
Problem Set 3 *Solutions*

Question 1. Return to the NELS-88 data used in Problem Set 2 to estimate the academic benefits to attending a Catholic high school. This time—rather than exact or nearest neighbor matching based on covariates—we will use propensity scores. **(30 points)**

- (a) For this analysis, use the “continuous” family income variable you created in Problem Set 2 and the dummy variables for parents’ highest level of education. In addition, create *z*-scores for the 8th and 12th grade reading and math scores. **(3 points)**

See the attached log file for creation of additional variables.

- (b) Use `teffects psmatch` or the `psmatch2` commands to estimate a propensity score model where the “treatment” is attending a Catholic high school. The goal will ultimately be (in part c) to estimate the ATT on 12th grade test scores, high school graduation, and post-secondary enrollment, using nearest neighbor matching (based on propensity scores). This will be an iterative process where you experiment with a propensity score model, check for balance, and then make adjustments to your propensity score model and matching rules as needed. I recommend using the `quietly` prefix with `teffects psmatch`, or omitting the `outcome()` option if you use the `psmatch2` command. (You do not want treatment effect estimates to guide your specification search). Here are a few tips/requirements: **(12 points)**
- Choose predictor variables that are likely to be associated with the “treatment” that you would ultimately like to see balanced between your treated and untreated group. You can use any variables in the dataset that you deem appropriate.
 - After fitting the propensity score model, check for balance on your predictor variables using `tebalance summarize`, `box` and `density`. (Or use `pstest` after `psmatch2`).
 - You may be able to improve balance by changing your propensity model specification—e.g., omitting or including variables (depending on how predictive or theoretically important they are), entering variables as continuous or categorical, adding interactions or nonlinear terms (e.g., quadratic)—and/or by tinkering with the number of nearest neighbors or caliper. Use your own judgment when deciding on “good enough” balance.
 - You do not need to provide results for all of the iterations you attempt. Just include a short written explanation justifying your choice, and provide balance tests/figures for your final specification. (You can refer to other specifications you tried in your write-up).

- Lastly, once you have settled on a propensity score model, check for overlap in the distribution of propensity scores between your treated and untreated group. (E.g., `teoverlap` or `tebalance density` after `teffects psmatch`, or using code provided in class). Include your graphical results with your output. Presuming you have good overlap, you can proceed to the next step. If there is poor overlap, you should revisit your propensity score model.

My final model is shown in the attached log (yours will likely differ). Of the confounders, I prioritized balance on baseline test scores, family income, and parental education, given the results of prior studies which demonstrate the importance of these in explaining later outcomes. The logit model results confirm these are important predictors of Catholic school enrollment as well. I experimented with several different specifications and variable definitions; these included models linear in prior test scores, models that used separate categorical variables for the highest education of each parent, models with interactions between gender and race, and models with a continuous measure of risk factors. The covariate balance was quite good for most specifications, but this one seemed especially good, as the balance test results show. (The log file shows the `tebalance summarize` for the same propensity score match and the `tebalance box` and `tebalance density` for select variables).

The `teoverlap` and `tebalance density` plots are also shown in the attached. Note that the former uses `*all*` observations, not just the matched sample. The latter shows both the full and matched sample.

- (c) Once you are satisfied with your propensity score model, calculate the ATT for the four outcome variables: 12th grade reading and math *z*-scores, high school graduation, and post-secondary enrollment. Interpret the results in words. What assumption(s) are required for these estimates to be considered causal? (5 points)

The results are shown in the attached log and summarized in the table below. Attending a Catholic high school is estimated to have a 0.119 standard deviation effect on math scores and a 0.024 standard deviation effect on reading scores. Only the math effect is statistically significant. The ATT estimate is positive and marginally insignificant for high school graduation (3.0 percentage points) and positive and significant for post-secondary enrollment (7.3 ppts). Because these are ATT estimates they are interpreted as the average treatment effect for the population who attends Catholic high school. The key assumption is conditional independence—conditional on the covariates (here, factors used to create balance between the treated and untreated cases), treatment assignment is independent of potential outcomes.

- (d) Rather than nearest neighbor matching, propensity scores can also be used in weighting estimators. Using the same propensity score model you settled on in part (b), estimate the ATT and ATE using inverse probability weighting (`teffects ipw`). How do your results differ from those in part (c), if at all? **(5 points)**

The results are shown in the attached log and summarized in the table below. The ATT results are very similar to those using propensity score matching.

- (e) Imbens (2015) proposed an algorithm for estimating propensity score models. The algorithm iteratively adds linear and quadratic terms (and interactions), keeping terms that improve the predictive fit of the model. The user-written command `pselect` executes this algorithm and outputs the resulting propensity scores to your dataset. (You will need to install it using `ssc install pselect`). The syntax of the command is:

```
pselect treat, tottry(varnames) genpscore(newvarname)
```

where *treat* is the treatment variable, *varnames* is a list of predictor variables you would like to try in the algorithm, and *newvarname* will be the new variable containing the propensity score. Choose a set of variables for the algorithm to try. (Note if you choose a long list it may take quite awhile for the algorithm to run. If it takes an exceedingly long time, start with a shorter list). What specification did the algorithm end up with? **(5 points)**

Note: the resulting propensity scores from part (e) could then be used for matching, stratification, or weighting.

The resulting model specification is shown in the attached log. I had the algorithm try the same set of variables used in the earlier steps. The resulting specification included some nonlinear terms (e.g., a quadratic in prior math scores) and many interactions (e.g., Black and family income).

```

.
. // *****
. //
. // Regression II - Problem set 3
. // Last updated: September 20, 2024
. //
. // *****
.
. // *****
. // Question 1
. // *****
.
. use https://stats.idre.ucla.edu/stat/stata/examples/methods_matter/chapter12/catholic, c
> lear

```

```

.
. // *****
. // Part a - create some new vars
. // as in Problem Set 2
. // *****
.
.       *ssc install fre
.       fre faminc8

```

faminc8 -- total annual family income in 8th grade

		Freq.	Percent	Valid	Cum.
Valid	1 none	18	0.32	0.32	0.32
	2 <\$1000	42	0.74	0.74	1.06
	3 \$1000-\$2999	84	1.48	1.48	2.54
	4 \$3000-\$4999	85	1.50	1.50	4.04
	5 \$5000-\$7499	144	2.54	2.54	6.58
	6 7500-\$9999	175	3.09	3.09	9.66
	7 \$10000-\$14999	447	7.88	7.88	17.55
	8 \$15000-\$19999	441	7.78	7.78	25.32
	9 \$20000-\$24999	655	11.55	11.55	36.87
	10 \$25000-\$34999	1267	22.34	22.34	59.21
	11 35000-\$49999	1419	25.02	25.02	84.24
	12 50000-\$74999	894	15.76	15.76	100.00
	Total	5671	100.00	100.00	

```

.
. // "continuous" version of family income
. gen faminc8b=0 if faminc8==1
(5,653 missing values generated)

. replace faminc8b = (0+1000)/2 if faminc8==2
(42 real changes made)

. replace faminc8b = (1000+2999)/2 if faminc8==3
(84 real changes made)

. replace faminc8b = (3000+4999)/2 if faminc8==4
(85 real changes made)

. replace faminc8b = (5000+7499)/2 if faminc8==5
(144 real changes made)

. replace faminc8b = (7500+9999)/2 if faminc8==6
(175 real changes made)

. replace faminc8b = (10000+14999)/2 if faminc8==7
(447 real changes made)

