



Fondo Europeo Agrícola de Desarrollo Rural
Europa invierte en las zonas rurales

ANEXO III

DETALLES ANÁLISIS CONTRAFCTUAL

**EVALUACIÓN EX POST DEL
PROGRAMA DE DESARROLLO RURAL DE
CASTILLA-LA MANCHA
(2007-2013)**



Diciembre de 2016

PROPSENSITY SCORE MATCHING (PSM)

MEDIDA 112

 Algorithm to estimate the propensity score

The treatment is grupo

GRUPO	Freq.	Percent	Cum.
0	2,066	41.82	41.82
1	2,874	58.18	100.00
Total	4,940	100.00	

Estimation of the propensity score

Iteration 0: log likelihood = -1461.0299
 Iteration 1: log likelihood = -1441.5545
 Iteration 2: log likelihood = -1441.4057
 Iteration 3: log likelihood = -1441.4056

Probit regression	Number of obs	=	3320
	LR chi2(6)	=	39.25
	Prob > chi2	=	0.0000
Log likelihood = -1441.4056	Pseudo R2	=	0.0134

grupo	Coef.	Std. Err.	z	P> z	[95% Conf. Interval]
ote	-.0000554	.0000115	-4.82	0.000	-.0000779 - .0000329
hatotales	.0000731	.0001108	0.66	0.509	-.000144 .0002902
uta	.1548476	.1420403	1.09	0.276	-.1235462 .4332415
importesol~o	2.02e-06	8.23e-07	2.46	0.014	4.11e-07 3.64e-06
edadfsol	-.0111786	.0041801	-2.67	0.007	-.0193715 -.0029857
provinciae~n	.0006326	.001758	0.36	0.719	-.0028129 .0040782
_cons	1.265148	.1949963	6.49	0.000	.8829624 1.647334

Note: the common support option has been selected
 The region of common support is [.69937608, .99615382]

Description of the estimated propensity score
 in region of common support

Percentiles		Smallest		
1%	.7325935	.6993761		
5%	.7660293	.7031669		
10%	.7822688	.7081927	Obs	3320
25%	.8165129	.715501	Sum of wgt.	3320
50%	.8461493		Mean	.8397555
		Largest	Std. Dev.	.0398037
75%	.8669175	.9801105		
90%	.884921	.9839183	Variance	.0015843
95%	.893802	.98679	Skewness	-.4802913
99%	.9238238	.9961538	Kurtosis	3.471325

 Step 1: Identification of the optimal number of blocks
 Use option detail if you want more detailed output

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*****
Step 1: Identification of the optimal number of blocks
Use option detail if you want more detailed output
*****

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The final number of blocks is 8

This number of blocks ensures that the mean propensity score is not different for treated and controls in each blocks

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*****
Step 2: Test of balancing property of the propensity score
Use option detail if you want more detailed output
*****

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The balancing property is satisfied

This table shows the inferior bound, the number of treated and the number of controls for each block

Inferior of block of pscore	GRUPO		Total
	0	1	
.6	113	425	538
.8	228	1,041	1,269
.85	147	800	947
.875	32	438	470
.9	12	84	96
Total	532	2,788	3,320

Note: the common support option has been selected

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*****
End of the algorithm to estimate the pscore
*****

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El modelo resulta en un bajo valor explicativo, aunque según la bibliografía consultada cuanto más bajo es el pseudo R^2 , mejor es la semejanza entre los grupos de control y tratamiento. De forma comparativa, si se tratara de un diseño experimental con asignación aleatoria al tratamiento, ninguna variable observable podría explicar la asignación al mismo, por definición. En este sentido, un bajo poder explicativo del modelo puede ser interpretado como una medida indirecta del grado de efectividad de los grupos de control. No obstante, también podría ocurrir que la diferencia entre ambos grupos se debiera a variables no observables. Este último sesgo se ha intentado corregir con la combinación de PSM con DID.

