

# MATCHIT: Nonparametric Preprocessing for Parametric Causal Inference

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# 1 Introduction

MATCHIT implements the suggestions of Ho, Imai, King and Stuart (2005) for improving parametric statistical models and reducing model dependence by preprocessing data with semi- and non-parametric matching methods. After preprocessing with MATCHIT, researchers can use whatever parametric model they would have used without MATCHIT, but produce inferences that are substantially more robust and less sensitive to modeling assumptions. Matched data sets created by MATCHIT can also be entered easily into Zelig (Imai, King and Lau, 2004), or other programs, for subsequent parametric analyses. MATCHIT reduces the dependence of causal inferences on commonly made, but hard-to-justify, statistical modeling assumptions via a wide range of sophisticated matching methods. In addition, we have written MATCHIT so that adding methods to its structure is easy, if you have the inclination.

## 1.1 Software Requirements

MATCHIT works in conjunction with the R programming language and statistical software, and will run on any platform where R is installed (Windows, Unix, or Mac OS X). R is available free for download at the Comprehensive R Archive Network (CRAN) at <http://www.r-project.org/>. MATCHIT has been tested on the most recent version of R (2.1.1). A good way to learn R, if you don't know it already, is to learn Zelig (available at <http://gking.harvard.edu>) which includes a self-contained introduction to R and can then be used to analyze the data after running MATCHIT.

## 1.2 Installing MatchIt

To install MATCHIT for all platforms, type at the R command prompt:

```
> install.packages("MatchIt")
```

and MATCHIT will install itself onto your system automatically. During the process you may either decide to keep or discard the installation files, which will not affect the way MATCHIT runs. You only need to do this once. Some users may also find it helpful to install the package with version control (see Subsection 6.4).

## 1.3 Loading MatchIt

As with any R package, you need install MATCHIT only once, but you must load it prior to each use. You can do this for each R session by typing

```
> library(MatchIt)
```

at the R command prompt.

Alternatively, you can specify R to load MATCHIT automatically at launch so that you can skip the step of typing `library(MatchIt)` at the beginning of every R session. To do this, edit the `Rprofile` file located in the R program subdirectory, e.g. `C:/R/rw2011/etc/`, for Windows systems or the `.Rprofile` file located in the home directory for Unix/Linux and Mac OS X systems. Using a text editor such as Windows notepad and emacs, add the following line to the file:

```
options(defaultPackages = c(getOption("defaultPackages"), "MatchIt"))
```

For this change to take effect, you need to restart R.

## 1.4 Updating MatchIt

We recommend that you periodically update MATCHIT at the R prompt by typing:

```
> update.packages()
> library(MatchIt)
```

which will update all the libraries including MATCHIT.

## 2 Statistical Overview

MATCHIT is designed for studies with a dependent variable (or a set of dependent variables) that is a function of a dichotomous causal (or “treatment”) variable, with values known as the “treated” and “control” groups, and a set of “pretreatment” covariates, i.e., that are causally prior to the administration of the treatment. MATCHIT works for experimental data, but is also designed for observational designs where the treatment variable is observed rather than manipulated by the investigator. MATCHIT can be used for other types of causal variables by dichotomizing them, perhaps in multiple ways (see also Imai and van Dyk, 2004).

### 2.1 Preprocessing via Matching

The goal of matching is to adjust the data prior to the parametric analysis so that (1) the relationship between  $t_i$  and  $X_i$  is eliminated or reduced, and (2) no bias and little inefficiency is induced. This means that during matching we can select, duplicate, or selectively drop observations from an existing sample without inducing bias, as long as we do so using a rule that is a function only of  $t_i$  and  $X_i$ . MATCHIT provides, implements, and evaluates the choice of these rules. After matching, the preprocessed dataset will be such that  $t_i$  and  $X_i$  are unrelated or less related than in the raw data, meaning that the treatment and control groups have the same background characteristics, or in other words that this relationship holds:  $\tilde{p}(X|t = 1) \approx \tilde{p}(X|t = 0)$ , where  $\tilde{p}$  refers to the observed empirical density of the data (think histogram), rather than a population density.

The simplest way to obtain good matches (as defined above) is to use one-to-one exact matching, which pairs each treated unit with one control unit for which the values of  $X_i$  are identical. However, with many covariates and finite numbers of potential matches, it is often very difficult to obtain exact matches. Luckily, good matching only requires that the *distribution* of  $X$  given  $t = 0$  match the distribution of  $X$  given  $t = 1$ , and so individual matched pairs are not required. Indeed, many of the other methods implemented in MATCHIT only attempt to balance the overall covariate distributions, without necessarily finding one-to-one exact matches.

### 2.2 Checking Balance

The goal of a matching procedure is to replicate a randomized experiment in terms of finding units who look as if they could have been randomly assigned to treatment or control status. That is, we want the distribution of covariates to be the same in the matched treated and matched control groups. Thus, a crucial part of any matching procedure is assessing how close the matches are in the two groups (the “balance”). Because the outcome variable is not used in the matching procedure, a variety of matching methods can be assessed, and the matching procedure that leads to the best balance chosen. MATCHIT provides a number of ways to assess the balance of covariates after matching, including numerical summaries such as the standardized bias between the groups (difference in means divided by the treated group standard deviation) and graphical summaries such as quantile-quantile plots that compare the empirical distributions of each covariate. These diagnostics can be done on the covariates included in the matching procedure, as well as on other covariates on which close matches are desired.

### 2.3 Conducting Analyses after Matching

The most common way that parametric analyses are used to compute quantities of interest is by holding constant some explanatory variables, changing others, and computing predicted or expected values and taking the difference or ratio. In the case of causal inference, this would probably mean looking at the effect on the expected value of the outcome variable when changing  $T$  from 0 to 1, while holding constant the pretreatment control variables  $X$  at their means or medians. This, and indeed any other ordinary procedure, would be a perfectly reasonable way to proceed with analysis after matching.

Another way to proceed with analysis after MATCHIT is to compute the average treatment effect on the treated. For example, for the treated group, the potential outcomes under control,  $Y_{0i}$ , are missing, whereas

the outcomes under treatment,  $Y_{1i}$ , are observed, and the goal of the analysis is to impute the missing outcomes,  $Y_{0i}$  in observations where  $T_i = 1$ , which we do via simulation using a parametric statistical model (as described below). Once those potential outcomes are imputed from the model, the estimate of individual  $i$ 's treatment effect is  $Y_{1i} - \hat{Y}_{0i}$  where  $\hat{Y}_{0i}$  is a simulation of the average missing potential outcome for unit  $i$  (that is it is a simulation of the value of the dependent variable for unit  $i$  under the counterfactual condition where  $T_i = 0$ ). The in-sample average treatment effect for the treated individuals can then be obtained by averaging this difference over all observations  $i$  where in fact  $T_i = 1$ . (A similar procedure can also be used to estimate various other quantities of interest such as the average treatment effect for all observations.) An advantage of this simulation approach is that the uncertainty estimates such as standard errors and confidence intervals are obtained easily by the usual rules in fitting the parametric model.

The imputation from the model can be done in at least two ways. Recall that the model is used to impute *the value that the outcome variable would take among the treated units if those treated units were actually controls*. Thus, one reasonable approach would be to fit a model to the whole set of matched data and create simulated predicted values of the dependent variable for the treated units with  $T_i$  switched counterfactually from 1 to 0. An alternative approach would be to fit a model without  $T$  by using only the outcomes of the matched control units (i.e., using only observations where  $T_i = 0$ ). Then, given this fitted model, the missing outcomes  $Y_{0i}$  are imputed for the matched treated units by using the values of the explanatory variables for the treated units. The first approach will usually have lower variance, since all observations are used, and the second may have less bias, since no assumption of constant parameters is needed. See (Ho et al., 2005) for more details.

### 3 User's Guide to MatchIt

We adopt the same notation as in Ho, Imai, King and Stuart (2005). Unless otherwise noted, let  $i$  index the  $n$  units in the dataset,  $n_1$  denote the number of treated units,  $n_0$  denote the number of control units (such that  $n = n_0 + n_1$ ), and  $x_i$  indicate a vector of pretreatment (or control) variables for unit  $i$ . Let  $t_i = 1$  when unit  $i$  is assigned treatment, and  $t_i = 0$  when unit  $i$  is assigned control. (The labels "treatment" and "control" are arbitrary and can be switched for convenience.) Denote  $y_{1i}$  as the potential outcome of unit  $i$  under treatment and  $y_{0i}$  the potential outcome of unit  $i$  under control. The variables  $y_{1i}$  and  $y_{0i}$  are jointly unobservable, and for each  $i$ , we observe one  $y_i = t_i y_{1i} + (1 - t_i) y_{0i}$ , and not the other.

#### 3.1 Example Data: National Supported Work Demonstration

For a running example, we use data from the job training program analyzed in Lalonde (1986) and Dehejia and Wahba (1999). A subsample of the data consisting of the National Supported Work Demonstration (NSW) treated group and the comparison sample from the Population Survey of Income Dynamics (PSID) is included in MATCHIT.<sup>1</sup> The variables in this dataset are described in Table 1. One causal effect of interest is the impact that participation in the job training program, `treat == 1`, had on real earnings in 1978, `re78`, for those that participated in the program. The average treatment effect on the treated (ATT) is defined as,

$$ATT = \frac{1}{\sum_{i=1}^n t_i} \sum_{i:t_i=1} E[Y_i(1) - Y_i(0)], \quad (1)$$

where  $Y_i(1)$  represents the potential outcome under the treatment of the job program, and  $Y_i(0)$  under control. Note that the first term inside the expectation (the right hand side of Equation 1) is *observed*, whereas the second term is the *unobserved* counterfactual of real earnings if participants had not participated. The nature of causal inference is that one of the two terms in the difference will always be unobserved.

---

<sup>1</sup>This data set, `lalonde`, was created using `NSWRE74_TREATED.txt` and `CPS3_CONTROLS.txt` from <http://www.columbia.edu/~rd247/nswdata>.