```

```
.      replace faminc8b = (15000+19999)/2 if faminc8==8
(441 real changes made)

.      replace faminc8b = (20000+24999)/2 if faminc8==9
(655 real changes made)

.      replace faminc8b = (25000+34999)/2 if faminc8==10
(1,267 real changes made)

.      replace faminc8b = (35000+49999)/2 if faminc8==11
(1,419 real changes made)

.      replace faminc8b = (50000+74999)/2 if faminc8==12
(894 real changes made)

.      label var faminc8b "family income in 8th grade (dollars)"

.
.      // father's highest education
.      fre fathed8
```

fathed8 -- father's highest level of education

		Freq.	Percent	Valid	Cum.
Valid	1 not finish hs	873	15.39	15.39	15.39
	2 hs grad	1778	31.35	31.35	46.75
	3 junior coll	660	11.64	11.64	58.38
	4 coll <4	443	7.81	7.81	66.20
	5 coll grad	743	13.10	13.10	79.30
	6 masters	346	6.10	6.10	85.40
	7 doctorate	141	2.49	2.49	87.89
	8 dont know	687	12.11	12.11	100.00
	Total	5671	100.00	100.00	

```
.      gen fathed1 = fathed8==1 /* hs dropout */
.      gen fathed2 = fathed8==2 /* hs grad */
.      gen fathed3 = (fathed8>=3 & fathed8<=4) /* some college */
.      gen fathed4 = (fathed8>=5 & fathed8<=7) /* 4yr college or more */
.      label var fathed1 "father's highest ed: hs dropout"
.      label var fathed2 "father's highest ed: hs grad"
.      label var fathed3 "father's highest ed: some college"
.      label var fathed4 "father's highest ed: 4yr college or more"

.
.      // mother's highest education
.      fre mothed8
```

mothed8 -- mother's highest level of education

		Freq.	Percent	Valid	Cum.
Valid	1 not finish hs	815	14.37	14.37	14.37
	2 hs grad	2091	36.87	36.87	51.24
	3 junior coll	686	12.10	12.10	63.34
	4 coll <4	468	8.25	8.25	71.59
	5 coll grad	655	11.55	11.55	83.14
	6 masters	299	5.27	5.27	88.41
	7 doctorate	82	1.45	1.45	89.86
	8 dont know	575	10.14	10.14	100.00
	Total	5671	100.00	100.00	

```

.       gen mothed1 = mothed8==1 /* hs dropout */
.       gen mothed2 = mothed8==2 /* hs grad */
.       gen mothed3 = (mothed8>=3 & mothed8<=4) /* some college */
.       gen mothed4 = (mothed8>=5 & mothed8<=7) /* 4yr college or more */
.       label var mothed1 "mother's highest ed: hs dropout"
.       label var mothed2 "mother's highest ed: hs grad"
.       label var mothed3 "mother's highest ed: some college"
.       label var mothed4 "mother's highest ed: 4yr college or more"
.
.       forvalues j=1/4 {
2.         replace fathed`j'=. if fathed8==.
3.         replace mothed`j'=. if mothed8==.
4.       }
(0 real changes made)
(0 real changes made)
(0 real changes made)
(0 real changes made)
(0 real changes made)
(0 real changes made)
(0 real changes made)
(0 real changes made)

.       // highest education of two parents
.       egen pared8=rowmax(fathed8 mothed8)
.
.       gen pared1 = pared8==1 /* hs dropout */
.       gen pared2 = pared8==2 /* hs grad */
.       gen pared3 = (pared8>=3 & pared8<=4) /* some college */
.       gen pared4 = (pared8>=5 & pared8<=7) /* 4yr college or more */
.       label var pared1 "parent's highest ed: hs dropout"
.       label var pared2 "parent's highest ed: hs grad"
.       label var pared3 "parent's highest ed: some college"
.       label var pared4 "parent's highest ed: 4yr college or more"
.       label var pared8 "parent's highest education"
.
.       // z-scores for 8th and 12th grade reading and math scores
.       foreach g in 8 12 {
2.         foreach s in read math {
3.           egen `s'`g'z = std(`s'`g')
4.           label var `s'`g'z "z-score for `g'th grade `s'"
5.         }
6.       }

.       // parent expects child to go to college
.       codebook fhowfar mhowfar

-----
fhowfar                                     how far in schl r^s father wants r to go
-----

      Type: Numeric (byte)
      Label: farcat2

      Range: [1,6]                               Units: 1
Unique values: 6                               Missing .: 0/5,671

```

Tabulation:	Freq.	Numeric	Label
	47	1	not finish hs
	309	2	hs grad
	384	3	junior coll
	595	4	coll <4
	2,889	5	coll grad
	1,447	6	postsec ed

```
-----
mhowfar                                how far in schl r^s mother wants r to go
-----
```

```

Type: Numeric (byte)
Label: farcat2

```

```

Range: [1,6]                               Units: 1
Unique values: 6                           Missing .: 0/5,671

```

Tabulation:	Freq.	Numeric	Label
	42	1	not finish hs
	275	2	hs grad
	361	3	junior coll
	577	4	coll <4
	2,928	5	coll grad
	1,488	6	postsec ed

```

.   gen collegexp=(fhowfar>=5 & fhowfar<.) | (mhowfar>=5 & mhowfar<.)
.   label var collegexp "=1 if mother or father expects college+"
.
.   codebook riskdrop8

```

```
-----
riskdrop8                                # of risk factors for later dropout
-----
```

```

Type: Numeric (byte)

```

```

Range: [0,5]                               Units: 1
Unique values: 6                           Missing .: 0/5,671

```

Tabulation:	Freq.	Value
	3,369	0
	1,406	1
	623	2
	214	3
	52	4
	7	5

```

.   gen riskdrop1=riskdrop8==1
.   gen riskdrop2=(riskdrop8>=2 & riskdrop8<=5)
.   label var riskdrop1 "=1 if 1 dropout risk factor"
.   label var riskdrop2 "=1 if 2-5 dropout risk factors"
.
.   fre parmar8

```

```
parmar8 -- parents marital status in 8th grade
```

		Freq.	Percent	Valid	Cum.
Valid	1 divorced	543	9.58	9.58	9.58
	2 widowed	77	1.36	1.36	10.93
	3 separated	140	2.47	2.47	13.40
	4 never married	91	1.60	1.60	15.01
	5 not married but cohabit	93	1.64	1.64	16.65
	6 married	4727	83.35	83.35	100.00
	Total	5671	100.00	100.00	

```

.       gen byte parmarried=parmar8==6
.
.       label var parmarried "=1 if parents married in 8th grade"
.
.
. // *****
. // Part b - finding a propensity score
. // model for later use
. // *****
.
.       // Here I use psmatch2 (with logit, 1 nn match). I use the "ties"
.       // option to line up with teffects psmatch (used later in part c). If
.       // there are multiple nearest neighbors with the same pscore, all of
.       // them will be matched.
.
.       psmatch2 catholic c.math8z#c.math8z c.read8z#c.read8z female ///
>       black hisp api nativam riskdrop1 riskdrop2 disrupt nohw8 ///
>       c.faminc8b#c.faminc8b pared1-pared4 parmarried collegexp, ties logit

```

```

Logistic regression                                Number of obs =   5,671
                                                    LR chi2(20)    =  269.04
                                                    Prob > chi2    =  0.0000
                                                    Pseudo R2     =  0.0709
Log likelihood = -1763.1344

