)[1,"Difference"]
  cacte_male[i] <- cacte_fn(df)[2,"Difference"]
}

pow_ate <- mean(sig_ate<.05)
pow_acte_s <- mean(sig_acte_s<.05)
pow_acte_a <- mean(sig_acte_a<.05)
pow_cacte_female <-  mean(sig_cacte_female<.05)
pow_cacte_male <- mean(sig_cacte_male<.05)
mn_cor_select <- mean(cor_select)

mn_ate <- mean(ate)
mn_acte_s <- mean(acte_s)
mn_acte_a <- mean(acte_a)
mn_cacte_female <-  mean(cacte_female)
mn_cacte_male <- mean(cacte_male)
```

```
  results <- rbind(
    c(mn_ate,
      mn_acte_s,
      mn_acte_a,
      mn_cacte_female,
      mn_cacte_male,mn_cor_select),

    c(pow_ate,
      pow_acte_s,
      pow_acte_a,
      pow_cacte_female,
      pow_cacte_male,
      NA
    ))

  return(results)

}
```

- sim_power_fn(): Conduct power simulations over a range of treatment effects

```
# Simulate power for range of treatment effects
sim_power_fn <- function(
  s_sims = 500,
  s_N=1000,
  s_sigma = 1,
  s_p_treat=.5, #
  s_prop_select=.5,
  s_p_treat_select = c(.25,.5,.25),
  s_tau_st = .5,
  s_tau_af = -.5,
  s_tau_am = .5,
  s_select_effect = 0



) {
  # INPUTS:
    # s_*: arguments passed to power_fn()
  # OUTPUTS:
  # results: list containing
  #           - data frame of  power simulations
  #           - summary statititstics
  #           - range of correlation between selecting treatment and outcome

  # Create matrix to store values
  power_mat <- matrix(NA,nrow=5, ncol = length(s_tau_st),
                      dimnames = list(c("ATE","ACTE-Select","ACTE-Avoid",
                                        "CACTE-Female","CACTE-Male"),
                                      s_tau_st
                      )
  )
  bias_mat <- matrix(NA,nrow=5, ncol = length(s_tau_st),
                     dimnames = list(c("ATE","ACTE-Select","ACTE-Avoid",
```

```
                                        "CACTE-Female","CACTE-Male"),
                                      s_tau_st
                    )
  )
  tmp <- c()
  ave_cor <- c()
  tmp_df <- data.frame(Estimate=NULL,Tau=NULL)
  df <- data.frame(Estimate= NULL,
                   Tau_Select = NULL,
                   Tau_Avoid = NULL ,
                   Tau_Alt = NULL ,
                   Power = NULL )
  # Loop over possible values
  for(i in 1:length(s_tau_st)){
    tmp <- power_fn(sims = s_sims,
                    p_N = s_N,
                    p_sigma  = s_sigma,
                    p_p_treat = s_p_treat,
                    p_prop_select = s_prop_select,
                    p_p_treat_select  = s_p_treat_select,
                    p_tau_st  = s_tau_st[i],
                    p_tau_af  = s_tau_af[i],
                    p_tau_am  = s_tau_am[i],
                    p_select_effect  = s_select_effect
    )
    ave_cor[i] <- tmp[1,6]
    power_mat[,i] <- tmp[2,1:5]
    tmp2 <- data.frame(Estimate= c("ATE","ACTE-Select","ACTE-Avoid",
                                   "CACTE-Female","CACTE-Male"),
                       Type = c("ATE","ACTE","ACTE","CACTE","CACTE"),
                       Tau_Select = rep(s_tau_st[i],5),
                       Tau_Avoid = rep(s_tau_af[i],5),
                       Tau_Alt = rep(s_tau_am[i],5),
                       Power = tmp[2,1:5]
    )
    df <- rbind(tmp2,df)
  }
  return(list(df,power_mat,ave_cor))

}
```

- display_power_sim_fn(): Wrapper to display results of power simulations as figure and table

```
# Display results of power simulations
display_power_sim_fn <- function(
  p_s_sims = 1000,
  p_s_N=1000,
  p_s_sigma = 1,
  p_s_p_treat=.4,
  p_s_prop_select=.5,
  p_s_p_treat_select = c(.25,.5,.25),
  p_s_tau_st = .5,
  p_s_tau_af = -.5,
  p_s_tau_am = .5,
```

```
  p_s_select_effect = 0,
  lab_effects = "Effects = Equal & offsetting"

){
  # INPUTS:
  # p_s_*: arguments passed to sim_power_fn()
  # OUTPUTS:
  # results: list containing
  #           - figure displaying results
  #           - table formatted for LaTeX

  pow <- sim_power_fn(
    s_sims = p_s_sims,
    s_N= p_s_N,
    s_sigma = p_s_sigma,
    s_p_treat= p_s_p_treat,
    s_prop_select= p_s_prop_select,
    s_p_treat_select = p_s_p_treat_select,
    s_tau_st = p_s_tau_st,
    s_tau_af = p_s_tau_af,
    s_tau_am = p_s_tau_am,
    s_select_effect = p_s_select_effect


  )
  rhos.min <- round(range(pow[[3]]),2) [1]
  rhos.max <- round(range(pow[[3]]),2) [2]

  p <- pow[[1]] %>%
    mutate(
      Estimate=factor(Estimate,
                      levels = c("ATE","ACTE-Select","ACTE-Avoid",
                                 "CACTE-Female","CACTE-Male")
      ),
      Type = factor(Type,
                    levels = c("ATE","ACTE","CACTE")
      )
    )%>%
    ggplot(aes(Tau_Select,Power, col=Estimate,linetype=Type))+
    geom_line()+
    ylim(0,1.05) +
    xlim(0,.7) +
    geom_hline(yintercept = .8,linetype = "dashed",col="grey")+
    xlab(expression(tau[Select]))+
    ylab("Power (Probability of Statistical Significance)")+
    annotate(geom = "text",
             hjust = 0,
             y = 1.05,
             x = 0,
             label = paste("Simulations =",scales::comma(p_s_sims))
    )+
    annotate(geom = "text",
             hjust = 0,
```

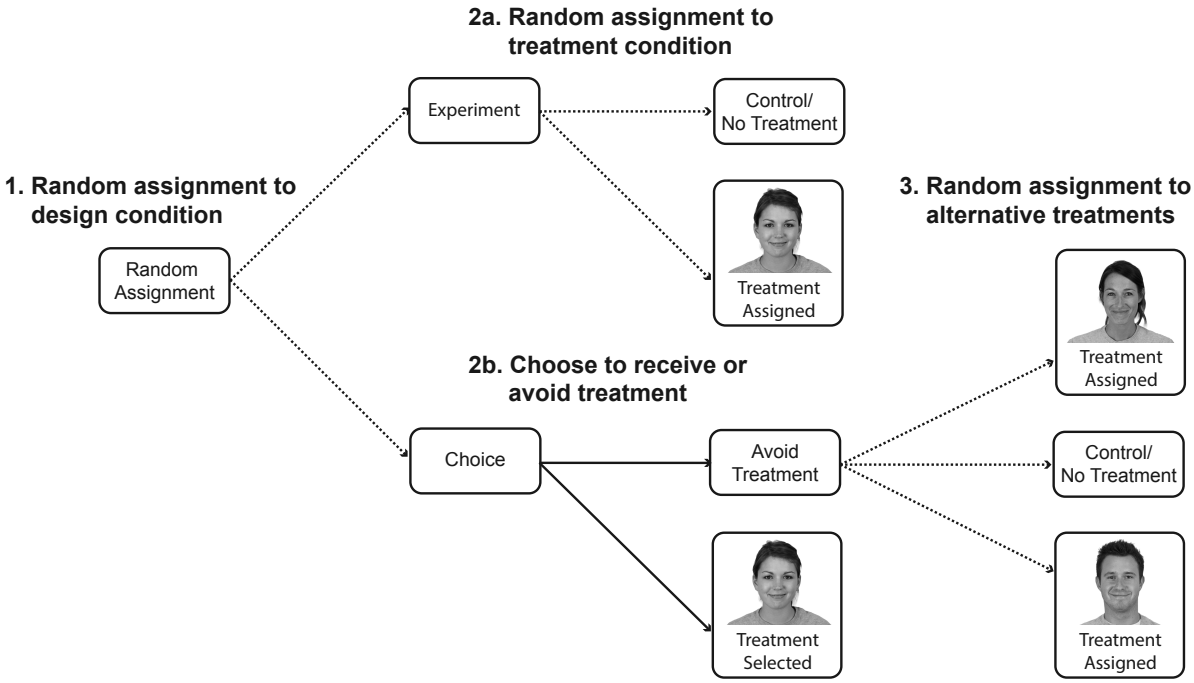
```
            y = 1,
            x = 0,
            label = lab_effects
    )+
    annotate(geom = "text",
            hjust = 0,
            y = .95,
            x = 0,
            label =paste("Prop Select =", round(p_s_prop_select,2))
    ) +
    annotate(geom = "text",
            hjust = 0,
            y = .90,
            x = 0,
            label = paste("Cor = [",rhos.min,", ",rhos.max,"]",sep="")
    )
  tab <- kable(pow[[2]],
               caption = "Power Analysis",
               format = "latex",
               booktabs=T,
               linesep = "",
               digits=2) %>%
    add_header_above(c("","Hypothesized Effect Among Selectors"=dim(pow[[2]])[2])) %>%
    kable_styling(latex_options = c("hold_position",font_size=10))

  return(list(p,tab))


}
```

Main Figures

Figure 1: Triply Randomized Parallel Design



Note: Figure created using Adobe Illustrator

Figure 2: Statistical Power with More Selectors than Avoiders, Equal and Offsetting Effects

```
# Uncomment to run. 500 Simulation takes ~ 30-40 minutes
# Set random seed
# set.seed(123)
#
# fig2_power_sim <- display_power_sim_fn(
#                       p_s_sims = 500,
#                       p_s_prop_select = 2/3,
#                       p_s_tau_st = seq(.1,.7,by=.05),
#                       p_s_tau_af = seq(-.1,-.7,by=-.05),
#                       p_s_tau_am = seq(.1,.7,by=.05)
#                       )

# Format Figure 2
fig2 <- fig2_power_sim [[1]]+
  theme_bw()+
  theme(
    panel.grid.minor = element_blank(),
  )+
  scale_color_grey(start = 0, end = .75)

# Display Figure 2
```

```
fig2
```

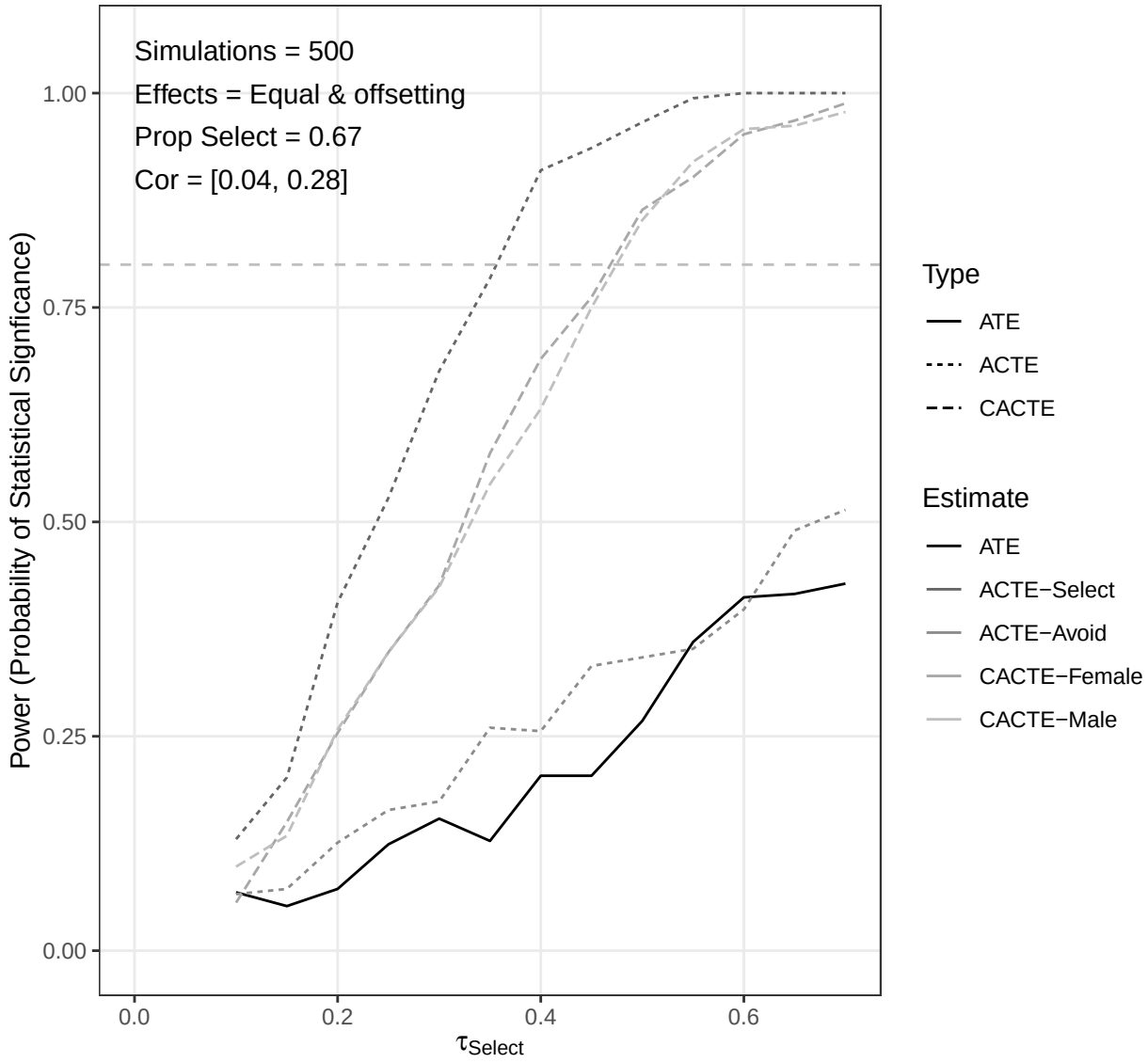


Figure 2: Statistical Power with More Selectors than Avoiders, Equal and Offsetting Effects

Figure 3: Who is Likely to Seek Out or Avoid the Message of the #MeToo Movement?

