Running Propensity Score Matching with STATA/PSMATCH2
(For Workshop Conducted at the School of Social Work, UIUC)

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STATA Basics

The Stata Interface

- The command window
- The results window
- The review window
- The variable window

Two Ways to Run Stata:

- Interactive mode
- Do-file

Update and Access Data online

- `. update all` – update Stata packages (routines created by other users)
- Example of accessing data online

```
. net search spost
. dir *dta
. use binlfp2
. sum
. tab lfp
```

Abbreviations

- Any variable names can be abbreviated to the shortest string that uniquely identifies it (e.g., age => ag => a
- Most common and general command names can be abbreviated:
  `summarize => sum` (you use this to get descriptive statistics)
  `tabulate => ta` (you use get frequency distribution or cross-tabulation)
  `generate => gen` or `g` (you use this to generate or create new variables)
  `regress => reg` (regression analysis)

Working Directory

- The working directory is the default directory for any file operations such as using data, saving data, or logging output.
- Type `cd` to see the name of current working directory.
- Change working direction, you may do:
  `cd "d:\my work"`

Get Online Help

```
. whelp psmatch2
. help psmatch2
```

Stata File Types (Extension Naming Conventions)

Most Important Types:

.dta Data files in Stata's format
.do Batch files that execute a set of Stata commands
.wmf Graphs saved as Window Metafiles
.log Output save as plain text by the log using command

Other Types

.ado Programs that add commands to Stata
.class Files that define classes in the Stata class system
.gph Graphs saved in Stata's proprietary format
.dlg Programs that define the appearance and functionality of dialog boxes
.hlp The text displayed when you use the help command
.smcl Output saved in the SMCL format by the log using command

Adding Comments

Stata treats everything that comes after // or after * as comments that are simply echoed to the output. On any given line, Stata ignores whatever comes after /// and treats the next line as a continuation of the current line.

PSMATCH2

There is currently no commercial software package that offers formal procedure for PSM. In SAS, Lori Parsons developed several Macros (e.g., the GREEDY macro does nearest neighbor within caliper matching). In SPSS, Dr. John Painter of Jordan Institute developed a SPSS macro to do similar works as GREEDY (http://sswnt5.sowo.unc.edu/VRC/Lectures/index.htm).

We have investigated several computing packages and found that PSMATCH2 (developed by Edwin Leuven and Barbara Sianesi [2003], as a user-supplied routine in STATA) is the most comprehensive package that allows users to fulfill most tasks for propensity score matching, and the routine is being continuously improved and updated.

Update PSMATCH2 (Do this periodically)

```
. ssc install psmatch2, replace
```

Important Issues Running PSMATCH2

- **Make sure your psmatch2 is a version later than Dec. 10, 2004:**
  . which psmatch2
  c:\ado\plus\p\psmatch2.ado
  *! version 2.0.8 10dec2004 E. Leuven, B. Sianesi
  We identified a bug recently, and contacted Edwin and Barbara. They just fixed it.

- When one treated case is found several nontreated case who all have the same values of propensity scores, these nontreated cases are tied. In 1-to-1 match, therefore, picking up which one from the tied cases as the identified match depends on the order of your data. Therefore, it's important to order your data observations randomly. You always do the following commands to begin with your matching:

```
. g x=uniform()
. sort x
```

- To guarantee same results from session to session, you want to control for seed number by using:
  - `set seed 1000`

  Different seed number generates different resample.
- For nearest neighbor and Mahalanobis matching, the literature (for instance, D'Agostino, R.B. [1998]. Propensity score methods for bias reduction in the comparison of a treatment to a non-randomized control group. *Statistics in Medicine 17*, 2265-2281) suggests the use of non-replacement. That is, once a treated case is matched to one nontreated case, both cases are removed from the pool. This can be done in nearest neighbor matching in PSMATCH2 by using "**noreplacment descending**".
- **You cannot do "noreplacement" for Mahalanobis matching.** Therefore, in the resample created by Mahalanobis, it's possible that one control case can be matched to several treated case. You need keep just one pair of the match and treated cases, and delete all pairs that use the match case more than once. **The shaded cases in the following example should be deleted:**

Treat	Match
205104	200042
203103	200285
203152	200285
203056	200315
200590	200339
202000	200347
201493	200375
205358	200375
204683	200397
202984	200399
203332	200399
204621	200463
200024	200676
201530	200676
200014	200694
201262	200694

More cases …

Illustrating Example 1

Research Questions

The association between parental substance abuse and child welfare system involvement is well-known but little understood. Policymakers and child welfare researchers are primarily concerned on: Whether or not these children are living in a safe environment? Does substance abuse treatment for caregivers affect the risk of child maltreatment re-report?

