ECON 211B: Homework 2

Carlos E. Dobkin

David Sungho Park

Problem 1

Table 1 compares the means between treatment and control groups. The last column displays the p-value for the mean difference tests. Our experimental data seems well balanced, except for *nodegree*. The p-value for *education* is also quite low. Such results suggest that our sample may not be fully randomized.

Table 1: Mean comparison between treatment and control

	Treatment group	Control group	Difference	p-value
age	24.63	24.45	0.18	0.721
education	10.38	10.19	0.19	0.136
black	0.80	0.80	0.00	0.965
hispanic	0.09	0.11	-0.02	0.422
married	0.17	0.16	0.01	0.701
nodegree	0.73	0.81	-0.08	0.008
re75	3,066.10	3,026.68	39.42	0.918
re78	5,976.35	5,090.05	886.30	0.061

[*] The source of dataset is the National Supported Work (NSW) Demonstration study. The treatment group and control group have 297 and 425 observations, respectively.

[**] The last column is the p-value for the two-tailed mean difference test.

Problem 2

Table 2 shows the evaluation of the NSW experiment on 1978 earnings. The first column shows the raw difference in the means between treatment and control, and the last column shows the difference in differences estimate. The first row displays each estimate of the treatment effect. As adding more covariates, the estimated treatment effect becomes smaller. Adding covariates does not result in getting closer to the difference in differences estimate but rather getting farther downwards. We need note that even though difference in differences is often used to mitigate selection biases, it can be still subject to biases.

Problem 3

The unbiasedness of the estimates depends on the randomization of the sample. In order for true randomization, no element of individual choice can be included in the determination of the treatment group. Although the eligibility to the NSW job training program was randomly assigned, the actual participation in the program should have been decided by the individuals. Therefore, our estimates of the treatment effect are still susceptible to selection biases.

Table 2: Evaluation of the effect of NSW

VARIABLES	(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8) DD
treat	886.3	882.2	831.0	826.4	824.4	820.4	793.6	846.9
	(472.1)	(472.3)	(472.1)	(469.5)	(470.0)	(470.2)	(471.9)	(560.1)
age		22.9	21.2	30.9	30.6	24.0	20.1	
		(35.1)	(35.0)	(35.0)	(35.1)	(36.1)	(36.5)	
education			267.7	294.8	291.9	287.7	205.9	
			(136.4)	(135.9)	(137.6)	(137.7)	(180.9)	
black				-1,750.7	-1,827.8	-1,835.6	-1,765.6	
				(581.0)	(796.7)	(796.9)	(803.5)	
hispanic					-148.8	-173.7	-133.9	
					(1,050.5)	(1,051.2)	(1,053.1)	
married						517.3	541.0	
						(643.9)	(645.0)	
nodegree							-522.3	
							(749.2)	
Constant	5,090.0	4,531.2	1,843.8	2,731.3	2,848.0	2,979.5	4,268.6	2,063.4
	(302.8)	(910.0)	(1,643.1)	(1,660.2)	(1,854.4)	(1,862.1)	(2,624.6)	(359.3)
Observations	722	722	722	722	722	722	722	722
R-squared	0.005	0.005	0.011	0.023	0.023	0.024	0.025	0.003

[*] The numbers in parentheses are the standard deviations.
[**] The last column displays the estimate using Difference in Differences.

