[Code] Impact of COVID Misinformation on Vaccination Intent - A Reanalysis Identifying and Addressing Covariate Imbalances

Stanford Stats 209 Project

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Full Report: https://www.overleaf.com/read/trngjhvnckrk

Covariate Names JSON Mapping: https://codebeautify.org/jsonviewer/cb92c22d

Import Data

```
# Download Relevant Files
system("gdown --id 1nWhtsofuJjDDm-qaiKVH0GvtEmmfGLC7") # full_orb_us.csv
system("gdown --id 1Zl1bHYKnZVCSKC3_e6-GXKk7Epzeukj8") # full_orb_uk.csv|
system("gdown --id 17Ta02ItPh5goVHnxZJku1H3Hh-sH8L-P") # utility.R
```

```
# Install Packages
if(!require(tidytext)){
  install.packages("tidytext")
}
if(!require(optmatch)){
  install.packages("optmatch")
}
if(!require(DOS2)){
  install.packages("DOS2")
}
if(!require(RItools)){
  install.packages("RItools")
}
if(!require(gridExtra)){
  install.packages("gridExtra")
}
if(!require(estimatr)){
  install.packages("estimatr")
}
if(!require(ggpubr)){
  install.packages("ggpubr")
}
if(!require(rstatix)){
  install.packages("rstatix")
}
```

```
}
if(!require(pROC)){
  install.packages("pROC")
}
```

```
Loading required package: tidytext

Warning message in library(package, lib.loc = lib.loc, character.only = TRUE, logica
“there is no package called ‘tidytext’”
Installing package into ‘/usr/local/lib/R/site-library’
(as ‘lib’ is unspecified)

also installing the dependencies ‘SnowballC’, ‘hunspell’, ‘janeaustenr’, ‘tokenizers


Loading required package: optmatch

Warning message in library(package, lib.loc = lib.loc, character.only = TRUE, logica
“there is no package called ‘optmatch’”
Installing package into ‘/usr/local/lib/R/site-library’
(as ‘lib’ is unspecified)

also installing the dependencies ‘SparseM’, ‘abind’, ‘xtable’, ‘svd’, ‘minqa’, ‘numD


Loading required package: DOS2

Warning message in library(package, lib.loc = lib.loc, character.only = TRUE, logica
“there is no package called ‘DOS2’”
Installing package into ‘/usr/local/lib/R/site-library’
(as ‘lib’ is unspecified)

also installing the dependencies ‘BiasedUrn’, ‘mvtnorm’, ‘sensitivity2x2xk’, ‘sensit


Loading required package: RItools

Loading required package: SparseM


Attaching package: ‘SparseM’


The following object is masked from ‘package:base’:

    backsolve


Loading required package: gridExtra

Warning message in library(package, lib.loc = lib.loc, character.only = TRUE, logica
“there is no package called ‘gridExtra’”
Installing package into ‘/usr/local/lib/R/site-library’
(as ‘lib’ is unspecified)

Loading required package: estimatr
```

```
Warning message in library(package, lib.loc = lib.loc, character.only = TRUE, logica
“there is no package called ‘estimatr’”
Installing package into ‘/usr/local/lib/R/site-library’
(as ‘lib’ is unspecified)
```

```
library(tidyverse)
library(tidytext)
library(optmatch)
library(DOS2)
library(RItools)
library(gridExtra)
library(estimatr)
library(ggpubr)
library(rstatix)
library(pROC)
source('utility.R')
```

```
Warning message in system("timedatectl", intern = TRUE):
“running command 'timedatectl' had status 1”
── Attaching packages ─────────────────────────────────────── tidyverse 1.3.1 ──

✓ ggplot2 3.3.5     ✓ purrr   0.3.4
✓ tibble  3.1.6     ✓ dplyr   1.0.7
✓ tidyr   1.1.4     ✓ stringr 1.4.0
✓ readr   2.1.0     ✓ forcats 0.5.1

── Conflicts ────────────────────────────────────────── tidyverse_conflicts() ──
✗ dplyr::filter() masks rstatix::filter(), stats::filter()
✗ dplyr::lag()    masks stats::lag()

Loading required package: survival

The optmatch package has an academic license. Enter relaxinfo() for more information.


Attaching package: ‘gridExtra’


The following object is masked from ‘package:dplyr’:

    combine
```

```
df_us <- read.csv("full_orb_us.csv")
```

```
head(df_us)
```

	X	Know.anyone.Nobody	Know.anyone.Myself	Know.anyone.Family.inside.HH	Know.a
	<int>	<int>	<int>	<int>	
1	0	0	0	0	
2	1	1	0	0	
3	2	0	0	0	
4	3	0	1	0	
5	4	1	0	0	
6	5	1	0	0	

```
# see https://github.com/sloomba/covid19-misinfo/blob/main/dat/orb_us.json for coding of the
str(df_us)
```

```
'data.frame':	4001 obs. of  137 variables:
 $ X                                                : int  0 1 2 3 4 5 6 7 8 9 ...
 $ Know.anyone.Nobody                               : int  0 1 0 0 1 1 1 0 1 0 ...
 $ Know.anyone.Myself                               : int  0 0 0 1 0 0 0 0 0 0 ...
 $ Know.anyone.Family.inside.HH                     : int  0 0 0 0 0 0 0 1 0 0 ...
 $ Know.anyone.Family.outside.HH                    : int  0 0 0 0 0 0 0 0 0 0 ...
 $ Know.anyone.Close.friend                         : int  0 0 0 0 0 0 0 0 0 0 ...
 $ Know.anyone.Colleague                            : int  1 0 1 0 0 0 0 0 0 1 ...
 $ COVID.19.Knowledge.Washing.hands                 : int  1 2 2 2 1 1 2 1 2 2 ...
 $ COVID.19.Knowledge.Staying.indoors.for.Self      : int  2 2 1 -2 1 -2 2 2 2 2 ...
 $ COVID.19.Knowledge.Staying.indoors.for.Others    : int  2 2 1 -1 -1 -2 2 -1 2 -1
 $ COVID.19.Knowledge.Spread.before.symptoms        : int  -1 2 2 -1 1 1 -1 1 2 2 ..
 $ COVID.19.Knowledge.R.Number                      : int  1 2 2 2 -1 -1 1 2 1 2 ...
 $ COVID.19.Knowledge.Treatments.already.exist      : int  2 2 -2 -1 -2 2 1 0 1 -2 .
 $ COVID.19.Knowledge.Wearing.masks                 : int  1 2 -1 -2 2 -1 -1 2 2 2 .
 $ COVID.19.VCI.COVID.19.Vax.Importance             : int  2 2 -1 -2 2 -2 0 2 2 2 ..
 $ COVID.19.VCI.COVID.19.Vax.Safety                 : int  1 2 1 1 1 -2 1 -2 2 1 ...
 $ COVID.19.VCI.COVID.19.Vax.Efficacy               : int  2 2 -1 -1 1 -2 1 1 1 2 ..
 $ COVID.19.VCI.COVID.19.Vax.Compatibility          : int  -1 2 -2 -2 -2 0 1 1 -2 -2
 $ COVID.19.VCI.Contract.via.COVID.19.Vax           : int  -2 2 -1 -2 0 -2 0 2 -2 0
 $ COVID.19.VCI.COVID.19.Vax.benefits.outweigh.risks: int  1 2 -2 -1 1 -2 -1 0 1 0 .
 $ General.VCI.Vax.Importance                       : int  2 2 2 2 0 -2 1 0 2 1 ...
 $ General.VCI.Vax.Safety                           : int  2 2 1 -1 0 2 0 2 2 0 ...
 $ General.VCI.Vax.Efficacy                         : int  1 2 1 -2 0 -2 1 -1 2 1 ..
 $ General.VCI.Vax.Compatibility                    : int  1 2 2 -2 1 -2 0 0 2 2 ...
 $ COVID.19.Impact.Mental.health                    : int  -1 2 2 -2 -2 -2 2 1 2 2 .
 $ COVID.19.Impact.Financial.stability              : int  1 2 -1 -1 -2 1 2 1 1 2 ..
 $ COVID.19.Impact.Daily.disruption                 : int  -1 2 2 1 -1 2 2 -2 2 1 ..
 $ COVID.19.Impact.Social.disruption                : int  1 2 2 1 -1 2 2 2 1 2 ...
 $ Social.Facebook.used                             : int  1 1 1 0 0 1 1 1 1 1 ...
 $ Social.Twitter.used                              : int  1 0 0 0 0 1 1 0 0 1 ...
 $ Social.YouTube.used                              : int  1 0 0 0 0 1 1 1 1 0 ...
 $ Social.WhatsApp.used                             : int  1 0 0 0 0 0 0 0 1 0 ...
 $ Social.Instagram.used                            : int  1 0 1 1 0 1 1 1 1 1 ...
 $ Social.Pinterest.used                            : int  0 0 0 0 0 1 0 1 1 1 ...
 $ Social.LinkedIN.used                             : int  0 0 1 0 0 1 0 0 0 0 ...
 $ Social.Other.used                                : int  0 0 0 0 0 0 1 1 1 0 ...
 $ Social.None.of.these.used                            : int  0 0 0 0 1 0 0 0 0 0 ...
 $ Social.Facebook.to.receive.info                      : int  1 1 0 0 0 1 1 1 0 0 ...
 $ Social.Twitter.to.receive.info                       : int  1 0 0 0 0 1 1 0 0 0 ...
 $ Social.YouTube.to.receive.info                       : int  0 0 0 0 0 0 1 0 0 0 ...
 $ Social.WhatsApp.to.receive.info                      : int  0 0 0 0 0 0 0 0 0 0 ...
 $ Social.Instagram.to.receive.info                     : int  0 0 0 1 0 0 1 0 0 0 ...
 $ Social.Pinterest.to.receive.info                     : int  0 0 0 0 0 0 0 0 0 0 ...
 $ Social.LinkedIN.to.receive.info                      : int  0 0 0 0 0 0 0 0 0 0 ...
 $ Social.Other.to.receive.info                         : int  0 0 0 0 0 0 1 0 0 0 ...
 $ Social.None.of.these.to.receive.info                 : int  0 0 1 0 1 0 0 0 1 1 ...
 $ Social.Facebook.to.share.info                        : num  1 1 0 0 0 NA 0 NA 0 0 ...
 $ Social.Twitter.to.share.info                         : num  1 0 0 0 0 NA 0 NA 0 0 ...
 $ Social.YouTube.to.share.info                         : num  0 0 0 0 0 NA 0 NA 0 0 ...
 $ Social.WhatsApp.to.share.info                        : num  1 0 0 0 0 NA 0 NA 0 0 ...
 $ Social.Instagram.to.share.info                       : num  1 0 0 1 0 NA 1 NA 0 0 ...
 $ Social.Pinterest.to.share.info                       : num  0 0 0 0 0 NA 0 NA 0 0 ...
 $ Social.LinkedIN.to.share.info                        : num  0 0 0 0 0 NA 0 NA 0 0 ...
 $ Social.Other.to.share.info                           : num  0 0 0 0 0 NA 0 NA 0 0 ...
 $ Social.None.of.these.to.share.info                   : num  0 0 1 0 1 NA 0 NA 1 1 ...
 $ Trust.Television                                     : int  0 0 0 1 0 0 0 0 0 0 ...
```

