Regression II
Vanderbilt University
Prof. Sean P. Corcoran **30 total points**

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 <u>not</u> 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 0.098 standard deviation effect on math scores and a -0.028 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 (1.7 percentage points) and positive and significant for post-secondary enrollment (6.8 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 similar to those using propensity score matching, though most effects are a little smaller. One exception is high school graduation, with an effect that is a bit larger and statistically significant.

(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 `psestimate` executes this algorithm and outputs the resulting propensity scores to your dataset. (You will need to install it using `ssc install psestimate`). The syntax of the command is:

`psestimate` *`treat`*`, totry(`*`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 make 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). See the log for an example of how to use the resulting model specification in a `teffects` command.

```
.
.
. // ************************************************************
. //
. // Regression II - Problem set 3
. // Last updated: September 19, 2025
. //
. // ************************************************************
.
. // *********************************
. // 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. Also create
. // z-scores for tests
. // *********************************
.
.         *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)"

.
.         // 3-category version of family income (following Murnane and Willett)
.         gen faminc8c = 1 if faminc8<=8
(4,235 missing values generated)

.         replace faminc8c = 2 if faminc8>=9 & faminc8<=10
(1,922 real changes made)

.         replace faminc8c = 3 if faminc8>=11 & faminc8~=.
(2,313 real changes made)

.         label var faminc8c "family income in 8th grade (three categories)"

.
.         // 4-category version of 8th grade math scores
.         egen math8b=cut(math8), at(30,38,44,51,80) icodes

.         replace math8b=math8b+1
(5,671 real changes made)

.         label var math8b "8th grade math score (four categories)

.
.         // father's highest education
.         // NOTE: code 8 is "don't know". Below set vars to missing in this case
.         codebook fathed8

-------------------------------------------------------------------------------------------
fathed8                                                  father^s highest level of education
-------------------------------------------------------------------------------------------

                  Type: Numeric (byte)
                 Label: farcat

                 Range: [1,8]                         Units: 1
         Unique values: 8                         Missing .: 0/5,671

            Tabulation: Freq.   Numeric  Label
                          873         1  not finish hs
                        1,778         2  hs grad
                          660         3  junior coll
                          443         4  coll <4
                          743         5  coll grad
                          346         6  masters
                          141         7  doctorate
                          687         8  dont know

.         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
.         // NOTE: code 8 is "don't know". Below set vars to missing in this case
.         codebook mothed8

-------------------------------------------------------------------------------------------
mothed8                                                   mother^s highest level of education
-------------------------------------------------------------------------------------------

                  Type: Numeric (byte)
                 Label: farcat

                 Range: [1,8]                         Units: 1
         Unique values: 8                         Missing .: 0/5,671

            Tabulation: Freq.   Numeric  Label
                          815         1  not finish hs
                        2,091         2  hs grad
                          686         3  junior coll
                          468         4  coll <4
                          655         5  coll grad
                          299         6  masters
                           82         7  doctorate
                          575         8  dont know

.         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==. | fathed8==8
  3.            replace mothed`j'=. if mothed8==. | mothed8==8
  4.            }
(687 real changes made, 687 to missing)
(575 real changes made, 575 to missing)
(687 real changes made, 687 to missing)
(575 real changes made, 575 to missing)
(687 real changes made, 687 to missing)
(575 real changes made, 575 to missing)
(687 real changes made, 687 to missing)
(575 real changes made, 575 to missing)

.
```

```
.         // highest education of two parents
.         // NOTE: code 8 is "don't know" so remove these first before taking max
.         gen ftemp = fathed8 if fathed8~=8
(687 missing values generated)

.         gen mtemp = mothed8 if mothed8~=8
(575 missing values generated)

.         egen pared8=rowmax(ftemp mtemp)
(406 missing values generated)

.         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"

.         drop ftemp mtemp

.
.         // 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 - estimating a propensity score
. // model using teffects psmatch
. // ************************************
.
.         // use of "quietly" to suppress ATE output. This model specification
.         // was the one I settled on--yours may differ
.         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 using tebalance summarize
```

```
.         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   -.0495814      .8200688   1.023323
         read8z |   .4356571     -.04546      .9223486   1.051909
         female |   .0496905    .0135434      .9955598   .9978893
          black |  -.1579425    .0219152      .6082682   1.087891
           hisp |  -.0974819     .030214      .7768816   1.094018
            api |  -.1926191    .0895978      .3939964   1.976068
        nativam |  -.0940456   -.0786986      .5998088   .6452951
      riskdrop1 |  -.0974069   -.0041294      .8844729   .9941924
      riskdrop2 |  -.4043775    -.045471      .3184886   .8323846
       disrupt8 |  -.0513382           0      .9158064          1
          nohw8 |  -.2800718   -.0330567      .4771307   .8944509
       faminc8b |   .4572743    .0162643      .8885848   .9480218
         pared1 |  -.3104968     .021481      .2860831   1.138903
         pared2 |  -.1167283   -.1011173      .8976232   .9077325
         pared3 |   .0275791    .0473309      1.034677   1.058908
         pared4 |   .2866933    .0172299      1.224495   1.007103
     parmarried |   .2616919     .051715      .5542313   .8669075
      collegexp |   .2563305   -.0160351      .6169925   1.040199
------------------------------------------------------------------