Variable name	Description
<b>Outcome variable (Y)</b>	
<b>re78</b>	Real earnings (1978)
<b>Treatment variable (T)</b>	
<b>treat</b>	Treated in job training program from March 1975-June 1977 (1 if treated, 0 if not treated)
<b>Pre-treatment covariates (X)</b>	
<b>age</b>	Age
<b>educ</b>	Years of education
<b>black</b>	Race black (1 if black, 0 otherwise)
<b>hispan</b>	Race hispanic (1 if Hispanic, 0 otherwise)
<b>married</b>	Marital status (1 if married, 0 otherwise)
<b>nodegree</b>	High school degree (1 if no degree, 0 otherwise)
<b>re74</b>	Real earnings (1974)
<b>re75</b>	Real earnings (1975)

Table 1: Description of Lalonde data

## 3.2 Preprocessing via Matching

`matchit()` implements a variety of matching procedures. A general syntax is

```
> m.out <- matchit(treat ~ x1 + x2, data = mydata)
```

where `treat` is the dichotomous treatment variable, and `x1` and `x2` are pre-treatment covariates. This command creates the `MATCHIT` object called `m.out`. A quick summary of the matching procedure can be printed on the screen by typing

```
> m.out
```

or

```
> print(m.out)
```

Examples of various matching procedures are given for the remainder of this section, and Section 4.1 lists all possible specifications of `matchit()`.

### 3.2.1 Exact Matching

The simplest version of matching is exact. This technique matches *each* treated unit to *all* possible control units with exactly the same value on all the covariates, forming subclasses such that within each subclass all units (treatment and control) have the same covariate values. Exact restrictions on a subset of covariates can also be specified in nearest neighbor matching (see Section 3.2.3).

The following example script can be run by typing `demo(exact)` at the R prompt:

```
> library(MatchIt)
> data(lalonde)
> m.out <- matchit(treat ~ educ + black + hispan, data = lalonde,
+   method = "exact")
```

The object `m.out` contains all the information on the matched units. The matching forms all possible subclasses based on unique values of the covariates in the right hand side of the formula; within each subclass, all units have the same covariate values. To obtain basic information about the matching procedure:

```
> m.out
```

```
Call: matchit(formula = treat ~ educ + black + hispan, data = lalonde, method = "exact")
```

```
Exact Subclasses: 25
```

```
Sample sizes:
```

	Control	Treated
Full	429	185
Matched	376	184
Unmatched	53	1

The printout includes the original call to MATCHIT and the fact that 184 treatment units were exactly matched to 376 control units on race and education. There was 1 treated unit and 53 control units that weren't matched, and therefore are excluded from the matched data set. See Sections 4.1.1 and 4.1.2 for a list of complete input options for exact matching. Now, proceed to Section 3.3 to learn about how the `summary()` command can be used with exact matching.

### 3.2.2 Subclassification

When there are many covariates (or many values of some covariates) on which matches are desired, finding sufficient exact matches will often be impossible. In that case, subclassification is sometimes desirable. Various subclassification schemes exist, including the one based on a scalar distance measure such as the estimated propensity score using the `distance` option (see Section 4.1.1). Subclassification will form subclasses based on this distance measure. Within each subclass, the distribution of covariates in the treatment and control groups should be similar.

Subclassification is implemented in MATCHIT using `method = "subclass"`. See also the sections on full matching (Section 3.2.4) and nearest-neighbor matching (Section 3.2.3), which provide additional ways of performing subclassification. The following example script can be run by typing `demo(subclass)` at the R prompt:

```
> data(lalonde)
> m.out <- matchit(treat ~ re74 + re75 + educ + black + hispan +
+   age, data = lalonde, method = "subclass")
```

The above syntax forms 6 subclasses, which is the default number of subclasses, based on a distance measure estimated using logistic regression. By default, each subclass will have approximately the same number of treated units. See Sections 4.1.1 and 4.1.3 for a complete list of input options for subclassification.

### 3.2.3 Nearest Neighbor Matching

Nearest neighbor matching selects the  $r$  best control matches for each individual in the treatment group (excluding those discarded using the `discard`) option. The matching is done using a distance measure specified by the `distance` option. Matches are chosen for each treated unit one at a time, and at each matching step we choose the control unit that is not yet matched but is closest to the treated unit on the distance measure. There are many variations on nearest neighbor matching, which are described in further detail in Sections 4.1.1 and 4.1.4.

Nearest neighbor matching is implemented in MATCHIT using the `method="nearest"` option. The following example script can be run by typing `demo(nearest)` at the R prompt.

To conduct propensity score matching with pre-treatment covariates composed of real earnings in 1974 and 1975, education, race, and age:

```
> m.out <- matchit(treat ~ re74 + re75 + educ + black + hispan +
+ age, data = lalonde, method = "nearest")
```

You may again check basic statistics of the MATCHIT object by the `print` command:

```
> print(m.out)
```

```
Call: matchit(formula = treat ~ re74 + re75 + educ + black + hispan + age, data = lalonde, method =
```

Sample sizes:

	Control	Treated
Full	429	185
Matched	185	185
Unmatched	244	0
Discarded	0	0

We see that 185 control units were matched to the 185 treated units (a “1-1” match).

**Additional Examples** Here, we illustrate various options of nearest neighbor matching by providing additional examples based on the Lalonde data. Users should refer to Sections 4.1.1 and 4.1.4 for a complete list of options for nearest neighbor matching.

1. Nearest neighbor matching on propensity score estimated using logistic regression where 2 matches are chosen for each treated unit.

```
> m.out1 <- matchit(treat ~ re74 + re75 + age + educ, data = lalonde, method = "nearest",
+ distance = "logit", ratio=2)
```

2. Mahalanobis matching on `re74` and `re75`.

```
> m.out <- matchit(treat ~ re74+re75, data=lalonde, method="nearest",
+ distance="mahalanobis")
```

3. Mahalanobis matching on `re74` and `re75` within nearest neighbor matching on distance measure (propensity score), with restriction of exact matches on `married`.

```
> m.out2 <- matchit(treat ~ re74 + re75 + age + educ, data = lalonde, method = "nearest",
+ distance = "logit", mahvars=c("re74", "re75"), exact=c("married"),
+ caliper=.25)
```

4. Nearest neighbor matching after discarding all units outside of the common support of the estimated distance measure.

```
> m.out3 <- matchit(treat ~ re74 + re75 + age + educ, data = lalonde, method = "nearest",
+ distance = "logit", discard= "both")
```

5. Nearest neighbor matching with replacement where two control units are matched with one treated unit.

```
> m.out4 <- matchit(treat ~ re74 + re75 + age + educ, data = lalonde, method = "nearest",
+ distance = "logit", replace = TRUE, ratio = 2)
```

6. Nearest neighbor matching followed by formation of 5 subclasses

```
m.out5 <- matchit(treat ~ re74 + re75 + age + educ, data = lalonde, method = "nearest",
distance = "logit", subclass=5)
```



### 3.2.4 Full Matching

Full matching is a particular type of subclassification that uses all treated and control units (Rosenbaum, 2002; Hansen, 2004). A fully matched sample is composed of matched sets, where each matched set contains either one treated unit and one or more controls (or one control unit and one or more treated units). The only units not placed into a subclass will be those discarded (if a `discard` option was specified) because they are outside of common support. Full matching is optimal in terms of minimizing a weighted average of the estimated distance measure between each treated subject and each control subject within each subclass. See Sections 4.1.1 and 4.1.5 for a complete list of optional inputs for full matching.

Full matching can be performed with MATCHIT by setting `method = "full"`. We use an add-on package called `optmatch` (Hansen, 2004), which must be installed separately by typing at the R command prompt,

```
> install.packages("optmatch", contriburl = "http://www.stat.lsa.umich.edu/~bbh/optmatch")
```

For more information about the package, see <http://www.stat.lsa.umich.edu/~bbh/optmatch.html>. The following example script can be run by typing `demo(full)` at the R prompt. We first load the Lalonde data, conduct full matching, and then print a short summary.

```
> m.out <- matchit(treat ~ age + educ + black + hispan + married +  
+   nodegree + re74 + re75, data = lalonde, method = "full",  
+   distance = "logit")  
> m.out
```

```
Call: matchit(formula = treat ~ age + educ + black + hispan + married +   nodegree + re74 + re75, data = lalonde, method = "full", distance = "logit")
```

Sample sizes:

	Control	Treated
Full	429	185
Matched	429	185
Unmatched	0	0
Discarded	0	0

We see that the matching has utilized all units (the treated and control group sample sizes are the same for the full and matched samples).

### 3.2.5 Optimal Matching

The default nearest neighbor matching method in MATCHIT is “greedy” matching, where the closest control match for each treated unit is chosen one at a time, without trying to minimize a global distance measure. Another method, “optimal” matching, finds the matched samples with the smallest average absolute distance between each matched pair. With large control pools, greedy and optimal matching may lead to very similar (or the same) sets of matches; Gu and Rosenbaum (1993) have shown that greedy and optimal matching generally choose the same sets of controls for the matched samples, but that optimal matching does a better job of minimizing the distance within each pair. In addition, optimal matching can be particularly helpful when there are not many appropriate control matches for the treated units. See Gu and Rosenbaum (1993) or Rosenbaum (2002) for more information on optimal matching. See Sections 4.1.1 and 4.1.6 for a complete list of optional inputs for optimal matching.

Optimal matching is performed with MATCHIT by setting `method = "optimal"`. We use an add-on package called `optmatch` (Hansen, 2004), which must be installed separately by typing at the R command prompt,

```
> install.packages("optmatch", contriburl = "http://www.stat.lsa.umich.edu/~bbh/optmatch")
```

For more information about the package, see <http://www.stat.lsa.umich.edu/~bbh/optmatch.html>. The following example script can be run by typing `demo(optimal)` at the R prompt.

```
> m.out <- matchit(treat ~ re74 + re75 + age + educ, data = lalonde,
+   method = "optimal", distance = "logit", ratio = 2)
> m.out
```

```
Call: matchit(formula = treat ~ re74 + re75 + age + educ, data = lalonde, method = "optimal", distar
```

Sample sizes:

	Control	Treated
Full	429	185
Matched	370	185
Unmatched	59	0
Discarded	0	0

### 3.3 Checking Balance

In MATCHIT, there are two ways to check balance after any matching procedure. Given the MATCHIT output object `m.out`, one can use the following commands

1. `summary(m.out)` gives numerical summaries of the resulting balance of covariates.
2. `plot(m.out)` gives graphical summaries to assess balance of covariates.

