CS112 Assignment 3, Spring 2021

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03/18/2021

A few important notes

Option 1 for submitting your assignment: *This method is actually preferred. This is an RMarkdown document. Did you know you can open this document in RStudio, edit it by adding your answers and code, and then knit it to a pdf? To submit your answers to this assignment, simply knit this file as a pdf and submit it as a pdf on Forum. All of your code must be included in the resulting pdf file, i.e., don't set echo = FALSE in any of your code chunks. This is a cheat sheet for using Rmarkdown. If you have questions about RMarkdown, please post them on Piazza. Try knitting this document in your RStudio. You should be able to get a pdf file. At any step, you can try knitting the document and recreate a pdf. If you get an error, you might have incomplete code.*

Option 2 for submitting your assignment: *If you are not comfortable with RMarkdown, you can also choose the Google Doc version of this assignment, make a copy of it and edit the Google doc (include your code, figures, results, and explanations) and at the end download your Google Doc as a pdf and submit the pdf file.*

Note: *Either way (if you use Rmd and knit as pdf OR if you use Google Doc and download as pdf) you should make sure you put your name on top of the document.*

Note: *The first time you run this document you may get an error that some packages don't exist. If you don't have the packages listed on top of this document, install them first and you won't get those errors.*

Note: *Don't change seed in the document. The function* `set.seed()` *has already been set at the beginning of this document to 928. Changing the see again to a different number will make your results not replicable.*

QUESTION 1: LEAD AND MORTALITY

Lead is a highly toxic metal that has really negative health outcomes, especially in young children. Unfortunately, traditionally lead has been used in paint in houses. Lead use in paint is now banned. In this exercise, you will be estimating the causal effect of lead on infant mortality based on data on 172 US cities in 1900 in the US. Read more about the data and the variables in it here and download the data by using the following package.

```
library(foreign)
main <- read.dta("https://wps.pearsoned.com/wps/media/objects/11422/11696965/data3eu/lead_mortality.dta
head(main)
```

```
##   year      city state      age hardness  ph   infrate typhoid_rate np_tub_rate
## 1 1900   Alameda    CA 28.95484       97 7.6 0.1097561   0.02439024 0.030487806
## 2 1900    Albany    NY 30.34768       43 7.3 0.2986185   0.04144527 0.013815090
## 3 1900 Allegheny    PA 27.08730      111 7.3 0.4468413   0.09399076 0.027734976
## 4 1900 Allentown    PA 27.76405      176 7.7 0.3841808   0.02824859 0.005649718
## 5 1900   Altoona    PA 27.03753      111 7.3 0.4678663   0.04370180 0.007712082
```

```
## 6 1900 Amsterdam    NY 28.60989       43 7.3 0.3062201   0.01435407 0.019138755
##    mom_rate population precipitation temperature lead foreign_share
## 1 0.1951219        164      1.850307    59.02617    0    0.19354838
## 2 0.1795962        941      3.278735    45.26791    1    0.18488371
## 3 0.1926040       1298      3.350943    48.97149    1    0.23730159
## 4 0.1977401        354      3.350943    48.97149    1    0.07865169
## 5 0.1825193        389      3.350943    48.97149    0    0.11260054
## 6 0.1626794        209      3.278735    45.26791    1    0.25274727
```

Specifically, the outcome variable is `infrate` and the treatment is `lead`.

STEP 1 Think about which one of the covariates in the data are relevant to your study and pick two of the most important ones. Specifically which ones are both correlated with the outcome and the treatment variable. Explain why these two variables made it to your list.

```
x =colnames(main)
y = c(x[4:15])
df = main[,y]
p = cor(df)
w = p[c(4,11),]
w
```

```
##                age   hardness         ph    infrate typhoid_rate np_tub_rate
## infrate -0.3993365 -0.3409013 -0.4832748 1.00000000    0.1807088   0.1714927
## lead    -0.1685794  0.2462254  0.1689401 0.06827977    0.1475322  -0.1390385
##            mom_rate population precipitation temperature       lead
## infrate  0.07033454 0.01160834     0.5076902   0.2175948 0.06827977
## lead    -0.06623375 0.13527625    -0.1006960   0.0861432 1.00000000
##         foreign_share
## infrate    0.20861505
## lead      -0.01542208
```

The variable I choose is age and precipitation because firstly they are correlated variables. The precipitation has the highest correlation with infrate. Also, the age has high correlation with infrate. In addition, I am interested in the child mortality versus mother's age because I did hear that the older the mother, the harder it is for her to give birth and at the same time, the child is less healthy than average children. It is not scientific informaton but still the assumption that I heard. Therefore, I included that variable here.

STEP 2 Are the two variables you picked in the step above balanced across the treatment and control groups? You can use any R function from any package to check this (for instance, you can check the cobalt package). You can also use the `MatchBalance()` function. Show your data visualization and explain.

Note: *This is optional but you can use the* ***gridExtra*** *package and its* ***grid.arrange()*** *function to put all the 4 graphs in one 2 x 2 graph. Read more about the package and how to use it here: https://cran.r-project.org/web/packages/egg/vignettes/Ecosystem.html. Set* ***nrow = 2****.*

```
# Your code here
MatchBalance(lead~age+precipitation,data=main)
```

```
##
## ***** (V1) age *****
## before matching:
## mean treatment........ 27.449
## mean control.......... 28.248
## std mean diff......... -35.472
##
```

```
## mean raw eQQ diff..... 0.88441
## med  raw eQQ diff..... 0.86823
## max  raw eQQ diff..... 2.41
##
## mean eCDF diff........ 0.10283
## med  eCDF diff........ 0.10645
## max  eCDF diff........ 0.2028
##
## var ratio (Tr/Co)..... 1.2017
## T-test p-value........ 0.022944
## KS Bootstrap p-value.. 0.068
## KS Naive p-value...... 0.092155
## KS Statistic.......... 0.2028
##
##
## ***** (V2) precipitation *****
## before matching:
## mean treatment........ 3.2888
## mean control.......... 3.4134
## std mean diff......... -20.881
##
## mean raw eQQ diff..... 0.16727
## med  raw eQQ diff..... 0.13831
## max  raw eQQ diff..... 0.8957
##
## mean eCDF diff........ 0.071693
## med  eCDF diff........ 0.030925
## max  eCDF diff........ 0.25066
##
## var ratio (Tr/Co)..... 1.2485
## T-test p-value........ 0.17219
## KS Bootstrap p-value.. 0.008
## KS Naive p-value...... 0.018166
## KS Statistic.......... 0.25066
##
##
## Before Matching Minimum p.value: 0.008
## Variable Name(s): precipitation  Number(s): 2
```

```
covs <- subset(main, select = c(age, precipitation))
#bal.tab(covs, treat = main$lead)
```

The balance of two covariates among two groups are very different. We can look at the p-value. The p-value for age is roughly less than 0.1 and the p-value for precipitation is also very small. The lower the p-value, the more unbalanced the distribution of the variates among two groups.

STEP 3 Write code that would simply calculate the Prima Facie treatment effect in the data above. What's the Prima Facie treatment effect?

```
# Your code here
#get the treatment group
treatgroup <- main[which(main$lead==1),]
#get the control group
controlgroup <- main[which(main$lead==0),]
#calculate the mean of outcome for treatment and control group (observational group)
```

```
mean(treatgroup$infrate) - mean(controlgroup$infrate)
```

```
## [1] 0.02208973
```

STEP 4 Explain why the Prima Facie effect is not the true average causal effect.

The true causal effect is measured when we see both outcomes at the same time. For instance, to measure the causal effect of treatment(taking medicine) for A, we need to observe the outcome of A both when he takes the medicine and when he does not take medicine. However, we never observe both outcomes in reality. We only observe one outcome.

The Prima Facie effect is what calculated above. You subtract and take the difference between two groups for the outcome. Those people in both groups are different people. So, we do not measure or have any concrete result about the treatment effect (lead). As they are different people in both groups, the control group might have very different distribution of covariates resulting from selection bias.

To calculate the average causal effect, we need to make sure that the distribution of covariates is similar for both groups. This is ensured when we use RCT due to randomization. So the distribution of covariates on average is balanced. Also, we can use other methods to calculate true causal effect after balancing between control and treatement groups (for observational study).

STEP 5 Use the two covariates that you identified in Step 1 above and use propensity score matching to create better balance across the two groups. Are the two variables you picked in the step above balanced across the treatment and control groups after propensity score matching? You can use any R function from any package to check this (for instance, you can check the cobalt package). You can also use the `MatchBalance()` function. Show your data visualization and explain.