```

	catholic	Coefficient	Std. err.	z	P> z	[95% conf. interval]	
	math8z	-.0605341	.0732046	-0.83	0.408	-.2040125	.0829443
	c.math8z#c.math8z	-.1680258	.0495161	-3.39	0.001	-.2650755	-.070976
	read8z	.3255739	.0679117	4.79	0.000	.1924695	.4586783
	c.read8z#c.read8z	.0100256	.0484394	0.21	0.836	-.0849138	.104965
	female	.0419112	.0950359	0.44	0.659	-.1443558	.2281781
	black	-.2319429	.1917082	-1.21	0.226	-.6076841	.1437983
	hisp	-.0828599	.1589371	-0.52	0.602	-.3943709	.2286512
	api	-1.165599	.2812792	-4.14	0.000	-1.716896	-.6143023
	nativam	-.4855327	.2864356	-1.70	0.090	-1.046936	.0758707
	riskdrop1	.0232422	.1225025	0.19	0.850	-.2168583	.2633426
	riskdrop2	-.4050387	.2595379	-1.56	0.119	-.9137236	.1036463
	disrupt8	.218962	.1285199	1.70	0.088	-.0329324	.4708563
	nohw8	-.6282156	.1773147	-3.54	0.000	-.975746	-.2806852
	faminc8b	.0000303	.0000145	2.09	0.036	1.93e-06	.0000587
	c.faminc8b#c.faminc8b	-2.12e-10	1.74e-10	-1.22	0.221	-5.52e-10	1.28e-10
	pared1	-.7369748	.3315306	-2.22	0.026	-1.386763	-.0871868
	pared2	.1017425	.156011	0.65	0.514	-.2040334	.4075184
	pared3	.0949015	.158119	0.60	0.548	-.215006	.4048091
	pared4	.3071211	.1506848	2.04	0.042	.0117842	.6024579
	parmarried	.2471734	.1803656	1.37	0.171	-.1063367	.6006836
	collegexp	.2901846	.1432064	2.03	0.043	.0095053	.5708639
	_cons	-3.252608	.377756	-8.61	0.000	-3.992996	-2.51222

```

.
.       // check for balance
.       pstest

```

Variable	Mean		%bias	t-test		V(T)/ V(C)
	Treated	Control		t	p> t	
math8z	.22418	.26686	-4.4	-0.79	0.429	0.93
c.math8z#c.math8z	.87985	.96325	-7.4	-1.28	0.200	0.96
read8z	.38086	.40004	-2.0	-0.35	0.729	1.01
c.read8z#c.read8z	1.0578	1.0631	-0.5	-0.08	0.937	0.92
female	.54223	.53209	2.0	0.35	0.727	.
black	.05912	.06588	-2.5	-0.48	0.631	.
hisp	.08953	.10473	-5.0	-0.88	0.378	.
api	.02365	.02365	0.0	0.00	1.000	.
nativam	.02365	.02534	-1.0	-0.19	0.851	.
riskdrop1	.21115	.19257	4.4	0.80	0.426	.
riskdrop2	.0473	.04223	1.7	0.42	0.674	.
disrupt8	.16216	.17061	-2.2	-0.39	0.697	.
nohw8	.06588	.05405	3.8	0.86	0.392	.
faminc8b	.39534	.40008	-2.8	-0.50	0.615	1.02

c.faminc8b#c.faminc8b		1.8e+09	1.9e+09	-2.6		-0.43	0.670		0.97
pared1		.02027	.02196	-0.8		-0.20	0.840		.
pared2		.25169	.24155	2.3		0.40	0.686		.
pared3		.22804	.23311	-1.2		-0.21	0.836		.
pared4		.38007	.375	1.1		0.18	0.857		.
parmarried		.91216	.91385	-0.5		-0.10	0.918		.
collegexp		.88514	.88176	0.9		0.18	0.856		.

```
-----
* if variance ratio outside [0.85; 1.18]
```

Ps	R2	LR	chi2	p>chi2	MeanBias	MedBias	B	R	%Var
0.004		6.95	0.997		2.3	2.0	15.3	0.91	0

```
-----
* if B>25%, R outside [0.5; 2]
```

```
.
.      // treated and matched untreated cases
.      tabulate _treated _weight

psmatch2: |
Treatment |      psmatch2: weight of matched controls
assignment |      1          2          3          4 |      Total
-----+-----
Untreated |      442          58          10          1 |      511
Treated   |      592           0           0           0 |      592
-----+-----
Total    |      1,034          58          10          1 |      1,103

.      count if _treated==0 & _weight~.
511

.
.      // propensity scores (pre-match)
.      psgraph, name(psg, replace) ///
>      title(Propensity score distributions: full sample)

.
.      // overlapping histograms of propensity scores, matched sample
.      twoway (histogram _pscore if catholic==0 [fweight= weight], bin(20) ///
>      fcolor(none) lcolor(blue)) (histogram _pscore if catholic==1, ///
>      bin(20) bin(20) fcolor(none) lcolor(red)), ///
>      legend(label(1 Untreated) label(2 Treated)) ///
>      name(psg2, replace) ///
>      title(Propensity score distributions: matched sample)

.
.      graph combine psq psq2, row(1) xsize(8) ysize(4) ///
>      name(graph1, replace) ///
>      title(Propensity score distributions: after psmatch2)

.      graph export graph1.pdf, name(graph1) as(pdf) replace
file graph1.pdf saved as PDF format

.
.      // now show tebalance and overlap after teffects psmatch--
.      // same model specification as above
.
.      capture drop _*
.
.      capture drop nn*

.      quietly teffects psmatch (math12z) (catholic c.math8z#c.math8z ///
>      c.read8z#c.read8z female black hisp api nativam riskdrop1 ///
>      riskdrop2 disrupt nohw8 c.faminc8b#c.faminc8b pared1-pared4 ///
>      parmarried collegexp, logit), atet gen(nn)
```

```
.
. // check for balance (now using tebalance)
. tebalance summarize math8z read8z female black hisp api nativam ///
> riskdrop1 riskdrop2 disrupt nohw8 faminc8b pared1-pared4 ///
> parmarried collegexp
```

Covariate balance summary

	Raw	Matched
Number of obs =	5,671	1,184
Treated obs =	592	592
Control obs =	5,079	592

	Standardized differences		Variance ratio	
	Raw	Matched	Raw	Matched
math8z	.2606656	-.0459574	.8200688	.9300023
read8z	.4356571	-.020112	.9223486	1.01078
female	.0496905	.0203104	.9955598	.9969744
black	-.1579425	-.0278925	.6082682	.9039273
hisp	-.0974819	-.051311	.7768816	.8693548
api	-.1926191	0	.3939964	1
nativam	-.0940456	-.0109189	.5998088	.9349509
riskdrop1	-.0974069	.0462655	.8844729	1.071258
riskdrop2	-.4043775	.0244877	.3184886	1.114074
disrupt8	-.0513382	-.0226605	.9158064	.9601742
nohw8	-.2800718	.0497759	.4771307	1.203516
faminc8b	.4572743	-.0292189	.8885848	1.018881
pared1	-.3007707	-.0117397	.2493092	.9246712
pared2	-.0780238	.0234947	.9231649	1.028034
pared3	.0180324	-.0120213	1.025671	.9847251
pared4	.2797614	.0104449	1.254392	1.005296
parmarried	.2616919	-.0059887	.5542313	1.017723
collegexp	.2563305	.0105195	.6169925	.9751505

```
.
. tebalance box math8z, name(balmath, replace)
.
. tebalance box read8z, name(balread, replace)
.
. tebalance density faminc8b, name(balinc, replace)
.
. graph combine balmath balread balinc, col(1) xsize(4) ysize(8) ///
> name(graph2, replace) ///
> title(Covariate balance: after teffects psmatch, size(medsmall))

. graph export graph2.pdf, as(pdf) replace
file graph2.pdf saved as PDF format

.
. // propensity scores (all observations)
. teffects overlap, ptlevel(1) name(graph3a, replace) ///
> title(Propensity score distribution: all obs, size(medsmall))

. capture drop ps0 ps1
.
. predict ps0 ps1, ps

.
. // propensity scores (all observations + matched sample)
. tebalance density, name(graph3b, replace) ///
> byopts(title(Propensity score distribution: all and matched sample, size
> (medsmall)))
```

```

.      // NOTE: the above tebalance density command shows the densities of
.      // pscore for the matched sample. FYI the code below will manually
.      // take the estimate pcores and produce overlapping densities. This
.      // is a bit cumbersome since it requires identifying the matches
.      // manually using the nn1 id
.      capture drop ob

.      gen ob=_n

.      preserve

.      tempfile treated

.      keep if catholic==1
(5,079 observations deleted)

.      keep nn1

.      bysort nn1: gen weight=_N

.      by nn1: keep if _n==1
(81 observations deleted)

.      rename nn1 ob

.      save `treated'
file C:\Users\corcorssp\AppData\Local\Temp\ST_ec14_000002.tmp saved as .dta format

.      restore

.      merge m:1 ob using `treated'
(variable ob was float, now double to accommodate using data's values)

      Result                                Number of obs
-----
Not matched                                5,160
   from master                            5,160   (_merge==1)
   from using                             0       (_merge==2)

Matched                                   511   (_merge==3)
-----

.      replace weight=1 if catholic==1
(592 real changes made)

.      tabstat  ps1 if weight~=., by(catholic)

Summary for variables: ps1
Group variable: catholic (attended catholic hs?)

catholic |      Mean
-----+-----
   no |   .1408498
   yes |   .145605
-----+-----
  Total |   .143402
-----

.      twoway (kdensity ps1 if catholic==0 & weight~=. ) ///
>      (kdensity ps1 if catholic==1) , name(graph3c, replace) ///
>      legend(label(1 Untreated) label(2 Treated)) xtitle(Propensity score) ///
>      title(Propensity score distribution: matched sample - manual, size(medsmall))

.      graph combine graph3a graph3b graph3c, col(1) xsize(4) ysize(8) ///
>      name(graph3, replace) ///
>      title(Propensity score distributions: after teffects psmatch, size(medium))
> m))