.
.         // BONUS: plotting the standardized differences (raw/matched)
.         mat     balance = r(table)

.         coefplot (matrix(balance[,1])) (matrix(balance[,2])), ///
>                 xline(0,lpattern(solid)) xline(-0.05 0.05,lcolor(red)) ///
>                 xlab(-0.45(0.05)0.45) xtitle("Standardized difference") ///
>                 legend(order(2 "Raw" 4 "Matched") position(6) rows(1)) ///
>                 sort(1) graphregion(margin(l+5)) title("Standardized differences: raw an
> d matched") ///
>                 xsize(10) ysize(4) name(graph1,replace)
(balance: could not determine CI1)
(balance: could not determine CI1)

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

.
.         // graphically compare distributions for continuous variables
.         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
```

```
.
.         // graphically compare distributions for propensity scores
.         // (all observations + matched sample only)
.         tebalance density, name(graph3, replace) ///
>                 byopts(title(Propensity score distribution: all observations and matched
>  sample, size(medsmall))) ///
>                 legend(order(1 "Untreated" 2 "Treated") position(6))

.
.         // graphically compare distributions of propensity scores (all observations
.         // using teoverlap)
.         teoverlap, ptlevel(1) name(graph4, replace) ///
>            title(Propensity score distribution: all observations using teoverlap, size(m
> edsmall))

.
.         graph combine graph3 graph4, col(1) xsize(6) ysize(8) ///
>                 name(graph5, replace)

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

.         graph close _all

.
.         // FYI to see actual logit results--which variables are significant
.         // predictors of treatment? How strong of a relationship?
.         logit 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

Iteration 0:  Log likelihood = -1897.6568
Iteration 1:  Log likelihood = -1779.3796
Iteration 2:  Log likelihood = -1763.2706
Iteration 3:  Log likelihood = -1763.0145
Iteration 4:  Log likelihood = -1763.0138
Iteration 5:  Log likelihood = -1763.0138

Logistic regression                                     Number of obs =  5,671
                                                        LR chi2(20)   = 269.29
                                                        Prob > chi2   = 0.0000
Log likelihood = -1763.0138                             Pseudo R2     = 0.0710

------------------------------------------------------------------------------
             catholic | Coefficient  Std. err.      z    P>|z|     [95% conf. interval]
----------------------+-------------------------------------------------------
               math8z |  -.0630993   .0732242    -0.86   0.389    -.2066161    .0804176
                      |
    c.math8z#c.math8z |  -.1692552   .0495166    -3.42   0.001    -.2663059   -.0722044
                      |
               read8z |   .3217844    .067893     4.74   0.000     .1887166    .4548523
                      |
    c.read8z#c.read8z |   .0104647   .0484315     0.22   0.829    -.0844593    .1053886
                      |
               female |   .0409147    .095074     0.43   0.667    -.1454269    .2272564
                black |  -.2491715   .1918147    -1.30   0.194    -.6251214    .1267785
                 hisp |  -.0945902   .1588538    -0.60   0.552     -.405938    .2167576
                  api |  -1.176192   .2813161    -4.18   0.000    -1.727561   -.6248225
              nativam |  -.4881439   .2865059    -1.70   0.088    -1.049685    .0733975
            riskdrop1 |   .0250028   .1227969     0.20   0.839    -.2156748    .2656803
            riskdrop2 |  -.4032556   .2596487    -1.55   0.120    -.9121577    .1056465
             disrupt8 |   .2221792   .1285998     1.73   0.084    -.0298717    .4742302
                nohw8 |  -.6271156   .1773633    -3.54   0.000    -.9747412     -.27949
             faminc8b |   .0000294   .0000145     2.03   0.042     1.07e-06    .0000578
                      |
c.faminc8b#c.faminc8b |  -2.06e-10   1.73e-10    -1.19   0.234    -5.46e-10    1.33e-10
                      |
               pared1 |  -.6229521   .3245582    -1.92   0.055    -1.259075    .0131703
               pared2 |   .0491702   .2057076     0.24   0.811    -.3540093    .4523496
               pared3 |   .1288713   .2068516     0.62   0.533    -.2765504     .534293
               pared4 |   .3233567   .2025939     1.60   0.110    -.0737201    .7204335
            parmarried |   .2604802   .1804001     1.44   0.149    -.0930976    .6140579
             collegexp |   .2769345   .1431216     1.93   0.053    -.0035785    .5574476
                 _cons |   -3.23417   .4041378    -8.00   0.000    -4.026266   -2.442075
------------------------------------------------------------------------------
```

```
.
.         // FYI to see logit results in terms of change in predicted probability
.         // of treatment (not logit coefficients)
.         margins, dydx(*) atmeans

Conditional marginal effects                              Number of obs = 5,671
Model VCE: OIM

Expression: Pr(catholic), predict()
dy/dx wrt:  math8z read8z female black hisp api nativam riskdrop1 riskdrop2 disrupt8
            nohw8 faminc8b pared1 pared2 pared3 pared4 parmarried collegexp
At: math8z     =  3.91e-10 (mean)
    read8z     = -1.01e-09 (mean)
    female     =  .5200141 (mean)
    black      =  .0975137 (mean)
    hisp       =  .1162053 (mean)
    api        =  .0585435 (mean)
    nativam    =  .0384412 (mean)
    riskdrop1  =  .2479281 (mean)
    riskdrop2  =  .1579968 (mean)
    disrupt8   =  .1795098 (mean)
    nohw8      =   .143361 (mean)
    faminc8b   =  32656.05 (mean)
    pared1     =  .0946923 (mean)
    pared2     =  .3091166 (mean)
    pared3     =   .241051 (mean)
    pared4     =  .2835479 (mean)
    parmarried =  .8335391 (mean)
    collegexp  =  .8012696 (mean)

------------------------------------------------------------------------------
             |            Delta-method
             |      dy/dx   std. err.      z    P>|z|     [95% conf. interval]
-------------+----------------------------------------------------------------
      math8z |  -.0057371   .0065909    -0.87   0.384     -.018655    .0071808
      read8z |   .0292574   .0065043     4.50   0.000     .0165092    .0420056
      female |   .0037201   .0086508     0.43   0.667    -.0132351    .0206752
       black |  -.0226553   .0173323    -1.31   0.191    -.0566259    .0113154
        hisp |  -.0086004   .0144423    -0.60   0.552    -.0369068    .0197061
         api |  -.1069421   .0256707    -4.17   0.000    -.1572558   -.0566285
     nativam |  -.0443832   .0261398    -1.70   0.090    -.0956163      .00685
   riskdrop1 |   .0022733   .0111812     0.20   0.839    -.0196414    .0241881
   riskdrop2 |  -.0366649   .0229526    -1.60   0.110    -.0816513    .0083214
    disrupt8 |   .0202011   .0117769     1.72   0.086    -.0028812    .0432833
       nohw8 |  -.0570188   .0160873    -3.54   0.000    -.0885494   -.0254883
