Toolkit for Weighting and Analysis of Nonequivalent Groups: A tutorial for the `twang` package

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1 Introduction

While working on an evaluation of drug treatment programs and writing up our methodology that appeared in McCaffrey *et al.* (2004), we developed several R scripts and functions throughout the experimentation. The `twang` package is the collection of functions that we found most useful. In fact, these are the functions that we now regularly use in our work. Since many of our colleagues at RAND have found them useful, we have made the package more generally available.

There are now numerous propensity scoring methods in the literature. They differ in how they estimate the propensity score (e.g. logistic regression, CART), the target estimand (e.g. treatment effect on the treated, population treatment effect), and how they utilize the resulting estimated propensity scores (e.g. stratification, matching, weighting). We originally developed the `twang` package with a particular process in mind, generalized boosted regression to estimate the propensity scores and weighting of the comparison cases to estimate a treatment effect on the treated. The main workhorse of `twang` is the `ps()` function that implements this. However, the framework of the package is flexible enough to allow the user to use propensity score estimates from other methods and implement new `stop.method` objects to assess the quality of balance between the treatment and control groups. The same set of functions are also useful for other tasks such as non-response weighting, discussed in section 4.

The propensity score is the probability that a particular case would be assigned or exposed to a treatment condition. Rosenbaum & Rubin (1983) showed that knowing the propensity score is sufficient to separate the effect of a treatment on an outcome from confounding factors that influence both treatment assignment and outcomes, provide the necessary conditions hold. The propensity score has the balancing property that given the propensity score the distribution of features for the treatment cases is the same as that for the control cases. While the treatment selection probabilities are generally not known, good estimates of them can be effective at removing confounding from treatment effect estimates. This package aims to compute good estimates of the propensity scores from the data, check their quality by assessing whether or not they have the balancing properties that we expect in theory, and use them in computing treatment effect estimates.

2 An example to start

If you have not already done so, install twang by typing `install.packages("twang")`. `twang` relies on other R packages, especially `gbm` and `survey`. You may have to run `install.packages()`

for these as well if they are not already installed. You will only need to do this step once. In the future running `update.packages()` regularly will ensure that you have the latest versions of the packages, including bug fixes and new features.

To start using `twang`, first load the package. You will have to do this step once for each R session that you run.

```
> library(twang)

Loading required package: gbm
Loading required package: survival
Loading required package: splines
Loading required package: lattice
Loading required package: mgcv
This is mgcv 1.3-13
Loaded gbm 1.5-5
Loading required package: survey
Loading required package: xtable
Loading required package: mlmRev
Loading required package: lme4
Loading required package: Matrix
Loading required package: Matrix
```

To demonstrate the package we utilize data from Lalonde's National Supported Work Demonstration analysis (Lalonde 1986, Dehejia & Wahba 1999, `http://www.columbia.edu/~rd247/nswdata.html`). This dataset is provided with the `twang` package.

```
> data(lalonde)
```

R can read data from many other sources. The manual "R Data Import/Export," available at `http://cran.r-project.org/doc/manuals/R-data.pdf`, describes that process in detail.

For the `lalonde` dataset, the variable `treat` is the 0/1 treatment indicator, 1 indicates "treatment" by being part of the National Supported Work Demonstration and 0 indicates "comparison" cases drawn from the Current Population Survey. We wish to adjust for eight other covariates: age, education, black, Hispanic, having no degree, married, earnings in 1974 (pretreatment), and earnings in 1975 (pretreatment). Note that we specify no outcome variables at this time. The `ps()` function is the primary method in twang for estimating propensity scores. This step is computationally intensive and can take a few minutes.

```
> par(mfrow = c(1, 2))
> ps.lalonde <- ps(treat ~ age + educ + black +
+     hispan + nodegree + married + re74 + re75,
+     data = lalonde, plots = "optimize", stop.method = stop.methods[c("es.stat.mean",
+         "ks.stat.max")], n.trees = 2000, interaction.depth = 2,
+     shrinkage = 0.01, perm.test.iters = 0, verbose = FALSE)
```

The arguments to `ps()` require some discussion. The first argument specifies a formula indicating that `treat` is the 0/1 treatment indicator and that the propensity score model should predict `treat` from the eight covariates listed there separated by "+". The "+" does *not* mean that these variables are being added together *nor* does it mean that model is linear. This is just R's notation for variables in the model. There is no need to specify interaction terms in the formula. There is also no need, and can be counterproductive, to create indicator variables to

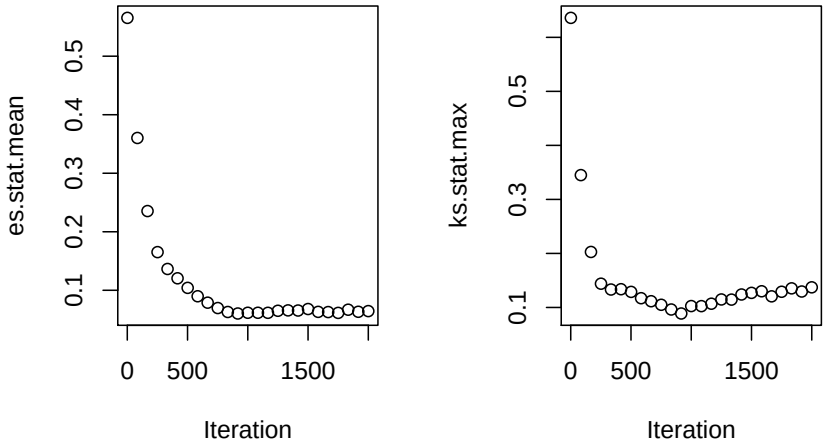


Figure 1: Optimization of `es.stat.mean` and `ks.stat.max`. The horizontal axes indicate the number of iterations and the vertical axes indicate the measure of imbalance between the two groups. For `es.stat.mean` the measure is the average effect size difference between the two groups and for `ks.stat.max` the measure is the largest of the KS statistics

represent categorical covariates (aka "dummy code"), provided the categorical variable is stored as a `factor` (see `help(factor)` for more details).

The next argument, `data`, indicates the dataset.

The `plots` controls the diagnostic plots that the `ps` function can create. They are described in more detail later. For now `plots="none"` skips the plots, but they can be created later using the `plot()` method. If the call to `ps()` includes an argument `pdf.plots=TRUE` then all the plots are written to a pdf file in the current working directory (use `getwd()` to learn what your working directory is and `setwd()` to set it). The default is `pdf.plots=FALSE`

`n.trees`, `interaction.depth`, and `shrinkage` are parameters for the gbm model that `ps()` computes and stores. The resulting `gbm` object describes a family of candidate propensity score models indexed by the number of gbm iterations from one to `n.trees`.