Data and Study Sample

This study is a secondary analysis of data of the National Survey of Child and Adolescent Well-Being (NSCAW) – a longitudinal study intended to answer a range of fundamental questions about the outcomes for abused and neglected children and their involvement in the child welfare system.

This study employed NSCAW data of two waves: baseline information between October 1999 and December 2000, and the 18-months follow-up. The sample for this study was limited to 2,758 children who lived at home (e.g., were not in foster care) and whose primary caregivers were female. The study was limited to female caregivers because the vast majority of primary caregivers in NSCAW were female (90%).

Measures

The choice of explanatory variables (i.e., conditioning variables) in the first-step model predicting propensity scores of service receipt serves a paramount important role in the whole propensity score analysis. We chose these variables based on a review of substance abuse literature to determine what characteristics were associated with treatment receipt. We found that these characteristics fall into four categories.

Demographic characteristics:

marital status (yes/no),
education (less than high school degree, high school degree, bachelor's degree or higher),
percentage in comparison with poverty line (<50%, 50% to 100%, … and 200% or higher),
employment (yes/no),
child race/ethnicity (Black/non-Hispanic, White/non-Hispanic, Hispanic, Native American),
child age (0 to 2 years, 3 to 5 years, 6 to 10 years, 11 and older),
caregiver age (less than 35 years, 35 to 44 years, 45 to 54 years, over 54 years), and
"trouble paying for basic necessities" (yes/no).

Risks:

caregiver mental health problems (yes/no), history of arrest (yes/no), and
type of maltreatment that the child experienced (physical abuse, sexual abuse, failure to provide, failure to supervise, other).

Prior Receipt of Substance Abuse Treatment (yes/no).

Need for substance abuse services:

Analytic Plan

"3 x 2 x 2 design" = 12 Matching Schemes:

Three logistic regression models (i.e., each model specified a different set of conditioning variables to predict the propensity scores of receiving treatment),
Two matching algorithms (i.e., nearest neighbor within caliper and Mahalanobis), and
Two matching specifications (i.e., for nearest neighbor we used two different specifications on caliper size, and for Mahalanobis we used one with and one without propensity score as a covariate to calculate the Mahalanobis metric distances).

We defined the ***logit*** or ***log[(1-p)/p]*** as propensity score.

Outcome Measure and Step-3 Analysis: Timing of first maltreatment re-report 18 months after baseline. We conducted survival analysis (i.e., the Kaplan-Meier product limit method) after matching to assess difference in timing of re-report between treatment and nontreatment groups.

Running PSMATCH2:

Step 1: Logistic regression predicting propensity score (using SAS)