Problem 4

Figure 1: Kernel density functions of 1978 earnings
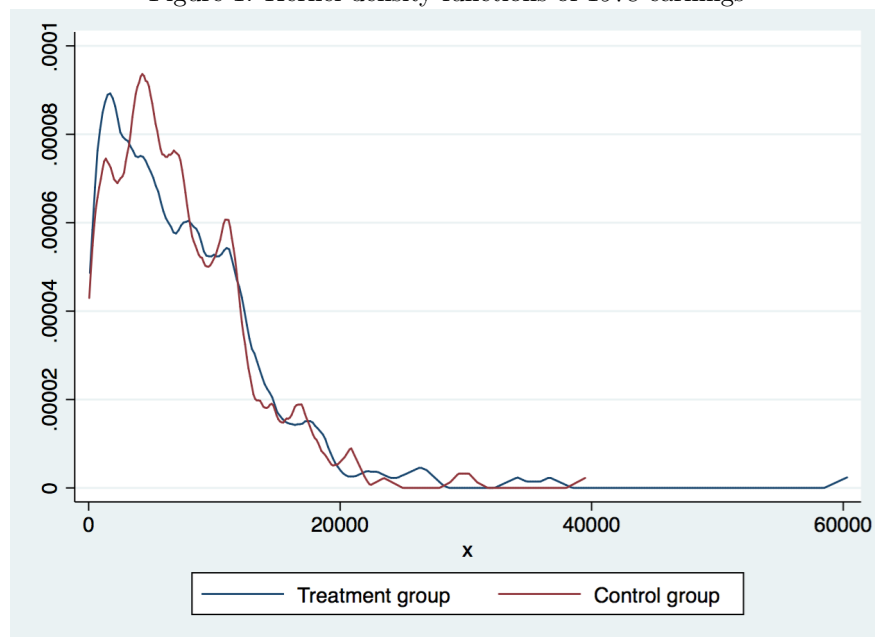
Note: The plot is estimated using the triangular kernel function.

Problem 5

Table 3 shows the means between the treatment and comparison groups. Contrary to Table 1, we can see the dataset is not well balanced and thus not consistent with the randomization. Therefore, any estimation of treatment effects with this dataset should be biased.

Table 3: Mean comparison between treatment and comparison

	Treatment (NSW)	Comparison (PSID)	Difference	p-value
age	24.63	34.85	-10.22	0.000
education	10.38	12.12	-1.74	0.000
black	0.80	0.25	0.55	0.000
hispanic	0.09	0.03	0.06	0.000
married	0.17	0.87	-0.70	0.000
nodegree	0.73	0.31	0.43	0.000
re75	3,066.10	19,063.34	-15,997.24	0.000
re78	5,976.35	21,553.92	-15,577.57	0.000

[*] The comparison group is the data from the Panel Study of Income Dynamics (PSID). The treatment group and comparison group have 297 and 2490 observations, respectively.
[**] The last column is the p-value for the two-tailed mean difference test.

Problem 6

Table 4: Estimated treatment effect against comparison group (PSID)

VARIABLES	(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8) DD
treat	-15,577.6	-14,756.3	-10,180.2	-8,834.2	-8,896.1	-6,326.6	-6,410.4	419.7
	(913.3)	(955.6)	(914.8)	(950.3)	(959.1)	(1,054.7)	(1,070.2)	(650.6)
age		80.3	206.5	192.3	192.9	163.2	162.0	
		(27.9)	(26.6)	(26.6)	(26.7)	(27.0)	(27.2)	
education			1,892.3	1,742.4	1,749.6	1,755.0	1,798.9	
			(90.4)	(94.9)	(96.1)	(95.5)	(134.7)	
black				-3,180.6	-3,109.4	-2,706.9	-2,725.0	
				(639.6)	(656.4)	(656.6)	(657.8)	
hispanic					670.9	621.6	612.6	
					(1,391.2)	(1,383.4)	(1,383.7)	
married						4,416.3	4,431.7	
						(774.1)	(774.9)	
nodegree							396.1	
							(856.0)	
Constant	21,553.9	18,754.5	-8,572.5	-5,463.4	-5,611.1	-8,567.3	-9,185.4	2,490.6
	(298.2)	(1,015.4)	(1,610.6)	(1,721.3)	(1,748.6)	(1,814.3)	(2,253.2)	(212.4)
Observations	2,787	2,787	2,787	2,787	2,787	2,787	2,787	2,787
R-squared	0.095	0.097	0.220	0.227	0.227	0.236	0.236	0.000

[*] The numbers in parentheses are the standard deviations.
[**] The last column displays the estimate using Difference in Differences.