```
# Create Figure 3
fig3 <- plot_balance_fn(df_mtg)

# Display Figure 3
fig3
```

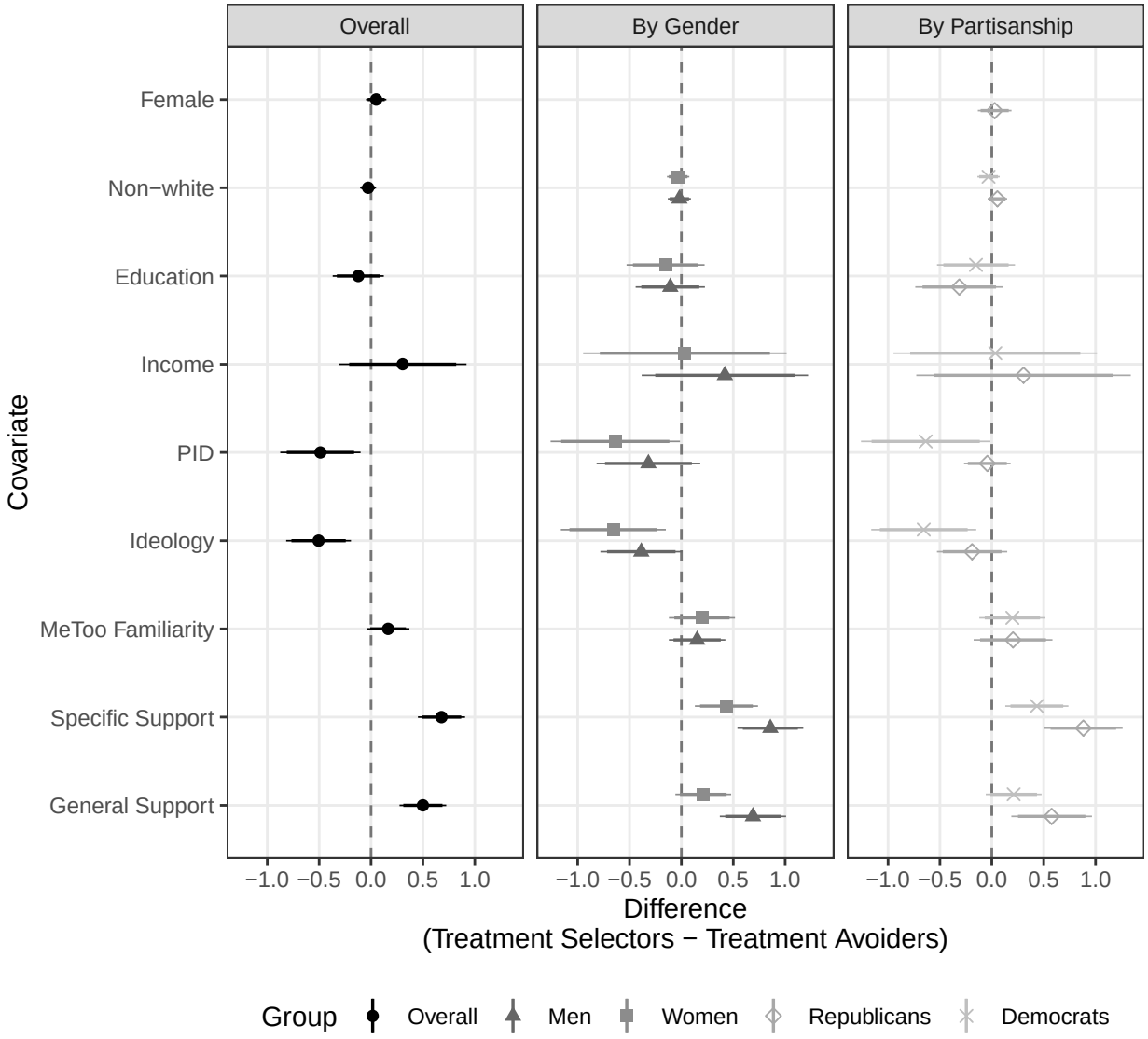


Figure 3: Who is Likely to Seek Out or Avoid the Message of the #MeToo Movement?

Figure 4: Heterogeneous Effects in the #MeToo MTurk Study

```
# Create Figure 4
fig4 <- plot_effects_fn(df_mtg,"dv_pca_metoo") + scale_color_grey(start = 0, end = .75)

# Display Figure 4
fig4
```

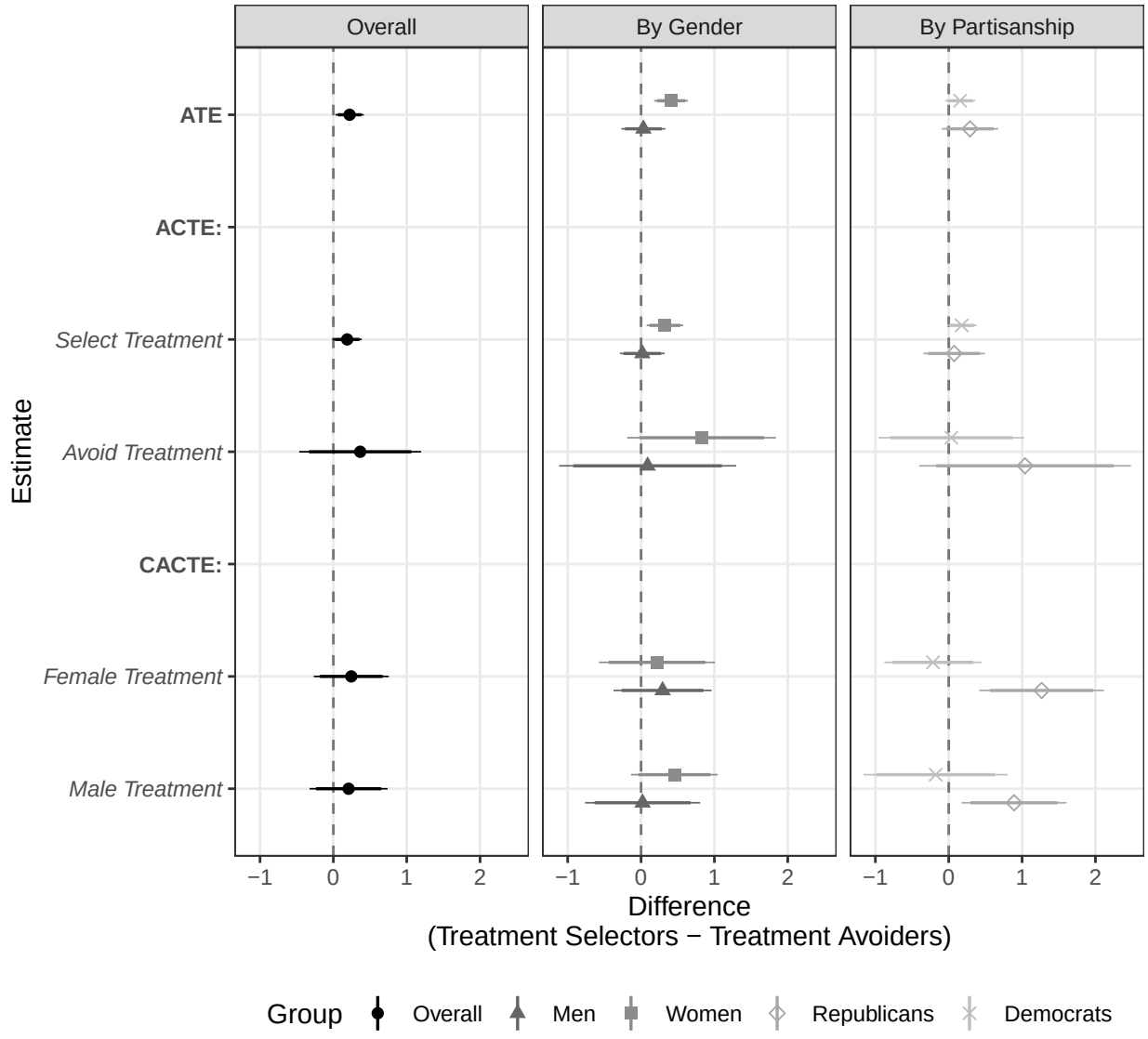


Figure 4: Heterogeneous Effects in the #MeToo MTurk Study

Figure 5: Who is Likely to Seek Out or Avoid the Message of the #MeToo Movement in a More Nationally Representative Sample?

```
# Create Figure 3
fig5 <- plot_balance_fn(df_qg)

# Display Figure 3
```

```
fig5
```

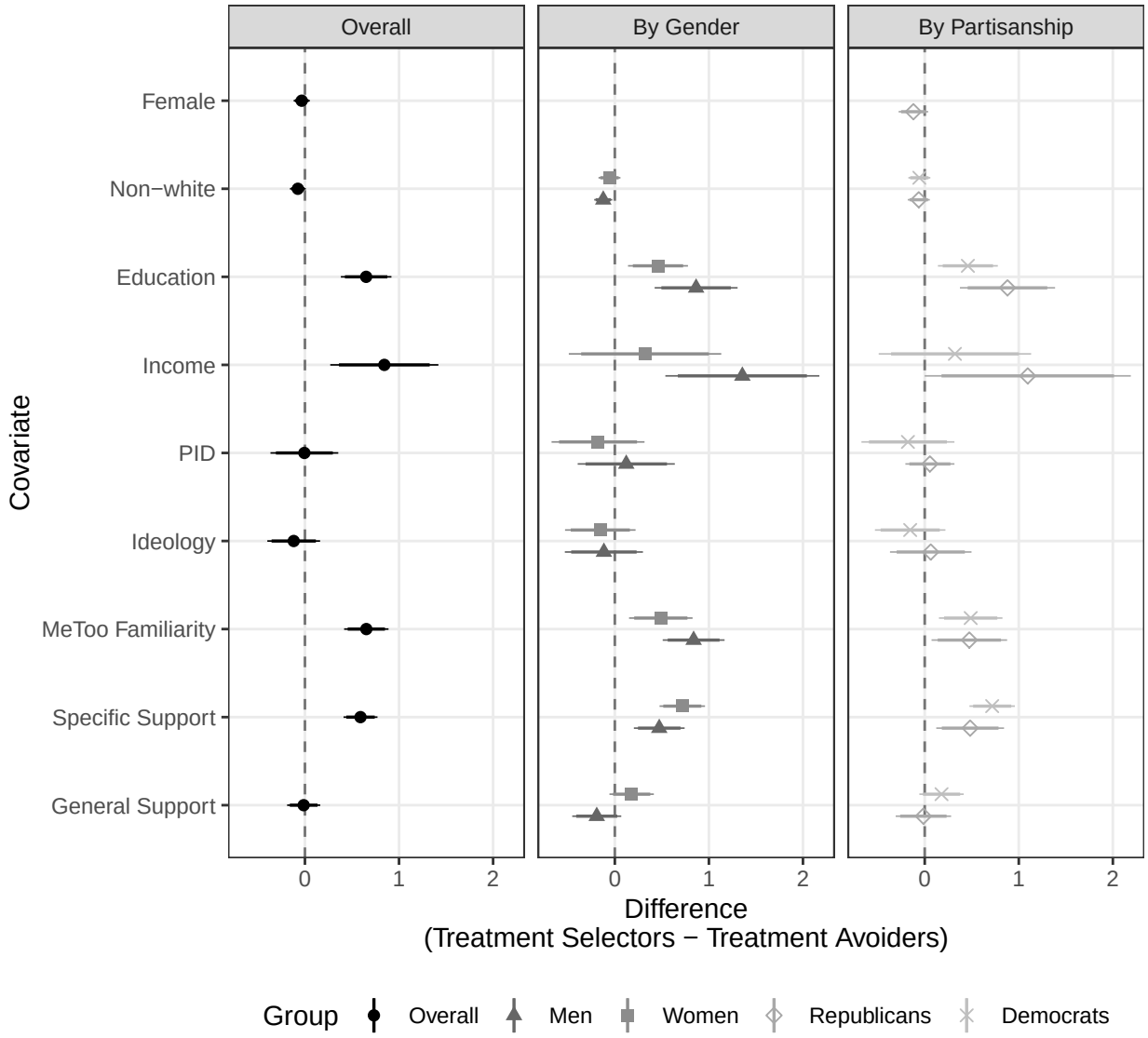


Figure 5: Who Seeks Out or Avoids the Message of the #MeToo Movement in a More Nationally Representative Sample?

Figure 6: Heterogeneous Effects in the #MeToo Qualtrics Study

```
# Create Figure 6
fig6 <- plot_effects_fn(df_qg,"dv_pca_metoo") + scale_color_grey(start = 0, end = .75)

# Display Figure 6
fig6
```

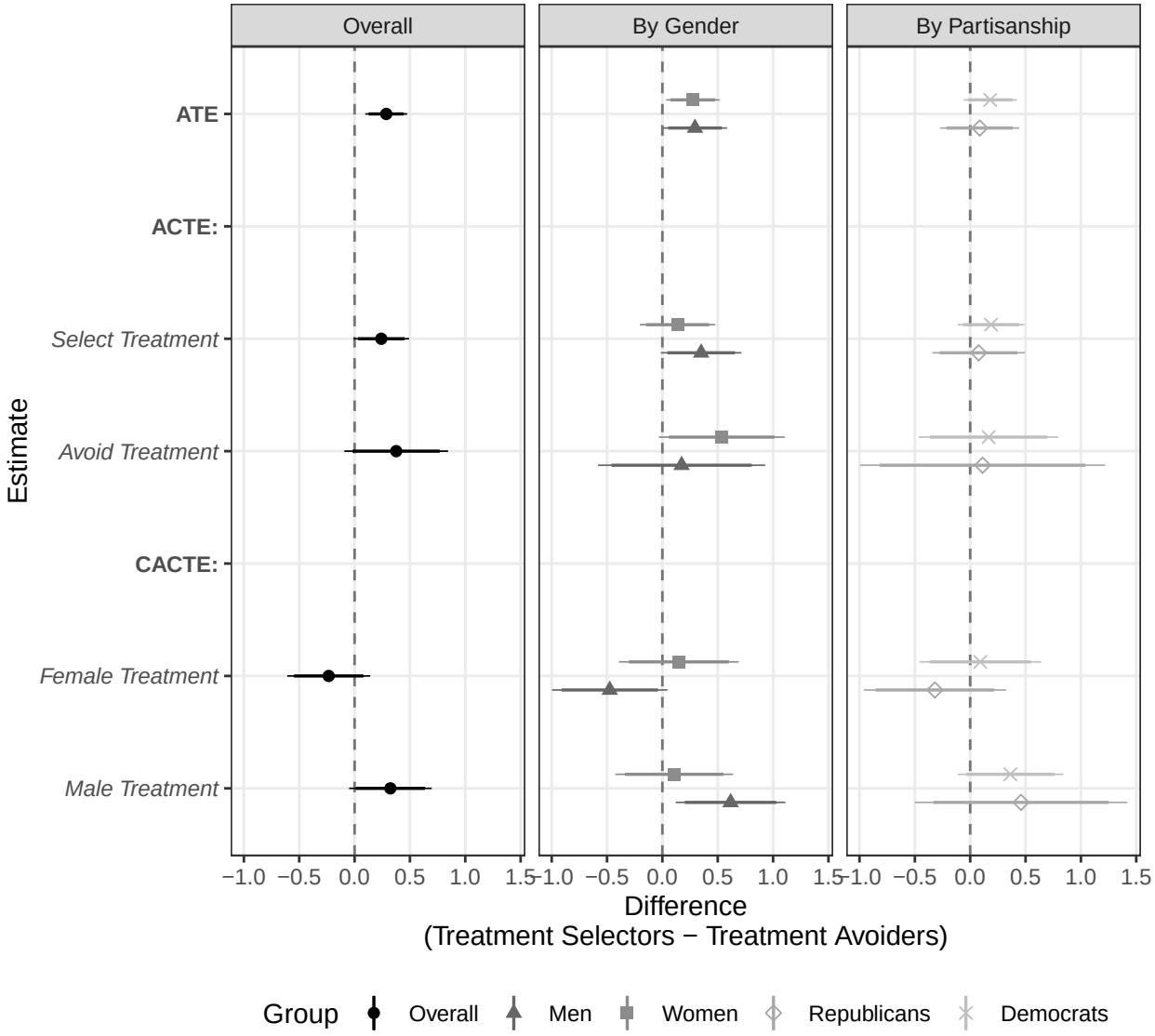


Figure 6: Heterogeneous Effects in the #MeToo Qualtrics Study

Main Tables

Table 1