    faminc8b |   1.45e-06   4.24e-07     3.42   0.001     6.19e-07    2.28e-06
      pared1 |  -.0566403   .0294206    -1.93   0.054    -.1143036    .0010231
      pared2 |   .0044707    .018696     0.24   0.811    -.0321728    .0411142
      pared3 |   .0117173   .0187864     0.62   0.533    -.0251034    .0485379
      pared4 |   .0294003   .0184974     1.59   0.112    -.0068538    .0656545
  parmarried |   .0236835   .0164338     1.44   0.150    -.0085262    .0558931
   collegexp |   .0251795   .0129571     1.94   0.052     -.000216     .050575
------------------------------------------------------------------------------

.
.         // BONUS: while it is very easy to see balance expressed as standardized
.         // differences (using tebalance summarize) it is less obvious how to get a
.         // balance table in the original units. teffects doesn't tag the matched
.         // observations in the same way psmatch2 does, so you have to manually ID
.         // the matches. There may be other ways to do it, but the below works.
.
.         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
(63 observations deleted)

.         rename nn1 ob

.         save `treated'
file C:\Users\corcorsp\AppData\Local\Temp\ST_3d28_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                         5,142
        from master                     5,142  (_merge==1)
        from using                          0  (_merge==2)

    Matched                               529  (_merge==3)
    -----------------------------------------

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

.         // this new "weight" variable is equal to 1 for all treated cases and
.         // equal to an integer value 1+ for MATCHED untreated cases (it is >1 if
.         // the observation was matched more than once). You can now condition
.         // (and use fweights) using this weight variable.
.
.         // balance table using new dtable command (with p-values)
.         // use the below for labeling purposes
.         gen catholic2=catholic

.         label define catholic2 0 "Matched untreated" 1 "Treated"

.         label values catholic2 catholic2

.         label var catholic2 "Attended Catholic HS"

.
.         dtable math8z read8z faminc8b female black hisp api nativam riskdrop1 ///
>                 riskdrop2 disrupt nohw8 pared1 pared2 pared3 pared4 parmarried ///
>                 collegexp if weight~=. [fweight=weight], ///
>                 by(catholic2, nototal tests) nosample col(test(pvalue)) ///
>                 cont(,stat(mean))
note: using test regress across levels of catholic2 for math8z, read8z, faminc8b,
      female, black, hisp, api, nativam, riskdrop1, riskdrop2, disrupt8, nohw8, pared1,
      pared2, pared3, pared4, parmarried, and collegexp.

------------------------------------------------------------------------------
                                          Attended Catholic HS
                                Matched untreated   Treated  pvalue
------------------------------------------------------------------------------
z-score for 8th grade math                  0.269      0.224  0.394
z-score for 8th grade read                  0.424      0.381  0.434
family income in 8th grade (dollars)   39,265.549 39,534.130  0.780
student is female?                          0.535      0.542  0.816
student is black?                           0.054      0.059  0.706
student is hispanic?                        0.081      0.090  0.603
student is asian/pacific islander?          0.012      0.024  0.123
student is native american?                 0.037      0.024  0.176
=1 if 1 dropout risk factor                 0.213      0.211  0.943
=1 if 2-5 dropout risk factors              0.057      0.047  0.434
student frequently disruptive               0.162      0.162  1.000
student rarely completes homework           0.074      0.066  0.570
parent's highest ed: hs dropout             0.024      0.027  0.712
parent's highest ed: hs grad                0.307      0.262  0.082
parent's highest ed: some college           0.231      0.252  0.416
parent's highest ed: 4yr college or more    0.395      0.404  0.767
=1 if parents married in 8th grade          0.897      0.912  0.374
=1 if mother or father expects college+     0.890      0.885  0.783
------------------------------------------------------------------------------
```

```
.
.         drop nn1 nn2 ob weight _merge catholic2

.
.
. // *********************************
. // Part c - estimate ATT using model
. // specification chosen above
. // *********************************
.
.         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.         }
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 =          2
------------------------------------------------------------------------------
             |               AI robust
     math12z | Coefficient  std. err.      z    P>|z|     [95% conf. interval]
-------------+----------------------------------------------------------------
ATET         |
    catholic |
(yes vs no)  |   .0976228   .0389805     2.50   0.012     .0212223    .1740232
------------------------------------------------------------------------------
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 =          2
------------------------------------------------------------------------------
             |               AI robust
     read12z | Coefficient  std. err.      z    P>|z|     [95% conf. interval]
-------------+----------------------------------------------------------------
ATET         |
    catholic |
(yes vs no)  |  -.0279133   .0394335    -0.71   0.479    -.1052015    .0493749
------------------------------------------------------------------------------
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 =          2
------------------------------------------------------------------------------
             |               AI robust
      hsgrad | Coefficient  std. err.      z    P>|z|     [95% conf. interval]
-------------+----------------------------------------------------------------
ATET         |
    catholic |
(yes vs no)  |   .0168919   .0108328     1.56   0.119      -.00434    .0381238
------------------------------------------------------------------------------
Outcome: inpse

Treatment-effects estimation                    Number of obs      =      5,671
Estimator      : propensity-score matching      Matches: requested =          1
Outcome model  : matching                                   min =          1
Treatment model: logit                                      max =          2
------------------------------------------------------------------------------
             |               AI robust
       inpse | Coefficient  std. err.      z    P>|z|     [95% conf. interval]
-------------+----------------------------------------------------------------
ATET         |
    catholic |
(yes vs no)  |   .0675676   .0208701     3.24   0.001     .0266628    .1084723
------------------------------------------------------------------------------
```

