



临床预测模型构建&机器学习(R语言进阶)

第4章倾向性匹配得分PSM 分析与R语言实现

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PSM定义



- ▶ 通过一定的统计学方法对试验组与对照组进行筛选,使筛选出来的研究对象在某些重要临床特征(潜在的混杂因素)上具有可比性。
- 一般是通过某种统计学模型求得每个观测的多个协变量的综合倾向性得分,再按照倾向性得分是否接近进行匹配。
- ▶ 最常用的统计模型一般是以分组变量为因变量,其他可能影响结果的混杂因素为协变量构建Logistic回归模型。
- 计算每个观测的倾向得分,按照得分大小进行匹配。

PSM概念解释



> 举个例子:

- ▶ 比如替某大龄女孩找对象,该女孩列出以下3个条件: 1. 年龄要与自己相差不大(±2岁);
- 2. 民族与自己一致; 3. 学历与自己一致。
- ▶ 那么如果是经典的匹配方法,首先是按照这些条件删选男生,然后在符合条件的男生中随机抽取一个男孩介绍给这个女孩。
- ➤ 如果是PSM呢,首先给出一个评分方法,比如总分 = 0.8*年龄+2.3*民族+1.6*学历,然后对该女孩和众多男孩分别求得分,找出一个得分与该女孩最为接近的男孩,介绍他们认识。
- ▶ 如果得分接近的有很多怎么办?选择多个还是选择一个?这是一个问题!

PSM概念解释



Table 1 Baseline clinical characteristics and procedure characteristics before and after matching on the propensity score

	Before n	natching		After m	atching	
Variables	Anemia,	No anemia,	P value	Anemia,	No anemia,	P value
	n=581 (%)	n=8,244 (%)		n=436 (%)	n=436 (%)	
Male	355 (61.10)	6,223 (75.49)	<0.001	276 (63.30)	276 (63.30)	1.000
Elders	386 (66.44)	2,881 (34.95)	<0.001	286 (65.60)	300 (68.81)	0.313
ВМІ	24.06±3.03	24.78±3.15	<0.001	24.22±3.02	24.17±3.25	0.835
Smoker	314 (54.04)	4,265 (51.73)	0.281	232 (53.21)	216 (49.54)	0.278
Drinker	186 (32.01)	2,517 (30.53)	0.454	142 (32.57)	133 (30.50)	0.512
Hypertension	358 (61.62)	4,687 (56.85)	0.025	274 (62.84)	274 (62.84)	1.000
Arrhythmia	68 (11.70)	772 (9.36)	0.063	55 (12.61)	53 (12.16)	0.837
Diabetes	581 (100.00)	8,244 (100.00)	0.003	436 (100.00)	436 (100.00)	0.528
Non-diabetes	396 (68.16)	6,140 (74.48)		291 (66.74)	304 (69.72)	
Diet-therapy	34 (5.85)	370 (4.49)		26 (5.96)	20 (4.59)	
Drug-therapy	151 (25.99)	1,734 (21.03)		119 (27.29)	112 (25.69)	
Hyperlipidemia	173 (29.78)	3,865 (46.88)	<0.001	134 (30.73)	126 (28.90)	0.554
PVD	18 (3.10)	126 (1.53)	0.004	14 (3.21)	14 (3.21)	1.000
History of cardiovascular and cerebrovascular diseases	238 (40.96)	2,884 (34.98)	0.004	180 (41.28)	177 (40.60)	0.836

PSM实战【案例1】



▶ 下图所示数据中共有10个变量,614个观测,试验组185例,对照组429例。treat变量即为分组变量,"1"=试验组(接受职业培训),"0"=对照组(未接受职业培训)。age, educ, black, hispan, married, nodegree, re74, re75为协变量, re78为结局变量(年总收入)。事实上,倾向性匹配得分分析是要建立一个以分组变量(treat)为因变量,各个协变量(age, educ, black, hispan, married, nodegree, re74, re75)为自变量的回归方程。而结局变量(re78)在PSM过程中几乎不参与建模。

SPSS? Stata? R?



软件名称	优点	不足	推荐级别
SPSS	1. 菜单操作; 2. 简便医	1. 仅能实现1:1匹配; 2.	****
	学; 3. 可直接导出匹配	导出数据集后需要手动	
	好的数据集	进行均衡性检验; 3. 不	
		能导出匹配结果的直观	
		图形	
Stata	1. 操作灵活; 2. 可实现	1. 命令行操作,需要一	****
	1:2及以上比例的匹配; 3.	定的Stata基础; 2. 匹配	
	自动均衡性检验; 4. 导	完成的数据集导出较麻	
	出匹配结果的直观图形	烦	