```
table_fn(fig4$data,
    "Table 1: Treatment Effect Estimates on Specific Support for \\#MeToo (MTurk Sample)")
```

Table 1: Table 1: Treatment Effect Estimates on Specific Support for #MeToo (MTurk Sample)

	Overall	Men	Women	Republicans	Democrats
ATE					
ATE	0.22	0.03	0.41	0.29	0.16
	[0.03, 0.41]	[-0.27, 0.33]	[0.18, 0.64]	[-0.10, 0.68]	[-0.05, 0.36]
ACTE					
Select Treatment	0.19	0.02	0.33	0.07	0.18
	[-0.01, 0.39]	[-0.29, 0.32]	[0.08, 0.58]	[-0.35, 0.49]	[-0.02, 0.38]
Avoid Treatment	0.37	0.09	0.83	1.04	0.04
	[-0.47, 1.20]	[-1.12, 1.30]	[-0.19, 1.84]	[-0.40, 2.48]	[-0.96, 1.03]
CACTE					
Female Treatment	0.24	0.29	0.22	1.27	-0.22
	[-0.27, 0.75]	[-0.38, 0.96]	[-0.57, 1.01]	[0.42, 2.12]	[-0.88, 0.45]
Male Treatment	0.21	0.02	0.46	0.89	-0.18
	[-0.32, 0.74]	[-0.76, 0.81]	[-0.14, 1.05]	[0.18, 1.60]	[-1.16, 0.81]

Note:
The table provides point estimates and 95% confidence intervals for treatment effect estimated from the full sample and separately by gender and partisanship

Table 2

```
table_fn(fig6$data,
    "Table 2: Treatment Effect Estimates on Specific Support for \\#MeToo (Qualtrics Sample)")
```

Table 2: Table 2: Treatment Effect Estimates on Specific Support for #MeToo (Qualtrics Sample)

	Overall	Men	Women	Republicans	Democrats
ATE					
ATE	0.29	0.29	0.28	0.09	0.18
	[0.10, 0.48]	[0.01, 0.58]	[0.03, 0.52]	[-0.27, 0.44]	[-0.06, 0.42]
ACTE					
Select Treatment	0.24	0.35	0.14	0.08	0.19
	[-0.01, 0.49]	[-0.01, 0.71]	[-0.20, 0.48]	[-0.34, 0.49]	[-0.11, 0.49]
Avoid Treatment	0.38	0.17	0.54	0.11	0.17
	[-0.09, 0.84]	[-0.58, 0.93]	[-0.03, 1.10]	[-0.99, 1.22]	[-0.47, 0.80]
CACTE					
Female Treatment	-0.23	-0.48	0.15	-0.32	0.09
	[-0.61, 0.14]	[-1.00, 0.05]	[-0.39, 0.69]	[-0.96, 0.32]	[-0.46, 0.64]
Male Treatment	0.32	0.62	0.11	0.46	0.36
	[-0.05, 0.70]	[0.12, 1.11]	[-0.43, 0.64]	[-0.50, 1.42]	[-0.11, 0.84]

Note:
The table provides point estimates and 95% confidence intervals for treatment effect estimated from the full sample and separately by gender and partisanship

Online Appendix

Appendix C Power Simulations

Figure and Table C.1: Statistical Power with Equal Number of Selectors than Avoiders, Equal and Offsetting Effects

```
# Uncomment to run. 500 Simulation takes ~ 30-40 minutes
# Set random seed
# set.seed(123)
# figC1_power_sim <- display_power_sim_fn(
#                       p_s_sims = 500,
#                       p_s_prop_select = .5,
#                       p_s_tau_st = seq(.1,.7,by=.05),
#                       p_s_tau_af = seq(-.1,-.7,by=-.05),
#                       p_s_tau_am = seq(.1,.7,by=.05)
#                       )

figC1_power_sim[[1]]
```

```
figC1_power_sim[[2]]
```

Figure and Table C.2: Statistical Power with More Selectors than Avoiders, Equal and Offsetting Effects

```
# Same as Figure 2
fig2_power_sim[[1]]
```

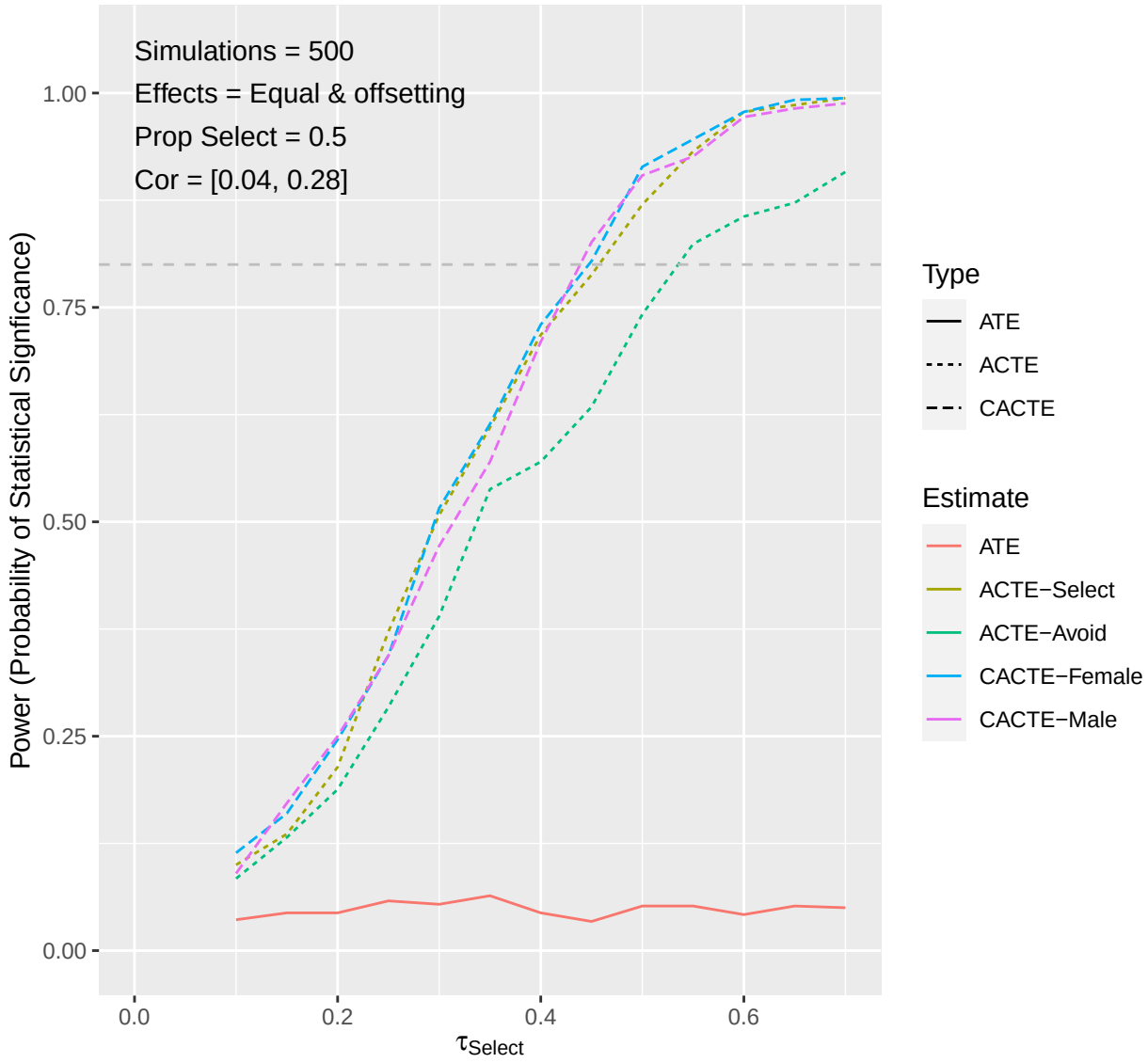


Figure C.1: Statistical Power with Equal Number of Selectors than Avoiders, Equal and Offsetting Effects

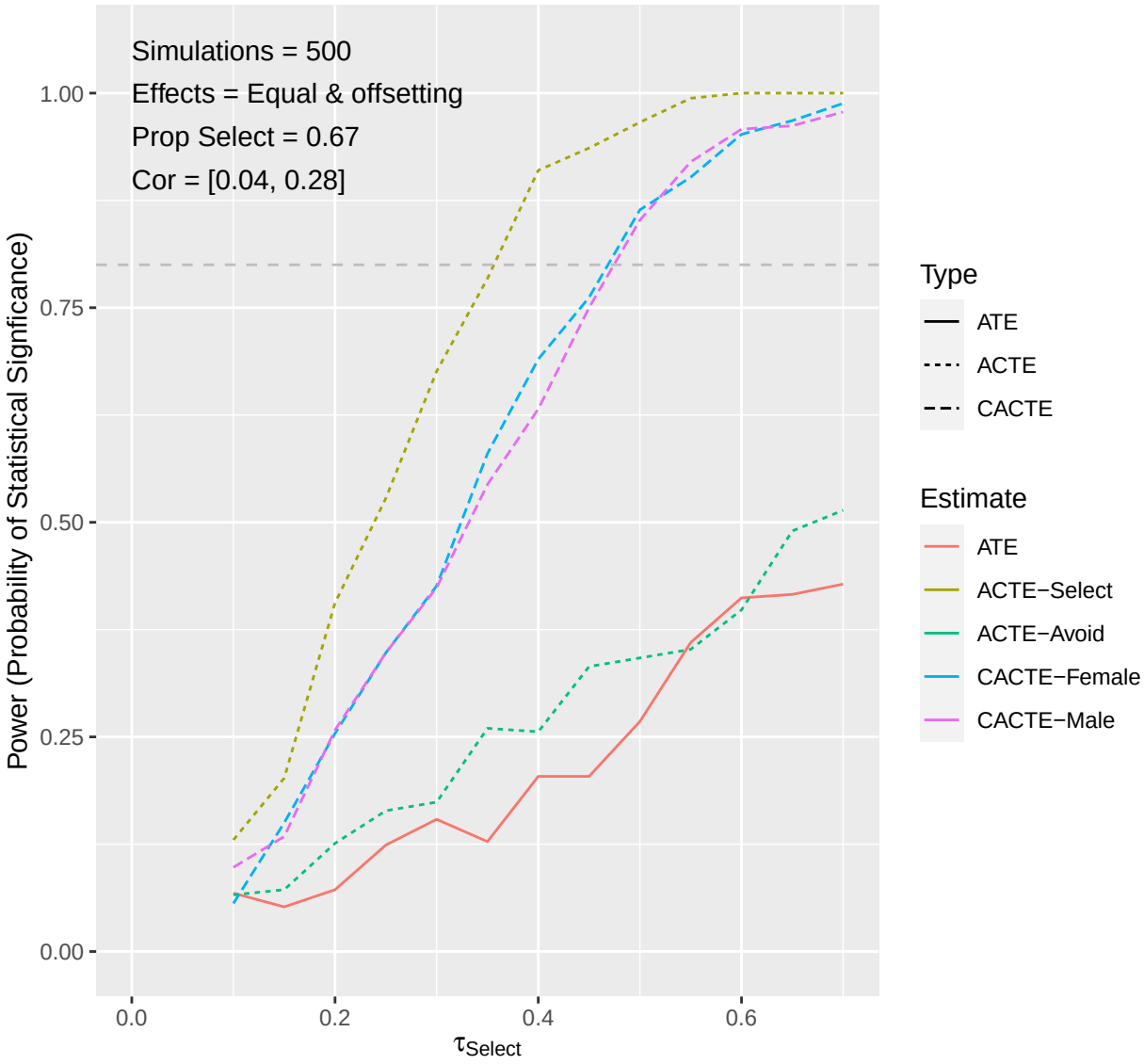


Figure C.2: Statistical Power with More Selectors than Avoiders, Equal and Offsetting Effects

Table C.1: Power Analysis

	Hypothesized Effect Among Selectors												
	0.1	0.15	0.2	0.25	0.3	0.35	0.4	0.45	0.5	0.55	0.6	0.65	0.7
ATE	0.04	0.04	0.04	0.06	0.05	0.06	0.04	0.03	0.05	0.05	0.04	0.05	0.05
ACTE-Select	0.10	0.14	0.21	0.37	0.51	0.61	0.72	0.79	0.87	0.93	0.98	0.99	0.99
ACTE-Avoid	0.08	0.13	0.19	0.28	0.39	0.54	0.57	0.63	0.74	0.82	0.86	0.87	0.91
CACTE-Female	0.11	0.16	0.25	0.34	0.52	0.61	0.73	0.80	0.91	0.95	0.98	0.99	0.99
CACTE-Male	0.09	0.17	0.25	0.34	0.47	0.57	0.71	0.83	0.90	0.93	0.97	0.98	0.99

Table C.2: Power Analysis

	Hypothesized Effect Among Selectors												
	0.1	0.15	0.2	0.25	0.3	0.35	0.4	0.45	0.5	0.55	0.6	0.65	0.7
ATE	0.07	0.05	0.07	0.12	0.15	0.13	0.20	0.20	0.27	0.36	0.41	0.42	0.43
ACTE-Select	0.13	0.20	0.41	0.53	0.68	0.78	0.91	0.94	0.97	0.99	1.00	1.00	1.00
ACTE-Avoid	0.07	0.07	0.13	0.16	0.17	0.26	0.26	0.33	0.34	0.35	0.40	0.49	0.51
CACTE-Female	0.06	0.15	0.25	0.35	0.43	0.58	0.69	0.76	0.86	0.90	0.95	0.97	0.99
CACTE-Male	0.10	0.13	0.26	0.35	0.42	0.54	0.63	0.75	0.85	0.92	0.96	0.96	0.98

```
fig2_power_sim[[2]]
```

Figure and Table C.3: Statistical Power with More Selectors than Avoiders, Equal and Offsetting Effects, and Selection Correlated with Outcome