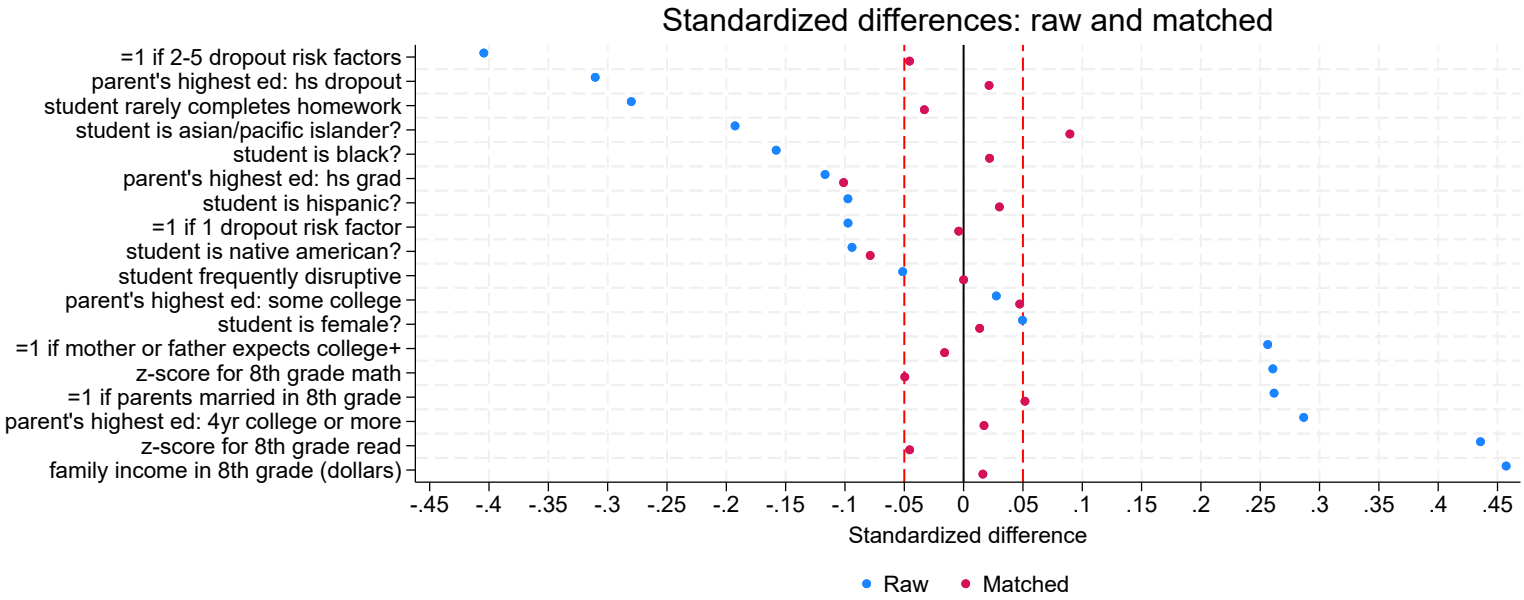
```
.
.
. // ****************************************
. // Part d - estimate ATT and ATE using IPW and
. // pscore model decided above
. // ****************************************
.
.         foreach j in math12z read12z hsgrad inpse {
  2.            display in red "Outcome: `j'"
  3.
.            _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 = 5.352e-23
Iteration 1:  EE criterion = 4.373e-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
------------------------------------------------------------------------------
                     |               Robust
          math12z    | Coefficient  std. err.      z    P>|z|     [95% conf. interval]
---------------------+--------------------------------------------------------
ATET                 |
            catholic |
     (yes vs no)     |   .1188871   .0230871     5.15   0.000     .0736373    .1641369
---------------------+--------------------------------------------------------
POmean               |
            catholic |
                 no  |   .2482061   .0318171     7.80   0.000     .1858458    .3105664
------------------------------------------------------------------------------
Warning: Convergence not achieved.

Iteration 0:  EE criterion = 5.352e-23
Iteration 1:  EE criterion = 6.474e-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
------------------------------------------------------------------------------
                     |               Robust
          math12z    | Coefficient  std. err.      z    P>|z|     [95% conf. interval]
---------------------+--------------------------------------------------------
ATE                  |
            catholic |
     (yes vs no)     |   .1095981   .0527149     2.08   0.038     .0062788    .2129174
---------------------+--------------------------------------------------------
POmean               |
            catholic |
                 no  |  -.0124144   .0134565    -0.92   0.356    -.0387886    .0139599
------------------------------------------------------------------------------
Warning: Convergence not achieved.
Outcome: read12z

Iteration 0:  EE criterion = 5.352e-23
Iteration 1:  EE criterion = 1.143e-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
------------------------------------------------------------------------------
                     |               Robust
          read12z | Coefficient  std. err.      z    P>|z|     [95% conf. interval]
---------------------+--------------------------------------------------------------
ATET                 |
            catholic |
         (yes vs no) |   .0399424   .0277714     1.44   0.150    -.0144886    .0943734
---------------------+--------------------------------------------------------------
POmean               |
            catholic |
                 no |   .2883356   .0292549     9.86   0.000     .2309969    .3456742
------------------------------------------------------------------------------
Warning: Convergence not achieved.

Iteration 0:  EE criterion = 5.352e-23
Iteration 1:  EE criterion = 7.017e-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
------------------------------------------------------------------------------
                     |               Robust
          read12z | Coefficient  std. err.      z    P>|z|     [95% conf. interval]
---------------------+--------------------------------------------------------------
ATE                  |
            catholic |
         (yes vs no) |   .0360945   .0584572     0.62   0.537    -.0784794    .1506685
---------------------+--------------------------------------------------------------
POmean               |
            catholic |
                 no |  -.0041737    .013563    -0.31   0.758    -.0307568    .0224093
------------------------------------------------------------------------------
Warning: Convergence not achieved.
Outcome: hsgrad

Iteration 0:  EE criterion = 5.352e-23
Iteration 1:  EE criterion = 2.555e-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
------------------------------------------------------------------------------
                     |               Robust
           hsgrad | Coefficient  std. err.      z    P>|z|     [95% conf. interval]
---------------------+--------------------------------------------------------------
ATET                 |
            catholic |
         (yes vs no) |   .0221237   .0071391     3.10   0.002     .0081314     .036116
---------------------+--------------------------------------------------------------
POmean               |
            catholic |
                 no |   .9525385   .0038179   249.49   0.000     .9450556    .9600214
------------------------------------------------------------------------------
Warning: Convergence not achieved.

Iteration 0:  EE criterion = 5.352e-23
Iteration 1:  EE criterion = 1.472e-32
    The Gauss-Newton stopping criterion has been met but missing standard errors
    indicate some of the parameters are not identified.
```