The `stop.method` argument takes a `stop.method` object which contains a set of rules and measures for assessing the quality of the balance between the treatment and comparison groups. The `ps` function selects the optimal number of gbm iterations to minimize the differences between the treatment and control groups as measured by the rules of the given `stop.method` object. Figure 1 illustrates this process. For each panel, the number of gbm iterations is plotted on the horizontal axis plots the measure of balance is plotted on the vertical axis. Each iteration adds model complexity to the propensity score model giving it greater modeling flexibility. The increased flexibility improves the balance of the two groups up to a certain point at which additional iterations offer no improvement or actually make the balance worse. In this example, iterating gbm for 946 iterations minimized the average effect size difference and 946 iterations minimized the largest of the eight Kolmogorov-Smirnov (KS) statistics computed for the eight covariates. `n.trees` is the maximum number of iterations that `ps()` will run and it will issue a warning if the estimated optimal number of iterations is too close to the bound. Increase

`n.trees` if this warning appears.

The `gbm` package has various tools for exploring the relationship between the covariates and the treatment assignment indicator if these are of interest. `summary()` computes the relative influence of each variable for estimating the probability of treatment assignment. The gbm estimates depend on the number of iterations, which is specified by the `n.trees` argument in the `summary` method for gbm. In this example, we choose the number of iterations to be the optimal number for minimizing the maximum KS statistics. This value can be found in the `n.trees` elementof the `ks.stat.max` element of the `desc` element of the `ps` object `ps.lalonde`. Figure 2 shows the barchart of the relative influence if `plot=TRUE`.

```
> summary(ps.lalonde$gbm.obj, n.trees = ps.lalonde$desc$ks.stat.max$n.trees,
+     plot = FALSE)

       var    rel.inf
1    black 46.9866311
2      age 21.3639461
3     re74 16.9928215
4     re75  5.0567355
5     educ  4.5293987
6  married  3.8981933
7 nodegree  0.6554839
8   hispan  0.5167900
```

2.1 Assessing "balance" using balance tables

Having estimated the propensity scores, `bal.table` produces a table that shows how well the resulting propensity score weights balance the treatment and comparison groups.

```
> lalonde.balance <- bal.table(ps.lalonde)
> lalonde.balance

$unw
            tx.mn    tx.sd    ct.mn    ct.sd std.eff.sz   stat     p    ks ks.pval
age        25.816    7.155   28.030   10.787     -0.309 -2.994 0.003 0.158   0.003
educ       10.346    2.011   10.235    2.855      0.055  0.547 0.584 0.111   0.075
black       0.843    0.365    0.203    0.403      1.757 19.371 0.000 0.640   0.000
hispan      0.059    0.237    0.142    0.350     -0.349 -3.413 0.001 0.083   0.319
nodegree    0.708    0.456    0.597    0.491      0.244  2.716 0.007 0.111   0.075
married     0.189    0.393    0.513    0.500     -0.824 -8.607 0.000 0.324   0.000
re74     2095.574 4886.620 5619.237 6788.751     -0.721 -7.254 0.000 0.447   0.000
re75     1532.055 3219.251 2466.484 3291.996     -0.290 -3.282 0.001 0.288   0.000

$es.stat.mean
            tx.mn    tx.sd    ct.mn    ct.sd std.eff.sz   stat     p    ks ks.pval
age        25.816    7.155   25.787    7.737      0.004  0.030 0.976 0.088   0.983
educ       10.346    2.011   10.524    2.238     -0.089 -0.600 0.549 0.084   0.989
black       0.843    0.365    0.843    0.364      0.000  0.002 0.998 0.000   1.000
hispan      0.059    0.237    0.046    0.210      0.056  0.634 0.527 0.013   1.000
nodegree    0.708    0.456    0.625    0.485      0.183  0.919 0.359 0.084   0.989
married     0.189    0.393    0.192    0.395     -0.008 -0.061 0.951 0.003   1.000
re74     2095.574 4886.620 1800.480 4253.284      0.060  0.527 0.598 0.054   1.000
```

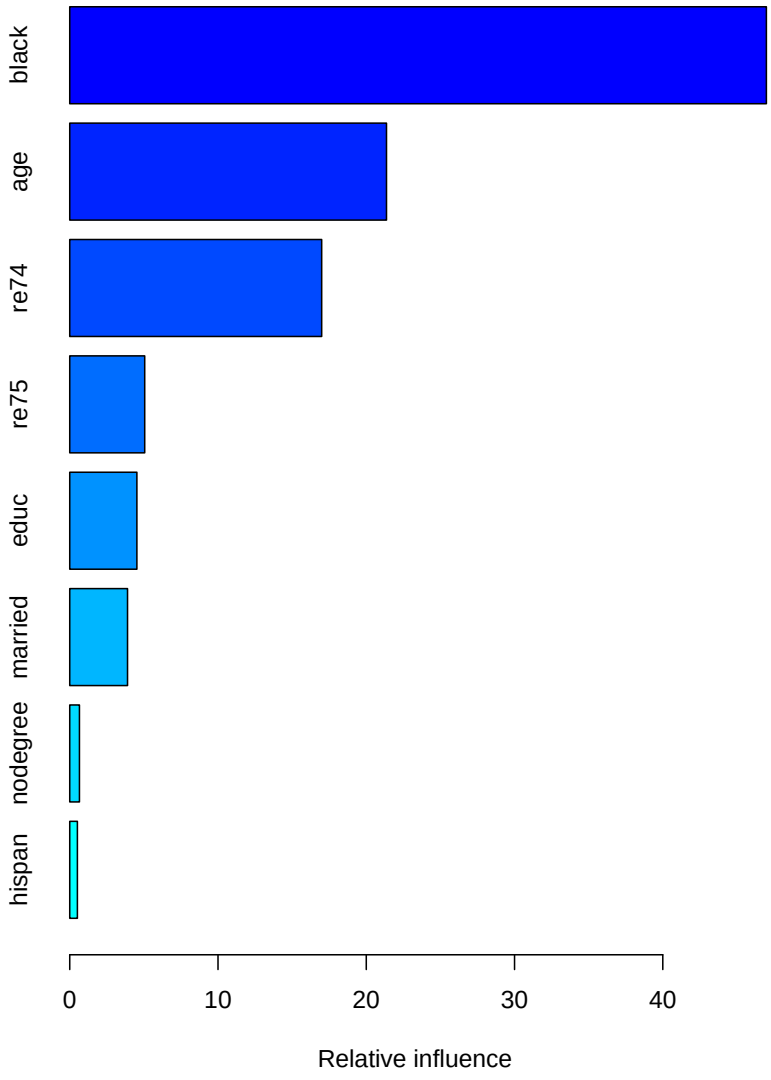


Figure 2: Relative influence of the covariates on the estimated propensity score

```
re75     1532.055 3219.251 1349.576 2795.808      0.057  0.461 0.645 0.072   0.998

$ks.stat.max
            tx.mn    tx.sd    ct.mn    ct.sd std.eff.sz   stat     p    ks ks.pval
age        25.816    7.155   25.787    7.737      0.004  0.030 0.976 0.088   0.983
educ       10.346    2.011   10.524    2.238     -0.089 -0.600 0.549 0.084   0.989
black       0.843    0.365    0.843    0.364      0.000  0.002 0.998 0.000   1.000
hispan      0.059    0.237    0.046    0.210      0.056  0.634 0.527 0.013   1.000
nodegree    0.708    0.456    0.625    0.485      0.183  0.919 0.359 0.084   0.989
married     0.189    0.393    0.192    0.395     -0.008 -0.061 0.951 0.003   1.000
re74     2095.574 4886.620 1800.480 4253.284      0.060  0.527 0.598 0.054   1.000
re75     1532.055 3219.251 1349.576 2795.808      0.057  0.461 0.645 0.072   0.998
```