```

```
. graph export graph3.pdf, as(pdf) replace
file graph3.pdf saved as PDF format
```

```
. graph close _all
```

```
. drop nn1 ps0 ps1 ob weight _merge
```

```
.
. // *****
. // Part c - estimate ATT using model
. // decided above
. // *****
. // show using both teffects psmatch and psmatch2
.
. foreach j in math12z read12z hsgrad inpse {
2. display in red "Outcome: `j'"
3.
. _eststo psm`j': teffects psmatch (`j') (catholic ///
> c.math8z#c.math8z c.read8z#c.read8z female black ///
> hisp api nativam riskdrop1 riskdrop2 disrupt nohw8 ///
> c.faminc8b#c.faminc8b pared1-pared4 ///
> parmarried collegexp, logit), atet
4.
. psmatch2 catholic c.math8z#c.math8z c.read8z#c.read8z ///
> female black hisp api nativam riskdrop1 riskdrop2 disrupt ///
> nohw8 c.faminc8b#c.faminc8b pared1-pared4 ///
> parmarried collegexp, logit outcome(`j')
5. }
```

```
Outcome: math12z
```

```
Treatment-effects estimation      Number of obs =      5,671
Estimator      : propensity-score matching      Matches: requested =      1
Outcome model  : matching                      min =      1
Treatment model: logit                      max =      1
```

	math12z	Coefficient	AI robust std. err.	z	P> z	[95% conf. interval]	
ATET							
catholic							
(yes vs no)		.1190682	.0423528	2.81	0.005	.0360583	.2020782

```
Logistic regression      Number of obs =      5,671
LR chi2(20) =      269.04
Prob > chi2 =      0.0000
Pseudo R2 =      0.0709
```

	catholic	Coefficient	Std. err.	z	P> z	[95% conf. interval]	
math8z		-.0605341	.0732046	-0.83	0.408	-.2040125	.0829443
c.math8z#c.math8z		-.1680258	.0495161	-3.39	0.001	-.2650755	-.070976
read8z		.3255739	.0679117	4.79	0.000	.1924695	.4586783
c.read8z#c.read8z		.0100256	.0484394	0.21	0.836	-.0849138	.104965
female		.0419112	.0950359	0.44	0.659	-.1443558	.2281781
black		-.2319429	.1917082	-1.21	0.226	-.6076841	.1437983
hisp		-.0828599	.1589371	-0.52	0.602	-.3943709	.2286512
api		-1.165599	.2812792	-4.14	0.000	-1.716896	-.6143023
nativam		-.4855327	.2864356	-1.70	0.090	-1.046936	.0758707
riskdrop1		.0232422	.1225025	0.19	0.850	-.2168583	.2633426
riskdrop2		-.4050387	.2595379	-1.56	0.119	-.9137236	.1036463
disrupt8		.218962	.1285199	1.70	0.088	-.0329324	.4708563
nohw8		-.6282156	.1773147	-3.54	0.000	-.975746	-.2806852
faminc8b		.0000303	.0000145	2.09	0.036	1.93e-06	.0000587
c.faminc8b#c.faminc8b		-2.12e-10	1.74e-10	-1.22	0.221	-5.52e-10	1.28e-10
pared1		-.7369748	.3315306	-2.22	0.026	-1.386763	-.0871868
pared2		.1017425	.156011	0.65	0.514	-.2040334	.4075184
pared3		.0949015	.158119	0.60	0.548	-.215006	.4048091
pared4		.3071211	.1506848	2.04	0.042	.0117842	.6024579
parmarried		.2471734	.1803656	1.37	0.171	-.1063367	.6006836
collegexp		.2901846	.1432064	2.03	0.043	.0095053	.5708639

	_cons		-3.252608	.377756	-8.61	0.000	-3.992996	-2.51222

	Variable	Sample		Treated	Controls	Difference	S.E.	T-stat

	math12z	Unmatched		.367093217	-.04278779	.409881007	.043090321	9.51
		ATT		.367093217	.248024987	.11906823	.056728857	2.10

Note: S.E. does not take into account that the propensity score is estimated.

		psmatch2:
psmatch2:		Common
Treatment		support
assignment		On suppor
		Total

Untreated		5,079
Treated		592

Total		5,671

Outcome: read12z

Treatment-effects estimation	Number of obs	=	5,671
Estimator : propensity-score matching	Matches: requested	=	1
Outcome model : matching	min	=	1
Treatment model: logit	max	=	1

		AI robust				
read12z		Coefficient	std. err.	z	P> z	[95% conf. interval]

ATET						
catholic						
(yes vs no)		.0242824	.0426474	0.57	0.569	-.0593049 .1078698

Logistic regression

Number of obs	=	5,671
LR chi2(20)	=	269.04
Prob > chi2	=	0.0000
Pseudo R2	=	0.0709

Log likelihood = -1763.1344

	catholic		Coefficient	Std. err.	z	P> z	[95% conf. interval]

	math8z		-.0605341	.0732046	-0.83	0.408	-.2040125 .0829443
	c.math8z#c.math8z		-.1680258	.0495161	-3.39	0.001	-.2650755 -.070976
	read8z		.3255739	.0679117	4.79	0.000	.1924695 .4586783
	c.read8z#c.read8z		.0100256	.0484394	0.21	0.836	-.0849138 .104965
	female		.0419112	.0950359	0.44	0.659	-.1443558 .2281781
	black		-.2319429	.1917082	-1.21	0.226	-.6076841 .1437983
	hisp		-.0828599	.1589371	-0.52	0.602	-.3943709 .2286512
	api		-1.165599	.2812792	-4.14	0.000	-1.716896 -.6143023
	nativam		-.4855327	.2864356	-1.70	0.090	-1.046936 .0758707
	riskdrop1		.0232422	.1225025	0.19	0.850	-.2168583 .2633426
	riskdrop2		-.4050387	.2595379	-1.56	0.119	-.9137236 .1036463
	disrupt8		.218962	.1285199	1.70	0.088	-.0329324 .4708563
	nohw8		-.6282156	.1773147	-3.54	0.000	-.975746 -.2806852
	faminc8b		.0000303	.0000145	2.09	0.036	1.93e-06 .0000587
	c.faminc8b#c.faminc8b		-2.12e-10	1.74e-10	-1.22	0.221	-5.52e-10 1.28e-10
	pared1		-.7369748	.3315306	-2.22	0.026	-1.386763 -.0871868
	pared2		.1017425	.156011	0.65	0.514	-.2040334 .4075184
	pared3		.0949015	.158119	0.60	0.548	-.215006 .4048091
	pared4		.3071211	.1506848	2.04	0.042	.0117842 .6024579
	parmarried		.2471734	.1803656	1.37	0.171	-.1063367 .6006836
	collegexp		.2901846	.1432064	2.03	0.043	.0095053 .5708639
	_cons		-3.252608	.377756	-8.61	0.000	-3.992996 -2.51222