Data Processing

```
# US
df_us_cleaned <- df_us %>%
  mutate(
    z = Treatment,
    inv_z = 1 - Treatment,

    # Pre-Treatment Covariates
    Shielding = ifelse(Shielding == 2, 0, 1),
    know.anyone.covid = (1 - Know.anyone.Nobody),

    # Derived Personas

    ## Bad Covid Knowledge
    ## only including these 5 which should be broadly known. Other 2 may not be well known.
    covid_knowledge_avg = (
      (COVID.19.Knowledge.Washing.hands) +
      (COVID.19.Knowledge.Staying.indoors.for.Self) +
      (COVID.19.Knowledge.Staying.indoors.for.Others) +
      (COVID.19.Knowledge.Spread.before.symptoms) +
      (COVID.19.Knowledge.Wearing.masks)
    )/5,
    bad_covid_knowledge = ifelse(covid_knowledge_avg < 0, 1, 0),

    ## Distrust of Covid Vax
    ## flip these two since their wording is opposite (agree is bad)
    COVID.19.VCI.COVID.19.Vax.Compatibility = COVID.19.VCI.COVID.19.Vax.Compatibility * -1,
COVID.19.VCI.Contract.via.COVID.19.Vax = COVID.19.VCI.Contract.via.COVID.19.Vax *
  -1,
covid_vax_trust_avg = (
  COVID.19.VCI.COVID.19.Vax.Importance +
    COVID.19.VCI.COVID.19.Vax.Safety +
    COVID.19.VCI.COVID.19.Vax.Efficacy +
    COVID.19.VCI.COVID.19.Vax.benefits.outweigh.risks +
    COVID.19.VCI.COVID.19.Vax.Compatibility +
    COVID.19.VCI.Contract.via.COVID.19.Vax
) / 6,
bad_covid_vax_trust = ifelse(covid_vax_trust_avg < 0, 1, 0),

## Distrust of General Vax
general_vax_trust_avg = (
  General.VCI.Vax.Importance +
    General.VCI.Vax.Safety +
    General.VCI.Vax.Efficacy +
    General.VCI.Vax.Compatibility
) / 4,
bad_general_vax_trust = ifelse(general_vax_trust_avg < 0, 1, 0),

# note this is post-treatment, but should technically be ok
# since should not have been affected by treatment
covid_disrupt = ifelse((
  COVID.19.Impact.Mental.health +
    COVID.19.Impact.Financial.stability +
    COVID.19.Impact.Daily.disruption +
    COVID.19.Impact.Social.disruption
) / 4 > 0,
1,
0
),

# Processed Questions
## Make questions -1, 0, 1 for more samples per bucket
COVID.19.Knowledge.Washing.hands.tri = ifelse(COVID.19.Knowledge.Washing.hands == 0, 0, i
COVID.19.Knowledge.Staying.indoors.for.Self.tri = ifelse(COVID.19.Knowledge.Staying.indoo
COVID.19.Knowledge.Staying.indoors.for.Others.tri = ifelse(COVID.19.Knowledge.Staying.indo
COVID.19.Knowledge.Spread.before.symptoms.tri = ifelse(COVID.19.Knowledge.Spread.before.s
COVID.19.Knowledge.Wearing.masks.tri = ifelse(COVID.19.Knowledge.Wearing.masks == 0, 0, i
COVID.19.VCI.COVID.19.Vax.Importance.tri = ifelse(COVID.19.VCI.COVID.19.Vax.Importance ==
COVID.19.VCI.COVID.19.Vax.Safety.tri = ifelse(COVID.19.VCI.COVID.19.Vax.Safety == 0, 0, i
COVID.19.VCI.COVID.19.Vax.Efficacy.tri = ifelse(COVID.19.VCI.COVID.19.Vax.Efficacy == 0,
COVID.19.VCI.COVID.19.Vax.benefits.outweigh.risks.tri = ifelse(COVID.19.VCI.COVID.19.Vax.
COVID.19.VCI.COVID.19.Vax.Compatibility.tri = ifelse(COVID.19.VCI.COVID.19.Vax.Compatibil
COVID.19.VCI.Contract.via.COVID.19.Vax.tri = ifelse(COVID.19.VCI.Contract.via.COVID.19.Va
General.VCI.Vax.Importance.tri = ifelse(General.VCI.Vax.Importance == 0, 0, ifelse(Genera
General.VCI.Vax.Safety.tri = ifelse(General.VCI.Vax.Safety == 0, 0, ifelse(General.VCI.Va
General.VCI.Vax.Efficacy.tri = ifelse(General.VCI.Vax.Efficacy == 0, 0, ifelse(General.VC
General.VCI.Vax.Compatibility.tri = ifelse(General.VCI.Vax.Compatibility == 0, 0, ifelse(
    # Outcomes

    ## Strict Decrease in Vaccine Intent
    ## note that 1 is the first answer choice which is Yes, so a "decrease" in vaccine intent
    Vaccine.Intent.for.self..Decrease = (Vaccine.Intent.for.self..Post. > Vaccine.Intent.for.
    Vaccine.Intent.for.others..Decrease = (Vaccine.Intent.for.others..Post. > Vaccine.Intent.

    pre_vaccine_no_intent = (Vaccine.Intent.for.self..Pre. == 4),

    ## Agreeing with Misinfo
    Image.NumAgree = ((Image.1.Agreement > 0) + (Image.2.Agreement > 0) + (Image.3.Agreement
    Image.NumDontKnow = ((Image.1.Agreement == 0) + (Image.2.Agreement == 0) + (Image.3.Agree
    Image.NumDisagree = (5 - Image.NumAgree - Image.NumDontKnow),
    NumMisinfoBelief = Treatment*Image.NumAgree + (1-Treatment)*(Image.NumDisagree),
    MisinfoBeliever = NumMisinfoBelief > 1,

    ## Sharing the Misinfo
    Image.NumShare = ((Image.1.Share > 0) + (Image.2.Share> 0) + (Image.3.Share > 0) + (Image
    Image.NumDontKnow = ((Image.1.Share == 0) + (Image.2.Share == 0) + (Image.3.Share == 0) +
    Image.NumNotShare = (5 - Image.NumShare - Image.NumDontKnow),
    NumMisinfoShare = Treatment*Image.NumShare + (1-Treatment)*(Image.NumNotShare),
    MisinfoShare = NumMisinfoShare > 1,

    ## Trusting the Misinfo Source
    Image.NumTrust = ((Image.1.Trust > 0) + (Image.2.Trust> 0) + (Image.3.Trust > 0) + (Image
    Image.NumDontKnow = ((Image.1.Trust == 0) + (Image.2.Trust == 0) + (Image.3.Trust == 0) +
    Image.NumNotTrust = (5 - Image.NumTrust - Image.NumDontKnow),
    NumMisinfoTrust = Treatment*Image.NumTrust + (1-Treatment)*(Image.NumNotTrust),
    MisinfoTrust = NumMisinfoTrust > 1
  )

df_us_cleaned %>%
  select(
    z,
    inv_z,
    Treatment,
    Shielding,
    know.anyone.covid,
    bad_covid_knowledge,
    bad_covid_vax_trust,
    bad_general_vax_trust,
    covid_disrupt,
    Vaccine.Intent.for.self..Decrease,
    Vaccine.Intent.for.self..Post.,
    Vaccine.Intent.for.self..Pre.,
    Vaccine.Intent.for.others..Decrease,
    Vaccine.Intent.for.others..Post.,
    Vaccine.Intent.for.others..Pre.,
    NumMisinfoBelief,
    NumMisinfoShare,
    NumMisinfoTrust
  ) %>% head()
```