`bal.table()` returns a lot of information, not all of which is needed for all analyses. The returned component is a list with named components, one for an unweighted analysis (named `unw`) and one for each `stop.method` specified, here `es.stat.mean` and `ks.stat.max`. McCaffrey et al (2004) essentially used `es.stat.mean` for the analyses, but our more recent work has been utilizing `ks.stat.max`. See section XXX for a more detailed description of these choices.

The table contains the following items

tx.mn, ct.mn The treatment means and the propensity score weighted control means for each of the variables. The unweighted table (unw) shows the unweighted means

tx.sd, ct.sd The treatment standard deviations and the propensity score weighted control standard deviations for each of the variables. The unweighted table (unw) shows the unweighted standard deviations

std.eff.sz The standardized effect size, defined as the treatment group mean minus the comparison group mean divided by the treatment group standard deviation (this value is sometimes referred to as "standardized bias" when people discuss propensity scores)

stat, p Depending on whether the variable is continuous or categorical, `stat` is a t-statistic or a χ^2 statistic. `p` is the associated p-value

ks, ks.pval The Kolmogorov-Smirnov test statistic and its associated p-value. If in the call to `ps()` `perm.test.iters>0` then these p-values are Monte Carlo p-values. Otherwise they are analytic approximations that are not necessarily accurate when there are ties. For categorical variables this is just the χ^2 test

Components of these tables are likely to be useful in reports and presentations demonstrating that indeed the two groups have been balanced. The `xtable` package aids in formatting for LaTeXand Word documents. Table 1 shows the results for `ks.stat.max` reformatted for a LaTeXdocument. For Word documents, paste LaTeXdescription of the table into a Word document, highlight it, Table->Convert->Text to Table, then under "Separate text at" insert "&" in the Other: box. Additional formatting from there will finish it.

```
> library(xtable)
> pretty.tab <- lalonde.balance$ks.stat.max[, c("tx.mn",
+     "ct.mn", "ks")]
> pretty.tab <- cbind(pretty.tab, lalonde.balance$unw[,
+     "ct.mn"])
> names(pretty.tab) <- c("E(Y1|t=1)", "E(Y0|t=1)",
+     "KS", "E(Y0|t=0)")
```

```
> xtable(pretty.tab, caption = "Balance of the treatment and comparison groups",
+     label = "tab:balance", digits = c(0, 2, 2,
+         2, 2), align = c("l", "r", "r", "r", "r"))
```

	E(Y1|t=1)	E(Y0|t=1)	KS	E(Y0|t=0)
age	25.82	25.79	0.09	28.03
educ	10.35	10.52	0.08	10.23
black	0.84	0.84	0.00	0.20
hispan	0.06	0.05	0.01	0.14
nodegree	0.71	0.62	0.08	0.60
married	0.19	0.19	0.00	0.51
re74	2095.57	1800.48	0.05	5619.24
re75	1532.06	1349.58	0.07	2466.48

Table 1: Balance of the treatment and comparison groups

The `summary()` method for `ps` objects offers a compact summary of the sample sizes of the groups and the balance measures

```
> summary(ps.lalonde)
```

```
           type n.treat n.ctrl       ess   max.es
1           unw     185    429 429.00000 1.756775
11 es.stat.mean     185    429  28.09103 0.183351
12  ks.stat.max     185    429  28.09103 0.183351
      mean.es    max.ks max.ks.p    mean.ks iter
1  0.56872589 0.6404460       NA 0.27024507   NA
11 0.05724476 0.0875748       NA 0.04970737  946
12 0.05724476 0.0875748       NA 0.04970737  946
```

In general, weighted means have greater sampling variance than unweighted means from a sample of equal size. The effective sample size (ESS) of the weighted comparison group captures this increase in variance as

$$ESS = \frac{\left(\sum_{i \in C} w_i\right)^2}{\sum_{i \in C} w_i^2}. \tag{1}$$

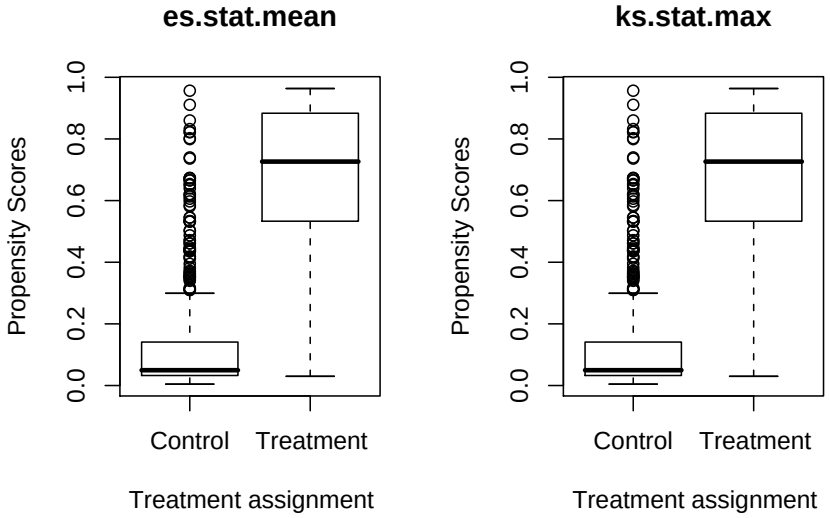
The ESS is approximately the number of observations from a simple random sample needed to obtain an estimate with sampling variation equal to the sampling variation obtained with the weighted comparison observations. Therefore, the ESS will give an estimate of the number of comparison participants that are comparable to the treatment group. The ESS is an accurate measure of the relative size of the variance of means when the weights are fixed or uncorrelated with outcomes otherwise the ESS underestimates the effective sample size (Little & Vartivarian, 2004). It is unlikely to be the case with propensity score weights that the weights are uncorrelated with outcomes. Hence the ESS might be an lower bound on the effective sample size, but it still serves as a useful measure on the effective number of control cases used in estimating weighted means.

The `ess` column in the summary results shows the ESS for the estimated propensity scores. Note that although the original comparison group had 429 cases, the propensity score estimates effectively utilize only 28.1 or 28.1 of the comparison cases, depending on the rules and measures used to estimate the propensity scores. While this may seem like a large loss of sample size, this indicates that many of the original cases were unlike the treatment cases and, hence, were not useful for isolating the treatment effect.