Aunque el modelo no explique en gran medida la participación en el Programa, sí permite definir los conjuntos de comparación para cada individuo del grupo de beneficiarios de la ayuda, para la estimación no paramétrica del efecto del tratamiento. La inclusión de variables con bajo poder explicativo en la estimación del propensity score tiene como propósito alcanzar la mayor calidad posible en el emparejamiento de tratados y controles.

CÁLCULO DEL EFECTO MEDIO DEL TRATAMIENTO SOBRE EL TRATADO (ATT)

EFECTO NETO SOBRE LA DIFERENCIA DE VALOR AÑADIDO BRUTO

ATT estimation with Nearest Neighbor Matching method
(random draw version)
Analytical standard errors

n. treat.	n. contr.	ATT	Std. Err.	t
2788	490	5.11e+05	38658.092	13.215

Note: the numbers of treated and controls refer to actual nearest neighbour matches

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ATT estimation with the Radius Matching method
Analytical standard errors

n. treat.	n. contr.	ATT	Std. Err.	t
2647	527	5.16e+05	28139.069	18.355

Note: the numbers of treated and controls refer to actual matches within radius

SUBMEDIDA 121.1: PERSONAS FÍSICAS

Algorithm to estimate the propensity score

The treatment is grupo

GRUPO	Freq.	Percent	Cum.
0	3,125	43.37	43.37
1	4,080	56.63	100.00
Total	7,205	100.00	

Estimation of the propensity score

Iteration 0: log likelihood = -700.84158
 Iteration 1: log likelihood = -643.40732
 Iteration 2: log likelihood = -638.65254
 Iteration 3: log likelihood = -638.57527
 Iteration 4: log likelihood = -638.57523

Probit regression Number of obs = 4246
LR chi2(7) = 124.53
Prob > chi2 = 0.0000
Pseudo R2 = 0.0888
 Log likelihood = -638.57523

grupo	Coef.	Std. Err.	z	P> z	[95% Conf. Interval]
edadfsol	.0133101	.0035048	3.80	0.000	.0064409 .0201793
impsol	-.0000299	3.09e-06	-9.68	0.000	-.000036 -.0000239
ayudaconc	.0000476	5.69e-06	8.36	0.000	.0000364 .0000587
importecert	.0000137	2.71e-06	5.03	0.000	8.33e-06 .000019
ote	-8.97e-06	.0000153	-0.59	0.557	-.0000389 .000021
hatot	-.0000245	.0000836	-0.29	0.770	-.0001884 .0001394
ineexplota-n	3.86e-08	2.61e-08	1.48	0.140	-1.27e-08 8.98e-08
_cons	1.04955	.1673984	6.27	0.000	.721455 1.377645

Note: the common support option has been selected
 The region of common support is [.25730116, .99997915]

Description of the estimated propensity score
 in region of common support

Estimated propensity score			
Percentiles	Smallest		
1%	.793759	.2573012	
5%	.9135526	.2874288	
10%	.9333333	.3013394	Obs 4246
25%	.952346	.3325635	Sum of wgt. 4246
50%	.9681609		Mean .961142
		Largest	Std. Dev. .0431439
75%	.9817805	.9999342	
90%	.9908539	.9999517	Variance .0018614
95%	.9946454	.9999619	Skewness -7.440405
99%	.9988119	.9999791	Kurtosis 91.28068

 Step 1: Identification of the optimal number of blocks
 Use option detail if you want more detailed output

The final number of blocks is 9

The final number of blocks is 9

This number of blocks ensures that the mean propensity score is not different for treated and controls in each blocks

```
*****  
Step 2: Test of balancing property of the propensity score  
Use option detail if you want more detailed output  
*****
```

The balancing property is satisfied

This table shows the inferior bound, the number of treated and the number of controls for each block