	z	inv_z	Treatment	Shielding	know.anyone.covid	bad_covid_knowledge	bad_covi
	<int>	<dbl>	<int>	<dbl>	<dbl>	<dbl>	
1	1	0	1	0	1	0	
2	1	0	1	1	0	0	
3	1	0	1	1	1	0	
4	1	0	1	0	1	1	
5	1	0	1	0	0	0	
6	1	0	1	1	0	1	

```
df_us_cleaned_removed_no_intent <- df_us_cleaned %>%
  filter(pre_vaccine_no_intent == 0)


final_covariates <- c(
  'Age',
  'Gender',
  'Education',
  'Employment',
  'Religion',
  'Political',
  'Ethnicity',
  'Income',
  'know.anyone.covid',
  'Shielding',
  'bad_covid_knowledge',
  'bad_covid_vax_trust',
  'bad_general_vax_trust',
  'covid_disrupt'
)

detailed_covariates <- c(
  final_covariates,
  'COVID.19.Knowledge.Washing.hands.tri',
  'COVID.19.Knowledge.Staying.indoors.for.Self.tri',
  'COVID.19.Knowledge.Staying.indoors.for.Others.tri',
  'COVID.19.Knowledge.Spread.before.symptoms.tri',
  'COVID.19.Knowledge.Wearing.masks.tri',
  'COVID.19.VCI.COVID.19.Vax.Importance.tri',
  'COVID.19.VCI.COVID.19.Vax.Safety.tri',
  'COVID.19.VCI.COVID.19.Vax.Efficacy.tri',
  'COVID.19.VCI.COVID.19.Vax.benefits.outweigh.risks.tri',
  'COVID.19.VCI.COVID.19.Vax.Compatibility.tri',
  'COVID.19.VCI.Contract.via.COVID.19.Vax.tri',
  'General.VCI.Vax.Importance.tri',
  'General.VCI.Vax.Safety.tri',
  'General.VCI.Vax.Efficacy.tri',
  'General.VCI.Vax.Compatibility.tri'
)


summary(df_us_cleaned)
```

```
       X         Know.anyone.Nobody Know.anyone.Myself
 Min.   :   0   Min.   :0.0000     Min.   :0.00000
 1st Qu.:1000   1st Qu.:0.0000     1st Qu.:0.00000
 Median :2000   Median :1.0000     Median :0.00000
 Mean   :2035   Mean   :0.5414     Mean   :0.07298
 3rd Qu.:3001   3rd Qu.:1.0000     3rd Qu.:0.00000
 Max.   :4995   Max.   :1.0000     Max.   :1.00000

 Know.anyone.Family.inside.HH Know.anyone.Family.outside.HH
 Min.   :0.00000              Min.   :0.0000
 1st Qu.:0.00000              1st Qu.:0.0000
```

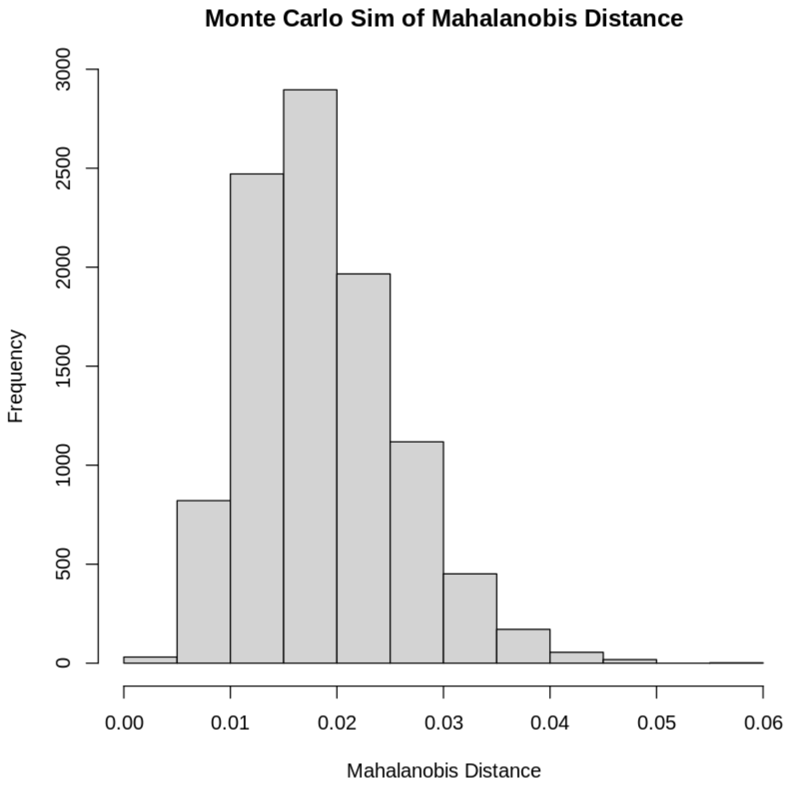
Imbalance

Mahalanobis Distance FRT

```
 Median :0.000            Median :0.0000
```

```
computeMahalanobis <- function(treatment.data, control.data) {
  total.data <- rbind(treatment.data, control.data)
  mean.treatment <- as.vector(colMeans(treatment.data))
  mean.control <- as.vector(colMeans(control.data))
  result <- mahalanobis(mean.treatment, mean.control, cov = cov(total.data))

  return(result)
}

simulate <- function(data) {
  # Build Random Vector
  data$random <- sample(data$z, replace=F, size=nrow(data))

  # Filter dataframes
  treatment_data = filter(data, random == 1)
  control_data = filter(data, random == 0)

  # Only select the relevant covariates
  treatment_data = treatment_data[, final_covariates]
  control_data = control_data[, final_covariates]

  distance <- computeMahalanobis(treatment_data, control_data)

  return(distance)
}

overall_mahal_sim <- c()

for(i in 1:10000) {
  overall_mahal_sim[i] <- simulate(df_us_cleaned)
}
```

```
orig_study_mahal <-
  computeMahalanobis(filter(df_us_cleaned, z == 1)[, final_covariates], filter(df_us_cleaned,
mahal_p_val <- mean(overall_mahal_sim > orig_study_mahal)

hist(overall_mahal_sim,
     main = 'Monte Carlo Sim of Mahalanobis Distance',
     xlab = 'Mahalanobis Distance')
abline(v = orig_study_mahal, lty = 2)
```



```
      Median : 1.0000        Median : 1.000          Median : 1.000
```

```
orig_study_mahal
mahal_p_val
```

```
0.415998496263431
0
```

```
      1st Qu.:-1.0000             1st Qu.:-1.0000
```

Visualizing the Imbalance

```
      Max.   : 2.0000             Max.   : 2.0000
```