2.2 Graphical assessments of balance

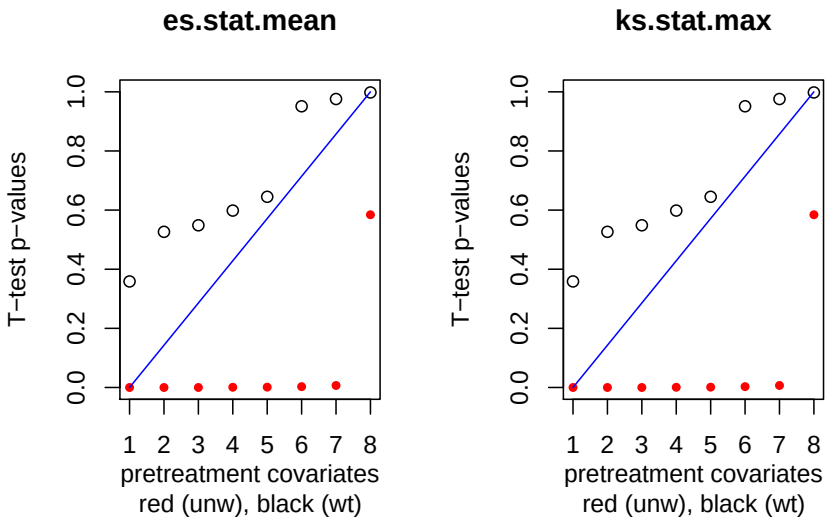
The `plot()` method can generate useful diagnostic plots from the propensity score objects. Boxplots comparing the estimated propensity score weights between the treatment and comparison groups checks for overlap in the groups.

```
> par(mfrow = c(1, 2))
> plot(ps.lalonde, plots = "ps boxplot")
> par(mfrow = c(1, 1))
```



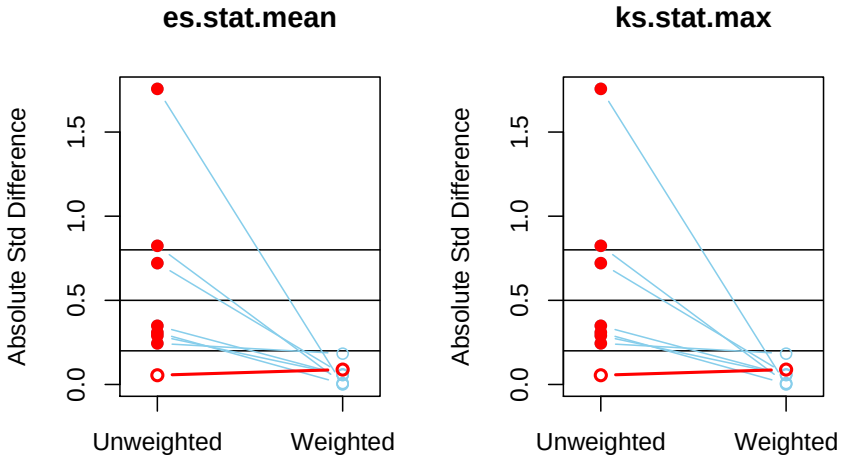
P-values from independent tests in which the null hypothesis is true have a uniform distribution. Therefore, a QQ plot comparing the quantiles of the observed p-values to the quantiles of the uniform distribution inform us of how similar the propensity score weighting makes the samples look like what we would expect from a randomized study. Setting `plots="t pvalues"` generates such QQ plots.

```
> par(mfrow = c(1, 2))
> plot(ps.lalonde, plots = "t pvalues")
> par(mfrow = c(1, 1))
```



Before weighting (closed circles), many variables have statistically significant differences between groups (i.e., with p-values near zero). After weighting (open circles) the p-values are above the 45-degree line, which represents the cumulative distribution of a uniform variable on [0,1]. This indicates that the p-values are even larger than would be expected in a randomized study. `plot()` can create similar figures for KS statistic p-values by setting `plots="ks pvalues"`.

```
> par(mfrow = c(1, 2))
> plot(ps.lalonde, plots = "spaghetti")
> par(mfrow = c(1, 1))
```



2.3 Analysis of outcomes

The `survey` package is useful for performing the outcomes analyses using propensity score weights. Its statistical methods properly account for the weights when computing standard error estimates.

```
> library(survey)
```

The `get.weights` function extracts the propensity score weights from a `ps` object. Those weights may then be used as case weights in a `svydesign` object.

```
> lalonde$w <- get.weights(ps.lalonde, type = "ATT",
+     stop.method = "ks.stat.max")
> design.ps <- svydesign(ids = ~1, weights = ~w,
+     data = lalonde)
```

The `type` argument to the `get.weights` function specifies whether the weights are for estimating the treatment effect on the treated, computed as 1 for the treatment cases and $p/(1-p)$ for the comparison cases, or for estimating the treatment effect on the population, computed as $1/p$ for the treatment cases and $1/(1-p)$ for the comparison cases. The third argument to `get.weights` selects which set of weights to utilize. If no `stop.method` is selected then it returns the first set of weights.

The `svydesign` function from the `survey` package creates an object that stores the dataset along with design information needed for analyses. See `help(svydesign)` for more details on setting up `svydesign` objects.

The aim of the National Supported Work Demonstration analysis is to determine whether the program was effective at increasing earnings in 1978. The propensity score adjusted test can be computed with `svyglm`.

```
> glm1 <- svyglm(re78 ~ treat, design = design.ps)
> summary(glm1)

Call:
svyglm(re78 ~ treat, design = design.ps)

Survey design:
svydesign(ids = ~1, weights = ~w, data = lalonde)

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)   5720.2      759.4   7.533 1.79e-13 ***
treat          628.9      953.9   0.659     0.51
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for gaussian family taken to be 49340405)

Number of Fisher Scoring iterations: 2
```

The analysis estimates an increase in earnings of $629 for those that participated in the NSW compared with similarly situated people observed in the CPS. The effect, however, does not appear to be statistically significant.