备注: R语言与SAS均可实现PSM, 请根据实际情况选择一种软件即可

R语言实现PSM代码{MatchIt}



- library(MatchIt)
- data(lalonde)
- head(lalonde)
- f=matchit(treat~re74+re75+educ+black+hispan+age+married+nodegree,data=lalonde,method="near est")
- #f=matchit(treat~re74+re75+educ+black+hispan+age+married+nodegree,data=lalonde,method="nearest",caliper=0.05)
- summary(f)
- matchdata=match.data(f)
- matchdata
- library(foreign)
- matchdata\$id<-1:nrow(matchdata)
- write.dta(matchdata,"d:/matchdata.dta")

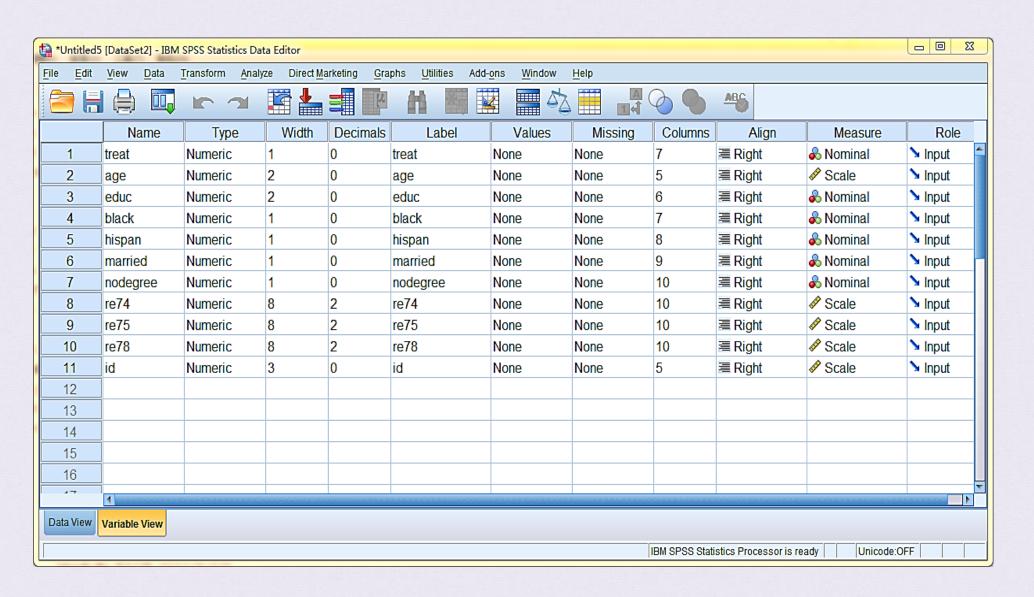
R语言实现PSM代码{nonrandom}



```
## plot.pscore {nonrandom}
library(nonrandom)
## STU1
data(stu1)
stu1.ps <- pscore(data = stu1,
        formula = therapie~tgr+age)
plot.pscore(x = stu1.ps,
     main = "PS distribution",
     xlab = "",
      par.1=list(col="red"),
      par.0=list(lwd=2),
      par.dens=list(kernel="gaussian"))
## STU1
data(stu1)
stu1.ps <- pscore(data = stu1,
        formula = therapie~tgr+age)
stu1.match <- ps.match(object = stu1.ps,
           ratio = 2,
           caliper = 0.05,
           givenTmatchingC = FALSE,
           matched.by = "pscore",
           setseed = 38902)
```