The estimations displayed in Table 4 are very different from those in Table 2. They even have different signs. By adding more covariates, the estimates are getting smaller in magnitude but still very far from the actual effect shown in the experimental data. On the other hand, the difference in differences estimate is rather comparable to its counterpart in Table 2. This shows how the difference in differences method can be used to mimic experimental results using observational data.

Problem 7

The estimates shown in Table 4 cannot have causal interpretations. This is mainly because the assumption of selection on observables has failed. Under such assumption of unconfoundedness, the treatment dummy variable should be exogenous, or independent of the observable covariates. However, all of the covariates of our sample are likely to affect whether an individual would be assigned to and decide to participate in the job training program.

Problem 8

We need to check the extent of the overlap in covariate distributions between the treatment and control groups, especially because without common support the estimates are very sensitive to model specification. Figures 2 to 4 present the histogram estimates for the propensity score distributions. We can see very small overlap in the covariate distributions between the treatment and comparison groups. Whereas the propensity score distribution of the treatment group is more spread out, the distribution for the comparison group is concentrated on a small interval below 0.1.

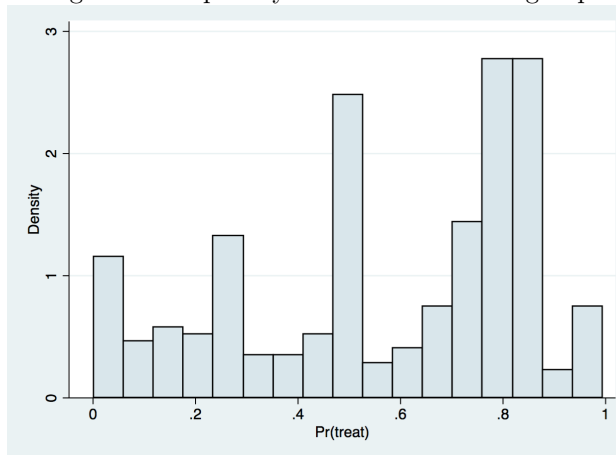Figure 2: Propensity score for treatment group

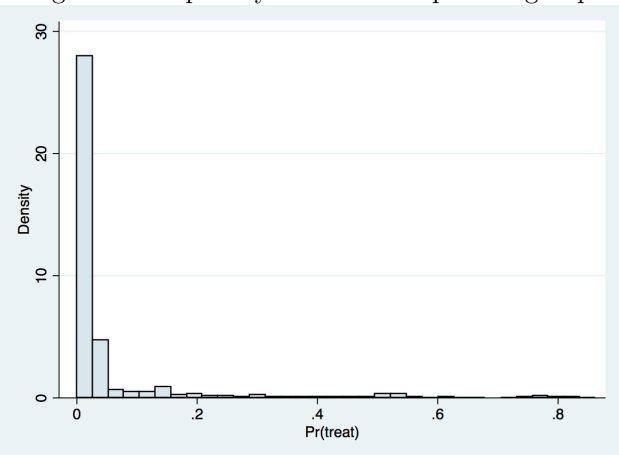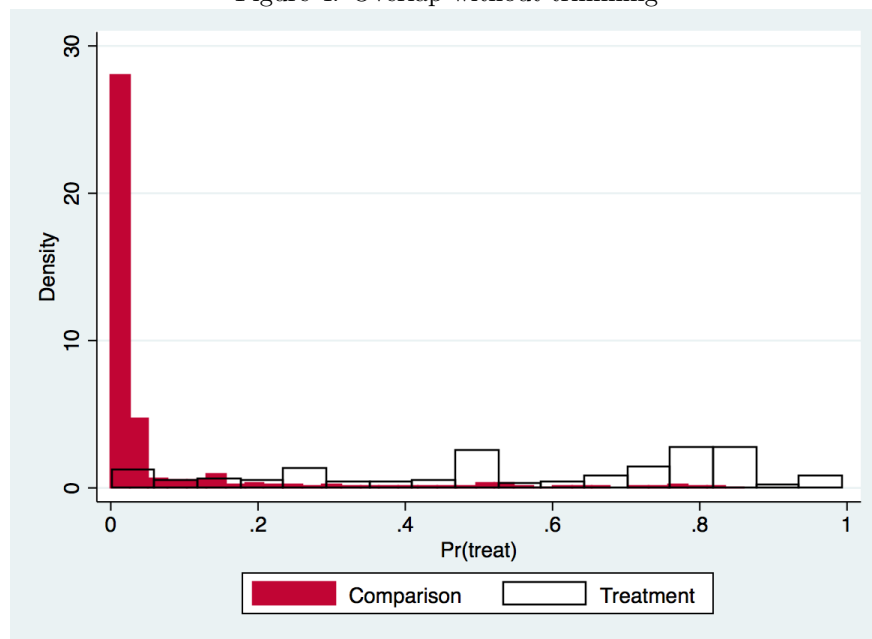Figure 3: Propensity score for comparison group