Below, we give three examples (exact matching, subclassification, and nearest neighbor matching) to illustrate the use of these two functions. Similar commands can be used for all other matching procedures, and they will give similar outputs. See Section 4.2 for details.

#### Examples

1. Using the example of exact matching from Section 3.2.1, we obtain more information on the matching using the `summary()` command. To include the covariates in each subclass, we also use the `covariates = TRUE` option:

```
> m.out <- matchit(treat ~ educ + black + hispan, data = lalonde,
+   method = "exact")
> summary(m.out, covariates = TRUE)
```

Call:

```
matchit(formula = treat ~ educ + black + hispan, data = lalonde, method = "exact")
```

Sample sizes for full and exactly matched data:

	Control	Treated
Full	429	185
Matched	376	184

Discarded        53        1

Matched sample sizes by subclass:

	Treated	Control	Total	educ	black	hispan
1	39	13	52	11	1	0
2	4	10	14	9	0	1
3	30	23	53	12	1	0
4	15	8	23	8	1	0
5	22	13	35	9	1	0
6	1	2	3	16	1	0
7	7	83	90	12	0	0
8	7	3	10	13	1	0
9	28	11	39	10	1	0
10	1	2	3	7	1	0
11	1	13	14	14	0	0
12	2	20	22	9	0	0
13	2	5	7	10	0	1
14	4	2	6	4	1	0
15	4	2	6	14	1	0
16	3	3	6	5	1	0
17	2	7	9	8	0	1
18	4	29	33	11	0	0
19	1	21	22	7	0	0
20	1	2	3	6	1	0
21	1	14	15	13	0	0
22	2	12	14	12	0	1
23	1	29	30	8	0	0
24	1	40	41	10	0	0
25	1	9	10	11	0	1

MATCHIT has created 25 subclasses where the values of the race and education covariates are equal. The MATCHIT output object will include **weights** and **subclass**, which can be used to identify which units were put into the same subclass. Units that did not have the same covariate values as anyone in the other treatment group have **subclass = NA**.

For example, we can use the **subclass** component of **m.out** to identify which units are in each subclass and to verify their covariate values. To see ID numbers of the first 10 units in subclass 1, in which all subjects are black and have 11 years of education (“NSW” refers to the National Supported Work Demonstration participants):

```
> row.names(m.out$X)[m.out$subclass == 1][1:10]

[1] "NSW1" "NSW4" "NSW8" "NSW21" "NSW24" "NSW26" "NSW27" "NSW30" "NSW33"
[10] "NSW45"
```

We can also confirm the covariate values of the units in each subclass. For example, to see the covariate values of the first 5 units in subclass 2 (“PSID” refers to individuals in the Panel Survey of Income Dynamics):

```
> m.out$X[m.out$subclass == 2 & !is.na(m.out$subclass), ][1:5,
+      ]
```

```
      educ black hispan
NSW2      9      0      1
NSW100     9      0      1
NSW112     9      0      1
NSW173     9      0      1
PSID9      9      0      1
```

2. Using the example of subclassification from Section 3.2.2, we check the balance of covariates.

```
> m.out <- matchit(treat ~ re74 + re75 + educ + black + hispan +
+      age, data = lalonde, method = "subclass")
> summary(m.out)
```

Call:

```
matchit(formula = treat ~ re74 + re75 + educ + black + hispan +      age, data = lalonde, method = "
```

Summary of balance for all data:

	Means Treated	Means Control	Pooled SD	QQ Med	QQ Mean	QQ Max
distance	5.66e-01	0.187	0.284	0.732	0.535	0.84
re74	2.10e+03	5619.237	6477.964	3430.277	5155.851	13044.16
re75	1.53e+03	2466.484	3295.679	1373.280	1511.706	9609.60
educ	1.03e+01	10.235	2.628	1.414	0.962	5.66
black	8.43e-01	0.203	0.489	1.414	0.903	1.41
hispan	5.95e-02	0.142	0.322	0.000	0.119	1.41
age	2.58e+01	28.030	9.881	1.414	4.650	14.14

	Std. Bias
distance	1.792
re74	-0.721
re75	-0.290
educ	0.055
black	1.757
hispan	-0.349
age	-0.309

Summary of balance by subclasses:

, , Subclass 1

	Means Treated	Means Control	Pooled SD	QQ Med	QQ Mean	QQ Max
distance	1.22e-01	7.62e-02	5.22e-02	5.48e-02	6.51e-02	1.23e-01
re74	3.63e+03	6.33e+03	7.15e+03	4.59e+03	5.18e+03	1.30e+04
re75	2.23e+03	2.62e+03	3.30e+03	6.63e+02	1.15e+03	9.63e+03
educ	1.06e+01	1.03e+01	2.80e+00	1.41e+00	1.37e+00	9.90e+00
black	6.45e-02	5.81e-03	1.03e-01	0.00e+00	4.56e-02	1.41e+00
hispan	3.55e-01	1.77e-01	3.94e-01	0.00e+00	2.28e-01	1.41e+00
age	2.50e+01	2.86e+01	1.05e+01	2.83e+00	6.56e+00	1.98e+01

	Std. Bias
distance	7.79e-01
re74	-3.38e-01
re75	-1.17e-01
educ	1.93e-01
black	2.35e-01
hispan	3.65e-01
age	-5.85e-01

, , Subclass 2

	Means Treated	Means Control	Pooled SD	QQ Med	QQ Mean	QQ Max
distance	5.39e-01	5.34e-01	6.46e-02	1.62e-02	1.99e-02	6.55e-02
re74	7.53e+03	7.21e+03	5.92e+03	6.57e+02	1.23e+03	4.51e+03
re75	4.11e+03	3.48e+03	5.01e+03	1.71e+03	2.12e+03	1.61e+04
educ	9.00e+00	8.69e+00	3.47e+00	7.07e-01	1.29e+00	5.66e+00
black	1.00e+00	1.00e+00	0.00e+00	0.00e+00	0.00e+00	0.00e+00
hispan	0.00e+00	0.00e+00	0.00e+00	0.00e+00	0.00e+00	0.00e+00
age	2.81e+01	3.33e+01	1.03e+01	9.33e+00	8.05e+00	1.98e+01

	Std. Bias
distance	6.29e-02
re74	5.56e-02
re75	1.10e-01
educ	1.03e-01
black	
hispan	
age	-6.36e-01

, , Subclass 3

	Means Treated	Means Control	Pooled SD	QQ Med	QQ Mean	QQ Max
distance	6.46e-01	6.45e-01	1.16e-02	1.32e-03	2.86e-03	1.30e-02
re74	8.92e+02	1.40e+03	1.82e+03	5.43e+02	8.26e+02	2.12e+03
re75	7.07e+02	1.46e+03	2.19e+03	2.91e+02	9.44e+02	8.97e+03
educ	8.93e+00	9.12e+00	1.32e+00	0.00e+00	4.37e-01	2.83e+00
black	1.00e+00	1.00e+00	0.00e+00	0.00e+00	0.00e+00	0.00e+00
hispan	0.00e+00	0.00e+00	0.00e+00	0.00e+00	0.00e+00	0.00e+00
age	2.39e+01	1.96e+01	7.08e+00	3.80e+00	6.26e+00	2.00e+01

	Std. Bias
distance	7.54e-02
re74	-3.15e-01
re75	-5.02e-01
educ	-1.57e-01
black	
hispan	
age	5.47e-01

, , Subclass 4

	Means Treated	Means Control	Pooled SD	QQ Med	QQ Mean	QQ Max
distance	6.77e-01	6.78e-01	8.23e-03	4.31e-03	4.32e-03	1.19e-02

re74	3.90e+02	7.11e+02	8.22e+02	0.00e+00	4.42e+02	1.68e+03
re75	1.19e+03	6.84e+02	1.47e+03	1.52e+02	7.70e+02	3.23e+03
educ	1.00e+01	1.06e+01	9.21e-01	1.41e+00	8.08e-01	2.83e+00
black	1.00e+00	1.00e+00	0.00e+00	0.00e+00	0.00e+00	0.00e+00
hispan	0.00e+00	0.00e+00	0.00e+00	0.00e+00	0.00e+00	0.00e+00
age	2.35e+01	2.22e+01	7.99e+00	2.83e+00	4.48e+00	1.13e+01

	Std. Bias
distance	-7.99e-02
re74	-4.35e-01
re75	3.06e-01
educ	-7.38e-01
black	
hispan	
age	1.95e-01

, , Subclass 5

	Means Treated	Means Control	Pooled SD	QQ Med	QQ Mean	QQ Max
distance	6.94e-01	6.97e-01	3.20e-03	1.09e-03	3.37e-03	1.07e-02
re74	9.41e+01	3.26e+02	4.43e+02	0.00e+00	1.58e+02	8.01e+02
re75	4.05e+02	3.08e+02	1.23e+03	0.00e+00	1.27e+03	7.78e+03
educ	1.10e+01	1.14e+01	4.28e-01	0.00e+00	6.06e-01	1.41e+00
black	1.00e+00	1.00e+00	0.00e+00	0.00e+00	0.00e+00	0.00e+00
hispan	0.00e+00	0.00e+00	0.00e+00	0.00e+00	0.00e+00	0.00e+00
age	2.67e+01	2.23e+01	6.11e+00	9.90e+00	6.87e+00	1.27e+01

	Std. Bias
distance	-9.86e-01
re74	-6.03e-01
re75	7.26e-02
educ	-1.66e+00
black	
hispan	
age	8.19e-01

, , Subclass 6

	Means Treated	Means Control	Pooled SD	QQ Med	QQ Mean	QQ Max
distance	7.20e-01	7.24e-01	1.81e-02	2.63e-03	5.47e-03	2.88e-02
re74	0.00e+00	2.70e+02	3.97e+02	0.00e+00	3.82e+02	3.63e+03
re75	5.19e+02	1.66e+03	2.34e+03	0.00e+00	1.33e+03	6.83e+03
educ	1.25e+01	1.26e+01	1.20e+00	0.00e+00	2.33e-01	1.41e+00
black	1.00e+00	1.00e+00	0.00e+00	0.00e+00	0.00e+00	0.00e+00
hispan	0.00e+00	0.00e+00	0.00e+00	0.00e+00	0.00e+00	0.00e+00
age	2.76e+01	2.70e+01	7.84e+00	2.45e+00	3.32e+00	1.13e+01

