**Answers to Study Questions for Chapter 3**

1. The most common propensity score methods include matching, stratification, weighting, and covariate adjustment.
2. Although all matching procedures match cases across groups based on the proximity of the propensity scores, nearest neighbor matches cases based solely on the absolute distance. Typically, the first match is made from the cases with the least distance between the propensity scores and subsequent matches are made based on the closest matches in the remaining cases. Optimal matching is different from this approach in that it considers all possible paired matches and selects a set of matched cases that has the smallest global distance. In this approach, some of the matched pairs may have less proximal propensity scores than those in the nearest neighbor procedure, but the average distance between pairs will be smaller. Like optimal matching, full matching considers the global distance of all matches, but creates subclasses rather than matched pairs. Therefore, more than one case in the treatment group can be matched to more than one case in the control group and vice versa.

Caliper matching is used with other matching methods (usually nearest neighbor), rather than as a stand-alone procedure. This approach simply sets a criterion for how much of a distance between the matched pairs is allowable. Without a caliper, some of the later matches created with nearest neighbor matching may be poorly matched. Therefore, by setting a caliper, any matches that are not within a specified distance (e.g., differences between propensity scores cannot be greater than .25*SD*) will be dropped from the matched data set.

1. Matching with replacement, ratio matching, and a sample with more control cases than treatment cases are all good approaches when there is a limited number of cases available for matching. Available matches can be limited with small sample sizes or poor common support (i.e., little overlap between propensity score distributions for each group).
2. Table 3.1 shows the matched cases from three matching procedures using propensity scores that were estimated from all 10 covariates in the *First Year Seminar* data set. Using paired (1 to 1) matching without replacement, how do the matches change when you use:
   1. Nearest neighbor matching includes all 30 treatment cases, but only 30 control cases;
   2. Caliper matching includes only 20 of the treated cases and 20 control cases;
   3. Optimal matching also includes all 30 treatment cases and 30 control cases. However, the control case matched to each treatment case is not the same one that was matched to those respective treatment cases in the nearest neighbor matching procedure.