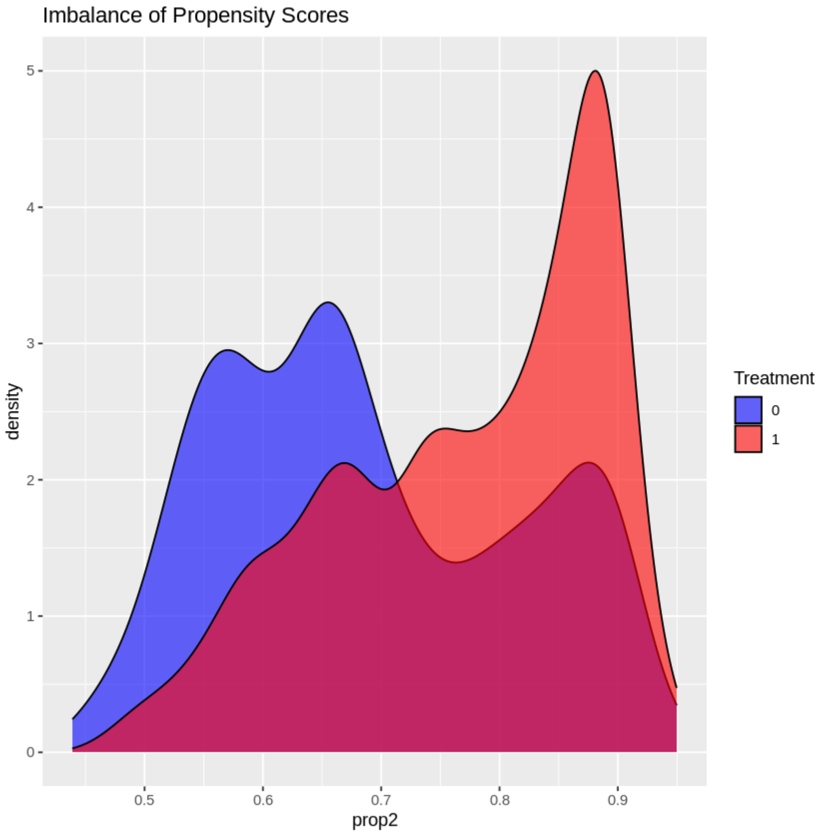
Propensity Score

```
      1st Qu.:-1.0000                1st Qu.: 1.0000
```

```
df_us_cleaned$prop2  <-
  glm(as.formula(paste("z ~", paste(
    final_covariates, collapse = " + "
  ))),
  family = binomial(link = "logit"),
  data = df_us_cleaned)$fitted.values

auc(df_us_cleaned$z, df_us_cleaned$prop2)
```

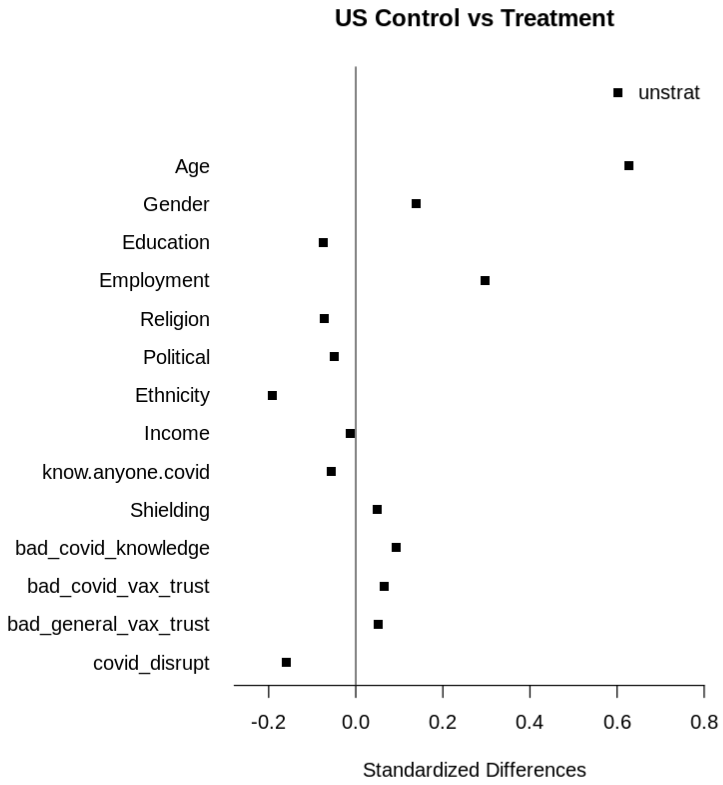
```
Setting levels: control = 0, case = 1

Setting direction: controls < cases

0.687015994668444
```

```
df_us_cleaned %>%
  mutate(Treatment = as.factor(Treatment)) %>%
  ggplot(aes(x = prop2, fill = Treatment)) +
  geom_density(alpha=0.6) +
  scale_fill_manual(values = c("blue","red")) +
  ggtitle('Imbalance of Propensity Scores')
```



Matching Plots

```
plot(
  xBalance(
    as.formula(paste("Treatment ~", paste(final_covariates, collapse = " + "))),
    data = df_us_cleaned
  ),
  main="US Control vs Treatment"
)
```



Individual Covariate T-Tests

```
df_us_cleaned.long <-
  select_if(df_us_cleaned[, c('z', final_covariates)], is.numeric)   %>%
  pivot_longer(-z, names_to = "variables", values_to = "value")

stat.test <- df_us_cleaned.long %>%
  group_by(variables) %>%
  t_test(value ~ z) %>%
  adjust_pvalue(method = "bonferroni") %>%
  add_significance()

stat.test[, c('variables', 'statistic', 'p.adj', 'p.adj.signif')] %>%
  arrange(p.adj)
```

A rstatix_test: 14 × 4

variables	statistic	p.adj	p.adj.signif
<chr>	<dbl>	<dbl>	<chr>
Age	-17.2654778	1.3370e-60	****
Employment	-8.7647881	5.5300e-17	****
Ethnicity	4.9574744	1.1074e-05	****
covid_disrupt	4.4650867	1.1900e-04	***
Gender	-3.7735170	2.3240e-03	**
bad_covid_knowledge	-2.7140540	9.3940e-02	ns
Education	2.0158926	6.1600e-01	ns
Religion	1.9627419	6.9720e-01	ns
bad_covid_vax_trust	-1.8518380	8.9880e-01	ns
bad_general_vax_trust	1.4297878	1.0000e+00	ns

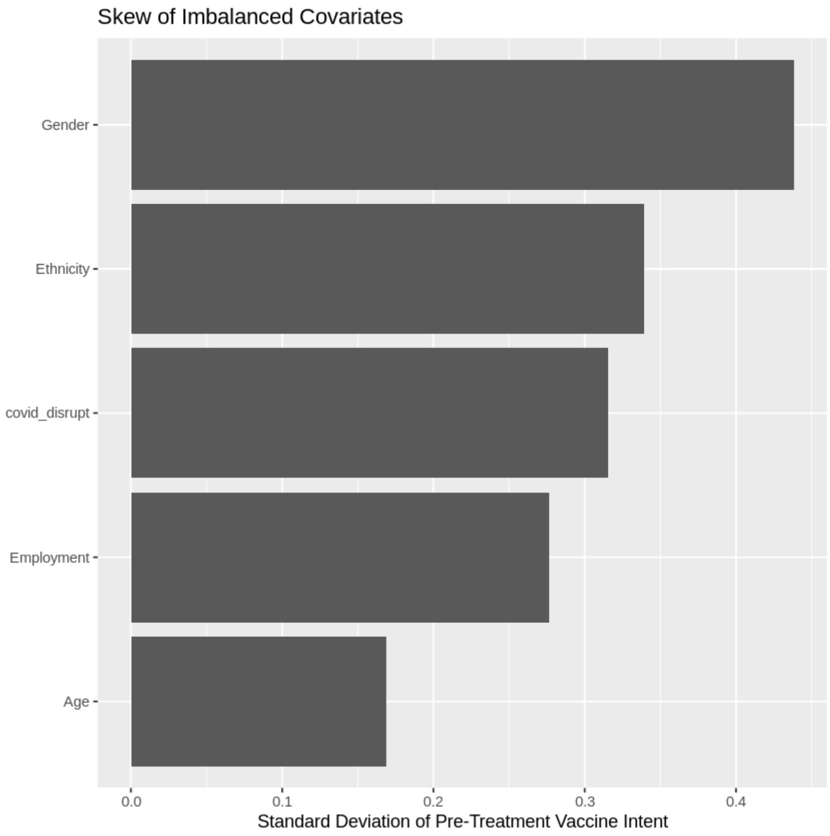
```
imbalanced_covariates <- stat.test %>%
  filter(p.adj.signif != 'ns') %>%
  pull(variables)
```