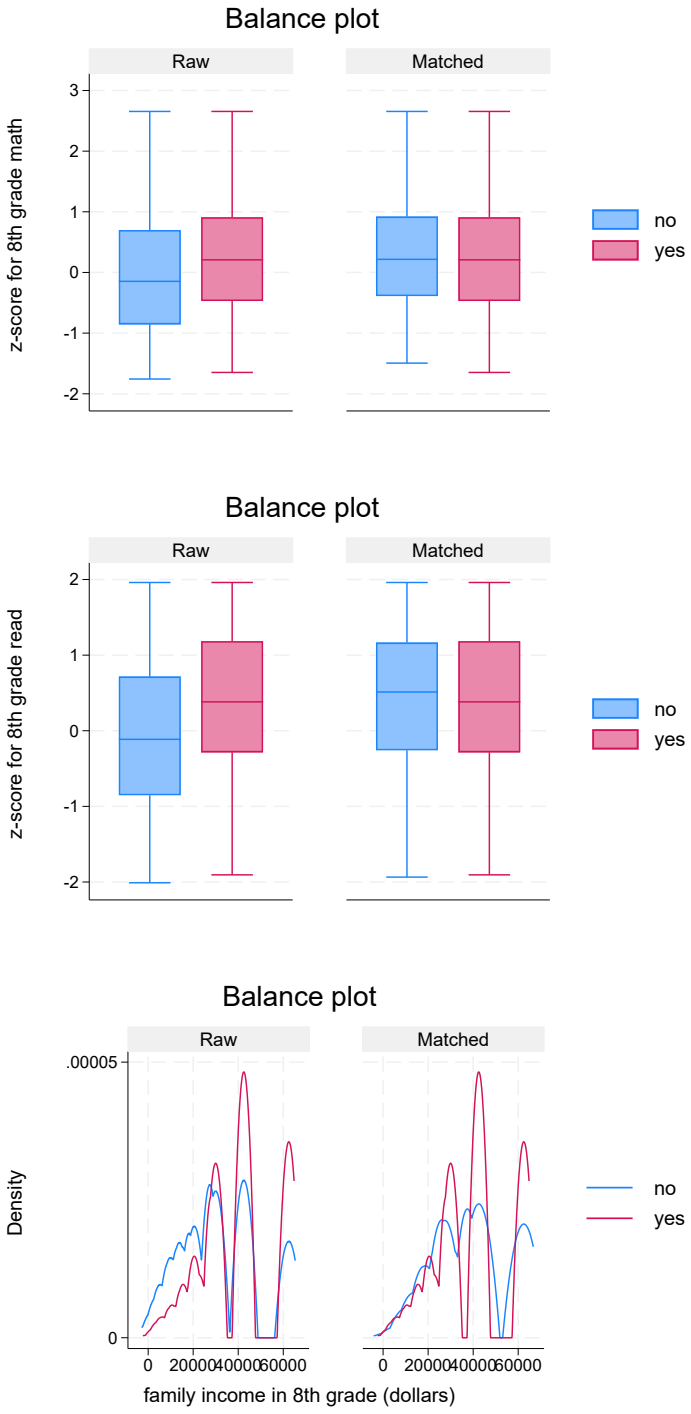
```
Treatment-effects estimation                    Number of obs     =      5,671
Estimator      : inverse-probability weights
Outcome model  : weighted mean
Treatment model: logit
------------------------------------------------------------------------------
             |               Robust
     hsgrad | Coefficient  std. err.      z    P>|z|     [95% conf. interval]
-------------+----------------------------------------------------------------
ATE          |
    catholic |
 (yes vs no) |   .0307212   .0196568     1.56   0.118    -.0078054    .0692477
-------------+----------------------------------------------------------------
POmean       |
    catholic |
          no |   .9146358   .0038232   239.23   0.000     .9071425    .9221292
------------------------------------------------------------------------------
Warning: Convergence not achieved.
Outcome: inpse

Iteration 0:  EE criterion = 5.352e-23
Iteration 1:  EE criterion = 3.517e-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
------------------------------------------------------------------------------
             |               Robust
       inpse | Coefficient  std. err.      z    P>|z|     [95% conf. interval]
-------------+----------------------------------------------------------------
ATET         |
    catholic |
 (yes vs no) |   .0620777   .0148643     4.18   0.000     .0329441    .0912112
-------------+----------------------------------------------------------------
POmean       |
    catholic |
          no |   .7994088   .0089341    89.48   0.000     .7818984    .8169193
------------------------------------------------------------------------------
Warning: Convergence not achieved.

Iteration 0:  EE criterion = 5.352e-23
Iteration 1:  EE criterion = 1.188e-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
------------------------------------------------------------------------------
             |               Robust
       inpse | Coefficient  std. err.      z    P>|z|     [95% conf. interval]
-------------+----------------------------------------------------------------
ATE          |
    catholic |
 (yes vs no) |   .1274161   .0201821     6.31   0.000     .0878599    .1669723
-------------+----------------------------------------------------------------
POmean       |
    catholic |
          no |   .7027407    .006283   111.85   0.000     .6904263     .715055
------------------------------------------------------------------------------
Warning: Convergence not achieved.

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