	Variable	Sample		Treated	Controls	Difference	S.E.	T-stat

	read12z	Unmatched		.328277963	-.038263548	.366541511	.043159142	8.49
		ATT		.328277963	.303995523	.02428244	.057104586	0.43

Note: S.E. does not take into account that the propensity score is estimated.

```

      | psmatch2:
psmatch2: | Common
Treatment | support
assignment | On suppor | Total
-----+-----+-----
Untreated | 5,079 | 5,079
Treated | 592 | 592
-----+-----+-----
Total | 5,671 | 5,671
Outcome: hsgrad

```

```

Treatment-effects estimation      Number of obs = 5,671
Estimator : propensity-score matching  Matches: requested = 1
Outcome model : matching              min = 1
Treatment model: logit                max = 1

```

```

      | AI robust
hsgrad | Coefficient std. err. z P>|z| [95% conf. interval]
-----+-----
ATET
catholic |
(yes vs no) | .0304054 .0121141 2.51 0.012 .0066622 .0541486
-----+-----

```

```

Logistic regression      Number of obs = 5,671
                        LR chi2(20) = 269.04
                        Prob > chi2 = 0.0000
Log likelihood = -1763.1344      Pseudo R2 = 0.0709

```

```

-----+-----+-----
catholic | Coefficient Std. err. z P>|z| [95% conf. interval]
-----+-----+-----
math8z | -.0605341 .0732046 -0.83 0.408 -.2040125 .0829443
c.math8z#c.math8z | -.1680258 .0495161 -3.39 0.001 -.2650755 -.070976
read8z | .3255739 .0679117 4.79 0.000 .1924695 .4586783
c.read8z#c.read8z | .0100256 .0484394 0.21 0.836 -.0849138 .104965
female | .0419112 .0950359 0.44 0.659 -.1443558 .2281781
black | -.2319429 .1917082 -1.21 0.226 -.6076841 .1437983
hisp | -.0828599 .1589371 -0.52 0.602 -.3943709 .2286512
api | -1.165599 .2812792 -4.14 0.000 -1.716896 -.6143023
nativam | -.4855327 .2864356 -1.70 0.090 -1.046936 .0758707
riskdrop1 | .0232422 .1225025 0.19 0.850 -.2168583 .2633426
riskdrop2 | -.4050387 .2595379 -1.56 0.119 -.9137236 .1036463
disrupt8 | .218962 .1285199 1.70 0.088 -.0329324 .4708563
nohw8 | -.6282156 .1773147 -3.54 0.000 -.975746 -.2806852
faminc8b | .0000303 .0000145 2.09 0.036 1.93e-06 .0000587
c.faminc8b#c.faminc8b | -2.12e-10 1.74e-10 -1.22 0.221 -5.52e-10 1.28e-10
pared1 | -.7369748 .3315306 -2.22 0.026 -1.386763 -.0871868
pared2 | .1017425 .156011 0.65 0.514 -.2040334 .4075184
pared3 | .0949015 .158119 0.60 0.548 -.215006 .4048091
pared4 | .3071211 .1506848 2.04 0.042 .0117842 .6024579
parmarried | .2471734 .1803656 1.37 0.171 -.1063367 .6006836
collegexp | .2901846 .1432064 2.03 0.043 .0095053 .5708639
_cons | -3.252608 .377756 -8.61 0.000 -3.992996 -2.51222
-----+-----+-----

```

```

-----+-----+-----
Variable Sample | Treated Controls Difference S.E. T-stat
-----+-----+-----
hsgrad Unmatched | .974662162 .910218547 .064443615 .01195636 5.39
ATT | .974662162 .944256757 .030405405 .012694851 2.40
-----+-----+-----

```

Note: S.E. does not take into account that the propensity score is estimated.

```

      | psmatch2:
psmatch2: | Common
Treatment | support
assignment | On suppor | Total
-----+-----+-----
Untreated | 5,079 | 5,079
Treated | 592 | 592
-----+-----+-----
Total | 5,671 | 5,671
Outcome: inpspe

```

Treatment-effects estimation	Number of obs	=	5,671
Estimator : propensity-score matching	Matches: requested	=	1
Outcome model : matching	min	=	1
Treatment model: logit	max	=	1

	inpse	Coefficient	AI robust std. err.	z	P> z	[95% conf. interval]	
ATET							
catholic							
(yes vs no)		.0726351	.0219293	3.31	0.001	.0296544	.1156158

Logistic regression	Number of obs	=	5,671
	LR chi2(20)	=	269.04
	Prob > chi2	=	0.0000
Log likelihood = -1763.1344	Pseudo R2	=	0.0709

	catholic	Coefficient	Std. err.	z	P> z	[95% conf. interval]	
math8z		-.0605341	.0732046	-0.83	0.408	-.2040125	.0829443
c.math8z#c.math8z		-.1680258	.0495161	-3.39	0.001	-.2650755	-.070976
read8z		.3255739	.0679117	4.79	0.000	.1924695	.4586783
c.read8z#c.read8z		.0100256	.0484394	0.21	0.836	-.0849138	.104965
female		.0419112	.0950359	0.44	0.659	-.1443558	.2281781
black		-.2319429	.1917082	-1.21	0.226	-.6076841	.1437983
hisp		-.0828599	.1589371	-0.52	0.602	-.3943709	.2286512
api		-1.165599	.2812792	-4.14	0.000	-1.716896	-.6143023
nativam		-.4855327	.2864356	-1.70	0.090	-1.046936	.0758707
riskdrop1		.0232422	.1225025	0.19	0.850	-.2168583	.2633426
riskdrop2		-.4050387	.2595379	-1.56	0.119	-.9137236	.1036463
disrupt8		.218962	.1285199	1.70	0.088	-.0329324	.4708563
nohw8		-.6282156	.1773147	-3.54	0.000	-.975746	-.2806852
faminc8b		.0000303	.0000145	2.09	0.036	1.93e-06	.0000587
c.faminc8b#c.faminc8b		-2.12e-10	1.74e-10	-1.22	0.221	-5.52e-10	1.28e-10
pared1		-.7369748	.3315306	-2.22	0.026	-1.386763	-.0871868
pared2		.1017425	.156011	0.65	0.514	-.2040334	.4075184
pared3		.0949015	.158119	0.60	0.548	-.215006	.4048091
pared4		.3071211	.1506848	2.04	0.042	.0117842	.6024579
parmarried		.2471734	.1803656	1.37	0.171	-.1063367	.6006836
collegexp		.2901846	.1432064	2.03	0.043	.0095053	.5708639
_cons		-3.252608	.377756	-8.61	0.000	-3.992996	-2.51222

Variable	Sample	Treated	Controls	Difference	S.E.	T-stat
inpse	Unmatched	.861486486	.6914747	.170011787	.019595842	8.68
	ATT	.861486486	.788851351	.072635135	.024156682	3.01

Note: S.E. does not take into account that the propensity score is estimated.

	psmatch2:
psmatch2:	Common
Treatment	support
assignment	On suppor
	Total
Untreated	5,079
Treated	592
Total	5,671

```
.
.      table _treated _weight
```

	psmatch2: weight of matched controls				
	1	2	3	4	Total
psmatch2: Treatment assignment					
Untreated	442	58	10	1	511
Treated	592				592
Total	1,034	58	10	1	1,103

```
.      count if _treated==0 & _weight~=.
.      511
```

```
.
.
.  // *****
.  // Part d - estimate ATT and ATE using IPW and
.  // pscore model decided above
.  // *****
.
.      foreach j in math12z read12z hsgrad inpse {
.      2.          display in red "Outcome: `j'"
.      3.
.          _eststo ipwatt`j': teffects ipw (`j') (catholic ///
.              c.math8z##c.math8z c.read8z##c.read8z female black ///
.              hisp api nativam riskdrop1 riskdrop2 disrupt nohw8 ///
.              c.faminc8b##c.faminc8b pared1-pared4 ///
.              parmarried collegexp, logit), atet
.      4.
.          _eststo ipwate`j': teffects ipw (`j') (catholic ///
.              c.math8z##c.math8z c.read8z##c.read8z female black ///
.              hisp api nativam riskdrop1 riskdrop2 disrupt nohw8 ///
.              c.faminc8b##c.faminc8b pared1-pared4 ///
.              parmarried collegexp, logit), ate
.      5.      }
Outcome: math12z
```

Iteration 0: EE criterion = 7.819e-21

Iteration 1: EE criterion = 1.322e-32

The Gauss-Newton stopping criterion has been met but missing standard errors indicate some of the parameters are not identified.