	Std. Bias
distance	-2.90e-01
re74	-Inf
re75	-6.96e-01
educ	-1.35e-01
black	
hispan	

age 8.69e-02

Sample sizes by subclasses:

	Subclass 1	Subclass 2	Subclass 3	Subclass 4	Subclass 5	Subclass 6
Treated	31	31	30	31	31	31
Control	344	26	17	21	7	14
Total	375	57	47	52	38	45

Summary of balance across subclasses

	Means Treated	Means Control	Pooled SD	QQ Med	QQ Mean	QQ Max
distance	5.66e-01	5.59e-01	1.44e-02	0.0135	1.69e-02	4.23e-02
re74	2.10e+03	2.72e+03	1.59e+03	967.1902	1.37e+03	4.30e+03
re75	1.53e+03	1.71e+03	1.18e+03	470.4902	1.26e+03	8.75e+03
educ	1.03e+01	1.05e+01	8.20e-01	0.5924	7.93e-01	4.01e+00
black	8.43e-01	8.33e-01	1.72e-02	0.0000	7.64e-03	2.37e-01
hispan	5.95e-02	2.97e-02	6.61e-02	0.0000	3.82e-02	2.37e-01
age	2.58e+01	2.55e+01	3.46e+00	5.1973	5.92e+00	1.58e+01
	Std. Bias					
distance	-0.0741					
re74	-Inf					
re75	-0.1360					
educ	-0.4002					
black	NaN					
hispan	NaN					
age	0.0687					

Percent Balance Improvement:

	Mean	QQ Med	QQ Mean	QQ Max	Std. Bias
distance	0	0	0	0	0
re74	0	0	0	0	0
re75	0	0	0	0	0
educ	0	0	0	0	0
black	0	0	0	0	0
hispan	0	0	0	0	0
age	0	0	0	0	0

For each set of units (full data set, matched data set, subclasses), the "Means Treated" and "Means Control" columns show the weighted means in the treated and control groups. The "Pooled SD" is the standard deviation of the covariate in the pooled group of treated and control units. The "Std. Bias" is the difference in means in the treated and control groups, divided by the "Pooled SD" in the full data set. Good matches will generally have standardized biases less than approximately 0.25; values greater than that imply that the groups have means that are more than a quarter of a standard deviation apart.

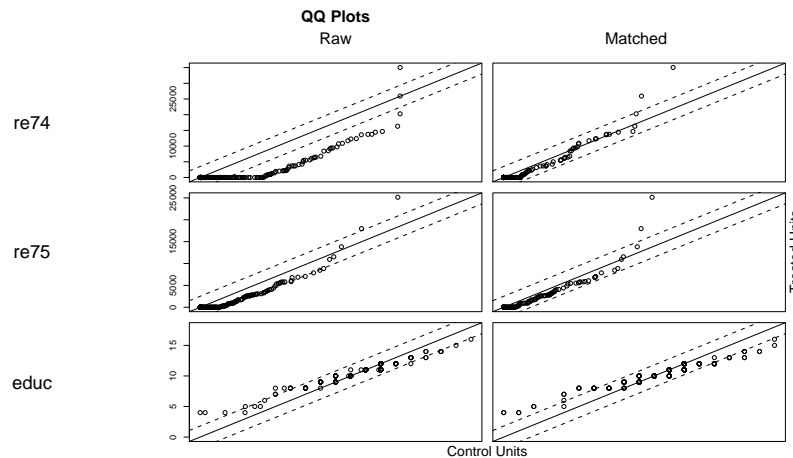
Finally, the final three columns gives summary statistics of a Quantile-Quantile (Q-Q) plot (see below for more information on these plots). Those columns give the median, mean, and maximum orthogonal deviations from the 45-degree line of the Q-Q plot. If the empirical distributions of the two groups

(treated and control) were exactly the same, all points would lie on the 45-degree line and thus all of these distances would be 0. Values greater than 0 indicate deviations between the groups in some part of the empirical distributions. The plots themselves, described below, can provide further insight into which part of the covariate distribution has differences between the groups.

As mentioned, we can also assess balance visually via the `plot` command, which provides two types of plots: jitter plots of the distance measure, and Q-Q plots of each covariate.

```
> plot(m.out)
> plot(m.out, type = "jitter")

[1] "To identify the units, use first mouse button; to stop, use second."
numeric(0)
```



```
> ## balance diagnostics through graphics
> plot(m.out)
> plot(m.out, type="jitter")
```

Figures 1 and 2 display these two diagnostic plots, respectively.

Lastly, subclassification may also be used in conjunction with nearest neighbor matching described below in Subsection 3.2.3, by specifying leaving the default of `method = "nearest"` but adding the option `subclass`. When you choose this command, `MATCHIT` matches in the same way, but it also adds a variable to the output object with the subclass number.

3. The `summary()` command first gives measures of the balance between the treated and control groups in the full (original) data set, and then the same measures of balance in the matched data set. If the matching worked well, the standardized bias and QQ plot statistics should be smaller in the matched data set as compared with the full data set. We could also use the `addlvars` option to examine the balance in variables not included in the distance model; it may be beneficial to include in the distance model any variables that are not well balanced in the matched data sets.

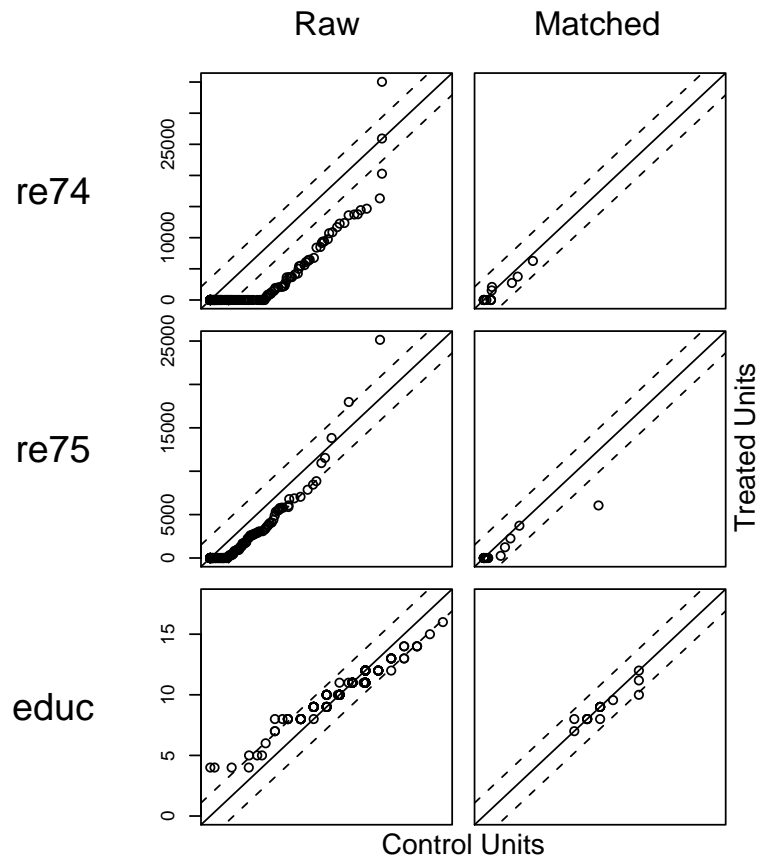
```
> summary(m.out)
```

Call:

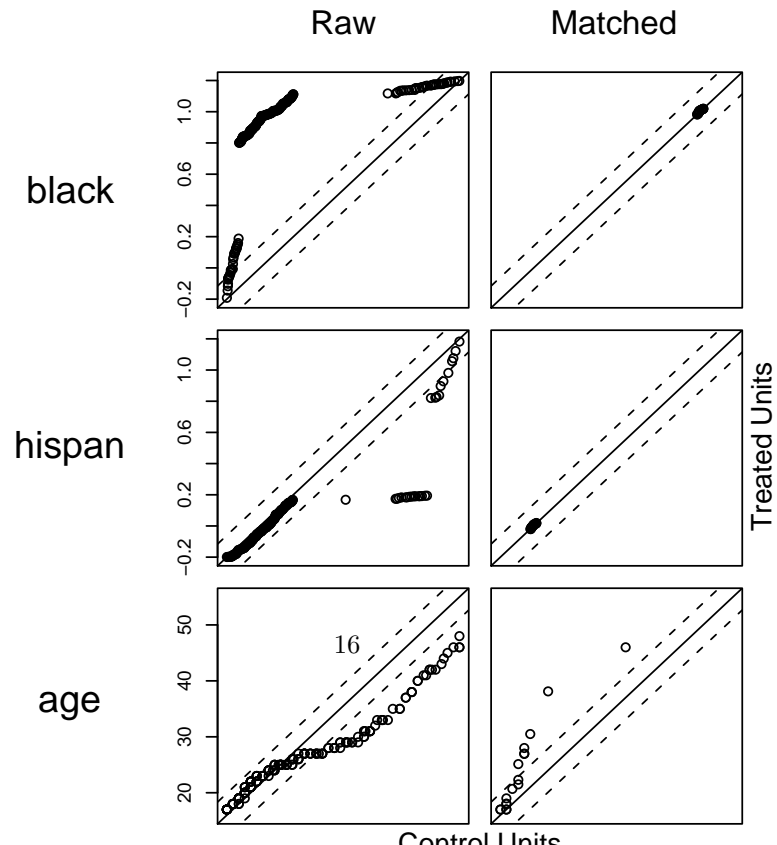
```
matchit(formula = treat ~ re74 + re75 + educ + black + hispan +      age, data = lalonde, method = "
```



### QQ Plots (Subclass 3)



### QQ Plots (Subclass 3)



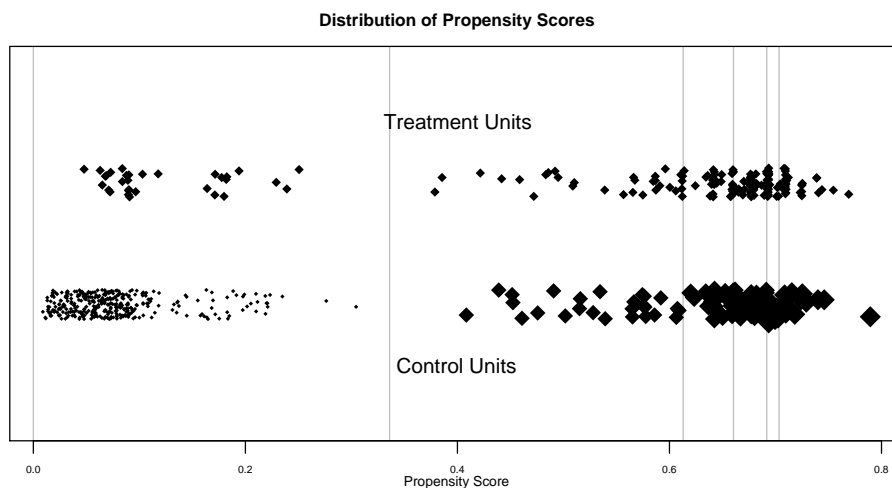


Figure 2: Sample diagnostic jitter plot: Subclassification with MATCHIT call `matchit(treat re74 + re75 + educ + black + hispan + age, data = lalonde, method = "subclass")`. Vertical lines indicate the subclass cut points and the area of each diamond is proportional to the weights of the matched units for each subclass.