Impact of Imbalanced Covariates

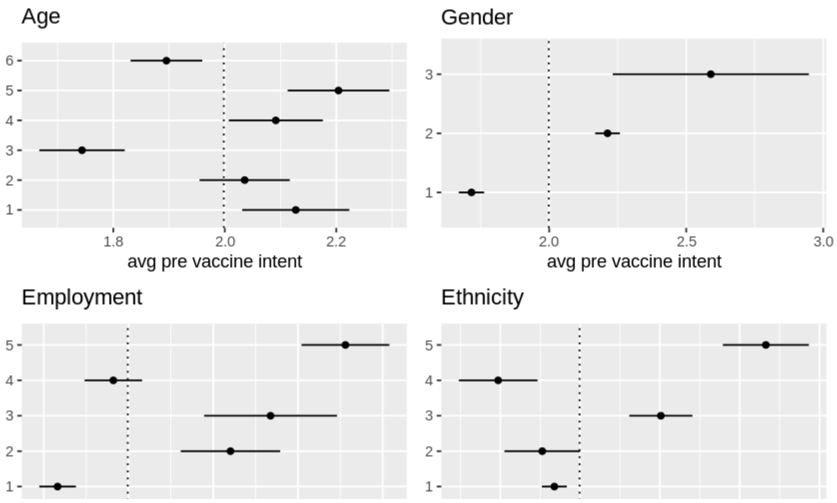
```
pre_intent_plot <- function(df, group, y, item = 'plot') {
  lower_limit <- ifelse(y == 'NumMisinfoBelief',-1.25,-0.5)
  upper_limit <- ifelse(y == 'NumMisinfoBelief', 3.25, 0.5)

  group = sym(group)
  y = sym(y)

  benchmark <- mean(df %>% pull(!!y))

  processed_df <- df %>%
    mutate(!!group := as.factor(!!group)) %>%
    group_by(!!group) %>%
    summarize(
      .groups = 'keep',
      t = mean(!!y),
      v = var(!!y) / n(),
      t_lower = t - 1.96 * sqrt(v),
      t_upper = t + 1.96 * sqrt(v)
    ) %>%
    select(!!group, t, v, t_lower, t_upper)

  se <- processed_df %>%
    ungroup() %>%
    summarize(se = sqrt(var(t))) %>%
    pull(se)

  p <- processed_df %>%
    ggplot(aes(
      x = t,
      y = !!group,
      group = !!group
    )) +
    #draws the means
    # geom_point(position = position_dodge(1)) +
    geom_point() +
    #draws the CI error bars
    geom_errorbarh(aes(xmin = t_lower, xmax = t_upper),
                   # color = !!group),
                   show.legend = FALSE,
                   height = 0) +
    # position = position_dodge(0.78)) +
    # xlim(lower_limit, upper_limit) +
    geom_vline(xintercept = benchmark, linetype = "dotted") +
    labs(
      title = group,
      x = 'avg pre vaccine intent') +
    theme(axis.title.y = element_blank())

  return(if (item == 'se') {
    se
  } else{
    p
  })
}


pre_vaccine_intent_se <- data.frame(covariate = character(),
                                      se = double())
pre_vaccine_intent_plots <- list()

i = 1
for (c in detailed_covariates) {
  pre_vaccine_intent_se <- pre_vaccine_intent_se %>%
    add_row(
      covariate = c,
      se = pre_intent_plot(df_us_cleaned, c, 'Vaccine.Intent.for.self..Pre.', 'se')
    )
  pre_vaccine_intent_plots[[i]] <-
    pre_intent_plot(df_us_cleaned, c, 'Vaccine.Intent.for.self..Pre.', 'plot')
  i = i + 1
}
```

Imbalanced Covariates

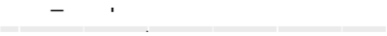
```
pre_vaccine_intent_se %>%
  filter(covariate %in% imbalanced_covariates) %>%
  ggplot(aes(x = reorder(covariate, se), y = se)) +
  geom_bar(stat = 'identity') +
  coord_flip() +
  theme(
    axis.title.y = element_blank()
  ) +
  labs(
    title='Skew of Imbalanced Covariates',
    y='Standard Deviation of Pre-Treatment Vaccine Intent'
  )
```



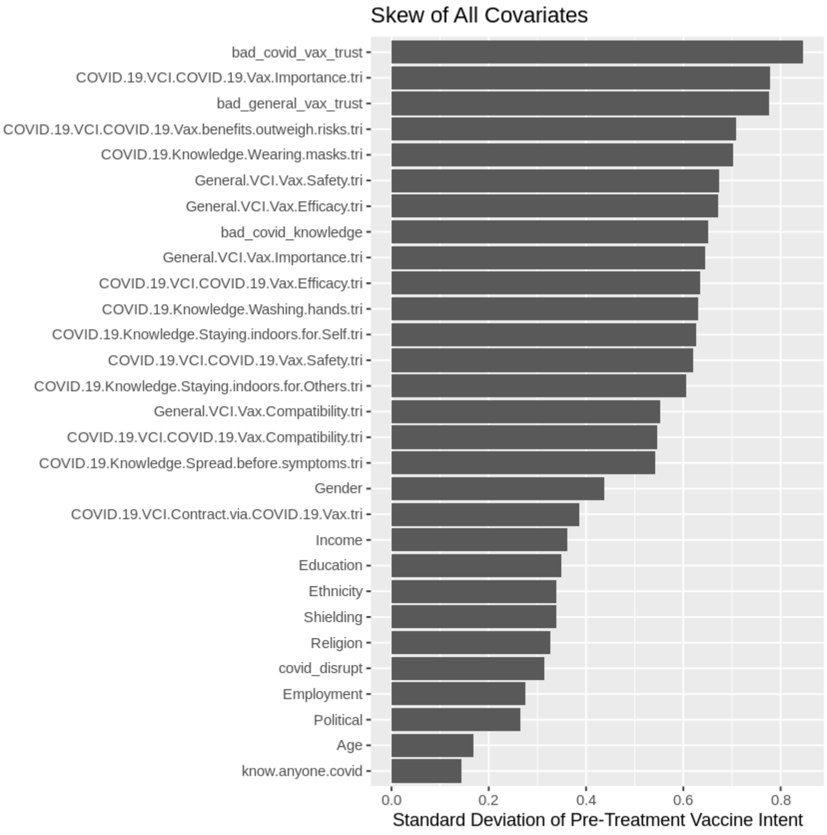
```
grid.arrange(grobs = pre_vaccine_intent_plots[c(1,2,4,7,14)], ncol = 2)
```



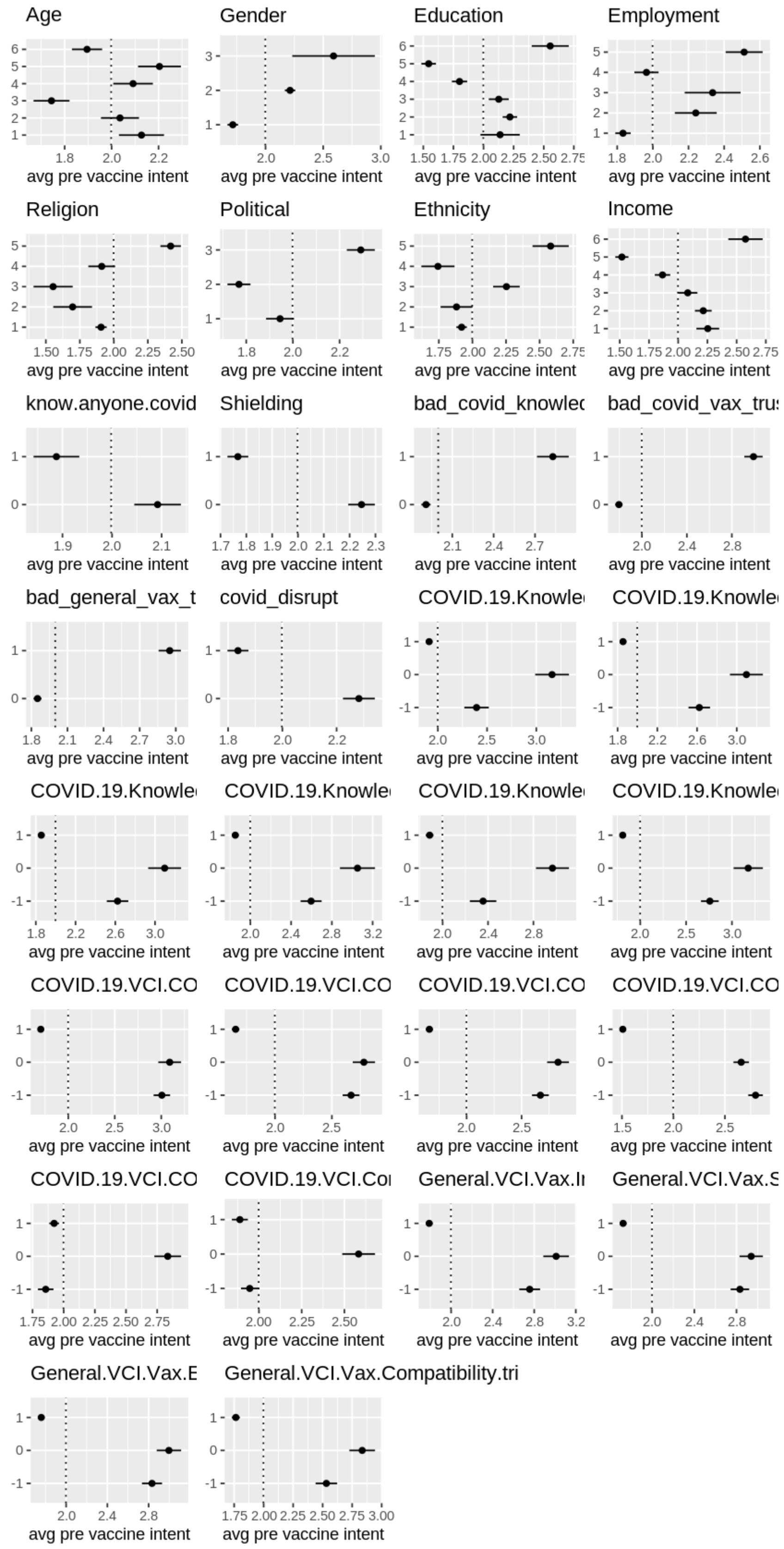
All Explored Covariates



```
pre_vaccine_intent_se %>%
  ggplot(aes(x = reorder(covariate, se), y = se)) +
  geom_bar(stat = 'identity') +
  coord_flip() +
  theme(
    axis.title.y = element_blank()
  ) +
  labs(
    title='Skew of All Covariates',
    y='Standard Deviation of Pre-Treatment Vaccine Intent'
  )
```



```
grid.arrange(grobs = pre_vaccine_intent_plots[1:16], ncol = 4)
grid.arrange(grobs = pre_vaccine_intent_plots[16:length(pre_vaccine_intent_plots)], ncol = 4)
```