Note: *This is optional but you can use the* ***gridExtra*** *package and its* ***grid.arrange()*** *function to put all the 4 graphs in one 2 x 2 graph. Read more about the package and how to use it here: https://cran.r-project.org/web/packages/egg/vignettes/Ecosystem.html. Set* ***nrow = 2****.*

```
# Your code here
#create a model to calculate propensity score
glm= glm(lead~age+precipitation,data =main,family = binomial)

#create another column called ps and use the model above to get the score for the column
main$ps <- predict(glm,type="response")

#use Match function to match both groups based on the propensity score
match_result <- Match(Y=main$infrate,Tr=main$lead,X=main$ps,M=1)

#Use MatchBalance to measure the balance between matched data.
mb  <- MatchBalance(lead~age+ precipitation, data=main, match.out=match_result)
```

```
##
## ***** (V1) age *****
##                        Before Matching        After Matching
## mean treatment........     27.449             27.449
## mean control..........     28.248             27.321
## std mean diff.........    -35.472             5.6725
##
## mean raw eQQ diff.....    0.88441            0.43524
## med  raw eQQ diff.....    0.86823            0.31016
## max  raw eQQ diff.....       2.41               2.41
##
```

```
## mean eCDF diff........    0.10283          0.039401
## med  eCDF diff........    0.10645          0.033898
## max  eCDF diff........     0.2028           0.12712
##
## var ratio (Tr/Co).....     1.2017            1.2377
## T-test p-value........   0.022944            0.4615
## KS Bootstrap p-value..       0.05             0.252
## KS Naive p-value......   0.092155           0.29616
## KS Statistic..........     0.2028           0.12712
##
##
## ***** (V2) precipitation *****
##                         Before Matching        After Matching
## mean treatment........     3.2888             3.2888
## mean control..........     3.4134              3.401
## std mean diff.........    -20.881            -18.795
##
## mean raw eQQ diff.....    0.16727            0.14105
## med  raw eQQ diff.....    0.13831           0.085197
## max  raw eQQ diff.....     0.8957             0.8957
##
## mean eCDF diff........   0.071693           0.055984
## med  eCDF diff........   0.030925           0.025424
## max  eCDF diff........    0.25066            0.20339
##
## var ratio (Tr/Co).....     1.2485             1.4284
## T-test p-value........    0.17219            0.10178
## KS Bootstrap p-value..      0.004              0.004
## KS Naive p-value......   0.018166           0.015173
## KS Statistic..........    0.25066            0.20339
##
##
## Before Matching Minimum p.value: 0.004
## Variable Name(s): precipitation  Number(s): 2
##
## After Matching Minimum p.value: 0.004
## Variable Name(s): precipitation  Number(s): 2
```

```
#see the summary of mb- balance of matched data and match_result
summary(mb)
```

```
##                     Length Class  Mode
## BeforeMatching      2      -none- list
## AfterMatching       2      -none- list
## BMsmallest.p.value  1      -none- numeric
## BMsmallestVarName   1      -none- character
## BMsmallestVarNumber 1      -none- numeric
## AMsmallest.p.value  1      -none- numeric
## AMsmallestVarName   1      -none- character
## AMsmallestVarNumber 1      -none- numeric
```

```
summary(match_result)
```

```
##
## Estimate...  -0.049769
```

```
## AI SE......  0.041291
## T-stat.....  -1.2053
## p.val......  0.22808
##
## Original number of observations..............  172
## Original number of treated obs...............  117
## Matched number of observations...............  117
## Matched number of observations  (unweighted).  118
```

For the age covariate, the propensity score helps to improve the balance between two groups. We can test by looking at the p-score after matching. T-test p-value of age goes up from 0.022944 to 0.4615. However, for the precipitation covariate, the propensity score does not help to improve the balance.

STEP 6

What is the treatment effect after propensity score matching?

The treatment effect after propensity score matching is -0.049769. The p-value is bigger than 0.05, therefore, the treatment effect is not statistically significant, which indicates that the treatment- lead- has little effect on the outcome variable.

STEP 7 Use any package to perform sensitivity analysis on the matched units using Rosenbaum's method. What is the critical value of the parameter gamma (i.e., the gamma for which statistical significance goes away)? Does this imply that your treatment effect is sensitive? Explain!

```
# Your code here
library('rbounds')
```

```
## Warning: package 'rbounds' was built under R version 4.0.4
```

```
psens(match_result,Gamma=1.5,GammaInc=.1)
```

```
##
##  Rosenbaum Sensitivity Test for Wilcoxon Signed Rank P-Value
##
## Unconfounded estimate ....  0.0063
##
##  Gamma Lower bound Upper bound
##    1.0      0.0063      0.0063
##    1.1      0.0016      0.0203
##    1.2      0.0004      0.0502
##    1.3      0.0001      0.1012
##    1.4      0.0000      0.1748
##    1.5      0.0000      0.2675
##
##  Note: Gamma is Odds of Differential Assignment To
##  Treatment Due to Unobserved Factors
##
```

The critical value of the parameter gamma is 1.2, it is when the p value of upper bound is larger than 0.05. It implies that the treatment effect is sensitive to hidden biases because at the level of gamma is 1.2, pretty low gamma level. The result is already not significant. So, we can say that we have not statistically significant results.

STEP 8 Use the two covariates that you identified in Step 1 above and use genetic matching (multivariate distance matching, i.e., matching on the variables) to try to create better balance across the two groups. Are the two variables you picked in the step above balanced across the treatment and control groups after genetic matching? You can use any R function from any package to check this (for instance, you can check the cobalt package). You can also use the `MatchBalance()` function. Show your data visualization and explain.

Note: *This is optional but you can use the* ***gridExtra*** *package and its* ***grid.arrange()*** *function to put all the 4 graphs in one 2 x 2 graph. Read more about the package and how to use it here: https://cran.r-project.org/web/packages/egg/vignettes/Ecosystem.html. Set* ***nrow = 2****.*