**Table 3.1** Conditions, identification numbers, and propensity scores for each matching method.

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Nearest Neighbor | | | | Caliper Matching | | | | Optimal Matching | | | |
| Treatment | | Control | | Treatment | | Control | | Treatment | | Control | |
| ID | PS | ID | PS | ID | PS | ID | PS | ID | PS | ID | PS |
| 12 | 0.398 | 94 | 0.274 | 12 | 0.398 | 47 | 0.412 | 12 | 0.398 | 77 | 0.278 |
| 13 | 0.938 | 64 | 0.615 | 14 | 0.147 | 24 | 0.192 | 13 | 0.938 | 16 | 0.351 |
| 14 | 0.147 | 42 | 0.145 | 15 | 0.184 | 53 | 0.134 | 14 | 0.147 | 42 | 0.145 |
| 15 | 0.184 | 24 | 0.192 | 25 | 0.236 | 84 | 0.174 | 15 | 0.184 | 24 | 0.192 |
| 25 | 0.236 | 80 | 0.255 | 27 | 0.453 | 85 | 0.402 | 25 | 0.236 | 74 | 0.248 |
| 27 | 0.453 | 48 | 0.287 | 32 | 0.586 | 96 | 0.553 | 27 | 0.453 | 48 | 0.287 |
| 28 | 0.973 | 73 | 0.783 | 33 | 0.467 | 95 | 0.409 | 28 | 0.973 | 73 | 0.783 |
| 29 | 0.534 | 43 | 0.341 | 34 | 0.41 | 90 | 0.394 | 29 | 0.534 | 41 | 0.258 |
| 32 | 0.586 | 36 | 0.378 | 38 | 0.424 | 36 | 0.378 | 32 | 0.586 | 96 | 0.553 |
| 33 | 0.467 | 72 | 0.314 | 44 | 0.437 | 8 | 0.454 | 33 | 0.467 | 37 | 0.454 |
| 34 | 0.41 | 77 | 0.278 | 45 | 0.839 | 73 | 0.783 | 34 | 0.41 | 95 | 0.409 |
| 35 | 0.939 | 6 | 0.744 | 57 | 0.239 | 26 | 0.27 | 35 | 0.939 | 36 | 0.378 |
| 38 | 0.424 | 76 | 0.278 | 60 | 0.673 | 64 | 0.615 | 38 | 0.424 | 43 | 0.341 |
| 44 | 0.437 | 59 | 0.287 | 65 | 0.365 | 43 | 0.341 | 44 | 0.437 | 47 | 0.412 |
| 45 | 0.839 | 46 | 0.611 | 68 | 0.395 | 37 | 0.454 | 45 | 0.839 | 85 | 0.402 |
| 57 | 0.239 | 74 | 0.248 | 75 | 0.008 | 79 | 0.011 | 57 | 0.239 | 80 | 0.255 |
| 60 | 0.673 | 95 | 0.409 | 83 | 0.643 | 46 | 0.611 | 60 | 0.673 | 94 | 0.274 |
| 62 | 0.782 | 98 | 0.518 | 88 | 0.176 | 31 | 0.204 | 62 | 0.782 | 98 | 0.518 |
| 65 | 0.365 | 41 | 0.258 | 93 | 0.800 | 6 | 0.744 | 65 | 0.365 | 59 | 0.287 |
| 66 | 0.718 | 8 | 0.454 | 97 | 0.546 | 98 | 0.518 | 66 | 0.718 | 8 | 0.454 |
| 68 | 0.395 | 26 | 0.270 |  |  |  |  | 68 | 0.395 | 90 | 0.394 |
| 70 | 0.583 | 40 | 0.352 |  |  |  |  | 70 | 0.583 | 26 | 0.270 |
| 75 | 0.008 | 3 | 0.008 |  |  |  |  | 75 | 0.008 | 49 | 0.008 |
| 78 | 0.726 | 37 | 0.454 |  |  |  |  | 78 | 0.726 | 72 | 0.314 |
| 82 | 0.718 | 47 | 0.412 |  |  |  |  | 82 | 0.718 | 46 | 0.611 |
| 83 | 0.643 | 85 | 0.402 |  |  |  |  | 83 | 0.643 | 76 | 0.278 |
| 88 | 0.176 | 87 | 0.175 |  |  |  |  | 88 | 0.176 | 87 | 0.175 |
| 93 | 0.8 | 96 | 0.553 |  |  |  |  | 93 | 0.8 | 6 | 0.744 |
| 97 | 0.546 | 16 | 0.351 |  |  |  |  | 97 | 0.546 | 40 | 0.352 |
| 100 | 0.623 | 90 | 0.394 |  |  |  |  | 100 | 0.623 | 64 | 0.615 |

1. Using the same propensity scores from Question 4, match students who participated in the first year seminar to those who did not using:
   1. Full matching with replacement includes all 30 treatment cases and all 70 control cases. Instead of identifying matched pairs, we are given propensity score weights. The first 20 cases are in Table 3.2:

**Table 3.2** Conditions, propensity scores and weights for the first 20 cases in the sample.

|  |  |  |  |
| --- | --- | --- | --- |
| ID | Univ101 | PS | psweight |
| 1 | 0 | .020 | .090 |
| 2 | 0 | .024 | .090 |
| 3 | 0 | .008 | .090 |
| 4 | 0 | .062 | .090 |
| 5 | 0 | .022 | .090 |
| 6 | 0 | .744 | 7.000 |
| 7 | 0 | .197 | .778 |
| 8 | 0 | .454 | 4.667 |
| 9 | 0 | .135 | .194 |
| 10 | 0 | .112 | .194 |
| 11 | 0 | .005 | .090 |
| 12 | 1 | .398 | 1.000 |
| 13 | 1 | .938 | 1.000 |
| 14 | 1 | .147 | 1.000 |
| 15 | 1 | .184 | 1.000 |
| 16 | 0 | .351 | .467 |
| 17 | 0 | .001 | .090 |
| 18 | 0 | .157 | .194 |
| 19 | 0 | .076 | .090 |
| 20 | 0 | .097 | .194 |

1. Nearest neighbor matching with replacement includes all 30 treatment cases, but only 17 control cases, which have varying weights. The matches are shown in Table 3.3.