Inferior of block of pscore	GRUPO		Total
	0	1	
.2	1	4	5
.4	2	5	7
.6	11	23	34
.8	19	84	103
.9	26	130	156
.925	33	603	636
.95	52	1,679	1,731
.975	22	1,552	1,574
Total	166	4,080	4,246

Note: the common support option has been selected

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*****  
End of the algorithm to estimate the pscore  
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CÁLCULO DEL EFECTO MEDIO DEL TRATAMIENTO SOBRE EL TRATADO (ATT)

EFECTO NETO SOBRE LA DIFERENCIA DE VALOR AÑADIDO BRUTO

ATT estimation with Nearest Neighbor Matching method
(random draw version)
Analytical standard errors

n. treat.	n. contr.	ATT	Std. Err.	t
4080	55	3.13e+05	3.40e+05	0.920

Note: the numbers of treated and controls refer to actual nearest neighbour matches

end of do-file

ATT estimation with the kernel Matching method

n. treat.	n. contr.	ATT	Std. Err.	t
4080	166	2.70e+05	.	.

Note: Analytical standard errors cannot be computed. Use the bootstrap option to get bootstrapped standard errors.

Bootstrapping of standard errors

command: attk dvab grupo , pscore(psvab2) comsup bwidth(.06)
statistic: attk = r(attack)

Bootstrap statistics

Number of obs	=	7205
Replications	=	50

Variable	Reps	observed	Bias	Std. Err.	[95% Conf. Interval]
attack	50	270417.3	60539.1	239624	-211125.2 (N)
					-107160 (P)
					-190765.1 (BC)

Note: N = normal
P = percentile
BC = bias-corrected

ATT estimation with the kernel Matching method
Bootstrapped standard errors

n. treat.	n. contr.	ATT	Std. Err.	t
4080	166	2.70e+05	2.40e+05	1.129

SUBMEDIDA 121.1: ENTIDADES JURÍDICAS

 Algorithm to estimate the propensity score

The treatment is grupo

GRUPO	Freq.	Percent	Cum.
0	3,953	97.60	97.60
1	97	2.40	100.00
Total	4,050	100.00	

Estimation of the propensity score

Iteration 0: log likelihood = -331.77018
 Iteration 1: log likelihood = -331.75715
 Iteration 2: log likelihood = -331.75603

Probit regression

Number of obs = 3971
 LR chi2(1) = 0.03
 Prob > chi2 = 0.8664
 Pseudo R2 = 0.0000

Log likelihood = -331.75603

grupo	Coef.	Std. Err.	z	P> z	[95% Conf. Interval]
vab0	3.15e-06	.0000174	0.18	0.856	-.0000309 .0000372
_cons	-2.135762	.0494201	-43.22	0.000	-2.232624 -2.0389

Note: the common support option has been selected
 The region of common support is [.0163455, .0165752]

Description of the estimated propensity score
 in region of common support

Estimated propensity score				
Percentiles		Smallest		
1%	.0163464	.0163455		
5%	.0163482	.0163455		
10%	.0163493	.0163456	Obs	3690
25%	.0163494	.0163457	Sum of wgt.	3690
50%	.0163494		Mean	.0163594
		Largest	Std. Dev.	.0000254
75%	.0163577	.0165661	Variance	6.45e-10
90%	.0163773	.0165666	Skewness	4.485789
95%	.0164023	.0165727	Kurtosis	27.55255
99%	.0164853	.0165752		

 Step 1: Identification of the optimal number of blocks
 Use option detail if you want more detailed output

The final number of blocks is 11

This number of blocks ensures that the mean propensity score
 is not different for treated and controls in each blocks

```

*****
Step 2: Test of balancing property of the propensity score
Use option detail if you want more detailed output
*****

```

The balancing property is satisfied

This table shows the inferior bound, the number of treated and the number of controls for each block

Inferior of block of pscore	GRUPO		Total
	0	1	
.0163452	2,203	8	2,211
.0163513	533	15	548
.0163574	729	36	765
.0164062	160	6	166
Total	3,625	65	3,690

