4 Matching

Stratification

We are going back to the language of the potential outcomes framework and assume that we are studying the causal effect of a binary variable D on an outcome variable Y. We do not wish to assume independence ($(Y^1, Y^0) \perp D$). However, we are willing to assume *conditional independence*, where conditioning is with respect to a set of observable variables S:

$$(Y^1, Y^0) \perp D \mid S$$

In other words, conditional on S, the potential outcomes do not depend on treatment exposure.

We are also going to assume *common support*

$$0 < \mathbb{P}(D = 1 \mid S) < 1.$$

This assumption rules out cases when for some values of S no one can be in the treatment state or no one is in the control state. The exact purpose of this assumption will be clarified once get to examples.

These assumptions imply that

$$\begin{aligned} \mathbb{E}[Y^0 \mid D = 1, S] &= \mathbb{E}[Y^0 \mid D = 0, S] \\ \mathbb{E}[Y^1 \mid D = 1, S] &= \mathbb{E}[Y^1 \mid D = 0, S], \end{aligned}$$

i.e., the potential outcomes in the treatment and control states do not depend on D once we condition on S.

> **Note**
>
> These assumptions *do not* imply that, e.g., $\mathbb{E}[Y^0 \mid D = 1, S] = \mathbb{E}[Y^1 \mid D = 1, S]$.

To simplify the exposition, assume that variables in S are discrete (or can be discretized) such that we can stratify our data. Our assumptions imply that knowledge and observation of S allow for a "perfect stratification" of the data. "Perfect" here means that individuals within groups defined by values of the variables in S are entirely indistinguishable from each other in all ways except for (1) observed treatment status and (2) differences in the potential outcomes that are independent of treatment status. Even though the naive treatment effect will be biased relative to the average treatment effect, the bias will disappear after conditioning on S. In this case we say that *treatment assignment is ignorable* or that *treatment selection is on observables*.

Conditioning on S allows us to derive the following identities:

$$
\begin{aligned}
NTE(S) &= \mathbb{E}[Y^1 \mid D=1, S] - \mathbb{E}[Y^0 \mid D=0, S] \\
ATT(S) &= \mathbb{E}[\delta \mid D=1, S] \\
&= \mathbb{E}[Y^1 \mid D=1, S] - \mathbb{E}[Y^0 \mid D=1, S] \\
&= \mathbb{E}[Y^1 \mid D=1, S] - \mathbb{E}[Y^0 \mid D=0, S] \\
ATU(S) &= \mathbb{E}[\delta \mid D=0, S] \\
&= \mathbb{E}[Y^1 \mid D=0, S] - \mathbb{E}[Y^0 \mid D=0, S] \\
&= \mathbb{E}[Y^1 \mid D=1, S] - \mathbb{E}[Y^0 \mid D=0, S] \\
ATE(S) &= \mathbb{E}[\delta \mid S] \\
&= \mathbb{P}(D=1)ATT(S) + (1-\mathbb{P}(D=1))ATU(S) \\
&= \mathbb{E}[Y^1 \mid D=1, S] - \mathbb{E}[Y^0 \mid D=0, S].
\end{aligned}
$$

Conditional on S, all four treatment effects are identical. In particular, the NTE within each stratum of S is unbiased relative to ATT, ATU, and ATE.

Note

This does not mean, however, that the unconditional $NTE = \mathbb{E}[Y^1 \mid D=1] - \mathbb{E}[Y^1 \mid D=0]$ is unbiased.

How do we get from conditional effects to unconditional ones? By appropriately weighting the conditional effects.

$$
\begin{aligned}
\mathbb{E}[\delta] &= \mathbb{E}_S[\mathbb{E}[\delta \mid S]] \\
\mathbb{E}[\delta \mid D=1] &= \mathbb{E}_{S|D=1}[\mathbb{E}[\delta \mid D=1, S]] \\
\mathbb{E}[\delta \mid D=0] &= \mathbb{E}_{S|D=0}[\mathbb{E}[\delta \mid D=0, S]].
\end{aligned}
$$

Math time

Let's take a closer look at how the conditional independence assumptions allows us to compute those expectations. For example, for the ATT we have (we assume that S defines discrete strata (a combination of values of the observable variables), indexed by $1, 2, \dots \bar{S}$.)

