CS112 Final Project Decision Memo

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To: The Electoral Service, Chile

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Re: Evaluation of E-voting as an Alternate System for Improving the Voters' Experience

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Executive Summary

There have been growing discussions about the impact of various voting technologies on the voting experience. One controversial debate is whether e-voting processes improve the legitimacy of the election process and the general voting experience. In their paper, 'Voting Made Safe and Easy: The impact of e-voting on Citizen Perceptions', Alvarez et. al use propensity score matching methods to measure the causal effect of replacing traditional voting technology with e-voting on the voting experience in Argentina. Extending their results using a genetic matching procedure, I was able to obtain a high degree of treatment/control-group balance on nearly all the covariates without discarding any of the treated units (as against Alvarez et. al, who discarded 284 treated units (32.8%) of the 866 treated units). Our results suggest that e-voters perceive the new technology as more efficient, easier to use, and more likely to register votes as intended. They also support replacing traditional voting with e-voting,

showing more confidence in ballot secrecy than traditional voters. This contradicts the original paper's finding regarding ballot secrecy. The results of this study could especially be significant to Chile as Chile and Argentina are reported to be extremely similar in terms of the covariates matched on in the study. Although there are certainly cultural differences between both countries, I recommend a gradual implementation (coupled with evaluation) of e-voting as it could be promising in Chile and help improve voters' experience.

Background

The recommendation to gradually implement e-voting into the current voting process in Chile follows from reliable evidence that Chile, in general, is very similar to Argentina in terms of crucial characteristics to the voting process e.g., age structure, education, school life expectancy, gender structure, technology adoption, etc[1]. Extrapolating from these similarities, we believe that e-voting could potentially have similar beneficial effects on the voting experience in Chile, especially as both countries operate under a democratic system.

The remainder of the memo is structured as follows:

Section A describes the original paper's benefits and presents a replication of the balance statistics obtained through the matching procedure (accompanied by a data visualization of the balance); Section B explains our genetic matching extension, justifying the decision to use genetic matching while outlining how exactly the procedure was carried out and the different matching attempts; Section C the final results obtained via matching; Section D presents our

[1] The comparison of Chile and Argentina on relevant characteristics was gotten from Index Mundi.

extension on Table 2 based on our genetic matching; Section E computes the causal effects of e-voting using the matched dataset obtained from our genetic matching we then compare our results to the original paper's; Section F outlines recommended additional analyses.

A. Discussion of the Original Paper

The original paper employs propensity score caliper matching to approximate a randomized field experiment by closely matching voters who used the traditional voting procedure to similar e-voters. To do so, propensity scores were first estimated, and then e-voters were matched with traditional voters that had an almost similar propensity score. A caliper of 0.05 was used to specify a maximum tolerated difference between matched units, ensuring that covariates were balanced across the e-voters and traditional voters samples. The matching procedure resulted in the discarding of 311 units (284 treated units and 27 control units). The discarding of 284 (32.8%) of the 866 treated units could especially bias the causal estimates as it represents a significant portion of the treated units. The balance statistics produced from the original paper are shown below:

	Before matching (N=1,475)				After matching (N=1,164)			
	EV	TV	Diff	p-value*	EV	TV	Diff	p-value*
Age group (1-5)	2.5	2.4	0.0	0.56	2.5	2.5	0.0	1.00
Education (1-8)	4.8	4.1	0.6	0.00	4.2	4.2	0.0	0.49
White collar (%)	30.3	27.6	2.7	0.29	29.4	27.3	2.1	0.47
Not full time worker (%)	27.7	33.5	-5.8	0.02	30.6	32.1	-1.5	0.61
Male (%)	49.7	49.1	0.6	0.87	49.0	49.8	-0.9	0.81
Technology count (1-6)	4.2	3.9	0.3	0.00	4.0	3.9	0.1	0.31
Political information (1-4)	1.5	1.3	0.2	0.00	1.4	1.3	0.0	0.63

Comparing the balance statistics before and after matching, there is a clear improvement in balance and now there are no significant differences between the treated and control samples after matching.