SAS Syntax: Predicting propensity scores, bivariate tests, data exporting

```
libname psm 'C:\Documents and Settings\Shenyang Guo\Desktop\PSM Workshop';
options nofmterr;
data data1;
set psm.sasdata;

/* Logistic regression model predicting propensity scores */
proc logistic descending;
      where chdset in(1,2) and phh8c=2;
      model aodserv= married high bahigh poverty2 poverty3
      poverty4 poverty5 employ open black hispanic natam chdage1 chdage2
      chdage3 cgrage1 cgrage2 cgrage3 cra47a mental arrest psh17a
      sexual provide supervis other ra cidi cgneed;
    output out=psm.pred1 pred=prob3;
run;

data data;
set psm.pred1;
if prob3=. then delete;  /*deleting missing data listwise */
logit3=log((1-prob3)/prob3);
      /* use logit rather than probability as propensity score */

/* create ASCII data file for Stata */
file 'C:\Documents and Settings\Shenyang Guo\Desktop\PSM Workshop\FROMSAS1.dat';
put  nscawid 1-7 (aodserv married high bahigh poverty2 poverty3
      poverty4 poverty5 employ open black hispanic natam chdage1 chdage2
      chdage3 cgrage1 cgrage2 cgrage3 cra47a mental arrest psh17a
      sexual provide supervis other ra cidi cgneed) (30*2.0)
      (prob3) (1*11.8) (logit3)(1*12.8);
run;

/* bivariate Chi-square test before matching */
proc freq;
tables (married high bahigh poverty2 poverty3
      poverty4 poverty5 employ open black hispanic natam chdage1 chdage2
      chdage3 cgrage1 cgrage2 cgrage3 cra47a mental arrest psh17a
      sexual provide supervis other ra cidi cgneed cwwrep)*aodserv /chisq;

/* Obtain descriptives so that we can verify data with Stata */
proc means;
var
    nscawid stratum nscawpsu
    aodserv married high bahigh poverty2 poverty3
    poverty4 poverty5 employ open black hispanic natam chdage1 chdage2
    chdage3 cgrage1 cgrage2 cgrage3 cra47a mental arrest psh17a
    sexual provide supervis other ra cidi cgneed
    prob3 logit3;
run;
```

Step 2: Matching with STATA/PSMATCH2

Run1: Input ASCII data and create STATA data file

```
infile nscawid aodserv married high bahigh poverty2 poverty3 poverty4 poverty5
  employ open black hispanic natam chdage1 chdage2 chdage3 cgrage1 cgrage2 cgrage3
  cra47a mental arrest psh17a sexual provide supervis other ra cidi cgneed prob3
```

```
  logit3 using "C:\...\fromsas1.dat"
summarize
save "C:\...\fromsas1.dta", replace
```

Other commands similar to **infile: insheet, infix**

Run2: 1-to-1 Match: Nearest Neighbor within Caliper, Mahalanobis with & without propensity score

```
clear
use "C:\Documents and Settings\Shenyang Guo\Desktop\PSM SSWR2005\fromsas1.dta"
set seed 1000
generate x=uniform()
sort x
// Nearest neighbor within caliper .1 - a narrowed caliper
psmatch2 aodserv, pscore(logit3) caliper(0.1) noreplacement descending
sort _id
g match=nscawid[_n1]
g treat=nscawid if _nn==1
drop if treat==.
outsheet treat match using "near1.dat", replace

clear
use "C:\Documents and Settings\Shenyang Guo\Desktop\PSM SSWR2005\fromsas1.dta"
set seed 1000
generate x=uniform()
sort x
// Nearest neighbor within caliper .25*SD
psmatch2 aodserv, pscore(logit3) caliper(0.401) noreplacement descending
sort _id
g match=nscawid[_n1]
g treat=nscawid if _nn==1
drop if treat==.
outsheet treat match using "near2.dat", replace

clear
use "C:\Documents and Settings\Shenyang Guo\Desktop\PSM SSWR2005\fromsas1.dta"
set seed 1000
generate x=uniform()
sort x
// Mahalanobis without propensity score
psmatch2 aodserv, mahal(married high bahigh poverty2 poverty3 poverty4 poverty5
employ open black hispanic natam chdage1 chdage2 chdage3 cgrage1 cgrage2 cgrage3
cra47a mental arrest psh17a sexual provide supervis other ra cidi cgneed)
sort _id
generate match=nscawid[_n1]
generate treat=nscawid if _n1 !=.
tab match
outsheet treat match using "mahal1.dat", replace

clear
use "C:\Documents and Settings\Shenyang Guo\Desktop\PSM SSWR2005\fromsas1.dta"
set seed 1000
generate x=uniform()
sort x
// Mahalanobis with propensity score
```

```
psmatch2 aodserv, mahal(married high bahigh poverty2 poverty3 poverty4 poverty5
employ open black hispanic natam chdage1 chdage2 chdage3 cgrage1 cgrage2 cgrage3
cra47a mental arrest psh17a sexual provide supervis other ra cidi cgneed) add
pscore(logit3)
sort _id
generate match=nscawid[_n1]
generate treat=nscawid if _n1 !=.
tab match
outsheet treat match using "mahal2.dat", replace
```