Summary of balance for all data:

	Means Treated	Means Control	Pooled SD	QQ Med	QQ Mean	QQ Max
distance	5.66e-01	0.187	0.284	0.732	0.535	0.84
re74	2.10e+03	5619.237	6477.964	3430.277	5155.851	13044.16
re75	1.53e+03	2466.484	3295.679	1373.280	1511.706	9609.60
educ	1.03e+01	10.235	2.628	1.414	0.962	5.66
black	8.43e-01	0.203	0.489	1.414	0.903	1.41
hispan	5.95e-02	0.142	0.322	0.000	0.119	1.41
age	2.58e+01	28.030	9.881	1.414	4.650	14.14
Std. Bias						
distance	1.792					
re74	-0.721					
re75	-0.290					
educ	0.055					
black	1.757					
hispan	-0.349					
age	-0.309					

Summary of balance for matched data:

	Means Treated	Means Control	Pooled SD	QQ Med	QQ Mean	QQ Max
distance	5.66e-01	0.365	0.257	0.150	0.284	6.93e-01
re74	2.10e+03	2466.304	4574.949	410.082	978.726	1.86e+04
re75	1.53e+03	1960.355	3089.993	638.038	887.982	1.61e+04
educ	1.03e+01	10.470	2.673	1.414	1.307	5.66e+00
black	8.43e-01	0.470	0.475	0.000	0.527	1.41e+00

hispan	5.95e-02	0.276	0.374	0.000	0.306	1.41e+00
age	2.58e+01	26.054	8.794	2.828	3.868	1.13e+01
	Std. Bias					
distance	0.9509					
re74	-0.0759					
re75	-0.1330					
educ	-0.0618					
black	1.0231					
hispan	-0.9118					
age	-0.0332					

Percent Balance Improvement:

	Mean	QQ	Med	QQ	Mean	QQ	Max	Std.	Bias
distance	46.9		79.4		46.8		17.6		46.9
re74	89.5		88.0		81.0		-42.3		89.5
re75	54.2		53.5		41.3		-67.3		54.2
educ	-12.5		0.0		-35.9		0.0		-12.5
black	41.8		100.0		41.6		0.0		41.8
hispan	-161.3		0.0		-157.7		0.0		-161.3
age	89.3		-100.0		16.8		20.0		89.3

Sample sizes:

	Control	Treated
All	429	185
Matched	185	185
Unmatched	244	0
Discarded	0	0

This reveals simple statistics of the propensity score and the covariates used in the propensity score specification for the full and matched samples, including means, QQ, and balance bias statistics used to assess whether there was a reduction in bias in the covariates. The univariate distance measure (propensity score, in this case) and the variables 1974 income, 1975 income, black, and age experienced reductions in bias due to the matching. For example, the original bias in 1974 income was  $-0.72$  standard deviations, but is only  $-0.076$  standard deviations in the matched samples. More specifically, job training participants on average earned roughly \$3,523 less in 1974 and \$934 less in 1975 than non-participants, respectively, in the full sample. In the matched sample, the earnings difference is reduced to \$370 in 1974 and \$428 in 1975. This one-to-one matching algorithm has thus chosen 185 control individuals who are more similar to the treated group in 1974 income and 1975 income, which is summarized by the 89.5 and 54.2 percent balance improvement.

The `summary` command will additionally report (a) the original call of the `MATCHIT` object, (b) how many units were discarded due to the `discard` option (described below), and (c) percent balance improvement.

For further information on the balance in the full and matched samples we can use the `interactions=T` option with `summary`, which shows the balance of all squares and interactions of the covariates used in the matching procedure. This is helpful for diagnosing whether balance across matched pairs has been attained. Significant differences in higher order interactions usually are a good indication that the assignment model needs to be respecified,

We can also examine the balance graphically:

```
> plot(m.out)
> plot(m.out, type="jitter")
```

Figures 3 and 4 display these two sample plots. In the jitter plot, you may identify units by observation name by clicking the first mouse button near the units.

Examining these graphs, we see that the matched samples are very well matched on the propensity score, but that there are some remaining imbalances in education, race, and age covariates.

### 3.4 Conducting Analyses after Matching

Once matching is complete and balance has been achieved, the `MATCHIT` object (output from the `matchit()` function) can be used with any other analysis procedure; `MATCHIT` is designed to make those analysis procedures less dependent on the modeling assumptions and thus work better. Therefore, any analysis you might have conducted using the original data set can be conducted with less model dependence using the matched data set. To obtain the matched data set, use `match.data(m.out)`, where `m.out` is a `MATCHIT` object. See Section 4.2.4 for more options and details.

In this section, we describe our recommended approach (Ho et al., 2005), which uses `Zelig` to conduct parametric causal inference after preprocessing the data through `MATCHIT`. The resulting matched data sets can also be exported to other statistical programs using commands such as `write.table()` and `write.csv()`. In addition, the commands in the `foreign` package allow users to save matched data sets as binary files for various statistical software including STATA and SPSS.

`Zelig` (Imai, King and Lau, 2004) is an easy-to-use R package that estimates a large variety of statistical models, gives easily interpretable results by simulating quantities of interest, provides numerical and graphical summaries, and is easily extensible. The package along with the complete documentation is available at <http://gking.harvard.edu/zelig/>. `MATCHIT` and `Zelig` can be easily used together to enable estimation of causal effects in very general settings with a variety of statistical models.

First, we use `match.data()` to create the matched data by excluding unmatched units from the original data, and including information about the particular matching procedure (i.e., weights, subclasses, and the distance measure).

```
> mdata <- matched.data(m.out)
```

where `m.out` is the `MATCHIT` object from `matchit()` and `mdata` is the resulting matched data. This matched data set can then be used for subsequent parametric analyses thorough `Zelig` or any other statistical programs. If one uses `Zelig`, then a syntax for least squares regression is

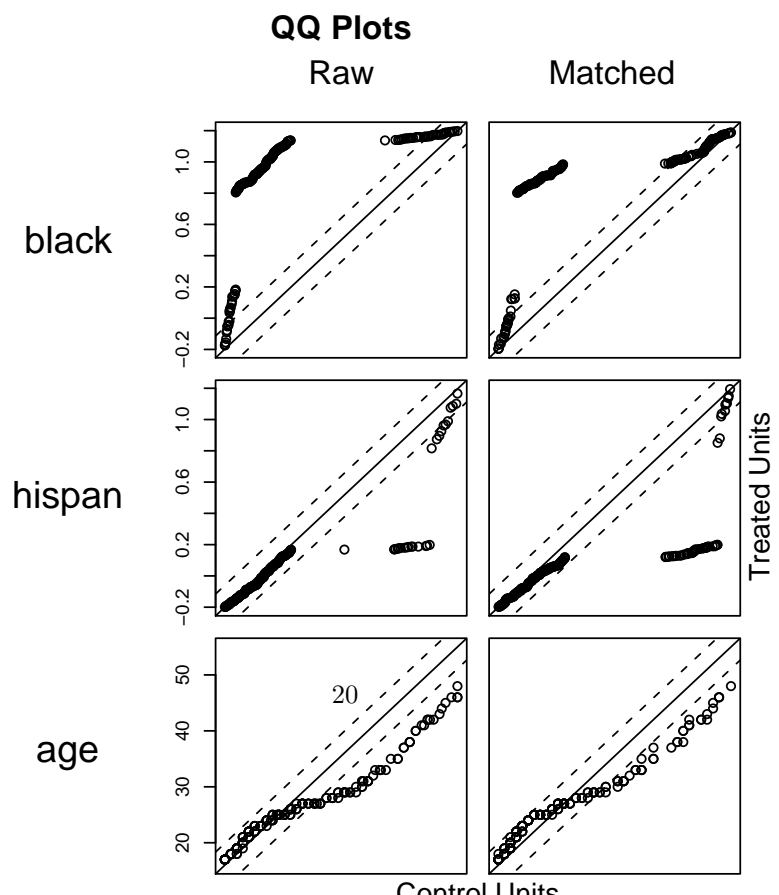
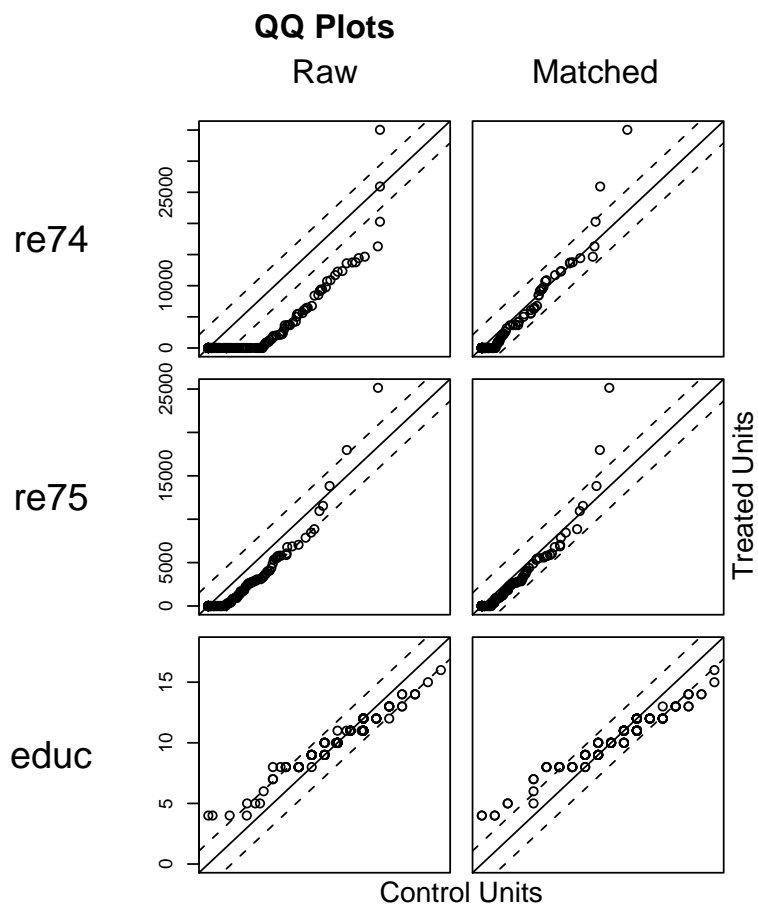
```
> z.out <- zelig(Y ~ treat + x1 + x2, model = "ls", data = mdata)
```

where `Y` is the outcome variable, and `z.out` is the output object from `zelig`. For more details, see Section 3.4.