We present a plot of the balance on covariates acheived by the matching procedure:

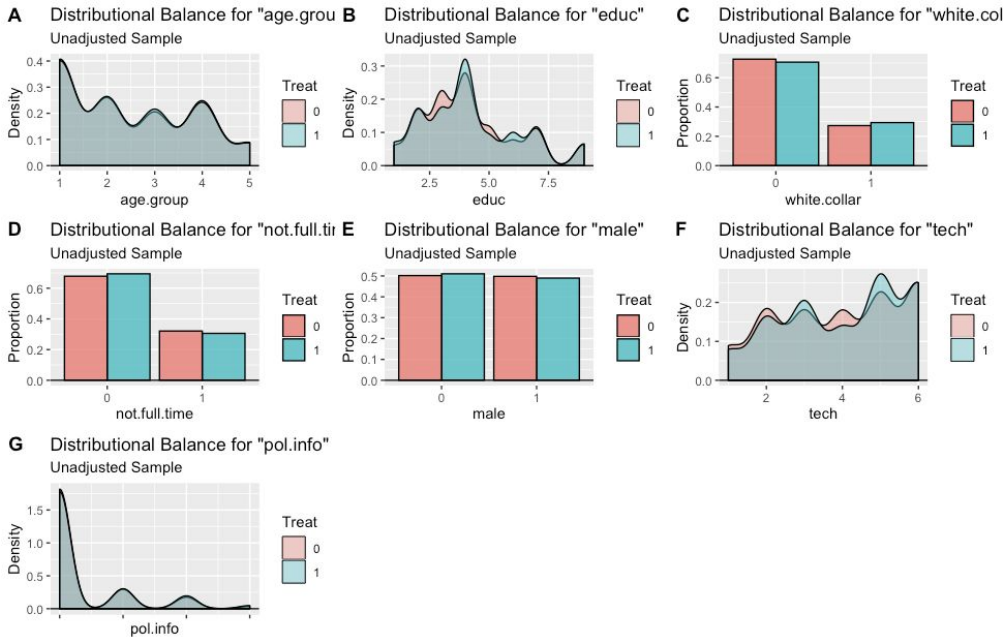

Figure 1. Plots Showing the Distributional Balance on Covariates After Matching. We can observe that covariate balance is better by noting the smaller thickness of green and red overlays in graphs A,B, F and C, and smaller differences in heights of bars C, D, and E.

B. Genetic Matching Trials and Justification

The decision to apply genetic matching stems from the fact that propensity score matching employs complete randomization and hence doesn't exactly balance all thecovariates. Genetic matching, on the other hand, employs blocked randomization and therefore is one step closer to exact balance on the covariates. Furthermore, propensity score matching leads to loss of information by condensing multiple dimensions in a single dimension represented by a propensity score (King & Nielsen, 2018), this is not the case with genetic matching.

Genetic matching was carried out on the same covariates that were used to compute the propensity scores in the original paper. These included quadratic and interaction terms:

age.group, I(age.group^2), I(age.group^3), age.group:educ, age.group:tech, educ, I(educ^2), tech, I(tech^2), pol.info, educ:pol.info, age.group:pol.info, tech:pol.info, white.collar, not.full.time, male.

Different matching arguments combinations were tried in the different genetic matching runs in a bid to identify the best possible balance across all the matching variables listed above. We tried over 25 matching algorithms over the span of 20 hours. Some of our attempts involved setting ties in the GenMatch function to FALSE, exact matching on various covariates including the single order covariates like age.group, pol.info, etc. We tried different calipers between 0.5 and 2 for different covariates and this worsened balance immensely compared to the default genetic matching. We also tried increasing the wait and maximum generations, but our minimum p-value varied greatly from run to run.