**Table 3.3** Conditions, identification numbers, and propensity scores for nearest neighbor with replacement.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Treatment | | Control | | |
| ID | PS | ID | PS | psweight |
| 75 | 0.008 | 3 | 0.008 | 0.567 |
| 66 | 0.718 | 6 | 0.744 | 1.700 |
| 78 | 0.726 |
| 82 | 0.718 |
| 27 | 0.453 | 8 | 0.454 | 1.133 |
| 44 | 0.437 |
| 15 | 0.184 | 24 | 0.192 | 0.567 |
| 33 | 0.467 | 37 | 0.454 | 0.567 |
| 65 | 0.365 | 40 | 0.352 | 0.567 |
| 14 | 0.147 | 42 | 0.145 | 0.567 |
| 32 | 0.586 | 46 | 0.611 | 1.133 |
| 70 | 0.583 |
| 38 | 0.424 | 47 | 0.412 | 0.567 |
| 60 | 0.673 | 64 | 0.615 | 1.7 |
| 83 | 0.643 |
| 100 | 0.623 |
| 13 | 0.938 | 73 | 0.783 | 3.4 |
| 28 | 0.973 |
| 35 | 0.939 |
| 45 | 0.839 |
| 62 | 0.782 |
| 93 | 0.8 |
| 25 | 0.236 | 74 | 0.248 | 1.133 |
| 57 | 0.239 |
| 88 | 0.176 | 87 | 0.175 | 0.567 |
| 12 | 0.398 | 90 | 0.394 | 1.133 |
| 68 | 0.395 |
| 34 | 0.41 | 95 | 0.409 | 0.567 |
| 97 | 0.546 | 96 | 0.553 | 0.567 |
| 29 | 0.534 | 98 | 0.518 | 0.567 |

1. Nearest neighbor, ratio (1:2) matching without replacement includes all 30treatment cases, but only 60 control cases.

**Table 3.4** Conditions, identification numbers, and propensity scores for nearest neighbor, ratio matching.

|  |  |  |  |
| --- | --- | --- | --- |
| Treatment | | Control | |
| ID | PS | ID | PS |
| 12 | 0.398 | 94 | 0.274 |
| 86 | 0.055 |
| 13 | 0.938 | 64 | 0.615 |
| 7 | 0.197 |
| 14 | 0.147 | 42 | 0.145 |
| 56 | 0.032 |
| 15 | 0.184 | 24 | 0.192 |
| 51 | 0.033 |
| 25 | 0.236 | 80 | 0.255 |
| 21 | 0.042 |
| 27 | 0.453 | 48 | 0.287 |
| 54 | 0.065 |
| 28 | 0.973 | 73 | 0.783 |
| 61 | 0.257 |
| 29 | 0.534 | 43 | 0.341 |
| 19 | 0.076 |
| 32 | 0.586 | 36 | 0.378 |
| 50 | 0.098 |
| 33 | 0.467 | 72 | 0.314 |
| 30 | 0.071 |
| 34 | 0.41 | 77 | 0.278 |
| 22 | 0.055 |
| 35 | 0.939 | 6 | 0.744 |
| 31 | 0.204 |
| 38 | 0.424 | 76 | 0.278 |
| 99 | 0.058 |
| 44 | 0.437 | 59 | 0.287 |
| 4 | 0.062 |
| 45 | 0.839 | 46 | 0.611 |
| 84 | 0.174 |
| 57 | 0.239 | 74 | 0.248 |
| 92 | 0.048 |
| 60 | 0.673 | 95 | 0.409 |
| 58 | 0.121 |
| 62 | 0.782 | 98 | 0.518 |
| 52 | 0.14 |
| 65 | 0.365 | 41 | 0.258 |
| 39 | 0.051 |
| 66 | 0.718 | 8 | 0.454 |
| 53 | 0.134 |
| 68 | 0.395 | 26 | 0.27 |
| 69 | 0.055 |
| 70 | 0.583 | 40 | 0.352 |
| 20 | 0.097 |
| 75 | 0.008 | 3 | 0.008 |
| 49 | 0.008 |
| 78 | 0.726 | 37 | 0.454 |
| 9 | 0.135 |
| 82 | 0.718 | 47 | 0.412 |
| 23 | 0.126 |
| 83 | 0.643 | 85 | 0.402 |
| 10 | 0.112 |
| 88 | 0.176 | 87 | 0.175 |
| 63 | 0.033 |
| 93 | 0.8 | 96 | 0.553 |
| 18 | 0.157 |
| 97 | 0.546 | 16 | 0.351 |
| 55 | 0.084 |
| 100 | 0.623 | 90 | 0.394 |
| 81 | 0.1 |