To illustrate this approach, we provide several examples using the Lalonde data. Users can run these example commands by typing `demo(Zelig)` at the R prompt. We use the linear least squares model in these examples. However, a wide range of other models are available in `Zelig` (for the list of supported models, see [http://gking.harvard.edu/zelig/docs/Models\\_Zelig\\_Can.html](http://gking.harvard.edu/zelig/docs/Models_Zelig_Can.html)), and they can be used in the exactly same way. If you have not installed `Zelig`, follow the installation procedure described at <http://gking.harvard.edu/zelig/docs/Installation.html>

1. Nearest neighbor matching using propensity scores:

```
> data(lalonde)
> library(Zelig)
> m.out1 <- matchit(treat ~ age + educ + black + hispan + nodegree +
```



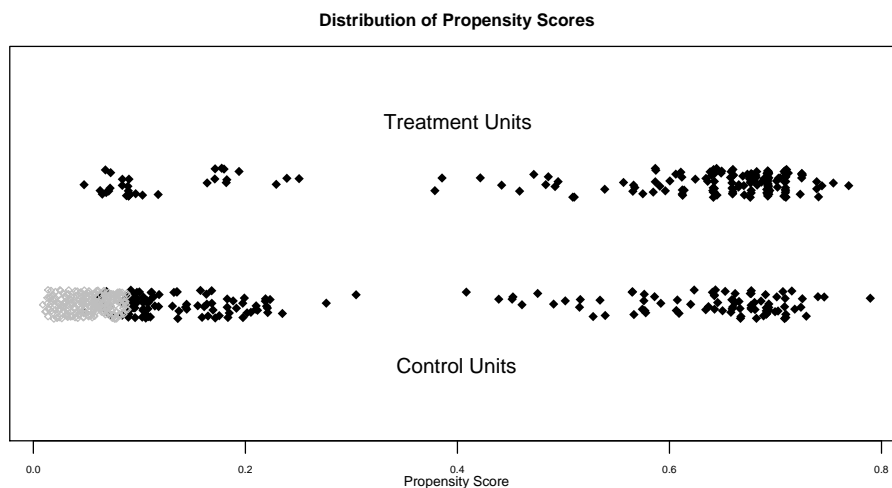


Figure 4: Sample diagnostic jitter plot: Nearest Neighbor matching with the MATCHIT call `matchit(treat re74 + re75 + educ + black + hispan + age, data=lalonde, method="nearest")`. Matched units shown in black, unmatched units shown in grey.

```
+ married + re74 + re75, method = "nearest", data = lalonde)
> z.out1 <- zelig(re78 ~ age + educ + black + hispan + nodegree +
+ married + re74 + re75 + distance, data = match.data(m.out1,
+ "control"), model = "ls")
> x.out1 <- setx(z.out1, data = match.data(m.out1, "treat"), fn = NULL,
+ cond = TRUE)
> s.out1 <- sim(z.out1, x = x.out1)
> summary(s.out1)
```

Model: ls

Number of simulations: 1000

Mean Values of Observed Data (n = 185)

(Intercept)	age	educ	black	hispan	nodegree
1.000e+00	2.582e+01	1.035e+01	8.432e-01	5.946e-02	7.081e-01
married	re74	re75	distance		
1.892e-01	2.096e+03	1.532e+03	5.774e-01		

Pooled Expected Values:  $E(Y|X)$

mean	sd	2.5%	97.5%
5018.9	2281.7	730.4	10046.4

Pooled Average Treatment Effect:  $Y - EV$

mean	sd	2.5%	97.5%
1330.3	568.7	236.7	2439.6

The estimated average treatment effect on the treated is thus \$1,355, with a 95% interval of (\$243, \$2,493).

2. Estimating the average treatment effects on both the treated and the control groups. We use the same `matchit()` output as in the first example above.

```
> z.out2 <- zelig(re78 ~ age + educ + black + hispan + nodegree +
+   married + re74 + re75 + distance, data = match.data(m.out1,
+   "control"), model = "ls")
> x.out2 <- setx(z.out2, data = match.data(m.out1, "control"),
+   fn = NULL, cond = TRUE)
> s.out2 <- sim(z.out2, x = x.out2)
> ate.all <- c(s.out1$qi$ate.ev, -s.out2$qi$ate.ev)
> mean(ate.all)
```

```
[1] 653
```

```
> sd(ate.all)
```

```
[1] 845.3
```

```
> quantile(ate.all, c(0.025, 0.975))
```

```
 2.5% 97.5%
-727.7 2215.3
```

3. Subclassification: In this case, the average treatment effect estimates are obtained for each subclass separately as well as for the overall sample. Estimating the treatment effects separately for each subclass, and then aggregating across subclasses, can significantly increase the robustness of the ultimate results since the parametric analysis within each subclass requires only local rather than global assumptions.

```
> m.out2 <- matchit(treat ~ age + educ + black + hispan + nodegree +
+   married + re74 + re75, data = lalonde, method = "subclass",
+   subclass = 4)
> z.out3 <- zelig(re78 ~ re74 + re75 + distance, data = match.data(m.out2,
+   "control"), model = "ls", by = "subclass")
> x.out3 <- setx(z.out3, data = match.data(m.out2, "treat"), fn = NULL,
+   cond = TRUE)
> s.out3 <- sim(z.out3, x = x.out3, num = 100)
> summary(s.out3)
```

```
Model: ls
```

```
Number of simulations: 25
```

```
Mean Values of Observed Data (n = 46)
```

(Intercept)	re74	re75	distance
1.0000	5430.5389	2929.0394	0.2392

```
Pooled Expected Values: E(Y|X)
```

mean	sd	2.5%	97.5%
4870	5170	-3657	16523

```

Pooled Average Treatment Effect: Y - EV
  mean      sd   2.5%  97.5%
1480.4 1354.3 -737.1 4396.5

```

```
> summary(s.out3, subset = 1)
```

Results for 1

```

Model: ls
Number of simulations: 25

Mean Values of Observed Data (n = 46)
(Intercept)      re74      re75  distance
      1.0000    5430.5389    2929.0394      0.2392

```

```

Pooled Expected Values: E(Y|X)
  mean      sd   2.5%  97.5%
6862   3930   2935 17574

```

```

Pooled Average Treatment Effect: Y - EV
  mean      sd   2.5%  97.5%
330.2   732.8 -973.6 1491.4

```

```
> summary(s.out3, subset = 2)
```

Results for 1

```

Model: ls
Number of simulations: 25

Mean Values of Observed Data (n = 45)
(Intercept)      re74      re75  distance
      1.0000    1777.4221    972.3441      0.6039

```

```

Pooled Expected Values: E(Y|X)
  mean      sd   2.5%  97.5%
4318.21 2437.01  -99.49 10061.82

```

```

Pooled Average Treatment Effect: Y - EV
  mean      sd   2.5%  97.5%
2168.1 1083.5  175.6 4099.1

```

```
> summary(s.out3, subset = 3)
```

Results for 1



```

Model: ls
Number of simulations: 25

Mean Values of Observed Data (n = 47)
(Intercept)      re74      re75      distance
      1.0000      939.9688      1217.4546      0.6934

Pooled Expected Values: E(Y|X)
      mean      sd      2.5%      97.5%
4095.9  5094.3   308.2 11508.9

Pooled Average Treatment Effect: Y - EV
      mean      sd      2.5%      97.5%
1797.5   794.2   425.0 3348.9

```

## 4 Reference Manual

### 4.1 Inputs

The main command, `matchit()`, can be used to implements any of the matching procedures:

```
m.out <- matchit(formula, data, method = "nearest", distance = "logit",
                 distance.options=list(), discard = "none", reestimate = FALSE, ...)
```

The command takes some inputs that are common to all matching procedures and other inputs specific to particular procedures. The outputs are standard across all procedures. We organize the reference manual in these categories.