$$
\begin{aligned}
ATT &= \mathbb{E}[Y^1 \mid D=1] - \mathbb{E}[Y^0 \mid D=1] \\
&= \sum_{s=1}^{\bar{S}} \mathbb{E}[Y^1 \mid D=1, S=s]\mathbb{P}(S=s \mid D=1) \\
&- \sum_{s=1}^{\bar{S}} \mathbb{E}[Y^0 \mid D=1, S=s]\mathbb{P}(S=s \mid D=1).
\end{aligned}
$$

The conditional independence assumption allows us to substitute counterfactual terms $\mathbb{E}[Y^0 \mid D=1, S=s]$ with observed terms $\mathbb{E}[Y^0 \mid D=0, S=s]$. This substitution yields

$$
\begin{aligned}
ATT &= \sum_{s=1}^{\bar{S}} \mathbb{E}[Y^1 \mid D=1, S=s]\mathbb{P}(S=s \mid D=1) \\
&\quad - \sum_{s=1}^{\bar{S}} \mathbb{E}[Y^0 \mid D=0, S=s]\mathbb{P}(S=s \mid D=1) \\
&= \sum_{s=1}^{\bar{S}} \big(\mathbb{E}[Y^1 \mid D=1, S=s] - \mathbb{E}[Y^0 \mid D=0, S=s]\big)\mathbb{P}(S=s \mid D=1) \\
&= \sum_{s=1}^{\bar{S}} NTE(S=s)\mathbb{P}(S=s \mid D=1).
\end{aligned}
$$

Thus, the ATT is simply a weighted average of the NTE in each stratum defined by S where the weights are given by the conditional distribution of S given $D=1$.

Notice the term $\sum_{s=1}^{\bar{S}} \mathbb{E}[Y^0 \mid D=0, S=s]\mathbb{P}(S=s \mid D=1)$. Here we are taking the expectation not with respect to the actual distribution $\mathbb{P}(S=s \mid D=0)$, but with respect to the distribution $\mathbb{P}(S=s \mid D=1)$. This ensures that the conditional distribution of S given $D=1$ is identical between the treatment and control units. You can think of it as weighting the control units in a way that achieves the covariate balance between the treatment and control groups. This is the main purpose of *matching*. We are weighting the control units to look like the treatment units in terms of S.

✓ **Math time**

We can derive the ATU similarly

$$
\begin{aligned}
ATU &= \mathbb{E}[Y^1 \mid D=0] - \mathbb{E}[Y^0 \mid D=0] \\
&= \sum_{s=1}^{\bar{S}} \mathbb{E}[Y^1 \mid D=0, S=s]\mathbb{P}(S=s \mid D=0) \\
&\quad - \sum_{s=1}^{\bar{S}} \mathbb{E}[Y^0 \mid D=0, S=s]\mathbb{P}(S=s \mid D=0) \\
&= \sum_{s=1}^{\bar{S}} \mathbb{E}[Y^1 \mid D=1, S=s]\mathbb{P}(S=s \mid D=0) \\
&\quad - \sum_{s=1}^{\bar{S}} \mathbb{E}[Y^0 \mid D=0, S=s]\mathbb{P}(S=s \mid D=0) \\
&= \sum_{s=1}^{\bar{S}} \big(\mathbb{E}[Y^1 \mid D=1, S=s] - \mathbb{E}[Y^0 \mid D=0, S=s]\big)\mathbb{P}(S=s \mid D=0) \\
&= \sum_{s=1}^{\bar{S}} NTE(S=s)\mathbb{P}(S=s \mid D=0).
\end{aligned}
$$

The ATU therefore is simply the weighted average of the NTE in each stratum defined by S where the weights are given by the conditional distribution of S given $D=0$. Notice

again the term $\sum_{s=1}^{\bar{S}} \mathbb{E}[Y^1 \mid D=1, S=s]\mathbb{P}(S=s \mid D=0)$. We are taking the expectation not with respect to the actual distribution of $\mathbb{P}(S=s \mid D=1)$ but with respect to the distribution $\mathbb{P}(S=s \mid D=0)$, thus ensuring the covariate balance between the treatment and control units. However, this time we are weighting the treatment units to look like the control units in terms of S.