1. Optimal matching with ratio matching, in which every person in the treatment group is matched with two people in the control group (1:2)

**Table 3.5** Conditions, identification numbers, and propensity scores for optimal, ratio matching.

|  |  |  |  |
| --- | --- | --- | --- |
| Treatment | | Control | |
| ID | PS | ID | PS |
| 12 | 0.398 | 92 | .048 |
| 94 | .274 |
| 13 | 0.938 | 69 | .055 |
| 99 | .058 |
| 14 | 0.147 | 10 | .112 |
| 58 | .121 |
| 15 | 0.184 | 9 | .135 |
| 42 | .145 |
| 25 | 0.236 | 22 | .055 |
| 51 | .033 |
| 27 | 0.453 | 41 | .258 |
| 48 | .287 |
| 28 | 0.973 | 6 | .744 |
| 73 | .783 |
| 29 | 0.534 | 20 | .097 |
| 24 | .192 |
| 32 | 0.586 | 26 | .270 |
| 55 | .084 |
| 33 | 0.467 | 37 | .454 |
| 77 | .278 |
| 34 | 0.41 | 16 | .351 |
| 40 | .352 |
| 35 | 0.939 | 39 | .051 |
| 50 | .098 |
| 38 | 0.424 | 43 | .341 |
| 80 | .255 |
| 44 | 0.437 | 47 | .412 |
| 85 | .402 |
| 45 | 0.839 | 86 | .055 |
| 87 | .175 |
| 57 | 0.239 | 31 | .204 |
| 54 | .065 |
| 60 | 0.673 | 46 | .611 |
| 24 | .192 |
| 62 | 0.782 | 4 | .062 |
| 19 | .076 |
| 65 | 0.365 | 59 | .287 |
| 84 | .174 |
| 66 | 0.718 | 52 | .140 |
| 53 | .134 |
| 68 | 0.395 | 18 | .157 |
| 74 | .248 |
| 70 | 0.583 | 8 | .454 |
| 96 | .553 |
| 75 | 0.008 | 3 | .008 |
| 49 | .008 |
| 78 | 0.726 | 72 | .314 |
| 76 | .278 |
| 82 | 0.718 | 36 | .378 |
| 95 | .409 |
| 83 | 0.643 | 61 | .257 |
| 90 | .394 |
| 88 | 0.176 | 23 | .126 |
| 81 | .100 |
| 93 | 0.8 | 7 | .197 |
| 21 | .042 |
| 97 | 0.546 | 56 | .032 |
| 98 | .518 |
| 100 | 0.623 | 30 | .071 |
| 63 | .033 |