Treatment-effects estimation Number of obs = 5,671

Estimator : inverse-probability weights

Outcome model : weighted mean

Treatment model: logit

	math12z	Coefficient	Robust std. err.	z	P> z	[95% conf. interval]	
ATET							
	catholic						
	(yes vs no)	.1208028	.0231066	5.23	0.000	.0755148	.1660909
POmean							
	catholic						
	no	.2462904	.0319048	7.72	0.000	.1837582	.3088226

Warning: Convergence not achieved.

Iteration 0: EE criterion = 7.819e-21

Iteration 1: EE criterion = 3.839e-34

The Gauss-Newton stopping criterion has been met but missing standard errors indicate some of the parameters are not identified.

Treatment-effects estimation Number of obs = 5,671

Estimator : inverse-probability weights

Outcome model : weighted mean

Treatment model: logit

	math12z	Coefficient	Robust std. err.	z	P> z	[95% conf. interval]	
ATE							
	catholic						
	(yes vs no)	.0983067	.0546021	1.80	0.072	-.0087113	.2053248

POmean							
	catholic						
	no	-.0126136	.0134597	-0.94	0.349	-.0389941	.0137669

Warning: Convergence not achieved.
Outcome: read12z

Iteration 0: EE criterion = 7.819e-21
Iteration 1: EE criterion = 6.888e-34
The Gauss-Newton stopping criterion has been met but missing standard errors indicate some of the parameters are not identified.

Treatment-effects estimation Number of obs = 5,671
Estimator : inverse-probability weights
Outcome model : weighted mean
Treatment model: logit

	read12z	Coefficient	Robust std. err.	z	P> z	[95% conf. interval]
ATET						
	catholic					
	(yes vs no)	.0412662	.0277719	1.49	0.137	-.0131658 .0956982
POmean						
	catholic					
	no	.2870117	.0293521	9.78	0.000	.2294827 .3445408

Warning: Convergence not achieved.

Iteration 0: EE criterion = 7.819e-21
Iteration 1: EE criterion = 1.166e-33
The Gauss-Newton stopping criterion has been met but missing standard errors indicate some of the parameters are not identified.

Treatment-effects estimation Number of obs = 5,671
Estimator : inverse-probability weights
Outcome model : weighted mean
Treatment model: logit

	read12z	Coefficient	Robust std. err.	z	P> z	[95% conf. interval]
ATE						
	catholic					
	(yes vs no)	.0210077	.0602739	0.35	0.727	-.0971271 .1391425
POmean						
	catholic					
	no	-.0043111	.0135662	-0.32	0.751	-.0309003 .0222782

Warning: Convergence not achieved.
Outcome: hsgrad

Iteration 0: EE criterion = 7.819e-21
Iteration 1: EE criterion = 7.463e-34
The Gauss-Newton stopping criterion has been met but missing standard errors indicate some of the parameters are not identified.

Treatment-effects estimation Number of obs = 5,671
Estimator : inverse-probability weights
Outcome model : weighted mean
Treatment model: logit

	hsgrad	Coefficient	Robust std. err.	z	P> z	[95% conf. interval]
ATET						
	catholic					
	(yes vs no)	.0221956	.0071377	3.11	0.002	.0082059 .0361853
POmean						
	catholic					
	no	.9524665	.003826	248.95	0.000	.9449677 .9599654

Warning: Convergence not achieved.

Iteration 0: EE criterion = 7.819e-21
 Iteration 1: EE criterion = 4.915e-34
 The Gauss-Newton stopping criterion has been met but missing standard errors
 indicate some of the parameters are not identified.

Treatment-effects estimation Number of obs = 5,671
 Estimator : inverse-probability weights
 Outcome model : weighted mean
 Treatment model: logit

	hsgrad	Coefficient	Robust std. err.	z	P> z	[95% conf. interval]	
ATE							
	catholic (yes vs no)	.0290058	.0209966	1.38	0.167	-.0121467	.0701584
POMean							
	catholic no	.9146284	.0038238	239.19	0.000	.9071339	.922123

Warning: Convergence not achieved.
 Outcome: inpse

Iteration 0: EE criterion = 7.819e-21
 Iteration 1: EE criterion = 1.478e-32
 The Gauss-Newton stopping criterion has been met but missing standard errors
 indicate some of the parameters are not identified.

Treatment-effects estimation Number of obs = 5,671
 Estimator : inverse-probability weights
 Outcome model : weighted mean
 Treatment model: logit

	inpse	Coefficient	Robust std. err.	z	P> z	[95% conf. interval]	
ATET							
	catholic (yes vs no)	.0636729	.0148925	4.28	0.000	.0344843	.0928616
POMean							
	catholic no	.7978135	.008995	88.70	0.000	.7801837	.8154434

Warning: Convergence not achieved.

Iteration 0: EE criterion = 7.819e-21
 Iteration 1: EE criterion = 2.078e-32
 The Gauss-Newton stopping criterion has been met but missing standard errors
 indicate some of the parameters are not identified.

Treatment-effects estimation Number of obs = 5,671
 Estimator : inverse-probability weights
 Outcome model : weighted mean
 Treatment model: logit

	inpse	Coefficient	Robust std. err.	z	P> z	[95% conf. interval]	
ATE							
	catholic (yes vs no)	.1301173	.0200468	6.49	0.000	.0908263	.1694082
POMean							
	catholic no	.7025744	.0062853	111.78	0.000	.6902554	.7148934