Figure 4: Overlap without trimming

We now trim the sample to account for the lack of common support. We try two rules: the 0.1 rule, where observations with the propensity score outside the interval $[0.1, 0.9]$ are dropped, and the 0.2 rule with symmetric procedures. Figures 5 and 6 show the overlap in distributions after trimming the sample. The sample represented by Figure 6 seems to have more common support. Tables 5 and 6 further compare the two trimming rules. Here as well, the sample trimmed by the 0.2 rule seems to be closer to the experimental benchmark in Table 1.

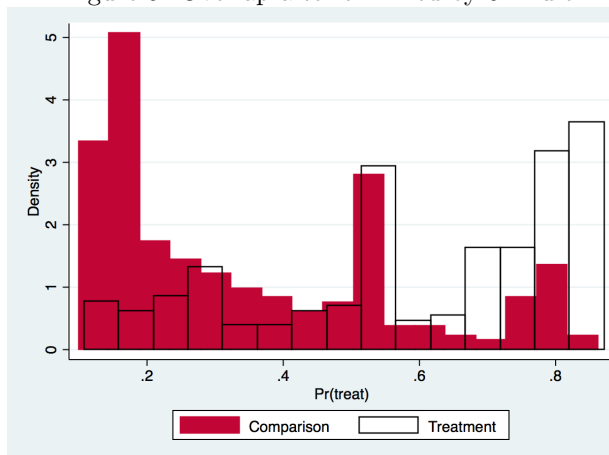Figure 5: Overlap after trimmed by 0.1 rule

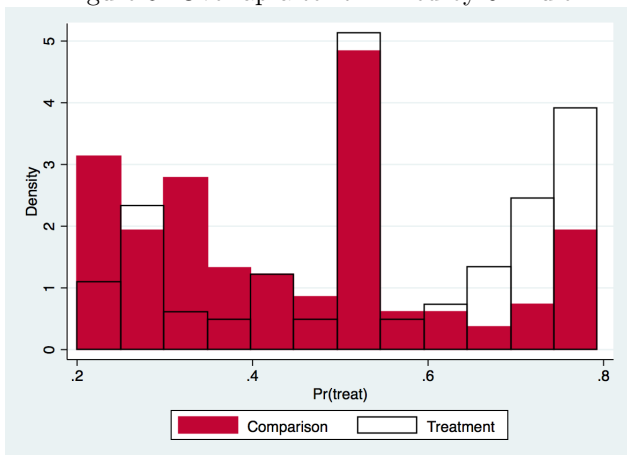Figure 6: Overlap after trimmed by 0.2 rule

Table 5: Mean comparison (0.1 rule)