Some authors have recommended utilizing both propensity score adjustment and additional covariate adjustment to minimize *mean square error* or to obtain "doubly robust" estimates of the treatment effect (Huppler-Hullsiek & Louis 2002, Bang & Robins 2005). These estimators are consistent if either the propensity scores are estimated correctly *or* the regression model is specified correctly. For example, note that the balance table for `ks.stat.max` made the two groups more similar on `nodegree`, but still some differences remained, 70.8% of the treatment group had no degree while 62.5% of the comparison group had no degree. While linear regression is sensitive to model misspecification when the treatment and comparison groups are dissimilar, the propensity score weighting has made them more similar, perhaps enough so that additional modeling with covariates can adjust for any remaining differences. In addition to potential bias reduction, the inclusion of additional covariates can reduce the standard error of the treatment effect if some of the covariates are strongly related to the outcome.

```
> glm2 <- svyglm(re78 ~ treat + nodegree, design = design.ps)
> summary(glm2)

Call:
svyglm(re78 ~ treat + nodegree, design = design.ps)

Survey design:
svydesign(ids = ~1, weights = ~w, data = lalonde)

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)   6890.9     1256.5   5.484 6.08e-08 ***
treat          785.6      980.3   0.801    0.423
nodegree     -1874.5     1141.4  -1.642    0.101
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for gaussian family taken to be 48568844)

Number of Fisher Scoring iterations: 2
```

Adjusting for the remaining group difference in degree slightly increased the estimate of the program's effect to $786, but the difference is still not statistically significant. We can covariate adjust for the other variables seeking additional bias and variance reduction, but that too in this case has no effect on the estimated program effect.

```
> glm3 <- svyglm(re78 ~ treat + age + educ + black +
+     hispan + nodegree + married + re74 + re75,
+     design = design.ps)
> summary(glm3)

Call:
svyglm(re78 ~ treat + age + educ + black + hispan + nodegree +
    married + re74 + re75, design = design.ps)

Survey design:
svydesign(ids = ~1, weights = ~w, data = lalonde)
```

```
Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept) -1.914e+03  4.033e+03  -0.475  0.63530
treat        6.674e+02  9.320e+02   0.716  0.47419
age          4.257e+00  5.213e+01   0.082  0.93494
educ         7.101e+02  2.405e+02   2.953  0.00327 **
black       -7.854e+02  9.577e+02  -0.820  0.41252
hispan       6.961e+02  1.642e+03   0.424  0.67178
nodegree     4.625e+02  1.504e+03   0.307  0.75861
married      5.215e+02  1.046e+03   0.498  0.61835
re74         4.487e-02  1.618e-01   0.277  0.78163
re75         1.566e-01  1.749e-01   0.895  0.37112
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for gaussian family taken to be 46719953)

Number of Fisher Scoring iterations: 2
```

2.4 Estimating the program effect using linear regression

The more traditional regression approach to estimating the program effect would fit a linear model with a treatment indicator and linear terms for each of the covariates.

```
> glm4 <- lm(re78 ~ treat + age + educ + black +
+     hispan + nodegree + married + re74 + re75,
+     data = lalonde)
> summary(glm4)

Call:
lm(formula = re78 ~ treat + age + educ + black + hispan + nodegree +
    married + re74 + re75, data = lalonde)

Residuals:
   Min     1Q Median     3Q    Max
-13595  -4894  -1662   3929  54570

Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept)  6.651e+01  2.437e+03   0.027   0.9782
treat        1.548e+03  7.813e+02   1.982   0.0480 *
age          1.298e+01  3.249e+01   0.399   0.6897
educ         4.039e+02  1.589e+02   2.542   0.0113 *
black       -1.241e+03  7.688e+02  -1.614   0.1071
hispan       4.989e+02  9.419e+02   0.530   0.5966
nodegree     2.598e+02  8.474e+02   0.307   0.7593
married      4.066e+02  6.955e+02   0.585   0.5590
re74         2.964e-01  5.827e-02   5.086 4.89e-07 ***
re75         2.315e-01  1.046e-01   2.213   0.0273 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
Residual standard error: 6948 on 604 degrees of freedom
Multiple R-Squared: 0.1478,        Adjusted R-squared: 0.1351
F-statistic: 11.64 on 9 and 604 DF,  p-value: < 2.2e-16
```

This model estimates a rather strong treatment effect, estimating a program effect of $1548 with a p-value=0.048. Several variations of this regression approach also estimate strong program effects. For example using square root transforms on the earnings variables yields a p-value=0.016. These estimates, however, are very sensitive to the model structure since the treatment and comparison subjects differ greatly as seen in the unweighted balance comparison ($unw) from `bal.table(ps.lalonde)`.

2.5 Propensity scores estimated from logistic regression

Propensity score analysis is intended to avoid these problems, but the quality of the balance and the treatment effect estimates can be sensitive to the method used to estimate the propensity scores. Consider estimating the propensity scores using logistic regression instead of `ps()`.

```
> ps.logit <- glm(treat ~ age + educ + black + hispan +
+     nodegree + married + re74 + re75, data = lalonde,
+     family = binomial)
> lalonde$w.logit <- rep(1, nrow(lalonde))
> lalonde$w.logit[lalonde$treat == 0] <- exp(predict(ps.logit,
+     subset(lalonde, treat == 0)))
```

`predict()` for logistic regression model produces estimates on the log-odds scale by default. Exponentiating those predictions for the comparison subjects gives the propensity score weights $p/(1-p)$. `dx.wts()` from the `twang` package diagnoses the balance for an arbitrary set of weights producing a balance table.

```
> bal.logit <- dx.wts(lalonde$w.logit, data = lalonde,
+     vars = c("age", "educ", "black", "hispan",
+         "nodegree", "married", "re74", "re75"),
+     treat.var = "treat", perm.test.iters = 0)



> print(bal.logit)

  type n.treat n.ctrl       ess    max.es    mean.es
1  unw     185    429 429.00000 1.7567745 0.56872589
2          185    429  99.81539 0.1188496 0.03188410
     max.ks    mean.ks iter
1 0.6404460 0.27024507   NA
2 0.3078039 0.09302319   NA
```

For propensity score weights estimated with logistic regression, the largest KS statistic was reduced from the unweighted sample's largest KS of 0.64 to 0.31, still quite a large KS statistic. Table 2 shows the details of the balance of the treatment and comparison groups. The means of the two groups appear to be quite similar while the KS statistic shows substantial differences in their distributions.

```
> pretty.tab <- bal.table(bal.logit)[[2]][, c("tx.mn",
+     "ct.mn", "ks")]
> pretty.tab <- cbind(pretty.tab, bal.table(bal.logit)[[1]]$ct.mn)
> names(pretty.tab) <- c("E(Y1|t=1)", "E(Y0|t=1)",
+     "KS", "E(Y0|t=0)")
> xtable(pretty.tab, caption = "Logistic regression estimates of the propensity scores",
+     label = "tab:balancelogit", digits = c(0,
+         2, 2, 2, 2), align = c("l", "r", "r",
+         "r", "r"))
```

	E(Y1|t=1)	E(Y0|t=1)	KS	E(Y0|t=0)
age	25.82	24.97	0.31	28.03
educ	10.35	10.40	0.04	10.23
black	0.84	0.84	0.00	0.20
hispan	0.06	0.06	0.00	0.14
nodegree	0.71	0.69	0.02	0.60
married	0.19	0.17	0.02	0.51
re74	2095.57	2106.05	0.23	5619.24
re75	1532.06	1496.54	0.13	2466.48

Table 2: Logistic regression estimates of the propensity scores

Table 3 compares the balancing quality of the propensity score weights directly with one another.