Step 3: Merge to Original Data and Step-3 Analysis (Survival Analysis)

SAS Syntax

- Merge the new sample (treat & match) with the original sample;
- Create a new variable (0/1) indicating "treatment" of the new sample;
- Use the new "treatment" variable to select valid cases – only use the resample;
- Run chi-square tests (we want all chi-squares are not significant, because this is after matching);
- Run survival analysis (Kaplan-Meier).

```
libname psm 'C:\Documents and Settings\Shenyang Guo\Desktop\psm workshop';
options nofmterr;

data n3;
input nt3 nm3;
datalines;
204869      202796
203309      201909
200725      204867
201516      204706
201646      204006
204017      203530
200098      205169
204479      203218
205411      203477
203103      200890
203316      205403
/* More cases */
;
run;

data n3_ (keep=nscawid n3treat);
set n3(keep=nt3) n3(keep=nm3);
nscawid=nt3;
if nt3=. then nscawid=nm3;
n3treat=1;
if nt3=. then n3treat=0;
run;

/*merge to the original data*/
data one;
set psm.pred1;
proc sort;
```

```
 by nscawid;
run;
data two ;
set n3_;
proc sort;
 by nscawid;
run;
data psm.final;
merge one two ;
 by nscawid;
run;

/*check chi-square after matching*/
data final;
set psm.final;
if n3treat=. then delete;
proc freq;
tables aodserv*(married high bahigh poverty2 poverty3
      poverty4 poverty5 employ open black hispanic natam chdage1 chdage2
      chdage3 cgrage1 cgrage2 cgrage3 cra47a mental arrest psh17a
      sexual provide supervis other ra cidi cgneed) /chisq;
run;

/* survival analysis: Kaplan-Meier*/
data final;
set psm.final;
if n3treat=. then delete;
proc lifetest data=data2 method=km plots=(s) graphics;
  time durm*rrpt(0);
  strata aodserv1;
  symbol1 v=none color=red line=1;
  symbol1 v=none color=blue line=2;
run;
```

Findings of Example 1:

Table 1
Table 2
Table 3
Figure 1

Table 1. Sample Description and Logistic Regression Models Predicting Propensity Scores