```
# Uncomment to run. 500 Simulation takes ~ 30-40 minutes

# Set random seed
# set.seed(123)
#
# figC3_power_sim <- display_power_sim_fn(
#                       p_s_sims = 500,
#                       p_s_prop_select = 2/3,
#                       p_s_select_effect = 0.5,
#                       p_s_tau_st = seq(.1,.7,by=.05),
#                       p_s_tau_af = seq(-.1,-.7,by=-.05),
#                       p_s_tau_am = seq(.1,.7,by=.05)
#                       )

figC3_power_sim[[1]]
```

```
figC3_power_sim[[2]]
```

```
# Uncomment to save results of power simulations
# save(figC1_power_sim, fig2_power_sim,figC3_power_sim,file = "power_simulations.rda")
```

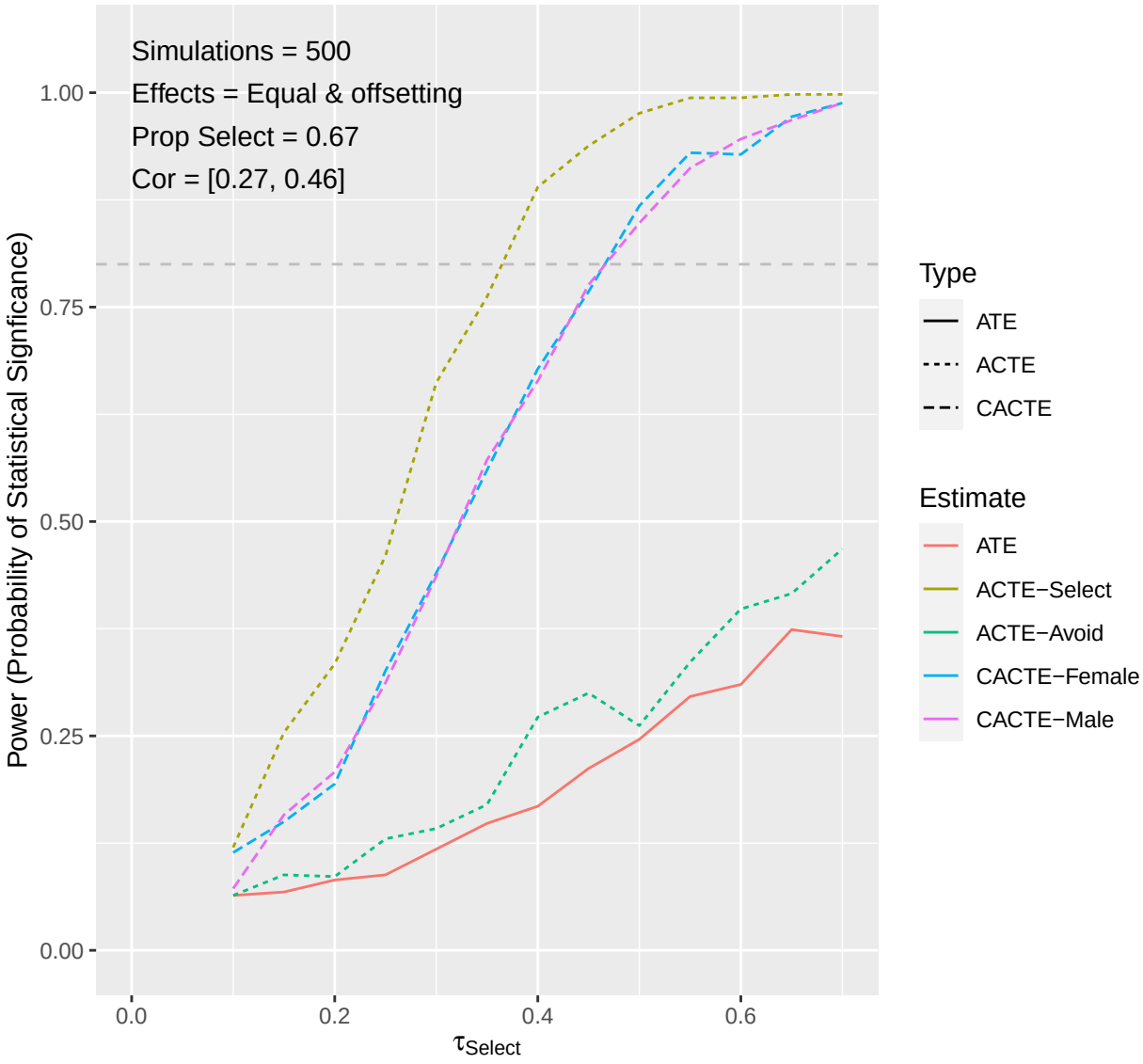


Figure C.3: Statistical Power with More Selectors than Avoiders, Equal and Offsetting Effects, and Selection Correlated with Outcome

Table C.3: Power Analysis

	Hypothesized Effect Among Selectors												
	0.1	0.15	0.2	0.25	0.3	0.35	0.4	0.45	0.5	0.55	0.6	0.65	0.7
ATE	0.06	0.07	0.08	0.09	0.12	0.15	0.17	0.21	0.25	0.30	0.31	0.37	0.37
ACTE-Select	0.12	0.25	0.33	0.46	0.66	0.76	0.89	0.94	0.98	0.99	0.99	1.00	1.00
ACTE-Avoid	0.06	0.09	0.09	0.13	0.14	0.17	0.27	0.30	0.26	0.34	0.40	0.42	0.47
CACTE-Female	0.11	0.15	0.19	0.33	0.44	0.56	0.68	0.77	0.87	0.93	0.93	0.97	0.99
CACTE-Male	0.07	0.16	0.21	0.31	0.44	0.57	0.66	0.78	0.85	0.91	0.95	0.97	0.99

Appendix D Descriptive Statistics

Table D.1: Descriptive Statistics for MTurk Sample

```
the_covariates <- c("female01", "age", "income", "education", "pid", "ideo",
                    "black", "latino", "asian", "fam_movement", "avoid01")
desc_tab_mt<- c()
for(i in 1:length(the_covariates)){
  desc_tab_mt <- cbind(desc_tab_mt,
                       summary(df_mtg[,the_covariates[i]])[1:6]
                       )
}
desc_tab_mt <- t(round(desc_tab_mt,2))
rownames(desc_tab_mt) <- c("Prop. Female", "Age", "Income", "Education",
                           "Party ID", "Ideology",
                           "Prop. Black",
                           "Prop. Latinx",
                           "Prop. Asian",
                           "Familiarity with MeToo",
                           "Prop Avoiding Treatment")


desc_tab_mt_tex <- kable(desc_tab_mt,
      booktabs = TRUE,
               caption = "Descriptive Statistics for MTurk Sample",
               digits=2,
  align = "l") %>%
  kable_styling(latex_options = c("hold_position",font_size=10))
desc_tab_mt_tex
```

Table D.2: Descriptive Statistics for Qualtrics Sample

```
desc_tab_q <- c()
df_qg <- data.frame(df_qg)
for(i in 1:length(the_covariates)){
  desc_tab_q <- cbind(desc_tab_q,
                       summary(na.omit(df_qg[,the_covariates[i]])))

}
desc_tab_q <- t(round(desc_tab_q,2))
rownames(desc_tab_q) <- c("Prop. Female", "Age", "Income", "Education",
```

Table D.1: Descriptive Statistics for MTurk Sample

	Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
Prop. Female	0	0	0	0.49	1	1
Age	18	29	35	38.12	45	82
Income	1	4	6	6.23	8	12
Education	1	3	5	4.31	5	7
Party ID	1	2	3	3.49	6	7
Ideology	1	2	3	3.53	5	7
Prop. Black	0	0	0	0.06	0	1
Prop. Latinx	0	0	0	0.07	0	1
Prop. Asian	0	0	0	0.09	0	1
Familiarity with MeToo	0	2	3	2.45	3	4
Prop Avoiding Treatment	0	0	0	0.19	0	1

```
                          "Party ID", "Ideology",
                          "Prop. Black",
                          "Prop. Latinx",
                          "Prop. Asian",
                          "Familiarity with MeToo",
                          "Prop Avoiding Treatment")



desc_tab_q_tex <- kable(desc_tab_q,
      booktabs = TRUE,
               caption = "Descriptive Statistics for Qualtrics Sample",
               digits=2,
  align = "l") %>%
  kable_styling(latex_options = c("hold_position",font_size=10))
desc_tab_q_tex
```

Table D.2: Descriptive Statistics for Qualtrics Sample

	Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
Prop. Female	0	0	1	0.51	1	1
Age	18	31	46	45.94	60	93
Income	1	3	5	5.38	8	12
Education	1	2	3	3.28	5	7
Party ID	1	2	4	3.62	6	7
Ideology	1	3	4	4.04	5	7
Prop. Black	0	0	0	0.17	0	1
Prop. Latinx	0	0	0	0.18	0	1
Prop. Asian	0	0	0	0.06	0	1
Familiarity with MeToo	0	1	2	2.05	3	4
Prop Avoiding Treatment	0	0	0	0.33	1	1

Appendix E Effects on General Support for Gender Equality

Figure and Table E.1: Effects on General Support for Gender Equality (MTurk Study)

```
# Create Figure E1
figE1 <- plot_effects_fn(df_mtg, "dv_pca_general")

# Display Figure 4
figE1
```

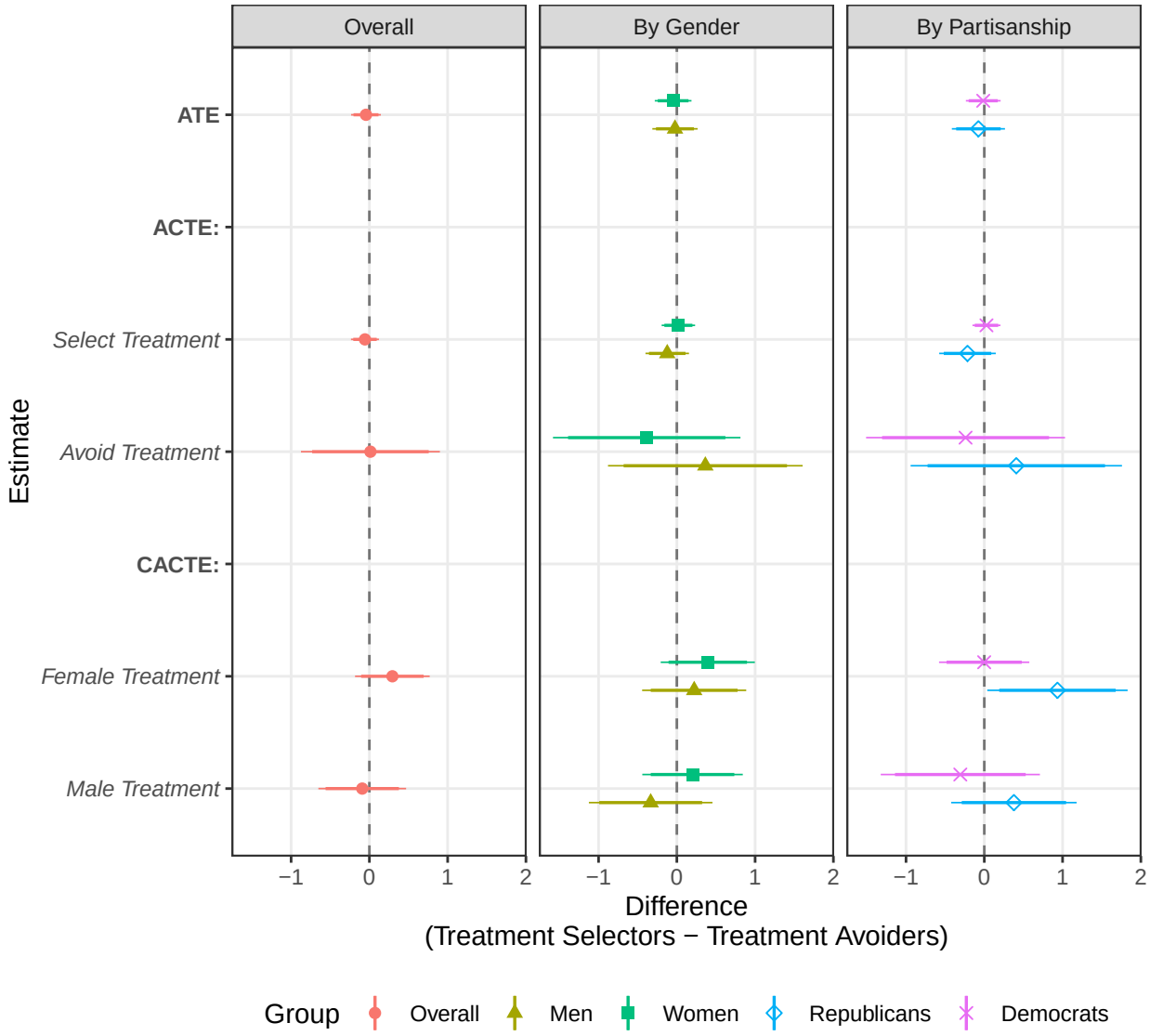


Figure E.1: Effects on General Support for Gender Equality (MTurk Study)

```
table_fn(figE1$data,
  "Treatment Effect Estimates on General Support for Gender Equality (MTurk Sample)"
  )
```

Table E.1: Treatment Effect Estimates on General Support for Gender Equality (MTurk Sample)

	Overall	Men	Women	Republicans	Democrats
ATE					
ATE	-0.04	-0.02	-0.05	-0.08	-0.01
	[-0.23, 0.15]	[-0.31, 0.27]	[-0.28, 0.19]	[-0.41, 0.26]	[-0.24, 0.21]
ACTE					
Select Treatment	-0.06	-0.12	0.02	-0.21	0.03
	[-0.23, 0.12]	[-0.40, 0.16]	[-0.19, 0.23]	[-0.58, 0.15]	[-0.15, 0.21]
Avoid Treatment	0.01	0.36	-0.38	0.41	-0.24
	[-0.87, 0.90]	[-0.88, 1.61]	[-1.58, 0.81]	[-0.94, 1.76]	[-1.51, 1.03]
CACTE					
Female Treatment	0.29	0.22	0.40	0.93	-0.00
	[-0.18, 0.77]	[-0.44, 0.89]	[-0.21, 1.00]	[0.04, 1.83]	[-0.58, 0.58]
Male Treatment	-0.09	-0.33	0.20	0.38	-0.31
	[-0.65, 0.47]	[-1.12, 0.46]	[-0.44, 0.84]	[-0.42, 1.18]	[-1.32, 0.71]

Note:
The table provides point estimates and 95% confidence intervals for treatment effect estimated from the full sample and separately by gender and partisanship

Figure and Table E.2: Effects on General Support for Gender Equality (Qualtrics Study)

```
# Create Figure E2
figE2 <- plot_effects_fn(df_qg, "dv_pca_general")