Adjusting for Imbalance

Setup

```
df_adj_summary <- data.frame(
  method = character(),
  outcome = character(),
  estimate = double(),
  std_err = double(),
  p_val = double()
)
```

```
ttest <- function(df, method_name, Y, treatment, control, alternative = 'greater'){
   results <- t.test(
    treatment,
    control,
    alternative = alternative
  )

  df <- df %>%
    add_row(
      method = method_name,
      outcome = Y,
      estimate = results$estimate[1] - results$estimate[2],
      std_err = results$stderr,
      p_val = results$p.value
    )
  return(df)
}
```

Baseline

```
# SELF US
df_adj_summary <- ttest(
  df_adj_summary,
  method_name = 'FRT',
  Y = 'Vaccine_Intent_Self',
  treatment = filter(df_us_cleaned_removed_no_intent, Treatment == 1)$Vaccine.Intent.for.self
  control = filter(df_us_cleaned_removed_no_intent, Treatment == 0)$Vaccine.Intent.for.self..
  alternative = 'greater'
)
df_adj_summary
```

A data.frame: 1 × 5

method	outcome	estimate	std_err	p_val
<chr>	<chr>	<dbl>	<dbl>	<dbl>
FRT	Vaccine_Intent_Self	0.08659778	0.01302287	1.920301e-11

Regression Adjustment

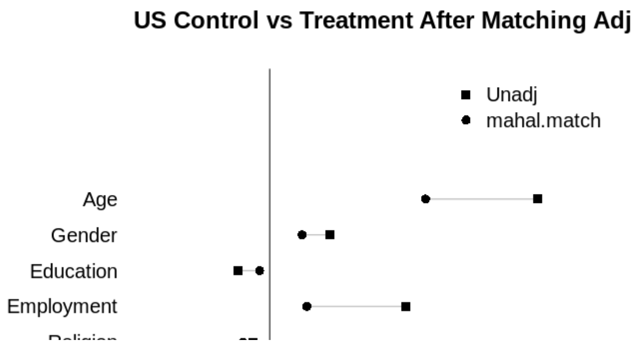
```
#### Prepare Dataset for doing Lin's estimator in US
df_us_Lin <- df_us_cleaned_removed_no_intent %>%
  select(
    c(
    'z',
    'Vaccine.Intent.for.self..Decrease',
    all_of(final_covariates)
    )
  )

#### Centralize covariates
lin_covariates <-
  subset(df_us_Lin, select = -c(z, Vaccine.Intent.for.self..Decrease))

lin_covariates_sub_mean = lin_covariates - colMeans(lin_covariates)
lin_adj_us = lm_robust(
  df_us_Lin$Vaccine.Intent.for.self..Decrease ~ df_us_Lin$z + . +
    df_us_Lin$z * . ,
  lin_covariates_sub_mean
)


df_adj_summary <- df_adj_summary %>%
    add_row(
      method = 'Lins Estimator',
      outcome = 'Vaccine_Intent_Self',
      estimate = lin_adj_us$coefficients['df_us_Lin$z'],
      std_err = lin_adj_us$std.error['df_us_Lin$z'],
      p_val = lin_adj_us$p.value['df_us_Lin$z']
    )
df_adj_summary
```

A data.frame: 2 × 5

method	outcome	estimate	std_err	p_val
<chr>	<chr>	<dbl>	<dbl>	<dbl>
FRT	Vaccine_Intent_Self	0.08659778	0.01302287	1.920301e-11
Lins Estimator	Vaccine_Intent_Self	0.07380057	0.03266724	2.393695e-02

Matching

```
matching_adj <- function(df,
                         covariates,
                         num_matches = 1,
                         match_from = 'control' # flip the z if matching from treatment, eg m
                         ){
  df$prop <-
    glm(
      as.formula(paste(ifelse(match_from == 'treatment', "inv_z ~", "z ~"), paste(covariates,
      family = binomial,
      data = df
    )$fitted.values

  mahal <- smahal(
      if(match_from == 'treatment'){df$inv_z} else{df$z},
      df[, covariates])

  mahal.match <- pairmatch(mahal, control = num_matches, data = df)
  match_summary <-
    summarize.match(df, mahal.match)
  p <- xBalance(
        as.formula(paste(paste("Treatment ~", paste(covariates, collapse = " + ")), '+ strata
        data = df
      )

  return_items <- list("summary" = match_summary, "mahal_match" = mahal.match, "xBalance" = p
  return(return_items)
}

match_results <- matching_adj(df_us_cleaned_removed_no_intent, final_covariates, num_matches


plot(match_results$xBalance,
  main="US Control vs Treatment After Matching Adj")
```



```
df_adj_summary <- ttest(
  df_adj_summary,
  method_name = 'matching',
  Y = 'Vaccine_Intent_Self',
  treatment = match_results$summary$Vaccine.Intent.for.self..Decrease.1,
  control = match_results$summary$Vaccine.Intent.for.self..Decrease.0,
  alternative = 'greater'
)
df_adj_summary
```

A data.frame: 3 × 5

method	outcome	estimate	std_err	p_val
<chr>	<chr>	<dbl>	<dbl>	<dbl>
FRT	Vaccine_Intent_Self	0.08659778	0.01302287	1.920301e-11
Lins Estimator	Vaccine_Intent_Self	0.07380057	0.03266724	2.393695e-02
matching	Vaccine_Intent_Self	0.07943925	0.01191567	1.530347e-11

▾ Placebo Benchmark

```
# train glm on the covariates (not depending on treatment at all)
glm_ber <- glm(as.formula(paste(
  "Vaccine.Intent.for.self..Decrease ~",
  paste(final_covariates, collapse = " + ")
)),
family = binomial,
data = df_us_cleaned)

# use trained glm to predict placebo Y's for full dataset
df_us_cleaned$placebo_y_prob <-
  predict(glm_ber, df_us_cleaned[, final_covariates], type = "response")
```

Baseline

```
df_adj_summary <- ttest(
  df_adj_summary,
  method_name = 'FRT',
  Y = 'Placebo_Y',
  treatment = filter(df_us_cleaned, Treatment == 1)$placebo_y_prob,
  control = filter(df_us_cleaned, Treatment == 0)$placebo_y_prob,
  alternative = 'two.sided'
)
df_adj_summary
```

A data.frame: 4 × 5

method	outcome	estimate	std_err	p_val
<chr>	<chr>	<dbl>	<dbl>	<dbl>
FRT	Vaccine_Intent_Self	0.086597782	0.013022871	1.920301e-11
Lins Estimator	Vaccine_Intent_Self	0.073800570	0.032667238	2.393695e-02
matching	Vaccine_Intent_Self	0.079439252	0.011915672	1.530347e-11
FRT	Placebo_Y	0.002514752	0.001380498	6.869553e-02

Lin's Estimator

```
placebo_lin_covariates <- df_us_cleaned[,final_covariates] - colMeans(df_us_cleaned[,final_cc

placebo_lin_fit <- lm_robust(df_us_cleaned$placebo_y_prob ~ df_us_cleaned$z + . +
          df_us_cleaned$z * . , placebo_lin_covariates)

df_adj_summary <- df_adj_summary %>%
    add_row(
      method = 'Lins Estimator',
      outcome = 'Placebo_Y',
      estimate = placebo_lin_fit$coefficients['df_us_cleaned$z'],
      std_err = placebo_lin_fit$std.error['df_us_cleaned$z'],
      p_val = placebo_lin_fit$p.value['df_us_cleaned$z']
    )
df_adj_summary
```

A data.frame: 5 × 5

method	outcome	estimate	std_err	p_val
FRT	Vaccine_Intent_Self	0.086597782	0.013022871	1.920301e-11