	n.treat	ess	max.es	mean.es	max.ks	mean.ks
unw	185	429.00	1.76	0.57	0.64	0.27
logit	185	99.82	0.12	0.03	0.31	0.09
es.stat.mean	185	28.09	0.18	0.06	0.09	0.05
ks.stat.max	185	28.09	0.18	0.06	0.09	0.05

Table 3: Summary of the balancing properties of logistic regression and gbm

```
> design.logit <- svydesign(ids = ~1, weights = ~w.logit,
+     data = lalonde)
> glm6 <- svyglm(re78 ~ treat, design = design.logit)
> summary(glm6)

Call:
svyglm(re78 ~ treat, design = design.logit)

Survey design:
svydesign(ids = ~1, weights = ~w.logit, data = lalonde)

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)   5135.1      588.9   8.719   <2e-16 ***
treat         1214.1      824.7   1.472    0.142
```

```
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for gaussian family taken to be 49598072)

Number of Fisher Scoring iterations: 2
```

The analysis estimates an increase in earnings of $1214 for those that participated in the NSW compared with similarly situated people observed in the CPS. Table 4 compares all of the treatment effect estimates

Treatment effect	PS estimate	Linear adjustment
$629	GBM, minimize KS	none
$786	GBM, minimize KS	nodegree
$667	GBM, minimize KS	all
$1548	None	all
$1214	Logistic regression	none
$1237	Logistic regression	all

Table 4: Treatment effect estimates by various methods

3 The details of `twang`

3.1 Propensity score weighting

Propensity score weighting Propensity score weighting (Rosenbaum 1987, Wooldridge 2002, Hirano and Imbens 2001, McCaffrey *et al.* 2004) addresses this problem by first reweighting the comparison cases so that the distribution of their features match the distribution of features of the treatment cases. Let $f(\mathbf{x}|t = 1)$ be the distribution of features for the treatment cases and $f(\mathbf{x}|t = 0)$ be the distribution of features for the comparison cases. If treatments were randomized then we would expect these two distributions to be similar. When they differ we will construct a weight, $w(\mathbf{x})$, so that

$$f(\mathbf{x}|t = 1) = w(\mathbf{x})f(\mathbf{x}|t = 0). \tag{2}$$

For example, if $f(\text{age=}65, \text{sex=F}|t = 1) = 0.10$ and $f(\text{age=}65, \text{sex=F}|t = 1) = 0.05$ (i.e. 10% of the treatment cases and 5% of the comparison cases are 65 year old females) then we need to give a weight of 2.0 to every 65 year old female in the comparison group so that they have the same representation as in the treatment group. More generally, we can solve (2) for $w(\mathbf{x})$ and apply Bayes Theorem to the numerator and the denominator to give an expression for the propensity score weight for comparison cases,

$$w(\mathbf{x}) = K\frac{f(t = 1|\mathbf{x})}{f(t = 0|\mathbf{x})} = K\frac{P(t = 1|\mathbf{x})}{1 - P(t = 1|\mathbf{x})}, \tag{3}$$

where K is a normalization constant that will cancel out in the outcomes analysis. Equation (3) indicates that if we assign a weight to comparison case i equal to the odds that a case with features $\mathbf{x}_i$ would be exposed to the treatment, then the distribution of their features would balance. Note that for comparison cases with features that are atypical of treatment cases, the propensity score $P(t = 1|\mathbf{x})$ would be near 0 and would produce a weight near 0. On the other hand, comparison cases with features typical of the treatment cases would receive larger weights.

3.2 Estimating the propensity score

In randomized studies $P(t = 1|\mathbf{x})$ is known and fixed in the study design. In observational studies the propensity score is unknown and must be estimated, but poor estimation of the propensity scores can cause just as much of a problem for estimating treatment effects as poor regression modeling of the outcome. Logistic regression is the common method for estimating propensity scores, and can suffice for many problems. Logistic regression for propensity scores estimates the log-odds of a case being in the treatment given $\mathbf{x}$ as

$$\log \frac{P(t = 1|\mathbf{x})}{1 - P(t = 1|\mathbf{x})} = \beta'\mathbf{x} \tag{4}$$

Usually, β is selected to maximize the logistic log-likelihood

$$\ell\beta = \frac{1}{n}\sum_{i=1}^{n} t_i\beta'\mathbf{x}_i - \log\left(1 + \exp(\beta'\mathbf{x}_i)\right) \tag{5}$$

Maximizing (5) provides the maximum likelihood estimates of β. However, in an attempt to remove as much confounding as possible, observational studies often record data on a large number of potential confounders, many of which can be correlated with one another. Standard methods for fitting logistic regression models to such data with the iteratively reweighted least squares algorithm can be statistically and numerically unstable. To improve the propensity score estimates we might also wish to include non-linear effects and interactions in $\mathbf{x}$. The inclusion of such terms only increases the instability of the models.

One increasingly popular method for fitting models with numerous correlated variables is the lasso (least absolute subset selection and shrinkage operator) introduced in statistics in Tibshirani (1996). For logistic regression, lasso estimation replaces (5) with a version that penalizes the absolute magnitude of the coefficients

$$\ell\beta = \frac{1}{n}\sum_{i=1}^{n} t_i\beta'\mathbf{x}_i - \log\left(1 + \exp(\beta'\mathbf{x}_i)\right) - \lambda\sum_{j=1}^{J}|\beta_j| \tag{6}$$

The second term on the right-hand side of the equation is the penalty term since it decreases the overall of $\ell\beta$ when there are coefficient that are large in absolute value. Setting $\lambda = 0$ returns the standard (and potentially unstable) logistic regression estimates of β. Setting λ to be very large essentially forces all of the β_j to be equal to 0 (the penalty excludes β_0). For a fixed value of λ the estimated $\hat{\beta}$ can have many coefficients exactly equal to 0, not just extremely small but precisely 0, and only the most powerful predictors of t will be non-zero. As a result the absolute penalty operates as a variable selection penalty. In practice, if we have several predictors of t that are highly correlated with each other, the lasso tends to include all of them in the model, shrink their coefficients toward 0, and produce a predictive model that utilizes all of the information in the covariates, producing a model with greater out-of-sample predictive performance than models fit using variable subset selection methods.

Our aim is to include as covariates all piecewise constant functions of the potential confounders and their interactions. That is, in $\mathbf{x}$ we will include indicator functions for continuous variables like $I(\text{age} < 15), I(\text{age} < 16), \ldots, I(\text{age} < 90)$, etc., for categorical variables like $I(\text{sex} = \text{male}), I(\text{prior MI} = \text{TRUE})$, and interactions among them like $I(\text{age} < 16)I(\text{sex} = \text{male})I(\text{prior MI} = \text{TRUE})$. This collection of basis functions spans a plausible set of propensity score functions, are computationally efficient, and are flat at the extremes of $\mathbf{x}$ reducing the likelihood of propensity score estimates near 0 and 1 that can occur with linear basis functions of $\mathbf{x}$. Theoretically with the lasso we can estimate the model in (6), selecting a λ small enough

so that it will eliminate most of the irrelevant terms and yield a sparse model with only the most important main effects and interactions. Boosting (Friedman 2001, 2003, Ridgeway 1999) effectively implements this strategy using a computationally efficient method that Efron *et al.* (2004) showed is equivalent to optimizing (6). With boosting it is possible to maximize (6) for a range of values of λ with no additional computational effort than for a specific value of λ. We use boosted logistic regression as implemented in the generalized boosted modeling (gbm) package in R (Ridgeway 2005).