Note: the common support option has been selected

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*****
End of the algorithm to estimate the pscore
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CÁLCULO DEL EFECTO MEDIO DEL TRATAMIENTO SOBRE EL TRATADO (ATT)

EFECTO NETO SOBRE LA DIFERENCIA DE VALOR AÑADIDO BRUTO

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ATT estimation with Nearest Neighbor Matching method
(random draw version)
Analytical standard errors

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n. treat.	n. contr.	ATT	Std. Err.	t
65	1268	7.837	52.533	0.149

Note: the numbers of treated and controls refer to actual nearest neighbour matches

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MEDIDA 123

Algorithm to estimate the propensity score

The treatment is grupo

GRUPO	Freq.	Percent	Cum.
0	3,953	86.46	86.46
1	619	13.54	100.00
Total	4,572	100.00	

Estimation of the propensity score

Iteration 0: log likelihood = -1345.5549
Iteration 1: log likelihood = -1299.6675
Iteration 2: log likelihood = -1299.7076 (backed up)
Iteration 3: log likelihood = -1299.7475 (backed up)
Iteration 4: log likelihood = -1299.7872 (backed up)
Iteration 5: log likelihood = -1299.8268 (backed up)
Iteration 6: log likelihood = -1299.8663 (backed up)
Iteration 7: log likelihood = -1299.9056 (backed up)
Iteration 8: log likelihood = -1299.9447 (backed up)
Iteration 9: log likelihood = -1299.9837 (backed up)
Iteration 10: log likelihood = -1300.0226 (backed up)
Iteration 11: log likelihood = -1300.0613 (backed up)
Iteration 12: log likelihood = -1300.0999 (backed up)
Iteration 13: log likelihood = -1300.1383 (backed up)
Iteration 14: log likelihood = -1300.1765 (backed up)
Iteration 15: log likelihood = -1300.2147 (backed up)
Iteration 16: log likelihood = -1300.2526 (backed up)
Iteration 17: log likelihood = -1300.3283
Iteration 18: log likelihood = -1300.4034
Iteration 19: log likelihood = -1300.478
Iteration 20: log likelihood = -1300.5519
Iteration 21: log likelihood = -1300.6253
Iteration 22: log likelihood = -1300.6981
Iteration 23: log likelihood = -1300.7704
Iteration 24: log likelihood = -1300.8421
Iteration 25: log likelihood = -1300.9133
Iteration 26: log likelihood = -1300.9839
Iteration 27: log likelihood = -1301.0539
Iteration 28: log likelihood = -1301.1235
Iteration 29: log likelihood = -1301.1924
Iteration 30: log likelihood = -1301.2609
Iteration 31: log likelihood = -1301.3288
Iteration 32: log likelihood = -1301.3962
Iteration 33: log likelihood = -1301.4631
Iteration 34: log likelihood = -1301.5294
Iteration 35: log likelihood = -1301.5952
Iteration 36: log likelihood = -1301.6605
Iteration 37: log likelihood = -1301.7253
Iteration 38: log likelihood = -1301.7896
Iteration 39: log likelihood = -1301.8534
Iteration 40: log likelihood = -1301.9166
Iteration 41: log likelihood = -1301.9794
Iteration 42: log likelihood = -1302.0417
Iteration 43: log likelihood = -1302.1035
Iteration 44: log likelihood = -1302.1648
Iteration 45: log likelihood = -1302.2256
Iteration 46: log likelihood = -1302.286
Iteration 47: log likelihood = -1302.3458
Iteration 48: log likelihood = -1302.4052
Iteration 49: log likelihood = -1302.4641
Iteration 50: log likelihood = -1302.5225
Iteration 51: log likelihood = -1302.5805
Iteration 52: log likelihood = -1302.6388
Iteration 53: log likelihood = -1302.6951