# Display Figure E2
figE2
```

```
table_fn(figE2$data,
  "Treatment Effect Estimates on General Support for Gender Equality (MTurk Sample)"
  )
```

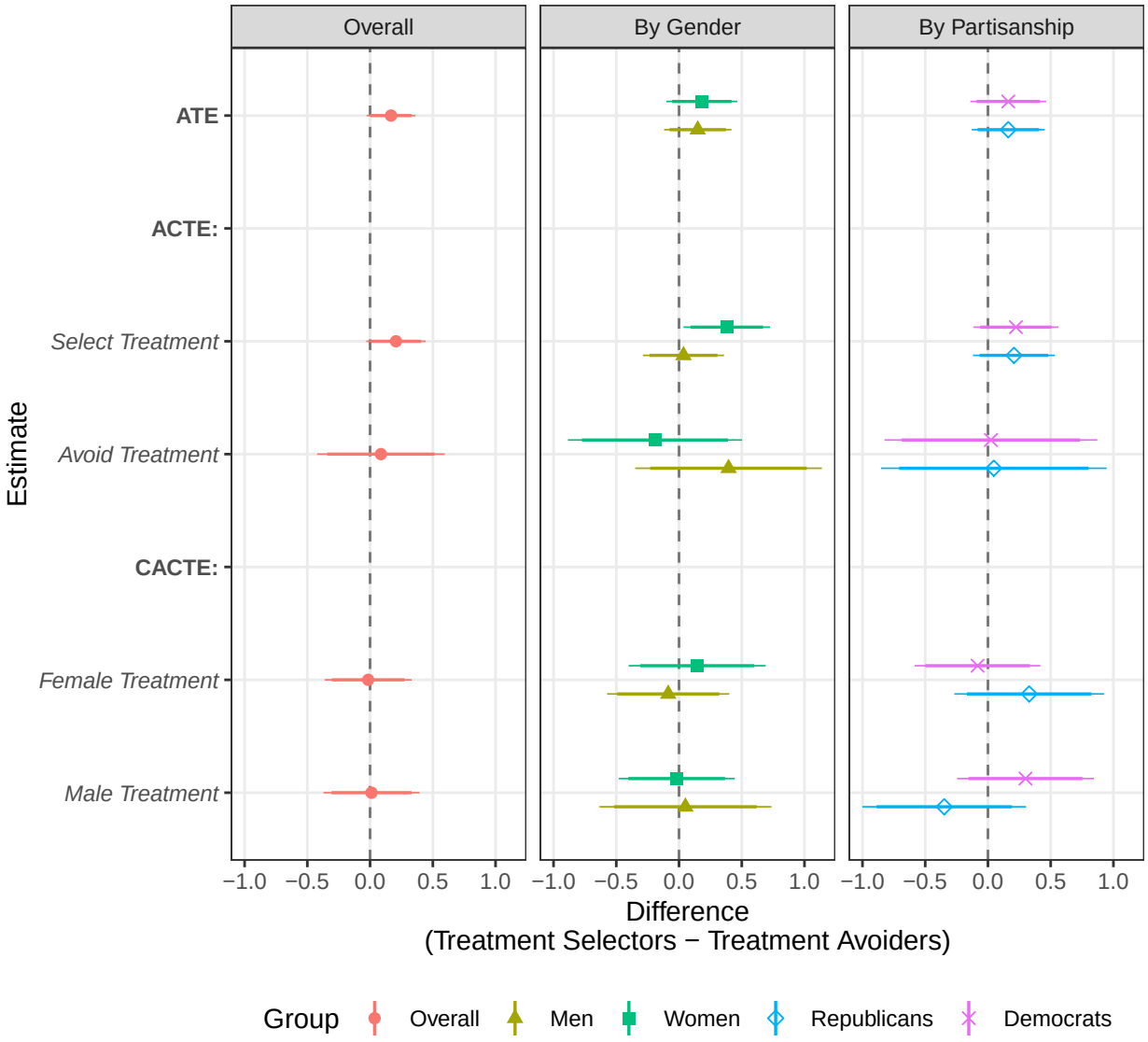


Figure E.2: Effects on General Support for Gender Equality (Qualtrics Study)

Table E.2: Treatment Effect Estimates on General Support for Gender Equality (MTurk Sample)

	Overall	Men	Women	Republicans	Democrats
ATE					
ATE	0.17	0.15	0.18	0.16	0.16
	[-0.03, 0.36]	[-0.12, 0.42]	[-0.10, 0.46]	[-0.13, 0.45]	[-0.14, 0.46]
ACTE					
Select Treatment	0.21	0.04	0.38	0.21	0.22
	[-0.03, 0.44]	[-0.29, 0.36]	[0.04, 0.73]	[-0.12, 0.53]	[-0.12, 0.56]
Avoid Treatment	0.09	0.39	-0.19	0.05	0.02
	[-0.42, 0.60]	[-0.35, 1.14]	[-0.89, 0.50]	[-0.85, 0.95]	[-0.82, 0.87]
CACTE					
Female Treatment	-0.02	-0.09	0.14	0.33	-0.08
	[-0.36, 0.33]	[-0.57, 0.40]	[-0.40, 0.69]	[-0.27, 0.92]	[-0.58, 0.42]
Male Treatment	0.01	0.05	-0.02	-0.35	0.30
	[-0.37, 0.39]	[-0.63, 0.74]	[-0.48, 0.44]	[-1.00, 0.30]	[-0.25, 0.84]

Note:
The table provides point estimates and 95% confidence intervals for treatment effect estimated from the full sample and separately by gender and partisanship

F Additional Analyses

Figure and Table F.1: Treatment Effect Estimates on Specific Support for #MeToo Conditional on Familiarity and Gender (MTurk Sample)

```
figF1_df <- rbind(
  data.frame(
  effects_fn(df_mtg[df_mtg$fam_movement>2,], "dv_pca_metoo"),
  Group = "Familiar",
  Type = "By Familiarity"),
  data.frame(
  effects_fn(df_mtg[df_mtg$fam_movement<3,], "dv_pca_metoo"),
  Group = "Unfamiliar",
  Type = "By Familiarity"),
  data.frame(
  effects_fn(df_mtg[df_mtg$fam_movement>2 & df_mtg$gender==0,], "dv_pca_metoo"),
  Group = "Familiar",
  Type = "Men"),
  data.frame(
  effects_fn(df_mtg[df_mtg$fam_movement<3& df_mtg$gender==0,], "dv_pca_metoo"),
  Group = "Unfamiliar",
  Type = "Men"),
    data.frame(
  effects_fn(df_mtg[df_mtg$fam_movement>2 & df_mtg$gender==1,], "dv_pca_metoo"),
  Group = "Familiar",
  Type = "Women"),
  data.frame(
  effects_fn(df_mtg[df_mtg$fam_movement<3& df_mtg$gender==1,], "dv_pca_metoo"),
  Group = "Unfamiliar",
  Type = "Women")
  )
```

```r
figF1 <- figF1_df %>%
  filter(Estimand != "CATE")%>%
  ggplot(aes(Estimate, Difference,col=Group,shape=Group))+
  geom_hline(yintercept = 0,linetype="dashed",alpha=.5)+
  facet_grid(~Type)+
  geom_point(aes(shape=Group),
                 position = position_dodge(width = .5),size=2
      )+
  geom_linerange(aes(ymin=ll,ymax=ul),size=.3,
                       position = position_dodge(width = .5))+
  geom_linerange(aes(ymin=ll90,ymax=ul90),size=.6,
                     position = position_dodge(width = .5))+
  coord_flip()+
  theme_bw()+
  theme(
    panel.grid.minor = element_blank(),
    legend.position = "bottom"
  )

figF1
```

```r
# Create Grouping Label
#df_mtg$Familiarity <- ifelse(df_mtg$fam_movement>2, "Familiar", "Unfamiliar")

table_app_fn(df_mtg, "dv_pca_metoo",
         "Familiarity",
         Familiarity,
         the_cap ="Treatment Effect Estimates on Specific Support for \\#MeToo Conditional On Familiarit
  footnote(general = "The table provides point estimates and 95% confidence intervals for treatment effe
           threeparttable = T,
           fixed_small_size = T)
```

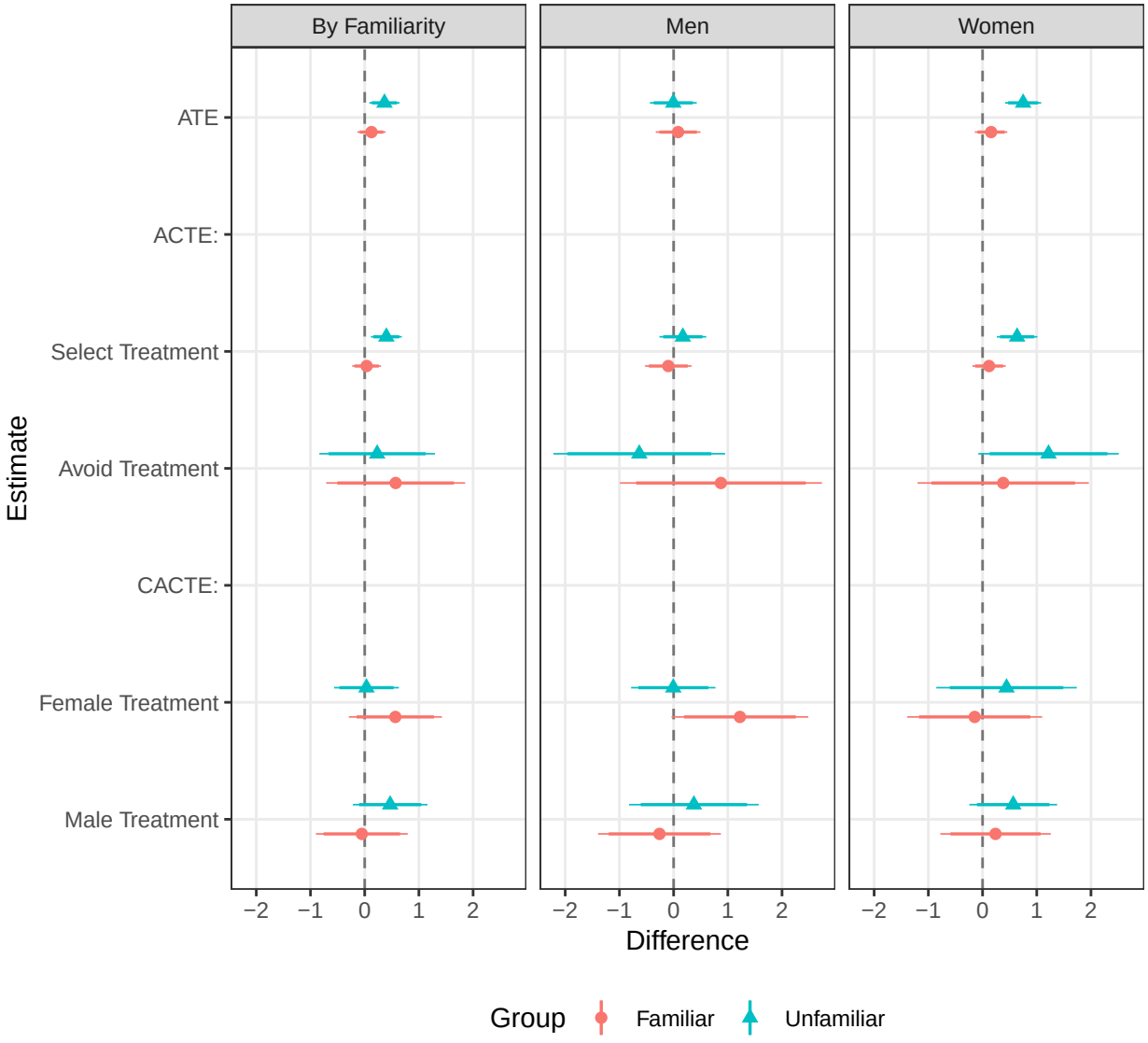


Figure F.1: Treatment Effect Estimates on Specific Support for #MeToo Conditional on Familiarity and Gender

Table F.1: Treatment Effect Estimates on Specific Support for #MeToo Conditional On Familiarity and Gender (MTurk Sample)

	Full Sample		Men		Women	
	Familiar	Unfamiliar	Familiar	Unfamiliar	Familiar	Unfamiliar
ATE						
ATE	0.13	0.36	0.08	-0.01	0.16	0.75
	[-0.14, 0.39]	[0.09, 0.64]	[-0.33, 0.50]	[-0.44, 0.43]	[-0.14, 0.46]	[0.42, 1.08]
ACTE						
Select Treatment	0.04	0.40	-0.10	0.17	0.12	0.64
	[-0.23, 0.30]	[0.11, 0.68]	[-0.53, 0.33]	[-0.26, 0.60]	[-0.19, 0.43]	[0.26, 1.01]
Avoid Treatment	0.57	0.23	0.87	-0.63	0.38	1.22
	[-0.71, 1.85]	[-0.84, 1.30]	[-0.99, 2.74]	[-2.22, 0.95]	[-1.20, 1.96]	[-0.08, 2.51]
CACTE						
Female Treatment	0.57	0.03	1.22	-0.01	-0.15	0.44
	[-0.29, 1.42]	[-0.57, 0.63]	[-0.04, 2.48]	[-0.78, 0.77]	[-1.39, 1.10]	[-0.85, 1.74]
Male Treatment	-0.05	0.47	-0.26	0.37	0.24	0.57
	[-0.90, 0.79]	[-0.22, 1.16]	[-1.39, 0.87]	[-0.82, 1.57]	[-0.78, 1.26]	[-0.24, 1.37]

Note:
The table provides point estimates and 95% confidence intervals for treatment effect estimated by level of pre-test familiarity with the movement overall and by gender

Figure and Table F.2: Treatment Effect Estimates on Specific Support for #MeToo Conditional on Familiarity and Gender (Qualtrics Study)

```
figF2_df <- rbind(
  data.frame(
  effects_fn(df_qg[df_qg$fam_movement>2,], "dv_pca_metoo"),
  Group = "Familiar",
  Type = "By Familiarity"),
  data.frame(
  effects_fn(df_qg[df_qg$fam_movement<3,], "dv_pca_metoo"),
  Group = "Unfamiliar",
  Type = "By Familiarity"),
  data.frame(
  effects_fn(df_qg[df_qg$fam_movement>2 & df_qg$gender==0,], "dv_pca_metoo"),
  Group = "Familiar",
  Type = "Men"),
  data.frame(
  effects_fn(df_qg[df_qg$fam_movement<3& df_qg$gender==0,], "dv_pca_metoo"),
  Group = "Unfamiliar",
  Type = "Men"),
    data.frame(
  effects_fn(df_qg[df_qg$fam_movement>2 & df_qg$gender==1,], "dv_pca_metoo"),
  Group = "Familiar",
  Type = "Women"),
  data.frame(
  effects_fn(df_qg[df_qg$fam_movement<3& df_qg$gender==1,], "dv_pca_metoo"),
  Group = "Unfamiliar",
  Type = "Women")
  )
```