C. Final Genetic Matching Results

Two different genetic matching runs resulted in the same minimum after-matching p-value. One of these run involved setting a population size of 2000 as well as setting ties to FALSE. The other employed exact matching on age.group:educ and tech:pol.info, after a realization that the covariate dataset produced from these interaction terms contained the same value for all units (regardless of whether they were treated or not). The minimum p-value presented by both of these models was 0.11048 for age.group:educ. Hence to decide on a genetic run, we extracted the matched dataset generated by both of these runs and ran MatchBalance to assess the balance on the covariates:

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[1] "age.group"     "educ"          "white.collar"  "not.full.time" "male"          "tech"
[7] "pol.info"
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The genetic matching run that did not employ exact matching, had a slightly higher minimum p-value when the matched dataset was fed into MatchBalance (0.528 vs. 0.513 on tech) and was therefore selected. The balance on covariates for this genetic matching run can be seen in Appendix A. We also present plots to visualize the balance on covariates:

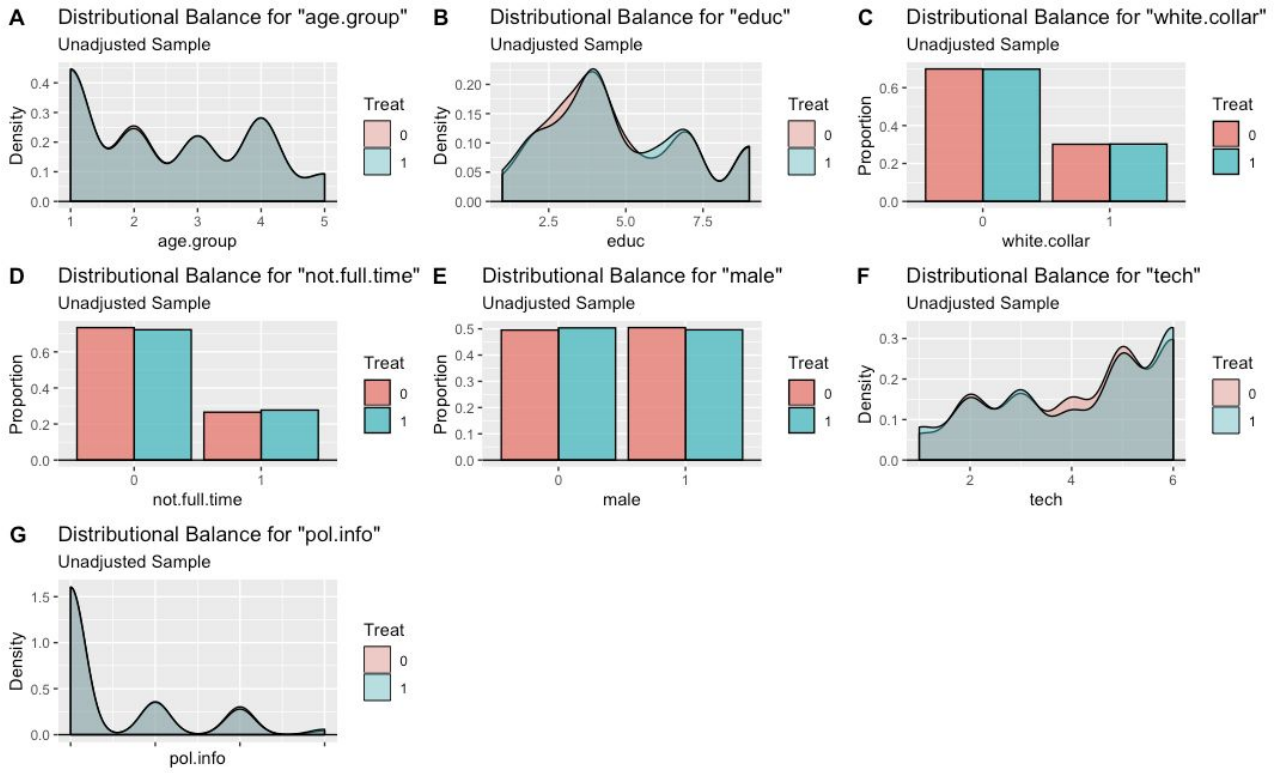

Figure 2. Plots Showing the Distributional Balance on Covariates After Genetic Matching. We can observe that covariate balance is better in our genetic matching procedure than the original paper's matching by noting the smaller thickness of green and red overlays in graphs A,B, F and C, and smaller differences in heights of bars C, D, and E in the former (see Fig. 1). [2]

No treated units were dropped in the process of attaining high balance on all the covariates. However, 201 control units were dropped.