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Iteration 53: log likelihood = -1302.6951
Iteration 54: log likelihood = -1302.7517
Iteration 55: log likelihood = -1302.8078
Iteration 56: log likelihood = -1302.8635
Iteration 57: log likelihood = -1302.9188
Iteration 58: log likelihood = -1302.9736
Iteration 59: log likelihood = -1303.0279
Iteration 60: log likelihood = -1303.0818
Iteration 61: log likelihood = -1303.1353
Iteration 62: log likelihood = -1303.1884
Iteration 63: log likelihood = -1303.241
Iteration 64: log likelihood = -1303.2932
Iteration 65: log likelihood = -1303.345
Iteration 66: log likelihood = -1303.3964
Iteration 67: log likelihood = -1303.4473
Iteration 68: log likelihood = -1303.4979
Iteration 69: log likelihood = -1303.548
Iteration 70: log likelihood = -1303.5977
Iteration 71: log likelihood = -1303.647
Iteration 72: log likelihood = -1303.6959
Iteration 73: log likelihood = -1303.7444
Iteration 74: log likelihood = -1303.7925
Iteration 75: log likelihood = -1303.8403
Iteration 76: log likelihood = -1303.8876
Iteration 77: log likelihood = -1303.9345
Iteration 78: log likelihood = -1303.9811
Iteration 79: log likelihood = -1304.0273
Iteration 80: log likelihood = -1304.0731
Iteration 81: log likelihood = -1304.1185
Iteration 82: log likelihood = -1304.1635
Iteration 83: log likelihood = -1304.2082
Iteration 84: log likelihood = -1304.2525
Iteration 85: log likelihood = -1304.2965
Iteration 86: log likelihood = -1304.3401
Iteration 87: log likelihood = -1304.3833
Iteration 88: log likelihood = -1304.4261
Iteration 89: log likelihood = -1304.4687
Iteration 90: log likelihood = -1304.5108
Iteration 91: log likelihood = -1304.5526
Iteration 92: log likelihood = -1304.5941
Iteration 93: log likelihood = -1304.6352
Iteration 94: log likelihood = -1304.676
Iteration 95: log likelihood = -1304.7164
Iteration 96: log likelihood = -1304.7565
Iteration 97: log likelihood = -1304.7963
Iteration 98: log likelihood = -1304.8352
Iteration 99: log likelihood = -1304.8752
Iteration 100: log likelihood = -1304.9152
Iteration 101: log likelihood = -1304.9528
Iteration 102: log likelihood = -1305.0291
Iteration 103: log likelihood = -1305.1041
Iteration 104: log likelihood = -1305.1778
Iteration 105: log likelihood = -1305.2504
Iteration 106: log likelihood = -1305.3217
Iteration 107: log likelihood = -1305.3918
Iteration 108: log likelihood = -1305.4607
Iteration 109: log likelihood = -1305.5284
Iteration 110: log likelihood = -1305.595
Iteration 111: log likelihood = -1305.6605
Iteration 112: log likelihood = -1305.7249
Iteration 113: log likelihood = -1305.7882
Iteration 114: log likelihood = -1305.8504
Iteration 115: log likelihood = -1305.9116
Iteration 116: log likelihood = -1305.9717
Iteration 117: log likelihood = -1306.0308
Iteration 118: log likelihood = -1306.0889
Iteration 119: log likelihood = -1306.146
Iteration 120: log likelihood = -1306.2021
Iteration 121: log likelihood = -1306.2573
Iteration 122: log likelihood = -1306.3115
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Iteration 120: log likelihood = -1306.3115
Iteration 121: log likelihood = -1306.3648
Iteration 122: log likelihood = -1306.4171
Iteration 123: log likelihood = -1306.4686
Iteration 124: log likelihood = -1306.5192
Iteration 125: log likelihood = -1306.5689
Iteration 126: log likelihood = -1306.6178
Iteration 127: log likelihood = -1306.6658
Iteration 128: log likelihood = -1306.713
Iteration 129: log likelihood = -1306.7594
Iteration 130: log likelihood = -1306.805
Iteration 131: log likelihood = -1306.8498
Iteration 132: log likelihood = -1306.8938
Iteration 133: log likelihood = -1306.9371
Iteration 134: log likelihood = -1306.9796
Iteration 135: log likelihood = -1307.0213
Iteration 136: log likelihood = -1307.0624
Iteration 137: log likelihood = -1307.1431
Iteration 138: log likelihood = -1307.2209
Iteration 139: log likelihood = -1307.2961
Iteration 140: log likelihood = -1307.3065
Iteration 141: log likelihood = -1307.3015

```

Probit regression