Variable	N	%	% Caregivers Treated (Service Users)	Bivariate x^2 Test	Logistic 1 B		Logistic 2 B		Logistic 3 B	
Marital status - Not married	1,926	69.8	11.5	.085						
Married (MARRIED)	832	30.2	9.3		.055		.397		.181	
Education - No degree	926	33.6	13.1	.005						
High school diploma or equivalent (HIGH)	1,232	44.7	10.6		-.161		.078		-.210	
B.A. or higher (BAHIGH)	600	21.8	7.8		-.424	*	-.064		-.253	
Poverty - < 50%	623	22.6	13.5	.014						
50% to <100% (POVERTY2)	898	32.6	11.7		-.146		-.206		-.088	
100% to <150% (POVERTY3)	503	18.2	8.0		-.329		-.220		-.221	
150% to <200% (POVERTY4)	339	12.3	8.9		-.125		-.099		.095	
< 200% or more (POVERTY5)	395	14.3	9.9		.095		-.277		.011	
Employment - Not employed	1,424	51.6	13.6	<.0001						
Employed (EMPLOY)	1,334	48.4	7.9		-.175		-.323		-.162	
Case status - Closed	1,211	43.9	5.7	<.0001						
Open (OPEN)	1,547	56.1	14.8		.807	***	.168		.509	**
Child race - White	1,504	54.5	9.8	.010						
African American (BLACK)	706	25.6	12.2		.167		-.367		.022	
Hispanic (HISPANIC)	404	14.7	9.7		.298		-.089		.332	
Native American (NATAM)	144	5.2	18.1		.882	**	.769	*	.819	**
Child Age - 11+	559	20.3	6.8	<.0001						
0-2 (CHDAGE1)	937	34.0	16.9		1.088	***	.739	*	1.027	***
3-5 (CHDAGE2)	452	16.4	9.1		.341		.223		.358	
6-10 (CHDAGE3)	810	29.4	7.5		.233		.179		.190	
Caregiver age - >54	43	1.6	18.6	.313						
< 35 (CGRAGE1)	1,904	69.0	10.4		-1.225	**	-.925		-1.210	*
35-44 (CGRAGE2)	653	23.7	11.3		-.755		-.460		-.813	
45-54 (CGRAGE3)	158	5.7	12.0		-.719		-.421		-.410	
Trouble paying for basic necessities - No	1,911	69.3	9.2	<.0001						
Yes (CRA47A)	847	30.7	14.5		.059		.195		.083	
Caregiver mental health - No problem	2,014	73.0	7.4	<.0001						
Mental health problem (METNAL)	744	27.0	20.2		.734	***	.203		.633	***
Caregiver arrest - Never arrested	1,837	66.6	6.1	<.0001						
Arrested (ARREST)	921	33.4	20.2		1.034	***	.767	***	.858	***
AOD treatment receipt - No treatment	2,469	89.5	8.1	<.0001						
Treatment (PSH17A)	289	10.5	33.9		-1.366	***	-.358		-.630	**
Maltreatment type - Physical abuse	681	24.7	7.8	<.0001						
Sexual abuse (SEXUAL)	356	12.9	3.7		-.667	*	-.422		-.422	
Failure to provide (PROVIDE)	596	21.6	17.0		.440	*	-.191		.276	
Failure to supervise (SUPERVIS)	764	27.7	11.9		.108		-.202		-.020	
Other (OTHER)	361	13.1	11.1		.211		-.569		.034	
Risk assessment - Risk absence	2,284	82.8	4.3	<.0001						
Risk precense (RA)	474	17.2	42.2				1.388	***	2.026	***
"CIDI-SF" - Absence	1,958	71.0	6.1	<.0001						
Presence (CIDI)	800	29.0	22.4				.971	***	.912	***
Caregiver report of need - No	2,635	95.5	9.3	<.0001						
Yes (CGNEED)	123	4.5	43.1				1.109	**	1.211	***
CWW report of need for service - No	2,425	87.9	3.1	<.0001						
Yes (CWWREP)	333	12.1	67.0				3.398	***		
Constant of the logistic regression					-.468		-3.607	***	-2.704	**

Reference group is show n next to the variable name. * p<.05, ** p<.01, *** p<.001

Table 2.Description of Matching Schemes and Resample Sizes

Scheme	Description of Matching Method	N of the New Sample	
		Treated	Nontreated
1. Nearest 1-1	Propensity scores predicted by **logistic 1,** Nearest 1-to-1 using caliper=.311 (.25σ_p)	273	273
2. Nearest 1-2	Propensity scores predicted by **logistic 1,** Nearest 1-to-1 using caliper=.1	272	272
3. Mahalanobis 1	Covariates used in the calculation of the Mahalanobis distances same as **logistic 1**	257	257
4. Mahalanobis 1 with p-score added	Mahalanobis 1 with propensity score added, Propensity scores predicted by **logistic 1**	256	256
5. Nearest 2-1	Propensity scores predicted by **logistic 2,** Nearest 1-to-1 using caliper=.490 (.25σ_p)	160	160
6. Nearest 2-2	Propensity scores predicted by **logistic 2,** Nearest 1-to-1 using caliper=.1	159	159
7. Mahalanobis 2	Covariates used in the calculation of the Mahalanobis distances same as **logistic 2**	177	177
8. Mahalanobis 2 with p-score added	Mahalanobis 2 with propensity score added, Propensity scores predicted by **logistic 2**	177	177
9. Nearest 3-1	Propensity scores predicted by **logistic 3,** Nearest 1-to-1 using caliper=.401 (.25σ_p)	237	237
10. Nearest 3-2	Propensity scores predicted by **logistic 3,** Nearest 1-to-1 using caliper=.1	237	237
11. Mahalanobis 3	Covariates used in the calculation of the Mahalanobis distances same as **logistic 3**	230	230
12. Mahalanobis 3 with p-score added	Mahalanobis 3 with propensity score added, Propensity scores predicted by **logistic 3**	230	230