D. Extension of Table 2 With Genetic Matching

[2] **#dataviz:** we interpreted data visualizations from the original paper and discussed them eg the tables. We created our own data visualizations to convey important discussions such as the differences between our genetic matching method and the original paper's. We provide a thorough interpretation of visualizations created. Additionally, we follow nuanced conventions of visualizations such as labelling, headers, legends etc.

Following the generation of the genetically matched dataset, balance statistics were computed using the same procedure employed in the Alvarez et. al's original paper. These balance statistics were then appended to the replication of the original paper's Table 2:

	Before matching (N=1,475)				After Original Paper's matching (N=1,164)				After Genetic matching (N=1,732)			
	EV	TV	Diff	p-value*	EV	TV	Diff	p-value*	EV	TV	Diff	p-value*
Age group (1-5)	2.5	2.4	0	0.55	2.5	2.5	0.0	1.00	2.5	2.5	0.0	1.00
Education (1-8)	4.8	4.1	0.6	0.00	4.2	4.2	0.0	0.45	4.8	4.8	0.0	0.68
White collar (%)	30.3	27.6	2.7	0.29	29.4	27.3	2.1	0.47	0.3	0.3	0.0	1.00
Not full time worker (%)	27.7	33.5	-5.8	0.02	30.6	32.1	-1.5	0.61	0.3	0.3	0.0	0.63
Male (%)	49.7	49.1	0.6	0.87	49	49.8	-0.9	0.81	0.5	0.5	0.0	0.77
Technology count (1-6)	4.2	3.9	0.3	0.00	4	3.9	0.1	0.32	4.2	4.2	0.0	0.55
Political information (1-4)	1.5	1.3	0.2	0.00	1.4	1.3	0.0	0.62	1.5	1.5	0.0	0.93

Comparing the balance statistics from the genetic match to the original paper's propensity score matching, we see that there are no observable differences between both the treated and control samples.[3] The result is also statistically significant as the p-value indicates. The genetic matching results in better balance on covariates than the propensity score matching from the original paper.

E. Extension of Table 3 With Genetic Matching and An Interpretation of the Results

[3] **#controlgroups:** we reference the significance of control groups in multiple facets, from the appropriateness of their choice, to the dropping of 201 units, to their use as measures of observable differences when contrasted with the treated units' balance statistics. We further attributed our matching results to careful consideration of the high degree of treatment/control group balance on nearly all the covariates thus reiterating the significance of this HC on this procedure.

Establishing that our Genetic matching leads to be balance on covariates, we estimate the causal impact of e-voting on voters' experience. Similar to the original paper, the causal effect is estimated using a difference in proportions test. We run the same algorithms used to estimate the causal impact from the original paper's matched dataset on our genetically matched dataset. The extension of Table is shown below:

	Before matching (N=1,475)					After Original Paper's matching (N=1,164)					After Genetic matching (N=1,732)				
	N	E-Voting (%)	Tradit. Voting (%)	Diff.	p-value *	N	E-Voting (%)	Tradit. Voting (%)	Diff.	p-value *	N	E-Voting (%)	Tradit. Voting (%)	Diff.	p-value*
Select candidates electronically	1388	83.8	53.4	30.4	0.000	1102	81.7	53.4	28.3	0.000	1674	85.1	76.2	9.0	0.000
Evaluation of voting experience	1460	46.3	21.3	25.0	0.000	1151	45.2	21.4	23.8	0.000	1715	46.3	22.0	24.4	0.000
Ease of voting procedure	1469	33.6	11.5	22.1	0.000	1159	32.0	11.4	20.6	0.000	1726	33.6	11.1	22.5	0.000
Agree substitute TV by EV	1409	84.1	62.4	21.7	0.000	1113	82.8	62.6	20.2	0.000	1657	86.3	75.7	10.7	0.000
Elections in Salta are clean	1284	58.0	41.0	17.0	0.000	1021	57.0	41.7	15.3	0.000	1684	77.1	86.4	-9.3	0.000
Sure vote was counted	1416	85.1	76.2	8.9	0.000	1123	84.7	76.5	8.1	0.001	1511	58.0	44.6	13.4	0.000
Qualification of poll workers	1418	86.3	77.0	9.3	0.000	1117	85.6	77.5	8.0	0.001	1704	84.1	78.1	5.9	0.002
Speed of voting process	1443	84.1	80.8	3.2	0.130	1135	83.0	81.0	2.0	0.412	1656	84.1	68.1	16.1	0.000
Confident ballot secret	1431	77.1	84.5	-7.4	0.001	1133	76.6	84.7	-8.1	0.001	1631	83.8	59.1	24.8	0.000

Table 3 presents the proportion of e-voters and traditional voters that gave positive responses to each question (questions are the row names). Comparing the difference in proportions after genetic matching to that after the original paper's matching, we see that the original paper underestimates or overestimates some of the effects. For example, the difference in proportions

of the e-voter and traditional voters when asked if they prefer to select candidates electronically greatly reduced (9% vs 28.3%), although the e-voters are still more likely to answer affirmatively. The original paper also underestimates the difference in the proportion of e-voters reporting a faster voting process (16.1% vs 2%), an easier voting procedure (22.5% vs 20.6%), and a more positive evaluation of the general voting experience (24.4% vs 23.8%). Interesting to note, is the change in valence when estimating the causal effect of e-voting on confidence in ballot secrecy. The original paper claims that e-voters are 8.1% less likely to report being confident in the ballot secrecy. Our results, however, find that the effect is a large opposite effect, suggesting that e-voters are 24.8% more likely to report confidence in ballot secrecy. Another important thing to note is that the genetic matching finds a significant difference in e-voters perception in the speed of voting compared to traditional voters, unlike the original paper. Lastly, we also see a change in the valence of the difference in proportion for perceptions on the cleanliness of elections in Salta. From my genetic matching results, e-voters consider Salta elections less clean than traditional voters, and the original paper finds the opposite. Despite, the number of differing results in my causal estimates compared to the original paper's, I am confident in our results for the following reasons:

a. The original matching procedure dropped about 30% of its treated units and this could greatly bias causal estimates. Our genetic matching on the other hand, drops no treated units.
b. We achieve better balance on covariates through our genetic matching than the original paper through its propensity score caliper matching (this is evident from Table 2). This

again points to the general problem of propensity score matching employing complete randomization as against blocked randomization.

F. Conclusion and Recommended additional analysis

The balance achieved (described above) through our genetic matching is superior on most variables when compared to the original paper's matching. In addition we do not discard any treated units, further conferring confidence in our results. From our causal effects (see Table 3 extension), we see that e-voting has a positive impact on the voting experience when compared to traditional voting. We see a positive difference in proportion for all but one question related to voting experience, indicating that for the most part, e-voters have more positive perceptions and evaluations of the voting experience. This suggests that e-voting does improve the legitimacy of elections and the general voting experience. To have more confidence in the results we obtain, our analysis will benefit from a sensitivity analysis to determine if the presence of an unmeasured covariate could significantly influence the conclusion drawn. The study replicated and extended above applied to an Argentine election. We have strong evidence that supports the claim that Chile is very similar to Argentina on characteristics and covariates that are relevant to electoral processes. Hence, we recommend that Chile gradually implement e-voting into its electoral processes.