The ATE can be simply found as

$$ATE = \sum_{s=1}^{\bar{S}} \mathbb{E}[\delta \mid S]\mathbb{P}(S=s) = \sum_{s=1}^{\bar{S}} NTE(S=s)\mathbb{P}(S=s).$$

✓ **Math time: Human capital**

Suppose we are interested in the causal effect of going to college (D) on income (Y). In the raw data, this effect is confounded by ability ($S \in \{1,2,3\}$) that jointly causes whether someone attends college or not and income. Suppose that the distribution of ability in the population is

S	$\mathbb{P}(S)$
1	0.44
2	0.24
3	0.32

Thus, high ability is less prevalent than low ability.

The conditional distribution of D given S is

	$S=1$	$S=2$	$S=3$
$\mathbb{P}(D=0 \mid S)$	9/11	1/2	3/8
$\mathbb{P}(D=1 \mid S)$	2/11	1/2	5/8

This distribution implies that for the low value of ability an individual is unlikely to go to college, for medium ability the chances are equal, and for high ability an individual is likely to go to college.

We can use these two tables to derive the joint distribution $\mathbb{P}(D,S)$:

$$\mathbb{P}(D=d, S=s) = \mathbb{P}(D=d \mid S=s)\mathbb{P}(S=s)$$

	$D=0$	$D=1$	$\mathbb{P}(S)$
$S=1$	0.36	0.08	0.44
$S=2$	0.12	0.12	0.24
$S=3$	0.12	0.2	0.32
$\mathbb{P}(D)$	0.6	0.4	1

Finally, let's derive the conditional distribution of S given D using the Bayes' rule:

$$\mathbb{P}(S = s \mid D = d) = \frac{\mathbb{P}(S = s, D = d)}{\mathbb{P}(D = d)}$$

	$D = 0$	$D = 1$
$\mathbb{P}(S = 1 \mid D)$	0.6	0.2
$\mathbb{P}(S = 2 \mid D)$	0.2	0.3
$\mathbb{P}(S = 3 \mid D)$	0.2	0.5

The potential outcomes for income are given by the following table. We are assuming conditional independence.

	$\mathbb{E}[Y^0 \mid D = 0, S]$	$\mathbb{E}[Y^1 \mid D = 1, S]$	$\mathbb{E}[\delta \mid S]$
$S = 1$	2	4	2
$S = 2$	6	8	2
$S = 3$	10	14	4

Thus, income increases with ability and college.

Now we can easily compute all the treatment effects.

$$ATT = \sum_{s=1}^{\bar{S}} \mathbb{E}[\delta \mid S]\mathbb{P}(S = s \mid D = 1) = 2 \times 0.2 + 2 \times 0.3 + 4 \times 0.5 = 3$$

$$ATU = \sum_{s=1}^{\bar{S}} \mathbb{E}[\delta \mid S]\mathbb{P}(S = s \mid D = 0) = 2 \times 0.6 + 2 \times 0.2 + 4 \times 0.2 = 2.4$$

$$ATE = \sum_{s=1}^{\bar{S}} \mathbb{E}[\delta \mid S]\mathbb{P}(S = s) = 2 \times 0.44 + 2 \times 0.24 + 4 \times 0.32 = 2.64.$$

One can also compute the ATE as

$$ATE = \mathbb{P}(D = 1)ATT + \mathbb{P}(D = 0)ATU = 0.4 \times 3 + 0.6 \times 2.4 = 2.64$$

Homework

Compute the unconditional NTE (is it biased?) and do the NTE decomposition. Hint: fill in the table of potential outcomes, like we did before

D	$\mathbb{E}[Y^1 \mid D]$	$\mathbb{E}[Y^0 \mid D]$	$\mathbb{E}[\delta \mid D]$	$\mathbb{P}(D)$
1	...	...	...	...
0	...	...	...	...

Then, e.g., you would compute $\mathbb{E}[Y^0 \mid D = 0]$ as

$$\mathbb{E}[Y^0 \mid D=0] = \sum_s \mathbb{E}[Y^0 \mid D=0, S=s]\mathbb{P}(S=s \mid D=0)$$

Matching

The stratification exercise that we have done illustrates what matching achieves but it does not show how matching, as an algorithm, actually works. There are two equivalent ways to implements matching: by selecting a matched sample or by weighting. We will first discuss selecting matched samples and then show that it can be thought of as a special case of weighting.