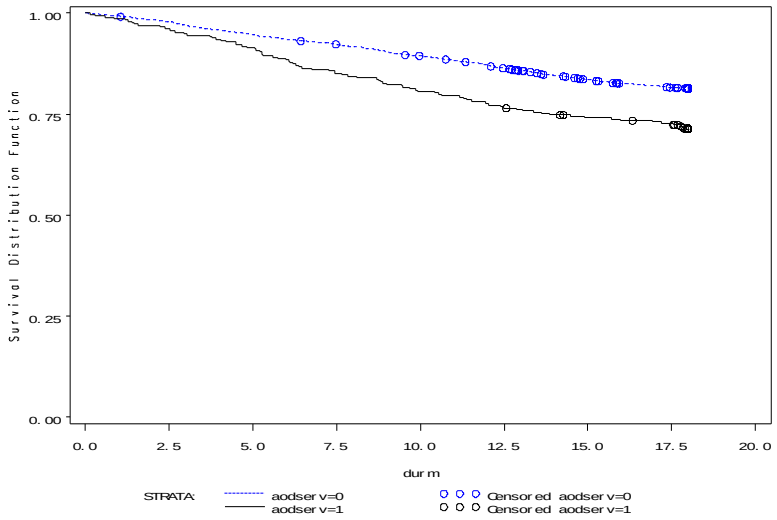
Table 3. Results of Sensitivity Analyses

Scheme	Covariate Distributions Did Not Overlap Sufficiently: Covariates Significant after Matching p<.05	Results of Survival Analysis on Timing of Re-report		
		85 Percentile of Survivor Function Months (Kaplan-Meier Estimtaion)		p-value Testing Group Difference (Wilcoxon)
		Treated	Nontreated	
Original Sample or All (n=2,723)[a]	BAHIGH, POVERTY3, EMPLOY, OPEN, NATAM, CHDAGE1, CHDAGE3, CRA47A, MENTAL, ARREST, PSH17A, SEXUAL, PROVIDE, RA, CIDI, CGNEED, CWWREP	7.4	13.6	<.0001
1. Nearest 1-1	RA, CIDI, CGNEED, CWWREP	7.4	8.9	.40
2. Nearest 1-2	RA, CIDI, CGNEED, CWWREP	7.4	9.1	.35
3. Mahalanobis 1	OPEN, MENTAL, ARREST, RA, CIDI, CGNEED, CWWREP	7.6	11.7	.04
4. Mahalanobis 1 with p-score added	OPEN, MENTAL, ARREST, RA, CIDI, CGNEED, CWWREP	7.5	11.7	.03
5. Nearest 2-1	None	7.4	9.5	.34
6. Nearest 2-2	None	8.8	9.5	.44
7. Mahalanobis 2	CGRAGE2, PSH17A, RA, CIDI, CWWREP	6.8	9.6	.60
8. Mahalanobis 2 with p-score added	CGRAGE2, PSH17A, RA, CIDI, CWWREP	8.1	9.6	.90
9. Nearest 3-1	CWWREP	7.3	12.7	.01
10. Nearest 3-2	CWWREP	7.3	12.7	.01
11. Mahalanobis 3	CGRAGE1, CGRAGE2, MENTAL, ARREST, RA, CIDI, CWWREP	9.4	11.1	.13
12. Mahalanobis 3 with p-score added	OPEN, CGRAGE1, CGRAGE2, MENTAL, ARREST, RA CIDI, CWWREP	8.3	10.8	.12