```

Number of obs   =      4312
LR chi2(1)      =       76.51
Prob > chi2     =       0.0000
Pseudo R2      =       0.0284

```

Log likelihood = -1307.3015

grupo	Coef.	Std. Err.	z	P> z	[95% Conf. Interval]	
vab0	.0000568	6.73e-06	8.44	0.000	.0000436	.0000699
_cons	-1.349484	.0270905	-49.81	0.000	-1.40258	-1.296388

Note: the common support option has been selected
The region of common support is [.03945294, .99879313]

Description of the estimated propensity score
in region of common support

Estimated propensity score					
Percentiles		Smallest			
1%	.0869906	.0394529			
5%	.0882271	.0568892			
10%	.0884972	.0583835	Obs	4310	
25%	.0885908	.0623672	Sum of wgt.	4310	
50%	.0885908		Mean	.0921357	
			Std. Dev.	.0305977	
75%	.0894312	.6433168			
90%	.092253	.7714787	Variance	.0009362	
95%	.0975608	.9696125	Skewness	19.71239	
99%	.1506368	.9987931	Kurtosis	473.9511	

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*****
Step 1: Identification of the optimal number of blocks
Use option detail if you want more detailed output
*****

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 Step 1: Identification of the optimal number of blocks
 Use option detail if you want more detailed output

The final number of blocks is 13

This number of blocks ensures that the mean propensity score is not different for treated and controls in each blocks

 Step 2: Test of balancing property of the propensity score
 Use option detail if you want more detailed output

The balancing property is satisfied

This table shows the inferior bound, the number of treated and the number of controls for each block

Inferior of block of pscore	GRUPO		Total
	0	1	
.0394529	0	1	1
.05	4	0	4
.075	64	7	71
.0875	2,810	42	2,852
.0890625	466	41	507
.0898438	182	33	215
.090625	229	103	332
.09375	92	58	150
.1	51	103	154
.2	5	11	16
.4	1	2	3
.6	0	3	3
.8	0	2	2
Total	3,904	406	4,310

Note: the common support option has been selected

 End of the algorithm to estimate the pscore

CÁLCULO DEL EFECTO MEDIO DEL TRATAMIENTO SOBRE EL TRATADO (ATT)

EFECTO NETO SOBRE LA DIFERENCIA DE VALOR AÑADIDO BRUTO

ATT estimation with Nearest Neighbor Matching method
 (random draw version)
 Analytical standard errors

n. treat.	n. contr.	ATT	Std. Err.	t
406	1433	557.375	185.120	3.011

Note: the numbers of treated and controls refer to actual nearest neighbour matches

EJE 4: LEADER

*****PSCORE*****

 Algorithm to estimate the propensity score

The treatment is t_c

T_c	Freq.	Percent	Cum.
0	225	6.19	6.19
1	3,409	93.81	100.00
Total	3,634	100.00	

Estimation of the propensity score

Iteration 0: log likelihood = -843.83365
 Iteration 1: log likelihood = -714.51507
 Iteration 2: log likelihood = -649.18783
 Iteration 3: log likelihood = -638.23105
 Iteration 4: log likelihood = -636.35115
 Iteration 5: log likelihood = -636.18194
 Iteration 6: log likelihood = -636.17952
 Iteration 7: log likelihood = -636.17952

Probit regression

Number of obs = 606
 LR chi2(4) = 109.82
 Prob > chi2 = 0.0000
 Pseudo R2 = 0.1579

Log likelihood = -292.82212