Exact Matching

For the treatment effect for the treated, exact matching constructs the counterfactual for each treatment case using the control cases with *identical* values on the variables in S. If there are several matches, one can average them using weights equal to $1/k$ for matched control cases, where k is the number of matches selected for each target treatment case. Another possibility is to randomly choose one match from among possible exact matches.

One can then estimate the ATT as follows

$$\widehat{ATT} = \frac{1}{n^1} \sum_{i \in I} \left(y_i - y_{j(i)} \right),$$

where n^1 is the number of treatment units, I is the set of indices of treatment units, y_i is the observed outcome of the treatment unit i, and $y_{j(i)}$ is the observed outcome of the control unit j that is matched to i.

> **Note**
>
> In case there are several matches, replace $y_j(i)$ with the average $\frac{1}{||J(i)||} \sum_{j \in J(i)} y_j$, where $J(i)$ is the set of indices of control units that are matched to the treatment unit i .

For the treatment effect for the untreated, this works exactly the same, with the only difference that we are constructing the counterfactuals for each control case using the treatment cases with identical values of S.

$$\widehat{ATU} = \frac{1}{n^0} \sum_{j \in J} \left(y_{i(j)} - y_j \right),$$

where n^0 is the number of control units, J is the set of indices of control units, y_j is the observed outcome of the control unit j, and $y_{i(j)}$ is the observed outcome of the treatment unit i that is matched to j.

The ATE can be estimated as

$$
\begin{aligned}
\widehat{ATE} &= \frac{n^1}{n^0+n^1}\widehat{ATT} + \frac{n^0}{n^0+n^1}\widehat{ATU} \\
&= \frac{n^1}{n^0+n^1}\frac{1}{n^1}\sum_{i\in I}\left(y_i - y_{j(i)}\right) + \frac{n^0}{n^0+n^1}\frac{1}{n^0}\sum_{j\in J}\left(y_{i(j)} - y_j\right) \\
&= \frac{1}{n^0+n^1}\left[\sum_{i\in I}(2d_i-1)(y_i - y_{j(i)}) + \sum_{j\in J}(2d_j-1)(y_j - y_{i(j)})\right] \\
&= \frac{1}{n}\sum_{k=1}^{n}(2d_k-1)\left(y_k - y_{l(k)}\right),
\end{aligned}
$$

where $d_k \in \{0,1\}$ is the treatment status of observation k, n is the total number of observations, k is a running index of all observations, and $l(k)$ is an index of an observation that is matched to an observation k.

The limitation of exact matching is that if we have a lot of covariates that take many values we will often not be able to find matches. In this scenario, there may be many strata in the available data in which no treatment or control cases are observed, even though the true probability of being treated is between 0 and 1 for every stratum in the population. This problem is called *sparseness*.

One way to deal with sparseness while preserving the core idea of exact matching is to use *coarsened exact matching* (Iacus, King, and Porro 2012). It's based on the idea that sometimes it's possible to do exact matching once we coarsen the data enough. We coarsen the data by binning the values of continuous (or even categorical) variables, then try to find exact matches.

Nearest-Neighbor Matching

For the treatment effect for the treated, nearest-neighbor matching constructs the counterfactual for each treatment case using the control cases that are "closest" to the treatment case on a unidimensional measure ("distance") constructed from the variables in S. The traditional algorithm randomly orders the treatment cases and then selects for each treatment case the control case with the smallest distance. The algorithm can be run with or without replacement. With replacement, a control case is returned to the pool after a match and can be matched later to another treatment case. Without replacement, a control case is taken out of the pool once it is matched.

One can select either just one nearest neighbor for each treatment case (one-to-one matching) or match the top *k* nearest neighbors (k-nearest-neighbor matching) to each target treatment case, in which case we average over the matched nearest neighbors. Matching more control cases to each treatment case results in lower expected variance of the treatment effect estimate but also raises the possibility of greater bias, because the probability of making more poor matches increases.

A danger with nearest-neighbor matching is that it may result in some very poor matches for treatment cases. A version of nearest-neighbor matching, known as *caliper matching*, is designed to remedy this drawback by restricting matches to some maximum distance. With

this type of matching, some treatment cases may not receive matches, and thus the effect estimate will apply to only the subset of the treatment cases matched.