```
.
. // **********************************
. // Part e - try psestimate
. // **********************************
.
.         *ssc install psestimate
.         psestimate catholic, totry(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..    50
...........s...........s...........s..........s..   100
.......s.......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
.........................................
Selected second order covariates are: c.math8z#c.math8z c.pared1#c.read8z c.disrupt8#c.col
> legexp c.black#c.collegexp c.black#c.faminc8b c.math8z#c.api 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.pared1#c.read8z c.disrupt8#c.collegexp c.black#c.
> collegexp c.black#c.faminc8b c.math8z#c.api c.disrupt8#c.black

.
.         // This is used below - resulting model specification from above
.         global fullmodel="`r(h)'"

.         display "$fullmodel"
faminc8b read8z api riskdrop2 nohw8 pared1 math8z collegexp pared4 black parmarried disrup
> t8 c.math8z#c.math8z c.pared1#c.read8z c.disrupt8#c.collegexp c.black#c.collegexp c.blac
> k#c.faminc8b c.math8z#c.api c.disrupt8#c.black

.
.         // You can use the new variable pscore as propensity scores for matching
.         // or weighting. Unfortunately it cannot be passed through to teffects,
.         // but you could use it in psmatch2 or for manual calculations. Example
.         // using psmatch2:
.         psmatch2 catholic, pscore(pscore) ties out(math12z)
------------------------------------------------------------------------------
        Variable     Sample |    Treated     Controls   Difference         S.E.   T-stat
-----------------------------+------------------------------------------------------------
         math12z  Unmatched | .367093217   -.04278779   .409881007   .043090321     9.51
                        ATT | .367093217   .243305348   .123787869   .056747299     2.18
-----------------------------+------------------------------------------------------------
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
```

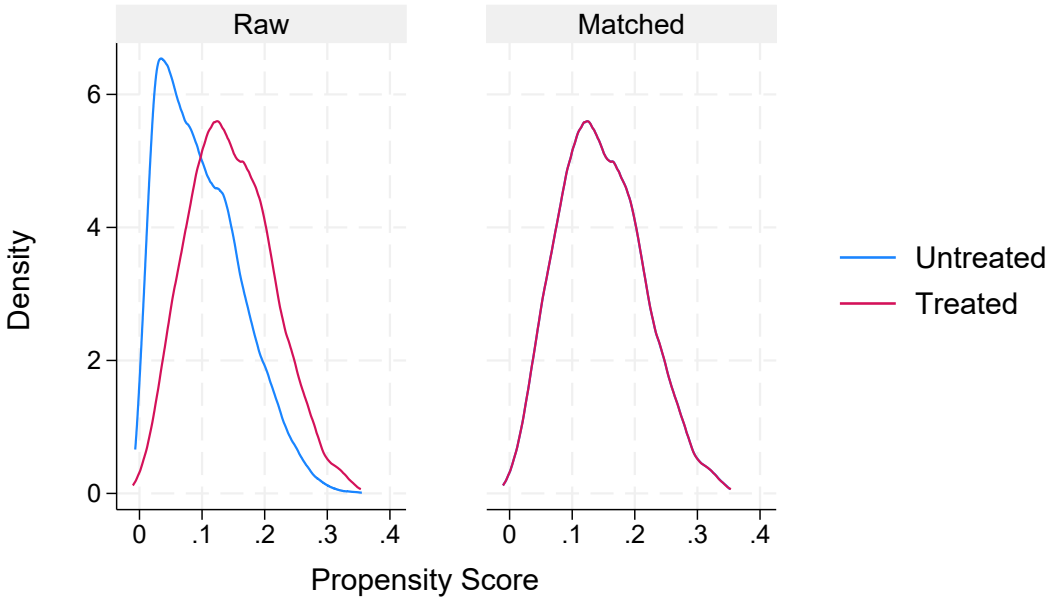
```
.
.         // OR, you can take the model specification that results from psestimate
.         // and put it into your teffects command:
.         foreach j in math12z read12z hsgrad inpse {
  2.            display in red "Outcome: `j'"
  3.            teffects psmatch (`j') (catholic $fullmodel, logit), atet
  4.        }
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
------------------------------------------------------------------------------
             |               AI robust
     math12z | Coefficient  std. err.      z    P>|z|     [95% conf. interval]
-------------+----------------------------------------------------------------
ATET         |
    catholic |
(yes vs no)  |   .1237879   .0439014     2.82   0.005     .0377427     .209833
------------------------------------------------------------------------------
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)  |   .1081204   .0455281     2.37   0.018      .018887    .1973538
------------------------------------------------------------------------------
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)  |   .0236486   .0117346     2.02   0.044     .0006492    .0466481
------------------------------------------------------------------------------
Outcome: inpse