	Treatment (NSW)	Comparison (PSID)	Difference	p-value
age	24.13	27.40	-3.27	0.000
education	10.41	10.69	-0.28	0.080
black	0.87	0.73	0.14	0.000
hispanic	0.04	0.03	0.00	0.922
married	0.11	0.34	-0.23	0.000
nodegree	0.75	0.62	0.13	0.001
re75	2,761.48	11,621.24	-8,859.76	0.000
re78	5,878.18	13,915.28	-8,037.11	0.000

Table 6: Mean comparison (0.2 rule)

	Treatment (NSW)	Comparison (PSID)	Difference	p-value
age	25.80	26.24	-0.44	0.475
education	10.67	10.73	-0.06	0.774
black	0.89	0.87	0.02	0.528
hispanic	0.02	0.03	-0.01	0.750
married	0.13	0.28	-0.15	0.000
nodegree	0.68	0.67	0.01	0.785
re75	3,054.25	10,062.27	-7,008.02	0.000
re78	5,889.99	12,264.23	-6,374.24	0.000

Problem 9

Table 7 presents the estimated job training effects using the sample trimmed by the 0.2 rule. The estimates are still very far from those in Table 2; they are even still negative. Yet they are at least closer to the experimental benchmark than the results in Table 4. By the 0.2 rule, we have dropped $2453(= 2787 - 334)$ observations. However, this seemingly unreasonable cost is justifiable by the improved balance in the selected sample and (slightly) better estimates of the treatment effect.

Table 7: Evaluation of the effect of NSW

VARIABLES	(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8) DD
treat	-6,374.2	-6,360.8	-6,279.5	-6,206.3	-6,206.0	-5,946.4	-5,821.7	633.8
	(890.2)	(892.1)	(872.0)	(870.7)	(871.2)	(891.9)	(897.7)	(930.9)
age		30.3	85.8	121.5	122.3	147.2	160.8	
		(79.1)	(78.5)	(81.1)	(81.2)	(83.2)	(84.0)	
education			988.0	1,068.7	1,087.6	1,157.4	920.1	
			(242.4)	(246.6)	(247.8)	(253.1)	(324.2)	
black				-2,339.9	-2,905.2	-3,425.5	-3,956.6	
				(1,403.4)	(1,570.2)	(1,616.6)	(1,678.2)	
hispanic					-2,429.8	-3,364.3	-3,802.4	
					(3,021.0)	(3,098.5)	(3,119.3)	
married						1,553.4	2,206.3	
						(1,170.0)	(1,295.6)	
nodegree							-1,624.2	
							(1,387.9)	
Constant	12,264.2	11,468.1	-590.0	-360.9	-18.8	-1,376.8	2,189.1	2,202.0
	(627.6)	(2,167.9)	(3,639.0)	(3,631.8)	(3,658.6)	(3,794.8)	(4,865.1)	(656.2)
Observations	334	334	334	334	334	334	334	334
R-squared	0.134	0.134	0.176	0.183	0.184	0.189	0.192	0.001

[*] The numbers in parentheses are the standard deviations.

[**] The last column displays the estimate using Difference in Differences.