Note: *In the matching assignment, you may find that the Genetic Matching step takes a while. If you have to reduce pop.size to e.g., 10 or 16 to ensure it stops after only an hour or two, that's fine. Running your computer for an hour or two is a good thing. Running it for a full day or more is unnecessary overkill (and if this is your situation, change hyperparameters like pop.size to reduce run-time). For example, we suggest you modify the pop.size (e.g., you can set it to 20, 30, etc.!), max.generations (set it to 10, 20 etc.!), and wait.generations (set it to 2, 5, etc.!) and that should expedite things.*

```
# Your code here
attach(main)
```

```
## The following object is masked from package:tidyr:
##
##     population
```

```
#outcome variable
Y <- main$infrate
#treatment variable
Tr <- main$lead
#covariates
X <- cbind(main$age,main$precipitation)
#genetic matching to find optimal weights/scales.
genout <- GenMatch(Tr = Tr, X = X,max.generations = 100,wait.generations = 5,pop.size = 100)
```

```
## Loading required namespace: rgenoud
```

```
##
##
## Thu Apr 08 14:30:36 2021
## Domains:
##  0.000000e+00   <=  X1   <=    1.000000e+03
##  0.000000e+00   <=  X2   <=    1.000000e+03
##
## Data Type: Floating Point
## Operators (code number, name, population)
##  (1) Cloning.....................  15
##  (2) Uniform Mutation............  12
##  (3) Boundary Mutation...........  12
##  (4) Non-Uniform Mutation........  12
##  (5) Polytope Crossover..........  12
##  (6) Simple Crossover............  12
##  (7) Whole Non-Uniform Mutation..  12
##  (8) Heuristic Crossover.........  12
##  (9) Local-Minimum Crossover.....  0
##
## SOFT Maximum Number of Generations: 100
## Maximum Nonchanging Generations: 5
## Population size       : 100
```

```
## Convergence Tolerance: 1.000000e-03
##
## Not Using the BFGS Derivative Based Optimizer on the Best Individual Each Generation.
## Not Checking Gradients before Stopping.
## Using Out of Bounds Individuals.
##
## Maximization Problem.
## GENERATION: 0 (initializing the population)
## Lexical Fit..... 3.409931e-01  3.548040e-01  7.862280e-01  7.862280e-01
## #unique......... 100, #Total UniqueCount: 100
## var 1:
## best............ 6.527786e+02
## mean............ 5.385620e+02
## variance........ 8.216224e+04
## var 2:
## best............ 2.694355e+02
## mean............ 4.820760e+02
## variance........ 8.958860e+04
##
## GENERATION: 1
## Lexical Fit..... 3.409931e-01  3.548040e-01  7.862280e-01  7.862280e-01
## #unique......... 64, #Total UniqueCount: 164
## var 1:
## best............ 6.527786e+02
## mean............ 6.721032e+02
## variance........ 3.057804e+04
## var 2:
## best............ 2.694355e+02
## mean............ 3.353476e+02
## variance........ 4.920579e+04
##
## GENERATION: 2
## Lexical Fit..... 3.409931e-01  3.548040e-01  7.862280e-01  7.862280e-01
## #unique......... 68, #Total UniqueCount: 232
## var 1:
## best............ 6.527786e+02
## mean............ 6.435759e+02
## variance........ 1.850818e+04
## var 2:
## best............ 2.694355e+02
## mean............ 2.977376e+02
## variance........ 1.510685e+04
##
## GENERATION: 3
## Lexical Fit..... 3.409931e-01  3.548040e-01  7.862280e-01  7.862280e-01
## #unique......... 59, #Total UniqueCount: 291
## var 1:
## best............ 6.527786e+02
## mean............ 6.488569e+02
## variance........ 1.742497e+04
## var 2:
## best............ 2.694355e+02
## mean............ 2.983642e+02
## variance........ 1.807687e+04
```

```
##
## GENERATION: 4
## Lexical Fit..... 3.409931e-01  3.548040e-01  7.862280e-01  7.862280e-01
## #unique......... 56, #Total UniqueCount: 347
## var 1:
## best............ 6.527786e+02
## mean............ 6.492073e+02
## variance........ 6.792589e+03
## var 2:
## best............ 2.694355e+02
## mean............ 2.996154e+02
## variance........ 1.276970e+04
##
## GENERATION: 5
## Lexical Fit..... 3.409931e-01  3.548040e-01  7.862280e-01  7.862280e-01
## #unique......... 57, #Total UniqueCount: 404
## var 1:
## best............ 6.527786e+02
## mean............ 6.495686e+02
## variance........ 8.107406e+03
## var 2:
## best............ 2.694355e+02
## mean............ 2.889946e+02
## variance........ 1.043028e+04
##
## GENERATION: 6
## Lexical Fit..... 3.409931e-01  3.548040e-01  7.862280e-01  7.862280e-01
## #unique......... 58, #Total UniqueCount: 462
## var 1:
## best............ 6.527786e+02
## mean............ 6.580603e+02
## variance........ 1.712426e+04
## var 2:
## best............ 2.694355e+02
## mean............ 2.863352e+02
## variance........ 5.927309e+03
##
## 'wait.generations' limit reached.
## No significant improvement in 5 generations.
##
## Solution Lexical Fitness Value:
## 3.409931e-01  3.548040e-01  7.862280e-01  7.862280e-01
##
## Parameters at the Solution:
##
##  X[ 1] : 6.527786e+02
##  X[ 2] : 2.694355e+02
##
## Solution Found Generation 1
## Number of Generations Run 6
##
## Thu Apr 08 14:30:38 2021
## Total run time : 0 hours 0 minutes and 2 seconds
```

```r
#match based on the optimal weights found above
mout <- Match(Y=Y,Tr = Tr, X = X, Weight.matrix = genout)
#summary of matching
summary(mout)
```

```
##
## Estimate...  0.0052926
## AI SE......  0.025371
## T-stat.....  0.20861
## p.val......  0.83475
##
## Original number of observations..............  172
## Original number of treated obs...............  117
## Matched number of observations...............  117
## Matched number of observations  (unweighted).  117
```

```r
mout$index.treated
```

```
##   [1]   2   3   4   6   8  15  16  17  20  21  23  24  27  29  30  31  32  33
##  [19]  34  35  36  38  39  40  41  46  47  51  53  54  56  57  58  59  60  61
##  [37]  63  64  66  67  68  69  70  71  72  74  75  76  77  79  80  81  82  84
##  [55]  86  87  89  93  94  95  96  97  99 100 101 102 103 105 107 109 110 111
##  [73] 112 114 116 117 118 119 120 121 123 125 127 128 129 130 131 132 133 134
##  [91] 135 136 137 138 140 141 142 144 145 146 147 148 149 150 152 154 155 156
## [109] 158 160 162 163 165 167 169 171 172
```

```r
mout$index.control
```

```
##   [1] 126   5  28  10 164  49  90  90 143  98  44  73 159  85  50  44 153  19
##  [19] 104  44  28 164 104   1  52  14  18   7  28 166 151  90 164  18 166  49
##  [37]  90  49  43  45  73  22 139  44  52 139  98 143  90  52  11 170  90 164
##  [55]  90  52   9 164 161  90 108  90   9  62  44  44 159  73   9 161  90  12
##  [73]  73 106  91 108 113  85  45  44   9   7  10  28 106 157  19  78 164   5
##  [91]  73  26  10  73  52  44  52  52 139  85  10  90  73  91 104   9  52  19
## [109] 104  43  90  11 159 161  18 104  90
```

```r
mout$weights
```

```
##   [1] 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
##  [38] 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
##  [75] 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
## [112] 1 1 1 1 1 1
```

```r
#check balance after matching
Mb2 = MatchBalance(lead ~age+precipitation , match.out = mout)
```

```
##
## ***** (V1) age *****
##                           Before Matching        After Matching
## mean treatment........     27.449             27.449
## mean control..........     28.248             27.501
## std mean diff.........    -35.472            -2.2905
##
## mean raw eQQ diff.....    0.88441            0.26349
## med  raw eQQ diff.....    0.86823            0.17318
## max  raw eQQ diff.....       2.41               2.41
##
```

```
## mean eCDF diff........    0.10283           0.024874
## med  eCDF diff........    0.10645           0.017094
## max  eCDF diff........     0.2028            0.08547
##
## var ratio (Tr/Co).....     1.2017             1.2303
## T-test p-value........   0.022944            0.34099
## KS Bootstrap p-value..      0.062              0.718
## KS Naive p-value......   0.092155            0.78623
## KS Statistic..........     0.2028            0.08547
##
##
## ***** (V2) precipitation *****
##                         Before Matching        After Matching
## mean treatment........     3.2888             3.2888
## mean control..........     3.4134              3.312
## std mean diff.........    -20.881            -3.8867
##
## mean raw eQQ diff.....    0.16727            0.10214
## med  raw eQQ diff.....    0.13831           0.023246
## max  raw eQQ diff.....     0.8957             0.8957
##
## mean eCDF diff........   0.071693           0.032375
## med  eCDF diff........   0.030925           0.034188
## max  eCDF diff........    0.25066            0.08547
##
## var ratio (Tr/Co).....     1.2485             1.7291
## T-test p-value........    0.17219             0.3548
## KS Bootstrap p-value..      0.002              0.558
## KS Naive p-value......   0.018166            0.78623
## KS Statistic..........    0.25066            0.08547
##
##
## Before Matching Minimum p.value: 0.002
## Variable Name(s): precipitation  Number(s): 2
##
## After Matching Minimum p.value: 0.34099
## Variable Name(s): age  Number(s): 1
```

```
summary(Mb2)
```

```
##                     Length Class  Mode
## BeforeMatching      2      -none- list
## AfterMatching       2      -none- list
## BMsmallest.p.value  1      -none- numeric
## BMsmallestVarName   1      -none- character
## BMsmallestVarNumber 1      -none- numeric
## AMsmallest.p.value  1      -none- numeric
## AMsmallestVarName   1      -none- character
## AMsmallestVarNumber 1      -none- numeric
```

After genetic matching, the age variable has the following result: T-test p-value..... 0.022944 0.34099 KS Bootstrap p-value.. 0.062 0.718 KS Naive p-value..... 0.092155 0.78623

Before matching, the p-value is small, which means there is a huge difference between the distribution of age among two groups. After matching, p-value becomes much larger, which means that there is an increase in the balance between the distribution of variable age among two groups.

After the genetic, the precipitation variable has the following result: T-test p-value..... 0.17219 0.3548 KS Bootstrap p-value.. 0.002 0.558 KS Naive p-value..... 0.018166 0.78623

Before matching, the p-value is small, which means there is a huge difference between the distribution of variable precipitation among two groups. After matching, p-value becomes much larger, which means that there is an increase in the balance between the distribution of variable precipitation among two groups.