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
       inpse | Coefficient  std. err.      z    P>|z|     [95% conf. interval]
-------------+----------------------------------------------------------------
ATET         |
    catholic |
(yes vs no)  |   .0793919   .0220244     3.60   0.000     .0362248     .122559
------------------------------------------------------------------------------

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


Standardized differences: raw and matched
=1 if 2-5 dropout risk factors
parent's highest ed: hs dropout
student rarely completes homework
student is asian/pacific islander?
student is black?
parent's highest ed: hs grad
student is hispanic?
=1 if 1 dropout risk factor
student is native american?
student frequently disruptive
parent's highest ed: some college
student is female?
=1 if mother or father expects college+
z-score for 8th grade math
=1 if parents married in 8th grade
parent's highest ed: 4yr college or more
z-score for 8th grade read
family income in 8th grade (dollars)
-.45 -.4 -.35 -.3 -.25 -.2 -.15 -.1 -.05 0 .05 .1 .15 .2 .25 .3 .35 .4 .45
Standardized difference
Raw
Matched

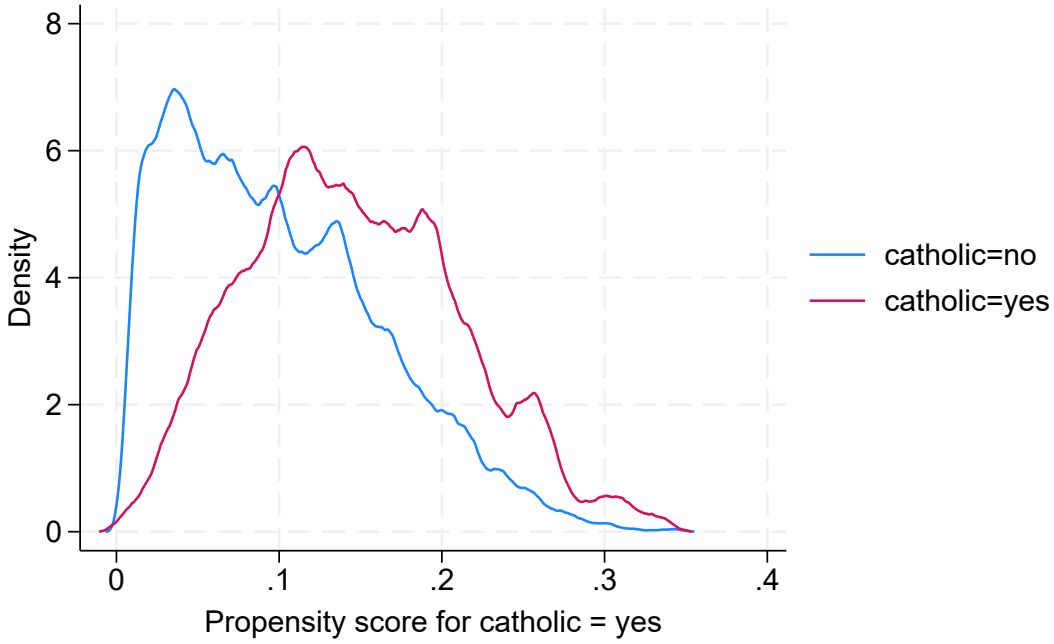
Covariate balance: after teffects psmatch