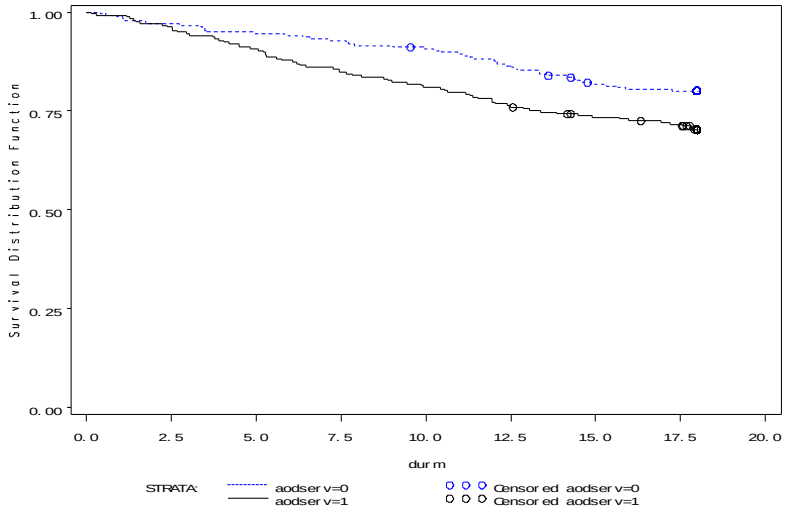
a. Thiry-five study subjects were eliminated in the analysis of the original sample due to missing data.

Figure 1. Survivor Functions: Percentage Remaining no Re-report

Original Sample (n=2,723)



Sample Based on Matching Scheme 10 (n=474)



Conclusion: The propensity score matching analysis indicates that children whose caregivers receiving substance abuse services were not faring better than children of non-service users - they are more likely to have maltreatment re-report. Child welfare practitioners, policymakers, and service providers need pay attention to the safety and well-being issues for these children.

Illustrating Example 2

Research Question

Does substance abuse treatment affect child's developmental well-being?

Data, Study Sample, and Measures

The study employed the same NSCAW data. To answer the research question, we used the Achenbach Children's Behavioral Checklist (CBCL/4-18, including externalizing, internalizing, and total scores) as the outcome measures. A high score on each of these measures indicates more behavioral problems. The study only analyzed CBCL/4-18, and therefore, excluded children who aged younger than 4 at baseline, and the study sample for this analysis consisted of 1,407 children.

Analytic Plan

Because the outcome variable is a continuous variable, we employed the difference-in-differences method with local linear regression and a tricube kernel. We also conducted sensitivity analysis to test how study results vary by different specifications on bandwidth value and trimming.

Running PSMATCH2:

Step 1: Logistic regression predicting propensity score (using SAS)

SAS Syntax: Predicting propensity scores, bivariate tests, data exporting

```
libname psm6 'C:\Documents and Settings\Shenyang Guo\Desktop\psm6';
options nofmterr;

data data2;
set psm6.pred1;

proc logistic descending;
      where chdset in(1,2) and phh8c=2;
      model aodserv= married high bahigh poverty2 poverty3
      poverty4 poverty5 employ open black hispanic natam chdage2
      chdage3 cgrage1 cgrage2 cgrage3 cra47a mental arrest psh17a
      sexual provide supervis other ra cidi cgneed;
    output out=psm6.pred1 pred=prob4;
proc means;
var ext int tot;
proc ttest;
 class aodserv;
 var ext int tot;
run;

data data;
set psm6.pred1;
if prob4=. then delete;

file 'C:\Documents and Settings\shenyang\Desktop\psm6\FROMSAS2.dat';
put  nscawid 1-7 (aodserv married high bahigh poverty2 poverty3
      poverty4 poverty5 employ open black hispanic natam chdage1 chdage2
      chdage3 cgrage1 cgrage2 cgrage3 cra47a mental arrest psh17a
      sexual provide supervis other ra cidi cgneed) (30*2.0)
      (prob4) (1*10.7) (bc3_ept pbc_ept bc3_ipt pbc_ipt bc3_tpt pbc_tpt) (6*3.0);
run;
```

```
proc means;
var
    nscawid aodserv married high bahigh poverty2 poverty3
      poverty4 poverty5 employ open black hispanic natam chdage1 chdage2
      chdage3 cgrage1 cgrage2 cgrage3 cra47a mental arrest psh17a
      sexual provide supervis other ra cidi cgneed prob4
    bc3_ept pbc_ept bc3_ipt pbc_ipt bc3_tpt pbc_tpt ext int tot prob4 logit4;
run;
```

Step 2: Running Difference-in-differences (STATA Syntax)