3.3 Evaluating the propensity score weights

As with regression analyses, propensity score methods cannot adjust for unmeasured covariates that are uncorrelated with the observed covariates. Nonetheless, the quality of the adjustment for the observed covariates achieved by propensity score weighting is easy to evaluate. The estimated propensity score weights should equalize the distributions of the cases' features as in (2). This implies that weighted statistics of the covariates of the comparison group should equal the same statistics for the treatment group. For example, the weighted average of the age of comparison cases should equal the average age of the treatment cases. To assess the quality of the propensity score weights one could compare a variety of statistics such as means, medians, variances, and Kolmogorov-Smirnov statistics for each covariate as well as interactions. The `twang` package provides both the standardized effect sizes and KS statistics and p-values testing for differences in the means and distributions of the covariates for analysts to use in assessing balance. In addition, the package encodes decisions on how to assess the quality of the balance in `stop.method` objects which determine how to select the gbm iterations and tune the weights. There are three `stop.method` objects included with `twang`, described in more detail later, that compare means, KS statistics, and within propensity score strata mean differences.

3.4 Analysis of outcomes

With propensity score analyses the final outcomes analysis is generally straightforward, while the propensity score estimation may require complex modeling. Once we have propensity score weights that equalize the distribution of features of treatment and control cases, we give each treatment case a weight of 1 and each comparison case a weight $w_i = p(\mathbf{x}_i)/(1-p(\mathbf{x}_i))$. We then estimate the treatment effect estimate with a weighted regression model that contains only a treatment indicator. No additional covariates are needed if the propensity score weights account for differences in $\mathbf{x}$.

A combination of propensity score weighting and covariate adjustment can be useful for several reasons. First, the propensity scores may not have been able to completely balance all of the covariates. The inclusion of these covariates in addition to the treatment indicator in a weighted regression model may correct this if the imbalance is relatively small. Second, in addition to exposure, the relationship between some of the covariates and the outcome may also be of interest. Their inclusion can provide coefficients that can estimate the direction and magnitude of the relationship. Third, as with randomized trials, stratifying on covariates that are highly correlated with the outcome can improve the precision of estimates. Lastly, the inclusion of covariates can make the treatment effect estimate more robust in the sense that if either the propensity score model is correct or the regression model is correct then the treatment effect estimator will be unbiased (Kuppler Hullsiek & Louis 2004).

4 Non-response weights

The `twang` package was designed to estimate propensity score weights for estimating treatment effects in observational or quasi-experimental studies. However, the package can be used in other applications. For example, it can be used to generate and diagnose nonresponse weights for survey nonresponse or study attrition. We now present an example that uses the tools in `twang`. This example uses the subset of the US Sustaining Effects Study data distributed with the HLM software (Bryk, Raudenbush, Congdon, 1996) and also available in the R package `mlmRev`. The data include mathematics test scores for 1721 students in kindergarten to fourth grade. They also include the students race (Black, Hispanic, or other), gender, an indicator for whether or not the student had been retained in grade, the percent low income students at the school, the school size, the percent of mobile student, the students' grade-levels,student and school IDs, and grades converted to year by centering. The study analysis plans to analyze growth in math achievement from grade 1 to grade 4 using only students with complete data. However, the student with complete data differ from other students and reduce the potential for bias from excluding incomplete cases, the analysis plans to weight complete cases with nonresponse weights.

Nonresponse weights equal the reciprocal of the probability of response and are applied only to respondents. Let p denote the probability of response and and $1/p$ denote the nonresponse weight. Using basic algebra we can rewrite the nonresponse weights:

$$\frac{1}{p} = 1 + \frac{1-p}{p} \tag{7}$$

This formula shows that the weight has a component for respondent (which equals 1) and component for the nonrespondents ($(1-p)/p$). The goal of nonresponse weighting is to develop the weights so that the weighted respondents look like the entire sample – both the respondents and nonrespondents. Since, the respondents already look like themselves, we must find good estimates of the second component of the weight, $(1-p)/p$. We want to find weights that make the respondents look like the nonrespondents. The `ps()` function finds weights that make the control group like the the treatment group in terms of the distribution of covariates by estimating the treatment on the treated weight. Hence if we call the nonrespondents the "treatment" group and respondents the "control" group then `ps()` function can provide estimates of $(1-p)/p$ and the diagnostic tools in `twang` can be used to diagnosis the weights. To obtain the final nonresponse weight we just add 1 to the weights from `ps()`.

Before we can generate nonresponse weights, we need to prepare the data using the following commands.

First we read in the data

```
> library(mlmRev)
> data(egsingle)
```

Next we create the patterns of grades for which students have responses

```
> tmp <- sapply(split(egsingle, egsingle$childid),
+     function(x) {
+         paste(as.character(x$grade), collapse = "")
+     })
```

identify students with test scores for every grade from 1 to 4

```
> tmp <- data.frame(childid = names(tmp), gpatt = tmp,
+     resp = as.numeric((1:length(tmp)) %in% grep("1234",
+         as.character(tmp))))
```

and merge this back to create a single data frame

```
> egsingle <- merge(egsingle, tmp)
```

Because nonresponse is a student-level variable rather than a student-by-year-level variable we create one record per student.

```
> egsingle.one <- unique(egsingle[, -c(3:6)])
```

We also create a race variable

```
> egsingle.one$race <- as.factor(race <- ifelse(egsingle.one$black ==
+     1, 1, ifelse(egsingle.one$hispanic == 1, 2,
+     3)))
```