```
figF2 <- figF2_df %>%
  filter(Estimand != "CATE")%>%
  ggplot(aes(Estimate, Difference,col=Group,shape=Group))+
  geom_hline(yintercept = 0,linetype="dashed",alpha=.5)+
  facet_grid(~Type)+
  geom_point(aes(shape=Group),
                 position = position_dodge(width = .5),size=2
      )+
  geom_linerange(aes(ymin=ll,ymax=ul),size=.3,
                       position = position_dodge(width = .5))+
  geom_linerange(aes(ymin=ll90,ymax=ul90),size=.6,
                     position = position_dodge(width = .5))+
  coord_flip()+
  theme_bw()+
  theme(
    panel.grid.minor = element_blank(),
    legend.position = "bottom"
  )

figF2
```

```
table_app_fn(df_qg, "dv_pca_metoo",
         "Familiarity",
         Familiarity,
         the_cap ="Treatment Effect Estimates on Specific Support for \\#MeToo Conditional On Familiari
  footnote(general = "The table provides point estimates and 95% confidence intervals for treatment eff
           threeparttable = T,
           fixed_small_size = T)
```

Table F.2: Treatment Effect Estimates on Specific Support for #MeToo Conditional On Familiarity and Gender (Qualtrics Sample)

	Full Sample		Men		Women	
	Unfamiliar	Familiar	Unfamiliar	Familiar	Unfamiliar	Familiar
ATE						
ATE	0.37	0.16	0.39	0.11	0.35	0.19
	[0.14, 0.61]	[-0.16, 0.48]	[0.05, 0.72]	[-0.44, 0.66]	[0.05, 0.65]	[-0.19, 0.58]
ACTE						
Select Treatment	0.16	0.30	0.42	0.17	-0.16	0.42
	[-0.20, 0.51]	[-0.05, 0.64]	[-0.07, 0.92]	[-0.36, 0.71]	[-0.65, 0.33]	[-0.04, 0.89]
Avoid Treatment	0.70	-0.28	0.33	-0.14	1.10	-0.41
	[0.20, 1.19]	[-1.33, 0.77]	[-0.39, 1.05]	[-2.38, 2.10]	[0.45, 1.75]	[-1.49, 0.68]
CACTE						
Female Treatment	-0.12	-0.21	-0.39	-0.49	0.29	-0.00
	[-0.52, 0.28]	[-1.09, 0.67]	[-0.96, 0.17]	[-2.08, 1.10]	[-0.26, 0.84]	[-1.26, 1.25]
Male Treatment	0.41	0.10	0.69	0.31	0.23	-0.03
	[-0.07, 0.89]	[-0.45, 0.65]	[0.05, 1.34]	[-0.63, 1.26]	[-0.45, 0.91]	[-0.79, 0.74]

Note:
The table provides point estimates and 95% confidence intervals for treatment effect estimated by level of pre-test familiarity with the movement overall and by gender

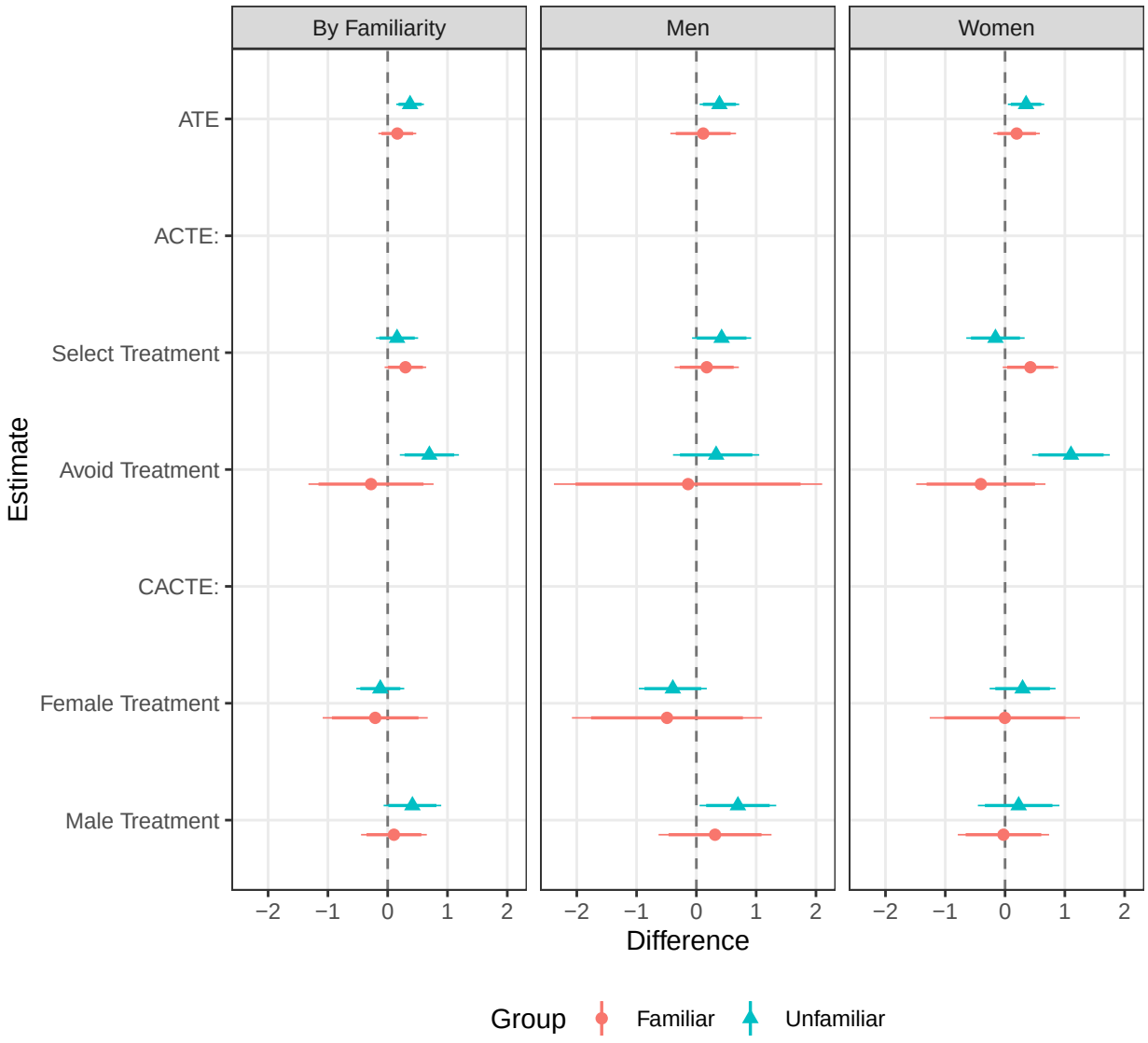


Figure F.2: Treatment Effect Estimates on Specific Support for #MeToo Conditional on Familiarity and Gender (Qualtrics Study)

Figure and Table F.3: Treatment Effect Estimates on Specific Support for #MeToo Conditional On Partisanship and Gender (MTurk Sample)

```
figF3_df <- rbind(
  data.frame(
  effects_fn(df_mtg[df_mtg$pid>4,], "dv_pca_metoo"),
  Group = "Republicans",
  Type = "By Partisanship"),
  data.frame(
  effects_fn(df_mtg[df_mtg$pid<4,], "dv_pca_metoo"),
  Group = "Democrats",
  Type = "By Partisanship"),
  data.frame(
  effects_fn(df_mtg[df_mtg$pid>4 & df_mtg$gender==0,], "dv_pca_metoo"),
  Group = "Republicans",
  Type = "Men"),
  data.frame(
  effects_fn(df_mtg[df_mtg$pid<4& df_mtg$gender==0,], "dv_pca_metoo"),
  Group = "Democrats",
  Type = "Men"),
    data.frame(
  effects_fn(df_mtg[df_mtg$pid>4 & df_mtg$gender==1,], "dv_pca_metoo"),
  Group = "Republicans",
  Type = "Women"),
  data.frame(
  effects_fn(df_mtg[df_mtg$pid<4& df_mtg$gender==1,], "dv_pca_metoo"),
  Group = "Democrats",
  Type = "Women")
  )

figF3_df$Group <- factor(figF3_df$Group,
                         levels = unique(figF3_df$Group) )

figF3 <- figF3_df %>%
  filter(Estimand != "CATE")%>%
  ggplot(aes(Estimate, Difference,col=Group,shape=Group))+
  geom_hline(yintercept = 0,linetype="dashed",alpha=.5)+
  facet_grid(~Type)+
  geom_point(aes(shape=Group),
                 position = position_dodge(width = .5),size=2
      )+
  geom_linerange(aes(ymin=ll,ymax=ul),size=.3,
                       position = position_dodge(width = .5))+
  geom_linerange(aes(ymin=ll90,ymax=ul90),size=.6,
                     position = position_dodge(width = .5))+
  coord_flip()+
  theme_bw()+
  theme(
    panel.grid.minor = element_blank(),
    legend.position = "bottom"
  )

figF3
```

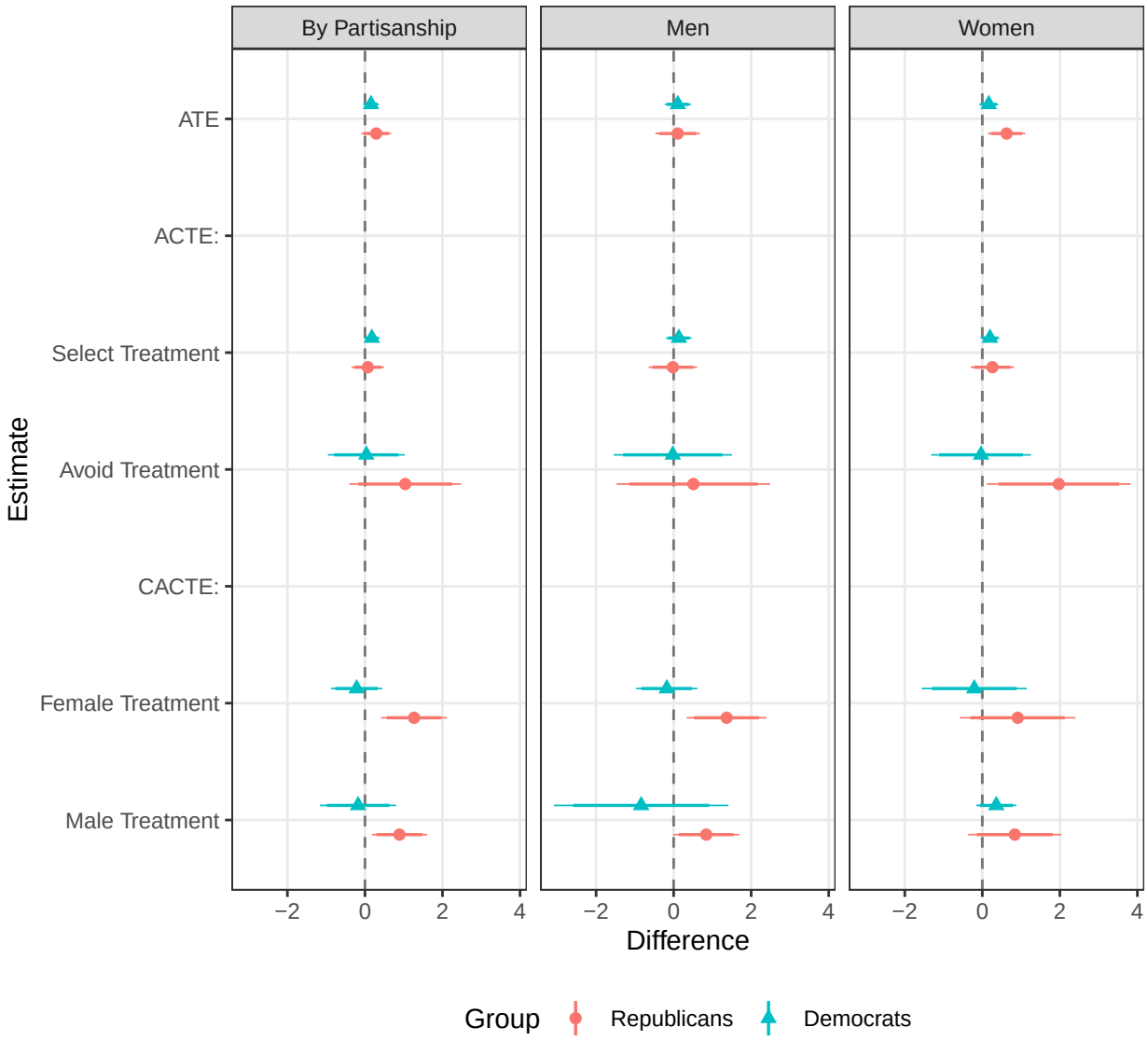


Figure F.3: Treatment Effect Estimates on Specific Support for #MeToo Conditional On Partisanship and Gender (MTurk Sample)

```
# Create Grouping Label

table_app_fn(df_mtg, "dv_pca_metoo",
         "Partisanship",
         Partisanship,
         the_cap ="Treatment Effect Estimates on Specific Support for \\#MeToo Conditional On Partisansh
  footnote(general = "The table provides point estimates and 95% confidence intervals for treatment effe
           threeparttable = T,
           fixed_small_size = T)
```

Table F.3: Treatment Effect Estimates on Specific Support for #MeToo Conditional On Partisanship and Gender (MTurk Sample)

	Full Sample		Men		Women	
	Democrats	Republicans	Democrats	Republicans	Democrats	Republicans
ATE						
ATE	0.16	0.29	0.11	0.10	0.17	0.63
	[-0.05, 0.36]	[-0.10, 0.68]	[-0.23, 0.45]	[-0.47, 0.68]	[-0.08, 0.41]	[0.15, 1.10]
ACTE						
Select Treatment	0.18	0.07	0.13	-0.02	0.20	0.26
	[-0.02, 0.38]	[-0.35, 0.49]	[-0.20, 0.46]	[-0.64, 0.60]	[-0.04, 0.44]	[-0.30, 0.82]
Avoid Treatment	0.04	1.04	-0.02	0.51	-0.03	1.97
	[-0.96, 1.03]	[-0.40, 2.48]	[-1.55, 1.50]	[-1.47, 2.49]	[-1.32, 1.25]	[0.12, 3.83]
CACTE						
Female Treatment	-0.22	1.27	-0.18	1.37	-0.21	0.91
	[-0.88, 0.45]	[0.42, 2.12]	[-0.97, 0.61]	[0.34, 2.40]	[-1.56, 1.15]	[-0.58, 2.40]
Male Treatment	-0.18	0.89	-0.84	0.84	0.36	0.84
	[-1.16, 0.81]	[0.18, 1.60]	[-3.09, 1.41]	[-0.01, 1.70]	[-0.16, 0.88]	[-0.36, 2.04]

Note:
The table provides point estimates and 95% confidence intervals for treatment effect estimated by partisanship overall and partisanship by gender

Figure and Table F.4: Treatment Effect Estimates on Specific Support for #MeToo Conditional On Partisanship and Gender (Qualtrics Sample)

```
figF4_df <- rbind(
  data.frame(
  effects_fn(df_qg[df_qg$pid>4,], "dv_pca_metoo"),
  Group = "Republicans",
  Type = "By Partisanship"),
  data.frame(
  effects_fn(df_qg[df_qg$pid<4,], "dv_pca_metoo"),
  Group = "Democrats",
  Type = "By Partisanship"),
  data.frame(
  effects_fn(df_qg[df_qg$pid>4 & df_qg$gender==0,], "dv_pca_metoo"),
  Group = "Republicans",
  Type = "Men"),
  data.frame(
  effects_fn(df_qg[df_qg$pid<4& df_qg$gender==0,], "dv_pca_metoo"),
  Group = "Democrats",
```