A related form of matching, *radius matching* (Dehejia and Wahba 2002), matches all control cases within a particular distance–the "radius"–from the treatment case and gives the selected control cases equal weight. If there are no control cases within the radius of a particular treatment case, then the nearest available control case is used as the match.

The treatment effect for the untreated is derived similarly, except that we match treatment cases to each control case. The formulas for estimating the ATT, ATU, and ATE are identical to the exact matching.

How can we define the "distance" between cases? There are two popular approaches. The first approach uses the values of covariates to compute the *Mahalanobis distance*, which is a scale-invariant distance metric:

$$d(S_i, S_j) = \sqrt{(S_i - S_j)' \Sigma^{-1} (S_i - S_j)},$$

where S_i and S_j are vectors of values of covariates for the two compared cases, i and j, and Σ is the variance-covariance matrix of S.

Another popular approach is to use the *propensity score*. Propensity score matching (Rosenbaum and Rubin 1983) uses variables in S to estimate the probability of treatment conditional on S, $\mathbb{P}(D = 1 \mid S)$ (e.g., using logit) and then uses the predicted values from that estimation to collapse the covariates into a single scalar called the *propensity score*. All comparisons between the treatment and control group are then based on that value.

> **Note**
>
> Although propensity score matching is a popular technique, there is some pushback against using it (King and Nielsen 2019). The general advice is to use propensity scores to construct weights, not select matches.

Weighting

Exact matching or nearest-neighbor-matching can be thought of as a special case of weighting. For example, the treatment effect for the treated can be defined as

$$\widehat{ATT} = \frac{1}{n^1} \sum_{i \in I} \left[y_i - \sum_{j \in J} w_{ij} y_j \right],$$

where w_{ij} is the weight of the control case j for the treatment case i. In the case of exact matching, the control unit j that is matched to the treatment unit i gets a weight of 1, while all other control units receive a weight of 0. If there are several matched control cases, each of them receives an equal weight.

In case of exact or nearest-neighbor matching, therefore, some units get a weight of 1, while all others get a weight of 0. In general, one can try to compute non-zero weights for each unit (not just for selected few). The weights should reflect how far a given control unit is from the treatment unit.

The treatment effect for the untreated can be defined as

$$\widehat{ATU} = \frac{1}{n^0} \sum_{j \in J} \left[\sum_{i \in I} w_{ji} y_i - y_j \right],$$

where w_{ji} is the weight of the treatment case i for the control case j.

The average treatment effect can be defined in one of the two ways:

$$\begin{aligned} \widehat{ATE} &= \frac{n^1}{n} \widehat{ATT} + \frac{n^0}{n} \widehat{ATU} \\ &= \frac{1}{n} \left(\sum_{i \in I} w_i y_i - \sum_{j \in J} w_j y_j \right), \end{aligned}$$

where w_i and w_j are the weights of units i and j.

The two main approaches to constructing weights are *kernel matching* and *inverse probability weighting*. In kernel matching, a *kernel function* is used to construct the weights (Heckman, Ichimura, Smith, and Todd (1998), also see Smith and Todd (2005) for a review). A kernel function G takes the distance between the two units and, together with a specified *bandwidth*, returns a value. The value will be the highest if the distance is zero. All control units are matched to each treatment unit but weighted so that those closest to the treatment unit are given the greatest weight. The weights of all the control units that are matched to the treatment unit i are given by

$$w_{ij} = \frac{G(d(S_i, S_j))}{\sum_{j \in J} G(d(S_i, S_j))}.$$

Inverse probability weighting uses *propensity scores* to construct weights (See, e.g., Horvitz and Thompson (1952), Hirano, Imbens, and Ridder (2003) or Busso, DiNardo, and McCrary (2014)). After estimating the propensity score $p(S) \equiv \mathbb{P}(D = 1 \mid S)$, the weights for the control units in the ATT formula are given by

$$w_{ij} = \frac{1}{n^1} \frac{p_j}{1 - p_j},$$

where p_j is the estimated propensity score for unit j. Notice that the weights do not depend on i. What do these weights do? For control observations with high propensity scores (high p_j) the weights are going to be high, and vice versa. Control observations with high propensity scores are basically the treatment observations that did not get treated (counterfactuals).