STEP 9 Demonstrate that you know how to perform matching within a narrow caliper (1e-2) caliper on one of the variables and a wide caliper (1e5) on the other one by repeating your analysis from the previous step.

```
#outcome variable
Y <- main$infrate
#treatment variable
Tr <- main$lead
#coveriates to match on
X <- cbind(main$age,main$precipitation)
#find optimal weights
genout <- GenMatch(Tr = Tr, X = X, replace = FALSE,max.generations = 100,wait.generations = 5,pop.size =
```

```
## Warning in GenMatch(Tr = Tr, X = X, replace = FALSE, max.generations = 100, :
## replace==FALSE, but there are more (weighted) treated obs than control obs. Some
## treated obs will not be matched. You may want to estimate ATC instead.
```

```
##
##
## Thu Apr 08 14:30:38 2021
## Domains:
##  0.000000e+00   <=  X1   <=    1.000000e+03
##  0.000000e+00   <=  X2   <=    1.000000e+03
##
## Data Type: Floating Point
## Operators (code number, name, population)
##  (1) Cloning.....................  15
##  (2) Uniform Mutation............  12
##  (3) Boundary Mutation...........  12
##  (4) Non-Uniform Mutation........  12
##  (5) Polytope Crossover..........  12
##  (6) Simple Crossover............  12
##  (7) Whole Non-Uniform Mutation..  12
##  (8) Heuristic Crossover.........  12
##  (9) Local-Minimum Crossover.....  0
##
## SOFT Maximum Number of Generations: 100
## Maximum Nonchanging Generations: 5
## Population size       : 100
## Convergence Tolerance: 1.000000e-03
##
## Not Using the BFGS Derivative Based Optimizer on the Best Individual Each Generation.
## Not Checking Gradients before Stopping.
## Using Out of Bounds Individuals.
##
## Maximization Problem.
## GENERATION: 0 (initializing the population)
## Lexical Fit..... 5.434409e-04  9.157989e-03  3.344789e-02  9.258026e-02
```

```
## #unique..... 100, #Total UniqueCount: 100
## var 1:
## best..... 7.974721e+02
## mean..... 5.138065e+02
## variance..... 8.068736e+04
## var 2:
## best..... 2.033883e+02
## mean..... 4.823751e+02
## variance..... 7.920175e+04
##
## GENERATION: 1
## Lexical Fit..... 5.434409e-04  9.157989e-03  3.344789e-02  9.258026e-02
## #unique..... 65, #Total UniqueCount: 165
## var 1:
## best..... 7.974721e+02
## mean..... 7.329019e+02
## variance..... 3.169862e+04
## var 2:
## best..... 2.033883e+02
## mean..... 2.266121e+02
## variance..... 1.767018e+04
##
## GENERATION: 2
## Lexical Fit..... 5.434409e-04  9.157989e-03  3.344789e-02  9.258026e-02
## #unique..... 64, #Total UniqueCount: 229
## var 1:
## best..... 7.974721e+02
## mean..... 7.595585e+02
## variance..... 2.057617e+04
## var 2:
## best..... 2.033883e+02
## mean..... 2.406200e+02
## variance..... 1.290289e+04
##
## GENERATION: 3
## Lexical Fit..... 5.434409e-04  9.157989e-03  3.344789e-02  9.258026e-02
## #unique..... 57, #Total UniqueCount: 286
## var 1:
## best..... 7.974721e+02
## mean..... 7.717237e+02
## variance..... 1.427134e+04
## var 2:
## best..... 2.033883e+02
## mean..... 2.565902e+02
## variance..... 2.170315e+04
##
## GENERATION: 4
## Lexical Fit..... 5.434409e-04  9.157989e-03  3.344789e-02  9.258026e-02
## #unique..... 58, #Total UniqueCount: 344
## var 1:
## best..... 7.974721e+02
## mean..... 7.817644e+02
## variance..... 1.213439e+04
## var 2:
```

```
## best..... 2.033883e+02
## mean..... 2.461689e+02
## variance..... 1.933112e+04
##
## GENERATION: 5
## Lexical Fit..... 5.442294e-04  3.344789e-02  4.345468e-02  9.258026e-02
## #unique..... 59, #Total UniqueCount: 403
## var 1:
## best..... 7.974721e+02
## mean..... 7.857375e+02
## variance..... 4.525148e+03
## var 2:
## best..... 3.529754e+00
## mean..... 2.326730e+02
## variance..... 1.339690e+04
##
## GENERATION: 6
## Lexical Fit..... 5.442294e-04  3.344789e-02  4.345468e-02  9.258026e-02
## #unique..... 64, #Total UniqueCount: 467
## var 1:
## best..... 7.974721e+02
## mean..... 7.747197e+02
## variance..... 1.428398e+04
## var 2:
## best..... 3.529754e+00
## mean..... 1.509859e+02
## variance..... 1.837358e+04
##
## GENERATION: 7
## Lexical Fit..... 5.443974e-04  3.344789e-02  4.338936e-02  9.258026e-02
## #unique..... 56, #Total UniqueCount: 523
## var 1:
## best..... 6.910468e+02
## mean..... 7.585720e+02
## variance..... 1.627123e+04
## var 2:
## best..... 3.529754e+00
## mean..... 7.333752e+01
## variance..... 2.495620e+04
##
## GENERATION: 8
## Lexical Fit..... 5.443974e-04  3.344789e-02  4.338936e-02  9.258026e-02
## #unique..... 59, #Total UniqueCount: 582
## var 1:
## best..... 6.910468e+02
## mean..... 6.601153e+02
## variance..... 1.995933e+04
## var 2:
## best..... 3.529754e+00
## mean..... 2.687119e+01
## variance..... 4.997237e+03
##
## GENERATION: 9
## Lexical Fit..... 5.443974e-04  3.344789e-02  4.338936e-02  9.258026e-02
```

```
## #unique......... 58, #Total UniqueCount: 640
## var 1:
## best............ 6.910468e+02
## mean............ 6.326088e+02
## variance........ 1.754840e+04
## var 2:
## best............ 3.529754e+00
## mean............ 5.315603e+01
## variance........ 2.310549e+04
##
## GENERATION: 10
## Lexical Fit..... 5.655368e-04  2.615226e-02  3.344789e-02  9.258026e-02
## #unique......... 61, #Total UniqueCount: 701
## var 1:
## best............ 1.807446e+02
## mean............ 6.416587e+02
## variance........ 1.668258e+04
## var 2:
## best............ 3.529754e+00
## mean............ 4.390970e+01
## variance........ 1.419133e+04
##
## GENERATION: 11
## Lexical Fit..... 5.655368e-04  2.615226e-02  3.344789e-02  9.258026e-02
## #unique......... 63, #Total UniqueCount: 764
## var 1:
## best............ 1.807446e+02
## mean............ 4.460758e+02
## variance........ 6.519161e+04
## var 2:
## best............ 3.529754e+00
## mean............ 5.754367e+01
## variance........ 3.039542e+04
##
## 'wait.generations' limit reached.
## No significant improvement in 5 generations.
##
## Solution Lexical Fitness Value:
## 5.655368e-04  2.615226e-02  3.344789e-02  9.258026e-02
##
## Parameters at the Solution:
##
##  X[ 1] : 1.807446e+02
##  X[ 2] : 3.529754e+00
##
## Solution Found Generation 5
## Number of Generations Run 11
##
## Thu Apr 08 14:30:41 2021
## Total run time : 0 hours 0 minutes and 3 seconds
```

```
#match based on optimal weights
#mout <- Match(Y=Y,Tr = Tr, X = X, replace = FALSE, Weight.matrix = genout,caliper =c(1e-2,1e5) )
```

```
#change the caliper so we can see the result with respect to different caliper.
mout3 <- Match(Y=Y,Tr = Tr, X = X, replace = FALSE, Weight.matrix = genout,caliper =1e5)
```

```
## Warning in Match(Y = Y, Tr = Tr, X = X, replace = FALSE, Weight.matrix =
## genout, : replace==FALSE, but there are more (weighted) treated obs than control
## obs. Some treated obs will not be matched. You may want to estimate ATC instead.
```

```
mout4 <- Match(Y=Y,Tr = Tr, X = X, replace = FALSE, Weight.matrix = genout,caliper = 1e-2)
```

```
## Warning in Match(Y = Y, Tr = Tr, X = X, replace = FALSE, Weight.matrix =
## genout, : replace==FALSE, but there are more (weighted) treated obs than control
## obs. Some treated obs will not be matched. You may want to estimate ATC instead.
```

STEP 10 Discuss your results in a paragraph, providing results. Explain how one could use the "exact" option (in Match) to accomplish almost the same thing as you accomplished with "caliper".

```
summary(mout3)
```

```
##
## Estimate...  0.021955
## SE.........  0.026106
## T-stat.....  0.841
## p.val......  0.40035
##
## Original number of observations..............  172
## Original number of treated obs...............  117
## Matched number of observations...............  55
## Matched number of observations  (unweighted).  55
##
## Caliper (SDs)........................................   1e+05 1e+05
## Number of obs dropped by 'exact' or 'caliper'  62
```

```
summary(mout4)
```

```
##
## Estimate...  0.057061
## SE.........  0.049192
## T-stat.....  1.16
## p.val......  0.24606
##
## Original number of observations..............  172
## Original number of treated obs...............  117
## Matched number of observations...............  3
## Matched number of observations  (unweighted).  3
##
## Caliper (SDs)........................................   0.01 0.01
## Number of obs dropped by 'exact' or 'caliper'  114
```

```
print("First Matching")
```

```
## [1] "First Matching"
```

```
result1 <- MatchBalance(lead ~age+precipitation , data = main, match.out = mout3)
```

```
##
## ***** (V1) age *****
##                        Before Matching        After Matching
```

```
## mean treatment........     27.449              27.2
## mean control..........     28.248             28.248
## std mean diff.........    -35.472              -49.6
##
## mean raw eQQ diff.....    0.88441             1.0485
## med  raw eQQ diff.....    0.86823            0.99786
## max  raw eQQ diff.....       2.41             1.9525
##
## mean eCDF diff........    0.10283            0.12377
## med  eCDF diff........    0.10645            0.12727
## max  eCDF diff........     0.2028            0.23636
##
## var ratio (Tr/Co).....     1.2017             1.0583
## T-test p-value........   0.022944         0.00056554
## KS Bootstrap p-value..       0.07              0.068
## KS Naive p-value......   0.092155            0.09258
## KS Statistic..........     0.2028            0.23636
##
##
## ***** (V2) precipitation *****
##                         Before Matching        After Matching
## mean treatment........     3.2888             3.2322
## mean control..........     3.4134             3.4134
## std mean diff.........    -20.881            -30.849
##
## mean raw eQQ diff.....    0.16727            0.19437
## med  raw eQQ diff.....    0.13831            0.15741
## max  raw eQQ diff.....     0.8957            0.66868
##
## mean eCDF diff........   0.071693           0.096552
## med  eCDF diff........   0.030925           0.036364
## max  eCDF diff........    0.25066            0.27273
##
## var ratio (Tr/Co).....     1.2485             1.2086
## T-test p-value........    0.17219            0.026152
## KS Bootstrap p-value..      0.008               0.018
## KS Naive p-value......   0.018166            0.033448
## KS Statistic..........    0.25066            0.27273
##
##
## Before Matching Minimum p.value: 0.008
## Variable Name(s): precipitation  Number(s): 2
##
## After Matching Minimum p.value: 0.00056554
## Variable Name(s): age  Number(s): 1
```

```
summary(result1)
```

```
##                     Length Class  Mode
## BeforeMatching      2      -none- list
## AfterMatching       2      -none- list
## BMsmallest.p.value  1      -none- numeric
## BMsmallestVarName   1      -none- character
## BMsmallestVarNumber 1      -none- numeric
## AMsmallest.p.value  1      -none- numeric
```

```
## AMsmallestVarName   1      -none- character
## AMsmallestVarNumber 1      -none- numeric
```

```
print("Second matching")
```

```
## [1] "Second matching"
```

```
result2 <- MatchBalance(lead ~age+precipitation , data = main, match.out = mout4)
```

```
##
## ***** (V1) age *****
##                          Before Matching        After Matching
## mean treatment........     27.449             27.912
## mean control.........     28.248             27.915
## std mean diff.........    -35.472           -0.17282
##
## mean raw eQQ diff.....    0.88441           0.011143
## med  raw eQQ diff.....    0.86823           0.013611
## max  raw eQQ diff.....       2.41           0.014868
##
## mean eCDF diff........    0.10283            0.16667
## med  eCDF diff........    0.10645            0.16667
## max  eCDF diff........     0.2028            0.33333
##
## var ratio (Tr/Co).....     1.2017             0.9786
## T-test p-value........   0.022944            0.79006
## KS Bootstrap p-value..        0.1               0.98
## KS Naive p-value......   0.092155                  1
## KS Statistic..........     0.2028            0.33333
##
##
## ***** (V2) precipitation *****
##                          Before Matching        After Matching
## mean treatment........     3.2888             3.362
## mean control.........     3.4134             3.362
## std mean diff.........    -20.881                 0
##
## mean raw eQQ diff.....    0.16727                 0
## med  raw eQQ diff.....    0.13831                 0
## max  raw eQQ diff.....     0.8957                 0
##
## mean eCDF diff........   0.071693                 0
## med  eCDF diff........   0.030925                 0
## max  eCDF diff........    0.25066                 0
##
## var ratio (Tr/Co).....     1.2485                 1
## T-test p-value........    0.17219                 1
## KS Bootstrap p-value..      0.002                 1
## KS Naive p-value......   0.018166                 1
## KS Statistic..........    0.25066                 0
##
##
## Before Matching Minimum p.value: 0.002
## Variable Name(s): precipitation  Number(s): 2
##
```

```
## After Matching Minimum p.value: 0.79006
## Variable Name(s): age  Number(s): 1
```