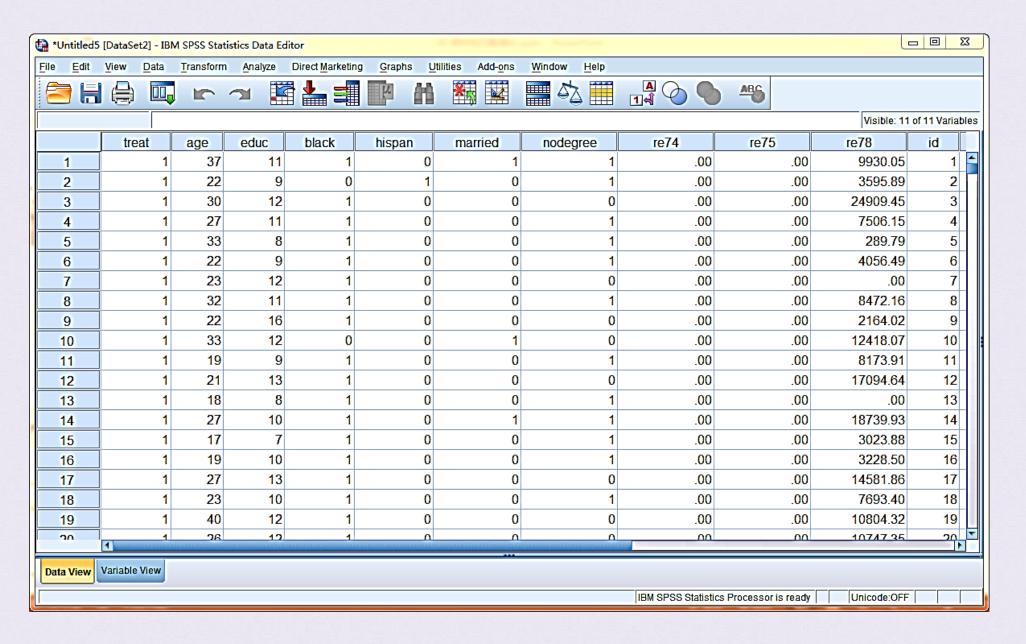
PSM实战 -- SPSS操作





PSM实战 -- SPSS操作





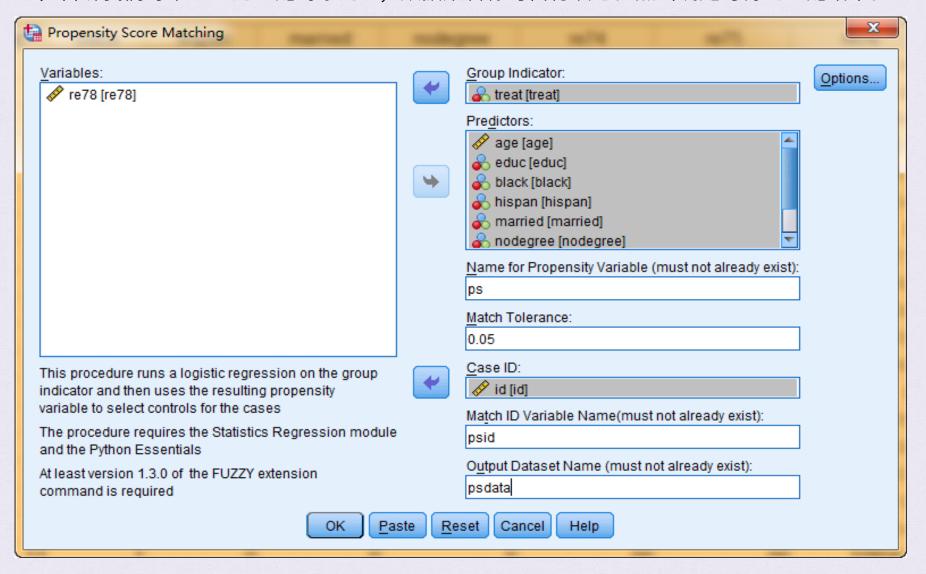
PSM实战 -- SPSS操作 1.点击"数据"-"倾向得分匹配",如下图:



🙀 *Untitled5 [DataS	et2] - IBM SPSS Statistics Data Editor	-			
<u>F</u> ile <u>E</u> dit <u>V</u> iew	<u>Data</u> <u>Transform</u> <u>Analyze</u> Direct <u>M</u> arket	ing <u>G</u> ra	aphs <u>U</u> tilities	Add- <u>o</u> ns	<u>W</u> indow <u>H</u> elp
	Define <u>V</u> ariable Properties	μ			
	Set Measurement Level for Unknown				
	<u> </u>				
tre	₽ New Custom Attri <u>b</u> ute	his		arried	nodegree
1	☐ Define Dates	_	0	1	1
2	Define Multiple Response Sets		1	0	1
3	Validation	-	0	0	0
4	ldentify Duplicate Cases		0	0	1
5	Identify Unusual Cases		0	0	1
6	Compare Datasets		0	0	1
7	Sort Cases		0	0	0
8	Sort Variables		0	0	1
9	Transpose		0	0	0
10	Merge Files	-	0	1	0
11	Restructure		0	0	1
12	Rake Weights		0	0	0
13	Propensity Score Matching		0	0	1
14	Case Control Matching		0	1	1
15	Aggregate		0	0	1
16	Split into Files	_	0	0	0
17	Orthogonal Design		0	0	1
18	Copy Dataset		0	0	0
19	Split File		0	0	0
20	⊞ Select Cases		U	U	U
	4∯ <u>W</u> eight Cases				
Data View Variable	View				
Propensity Score Mat	ching				

SPSS操作 2. 弹出下图对话框,组指示符选择"treat",即干预因素,须为二分类变量;预测变量框里 选入所有混杂因素,倾向变量名即每个个体的倾向评分得分变量名,可随意填写(字母或字母 加数字)、匹配容差可从较小的数值填写,根据情况填写;匹配id变量名,即可输出一个变 量,告诉我们每个case的匹配对象的id;数据集名称可自行填写。点击确定可得到匹配结果。





