



Propensity Score [brief introduction]



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Reference

Austin, P. C. (2011).

A tutorial and case study in propensity score analysis: an application to estimating the effect of in-hospital smoking cessation counseling on mortality.

Multivariate behavioral research, 46(1), 119-151.

Propensity score

1. **Definition:** the propensity score is
 - Probability of receiving treatment (exposure, A) given covariates (L).
 - $P(L) = \Pr(A=1|L)$
2. **Properties**
 - Balancing score.
 - $P(L)=0.5$ in RCT.
3. **Assumes**
 - no unmeasured confounding $Y(1), Y(0) \perp A \mid P(L)$.
 - positivity: $0 < P(L) < 1$.
 - Sufficient overlap. If there is no overlap, can't compare $Y(0), Y(1)$

Propensity score

- Modelling $P(L) = \Pr(A=1|L)$
 - Any method that gives good predictions is useful.
 - i. **Logistic regression** typically used
 - ii. **Machine learning** methods also reasonable
 - only the predictions matter, the coefficients (in the PS model) don't
 - model can be rich

Propensity score

- Variables to include (requires subject area-expertise)
 - Include only pre-baseline measures
 - **Confounders**: important to include
 - **Risk factors** /Predictors of Y : include to reduce SE
 - **Instruments**/Predictors of A only: avoid
 - **Noise**: avoid (increases SE)
 - Don't look at outcome data while modelling PS

Various Propensity score analyses approaches

How can I use propensity scores?

- Matching ✓
- Weighting ✓
- Stratification (will not cover)
- Propensity score as a covariate (will not cover)

[A tutorial and case study in propensity score analysis: an application to estimating the effect of in-hospital smoking cessation counseling on mortality](#)

PC Austin - Multivariate behavioral research, 2011 - Taylor & Francis

Propensity score methods allow investigators to estimate causal treatment effects using observational or nonrandomized data. In this article we provide a practical illustration of the appropriate steps in conducting **propensity score** analyses. For illustrative purposes, we use ...

☆ 𐀀 Cited by 227 Related articles All 12 versions Web of Science: 885

Propensity score Matching (ATT)

Propensity score matching

How to conduct propensity score matching?



For the purposes of illustration, we will first assume that our data was collected via SRS.

Propensity score matching: step 1

Step 1: Specify PS

Model and
fit that model

PS.model/formula specification: $A \sim L$

PS.fit = logistic($A \sim L$)

Predict from PS.fit

Get the predicted values from the fitted logistic regression

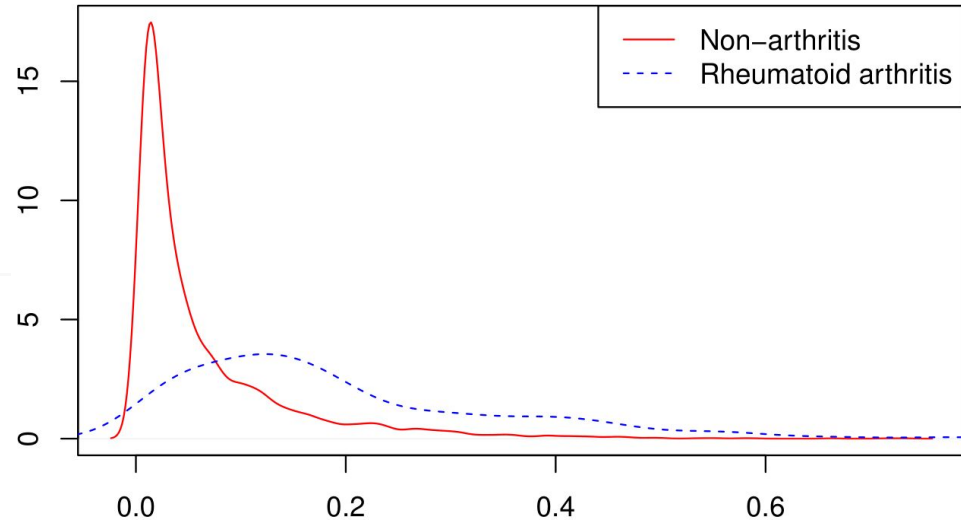
Propensity score matching: step 1

Step 1:

Plot the predicted values / propensity scores

Numerical summary of PS distribution

```
## $`Non-arthritis`  
##   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.  
## 0.001809 0.013710 0.031450 0.064314 0.080949 0.733198  
##  
## $`Rheumatoid arthritis`  
##   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.  
## 0.006047 0.087135 0.148875 0.190836 0.270072 0.792427
```



Propensity score matching: step 2

Step 2: Match subjects by PS

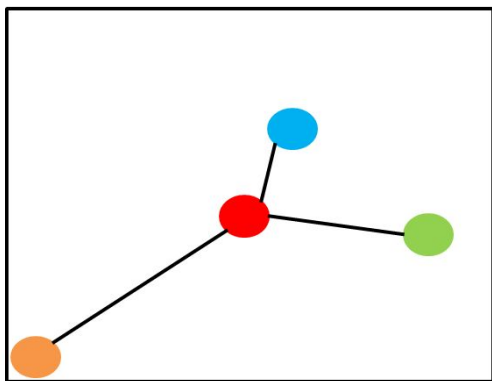
Different algorithms are available to match propensity scores

- Nearest Neighbor (NN) matching: selects the closet PS in the control
- NN & caliper matching: pre-defined bound
- Optimal matching
- Coarsened exact matching / CEM
- Full Matching

Propensity score matching: step 2

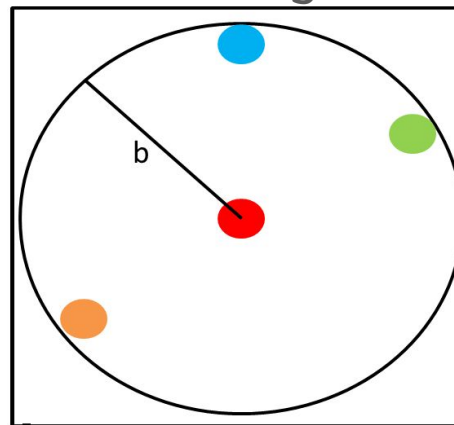
Step 2: Match subjects by PS

Nearest Neighbor



Treated ●
Control ● ● ●

Nearest Neighbor + caliper



Treated ●
Control ● ● ●

Randomness involved if tied

Propensity score matching: step 2

Step 2:

Match subjects
by PS

Good idea to set seed because some randomness is involved.

Match with the following criteria:

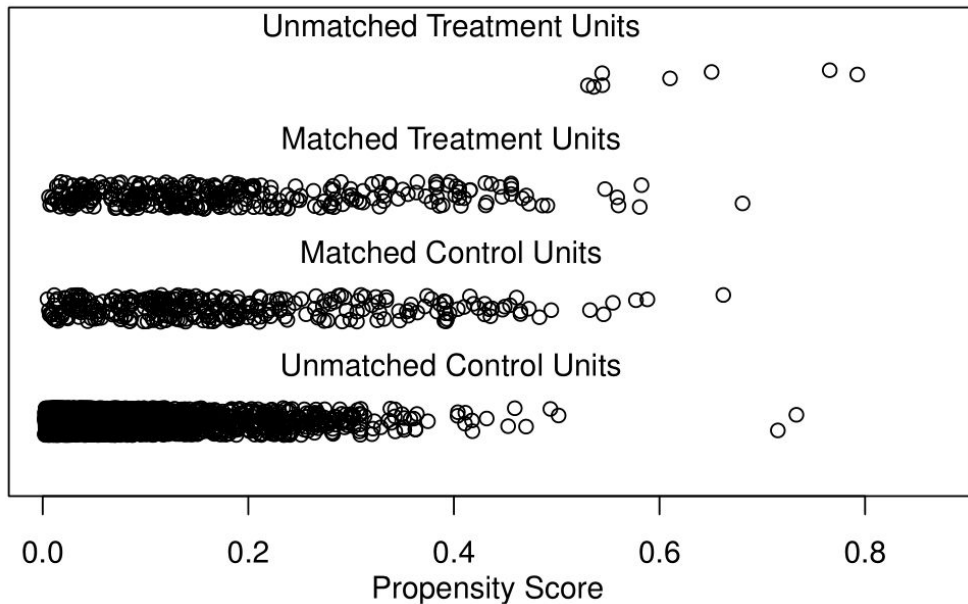
- First get PS from a logistic regression (logit link)
- Using those PS, perform nearest-neighbor matching
- Match without replacement
- Pair matching (ratio = 1:1 for RA vs. non-arthritis)
- Caliper = $0.2 * \text{sd}(\text{PS})$