When we use a large caliper (1e5), we get more matches from the control group for the treated units. In our case, 55 matches. The larger caliper, the higher the level of tolerance for differences between the covariates of treatment and control units when matching. In this case, the p-value after matching is very small, which means that the covariates are not balanced.

However, when we use a small caliper (1e-2) we get much fewer matches (3). The caliper determines how similar the algorithm needs the control unit to be to a treated unit before we can get a match.

Exact matching means that for a match to be made, the control unit must have exact values for the covariates as a treated unit.A very small caliper (maybe 1e-7) would leave little room for difference and would be virtually the same as exact matching.I do not know if we can set caliper to 0, but this would probably be the setting for an exact match.

The exact option is the same when we set the caliper to super small. In that case, the matched data would only consist of almost identical units.

STEP 11 What is the treatment effect after genetic matching? The first result: 0.0052926 With caliper 1e5: 0.022 With caliper 1e-2: 0.057

STEP 12 Use any package to perform sensitivity analysis on the matched units using Rosenbaum's method. What is the critical value of the parameter gamma (i.e., the gamma for which statistical significance goes away)? Does this imply that your treatment effect is sensitive? Explain!

```
# Your code here

print("Table1 with genetic matching")
```

```
## [1] "Table1 with genetic matching"
```

```
psens(mout,Gamma=1.5,GammaInc=0.05)
```

```
##
##  Rosenbaum Sensitivity Test for Wilcoxon Signed Rank P-Value
##
## Unconfounded estimate ....  0.3902
##
##  Gamma Lower bound Upper bound
##   1.00      0.3902      0.3902
##   1.05      0.3058      0.4801
##   1.10      0.2337      0.5669
##   1.15      0.1746      0.6469
##   1.20      0.1278      0.7180
##   1.25      0.0917      0.7791
##   1.30      0.0647      0.8299
##   1.35      0.0450      0.8712
##   1.40      0.0308      0.9039
##   1.45      0.0208      0.9293
##   1.50      0.0139      0.9486
##
##  Note: Gamma is Odds of Differential Assignment To
##  Treatment Due to Unobserved Factors
##
```

```
print("Table2 with genetic matching using caliper 1e5")
```

```
## [1] "Table2 with genetic matching using caliper 1e5"
```

```
psens(mout3,Gamma=1.5,GammaInc=0.05)
```

```
##
##  Rosenbaum Sensitivity Test for Wilcoxon Signed Rank P-Value
##
## Unconfounded estimate ....  0.2254
##
##  Gamma Lower bound Upper bound
##   1.00      0.2254      0.2254
##   1.05      0.1810      0.2753
##   1.10      0.1440      0.3273
##   1.15      0.1137      0.3803
##   1.20      0.0891      0.4332
##   1.25      0.0694      0.4851
##   1.30      0.0538      0.5351
##   1.35      0.0414      0.5828
##   1.40      0.0318      0.6277
##   1.45      0.0243      0.6694
##   1.50      0.0185      0.7079
##
##  Note: Gamma is Odds of Differential Assignment To
##  Treatment Due to Unobserved Factors
##
```

```
print("Table3 with genetic matching caliper 1e-2")
```

```
## [1] "Table3 with genetic matching caliper 1e-2"
```

```
psens(mout4,Gamma=1.5,GammaInc=0.05)
```

```
##
##  Rosenbaum Sensitivity Test for Wilcoxon Signed Rank P-Value
##
## Unconfounded estimate ....  0.1425
##
##  Gamma Lower bound Upper bound
##   1.00      0.1425      0.1425
##   1.05      0.1338      0.1514
##   1.10      0.1258      0.1602
##   1.15      0.1182      0.1687
##   1.20      0.1113      0.1769
##   1.25      0.1047      0.1850
##   1.30      0.0987      0.1929
##   1.35      0.0930      0.2006
##   1.40      0.0877      0.2081
##   1.45      0.0827      0.2154
##   1.50      0.0780      0.2225
##
##  Note: Gamma is Odds of Differential Assignment To
##  Treatment Due to Unobserved Factors
##
```

With the first genetic matching, the result shows that the treatment is sensitive because with the low level of gamma, 1.0, the upper bound of p-value is much larger than 0.05. Therefore, we can conclude that the treatment is sensitive. Also, our finding is not statistically significant.

With the second genetic matching using caliper of 1e5, we also say that the result is sensitive because with the low level of gamma, 1.0, the upper bound of p-value is much larger than 0.05. Therefore, we can conclude that the treatment is sensitive. Also, our finding is not statistically significant.

With the third genetic matching using caliper of 1e-2, we also say that the result is sensitive because with the low level of gamma, 1.0, the upper bound of p-value is much larger than 0.05. Therefore, we can conclude that the treatment is sensitive. Also, our finding is not statistically significant.

STEP 13 Summarize the three treatment effects you found (including the prima facie treatment effect) here. - Prima Facie treatment effect: 0.02208973 - Propensity score matching treatment effect: -0.049769 - Genetic Matching treatment effect: 0.0052926

STEP 14 Explain which matching method creates better balance across your two covariates.

Genetic Matching is the better method in this case. When we evaluate which method that creates better balance among two covariates, we look at the p-value before and after matching of two covariates.

For the propensity score, the age variable's p score after matching is: t-test p-value: 0.252 KS Bootstrap p-value: 0.29616 KS Naive p-value: 0.12712.

For the propensity score, the precipitation variable's p-value after matching is: T-test p-value : 0.10178 KS Bootstrap p-value: 0.004 KS Naive p-value. . . . . :0.015173

In contrast, the genetic matching generates different p-values after matching: For the age variable: T-test p-value: 0.34099 KS Bootstrap p-value: 0.718 KS Naive p-value: 0.78623

for the precipitation variable:

T-test p-value: 0.003024 KS Bootstrap p-value: 0.02 KS Naive p-value: 0.033448

Looking at the result, we can see that genetic matching is doing a better job at balancing the covariate age because the p-value after matching for covariate age is higher compared to p-value of covariate age using propensity score.

The p-value represents how balanced the covariates are. Normally, recalling the null hypothesis. When the p value is large, it means that there is no difference. When p-value is smaller than 0.05, we say that we can reject the null hypothesis that there is not difference. The p-value in matching is the same.

The higher p-value, the more similar the covariates between two groups(control and treatment group), meaning the more balanced the covariate. With balanced covariates, it means that the differences between two groups in terms of the covariate is not that much. Therefore, the selection bias is reduced.

The lower p-value, the more different the covariates between two groups. It means that the distribution of covariates are not balanced.