SPSS操作 3.如下图进行"选项设置"。Variable for Number of Eligible Case:输出新的变量(变量名自定义)显示实验组匹配几个满足条件的对照;Sampling:抽样;Without replacement:不放回抽;With replacement:放回抽样;Give priority…:优先精确匹配;Maxmize execution performance: 最大匹配(系统默认);Randomize case order when…: 当多个对照符合时随 机选择一个对象匹配; Random Number Seed: 设置随机种子数。

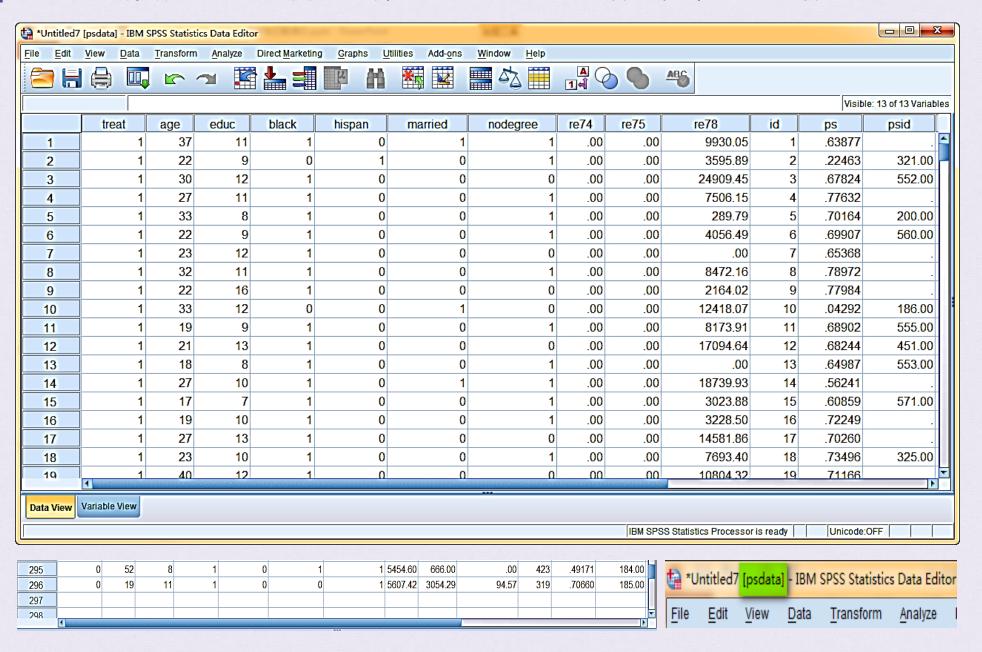


elicase		
Sampling		
Without replacement		
With replacement		
Give priority to exact match	es	
✓ Maximize execution perform	nance	
Randomize case order wh	en drawing matches	
Ra <u>n</u> dom Number Seed:		
20170713		

*Untitled	5 [DataSet2] - IBM SPSS Stati	istics Data Editor								X
<u>F</u> ile <u>E</u> dit	<u>V</u> iew <u>C</u>	ata <u>T</u> ransform	<u>A</u> nalyze Direct	Marketing Graphs	<u>U</u> tilities Add- <u>o</u> ns	<u>W</u> indow <u>H</u> elp					
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										Visible: 13 of 13 V	/ariables
	lack	hispan	married	nodegree	re74	re75	re78	id	ps	psid	١,
1	1	0	1	1	.00	.00	9930.05	1	.63877		<u> </u>
2	0	1	0	1	.00	.00	3595.89	2	.22463	321.00	
3	1	0	0	0	.00	.00	24909.45	3	.67824	552.00	
4	1	0	0	1	.00	.00	7506.15	4	.77632		
5	1	0	0	1	.00	.00	289.79	5	.70164	200.00	
6	1	0	0	1	.00	.00	4056.49	6	.69907	560.00	
7	1	0	0	0	.00	.00	.00	7	.65368		
8	1	0	0	1	.00	.00	8472.16	8	.78972		
9	1	0	0	0	.00	.00	2164.02	9	.77984		
10	0	0	1	0	.00	.00	12418.07	10	.04292	186.00	
11	1	0	0	1	.00	.00	8173.91	11	.68902	555.00	
12	1	0	0	0	.00	.00	17094.64	12	.68244	451.00	
13	1	0	0	1	.00	.00	.00	13	.64987	553.00	
14	1	0	1	1	.00	.00	18739.93	14	.56241		
15	1	0	0	1	.00	.00	3023.88	15	.60859	571.00	
16	1	0	0	1	.00	.00	3228.50	16	.72249		
17	1	0	0	0	.00	.00	14581.86	17	.70260		
18	1	0	0	1	00	00	7693 40	18	73496	325 00	- F
			Temperature Control Control			•••					
Data View	Variable Vi	ew									
							IBM SPSS	Statistics Proc	essor is ready U	nicode:OFF	