Summarize the PS

Propensity score matching: step 2

Step 2: Match subjects by PS

Distribution of Propensity Scores

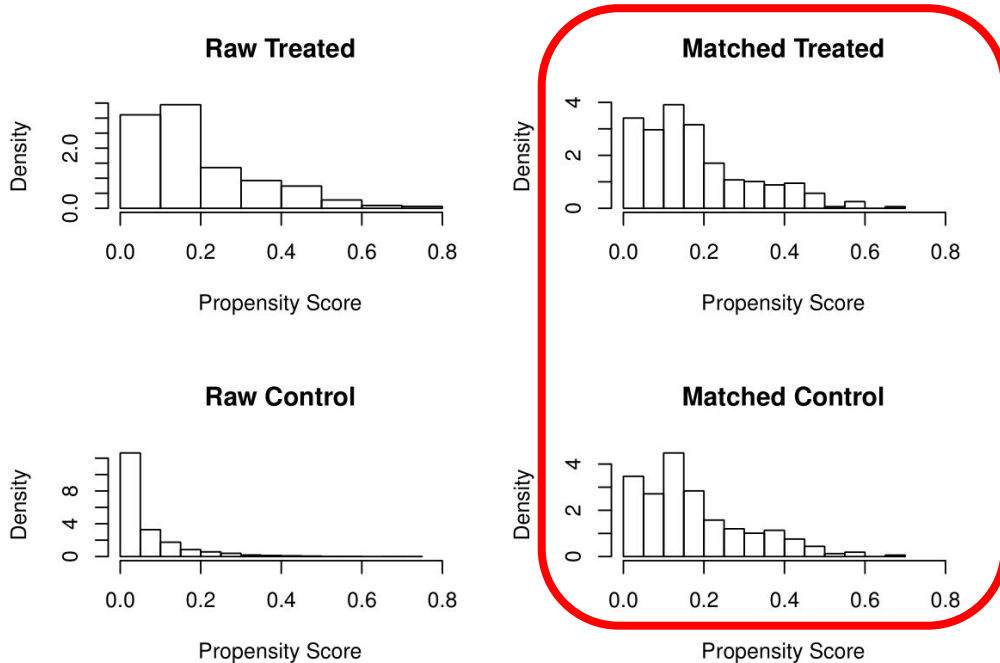


Sample sizes:

##	Control	Treated
## All	4089	325
## Matched	317	317
## Unmatched	3772	8
## Discarded	0	0

Propensity score matching: step 3

Step 3: Covariate balance in matched sample, **check graphically**



step 3

Step 3

Covariate balance checking using SMD (<0.2, Or <0.1)

```

## Unmatched Stratified by arthritis.type
## Non-arthritis Rheumatoid arthritis SMD
## n 4089 325
## gender = Female (%) 1960 (47.9) 194 (59.7) 0.238
## bmi = (25,80] (%) 2745 (67.1) 245 (75.4) 0.183
## diabetes = Yes (%) 358 ( 8.8) 87 (26.8) 0.485
## smoke = Yes (%) 1796 (43.9) 177 (54.5) 0.212
## age (%) 0.891
## (0,50] 2577 (63.0) 74 (22.8)
## (50,70] 1046 (25.6) 169 (52.0)
## 70+ 466 (11.4) 82 (25.2)
## race (%) 0.347
## White 1739 (42.5) 127 (39.1)
## Black 843 (20.6) 114 (35.1)
## Other 1507 (36.9) 84 (25.8)
## born = USborn (%) 0.221
## education (%) 0.160
## School 495 (12.1) 52 (16.0)
## College 1892 (46.3) 127 (39.1)
## High.School 1702 (41.6) 146 (44.9)
## marriage = Married (%) 0.275
## annualincome (%) 0.531
## <20k 820 (20.1) 135 (41.5)
## 20kto54k 1737 (42.5) 126 (38.8)
## 55k+ 1532 (37.5) 64 (19.7)
## physical.activity (%) 0.266
## No 2309 (56.5) 223 (68.6)
## High 871 (21.3) 43 (13.2)
## Moderate 909 (22.2) 59 (18.2)
## medical.access = Yes (%) 0.457
## blood.pressure = Yes (%) 0.801
## healthy.diet (%) 0.213
## Poor 210 ( 5.1) 34 (10.5)
## Fair 951 (23.3) 81 (24.9)
## Good 2928 (71.6) 210 (64.6)
## covered.health = Yes (%) 0.369