#### 4.1.1 All Matching Methods

1. **formula** takes the usual syntax of R formula, `treat ~ x1 + x2`, where **treat** is a binary treatment indicator and **x1** and **x2** are the pre-treatment covariates. Both the treatment indicator and pre-treatment covariates must be contained in the same data frame, which is specified as **data** (see below). All of the usual R syntax for formulas work here. For example, `x1:x2` represents the first order interaction term between **x1** and **x2**, and `I(x1 ^ 2)` represents the square term of **x1**. See `help(formula)` for details.
2. **data** specifies the data frame containing the variables called in **formula**. You may find it helpful for the diagnostics to specify observation names in the data frame (see Section 6.3).
3. **method** specifies a matching method. Currently, **exact** (exact matching), **full** (full matching), **nearest** (nearest neighbor matching), **optimal** (optimal matching), and **subclass** (subclassification) are available. The default is **nearest**. Note that within each of these matching methods, **MATCHIT** offers a variety of options. See Section 3 for more details.
4. **distance** specifies the method used to estimate the distance measure. The default is logistic regression, **logit**. Before using any of these techniques, it is best to understand the theoretical groundings of these techniques and to evaluate the results. Most of these methods (such as logistic or probit regression) are estimating the propensity score, defined as the probability of receiving treatment, conditional on the covariates (Rosenbaum and Rubin (1983)). The distance measures used are the predicted probabilities from the model (the propensity scores). Currently, the following methods are available:

- (a) `mahalanobis` computes the Mahalanobis distance measure (`mahalanobis()` in the `stats` package).
  - (b) binomial generalized linear models with various links (`glm()` in the `stats` package); `logit` (logistic link), `linear.logit` (logistic link with linear propensity score)<sup>2</sup>, `probit` (probit link), `linear.probit` (probit link with linear propensity score), `cloglog` (complementary log-log link), `linear.cloglog` (complementary log-log link with linear propensity score), `log` (log link), `linear.log` (log link with linear propensity score), `cauchit` (Cauchy CDF link), `linear.cauchit` (Cauchy CDF link with linear propensity score).
  - (c) binomial generalized additive model with various links (`gam()` in the `mgcv` package); `GAMlogit` (logistic link), `GAMlinear.logit` (logistic link with linear propensity score), `probit` (probit link), `GAMlinear.probit` (probit link with linear propensity score), `GAMcloglog` (complementary log-log link), `GAMlinear.cloglog` (complementary log-log link with linear propensity score), `GAMlog` (log link), `GAMlinear.log` (log link with linear propensity score), `GAMcauchit` (Cauchy CDF link), `GAMlinear.cauchit` (Cauchy CDF link with linear propensity score). Hastie and Tibshirani (1990); Beck and Jackman (1998) and many others discuss the generalized additive models.
  - (d) `nnet`, neural network model (`nnet()` in the `nnet` package). Beck, King and Zeng (2000); Bishop (1995); King and Zeng (2002); White (1992); Zeng (1999) among many others discuss neural networks.
  - (e) `rpart`, classification trees (`rpart()` in the `rpart` package). Breiman et al. (1984); Ruger et al. (2003) and many others discuss classification trees.
5. `distance.options` specifies the optional arguments that are passed to the model for estimating the distance measure. The input to this argument should be a list. For example, if the distance measure is estimated with a logistic regression, users can increase the maximum IWLS iterations by `distance.options = list(maxit = 5000)`.
6. `discard` specifies whether to discard units that fall outside some measure of support of the distance score before matching, and not allow them to be used at all in the matching procedure. Note that discarding units may change the quantity of interest being estimated.
- **none** (default) discards no units before matching. Use this option when the units to be matched are substantially similar, such as in the case of matching treatment and control units from a field experiment that was close to (but not fully) randomized (e.g., Imai 2005), when caliper matching will restrict the donor pool, or when you do not wish to change the quantity of interest and the parametric methods to be used post-matching can be trusted to extrapolate.
  - **both** discards all units (treated and control) that are outside the support of the distance measure. Use this option when the units to be matched are substantially different (when there is a large degree of non-overlapping support on the distance score), such as in the case of measuring the effect of democracy on economic growth.
  - **control** discards only control units outside the support of the distance measure of the treated units. Use this option when the average treatment effect on the treated is of most interest and when unwilling to discard non-overlapping treatment units (which would change the quantity of interest), such as possibly in the case of the effect of job training on those individuals that actually participated in a job evaluation program or a drug study where interest is in all patients treated with the drug.
  - **treat** discards only treated units outside the support of the distance measure of the control units. Use this option when the average treatment effect on the control units is of most interest and when unwilling to discard control units.
  - **convex.hull** discards control units not within the convex hull of the treated units using the method developed in (King and Zeng, 2004).

---

<sup>2</sup>The linear propensity scores are obtained by transforming back onto a linear scale

7. **reestimate** specifies whether the model for distance measure should be re-estimated after units are discarded. The input must be a logical value. The default is **FALSE**. Re-estimation may be desirable for efficiency reasons, especially if many units were discarded and so the post-discard samples are quite different from the original samples.
8. **verbose** specifies whether or not to print out comments indicating the status of the matching. The input must be a logical value. The default is **FALSE**.

#### 4.1.2 Exact Matching

Exact matching is implemented in **MATCHIT** using **method = "exact"**. Exact matching will be done on all covariates included on the right-hand side of the **formula** specified in the **MATCHIT** call. No **distance** option is used for exact matching, and there are no additional options for exact matching.

#### 4.1.3 Subclassification

1. **subclass** is either (1) a scalar, specifying the number of subclasses, or (2) a vector of probabilities bounded between 0 and 1, to create quantiles of the distance measure using the units in the group specified by **sub.by**. The default is **subclass = 6**.
2. **sub.by** specifies by what criteria to subclassify: **"treat"** indicates by the number of treatment units (default), **"control"** indicates by the number of control units, and **"all"** indicates by the total number of units.

#### 4.1.4 Nearest Neighbor Matching

1. **m.order** specifies the order in which to match treatment units with control units:
  - **"largest"** indicates matching from the largest value of the distance measure to the smallest. This is the default.
  - **"smallest"** indicates matching from the smallest value of the distance measure to the largest.
  - **"random"** indicates matching in random order.
2. **replace** specifies whether each control unit can be matched to more than one treated unit. For matching “with replacement”, **replace = TRUE**. If each control is to be used as a match at most once (“without replacement”), **replace = FALSE**. The default is **FALSE**.
3. **ratio** specifies the number of control units to match to each treated unit, default=1. If matching is done without replacement and there are fewer control units than ratio times the number of eligible treated units (i.e., there are not enough control units for the specified method), then the higher ratios will have NA in place of the matching unit number in **match.matrix**.
4. **exact** specifies variables on which to perform exact matching within the nearest neighbor matching. If **exact** is specified, only matches that exactly match on the covariates in **exact** will be allowed. Within the matches that match on the variables in **exact**, the match with the closest distance measure will be chosen. **exact** should be entered as a vector of variable names (**exact = c("X1", "X2")**) that are names of variables in **data**.
5. **caliper** specifies the number of standard deviations of the distance measure within which to draw control units, default=0. If a caliper is specified, the matches are restricted to being within the caliper and a control unit within the caliper for a treated unit is randomly selected as the match for that treated unit. If **caliper != 0**, there are two additional options:
  - **calclosest** specifies whether to take the nearest available match if no matches are available within the **caliper**. The default is **FALSE**.

- **mahvars** specifies variables on which to perform Mahalanobis-metric matching within each caliper (default=NULL). Variables should be entered as a vector of variable names (**mahvars=c("X1", "X2")**) that are names of variables in **data**. If **mahvars** is specified without **caliper**, the caliper is set to 0.25.
6. **subclass** and **sub.by**. See Section 3.2.2 for more details on these options. If a **subclass** is specified within **method = "nearest"**, the matched units will be placed into subclasses after the nearest neighbor matching is completed.

#### 4.1.5 Full Matching

1. ... represents additional inputs that can be passed to the **fullmatch()** function in the **optmatch** package. See **help(fullmatch)** for details.

#### 4.1.6 Optimal Matching

The available options are listed below.

1. **ratio** specifies the number of control units to be matched to each treatment unit, the default is 1.
2. ... represents additional inputs that can be passed to the **fullmatch()** function in the **optmatch** package. See **help(fullmatch)** for details.

### 4.2 Outputs

#### 4.2.1 Output Object Contents

Regardless of the type of matching performed, the **matchit** output object contains the following elements:

1. **call** provides the original **matchit()** call.
2. **formula** shows the formula used to specify the model for estimating the distance measure.
3. **model** stores the output of the model used to estimate the distance measure. **summary(m.out\$model)** will give the summary of the model where **m.out** is the output object from **matchit()**.
4. **match.matrix** is an  $n_1$  by **ratio** matrix where:
  - the row names, which can be obtained through **row.names(match.matrix)**, represent the names of the treatment units, which come from the data frame specified in **data** (to learn how to do this, see Section 6.3).
  - each column stores the name(s) of the control unit(s) matched to the treatment unit of that row. For example, when the **ratio** input for nearest neighbor or optimal matching is specified as 3, the three columns of **match.matrix** represent the three control units matched to one treatment unit).
  - NA indicates that the treatment unit was not matched.
5. **discarded** is a vector of length  $n$  that displays whether the units were ineligible for matching due to common support restrictions. It equals **TRUE** if unit  $i$  was discarded, and it is set to **FALSE** otherwise.
6. **distance** is a vector of length  $n$  with the estimated distance measure for each unit.
7. **weights** is a vector of length  $n$  that provides the weights assigned to each unit in the matching process. Unmatched units have weights equal to 0. Matched treated units have weight 1. Each matched control unit has weight proportional to the number of treatment units to which it was matched, and the sum of the control weights is equal to the number of uniquely matched control units. See Section 6.2 for more details.

8. **subclass** contains the subclass index in an ordinal scale from 1 to the total number of subclasses as specified in **subclass** (or the total number of subclasses from full or exact matching). Unmatched units have NA.
9. **q.cut** gives the subclass cut-points that classify the distance measure.
10. **treat** stores the treatment indicator from **data** (the left-hand side of **formula**).
11. **X** stores the covariates used for estimating the distance measure (the right-hand side of **formula**). When applicable, **X** is augmented by covariates contained in **mahvars** and **exact**.

#### 4.2.2 summary()

The **summary** command returns more information about the MATCHIT model. Optional inputs are:

1. **interactions**, which is an option to calculate summary statistics in **sum.all** and **sum.matched** for all covariates, their squares, and two-way interactions when **interactions=TRUE** and only the covariates themselves when **interactions=FALSE** (default).
2. **addlvariables**, which may contain additional variables on which to calculate the diagnostic statistics (in addition to the variables included in the matching procedure). By default, **addlvariables=NULL**. **addlvariables** must be specified as a data frame, with the same number of units and units in the same order as in the data set sent to MATCHIT.