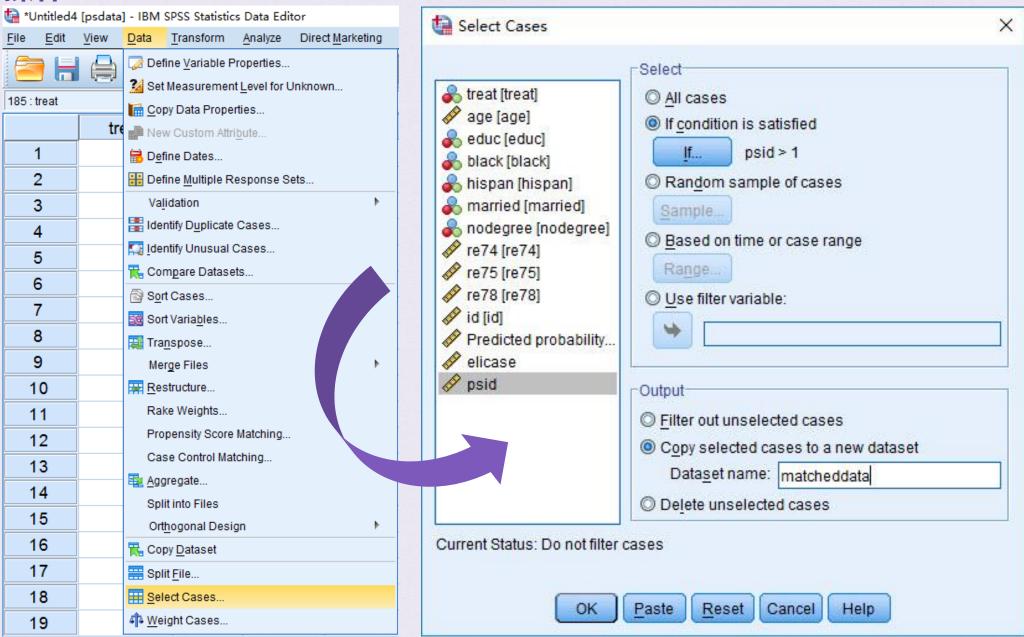
SPSS操作 5. SPSS会将所有匹配的对象重新筛选出来生成一个新的数据,即匹配后的数据。





SPSS操作 6. 如下图所示,筛选最终的成功匹配的数据集







匹配后的统计结果概览

Case Control Matching Statistics

Match Type	Count
Exact Matches	0
Fuzzy Matches	111
Unmatched Including Missing Keys	74
Unmatched with Valid Keys	74
Sampling	without replacement
Log file	none
Maximize Matching Performance	yes

Case Control Match Tolerances

Match Variables	Value	Fuzzy Match Tries	Incremental Rejection Percentage
Exact (All Variables)		35684.000	100.000
ps	.050	35684.000	99.689

Tries is the number of match comparisons before drawing.
Rejection percentage shows the match rejection rate. Rejections are attributed to the first variable in the BY list that causes rejection.

SPSS操作注意事项



在用SPSS做倾向评分匹配时应注意:

- ▶ 1. SPSS安装需要同意安装Python Essentials插件,否则无法使用;
- ▶ 2. 所有用于分析的变量名和界面填写的变量名必须是英文或英文加数字,不能是中文;
- ▶ 3. 匹配容差需要根据实际情况确定,如两组样本量差异较大(两组差10倍以上),可以用较小的容差,如0.001,如较小容差不能匹配,再将容差调大后重试,如0.01或0.05;
- ▶ 4. 完成匹配后应对两组进行均衡性检验,成组t检验或者普通卡方检验;
- ▶ 5. 如果一个观测有多个匹配对象,程序会从中随机选择,因此每次运行可能得到的匹配结果不同,如果设定固定随机种子数,结果应该一致;
- ▶ 6. SPSS程序只能进行1: 1匹配,其他比例可通过Stata实现。

完成匹配后均衡性检验(age nodegree)



Group Statistics

	treat	N	Mean	Std. Deviation	Std. Error Mean
age	1	185	25.82	7.155	.526
	0	111	27.41	10.831	1.028

treat * nodegree Crosstabulation

Count

		node		
		0	1	Total
treat	0	41	70	111
	1	54	131	185
Total		95	201	296

Independent Samples Test

		Levene's Test Varia			t-test for Equality of Means						
							Mean	Std. Error	95% Confidenc Differ		
		F	Sig.	t	df	Sig. (2-tailed)	Difference	Difference	Lower	Upper	
age	Equal variances assumed	34.106	.000	-1.519	294	.130	-1.589	1.046	-3.648	.470	
	Equal variances not assumed			-1.376	168.248	.171	-1.589	1.155	-3.869	.691	