Warning: Convergence not achieved.

```

.
.      esttab _all using PS3estimates.csv, se paren csv replace
(output written to PS3estimates.csv)

.
. // *****
. // Part e - try pestimate
. // *****
.
.      ssc install pestimate
checking pestimate consistency and verifying not already installed...
all files already exist and are up to date.

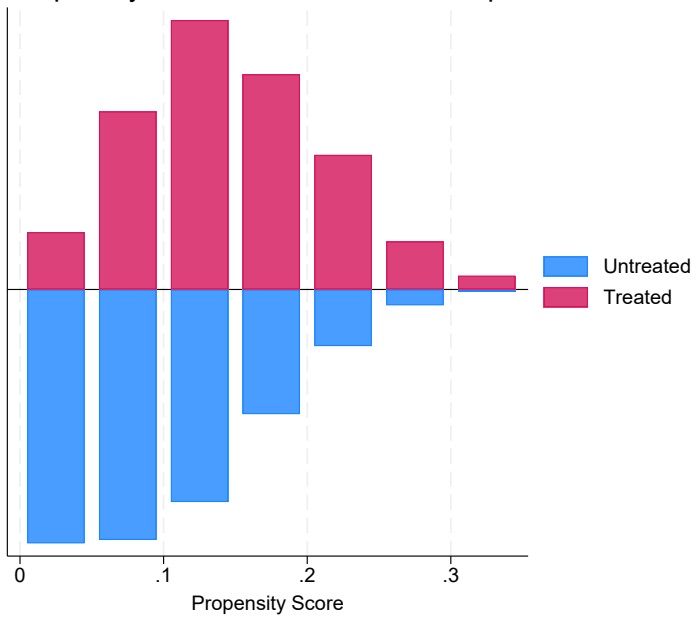
.      pestimate catholic, tottry(math8z read8z female black hisp ///
>      api riskdrop1 riskdrop2 disrupt nohw8 faminc8b pared1-pared4 ///
>      parmarried collegexp) genpscore(pscore)
Selecting first order covariates... (153)
-----+--- 1 -----+--- 2 -----+--- 3 -----+--- 4 -----+--- 5
.....s.....s.....s.....s..      50
.....s.....s.....s.....s..      100
.....s.....s.....s.....s.....
Selected first order covariates are: faminc8b read8z api riskdrop2 nohw8 pared1 math8z col
> legexp pared4 black parmarried disrupt8
Selecting second order covariates... (3,081)
-----+--- 1 -----+--- 2 -----+--- 3 -----+--- 4 -----+--- 5
.....      50
.....s.....      100
.....      150
.....s.....      200
.....s.....      250
.....      300
.....s.....      350
.....s.....      400
.....      450
.....s.....      500
.....s.....      550
.....s.....      600
.....      650
.....s.....      700
.....
Selected second order covariates are: c.math8z#c.math8z c.disrupt8#c.collegexp c.black#c.c
> ollegexp c.pared1#c.read8z c.black#c.faminc8b c.pared1#c.faminc8b c.math8z#c.api c.parma
> rried#c.riskdrop2 c.disrupt8#c.black
Final model is: faminc8b read8z api riskdrop2 nohw8 pared1 math8z collegexp pared4 black p
> armarried disrupt8 c.math8z#c.math8z c.disrupt8#c.collegexp c.black#c.collegexp c.pared1
> #c.read8z c.black#c.faminc8b c.pared1#c.faminc8b c.math8z#c.api c.parmarried#c.riskdrop2
> c.disrupt8#c.black

.
.      // Close log and convert to PDF
.      capture log close

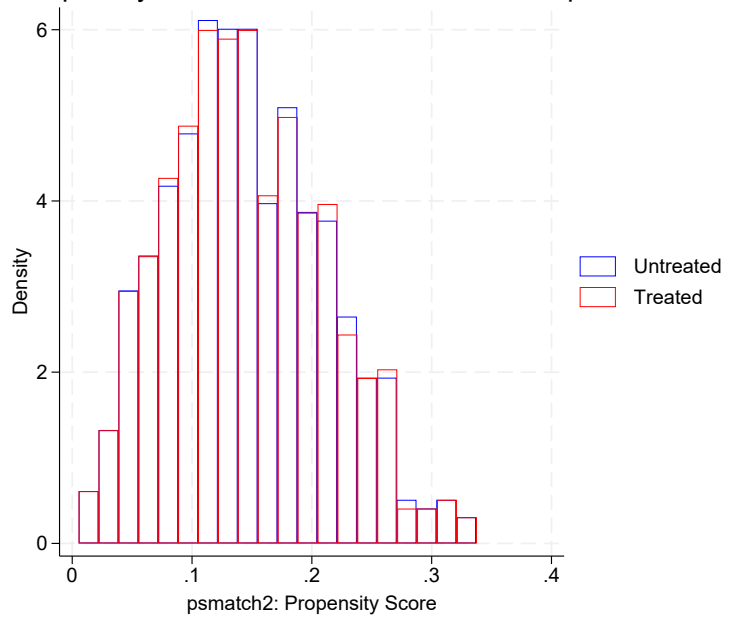
```

Propensity score distributions: after psmatch2

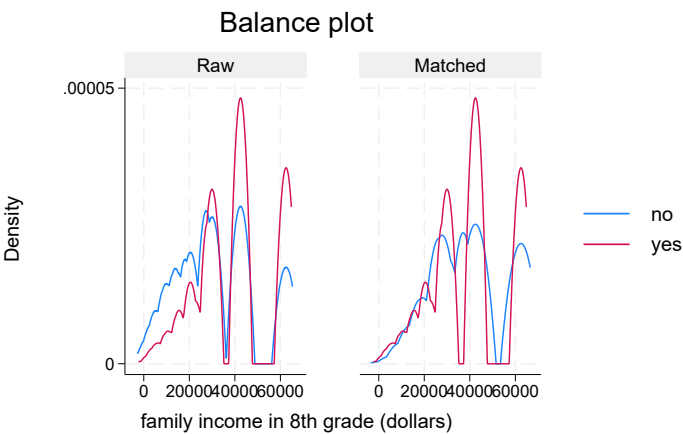
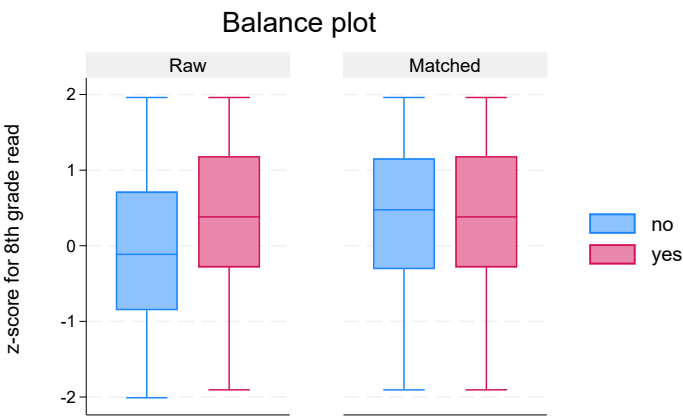
Propensity score distributions: full sample



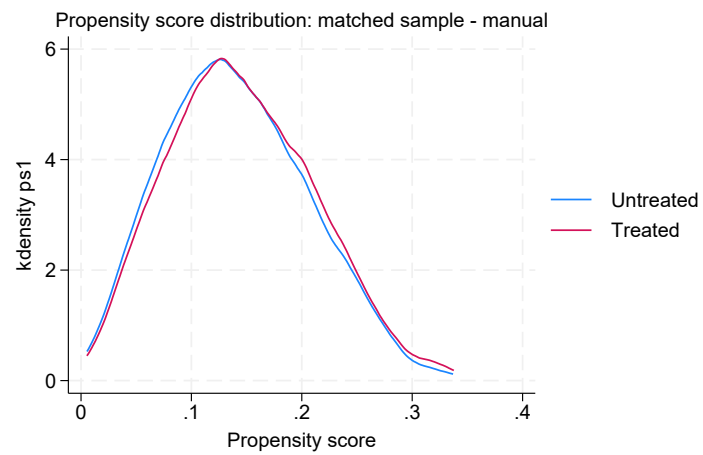
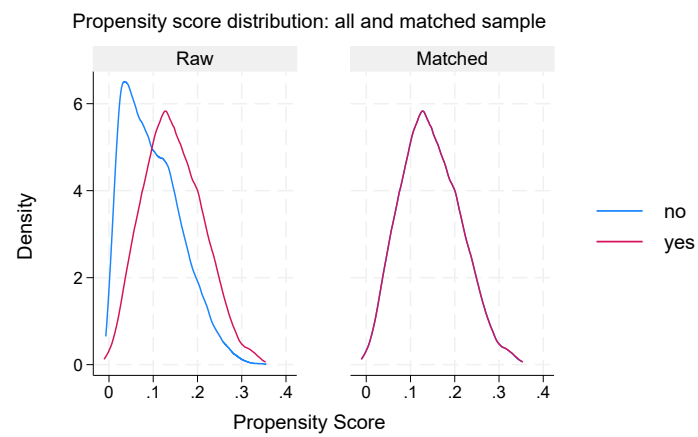
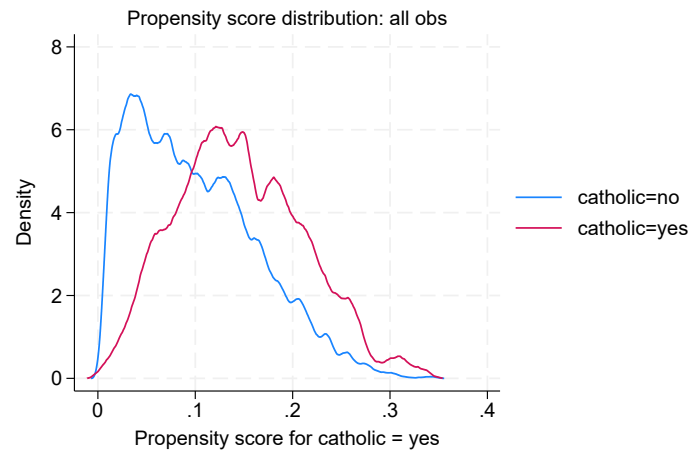
Propensity score distributions: matched sample