As discussed above, to use `ps()` to estimate nonresponse, we need to let nonrespondents be the treatment group by modeling an indicator of nonresponse rather than an indicator of response. We create this indicator and are set to estimate weights.

```
> egsingle.one$nresp <- 1 - egsingle.one$resp
```

```
> par(mfrow = c(1, 2))
> egsingle.ps <- ps(nresp ~ race + female + size +
+     lowinc + mobility, data = egsingle.one, plots = "optimize",
+     stop.method = stop.methods[c("es.stat.mean",
+         "ks.stat.max")], n.trees = 2500)

Fitting gbm model
Iter   TrainDeviance   ValidDeviance   StepSize   Improve
     1        1.3849             nan     0.0100    0.0004
     2        1.3841             nan     0.0100    0.0004
     3        1.3832             nan     0.0100    0.0005
     4        1.3820             nan     0.0100    0.0004
     5        1.3811             nan     0.0100    0.0004
     6        1.3800             nan     0.0100    0.0005
     7        1.3793             nan     0.0100    0.0002
     8        1.3784             nan     0.0100    0.0004
     9        1.3776             nan     0.0100    0.0003
    10        1.3769             nan     0.0100    0.0002
   100        1.3266             nan     0.0100    0.0001
   200        1.2992             nan     0.0100   -0.0000
   300        1.2832             nan     0.0100   -0.0000
   400        1.2709             nan     0.0100   -0.0001
   500        1.2621             nan     0.0100   -0.0000
   600        1.2550             nan     0.0100   -0.0001
   700        1.2496             nan     0.0100   -0.0000
   800        1.2451             nan     0.0100   -0.0002
   900        1.2410             nan     0.0100   -0.0001
  1000        1.2376             nan     0.0100   -0.0001
  1100        1.2345             nan     0.0100   -0.0001
  1200        1.2319             nan     0.0100   -0.0001
  1300        1.2295             nan     0.0100   -0.0001
```

```
  1400        1.2273            nan     0.0100   -0.0001
  1500        1.2253            nan     0.0100   -0.0000
  1600        1.2234            nan     0.0100   -0.0001
  1700        1.2215            nan     0.0100   -0.0001
  1800        1.2199            nan     0.0100   -0.0000
  1900        1.2183            nan     0.0100   -0.0001
  2000        1.2171            nan     0.0100   -0.0001
  2100        1.2159            nan     0.0100   -0.0001
  2200        1.2149            nan     0.0100   -0.0000
  2300        1.2136            nan     0.0100   -0.0001
  2400        1.2125            nan     0.0100   -0.0001
  2500        1.2114            nan     0.0100   -0.0001

Diagnosis of unweighted analysis
Optimizing with es.stat.mean stopping rule
   Optimized at 1013
Diagnosis of es.stat.mean weights
Optimizing with ks.stat.max stopping rule
   Optimized at 185
Diagnosis of ks.stat.max weights
```

The optimal number of iterations for gbm to minimize the maximum KS statistic is 2048 and the optimal number of iterations for gbm to minimize the average effect size is . The weights do an excellent job matching the distribution of the respondent group covariates to those of the nonrespondents.

```
> pretty.tab <- bal.table(egsingle.ps)$ks.stat.max[,
+     c("tx.mn", "ct.mn", "std.eff.sz", "ks")]
> names(pretty.tab) <- c("E(Y1|t=1)", "E(Y0|t=1)",
+     "Std.Eff.", "KS")
> xtable(pretty.tab, caption = "Balance of the nonrespondents and respondents",
+     label = "tab:balance2", digits = c(0, 2, 2,
+         2, 2), align = c("l", "r", "r", "r", "r"))
```

	E(Y1|t=1)	E(Y0|t=1)	Std.Eff.	KS
race:1	0.73	0.71	0.04	0.02
race:2	0.16	0.15	0.04	0.01
race:3	0.11	0.14	−0.10	0.03
female:Female	0.52	0.48	0.07	0.04
female:Male	0.48	0.52	−0.07	0.04
size	761.33	762.12	−0.00	0.04
lowinc	80.75	80.71	0.00	0.04
mobility	36.44	35.48	0.07	0.04

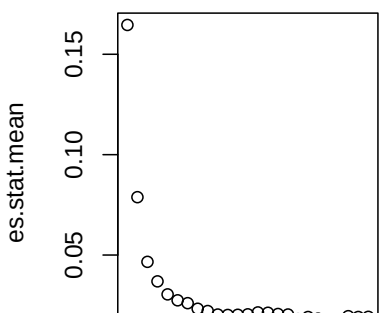
Table 5: Balance of the nonrespondents and respondents

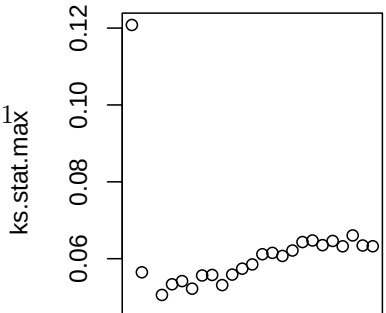
The final step is to add 1 to the weights to get the final nonresponse weight and then add the nonresponse weights to the respondent data so analyses can proceed.

```
> egsingle.one$wgt <- 1 + get.weights(egsingle.ps,
+     type = "ATT", stop.method = "ks.stat.max")
```

```
Fitting gbm model
Iter   TrainDeviance   ValidDeviance   StepSize   Improve
     1        1.3853             nan     0.0100    0.0002
     2        1.3845             nan     0.0100    0.0004
     3        1.3833             nan     0.0100    0.0004
     4        1.3823             nan     0.0100    0.0005
     5        1.3814             nan     0.0100    0.0004
     6        1.3804             nan     0.0100    0.0004
     7        1.3795             nan     0.0100    0.0003
     8        1.3789             nan     0.0100    0.0002
     9        1.3779             nan     0.0100    0.0005
    10        1.3773             nan     0.0100    0.0003
   100        1.3263             nan     0.0100    0.0001
   200        1.2984             nan     0.0100    0.0000
   300        1.2827             nan     0.0100   -0.0000
   400        1.2711             nan     0.0100   -0.0002
   500        1.2629             nan     0.0100   -0.0000
   600        1.2562             nan     0.0100   -0.0001
   700        1.2508             nan     0.0100   -0.0001
   800        1.2463             nan     0.0100   -0.0001
   900        1.2421             nan     0.0100   -0.0001
  1000        1.2391             nan     0.0100   -0.0001
  1100        1.2360             nan     0.0100   -0.0001
  1200        1.2329             nan     0.0100   -0.0001
  1300        1.2307             nan     0.0100   -0.0000
  1400        1.2283             nan     0.0100   -0.0001
  1500        1.2259             nan     0.0100   -0.0001
  1600        1.2240             nan     0.0100   -0.0001
  1700        1.2224             nan     0.0100   -0.0000
  1800        1.2209             nan     0.0100   -0.0001
  1900        1.2193             nan     0.0100   -0.0001
  2000        1.2177             nan     0.0100   -0.0001
  2100        1.2165             nan     0.0100   -0.0001
  2200        1.2151             nan     0.0100   -0.0001
  2300        1.2141             nan     0.0100   -0.0001
  2400        1.2130             nan     0.0100   -0.0001
  2500        1.2119             nan     0.0100   -0.0001

Diagnosis of unweighted analysis
Optimizing with es.stat.mean stopping rule
   Optimized at 1658
Diagnosis of es.stat.mean weights
Optimizing with ks.stat.max stopping rule
   Optimized at 182
Diagnosis of ks.stat.max weights
```





```
> egsinge.resp <- merge(subset(egsingle, subset = resp ==
+     1), subset(egsingle.one, subset = resp ==
+     1, select = c(childid, wgt)))
```

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