Run3: Input Data to STATA

```
clear
infile nscawid aodserv married high bahigh poverty2 poverty3 poverty4 poverty5
   employ open black hispanic natam chdage1 chdage2 chdage3 cgrage1 cgrage2
   cgrage3 cra47a mental arrest psh17a sexual provide supervis other ra cidi
   cgneed prob4 bc3_ept pbc_ept bc3_ipt pbc_ipt bc3_tpt pbc_tpt using
   "C:\Documents and Settings\Shenyang Guo\Desktop\PSM SSWR2005\fromsas2.dat"
gen logit4=log((1-prob4)/prob4)
gen extern=bc3_ept-pbc_ept
gen intern=bc3_ipt-pbc_ipt
gen total=bc3_tpt-pbc_tpt
sum
save "C:\Documents and Settings\Shenyang Guo\Desktop\PSM SSWR2005\fromsas2.dta",
   replace
```

Run4: Run difference-in-differences

```
// Local linear regression - Outcome externalizing change score
clear
use "C:\Documents and Settings\Shenyang Guo\Desktop\PSM SSWR2005\fromsas2.dta"
generate x=uniform()
sort x
set seed 1000
psmatch2 aodserv, outcome(extern) pscore(logit4) com llr
//Delete 2 "off support" cases for BS
drop if aodserv==1 & _weight==.
//Run bootstrapping to obtain standard error
bs "psmatch2 aodserv, outcome(extern) pscore(logit4) com llr" "r(att)"

//Change default bandwidth default .8 to a small bandwidth .02
clear
use "C:\Documents and Settings\Shenyang Guo\Desktop\PSM SSWR2005\fromsas2.dta"
generate x=uniform()
sort x
set seed 1000
psmatch2 aodserv, outcome(extern) pscore(logit4) com llr bwidth(.02)

//Trim - drop 5% treated cases at which Pscore for nontreated is the lowest
clear
use "C:\Documents and Settings\Shenyang Guo\Desktop\PSM SSWR2005\fromsas2.dta"
generate x=uniform()
sort x
set seed 1000
psmatch2 aodserv, outcome(extern) pscore(logit4) llr trim(5)
```

Findings of Example 2 (Table 4)

Table 4. Estimated Average Treatment Effects on CBCL Change:
Difference-in-Differences Estimation by Local Linear Regression

Group & Comparison	Outcome Measures: CBCL Scores		
	Externalizing	Internalizing	Total
Mean Difference between 18 Months and Baseline			
Children whose caregivers received services (n=112)	.15	-2.09	-.89
Children whose caregivers did not receive services (n=1,295)	-1.82	-1.44	-1.92
Unadjusted Mean Difference[a]	1.97	-.65	1.03
Adjusted Mean Difference			
DID[b] Point Estimate (Bias Corrected 95% Confidence Interval)	3.37 (.27, 5.43)	.84 (-1.85, 3.56)	2.76 (.96, 5.12)
Sensitivity Analyses			
DID[b] Point Estimate (Bias Corrected 95% Confidence Interval)			
Changing Bandwidth:			
Small - bandwidth = .01	3.97 (1.80, 6.59)	1.30 (-1.23, 3.30)	3.35 (1.13, 5.92)
Small - bandwidth = .05	3.52 (.55, 5.39)	.84 (-1.87, 3.58)	2.83 (1.01, 5.14)
Large - bandwidth = .8	2.77 (.18, 5.24)	.08 (-2.19, 2.05)	2.10 (.38, 4.58)
Trimming:			
2% (2 cases excluded)	3.31 (.17, 5.32)	.77 (-1.97, 3.31)	2.82 (.97, 5.23)
5% (5 cases excluded)	3.38 (.58, 5.46)	.89 (-1.40, 3.26)	2.99 (1.29, 5.35)
10% (11 cases excluded)	3.50 (.90, 5.89)	.58 (-2.29, 2.80)	3.01 (1.40, 5.75)

Note: a. T-tests show that all unadjusted mean differences are not statistically different.
b. DID - Difference-in-Differences.

Conclusion: The DID analysis indicates that children whose caregivers receiving substance abuse services were not faring better than children of non-service users- the mean externalizing score and the mean total score for the substance-abusing group increased (worsening), while these two scores for the non-substance abusing group decreased (improving), from baseline to 18 months. The difference-in-differences estimation just shows a greater difference between the two groups.