QUESTION 2

Load the "Matching" library, and then run the GerberGreenImai demo by typing:

```
library("Matching")
demo(GerberGreenImai)
```

```
##
##
##  demo(GerberGreenImai)
```

```
##  ---- ~~~~~~~~~~~~~~~
##
## > #
## > # Gerber, Alan S. and Donald P. Green. 2000. "The Effects of Canvassing, Telephone Calls, and
## > # Direct Mail on Voter Turnout: A Field Experiment." American Political Science Review 94: 653-663
## > #
## > # Imai, Kosuke. 2005. "Do Get-Out-The-Vote Calls Reduce Turnout? The Importance of
## > # Statistical Methods for Field Experiments".  American Political Science Review 99: 283-300.
## > #
## >
## > set.seed(10391)
##
## > data(GerberGreenImai)
##
## > #replication of Imai's propensity score matching model
## > pscore.glm<-glm(PHN.C1 ~ PERSONS + VOTE96.1 + NEW + MAJORPTY + AGE +
## +                 WARD + PERSONS:VOTE96.1 + PERSONS:NEW + AGE2,
## +                 family=binomial(logit), data=GerberGreenImai)
##
## > D<-GerberGreenImai$PHN.C1 #treatment phone calls
##
## > Y<-GerberGreenImai$VOTED98 #outcome, turnout
##
## > cat("\nTHIS MODEL FAILS TO BALANCE AGE\n")
##
## THIS MODEL FAILS TO BALANCE AGE
##
## > X  <- fitted(pscore.glm)
##
## > #propensity score matching estimator
## > r1  <- Match(Y=Y, Tr=D, X=X, M=3)
##
## > summary(r1)
##
## Estimate...  0.056143
## AI SE......  0.03244
## T-stat.....  1.7307
## p.val......  0.083505
##
## Original number of observations..............  10829
## Original number of treated obs...............  247
## Matched number of observations...............  247
## Matched number of observations  (unweighted).  4638
##
##
## > #check for balance before and after matching
## > mb1  <- MatchBalance(PHN.C1 ~ AGE + AGE2 + PERSONS + VOTE96.1 + NEW + MAJORPTY +
## +                      WARD + I(PERSONS*VOTE96.1) + I(PERSONS*NEW), match.out=r1,
## +                      data=GerberGreenImai)
##
## ***** (V1) AGE *****
##                        Before Matching        After Matching
## mean treatment........     58.308             58.308
## mean control..........     49.425             58.642
```

```
## std mean diff.........     44.752           -1.6835
##
## mean raw eQQ diff.....     8.9231              1.18
## med  raw eQQ diff.....          9                 1
## max  raw eQQ diff.....         19                 7
##
## mean eCDF diff........     0.1114           0.014937
## med  eCDF diff........    0.11774           0.010349
## max  eCDF diff........     0.2229           0.056274
##
## var ratio (Tr/Co).....     1.1228             0.9957
## T-test p-value........ 2.8173e-11            0.75534
## KS Bootstrap p-value.. < 2.22e-16         < 2.22e-16
## KS Naive p-value...... 7.6768e-11         8.3617e-07
## KS Statistic..........     0.2229           0.056274
##
##
## ***** (V2) AGE2 *****
##                         Before Matching        After Matching
## mean treatment........     37.921             37.921
## mean control..........     27.937             38.329
## std mean diff.........     44.468            -1.8158
##
## mean raw eQQ diff.....     10.019             1.1526
## med  raw eQQ diff.....       7.85               1.03
## max  raw eQQ diff.....      23.37              12.95
##
## mean eCDF diff........     0.1114           0.014937
## med  eCDF diff........    0.11774           0.010349
## max  eCDF diff........     0.2229           0.056274
##
## var ratio (Tr/Co).....       1.22            0.95603
## T-test p-value........ 3.5657e-11            0.72991
## KS Bootstrap p-value.. < 2.22e-16         < 2.22e-16
## KS Naive p-value...... 7.6768e-11         8.3617e-07
## KS Statistic..........     0.2229           0.056274
##
##
## ***** (V3) PERSONS *****
##                         Before Matching        After Matching
## mean treatment........     1.5182             1.5182
## mean control..........     1.5021             1.5063
## std mean diff.........     3.2235             2.3855
##
## mean raw eQQ diff.....   0.016194          0.0097025
## med  raw eQQ diff.....          0                  0
## max  raw eQQ diff.....          1                  1
##
## mean eCDF diff........  0.0080698          0.0048512
## med  eCDF diff........  0.0080698          0.0048512
## max  eCDF diff........    0.01614          0.0097025
##
## var ratio (Tr/Co).....     1.0027            0.99883
## T-test p-value........    0.61693            0.76319
```

```
##
##
## ***** (V4) VOTE96.1 *****
##                         Before Matching        After Matching
## mean treatment........    0.71255           0.71255
## mean control..........    0.53081           0.70365
## std mean diff.........     40.076            1.9617
##
## mean raw eQQ diff.....    0.18219         0.0099181
## med  raw eQQ diff.....          0                 0
## max  raw eQQ diff.....          1                 1
##
## mean eCDF diff........   0.090872          0.004959
## med  eCDF diff........   0.090872          0.004959
## max  eCDF diff........    0.18174         0.0099181
##
## var ratio (Tr/Co).....    0.82568           0.98224
## T-test p-value........ 2.0709e-09           0.78369
##
##
## ***** (V5) NEW *****
##                         Before Matching        After Matching
## mean treatment........    0.11336           0.11336
## mean control..........    0.20129           0.11609
## std mean diff.........    -27.677          -0.86004
##
## mean raw eQQ diff.....   0.089069          0.022208
## med  raw eQQ diff.....          0                 0
## max  raw eQQ diff.....          1                 1
##
## mean eCDF diff........   0.043962          0.011104
## med  eCDF diff........   0.043962          0.011104
## max  eCDF diff........   0.087925          0.022208
##
## var ratio (Tr/Co).....    0.62766           0.97948
## T-test p-value........ 2.7138e-05           0.91226
##
##
## ***** (V6) MAJORPTY *****
##                         Before Matching        After Matching
## mean treatment........    0.80162           0.80162
## mean control..........    0.74476           0.77714
## std mean diff.........     14.231            6.1256
##
## mean raw eQQ diff.....    0.05668          0.004959
## med  raw eQQ diff.....          0                 0
## max  raw eQQ diff.....          1                 1
##
## mean eCDF diff........   0.028432         0.0024795
## med  eCDF diff........   0.028432         0.0024795
## max  eCDF diff........   0.056864          0.004959
##
## var ratio (Tr/Co).....    0.83988            0.9182
## T-test p-value........   0.028254           0.45981
```

```
##
##
## ***** (V7) WARD3 *****
##                          Before Matching        After Matching
## mean treatment........   0.012146          0.012146
## mean control..........   0.025799          0.010816
## std mean diff.........    -12.439            1.2117
##
## mean raw eQQ diff.....   0.016194         0.0051746
## med  raw eQQ diff.....          0                 0
## max  raw eQQ diff.....          1                 1
##
## mean eCDF diff........  0.0068264         0.0025873
## med  eCDF diff........  0.0068264         0.0025873
## max  eCDF diff........   0.013653         0.0051746
##
## var ratio (Tr/Co).....    0.47929            1.1215
## T-test p-value........   0.057321           0.88578
##
##
## ***** (V8) WARD4 *****
##                          Before Matching        After Matching
## mean treatment........  0.0080972         0.0080972
## mean control..........   0.022113          0.010098
## std mean diff.........    -15.608           -2.2279
##
## mean raw eQQ diff.....   0.016194         0.0092712
## med  raw eQQ diff.....          0                 0
## max  raw eQQ diff.....          1                 1
##
## mean eCDF diff........  0.0070079         0.0046356
## med  eCDF diff........  0.0070079         0.0046356
## max  eCDF diff........   0.014016         0.0092712
##
## var ratio (Tr/Co).....    0.37289           0.80349
## T-test p-value........   0.018007           0.80933
##
##
## ***** (V9) WARD5 *****
##                          Before Matching        After Matching
## mean treatment........   0.016194          0.016194
## mean control..........     0.0189          0.010364
## std mean diff.........    -2.1392            4.6101
##
## mean raw eQQ diff.....  0.0040486        0.00064683
## med  raw eQQ diff.....          0                 0
## max  raw eQQ diff.....          1                 1
##
## mean eCDF diff........  0.0013528        0.00032342
## med  eCDF diff........  0.0013528        0.00032342
## max  eCDF diff........  0.0027057        0.00064683
##
## var ratio (Tr/Co).....    0.86262            1.5534
## T-test p-value........    0.74035           0.56994
```

```
##
##
## ***** (V10) WARD6 *****
##                        Before Matching        After Matching
## mean treatment........   0.020243          0.020243
## mean control..........   0.041108          0.022823
## std mean diff.........    -14.785           -1.8285
##
## mean raw eQQ diff.....   0.024291          0.014877
## med  raw eQQ diff.....          0                 0
## max  raw eQQ diff.....          1                 1
##
## mean eCDF diff........   0.010432         0.0074386
## med  eCDF diff........   0.010432         0.0074386
## max  eCDF diff........   0.020865          0.014877
##
## var ratio (Tr/Co).....    0.50515           0.88929
## T-test p-value........   0.023887           0.83806
##
##
## ***** (V11) WARD7 *****
##                        Before Matching        After Matching
## mean treatment........   0.012146          0.012146
## mean control..........   0.031847          0.012251
## std mean diff.........    -17.949         -0.095498
##
## mean raw eQQ diff.....   0.020243         0.0012937
## med  raw eQQ diff.....          0                 0
## max  raw eQQ diff.....          1                 1
##
## mean eCDF diff........  0.0098504        0.00064683
## med  eCDF diff........  0.0098504        0.00064683
## max  eCDF diff........   0.019701         0.0012937
##
## var ratio (Tr/Co).....    0.39069           0.99155
## T-test p-value........   0.006539            0.9902
##
##
## ***** (V12) WARD8 *****
##                        Before Matching        After Matching
## mean treatment........    0.02834           0.02834
## mean control..........    0.03402           0.02208
## std mean diff.........    -3.4159            3.7647
##
## mean raw eQQ diff.....  0.0080972         0.0090556
## med  raw eQQ diff.....          0                 0
## max  raw eQQ diff.....          1                 1
##
## mean eCDF diff........    0.00284         0.0045278
## med  eCDF diff........    0.00284         0.0045278
## max  eCDF diff........    0.00568         0.0090556
##
## var ratio (Tr/Co).....    0.84127            1.2753
## T-test p-value........    0.59687           0.64774
```

```
##
##
## ***** (V13) WARD9 *****
##                         Before Matching        After Matching
## mean treatment........   0.036437          0.036437
## mean control..........   0.036572          0.036173
## std mean diff.........  -0.071523           0.14083
##
## mean raw eQQ diff.....          0         0.0073307
## med  raw eQQ diff.....          0                 0
## max  raw eQQ diff.....          0                 1
##
## mean eCDF diff........ 6.7145e-05         0.0036654
## med  eCDF diff........ 6.7145e-05         0.0036654
## max  eCDF diff........ 0.00013429         0.0073307
##
## var ratio (Tr/Co).....     1.0004             1.007
## T-test p-value........    0.99114           0.98703
##
##
## ***** (V14) WARD10 *****
##                         Before Matching        After Matching
## mean treatment........   0.064777          0.064777
## mean control..........   0.042714            0.0572
## std mean diff.........     8.9458            3.0724
##
## mean raw eQQ diff.....   0.020243          0.013799
## med  raw eQQ diff.....          0                 0
## max  raw eQQ diff.....          1                 1
##
## mean eCDF diff........   0.011032         0.0068995
## med  eCDF diff........   0.011032         0.0068995
## max  eCDF diff........   0.022063          0.013799
##
## var ratio (Tr/Co).....     1.4875            1.1234
## T-test p-value........    0.16422           0.69738
##
##
## ***** (V15) WARD11 *****
##                         Before Matching        After Matching
## mean treatment........   0.076923          0.076923
## mean control..........    0.04262          0.081194
## std mean diff.........     12.847           -1.5994
##
## mean raw eQQ diff.....   0.032389         0.0062527
## med  raw eQQ diff.....          0                 0
## max  raw eQQ diff.....          1                 1
##
## mean eCDF diff........   0.017152         0.0031263
## med  eCDF diff........   0.017152         0.0031263
## max  eCDF diff........   0.034304         0.0062527
##
## var ratio (Tr/Co).....     1.7471            0.95181
## T-test p-value........   0.045949           0.83068
```

```
##
##
## ***** (V16) WARD12 *****
##                         Before Matching        After Matching
## mean treatment........   0.036437          0.036437
## mean control..........   0.034398           0.04132
## std mean diff.........     1.0861           -2.6005
##
## mean raw eQQ diff.....          0          0.0032342
## med  raw eQQ diff.....          0                  0
## max  raw eQQ diff.....          0                  1
##
## mean eCDF diff........  0.0010196          0.0016171
## med  eCDF diff........  0.0010196          0.0016171
## max  eCDF diff........  0.0020392          0.0032342
##
## var ratio (Tr/Co).....     1.0612            0.88632
## T-test p-value........    0.86605            0.76452
##
##
## ***** (V17) WARD13 *****
##                         Before Matching        After Matching
## mean treatment........   0.040486          0.040486
## mean control..........   0.041108          0.040446
## std mean diff.........    -0.3148          0.020252
##
## mean raw eQQ diff.....  0.0040486          0.022208
## med  raw eQQ diff.....          0                  0
## max  raw eQQ diff.....          1                  1
##
## mean eCDF diff........ 0.00031086          0.011104
## med  eCDF diff........ 0.00031086          0.011104
## max  eCDF diff........ 0.00062171          0.022208
##
## var ratio (Tr/Co).....    0.98943             1.0009
## T-test p-value........    0.96104            0.99801
##
##
## ***** (V18) WARD14 *****
##                         Before Matching        After Matching
## mean treatment........   0.024291          0.024291
## mean control..........   0.036194          0.018969
## std mean diff.........    -7.7153             3.4501
##
## mean raw eQQ diff.....   0.012146          0.0097025
## med  raw eQQ diff.....          0                  0
## max  raw eQQ diff.....          1                  1
##
## mean eCDF diff........   0.005951          0.0048512
## med  eCDF diff........   0.005951          0.0048512
## max  eCDF diff........   0.011902          0.0097025
##
## var ratio (Tr/Co).....    0.68214             1.2736
## T-test p-value........    0.23421            0.68269
```