```
  Type = "Men"),
    data.frame(
  effects_fn(df_qg[df_qg$pid>4 & df_qg$gender==1,], "dv_pca_metoo"),
  Group = "Republicans",
  Type = "Women"),
  data.frame(
  effects_fn(df_qg[df_qg$pid<4& df_qg$gender==1,], "dv_pca_metoo"),
  Group = "Democrats",
  Type = "Women")
  )

figF4_df$Group <- factor(figF4_df$Group,
                         levels = unique(figF4_df$Group) )

figF4 <- figF4_df %>%
  filter(Estimand != "CATE")%>%
  ggplot(aes(Estimate, Difference,col=Group,shape=Group))+
  geom_hline(yintercept = 0,linetype="dashed",alpha=.5)+
  facet_grid(~Type)+
  geom_point(aes(shape=Group),
                 position = position_dodge(width = .5),size=2
      )+
  geom_linerange(aes(ymin=ll,ymax=ul),size=.3,
                       position = position_dodge(width = .5))+
  geom_linerange(aes(ymin=ll90,ymax=ul90),size=.6,
                     position = position_dodge(width = .5))+
  coord_flip()+
  theme_bw()+
  theme(
    panel.grid.minor = element_blank(),
    legend.position = "bottom"
  )

figF4
```

```
# Create Grouping Label
table_app_fn(df_qg, "dv_pca_metoo",
         "Partisanship",
         Partisanship,
         the_cap ="Treatment Effect Estimates on Specific Support for \\#MeToo Conditional On Partisansh
  footnote(general = "The table provides point estimates and 95% confidence intervals for treatment effe
           threeparttable = T,
           fixed_small_size = T)
```

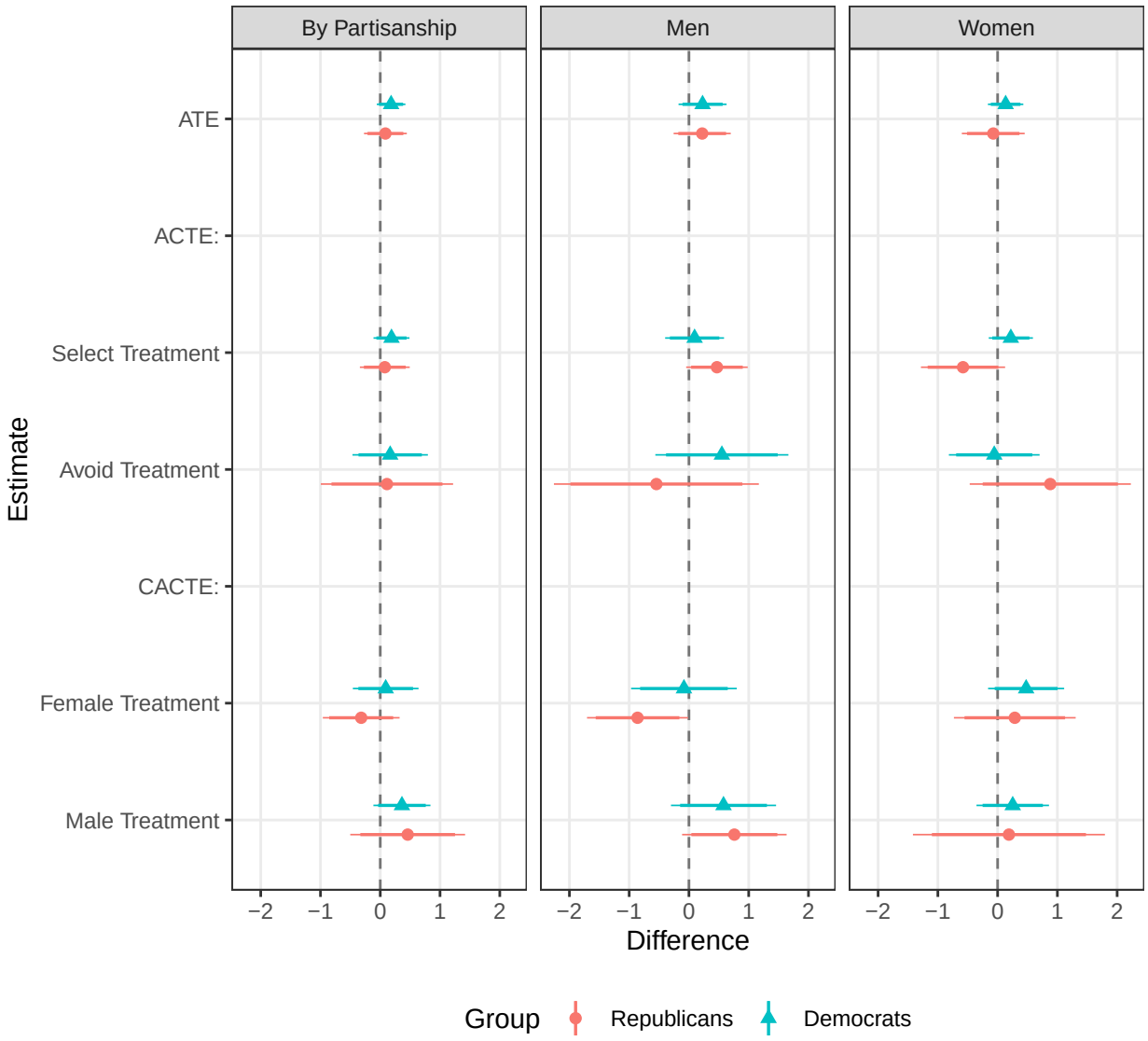


Figure F.4: Treatment Effect Estimates on Specific Support for #MeToo Conditional On Partisanship and Gender (Qualtrics Sample)

Table F.4: Treatment Effect Estimates on Specific Support for #MeToo Conditional On Partisanship and Gender (Qulatrics Sample)

	Full Sample		Men		Women	
	Republicans	Democrats	Republicans	Democrats	Republicans	Democrats
ATE						
ATE	0.09	0.18	0.22	0.23	-0.07	0.13
	[-0.27, 0.44]	[-0.06, 0.42]	[-0.26, 0.70]	[-0.17, 0.63]	[-0.60, 0.45]	[-0.16, 0.43]
ACTE						
Select Treatment	0.08	0.19	0.47	0.09	-0.58	0.22
	[-0.34, 0.49]	[-0.11, 0.49]	[-0.05, 0.98]	[-0.40, 0.59]	[-1.28, 0.13]	[-0.15, 0.59]
Avoid Treatment	0.11	0.17	-0.54	0.55	0.88	-0.06
	[-0.99, 1.22]	[-0.47, 0.80]	[-2.26, 1.17]	[-0.56, 1.66]	[-0.47, 2.23]	[-0.82, 0.70]
CACTE						
Female Treatment	-0.32	0.09	-0.86	-0.08	0.29	0.48
	[-0.96, 0.32]	[-0.46, 0.64]	[-1.71, -0.01]	[-0.97, 0.80]	[-0.73, 1.31]	[-0.16, 1.11]
Male Treatment	0.46	0.36	0.76	0.58	0.19	0.25
	[-0.50, 1.42]	[-0.11, 0.84]	[-0.11, 1.63]	[-0.30, 1.46]	[-1.42, 1.80]	[-0.35, 0.86]

Note:
The table provides point estimates and 95% confidence intervals for treatment effect estimated by partisanship overall and partisanship by gender

Figure and Table F.5: Treatment Effect Estimates on Knowledge of Sexual Assault Statistics (MTurk Sample)

```
# Create Figure 5
figF5 <- plot_effects_fn(df_mtg,"dv_fact01")

# Display Figure 5
figF5
```

```
table_fn(figF5$data,
    "Treatment Effect Estimates on Knowledge of Sexual Assault Statistics (MTurk Sample)")
```

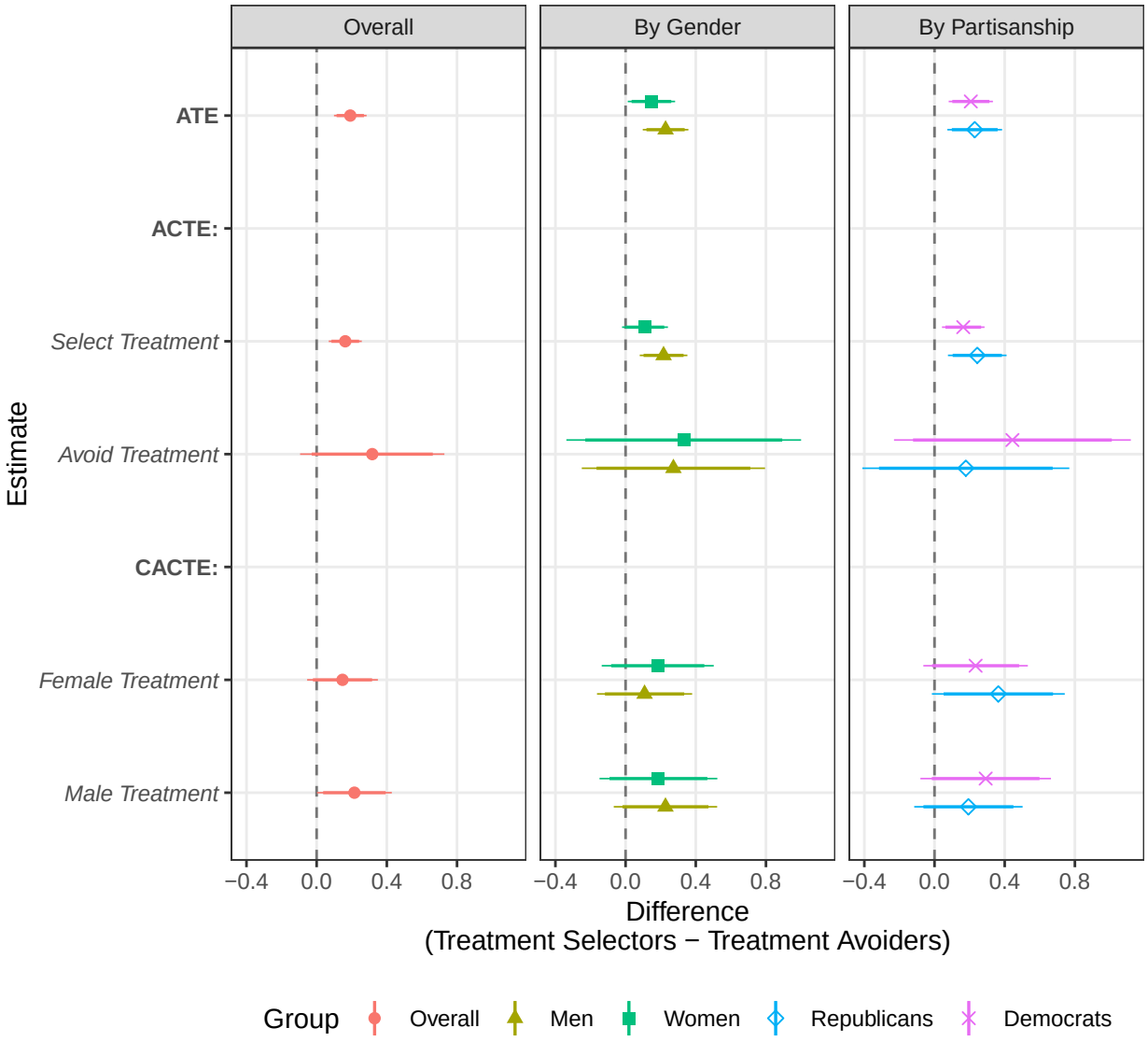


Figure F.5: Treatment Effect Estimates on Knowledge of Sexual Assault Statistics (MTurk Sample)

Table F.5: Treatment Effect Estimates on Knowledge of Sexual Assault Statistics (MTurk Sample)

	Overall	Men	Women	Republicans	Democrats
ATE					
ATE	0.19	0.23	0.15	0.23	0.21
	[0.10, 0.28]	[0.10, 0.36]	[0.01, 0.28]	[0.07, 0.39]	[0.08, 0.33]
ACTE					
Select Treatment	0.16	0.22	0.11	0.24	0.16
	[0.07, 0.26]	[0.08, 0.35]	[-0.02, 0.24]	[0.08, 0.41]	[0.04, 0.29]
Avoid Treatment	0.32	0.27	0.33	0.18	0.44
	[-0.09, 0.73]	[-0.25, 0.79]	[-0.34, 1.00]	[-0.41, 0.77]	[-0.23, 1.12]
CACTE					
Female Treatment	0.15	0.11	0.18	0.36	0.23
	[-0.05, 0.35]	[-0.16, 0.38]	[-0.14, 0.50]	[-0.02, 0.74]	[-0.06, 0.53]
Male Treatment	0.22	0.23	0.19	0.19	0.29
	[0.00, 0.43]	[-0.07, 0.52]	[-0.15, 0.52]	[-0.12, 0.50]	[-0.08, 0.66]

Note:
The table provides point estimates and 95% confidence intervals for treatment effect estimated from the full sample and separately by gender and partisanship

Figure and Table F.6: Treatment Effect Estimates on Knowledge of Sexual Assault Statistics (Qualtrics Sample)

```
# Create Figure 6
figF6 <- plot_effects_fn(df_qg,"dv_fact01")