Propensity score distribution: all observations and matched sample



Propensity score distribution: all observations using teoverlap



	(1) math12z	(2) read12z	(3) hsgrad	(4) inpse	(5) math12z	(6) math12z	(7) read12z	(8) read12z	(9) hsgrad	(10) hsgrad	(11) inpse	(12) inpse
main												
r1vs0.catholic	0.0976*	-0.0279	0.0169	0.0676**	0.119***	0.110*	0.0399	0.0361	0.0221**	0.0307	0.0621***	0.127***
	(0.0390)	(0.0394)	(0.0108)	(0.0209)	(0.0231)	(0.0527)	(0.0278)	(0.0585)	(0.00714)	(0.0197)	(0.0149)	(0.0202)
POmean												
0.catholic					0.248***	-0.0124	0.288***	-0.00417	0.953***	0.915***	0.799***	0.703***
					(0.0318)	(0.0135)	(0.0293)	(0.0136)	(0.00382)	(0.00382)	(0.00893)	(0.00628)
TME1												
math8z					-0.0631	-0.0631	-0.0631	-0.0631	-0.0631	-0.0631	-0.0631	-0.0631
					(0.0720)	(0.0720)	(0.0720)	(0.0720)	(0.0720)	(0.0720)	(0.0720)	(0.0720)
c.math8z#c.math8z					-0.169***	-0.169***	-0.169***	-0.169***	-0.169***	-0.169***	-0.169***	-0.169***
					(0.0504)	(0.0504)	(0.0504)	(0.0504)	(0.0504)	(0.0504)	(0.0504)	(0.0504)
read8z					0.322***	0.322***	0.322***	0.322***	0.322***	0.322***	0.322***	0.322***
					(0.0681)	(0.0681)	(0.0681)	(0.0681)	(0.0681)	(0.0681)	(0.0681)	(0.0681)
c.read8z#c.read8z					0.0105	0.0105	0.0105	0.0105	0.0105	0.0105	0.0105	0.0105
					(0.0490)	(0.0490)	(0.0490)	(0.0490)	(0.0490)	(0.0490)	(0.0490)	(0.0490)
female					0.0409	0.0409	0.0409	0.0409	0.0409	0.0409	0.0409	0.0409
					(0.0938)	(0.0938)	(0.0938)	(0.0938)	(0.0938)	(0.0938)	(0.0938)	(0.0938)
black					-0.249	-0.249	-0.249	-0.249	-0.249	-0.249	-0.249	-0.249
					(0.190)	(0.190)	(0.190)	(0.190)	(0.190)	(0.190)	(0.190)	(0.190)
hisp					-0.0946	-0.0946	-0.0946	-0.0946	-0.0946	-0.0946	-0.0946	-0.0946
					(0.158)	(0.158)	(0.158)	(0.158)	(0.158)	(0.158)	(0.158)	(0.158)
api					-1.176***	-1.176***	-1.176***	-1.176***	-1.176***	-1.176***	-1.176***	-1.176***
					(0.284)	(0.284)	(0.284)	(0.284)	(0.284)	(0.284)	(0.284)	(0.284)
nativam					-0.488	-0.488	-0.488	-0.488	-0.488	-0.488	-0.488	-0.488
					(0.283)	(0.283)	(0.283)	(0.283)	(0.283)	(0.283)	(0.283)	(0.283)
riskdrop1					0.0250	0.0250	0.0250	0.0250	0.0250	0.0250	0.0250	0.0250
					(0.118)	(0.118)	(0.118)	(0.118)	(0.118)	(0.118)	(0.118)	(0.118)
riskdrop2					-0.403	-0.403	-0.403	-0.403	-0.403	-0.403	-0.403	-0.403
					(0.245)	(0.245)	(0.245)	(0.245)	(0.245)	(0.245)	(0.245)	(0.245)
disrupt8					0.222	0.222	0.222	0.222	0.222	0.222	0.222	0.222
					(0.128)	(0.128)	(0.128)	(0.128)	(0.128)	(0.128)	(0.128)	(0.128)
nohw8					-0.627***	-0.627***	-0.627***	-0.627***	-0.627***	-0.627***	-0.627***	-0.627***
					(0.177)	(0.177)	(0.177)	(0.177)	(0.177)	(0.177)	(0.177)	(0.177)
faminc8b					0.0000294	0.0000294	0.0000294	0.0000294	0.0000294	0.0000294	0.0000294	0.0000294
					(0.000015(	(0.000015(	(0.000015(	(0.000015(	(0.000015(	(0.000015(	(0.000015(	(0.0000150)
c.faminc8b#c.faminc8b					-2.06e-10	-2.06e-10	-2.06e-10	-2.06e-10	-2.06e-10	-2.06e-10	-2.06e-10	-2.06e-10
					(1.79e-10)	(1.79e-10)	(1.79e-10)	(1.79e-10)	(1.79e-10)	(1.79e-10)	(1.79e-10)	(1.79e-10)
pared1					-0.623	-0.623	-0.623	-0.623	-0.623	-0.623	-0.623	-0.623
					(0.318)	(0.318)	(0.318)	(0.318)	(0.318)	(0.318)	(0.318)	(0.318)
pared2					0.0492	0.0492	0.0492	0.0492	0.0492	0.0492	0.0492	0.0492
					(0.205)	(0.205)	(0.205)	(0.205)	(0.205)	(0.205)	(0.205)	(0.205)
pared3					0.129	0.129	0.129	0.129	0.129	0.129	0.129	0.129
					(0.206)	(0.206)	(0.206)	(0.206)	(0.206)	(0.206)	(0.206)	(0.206)

pared4					0.323	0.323	0.323	0.323	0.323	0.323	0.323	0.323
					(0.201)	(0.201)	(0.201)	(0.201)	(0.201)	(0.201)	(0.201)	(0.201)
parmarried					0.260	0.260	0.260	0.260	0.260	0.260	0.260	0.260
					(0.171)	(0.171)	(0.171)	(0.171)	(0.171)	(0.171)	(0.171)	(0.171)
collegexp					0.277	0.277	0.277	0.277	0.277	0.277	0.277	0.277
					(0.146)	(0.146)	(0.146)	(0.146)	(0.146)	(0.146)	(0.146)	(0.146)
_cons					-3.234***	-3.234***	-3.234***	-3.234***	-3.234***	-3.234***	-3.234***	-3.234***
					(0.387)	(0.387)	(0.387)	(0.387)	(0.387)	(0.387)	(0.387)	(0.387)
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"