```
##
##
## ***** (V19) WARD15 *****
##                        Before Matching        After Matching
## mean treatment........   0.032389          0.032389
## mean control..........   0.031091          0.034104
## std mean diff.........     0.7318          -0.96678
##
## mean raw eQQ diff.....          0         0.00086244
## med  raw eQQ diff.....          0                  0
## max  raw eQQ diff.....          0                  1
##
## mean eCDF diff........ 0.00064907         0.00043122
## med  eCDF diff........ 0.00064907         0.00043122
## max  eCDF diff........  0.0012981         0.00086244
##
## var ratio (Tr/Co).....     1.0445             0.9514
## T-test p-value........    0.90953            0.91296
##
##
## ***** (V20) WARD16 *****
##                        Before Matching        After Matching
## mean treatment........   0.020243          0.020243
## mean control..........    0.02268          0.023083
## std mean diff.........     -1.727           -2.0123
##
## mean raw eQQ diff.....  0.0040486          0.0015093
## med  raw eQQ diff.....          0                  0
## max  raw eQQ diff.....          1                  1
##
## mean eCDF diff........  0.0012186         0.00075464
## med  eCDF diff........  0.0012186         0.00075464
## max  eCDF diff........  0.0024371          0.0015093
##
## var ratio (Tr/Co).....    0.89832            0.87953
## T-test p-value........    0.78894            0.82277
##
##
## ***** (V21) WARD17 *****
##                        Before Matching        After Matching
## mean treatment........   0.076923          0.076923
## mean control..........    0.04725           0.08248
## std mean diff.........     11.113           -2.0812
##
## mean raw eQQ diff.....    0.02834          0.0066839
## med  raw eQQ diff.....          0                  0
## max  raw eQQ diff.....          1                  1
##
## mean eCDF diff........   0.014837          0.003342
## med  eCDF diff........   0.014837          0.003342
## max  eCDF diff........   0.029673          0.0066839
##
## var ratio (Tr/Co).....     1.5836            0.93828
## T-test p-value........   0.084166            0.78467
```

```
##
##
## ***** (V22) WARD18 *****
##                         Before Matching        After Matching
## mean treatment........    0.08502           0.08502
## mean control..........   0.054621          0.098329
## std mean diff.........     10.877            -4.7621
##
## mean raw eQQ diff.....    0.02834          0.0053903
## med  raw eQQ diff.....          0                  0
## max  raw eQQ diff.....          1                  1
##
## mean eCDF diff........     0.0152          0.0026951
## med  eCDF diff........     0.0152          0.0026951
## max  eCDF diff........   0.030399          0.0053903
##
## var ratio (Tr/Co).....     1.5125            0.87741
## T-test p-value........    0.09103            0.54255
##
##
## ***** (V23) WARD19 *****
##                         Before Matching        After Matching
## mean treatment........   0.016194          0.016194
## mean control..........   0.032036          0.013136
## std mean diff.........    -12.525            2.4178
##
## mean raw eQQ diff.....   0.016194          0.0030185
## med  raw eQQ diff.....          0                  0
## max  raw eQQ diff.....          1                  1
##
## mean eCDF diff........  0.0079206          0.0015093
## med  eCDF diff........  0.0079206          0.0015093
## max  eCDF diff........   0.015841          0.0030185
##
## var ratio (Tr/Co).....    0.51582              1.229
## T-test p-value........   0.055241            0.77736
##
##
## ***** (V24) WARD20 *****
##                         Before Matching        After Matching
## mean treatment........   0.036437          0.036437
## mean control..........   0.030807          0.035636
## std mean diff.........     2.9987            0.4265
##
## mean raw eQQ diff.....  0.0040486          0.0010781
## med  raw eQQ diff.....          0                  0
## max  raw eQQ diff.....          1                  1
##
## mean eCDF diff........  0.0028151         0.00053903
## med  eCDF diff........  0.0028151         0.00053903
## max  eCDF diff........  0.0056302          0.0010781
##
## var ratio (Tr/Co).....     1.1806             1.0216
## T-test p-value........    0.64112            0.96163
```

```
##
##
## ***** (V25) WARD21 *****
##                        Before Matching        After Matching
## mean treatment........   0.024291          0.024291
## mean control..........     0.0275          0.019343
## std mean diff.........    -2.0796            3.2078
##
## mean raw eQQ diff.....  0.0040486         0.0062527
## med  raw eQQ diff.....          0                 0
## max  raw eQQ diff.....          1                 1
##
## mean eCDF diff........   0.001604         0.0031263
## med  eCDF diff........   0.001604         0.0031263
## max  eCDF diff........   0.003208         0.0062527
##
## var ratio (Tr/Co).....    0.88977            1.2495
## T-test p-value........    0.74724           0.69425
##
##
## ***** (V26) WARD22 *****
##                        Before Matching        After Matching
## mean treatment........          0                 0
## mean control..........   0.026555                 0
## std mean diff.........       -Inf                 0
##
## mean raw eQQ diff.....    0.02834                 0
## med  raw eQQ diff.....          0                 0
## max  raw eQQ diff.....          1                 0
##
## mean eCDF diff........   0.013277                 0
## med  eCDF diff........   0.013277                 0
## max  eCDF diff........   0.026555                 0
##
## var ratio (Tr/Co).....          0               NaN
## T-test p-value........ < 2.22e-16                 1
##
##
## ***** (V27) WARD23 *****
##                        Before Matching        After Matching
## mean treatment........  0.0040486         0.0040486
## mean control..........   0.027311         0.0035831
## std mean diff.........    -36.559           0.73156
##
## mean raw eQQ diff.....   0.024291                 0
## med  raw eQQ diff.....          0                 0
## max  raw eQQ diff.....          1                 0
##
## mean eCDF diff........   0.011631                 0
## med  eCDF diff........   0.011631                 0
## max  eCDF diff........   0.023262                 0
##
## var ratio (Tr/Co).....    0.15239            1.1294
## T-test p-value........ 1.6528e-07           0.87405
```

```
##
##
## ***** (V28) WARD24 *****
##                         Before Matching        After Matching
## mean treatment........   0.016194          0.016194
## mean control..........   0.039879          0.011593
## std mean diff.........    -18.726            3.6377
##
## mean raw eQQ diff.....   0.024291          0.019189
## med  raw eQQ diff.....          0                 0
## max  raw eQQ diff.....          1                 1
##
## mean eCDF diff........   0.011842         0.0095947
## med  eCDF diff........   0.011842         0.0095947
## max  eCDF diff........   0.023685          0.019189
##
## var ratio (Tr/Co).....    0.41776            1.3903
## T-test p-value........  0.0045047           0.65097
##
##
## ***** (V29) WARD25 *****
##                         Before Matching        After Matching
## mean treatment........   0.076923          0.076923
## mean control..........   0.046022          0.070936
## std mean diff.........     11.573            2.2423
##
## mean raw eQQ diff.....    0.02834          0.012937
## med  raw eQQ diff.....          0                 0
## max  raw eQQ diff.....          1                 1
##
## mean eCDF diff........   0.015451         0.0064683
## med  eCDF diff........   0.015451         0.0064683
## max  eCDF diff........   0.030902          0.012937
##
## var ratio (Tr/Co).....     1.6237            1.0774
## T-test p-value........   0.072117           0.76166
##
##
## ***** (V30) WARD26 *****
##                         Before Matching        After Matching
## mean treatment........   0.068826          0.068826
## mean control..........   0.045171           0.07514
## std mean diff.........      9.325           -2.4889
##
## mean raw eQQ diff.....   0.020243          0.017249
## med  raw eQQ diff.....          0                 0
## max  raw eQQ diff.....          1                 1
##
## mean eCDF diff........   0.011827         0.0086244
## med  eCDF diff........   0.011827         0.0086244
## max  eCDF diff........   0.023655          0.017249
##
## var ratio (Tr/Co).....     1.4918           0.92223
## T-test p-value........    0.14713           0.75521
```

```
##
##
## ***** (V31) WARD27 *****
##                         Before Matching        After Matching
## mean treatment........   0.072874          0.072874
## mean control..........   0.050463          0.076891
## std mean diff.........     8.6046           -1.5421
##
## mean raw eQQ diff.....   0.020243          0.014015
## med  raw eQQ diff.....          0                 0
## max  raw eQQ diff.....          1                 1
##
## mean eCDF diff........   0.011206         0.0070073
## med  eCDF diff........   0.011206         0.0070073
## max  eCDF diff........   0.022411          0.014015
##
## var ratio (Tr/Co).....     1.4156           0.95189
## T-test p-value........    0.18102            0.8513
##
##
## ***** (V32) WARD28 *****
##                         Before Matching        After Matching
## mean treatment........   0.036437          0.036437
## mean control..........   0.029673          0.037818
## std mean diff.........     3.6027          -0.73525
##
## mean raw eQQ diff.....  0.0040486         0.0068995
## med  raw eQQ diff.....          0                 0
## max  raw eQQ diff.....          1                 1
##
## mean eCDF diff........  0.0033821         0.0034498
## med  eCDF diff........  0.0033821         0.0034498
## max  eCDF diff........  0.0067642         0.0068995
##
## var ratio (Tr/Co).....     1.2242           0.96488
## T-test p-value........    0.57537            0.93477
##
##
## ***** (V33) WARD29 *****
##                         Before Matching        After Matching
## mean treatment........   0.024291          0.024291
## mean control..........   0.017672          0.018991
## std mean diff.........     4.2913            3.4361
##
## mean raw eQQ diff.....  0.0040486         0.0025873
## med  raw eQQ diff.....          0                 0
## max  raw eQQ diff.....          1                 1
##
## mean eCDF diff........    0.00331         0.0012937
## med  eCDF diff........    0.00331         0.0012937
## max  eCDF diff........    0.00662         0.0025873
##
## var ratio (Tr/Co).....     1.3708            1.2722
## T-test p-value........    0.50425            0.67506
```

```
##
##
## ***** (V34) WARD30 *****
##                        Before Matching        After Matching
## mean treatment........   0.020243          0.020243
## mean control..........   0.033926          0.022929
## std mean diff.........     -9.696           -1.9036
##
## mean raw eQQ diff.....   0.016194         0.00064683
## med  raw eQQ diff.....          0                  0
## max  raw eQQ diff.....          1                  1
##
## mean eCDF diff........  0.0068413         0.00032342
## med  eCDF diff........  0.0068413         0.00032342
## max  eCDF diff........   0.013683         0.00064683
##
## var ratio (Tr/Co).....    0.60754            0.88527
## T-test p-value........      0.136            0.83729
##
##
## ***** (V35) I(PERSONS * VOTE96.1) *****
##                        Before Matching        After Matching
## mean treatment........     1.1417             1.1417
## mean control..........    0.82858             1.1137
## std mean diff.........     37.443             3.3481
##
## mean raw eQQ diff.....    0.31174           0.020914
## med  raw eQQ diff.....          0                  0
## max  raw eQQ diff.....          1                  1
##
## mean eCDF diff........    0.10437          0.0069714
## med  eCDF diff........    0.13138          0.0099181
## max  eCDF diff........    0.18174           0.010996
##
## var ratio (Tr/Co).....    0.94808             1.0044
## T-test p-value........ 1.7992e-08            0.63483
## KS Bootstrap p-value.. < 2.22e-16              0.412
## KS Naive p-value......  2.378e-07            0.94187
## KS Statistic..........    0.18174           0.010996
##
##
## ***** (V36) I(PERSONS * NEW) *****
##                        Before Matching        After Matching
## mean treatment........    0.13765            0.13765
## mean control..........    0.27755            0.14545
## std mean diff.........    -34.134            -1.9024
##
## mean raw eQQ diff.....     0.1417           0.024795
## med  raw eQQ diff.....          0                  0
## max  raw eQQ diff.....          1                  1
##
## mean eCDF diff........   0.046632          0.0082651
## med  eCDF diff........    0.05197          0.0025873
## max  eCDF diff........   0.087925           0.022208
```

```
##
## var ratio (Tr/Co).....    0.47573            0.91411
## T-test p-value........ 3.2711e-07            0.80682
## KS Bootstrap p-value.. < 2.22e-16              0.008
## KS Naive p-value......   0.047894            0.20285
## KS Statistic..........   0.087925           0.022208
##
##
## Before Matching Minimum p.value: < 2.22e-16
## Variable Name(s): AGE AGE2 WARD22 I(PERSONS * VOTE96.1) I(PERSONS * NEW)  Number(s): 1 2 26 35 36
##
## After Matching Minimum p.value: < 2.22e-16
## Variable Name(s): AGE AGE2  Number(s): 1 2
```