# Display Figure 6
figF6
```

```
table_fn(figF6$data,
    "Treatment Effect Estimates on Knowledge of Sexual Assault Statistics (Qualtrics Sample)")
```

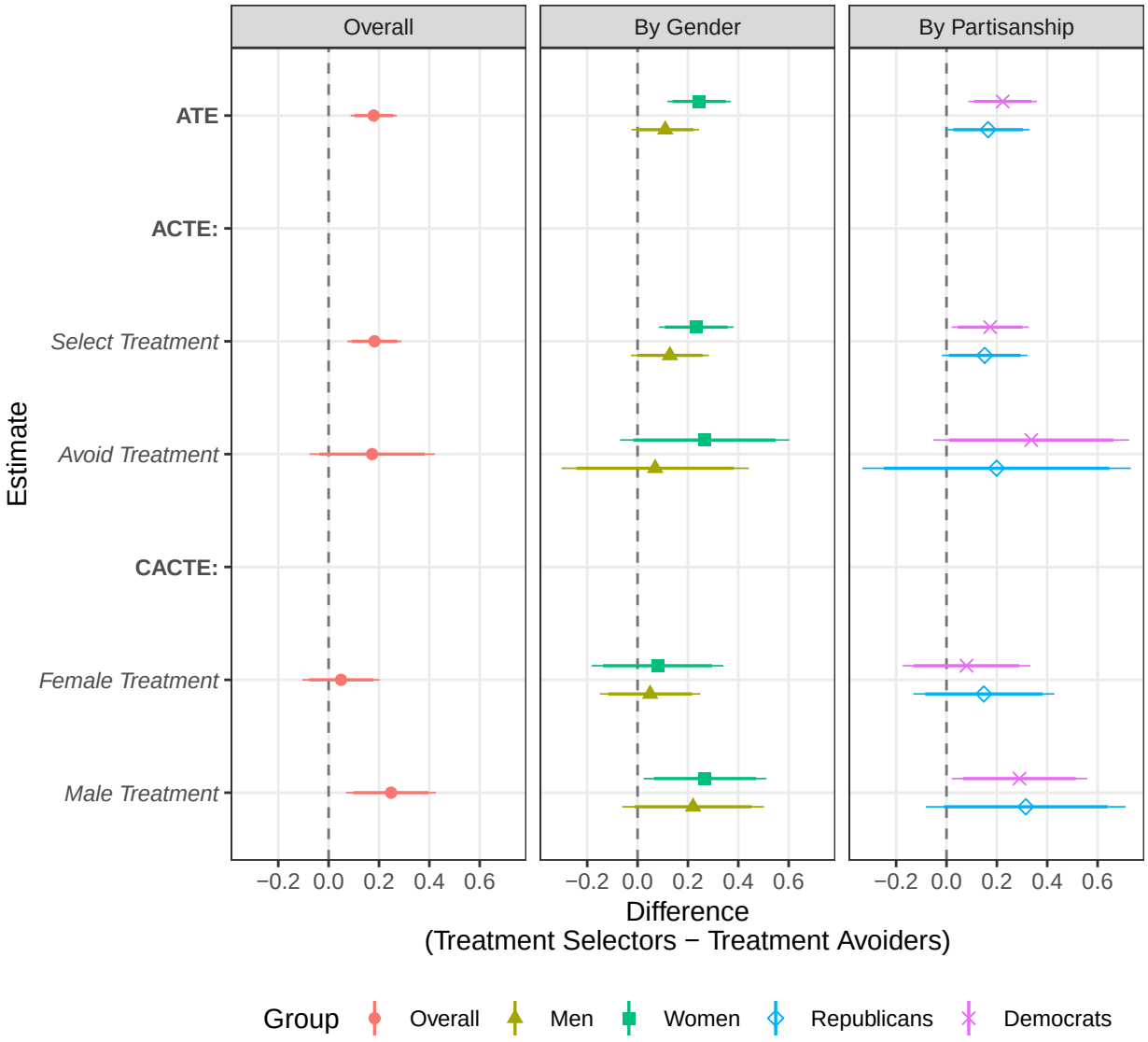


Figure F.6: Treatment Effect Estimates on Knowledge of Sexual Assault Statistics (Qualtrics Sample)

Table F.6: Treatment Effect Estimates on Knowledge of Sexual Assault Statistics (Qualtrics Sample)

	Overall	Men	Women	Republicans	Democrats
ATE					
ATE	0.18	0.11	0.24	0.17	0.22
	[0.09, 0.27]	[-0.02, 0.24]	[0.12, 0.37]	[-0.00, 0.33]	[0.09, 0.36]
ACTE					
Select Treatment	0.18	0.13	0.23	0.15	0.17
	[0.07, 0.29]	[-0.03, 0.28]	[0.08, 0.38]	[-0.02, 0.32]	[0.02, 0.33]
Avoid Treatment	0.17	0.07	0.27	0.20	0.34
	[-0.08, 0.42]	[-0.30, 0.44]	[-0.07, 0.60]	[-0.33, 0.73]	[-0.05, 0.73]
CACTE					
Female Treatment	0.05	0.05	0.08	0.15	0.08
	[-0.10, 0.20]	[-0.15, 0.25]	[-0.18, 0.34]	[-0.13, 0.43]	[-0.17, 0.33]
Male Treatment	0.25	0.22	0.27	0.31	0.29
	[0.07, 0.43]	[-0.06, 0.50]	[0.02, 0.51]	[-0.08, 0.71]	[0.02, 0.56]

Note:
The table provides point estimates and 95% confidence intervals for treatment effect estimated from the full sample and separately by gender and partisanship

Figure and Table F.7: Treatment Effect Estimates on Providing Written Responses about #MeToo (MTurk Sample)

```
# Create Figure 6
figF8 <- plot_effects_fn(df_mtg,"dv_response01")

# Display Figure 6
figF8
```

```
table_fn(figF8$data,
    "Treatment Effect Estimates on Providing Written Responses about \\#MeToo (MTurk Sample)")
```

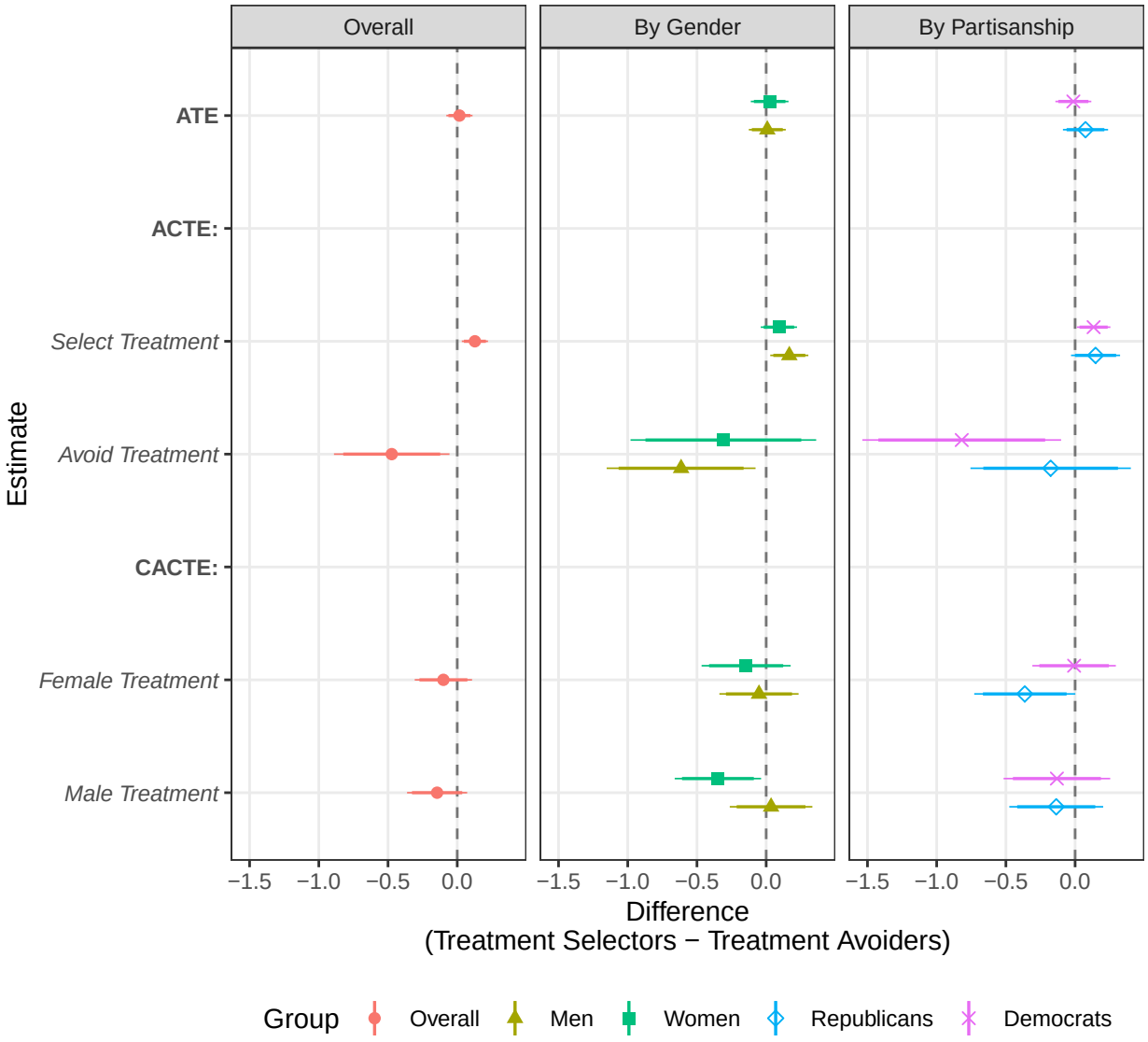


Figure F.7: Treatment Effect Estimates on Providing Written Responses about #MeToo (MTurk Sample)

Table F.7: Treatment Effect Estimates on Providing Written Responses about #MeToo (MTurk Sample)

	Overall	Men	Women	Republicans	Democrats
ATE					
ATE	0.02	0.01	0.03	0.08	-0.01
	[-0.08, 0.11]	[-0.13, 0.14]	[-0.11, 0.16]	[-0.09, 0.24]	[-0.14, 0.12]
ACTE					
Select Treatment	0.13	0.17	0.09	0.15	0.13
	[0.03, 0.22]	[0.03, 0.30]	[-0.04, 0.22]	[-0.03, 0.32]	[0.01, 0.25]
Avoid Treatment	-0.47	-0.61	-0.31	-0.18	-0.82
	[-0.89, -0.06]	[-1.15, -0.08]	[-0.98, 0.36]	[-0.76, 0.40]	[-1.54, -0.10]
CACTE					
Female Treatment	-0.10	-0.05	-0.14	-0.36	-0.01
	[-0.31, 0.11]	[-0.34, 0.23]	[-0.47, 0.18]	[-0.73, 0.00]	[-0.31, 0.29]
Male Treatment	-0.15	0.04	-0.35	-0.14	-0.13
	[-0.36, 0.07]	[-0.26, 0.33]	[-0.66, -0.04]	[-0.48, 0.20]	[-0.52, 0.25]

Note:
The table provides point estimates and 95% confidence intervals for treatment effect estimated from the full sample and separately by gender and partisanship

Figure and Table F.8: Treatment Effect Estimates on Providing Written Responses about #MeToo (Qualtrics Sample)

```
# Create Figure 6
figF8 <- plot_effects_fn(df_qg,"dv_response01")

# Display Figure 6
figF8
```

```
table_fn(figF8$data,
    "Treatment Effect Estimates on Providing Written Responses about \\#MeToo (Qualtrics Sample)")
```

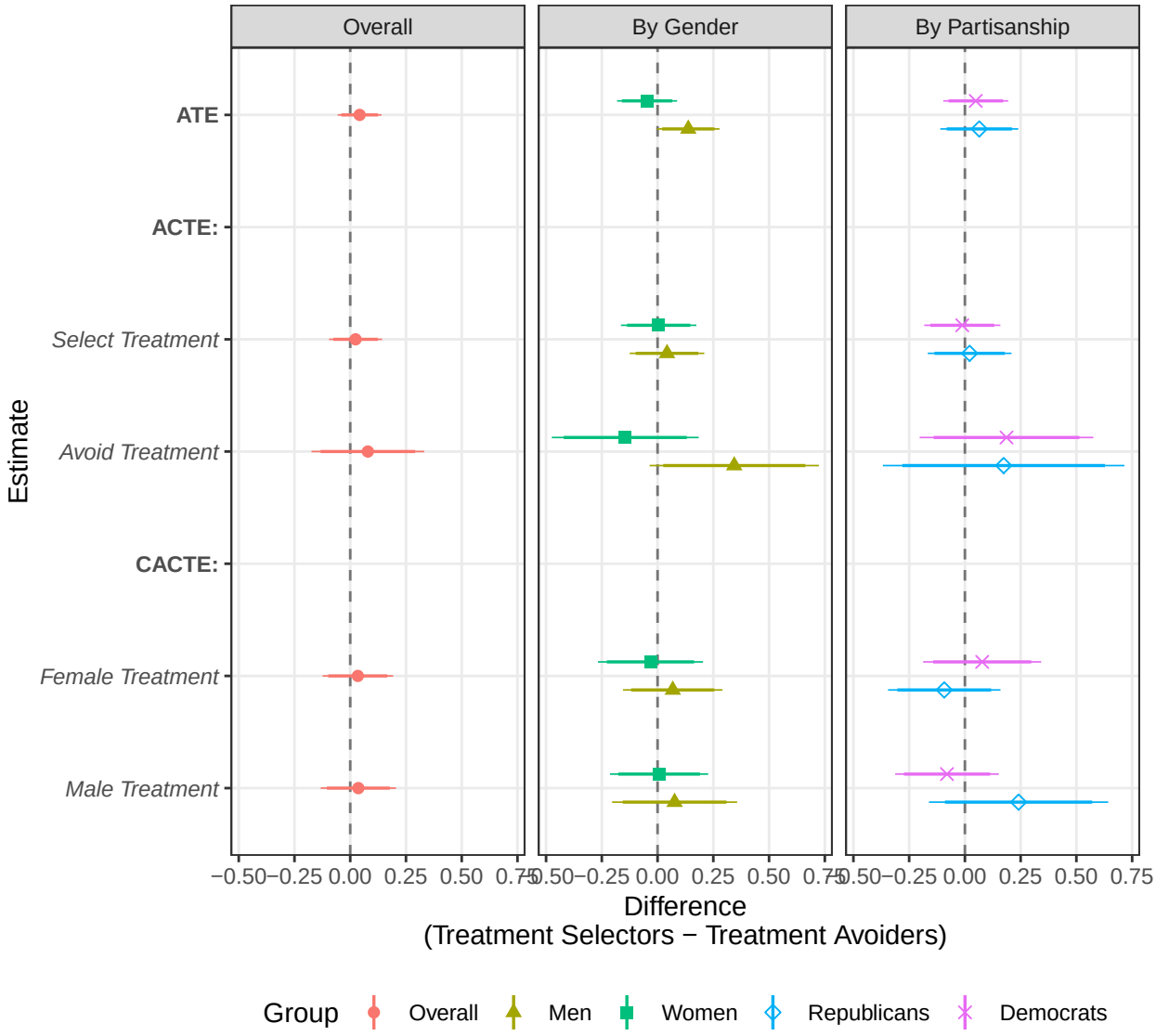


Figure F.8: Treatment Effect Estimates on Providing Written Responses about #MeToo (Qualtrics Sample)

Table F.8: Treatment Effect Estimates on Providing Written Responses about #MeToo (Qualtrics Sample)

	Overall	Men	Women	Republicans	Democrats
ATE					
ATE	0.04	0.14	-0.05	0.06	0.05
	[-0.06, 0.14]	[-0.00, 0.28]	[-0.18, 0.09]	[-0.11, 0.24]	[-0.10, 0.19]
ACTE					
Select Treatment	0.02	0.04	0.00	0.02	-0.01
	[-0.10, 0.14]	[-0.12, 0.21]	[-0.16, 0.17]	[-0.17, 0.21]	[-0.18, 0.16]
Avoid Treatment	0.08	0.34	-0.14	0.17	0.19
	[-0.17, 0.33]	[-0.04, 0.72]	[-0.47, 0.18]	[-0.37, 0.72]	[-0.20, 0.58]
CACTE					
Female Treatment	0.03	0.07	-0.03	-0.09	0.08
	[-0.12, 0.19]	[-0.15, 0.29]	[-0.27, 0.20]	[-0.34, 0.16]	[-0.19, 0.34]
Male Treatment	0.04	0.08	0.01	0.24	-0.08
	[-0.13, 0.21]	[-0.20, 0.36]	[-0.21, 0.23]	[-0.16, 0.64]	[-0.31, 0.15]

Note:
The table provides point estimates and 95% confidence intervals for treatment effect estimated from the full sample and separately by gender and partisanship