Matching

```
match_results_placebo <- matching_adj(df_us_cleaned,
                              final_covariates,
                              num_matches = 2,
                              match_from = 'treatment')

df_adj_summary <- ttest(
  df_adj_summary,
  method_name = 'matching',
  Y = 'Placebo_Y',
  treatment = match_results_placebo$summary$placebo_y_prob.1,
  control = match_results_placebo$summary$placebo_y_prob.0,
  alternative = 'two.sided'
)
df_adj_summary
```

A data.frame: 6 × 5

method	outcome	estimate	std_err	p_val
<chr>	<chr>	<dbl>	<dbl>	<dbl>
FRT	Vaccine_Intent_Self	0.0865977820	0.013022871	1.920301e-11
Lins Estimator	Vaccine_Intent_Self	0.0738005700	0.032667238	2.393695e-02
matching	Vaccine_Intent_Self	0.0794392523	0.011915672	1.530347e-11
FRT	Placebo_Y	0.0025147524	0.001380498	6.869553e-02
Lins Estimator	Placebo_Y	0.0093135764	0.005651380	9.942806e-02
matching	Placebo_Y	-0.0004977516	0.001179685	6.730946e-01

Summary Results

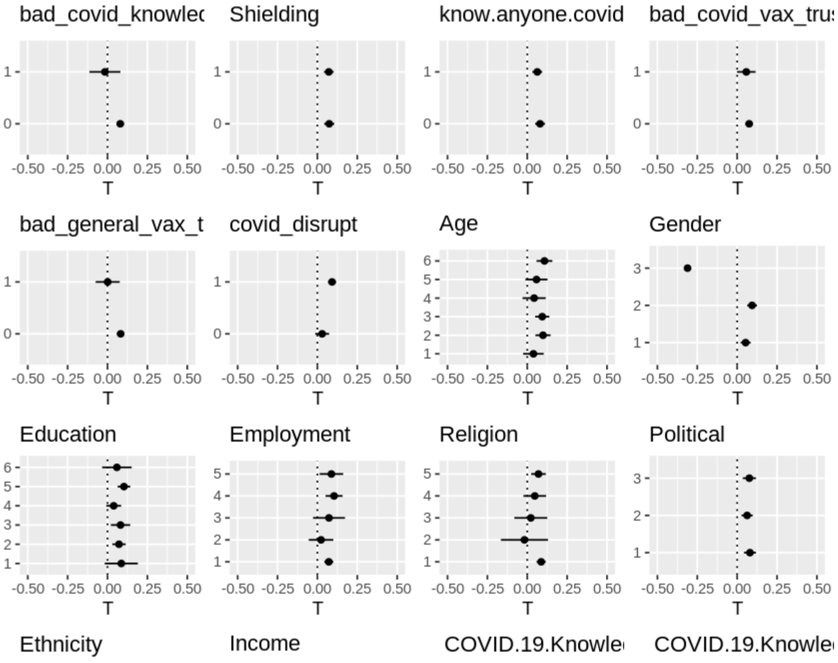
```
df_adj_summary %>%
  filter(outcome == 'Vaccine_Intent_Self')
```

A data.frame: 6 × 5

method	outcome	estimate	std_err	p_val
<chr>	<chr>	<dbl>	<dbl>	<dbl>
FRT	Vaccine_Intent_Self	0.0865977820	0.013022871	1.920301e-11
Lins Estimator	Vaccine_Intent_Self	0.0738005700	0.032667238	2.393695e-02
Lins Estimator	Placebo Y	0.0093135764	0.005651380	9.942806e-02

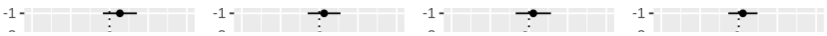
Heterogenous Treatment Effects

```
hte_plot <- function(df, group, y){
  lower_limit <- ifelse(y == 'NumMisinfoBelief', -1.25, -0.5)
  upper_limit <- ifelse(y == 'NumMisinfoBelief', 3.25, 0.5)

  group = sym(group)
  y = sym(y)

  p <- df %>%
    mutate(
      !!group := as.factor(!!group)
    ) %>%
    group_by(!!group, z) %>%
    summarize(
      .groups = 'keep',
      t = mean(!!y),
      v = var(!!y) / n()
    ) %>%
    pivot_wider(names_from = z, values_from = c(t, v)) %>%
    mutate(
      T = t_1 - t_0,
      var = v_0 + v_1,
      T_lower = T - 1.96 *sqrt(var),
      T_upper = T + 1.96*sqrt(var)
    ) %>%
    select(
      !!group, T, var, T_lower, T_upper
    ) %>%
    ggplot(aes(x=T, y = !!group, group = !!group)) +
    #draws the means
    # geom_point(position = position_dodge(1)) +
    geom_point() +
    #draws the CI error bars
    geom_errorbarh(
      aes(xmin = T_lower, xmax = T_upper),
          # color = !!group),
      show.legend = FALSE,
      height = 0
      # position = position_dodge(0.78)
    ) +
    xlim(lower_limit, upper_limit) +
    geom_vline(xintercept = 0, linetype="dotted") +
    ggtitle(group) +
    theme(axis.title.y=element_blank())

  return(p)
}

hte_plots_vaccine_intent_self <- list()
#hte_plots_vaccine_intent_others <- list()
#hte_plots_misinfo_belief <- list()

i = 1
for(c in detailed_covariates){
  hte_plots_vaccine_intent_self[[i]] <- (hte_plot(df_us_cleaned, c, 'Vaccine.Intent.for.self.
  #hte_plots_vaccine_intent_others[[i]] <- (hte_plot(df_us_cleaned, c, 'Vaccine.Intent.for.ot
  #hte_plots_misinfo_belief[[i]] <- (hte_plot(df_us_cleaned, c, 'NumMisinfoBelief'))
  i = i + 1
}

grid.arrange(grobs = hte_plots_vaccine_intent_self[1:16], ncol = 4)
grid.arrange(grobs = hte_plots_vaccine_intent_self[16:length(hte_plots_vaccine_intent_self)],
Warning message:
“Removed 1 rows containing missing values (geom_errorbarh).”
```



Appendix

Regression Adjustment for different Y



```
### Prepare Dataset for doing Lin's estimator in US
df_us_Lin_diffY <- df_us %>%
  mutate(


    Image.NumAgree = ((Image.1.Agreement > 0) + (Image.2.Agreement > 0) + (Image.3.Agreement
    Image.NumDontKnow = ((Image.1.Agreement == 0) + (Image.2.Agreement == 0) + (Image.3.Agree
    Image.NumDisagree = (5 - Image.NumAgree - Image.NumDontKnow),
    NumMisinfoBelief = Treatment*Image.NumAgree + (1-Treatment)*(Image.NumDisagree),
    MisinfoBeliever = NumMisinfoBelief > 1
  )

df_us_Lin_diffY <- df_us_Lin_diffY %>%
  select(
    Treatment,
    MisinfoBeliever,
    Age,
    Gender,
    Education,
    Employment,
    Religion,
    Political,
    Ethnicity,
    Income
  )

#### Centralize covariates
covariate <- subset(df_us_Lin_diffY, select=-c(Treatment, MisinfoBeliever))

covariate_sub_mean = covariate - colMeans(covariate)
fit_misinfo_us = lm_robust(df_us_Lin_diffY$MisinfoBeliever ~ df_us_Lin_diffY$Treatment + . +
          df_us_Lin_diffY$Treatment * . , covariate_sub_mean)

fit_misinfo_us
```

```
                                          Estimate  Std. Error     t value
(Intercept)                           0.1740396861 0.019694216  8.83709626
df_us_Lin_diffY$Treatment             0.1450791027 0.024768026  5.85751572
Age                                   0.0019454845 0.006695294  0.29057493
Gender                                0.0048258691 0.013019011  0.37067863
Education                            -0.0070584299 0.007794243 -0.90559528
Employment                            0.0114954266 0.008324136  1.38097543
Religion                              0.0072905918 0.006165036  1.18257086
Political                             0.0002926068 0.010903823  0.02683525
Ethnicity                             0.0031752055 0.007980987  0.39784622
Income                               -0.0129332051 0.006720612 -1.92440894
df_us_Lin_diffY$Treatment:Age        -0.0611937418 0.008410222 -7.27611521
df_us_Lin_diffY$Treatment:Gender     -0.0592343925 0.016061044 -3.68807865
df_us_Lin_diffY$Treatment:Education   0.0113309146 0.009528519  1.18915805
df_us_Lin_diffY$Treatment:Employment -0.0502178194 0.009683472 -5.18593109
df_us_Lin_diffY$Treatment:Religion   -0.0364020033 0.007597894 -4.79106513
df_us_Lin_diffY$Treatment:Political  -0.0533218053 0.013082245 -4.07589120
df_us_Lin_diffY$Treatment:Ethnicity   0.0041005302 0.009965155  0.41148686
```