The **summary** call returns, when applicable:

1. The original assignment model call.
2. **sum.all** is a data frame that contains variable names and interactions down the row names, and summary statistics on *all observations* in each of the columns. The columns in **sum.all** contain<sup>3</sup>:
  - means of all covariates  $X$  for treated and control units, where **Means Treated** =  $\mu_{X|T=1} = \frac{1}{n_1} \sum_{T=1} X_i$  and **Means Control** =  $\mu_{X|T=0} = \frac{1}{n_0} \sum_{T=0} X_i$ ,
  - pooled standard deviations for all covariates  $X$ , where  $SD = s_X = \sqrt{\frac{1}{n-1} \sum_i (X_i - \bar{X})^2}$ .
  - summary statistics from a Q-Q plot, which compares treated and control covariate distributions, where **QQ Med**, **QQ Mean**, and **QQ Max** indicate the median, mean, and maximum orthogonal deviations from the 45 degree line of a Q-Q plot.
  - standardized bias statistics,

$$\text{Std.Bias} = \frac{\mu_{X|T=1} - \mu_{X|T=0}}{s_{x|T=1}}, \quad \text{where} \quad s_{x|T=1} = \sqrt{\frac{\sum_{i \in \{i: T_i=1\}} X_i - \mu_{X|T=1}}{n_1 - 1}}.$$

3. **sum.matched** is a data frame which contains variable names down the row names, and summary statistics on only the *matched observations* in each of the columns. Specifically, the columns in **sum.matched** contain the following elements<sup>4</sup>:
  - weighted means for matched treatment units of all covariates  $X$  and their interactions, where **Means Treated** =  $\mu_{wX|T=1} = \frac{1}{n_1} \sum_{T=1} w_i X_i$  and **Means Control** =  $\mu_{wX|T=0} = \frac{1}{n_0} \sum_{T=0} w_i X_i$ ,
  - weighted standard deviations for all covariates  $X$  and their interactions of matched units, where  $SD = s_{wX} = \sqrt{\frac{1}{n} \sum_i (w_i X_i - \bar{X}^*)^2}$ , where  $\bar{X}^*$  is the weighted mean of  $X$ .

<sup>3</sup>The output for full matching is slightly different from that described here; see Section 3.2.4 for details.

<sup>4</sup>The values output for full matching are slightly different from that described here; see Section 3.2.4 for details

- standardized bias statistics  $\text{Std. Bias} = \frac{\mu_{wX|T=1} - \mu_{wX|T=0}}{s_{x|T=1}}$ , and

where  $w$  represents the vector of **weights**.

4. **reduction** shows the percent bias reduction achieved in each of the balance measures in **sum.all** and **sum.matched**, defined as  $100(|a| - |b|)/|a|$ , where  $a$  was the value of the balance measure before matching and  $b$  is the value of the balance measure after matching.
5. **nn** gives the sample sizes in the full and matched samples and the number of discarded units, by treatment and control.
6. **q.table** is an array that contains the same information as **sum.matched** by subclass.
7. **qn** gives the sample sizes in the full and matched samples and the number of discarded units, by subclass and by treatment and control.
8. **match.matrix** from the **matchit** output.

#### 4.2.3 plot()

The **plot** command allows you to check the distributions of covariates in the assignment model, squares, and interactions, and within each subclasses if specified. The graphs present:

1. Q-Q plots of each covariate to check balance of marginal distributions (**type="QQ"** (default)). This graph plots covariate values that fall in (approximately) the same quantile of treated and control distributions. Control unit quantile values are plotted on the x-axis, and treated unit quantile values are plotted on the y-axis. If values fall below the 45 degree line, control units generally take lower values of the covariate. Data points that fall exactly on the 45 degree line indicate that the marginal distributions are identical. Discrete covariates that take 5 or fewer values are jittered for visibility. This may be changed by setting the option **discrete.cutoff**.
2. Jitter plots of the propensity score for treated and control units (**type="jitter"**).

#### 4.2.4 match.data()

To extract the matched data set for subsequent analyses from the output object (see Section 3.4), we provide the function **match.data()**. This is used as follows:

```
m.data <- match.data(object, group = "all", distance = "distance", weights = "weights",
                     subclass = "subclass")
```

The output of the function **match.data()** is the original data frame where additional information about matching (i.e., distance measure as well as resulting weights and subclasses) is added, restricted to units that were matched.

**Inputs** **match.data()** takes the following inputs:

1. **object** is the output object from **matchit()**. This is a required input.
2. **group** specifies for which matched group the user wants to extract the data. Available options are **"all"** (all matched units), **"treat"** (matched units in the treatment group), and **"control"** (matched units in the control group). The default is **"all"**.
3. **distance** specifies the variable name used to store the distance measure. The default is **"distance"**.
4. **weights** specifies the variable name used to store the resulting weights from matching. The default is **"weights"**. See Section 6.2 for more details on the weights.
5. **subclass** specifies the variable name used to store the subclass indicator. The default is **"subclass"**.

**Examples** Here, we present examples for using `match.data()`. Users can run these commands by typing `demo(match.data)` at the R prompt.

```
## load the Lalonde data
data(lalonde)

## perform nearest neighbor matching
m.out1 <- matchit(treat ~ re74 + re75 + age + educ, data = lalonde, method = "nearest",
                 distance = "logit")

## obtain matched data
m.data1 <- match.data(m.out1)

## summarize the resulting matched data
summary(m.data1)

## obtain matched data for the treatment group
m.data2 <- match.data(m.out1, group = "treat")
summary(m.data2)

## obtain matched data for the control group
m.data3 <- match.data(m.out1, group = "control")
summary(m.data3)

## run a subclassification method
m.out2 <- matchit(treat ~ re74 + re75 + age + educ, data=lalonde, method = "subclass")

## specify different names
m.data4 <- match.data(m.out2, subclass = "block", weights = "w",
                    distance = "pscore")

## print the variable names of the matched data
names(m.data4)
```

## 5 What's New?

- **2.0-1** (??, 2005): Stable release for R 2.1. Major revisions.
- **1.0-2** (August 10, 2005): Stable release for R 2.1. Minor bug fixes (Thanks to Bart Bonikowski).
- **1.0-1** (January 3, 2005): Stable release for R 2.0. The first official version of MATCHIT

## 6 Frequently Asked Questions

### 6.1 Can I use a Difference-in-Difference Estimator for Matched Data?

A difference-in-differences (DID) analysis can be easily conducted with MATCHIT. If we were interested in the DID matching estimate in the Lalonde data, we could simply include `re75` as a covariate in the preprocessing step. Then the analysis can be performed on the change in income from 1975 to 1978: `re78-re75`. Time-varying covariates (of which none exist in the Lalonde data) should of course also be differenced for the DID estimator.

## 6.2 How Exactly are the Weights Created?

Each type of matching method can be thought of as creating groups of units with at least one treated unit and at least one control unit in each. In exact matching, subclassification, or full matching, these groups are the subclasses formed, and the number of treated and control units will vary quite a bit across subclasses. In nearest neighbor or optimal matching, the groups are the pairs (or sets) of treated and control units matched. In 1:1 nearest neighbor matching there will be one treated unit and one control unit in each group. In 2:1 nearest neighbor matching there will be one treated unit and two control units in each group. Unmatched units receive a weight of 0. All matched treated units receive a weight of 1.

The weights for matched control units are formed as follows:

1. Within each group, each control unit is given a preliminary weight of  $n_{ti}/n_{ci}$ , where  $n_{ti}$  and  $n_{ci}$  are the number of treated and control units in group  $i$ , respectively.
2. If matching is done with replacement, each control unit's weight is added up across the groups in which it was matched.
3. The control group weights are scaled to sum to the number of uniquely matched control units.

With subclassification, when the analysis is done separately within each subclass and then aggregated up across the subclasses, these weights will generally not be used, but they may be used for full matching or nearest neighbor matching if the number of control units matched to each treated unit varies.

## 6.3 How Do I Create Observation Names?

Since the diagnostics often make use of the observation names of the data frame, you may find it helpful to specify observation names for the data input. Use the `row.names` command to achieve this. For example, to assign the names "Dan", "Kosuke", "Liz" and "Gary" to a data frame with the first four observations in the Lalonde data, type:

```
> test <- lalonde[1:4,] #taking a lalonde subset
> row.names(test) <- c("Dan","Kosuke","Liz","Gary") #assigning row names
> print(test)
```

	treat	age	educ	black	hispan	married	nodegree	re74	re75	re78
Dan	1	37	11	1	0	1	1	0	0	9930.046
Kosuke	1	22	9	0	1	0	1	0	0	3595.894
Liz	1	30	12	1	0	0	0	0	0	24909.450
Gary	1	27	11	1	0	0	1	0	0	7506.146

## 6.4 How Do I Ensure Replicability As MatchIt Versions Develop?

As the literature on matching techniques is rapidly evolving, MATCHIT will strive to incorporate new developments. MATCHIT is thereby an evolving program. Users may be concerned that analysis written in a particular version may not be compatible with newer versions of the program. The primary way to ensure that replication archives remain valid is to record the version of MATCHIT that was used in the analysis. Our website maintains binaries of all public release versions, so that researchers can replicate results exactly with the appropriate version (for Unix-based platforms, see <http://gking.harvard.edu/src/contrib/>; for windows, see <http://gking.harvard.edu/bin/windows/contrib/>).

In addition, users may find it helpful to install packages with version control, using the `installWithVers` command with `install.packages`. So for example, in the windows R console, users may download the appropriate version from our website and install the package with version control by:

```
install.packages(choose.files('',filters=Filters[c('zip','All'),]),
  .libPaths()[1],installWithVers=T,CRAN=NULL)
```



R CMD INSTALL similarly permits users to specify this version using the `-with-package-versions` option. After having specified version control, different versions of the program may be called as necessary. Similar advice may also be appropriate for version control for R more generally.

## 6.5 What Do I Do about Missing Data?

MATCHIT requires complete data sets, with no missing values (other than potential outcomes of course). If there are missing values in the data set, imputation techniques should be used first to fill in (“impute”) the missing values (both covariates and outcomes), or the analysis should be done using only complete cases (which we do not in general recommend). For imputation software, see Amelia at (<http://gking.harvard.edu/stats.shtml>) or other programs at <http://www.multiple-imputation.com>. For more information on missing data and imputation methods, see King et al. (2001).

## 6.6 Why Preprocessing?

The purpose of matching is to approximate an experimental template, where the matching procedure approximates random assignment of treatment in order to balance covariates between treatment and control groups. Separation of the estimation procedure into two steps simulates the research design of an experiment, where no information on outcomes is known at the point of experimental design and randomization. Much like an experimenter cannot easily rerun an experiment if the outcome was not satisfactory, the separation of the balancing process in MATCHIT from the analysis process afterwards helps keep clear the goal of balancing control and treatment groups and makes it less likely that the user will inadvertently cook the books in his or her favor.

## References

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