```

Table 1 in unmatched data and corresponding SMD

	Non-Ar	RA	SMD
Diabetes	8.8%	26.8%	0.485
Smoke	43.9%	54.5%	0.212

```

## Sample sizes:
## Control Treated
## All 4089 325
## Matched 317 317
## Unmatched 3772 8
## Discarded 0 0

```


step 3

Unmatched

Table 1 in matched data and corresponding SMD

Step 3:

	Non-Ar	RA	SMD
Diabetes	21.8%	25.2%	0.082
Smoke	53.6%	53.6%	<0.001

```
## Sample sizes:
##           Control Treated
## All           4089     325
## Matched           317     317
## Unmatched       3772         8
## Discarded         0         0
```

SMD
(<0.2 ,
Or
 <0.1)

Matched

```
SMD
##
## n 317 317
0.238 ## gender = Female (%) 173 (54.6) 186 (58.7) 0.083
0.183 ## bmi = (25,80] (%) 241 (76.0) 238 (75.1) 0.022
0.485 ## diabetes = Yes (%) 69 (21.8) 80 (25.2) 0.082
0.212 ## smoke = Yes (%) 170 (53.6) 170 (53.6) <0.001
0.891 ## age (%) 0.052
## (0,50] 77 (24.3) 74 (23.3)
## (50,70] 166 (52.4) 162 (51.1)
## 70+ 74 (23.3) 81 (25.6)
0.347 ## race (%) 0.110
## White 139 (43.8) 126 (39.7)
## Black 108 (34.1) 107 (33.8)
## Other 70 (22.1) 84 (26.5)
0.221 ## born = USborn (%) 252 (79.5) 254 (80.1) 0.016
0.160 ## education (%) 0.066
## School 52 (16.4) 51 (16.1)
## College 133 (42.0) 124 (39.1)
## High.School 132 (41.6) 142 (44.8)
0.275 ## marriage = Married (%) 150 (47.3) 149 (47.0) 0.006
0.531 ## annualincome (%) 0.034
## <20k 125 (39.4) 127 (40.1)
## 20kto54k 131 (41.3) 126 (39.7)
## 55k+ 61 (19.2) 64 (20.2)
0.266 ## physical.activity (%) 0.083
## No 205 (64.7) 215 (67.8)
## High 52 (16.4) 43 (13.6)
## Moderate 60 (18.9) 59 (18.6)
0.457 ## medical.access = Yes (%) 300 (94.6) 302 (95.3) 0.029
0.801 ## blood.pressure = Yes (%) 202 (63.7) 196 (61.8) 0.039
0.213 ## healthy.diet (%) 0.049
## Poor 28 ( 8.8) 31 ( 9.8)
## Fair 74 (23.3) 78 (24.6)
## Good 215 (67.8) 208 (65.6)
0.369 ## covered.health = Yes (%) 265 (83.6) 272 (85.8) 0.061
```

Propensity score matching: step 4

Step 4: Estimate treatment effect

Logistic regression

$(Y \sim A)$ OR = 1.55

fit in matched data

Propensity score matching vs. regression

Estimates of the OR/CI from matching are not very different than what we got from regression. Why would we do this then?

- **Intuitive**: compare two similar groups
- **Diagnostics** (balance checking) much easier compared to residual plot/influence
- Exposure and outcome models are **seperate**
- Non-parametric (ML) approaches can be used to relax linearity assumption in estimating PS.

Propensity score matching directly gives you

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Thanks!



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