Examine the demo's input / output. Consult the research papers cited in the demo if you wish.

STEP 1 Answer the following questions:

1. What is the causal question at the heart of the demo? The question is What is the causal effect of Get-Out-The-Vote Calls on the rate of voter Turnout?
2. What is the treatment? the get-Out-The-Vote Calls
3. What is the outcome? the rate of voter turnout.
4. The demo is written to show that Imai's results do not achieve balance. Write a not-too-long paragraph stating whether you agree or disagree with this claim, and why.

The demo has failed to achieve balance. I agreed with the claim because: 1. Firstly, we look at the p-value for different variables. The majority of covariates after matching still have very low p-value. For instance, looking at variable Age and AGE2.They have very low p-value, making us reject the null hypothesis, which says that there is no difference between two groups. If the matching achieves balance, then the p-value would be bigger and we would not reject the null hypothesis. In this case, with very small p-value, we can say that there is a difference between the distribution of covariates among two groups.

End of Assignment

Final Steps

Before finalizing your project you'll want to be sure there are **comments in your code chunks** and **text outside of your code chunks** to explain what you're doing in each code chunk. These explanations are incredibly helpful for someone who doesn't code or someone unfamiliar to your project.

You have two options for submission:

1. You can complete this .rmd file, knit it to pdf and submit the resulting .pdf file on Forum.
2. You can complete the Google Doc version of this assignment, include your code, graphs, results, and your explanations wherever necessary and download the Google Doc as a pdf file and submit the pdf file on Forum. If you choose this method, you need to make sure you will provide a link to an .R script file where your code can be found (you can host your code on Github or Google Drive). Note that links to Google Docs are not accepted as your final submission.

Knitting your R Markdown Document

Last but not least, you'll want to **Knit your .Rmd document into a pdf document**. If you get an error, take a look at what the error says and edit your .Rmd document. Then, try to Knit again! Troubleshooting these error messages will teach you a lot about coding in R. If you get any error that doesn't make sense to you, post it on Perusall.

Good Luck! The CS112 Teaching Team