Link to Gist containing code:

https://gist.github.com/Korede2001/b1c7bf625b2c9b812ed8ef6e14623d3f

References

Alvarez M., Levin, I., Pomares, J., Leiras, M. (2013, June). Political Science Research and Methods 1(1): 117-37. Retrieved from: https://www-cambridge-org.ccl.idm.oclc.org/core/journals/political-science-research-and-methods/article/voting-made-safe-and-easy-the-impact-of-evoting-on-citizen-perceptions/A96562BA348433894BED1F2BA8BC3761

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Appendix A

***** (V1) age.group *****

	Before Matching	After Matching
mean treatment.....	2.4758	2.4758
mean control.....	2.4433	2.4723
std mean diff.....	2.4035	0.25697
mean raw eQQ diff.....	0.065681	0.010393
med raw eQQ diff.....	0	0
max raw eQQ diff.....	1	1
mean eCDF diff.....	0.013296	0.0020785
med eCDF diff.....	0.017038	0.0023095
max eCDF diff.....	0.026754	0.0034642
var ratio (Tr/Co).....	1.048	1.0091
T-test p-value.....	0.64508	0.69117
KS Bootstrap p-value..	0.568	1
KS Naive p-value.....	0.96005	1

KS Statistic.....	0.026754	0.0034642

***** (V2) I(age.group^2) *****

	Before Matching	After Matching
mean treatment.....	7.9446	7.9446
mean control.....	7.7011	7.9111
std mean diff.....	3.2799	0.45121
mean raw eQQ diff.....	0.33498	0.054273
med raw eQQ diff.....	0	0
max raw eQQ diff.....	7	9
mean eCDF diff.....	0.013296	0.0020785
med eCDF diff.....	0.017038	0.0023095
max eCDF diff.....	0.026754	0.0034642
var ratio (Tr/Co).....	1.034	1.0087
T-test p-value.....	0.53124	0.43589
KS Bootstrap p-value..	0.568	1
KS Naive p-value.....	0.96005	1
KS Statistic.....	0.026754	0.0034642

***** (V3) I(age.group^3) *****

	Before Matching	After Matching
mean treatment.....	29.469	29.469
mean control.....	28.217	29.271
std mean diff.....	3.4895	0.55032
mean raw eQQ diff.....	1.4154	0.24596
med raw eQQ diff.....	0	0
max raw eQQ diff.....	37	61
mean eCDF diff.....	0.013296	0.0020785
med eCDF diff.....	0.017038	0.0023095
max eCDF diff.....	0.026754	0.0034642
var ratio (Tr/Co).....	1.0225	1.0091
T-test p-value.....	0.50671	0.3564
KS Bootstrap p-value..	0.568	1
KS Naive p-value.....	0.96005	1
KS Statistic.....	0.026754	0.0034642

***** (V4) educ *****

	Before Matching	After Matching
mean treatment.....	4.7714	4.7714
mean control.....	4.1429	4.7587
std mean diff.....	27.294	0.55161
mean raw eQQ diff.....	0.62397	0.075058
med raw eQQ diff.....	0	0
max raw eQQ diff.....	2	2
mean eCDF diff.....	0.070303	0.0090935
med eCDF diff.....	0.085505	0.006351
max eCDF diff.....	0.1307	0.023095
var ratio (Tr/Co).....	1.3199	1.0128
T-test p-value.....	3.0007e-08	0.50407
KS Bootstrap p-value..	< 2.22e-16	0.733
KS Naive p-value.....	9.9039e-06	0.97503
KS Statistic.....	0.1307	0.023095

***** (V5) I(educ^2) *****

	Before Matching	After Matching
mean treatment.....	28.062	28.062
mean control.....	21.174	27.874
std mean diff.....	27.851	0.76104
mean raw eQQ diff.....	6.8539	0.62009
med raw eQQ diff.....	0	0
max raw eQQ diff.....	32	32
mean eCDF diff.....	0.070303	0.0090935
med eCDF diff.....	0.085505	0.006351
max eCDF diff.....	0.1307	0.023095
var ratio (Tr/Co).....	1.5002	0.99121
T-test p-value.....	5.3193e-09	0.27401
KS Bootstrap p-value..	< 2.22e-16	0.733
KS Naive p-value.....	9.9039e-06	0.97503
KS Statistic.....	0.1307	0.023095