Chi-Square Tests

	Value	df	Asymp. S (2-side		Exact Sig. (2- sided)	Exact Sig. (1- sided)
Pearson Chi-Square	1.911 ^a	1		.167		
Continuity Correction ^b	1.572	1	_	.210		
Likelihood Ratio	1.894	1		.169		
Fisher's Exact Test					.198	.105
Linear-by-Linear Association	1.904	1		.168		
N of Valid Cases	296					

- a. 0 cells (0.0%) have expected count less than 5. The minimum expected count is 35.63.
- b. Computed only for a 2x2 table



▶ 1. 安装psmatch2统计包,命令如下:

.ssc install psmatch2

#需要在联网状态下键入上述命令,然后软件自动搜索对应的程序包进行安装,成功安装后会有以下提示:

checking psmatch2 consistency and verifying not already installed...

installing into .\ado\plus\...

installation complete. (#出现此提示语句表示安装完成)

#为了验证是否成功安装以及查看psmatch2命令的帮助菜单,可在命令窗口键入

.help psmatch2

#如果能顺利弹出帮助文件,表示安装成功,可正常使用。

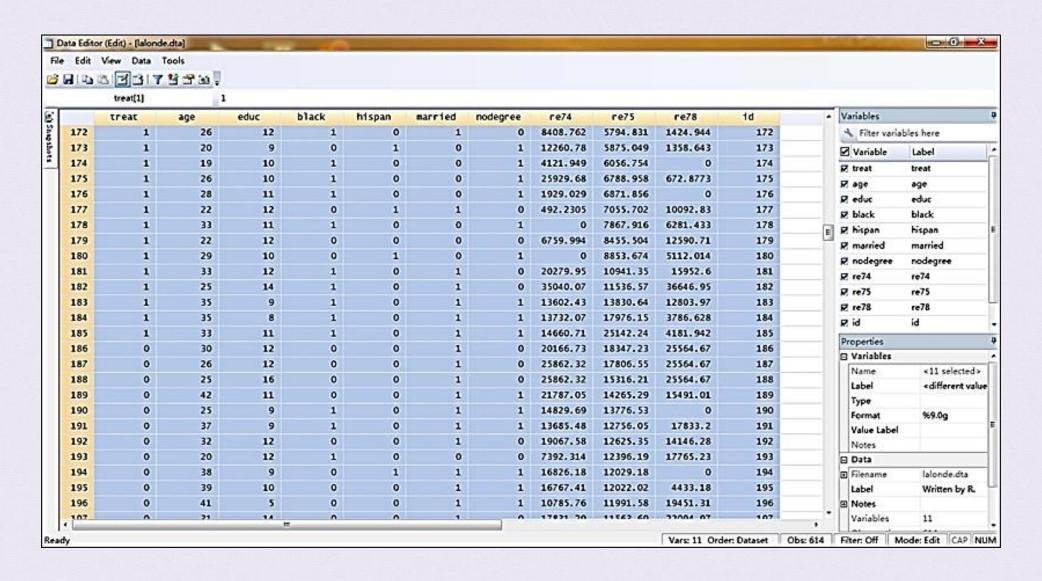


> 2. 数据准备

数据如下图所示,共有10个变量,614个观测,试验组185例,对照组429例。treat变量即为分组变量,"1"=试验组,"0"=对照组。age, educ, black, hispan, married, nodegree, re74, re75为协变量, re78为结局变量(总收入)。事实上,倾向性匹配得分分析是要建立一个以分组变量(treat)为因变量,各个协变量(age, educ, black, hispan, married, nodegree, re74, re75)为自变量的回归方程。而结局变量(re78)在PSM过程中几乎不参与建模。

Stata操作







> 3. 数据分析及命令解读,命令窗口键入如下命令:

```
.gen tmp = runiform()
.sort tmp
(# 以上两步对所有观测值进行随机排序)
.psmatch2 treat age educ black hispan married nodegree re74 re75, out(re78) logit neighbor(1) common caliper(.05) ties
.pstest, both
.psgraph
```



> 3.1 命令解读,以下是帮助菜单中psmatch2语法格式:

psmatch2 depvar [indepvars] [if exp] [in range] [, outcome(varlist) pscore(varname) neighbor(integer) radius caliper(real) mahalanobis(varlist) ai(integer) population altvariance kernel llr kerneltype(type) bwidth(real) spline nknots(integer) common trim(real) noreplacement descending odds index logit ties quietly w(matrix) ate]



▶ 3.2. 命令解读:

- ▶ psmatch2 因变量协变量,[选择项]
- ▶ 本例选择 "nearest neighbor matching within caliper" 匹配方法。out(re78) 指名结局变量。
- ➤ logit 指定使用logit模型进行拟合,默认的是probit模型。
- ▶ neighbor(1) 指定按照1:1进行匹配,如果要按照1:3进行匹配,则设定为neighbor(3),本例中因对照组 样本量有限,仅适合1:1进行匹配。
- > common 强制排除试验组中倾向值大于对照组最大倾向值或低于对照组最小倾向值的观测。
- ➤ caliper(.05) 试验组与匹配对照所允许的最大距离为0.05。
- ➤ ties强制当试验组观测有不止一个最优匹配时同时记录。



▶ 3.3. 命令解读:

- ➤ pstest, both 做匹配后均衡性检验,理论上说此处只能对连续变量做均衡性检验,对分类变量的均衡性检验应该重新整理数据后运用χ2检验或者秩和检验。但此处对于分类变量也有一定的参考价值。
- ▶ psgraph 对匹配的结果进行图示。



- ▶ 4. 结果解读
- > 4.1 模型拟合结果,此处无太多实际意义。

Logistic regre	ssion			Numbe	r of obs	3 =	614
				LR ch	i2(8)	=	263.65
				Prob	> chi2	=	0.0000
Log likelihood	= -243.9219	7		Pseud	lo R2	=	0.3508
treat	Coef.	Std. Err.	z	P> z	[95%	Conf.	Interval]
age	.0157771	.0135771	1.16	0.245	0108	3335	.0423876
educ	.1613069	.0651264	2.48	0.013	.0336	614	.2889524
black	3.065368	.2865262	10.70	0.000	2.503	3787	3.626949
hispan	.9836336	.425664	2.31	0.021	.1493	3476	1.81792
married	8321133	.2903292	-2.87	0.004	-1.401	148	2630786
nodegree	.7072969	.3376683	2.09	0.036	.0454	792	1.369115
re74	0000718	.0000287	-2.50	0.013	0001	281	0000154
re75	.0000534	.0000463	1.15	0.249	0000	374	.0001443
	-4.728649	1.017069	-4.65	0.000	-6.722		-2.73523



4.2 试验组可匹配的观测概览,按照命令中设定的匹配规则,试验组有8例患者 未能匹配到合适对照。

psmatch2:	psmatch2	: Common	
Treatment	sup	port	
assignment	Off suppo	On suppor	Total
Untreated	0	429	429
Treated	8	177	185
Total	8	606	614



- > 4.3 结果解读的重点应该是对Stata新生成的中间变量的解读。
 - ➤ 其中_pscore 是每个观测值对应的倾向值;
 - ▶ _id 是自动生成的每一个观测对象唯一的ID(事实上这列变量即是对_pscore 排序);
 - ▶ _treated 表示某个对象是否为试验组;
 - ▶ _n1表示的是他被匹配到的对照对象的_id(如果是1:3匹配,还会生成_n2,_n3);
 - ▶ _pdif表示一组匹配了的观察对象他们概率值的差。

为了观察方便可以按照id变量进行排序,排序后结果如下图所示:



	id	tmp	_pscore	_treated	_support	_weight	_re78	_id	_n1	_nn	_pdif	
1	1	.13698408	. 63876993	Treated	On support	1	14421.13	510	380	1	.00021577	0
2	2	. 64322067	. 22463424	Treated	On support	1	1525.014	456	332	1	.00055488	
3	3	. 5578017	. 67824388	Treated	On support	1	2158.959	531	394	1	.00054473	
4	4	. 60479494	.77632408	Treated	on support	1	701.9201	601	428	1	.00258745	
5	5	.68417598	.70163875	Treated	On support	1	14344.29	547	407	1	.00344627	
6	6	.10866794	. 6990699	Treated	On support	1	8900.347	546	406	1	.00559328	
7	7	.61845813	. 65368426	Treated	On support	1	0	521	387	1	.00192223	
8	8	.06106378	.78972311	Treated	Off support			607				
9	9	. 55523883	.77983825	Treated	On support	1	701.9201	605	428	1	.00092671	
10	10	. 87144908	. 04292461	Treated	On support	1	1202.869	432	131	1	. 00008751	
11	11	. 25514988	. 68901996	Treated	On support	1	582.2243	542	402	1	. 00068693	
12	12	. 0445188	. 682444	Treated	On support	1	17941.08	536	397	1	0	
13	13	.42415572	. 64986767	Treated	On support	1	0	519	386	1	.00024967	
14	14	.89834616	. 56241073	Treated	On support	1	0	483	369	1	.0008096	
15	15	. 52192476	. 60858629	Treated	On support	1	0	497	374	1	.00241071	
16	16	. 84140944	.72249036	Treated	On support	1	3794.063	566	414	2	.00317435	
17	17	. 21100766	.70259562	Treated	On support	1	14344.29	549	407	1	.00248939	
18	18	. 56440917	.73496416	Treated	On support	1	10122.43	571	416	1	.00020232	
19	19	. 26480209	.71166489	Treated	On support	1	1730.418	555	410	1	.00123646	
20	20	. 94774264	. 66431981	Treated	On support	1	422.6298	528	390	1	.00142205	
21	21	. 27691541	.76517492	Treated	On support	1	33.98771	589	427	1	.00104033	
22	22	.11801585	.13901525	Treated	On support	1	3392.86	451	305	1	.0016362	
23	23	. 40797025	.12238224	Treated	On support	1	12489.75	444	296	1	. 00026069	
24	24	.72194916	. 76799791	Treated	On support	1	33.98771	591	427	1	. 00386332	
25	25	. 87169105	.71931601	Treated	On support	1	3794.063	564	414	2	0	
76	76	46114700	60016715	Tenated	On CURRER	m 1	0	400	274	- 1	AA1 97095	