t_c	Coef.	Std. Err.	z	P> z	[95% Conf. Interval]
inversion	-3.94e-06	5.09e-07	-7.75	0.000	-4.94e-06 -2.94e-06
imp_neto_n~t	-.0000952	.000075	-1.27	0.204	-.0002421 .0000517
np_	1.005032	.4563767	2.20	0.028	.11055 1.899514
tamao	2.38e-06	4.98e-06	0.48	0.633	-7.38e-06 .0000121
_cons	.0721252	.4583376	0.16	0.875	-.8262 .9704504

Description of the estimated propensity score
in region of common support

Estimated propensity score				
1%	.6255857	Smallest		
5%	.835994	.0573989		
10%	.8732216	.0615859	Obs	3629
25%	.9001497	.0906207	Sum of wgt.	3629
50%	.9973334	.0911535	Mean	.9390917
75%	.9984636	Largest	Std. Dev.	.0880754
90%	.9985415	.9985836	Variance	.0077573
95%	.99856	.9985841	Skewness	-4.132426
99%	.9985769	.9985845	Kurtosis	32.8526
		.9985848		

Step 1: Identification of the optimal number of blocks
Use option detail if you want more detailed output

The final number of blocks is 16

This number of blocks ensures that the mean propensity score
is not different for treated and controls in each blocks

Step 2: Test of balancing property of the propensity score
Use option detail if you want more detailed output |

The balancing property is satisfied

This table shows the inferior bound, the number of treated
and the number of controls for each block

Inferior of block of pscore	T_C		Total
	0	1	
.0573989	9	1	10
.2	10	2	12
.4	11	2	13
.6	6	4	10
.7	13	57	70
.8	18	107	125
.85	38	620	658
.9	14	569	583
.90625	0	114	114
.9070312	0	19	19
.9074218	98	1	99
.95	3	1,913	1,916
Total	220	3,409	3,629

Note: the common support option has been selected

End of the algorithm to estimate the pscore

CÁLCULO DEL EFECTO MEDIO DEL TRATAMIENTO SOBRE EL TRATADO (ATT)

EFECTO NETO SOBRE LA DIFERENCIA DE VALOR AÑADIDO BRUTO

ATT estimation with Nearest Neighbor Matching method
(random draw version)
Analytical standard errors

n. treat.	n. contr.	ATT	Std. Err.	t
448	104	11.806	20.637	0.572

Note: the numbers of treated and controls refer to actual nearest neighbour matches

```
. attr diffvab t_c, pscore(ps005) radius(0.0001) comsup  
|
```

The program is searching for matches of treated units within radius.
This operation may take a while.

ATT estimation with the Radius Matching method
Analytical standard errors

n. treat.	n. contr.	ATT	Std. Err.	t
90	64	3.593	33.400	0.108

Note: the numbers of treated and controls refer to actual matches within radius

ATT estimation with the Kernel Matching method

n. treat.	n. contr.	ATT	Std. Err.	t
448	149	13.600	.	.

Note: Analytical standard errors cannot be computed. Use the bootstrap option to get bootstrapped standard errors.

EFEECTO NETO SOBRE LA DIFERENCIA DE EMPLEO

```
. attr difempleo T_C, pscore(ps002) radius(0.01) comsup
```

The program is searching for matches of treated units within radius.
This operation may take a while.

ATT estimation with the Radius Matching method
Analytical standard errors

n. treat.	n. contr.	ATT	Std. Err.	t
503	276	0.737	0.284	2.594

ATT estimation with the Kernel Matching method
Bootstrapped standard errors

n. treat.	n. contr.	ATT	Std. Err.	t
505	283	0.552	0.249	2.215