***** (V6) tech *****

	Before Matching	After Matching
mean treatment.....	4.1836	4.1836
mean control.....	3.9097	4.1813
std mean diff.....	16.549	0.13953
mean raw eQQ diff.....	0.26929	0.078522
med raw eQQ diff.....	0	0
max raw eQQ diff.....	1	1
mean eCDF diff.....	0.045652	0.013087
med eCDF diff.....	0.041212	0.013857
max eCDF diff.....	0.10917	0.027714
var ratio (Tr/Co).....	1.0529	1.0818
T-test p-value.....	0.0015253	0.92931
KS Bootstrap p-value..	0.001	0.513
KS Naive p-value.....	0.0003975	0.89357
KS Statistic.....	0.10917	0.027714

***** (V7) I(tech^2) *****

	Before Matching	After Matching

mean treatment.....	20.239	20.239
mean control.....	17.883	20.013
std mean diff.....	18.428	1.7706
mean raw eQQ diff.....	2.3218	0.61201
med raw eQQ diff.....	0	0
max raw eQQ diff.....	11	11
mean eCDF diff.....	0.045652	0.013087
med eCDF diff.....	0.041212	0.013857
max eCDF diff.....	0.10917	0.027714
var ratio (Tr/Co).....	1.0854	1.0699
T-test p-value.....	0.00037227	0.29018
KS Bootstrap p-value..	0.001	0.513
KS Naive p-value.....	0.0003975	0.89357
KS Statistic.....	0.10917	0.027714

***** (V8) pol.info *****

	Before Matching	After Matching
mean treatment.....	1.4746	1.4746

mean control.....	1.3103	1.4677
std mean diff.....	20.451	0.86268
mean raw eQQ diff.....	0.16256	0.011547
med raw eQQ diff.....	0	0
max raw eQQ diff.....	1	1
mean eCDF diff.....	0.041063	0.0028868
med eCDF diff.....	0.035125	0.0017321
max eCDF diff.....	0.094002	0.0080831
var ratio (Tr/Co).....	1.44	1.0456
T-test p-value.....	2.0928e-05	0.2568
KS Bootstrap p-value..	< 2.22e-16	0.917
KS Naive p-value.....	0.0036036	1
KS Statistic.....	0.094002	0.0080831

***** (V9) white.collar *****

	Before Matching	After Matching
mean treatment.....	0.30254	0.30254
mean control.....	0.27586	0.30139

std mean diff.....	5.8044	0.25123
mean raw eQQ diff.....	0.026273	0.0011547
med raw eQQ diff.....	0	0
max raw eQQ diff.....	1	1
mean eCDF diff.....	0.013339	0.00057737
med eCDF diff.....	0.013339	0.00057737
max eCDF diff.....	0.026678	0.0011547
var ratio (Tr/Co).....	1.0558	1.0022
T-test p-value.....	0.26506	0.91465

***** (V10) not.full.time *****

	Before Matching	After Matching
mean treatment.....	0.27714	0.27714
mean control.....	0.33498	0.26559
std mean diff.....	-12.915	2.5784
mean raw eQQ diff.....	0.059113	0.011547
med raw eQQ diff.....	0	0

max raw eQQ diff.....	1	1
mean eCDF diff.....	0.02892	0.0057737
med eCDF diff.....	0.02892	0.0057737
max eCDF diff.....	0.057839	0.011547
var ratio (Tr/Co).....	0.89885	1.0271
T-test p-value.....	0.018169	0.43771

***** (V11) male *****

	Before Matching	After Matching
mean treatment.....	0.49654	0.49654
mean control.....	0.49097	0.50462
std mean diff.....	1.1128	-1.6157
mean raw eQQ diff.....	0.0049261	0.0080831
med raw eQQ diff.....	0	0
max raw eQQ diff.....	1	1
mean eCDF diff.....	0.0027835	0.0040416
med eCDF diff.....	0.0027835	0.0040416

max eCDF diff.....	0.005567	0.0080831
var ratio (Tr/Co).....	0.99979	1
T-test p-value.....	0.83338	0.6088