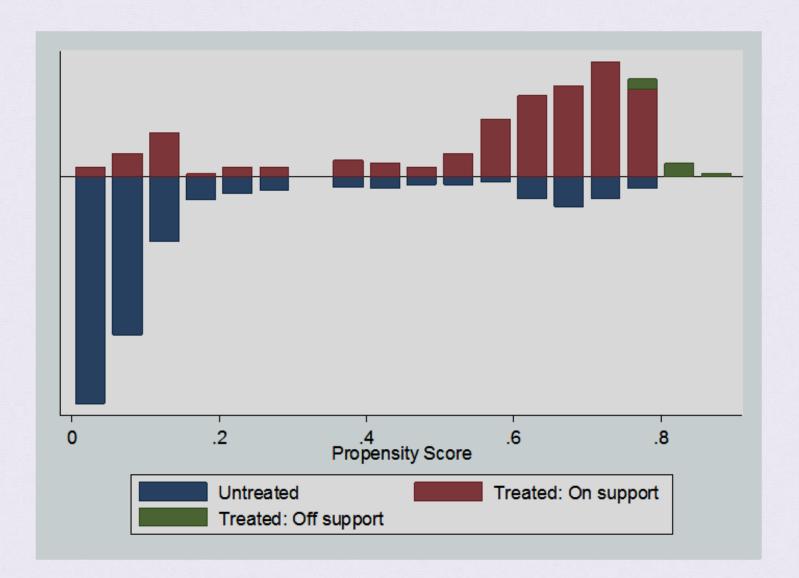


> 4.4 均衡性检验结果

	Unmatched	Mean			%reduct	t-test		V(T)/
Variable	Matched	Treated	Control	%bias	bias	t	p> t	V(C)
age	U	25.816	28.03	-24.2		-2.56	0.011	0.44*
	М	25.446	24.288	12.7	47.7	1.29	0.198	0.52*
educ	U	10.346	10.235	4.5		0.48	0.633	0.50*
	М	10.322	10.35	-1.1	74.4	-0.11	0.911	0.59*
black	U	.84324	.2028	166.8		18.60	0.000	0.82
	М	.83616	.83051	1.5	99.1	0.14	0.887	0.97
hispan	U	.05946	.14219	-27.7		-2.94	0.003	0.46*
	М	.06215	.0678	-1.9	93.2	-0.22	0.830	0.92
married	U	.18919	.51282	-71.9		-7.82	0.000	0.62*
	М	.19774	.13559	13.8	80.8	1.57	0.117	1.35*
nodegree	U	.70811	.59674	23.5		2.63	0.009	0.86
	М	.69492	.68927	1.2	94.9	0.11	0.909	0.99
re74	υ	2095.6	5619.2	-59.6		-6.38	0.000	0.52*
	М	2179.4	2442.1	-4.4	92.5	-0.50	0.615	1.06
re75	U	1532.1	2466.5	-28.7		-3.25	0.001	0.96
	М	1485.9	1414.6	2.2	92.4	0.24	0.808	2.15*



> 4.5 匹配结果的图示化





▶ 5. Stata命令汇总

- .ssc install psmatch2 #安装程序包
- .use "F:\lalonde.dta" #调用F盘存储数据
- .gen tmp = runiform()
- .sort tmp #对所有观测随机排序
- .psmatch2 treat age educ black hispan married nodegree re74 re75, out(re78) logit neighbor(1) common caliper(.05) ties #PSM分析
- .pstest, both #均衡性检验
- .psgraph #图示匹配结果

有关PSM的几点思考



1. PSM的适用条件:

对照组样本量足够大,对照组与试验组样本量之比5:1以上,确保绝大多数试验组对象可以匹配上合适的对照,最好所有试验组对象均得到良好匹配。

2. PSM与回归的关系

能用PSM的均可以用回归分析,可以用回归的未必可以用PSM,建议同时采用PSM与回归分析处理数据,当两者结果一致的时候说明结果较可信

请在此处输入小标题





感谢观看

THANKS



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