Covariate balance: after teffects psmatch



Propensity score distributions: after teffects psmatch



	PSM (1) math12z	PSM (2) read12z	PSM (3) hsgrad	PSM (4) inpse	IPW-ATT (5) math12z	IPW-ATE (6) math12z	IPW-ATT (7) read12z	IPW-ATE (8) read12z	IPW-ATT (9) hsgrad	IPW-ATE (10) hsgrad	IPW-ATT (11) inpse	IPW-ATE (12) inpse
main												
r1vs0.catholic	0.119** (0.0424)	0.0243 (0.0426)	0.0304* (0.0121)	0.0726*** (0.0219)	0.121*** (0.0231)	0.0983 (0.0546)	0.0413 (0.0278)	0.0210 (0.0603)	0.0222** (0.00714)	0.0290 (0.0210)	0.0637*** (0.0149)	0.130*** (0.0200)
POmean												
0.catholic					0.246*** (0.0319)	-0.0126 (0.0135)	0.287*** (0.0294)	-0.00431 (0.0136)	0.952*** (0.00383)	0.915*** (0.00382)	0.798*** (0.00900)	0.703*** (0.00629)
TME1												
math8z					-0.0605 (0.0720)	-0.0605 (0.0720)	-0.0605 (0.0720)	-0.0605 (0.0720)	-0.0605 (0.0720)	-0.0605 (0.0720)	-0.0605 (0.0720)	-0.0605 (0.0720)
c.math8z#c.math8z					-0.168*** (0.0504)	-0.168*** (0.0504)	-0.168*** (0.0504)	-0.168*** (0.0504)	-0.168*** (0.0504)	-0.168*** (0.0504)	-0.168*** (0.0504)	-0.168*** (0.0504)
read8z					0.326*** (0.0681)	0.326*** (0.0681)	0.326*** (0.0681)	0.326*** (0.0681)	0.326*** (0.0681)	0.326*** (0.0681)	0.326*** (0.0681)	0.326*** (0.0681)
c.read8z#c.read8z					0.0100 (0.0491)	0.0100 (0.0491)	0.0100 (0.0491)	0.0100 (0.0491)	0.0100 (0.0491)	0.0100 (0.0491)	0.0100 (0.0491)	0.0100 (0.0491)
female					0.0419 (0.0939)	0.0419 (0.0939)	0.0419 (0.0939)	0.0419 (0.0939)	0.0419 (0.0939)	0.0419 (0.0939)	0.0419 (0.0939)	0.0419 (0.0939)
black					-0.232 (0.190)	-0.232 (0.190)	-0.232 (0.190)	-0.232 (0.190)	-0.232 (0.190)	-0.232 (0.190)	-0.232 (0.190)	-0.232 (0.190)
hisp					-0.0829 (0.157)	-0.0829 (0.157)	-0.0829 (0.157)	-0.0829 (0.157)	-0.0829 (0.157)	-0.0829 (0.157)	-0.0829 (0.157)	-0.0829 (0.157)
api					-1.166*** (0.282)	-1.166*** (0.282)	-1.166*** (0.282)	-1.166*** (0.282)	-1.166*** (0.282)	-1.166*** (0.282)	-1.166*** (0.282)	-1.166*** (0.282)
nativam					-0.486 (0.283)	-0.486 (0.283)	-0.486 (0.283)	-0.486 (0.283)	-0.486 (0.283)	-0.486 (0.283)	-0.486 (0.283)	-0.486 (0.283)
riskdrop1					0.0232 (0.117)	0.0232 (0.117)	0.0232 (0.117)	0.0232 (0.117)	0.0232 (0.117)	0.0232 (0.117)	0.0232 (0.117)	0.0232 (0.117)
riskdrop2					-0.405 (0.242)	-0.405 (0.242)	-0.405 (0.242)	-0.405 (0.242)	-0.405 (0.242)	-0.405 (0.242)	-0.405 (0.242)	-0.405 (0.242)
disrupt8					0.219 (0.127)	0.219 (0.127)	0.219 (0.127)	0.219 (0.127)	0.219 (0.127)	0.219 (0.127)	0.219 (0.127)	0.219 (0.127)
nohw8					-0.628*** (0.177)	-0.628*** (0.177)	-0.628*** (0.177)	-0.628*** (0.177)	-0.628*** (0.177)	-0.628*** (0.177)	-0.628*** (0.177)	-0.628*** (0.177)
faminc8b					0.0000303 (0.0000151)	0.0000303 (0.0000151)	0.0000303 (0.0000151)	0.0000303 (0.0000151)	0.0000303 (0.0000151)	0.0000303 (0.0000151)	0.0000303 (0.0000151)	0.0000303 (0.0000151)
c.faminc8b#c.faminc					-2.12e-10 (1.80e-10)	-2.12e-10 (1.80e-10)	-2.12e-10 (1.80e-10)	-2.12e-10 (1.80e-10)	-2.12e-10 (1.80e-10)	-2.12e-10 (1.80e-10)	-2.12e-10 (1.80e-10)	-2.12e-10 (1.80e-10)
pared1					-0.737* (0.323)	-0.737* (0.323)	-0.737* (0.323)	-0.737* (0.323)	-0.737* (0.323)	-0.737* (0.323)	-0.737* (0.323)	-0.737* (0.323)
pared2					0.102 (0.156)	0.102 (0.156)	0.102 (0.156)	0.102 (0.156)	0.102 (0.156)	0.102 (0.156)	0.102 (0.156)	0.102 (0.156)
pared3					0.0949 (0.158)	0.0949 (0.158)	0.0949 (0.158)	0.0949 (0.158)	0.0949 (0.158)	0.0949 (0.158)	0.0949 (0.158)	0.0949 (0.158)

	PSM (1) math12z	PSM (2) read12z	PSM (3) hsgrad	PSM (4) inpse	IPW-ATT (5) math12z	IPW-ATE (6) math12z	IPW-ATT (7) read12z	IPW-ATE (8) read12z	IPW-ATT (9) hsgrad	IPW-ATE (10) hsgrad	IPW-ATT (11) inpse	IPW-ATE (12) inpse
pared4					0.307* (0.151)	0.307* (0.151)	0.307* (0.151)	0.307* (0.151)	0.307* (0.151)	0.307* (0.151)	0.307* (0.151)	0.307* (0.151)
parmarried					0.247 (0.170)	0.247 (0.170)	0.247 (0.170)	0.247 (0.170)	0.247 (0.170)	0.247 (0.170)	0.247 (0.170)	0.247 (0.170)
collegexp					0.290* (0.147)	0.290* (0.147)	0.290* (0.147)	0.290* (0.147)	0.290* (0.147)	0.290* (0.147)	0.290* (0.147)	0.290* (0.147)
_cons					-3.253*** (0.362)	-3.253*** (0.362)	-3.253*** (0.362)	-3.253*** (0.362)	-3.253*** (0.362)	-3.253*** (0.362)	-3.253*** (0.362)	-3.253*** (0.362)
N	5671	5671	5671	5671	5671	5671	5671	5671	5671	5671	5671	5671

Standard errors in parentheses

=** p<0.05

** p<0.01*** p<0.001"