For the ATU, we have the following weights:

$$w_{ji} = \frac{1}{n^0}\frac{1-p_i}{p_i},$$

where p_i is the estimated propensity score for unit i. Notice again that the weights do not depend on j. For treatment observations with low propensity scores (high p_j) the weights are going to be high, and vice versa. Likewise, treatment observations with low propensity scores are like the control observations that did get treated (counterfactuals).

For the ATE, the weights are:

$$w_i = \frac{1}{p_i}, w_j = \frac{1}{1-p_j}.$$

The inverse probability weight also has some modifications, for example the normalized weighting (Hirano and Imbens, 2001, Millimet and Tchernis, 2009). Abadie and Imbens (2011) develop the bias-correction method for matching estimators.

Where do those weights come from? One can prove the following identities

$$\begin{aligned}
ATE &= \mathbb{E}\left[Y\frac{D-p(S)}{p(S)(1-p(S))}\right],\\
ATT &= \frac{1}{\mathbb{P}(D=1)}\mathbb{E}\left[Y\frac{D-p(S)}{1-p(S)}\right],\\
ATU &= \frac{1}{\mathbb{P}(D=0)}\mathbb{E}\left[Y\frac{1-p(S)}{D-(1-p(S))}\right].
\end{aligned}$$

✓ **Math time: Proof for ATT**

Consider the following term

$$\begin{aligned}
\mathbb{E}\left[Y\frac{D-p(S)}{1-p(S)} \mid S\right] &= \mathbb{E}\left[Y\frac{D-p(S)}{1-p(S)} \mid S, D=1\right]\mathbb{P}(D=1 \mid S)\\
&\quad + \mathbb{E}\left[Y\frac{D-p(S)}{1-p(S)} \mid S, D=0\right]\mathbb{P}(D=0 \mid S)\\
&= \mathbb{E}[Y \mid S, D=1]p(S) - \frac{p(S)}{1-p(S)}\mathbb{E}[Y \mid S, D=0](1-p(S))\\
&= p(S)\left(\mathbb{E}[Y \mid D=1, S] - \mathbb{E}[Y \mid D=0, S]\right)\\
&= p(S)ATT(S).
\end{aligned}$$

Now we have the following expression for the conditional ATT

$$ATT(S) = \frac{\mathbb{E}\left[Y\frac{D-p(S)}{1-p(S)} \mid S\right]}{\mathbb{P}(D=1 \mid S)}.$$

The unconditional ATT obtains after taking the expectation:

$$
\begin{aligned}
ATT &= \mathbb{E}_{S|D=1} ATT(S) \\
&= \sum_{k=1}^{\bar{S}} \frac{\mathbb{E}\left[Y \frac{D-p(S)}{1-p(S)} \mid S=k\right]}{\mathbb{P}(D=1 \mid S=k)} \mathbb{P}(S=k \mid D=1) \\
&= \sum_{k=1}^{\bar{S}} \mathbb{E}\left[Y \frac{D-p(S)}{1-p(S)} \mid S=k\right] \frac{\mathbb{P}(S=k)}{\mathbb{P}(D=1)} \\
&= \frac{1}{\mathbb{P}(D=1)} \sum_{k=1}^{\bar{S}} \mathbb{E}\left[Y \frac{D-p(S)}{1-p(S)} \mid S=k\right] \mathbb{P}(S=k) \\
&= \frac{1}{\mathbb{P}(D=1)} \mathbb{E}\left[Y \frac{D-p(S)}{1-p(S)}\right]
\end{aligned}
$$

The sample equivalent of the ATT formula is

$$
\begin{aligned}
\widehat{ATT} &= \frac{n}{n^1} \frac{1}{n} \sum_{k=1}^{n} y_k \frac{d_k - p_k}{1-p_k} = \frac{1}{n^1} \left(\sum_{i \in I} y_i - \sum_{j \in J} \frac{p_j}{1-p_j} y_j \right) \\
&= \frac{1}{n^1} \sum_{i \in I} \left(y_i - \sum_{j \in J} \frac{1}{n^1} \frac{p_j}{1-p_j} y_j \right).
\end{aligned}
$$

Therefore, we can see that the weights on the control units are

$$
w_{ij} = \frac{1}{n^1} \frac{p_j}{1-p_j}.
$$

Homework

1. Prove the formulas for ATU and ATE
2. Using the sample equivalents of the formulas for ATU and ATE, derive the weights and show that they are equal to the ones we defined above.