Stata Codes

```
***************************************** Problem 1 *****************************************
use "211b_hw2_NSW_PSID.dta", replace
keep if data_id=="Lalonde Sample"


* Creating an 8x4 matrix
mat T = J(8,4,.)


* Filling in the matrix
local i = 1
local list "age education black hispanic married nodegree re75 re78"
foreach x of local list {
    ttest `x', by(treat)
    mat T[`i',1] = r(mu_2)
    mat T[`i',2] = r(mu_1)
    mat T[`i',3] = r(mu_2) - r(mu_1)
    mat T[`i',4] = r(p)
    local i = `i' + 1
     }


* Naming rows/columns
mat rownames T = age education black hispanic married nodegree re75 re78
mat colnames T = "Treatment group" "Control group" "Difference" "p-value"


* Exporting to LaTeX
frmttable using "mean_diff.tex",statmat(T) tex fr nocenter sdec(2,2,2,3) replace



***************************************** Problem 2 *****************************************
use "211b_hw2_NSW_PSID.dta", replace
keep if data_id=="Lalonde Sample"


* Raw difference
reg re78 treat
outreg2 using "reg1.tex", tex(fr) replace se bdec(1) sdec(1) noaster nonote ctitle(" ")


* Adding estimation results sequentially
local list "age education black hispanic married nodegree"
foreach x of local list {
    reg re78 treat-`x'
    outreg2 using "reg1.tex", tex(fr) append se bdec(1) sdec(1) noaster nonote ctitle(" ")
    }
```

```
* Diff-in-Diff (DD)
gen diff = re78 - re75
reg diff treat
outreg2 using "reg1.tex", tex(fr) append se bdec(1) sdec(1) noaster nonote ctitle("DD")


* Alternative: DD estimation (by def)
su re78 if treat==1
gen re78_T = r(mean)
su re75 if treat==1
gen re75_T = r(mean)
su re78 if treat==0
gen re78_C = r(mean)
su re75 if treat==0
gen re75_C = r(mean)
gen DD = (re78_T - re75_T)-(re78_C-re75_C)
di DD



*********************************** Problem 4 ****************************************
use "211b_hw2_NSW_PSID.dta", replace
keep if data_id=="Lalonde Sample"

* Kernel density plots
gen earnings_1978_t = treat*re78
gen earnings_1978_c = (1-treat)*re78
replace earnings_1978_t =. if earnings_1978_t ==0
replace earnings_1978_c =. if earnings_1978_c ==0

twoway (kdensity earnings_1978_t, kernel(triangle))(kdensity earnings_1978_c,
kernel(triangle)), legend(on order(1 "Treatment group" 2 "Control group"))
graph export "kernel_density.png", replace



*********************************** Problem 5 ****************************************
use "211b_hw2_NSW_PSID.dta", replace
drop if data_id=="Lalonde Sample" & treat==0

* Creating an 8x4 matrix
mat T = J(8,4,.)

* Filling in the matrix
local i = 1
local list "age education black hispanic married nodegree re75 re78"
```

```
foreach x of local list {
    ttest `x', by(treat)
    mat T[`i',1] = r(mu_2)
    mat T[`i',2] = r(mu_1)
    mat T[`i',3] = r(mu_2) - r(mu_1)
    mat T[`i',4] = r(p)
    local i = `i' + 1
  }


* Naming rows/columns
mat rownames T = age education black hispanic married nodegree re75 re78
mat colnames T = "Treatment (NSW)" "Comparison (PSID)" "Difference" "p-value"


* Exporting to LaTeX
frmttable using "mean_diff_PSID.tex",statmat(T) tex fr nocenter sdec(2,2,2,3) replace



************************************** Problem 6 **************************************
use "211b_hw2_NSW_PSID.dta", replace
drop if data_id=="Lalonde Sample" & treat==0


* Raw difference
reg re78 treat
outreg2 using "reg2.tex", tex(fr) replace se bdec(1) sdec(1) noaster nonote ctitle(" ")


* Adding estimation results sequentially
local list "age education black hispanic married nodegree"
foreach x of local list {
    reg re78 treat-`x'
    outreg2 using "reg2.tex", tex(fr) append se bdec(1) sdec(1) noaster nonote ctitle(" ")
    }