***** (V12) age.group:educ *****

	Before Matching	After Matching
mean treatment.....	11.179	11.179
mean control.....	9.4171	11.033
std mean diff.....	20.67	1.7069
mean raw eQQ diff.....	1.757	0.27252
med raw eQQ diff.....	1	0
max raw eQQ diff.....	9	9
mean eCDF diff.....	0.04605	0.0070208
med eCDF diff.....	0.050841	0.0057737
max eCDF diff.....	0.084371	0.016166
var ratio (Tr/Co).....	1.5823	1.0833
T-test p-value.....	1.0875e-05	0.11048

KS Bootstrap p-value..	0.004	0.979
KS Naive p-value.....	0.012309	0.99986
KS Statistic.....	0.084371	0.016166

***** (V13) age.group:tech *****

	Before Matching	After Matching
mean treatment.....	9.4342	9.4342
mean control.....	8.6552	9.4134
std mean diff.....	13.247	0.35344
mean raw eQQ diff.....	0.77997	0.22633
med raw eQQ diff.....	0	0
max raw eQQ diff.....	5	6
mean eCDF diff.....	0.027816	0.0062492
med eCDF diff.....	0.034022	0.0034642
max eCDF diff.....	0.056675	0.026559
var ratio (Tr/Co).....	1.2074	1.0947
T-test p-value.....	0.0083461	0.82181
KS Bootstrap p-value..	0.107	0.67

KS Naive p-value.....	0.20092	0.92013
KS Statistic.....	0.056675	0.026559

***** (V14) educ:pol.info *****

	Before Matching	After Matching
mean treatment.....	7.6536	7.6536
mean control.....	5.9163	7.6074
std mean diff.....	24.798	0.65928
mean raw eQQ diff.....	1.7274	0.23788
med raw eQQ diff.....	1	0
max raw eQQ diff.....	9	9
mean eCDF diff.....	0.064052	0.0067085
med eCDF diff.....	0.053076	0.0057737
max eCDF diff.....	0.15014	0.024249
var ratio (Tr/Co).....	1.5246	1.0029
T-test p-value.....	1.7567e-07	0.44366
KS Bootstrap p-value..	< 2.22e-16	0.775
KS Naive p-value.....	1.9961e-07	0.96093

KS Statistic..... 0.15014 0.024249

***** (V15) age.group:pol.info *****

	Before Matching	After Matching
mean treatment.....	3.8303	3.8303
mean control.....	3.289	3.8025
std mean diff.....	15.705	0.80414
mean raw eQQ diff.....	0.5353	0.062356
med raw eQQ diff.....	0	0
max raw eQQ diff.....	4	4
mean eCDF diff.....	0.031924	0.0032866
med eCDF diff.....	0.034293	0.0034642
max eCDF diff.....	0.068046	0.0069284
var ratio (Tr/Co).....	1.5764	1.0512
T-test p-value.....	0.00082568	0.38402
KS Bootstrap p-value..	0.018	1
KS Naive p-value.....	0.072946	1
KS Statistic.....	0.068046	0.0069284

***** (V16) tech:pol.info *****

	Before Matching	After Matching
mean treatment.....	6.485	6.485
mean control.....	5.3727	6.4515
std mean diff.....	22.09	0.66507
mean raw eQQ diff.....	1.0985	0.14896
med raw eQQ diff.....	1	0
max raw eQQ diff.....	6	4
mean eCDF diff.....	0.053642	0.0075443
med eCDF diff.....	0.042683	0.0057737
max eCDF diff.....	0.11947	0.024249
var ratio (Tr/Co).....	1.3954	1.0444
T-test p-value.....	5.1807e-06	0.55519
KS Bootstrap p-value..	< 2.22e-16	0.736
KS Naive p-value.....	7.3805e-05	0.96093
KS Statistic.....	0.11947	0.024249