Old Placebo Code

```
df us Lin diffY$Treatment            5.078078e-09  0.096519907  0.1936382982
```

Without covariate adjustment

```
Education                            3.652049e-01 -0.022339510  0.0082226498
```

```
df_us_cleaned_control <- df_us_cleaned[df_us_cleaned$Treatment == 0,]
df_us_cleaned_treatment <- df_us_cleaned[df_us_cleaned$Treatment == 1,]
#### fit bernoulli glm on control:
glm_ber <- glm(Vaccine.Intent.for.self..Decrease ~ Age + Gender + Education + Employment + Re
+ Political + Ethnicity + Income + know.anyone.covid + Shielding + bad_covid_knowledge + bad_
+ bad_general_vax_trust + covid_disrupt,
       family=binomial(link=logit),
       data=df_us_cleaned_control)

prob_control <- predict(glm_ber, df_us_cleaned_control[,final_covariates], type = "response"
fake_outcome_control <- rbernoulli(length(prob_control), p = prob_control)

prob_treatment <- predict(glm_ber, df_us_cleaned_treatment[,final_covariates], type = "respor
fake_outcome_treatment <- rbernoulli(length(prob_treatment), p = prob_treatment)

#### Compute difference in mean:
mean(fake_outcome_control) - mean(fake_outcome_treatment)
```

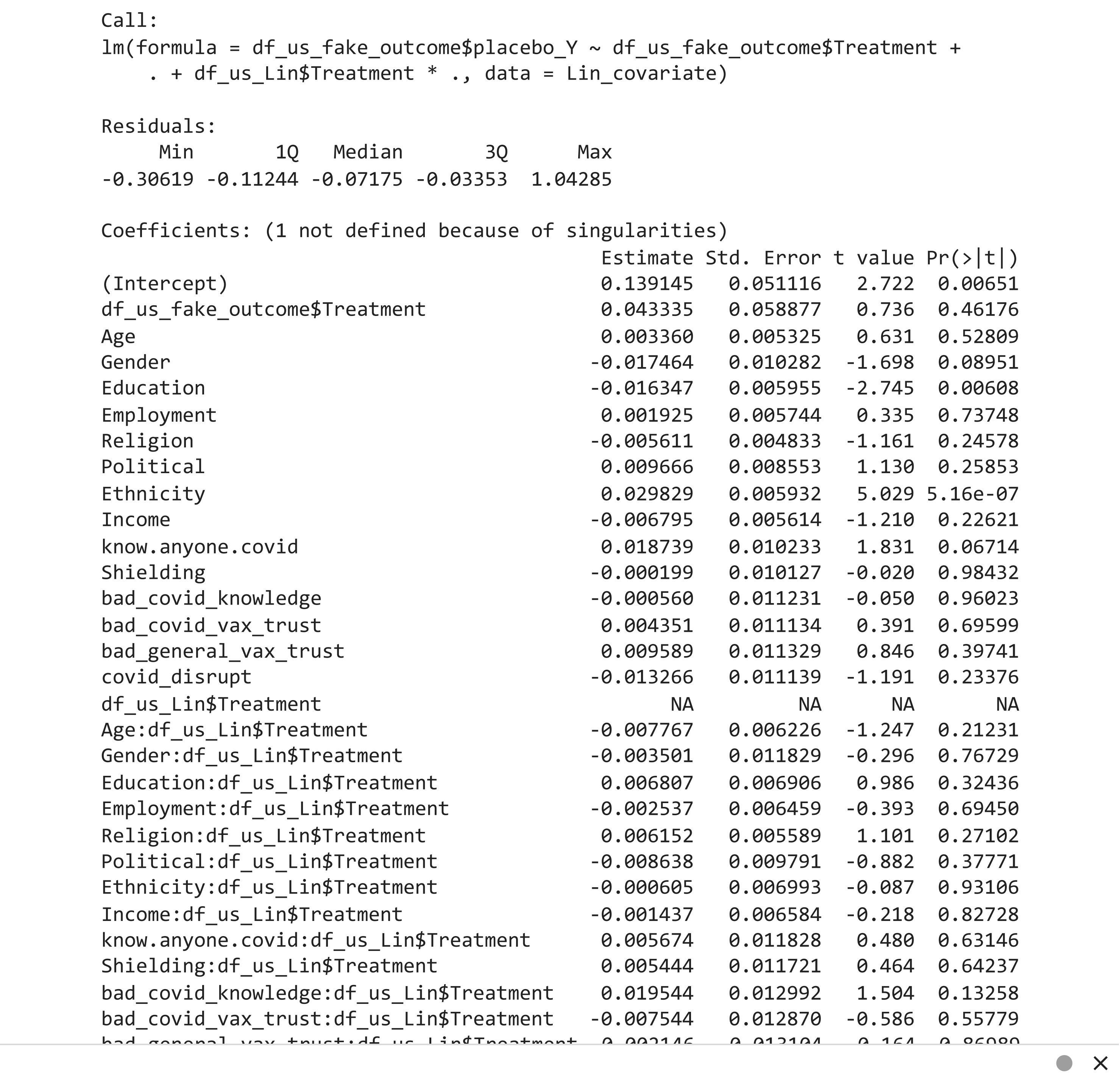
```
-0.00397034321892702
```

```
Ethnicity                            3983
```

With covariate adjustment

```
df us Lin diffY$Treatment:Gender     3983
```

```
# glm_ber_Lin <- glm(df_us_cleaned_control$Vaccine.Intent.for.self..Decrease ~
#        family=binomial(link=logit),
#        data=df_us_cleaned_control)

df_us_fake_outcome <- df_us_cleaned %>%
  mutate(
    placebo_Y <- c(fake_outcome_treatment, fake_outcome_control)
  )

Lin_covariate <- df_us_fake_outcome[,final_covariates] - colMeans(df_us_fake_outcome[,final_c

placebo_lin_fit= lm(df_us_fake_outcome$placebo_Y ~ df_us_fake_outcome$Treatment + . +
          df_us_Lin$Treatment * . , Lin_covariate)

summary(placebo_lin_fit)
```



```
Call:
lm(formula = df_us_fake_outcome$placebo_Y ~ df_us_fake_outcome$Treatment +
    . + df_us_Lin$Treatment * ., data = Lin_covariate)

Residuals:
     Min       1Q   Median       3Q      Max
-0.30619 -0.11244 -0.07175 -0.03353  1.04285

Coefficients: (1 not defined because of singularities)
                                           Estimate Std. Error t value Pr(>|t|)
(Intercept)                                0.139145   0.051116   2.722  0.00651
df_us_fake_outcome$Treatment               0.043335   0.058877   0.736  0.46176
Age                                        0.003360   0.005325   0.631  0.52809
Gender                                    -0.017464   0.010282  -1.698  0.08951
Education                                 -0.016347   0.005955  -2.745  0.00608
Employment                                 0.001925   0.005744   0.335  0.73748
Religion                                  -0.005611   0.004833  -1.161  0.24578
Political                                  0.009666   0.008553   1.130  0.25853
Ethnicity                                  0.029829   0.005932   5.029 5.16e-07
Income                                    -0.006795   0.005614  -1.210  0.22621
know.anyone.covid                          0.018739   0.010233   1.831  0.06714
Shielding                                 -0.000199   0.010127  -0.020  0.98432
bad_covid_knowledge                       -0.000560   0.011231  -0.050  0.96023
bad_covid_vax_trust                        0.004351   0.011134   0.391  0.69599
bad_general_vax_trust                      0.009589   0.011329   0.846  0.39741
covid_disrupt                             -0.013266   0.011139  -1.191  0.23376
df_us_Lin$Treatment                              NA         NA      NA       NA
Age:df_us_Lin$Treatment                   -0.007767   0.006226  -1.247  0.21231
Gender:df_us_Lin$Treatment                -0.003501   0.011829  -0.296  0.76729
Education:df_us_Lin$Treatment              0.006807   0.006906   0.986  0.32436
Employment:df_us_Lin$Treatment            -0.002537   0.006459  -0.393  0.69450
Religion:df_us_Lin$Treatment               0.006152   0.005589   1.101  0.27102
Political:df_us_Lin$Treatment             -0.008638   0.009791  -0.882  0.37771
Ethnicity:df_us_Lin$Treatment             -0.000605   0.006993  -0.087  0.93106
Income:df_us_Lin$Treatment                -0.001437   0.006584  -0.218  0.82728
know.anyone.covid:df_us_Lin$Treatment      0.005674   0.011828   0.480  0.63146
Shielding:df_us_Lin$Treatment              0.005444   0.011721   0.464  0.64237
bad_covid_knowledge:df_us_Lin$Treatment    0.019544   0.012992   1.504  0.13258
bad_covid_vax_trust:df_us_Lin$Treatment   -0.007544   0.012870  -0.586  0.55779
bad_general_vax_trust:df_us_Lin$Treatment  0.002146   0.013104   0.164  0.86989
```