* Diff-in-Diff (DD)
gen diff = re78 - re75
reg diff treat
outreg2 using "reg2.tex", tex(fr) append se bdec(1) sdec(1) noaster nonote ctitle("DD")



************************************** Problem 8 **************************************
use "211b_hw2_NSW_PSID.dta", replace
drop if data_id=="Lalonde Sample" & treat==0


* Estimating p-score using logit and polynomials and interaction terms
```

```
logit treat age-nodegree c.age#(c.age c.education black hispanic married nodegree)
c.education#(c.education black hispanic married nodegree) black#(hispanic married nodegree)
hispanic#(married nodegree) married#nodegree
predict pscore, pr


* Plotting histograms
histogram pscore if treat==1, fcolor(bluishgray) lcolor(black)
graph export "pscore_PSID_t.png", replace


histogram pscore if treat==0, fcolor(bluishgray) lcolor(black)
graph export "pscore_PSID_c.png", replace


* Plotting overlap (before trimming)
twoway (histogram pscore if treat==0, color(cranberry))(histogram pscore if treat==1,
fcolor(none) lcolor(black)), legend(order(1 "Comparison" 2 "Treatment"))
graph export "pscore_PSID_overlap.png", replace


* Trimming by "0.1 Rule"
keep if pscore > 0.1 & pscore < 0.9


twoway (histogram pscore if treat==0, color(cranberry))(histogram pscore if treat==1,
fcolor(none) lcolor(black)), legend(order(1 "Comparison" 2 "Treatment"))
graph export "pscore_overlap_PSID_1-9.png", replace

mat T = J(8,4,.)
local i = 1
local list "age education black hispanic married nodegree re75 re78"
foreach x of local list {
    ttest `x', by(treat)
    mat T[`i',1] = r(mu_2)
    mat T[`i',2] = r(mu_1)
    mat T[`i',3] = r(mu_2) - r(mu_1)
    mat T[`i',4] = r(p)
    local i = `i' + 1
     }
mat rownames T = age education black hispanic married nodegree re75 re78
mat colnames T = "Treatment (NSW)" "Comparison (PSID)" "Difference" "p-value"
mat list T
frmttable using "mean_diff_PSID_1-9.tex",statmat(T) tex fr nocenter sdec(2,2,2,3) replace


* Trimming by "0.2 Rule"
keep if pscore > 0.2 & pscore < 0.8
```

```
twoway (histogram pscore if treat==0, color(cranberry))(histogram pscore if treat==1,
fcolor(none) lcolor(black)), legend(order(1 "Comparison" 2 "Treatment"))
graph export "pscore_overlap_PSID_2-8.png", replace


mat T = J(8,4,.)
local i = 1
local list "age education black hispanic married nodegree re75 re78"
foreach x of local list {
    ttest `x', by(treat)
    mat T[`i',1] = r(mu_2)
    mat T[`i',2] = r(mu_1)
    mat T[`i',3] = r(mu_2) - r(mu_1)
    mat T[`i',4] = r(p)
    local i = `i' + 1
     }
mat rownames T = age education black hispanic married nodegree re75 re78
mat colnames T = "Treatment (NSW)" "Comparison (PSID)" "Difference" "p-value"
frmttable using "mean_diff_PSID_2-8.tex",statmat(T) tex fr nocenter sdec(2,2,2,3) replace



************************************** Problem 9 ***************************************
use "211b_hw2_NSW_PSID.dta", replace
drop if data_id=="Lalonde Sample" & treat==0
logit treat age-nodegree c.age#(c.age c.education black hispanic married nodegree)
c.education#(c.education black hispanic married nodegree) black#(hispanic married nodegree)
hispanic#(married nodegree) married#nodegree
predict pscore, pr
keep if pscore > 0.2 & pscore < 0.8


* Estimation
reg re78 treat
outreg2 using "reg3.tex", tex(fr) replace se bdec(1) sdec(1) noaster nonote ctitle(" ")


local list "age education black hispanic married nodegree"
foreach x of local list {
    reg re78 treat-`x'
    outreg2 using "reg3.tex", tex(fr) append se bdec(1) sdec(1) noaster nonote ctitle(" ")
    }


gen diff = re78 - re75
reg diff treat
outreg2 using "reg3.tex", tex(fr) append se bdec(1) sdec(1) noaster nonote ctitle("DD")
```