# On Assessing the Specification of Propensity Score Models

Wang-Sheng Lee*

Melbourne Institute of Applied Economic and Social Research
The University of Melbourne

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**Abstract**

This paper discusses a graphical method and a closely related regression test for assessing the specification of the propensity score, an area where the literature currently offers little guidance. The approach involves non-parametric combination of separate *F*-tests so that an omnibus statistic is obtained. Based on a Monte Carlo study, it is found that the proposed regression test has considerable power to detect a misspecification in the link function used to estimate the propensity score, but has little power to detect omitted variables. A possible strategy for applied researchers would be to use the proposed tests in this paper in conjunction with sensitivity tests that check for the influence of unobserved variables. Such a strategy is shown to be helpful in limiting the bias one obtains when estimating average treatment effects in observational studies.

JEL Classifications: C21, C52
Key words: Propensity score, Specification, Monte Carlo, Non-parametric Combination

*Research Fellow, Melbourne Institute of Applied Economic and Social Research, The University of Melbourne, Level 7, 161 Barry Street, Carlton, Victoria 3010, Australia. E-mail: wang.lee@unimelb.edu.au. Thanks to Jeff Borland, Michael Lechner, Jim Powell and Chris Skeels for comments on an earlier version of this paper. I am also grateful to Carlos Flores, Alfonso Flores-Lagunes, Agne Lauzadyte, Gerard van den Berg, and other participants at the 3rd Annual IZA Conference on the Evaluation of Labor Market Programs (2007) for useful comments. All errors are my own.

## 1. Introduction

Despite being an important first step in implementing propensity score methods, the effect of misspecification of the propensity score model has not been subject to much scrutiny by researchers. In general, if the propensity score model is misspecified, the estimator of the propensity score will be inconsistent for the true propensity score and the resulting propensity score matching estimator may be inconsistent for estimating the average treatment effect. Recent papers that discuss the issue of the misspecification of propensity scores include Kordas and Lehrer (2004), who consider the application of semi-parametric methods to allow more flexibility in estimating the propensity score; Millimet and Tchernis (2007), whose Monte Carlo findings suggest that over-specifying the propensity score model might be beneficial; Shaikh et al. (2006), who propose a specification test based on a certain restriction between the estimated densities of the treatment and comparison groups; and Zhao (2007), who finds that the estimated average treatment effects are not sensitive to the specification of the propensity score if the conditional independence assumption underlying matching estimators holds. In current practice, a heuristic approach used by some applied researchers to check the specification of the propensity score is the propensity score specification test first suggested by Rosenbaum and Rubin (1984) and elaborated in more detail by Dehejia and Wahba (1999, 2002) (henceforth referred to as the DW algorithm). However, with the possible exception of Lee (2006), the properties of the DW algorithm have to date not been subject to much investigation and its use as a specification test is by no means universally accepted.[1]

This paper discusses a graphical method and a closely related regression test for assessing the specification of the propensity score, an area where the literature currently

[1] For example, many papers in the applied economics literature that use propensity score methods do not use the DW algorithm as a specification test. Many others also do not conduct any specification tests and rely on ad hoc specifications of the propensity score.

offers little guidance. The graphical method is an original proposal that integrates a suggestion of Rubin (1984) with the ideas of regression graphics for binary responses in Cook (1996), Cook (1998) and Cook and Weisburg (1999). It is based on using two-dimensional scatter plots and is useful for visualising balance in continuous covariates. In addition, a more general regression interpretation of the graphical method is made involving the use of non-parametric combination (Pesarin 2001). Based on a Monte Carlo study, it is found that the proposed regression test has considerable power to detect a misspecification in the link function used to estimate the propensity score, although it is found that it has little power to detect omitted variables. However, note that balancing tests in general should not be expected to be able to detect omitted variables as balancing tests are not tests for the Conditional Independence Assumption (CIA). Hence, finding such a limitation in the proposed test is not entirely surprising. A possible strategy for applied researchers would be to use the proposed tests in this paper in conjunction with sensitivity tests that check for the influence of unobserved variables. Such a strategy is shown to be helpful in limiting the bias one obtains when estimating average treatment effects in observational studies.

The layout of the paper is as follows. In section 2, some background information is provided on diagnostics for propensity score methods to set the context for understanding where the graphical diagnostics fit in. In section 3, we introduce the use of two-dimensional scatter plots to guide in the specification of the propensity score. In section 4, we use simulated data to illustrate the graphical test. Section 5 discusses a regression interpretation of the graphical test and performs a Monte Carlo study. Section 6 discusses other possible applications of the proposed regression test. Finally, section 7 concludes.

## 2. Propensity Score Diagnostics

One advantage of matching over regression based methods for estimating average treatment effects is that diagnostics are available for the former that do not involve use of the outcome variable. Only information on the observable covariates are needed for such a diagnostic so there is no way that performing these diagnostics can systematically influence estimates of the average causal effect. In the case of propensity score matching, balancing tests are often performed to check if the treatment and comparison group are comparable. More specifically, the idea behind balancing tests is to verify if *X* has the same distribution for the treatment and comparison groups conditional on the propensity score:

$$D \perp X \mid p(X)$$

where *D* is the binary treatment group indicator, *X* is a set of covariates that are chosen to fulfil the CIA and $p(X) = \Pr(D = 1 \mid X)$ is the true propensity score. The basic intuition is that after conditioning on *p(X)*, additional conditioning on *X* should not provide new information on *D*.

### 2.1 *How Well is the Propensity Score Estimated?*

In practice, of course, the true propensity score is unknown and needs to be estimated. In general, the literature has placed much less attention on the specification of the propensity score (both the choice of variables and functional form), compared with the issues regarding how the propensity score is to be used (choice of matching algorithm and matching structure).[2] In part, this could be because the results of Drake (1993) suggest that misspecification of the propensity score model does not lead to large biases relative to misspecification of the response model. In addition, Rubin and

[2] See, for example, Augurzky and Kluve (2007), Frölich (2004), and Zhao (2004) who all emphasize the latter.

Thomas (1992a, 1996) and Gu and Rosenbaum (1993) show that much of the balance resulting from matching on *p(X)* alone can be achieved with relatively coarse matching. For example, when stratification (or blocking) on the propensity score is done, the intuition is that there is less reliance on correct specification of the model used to estimate the propensity score since the probabilities are used only to partially order the sample.

However, estimating the propensity score accurately and correctly can be important in some cases. For example, in the case when the propensity score is used as a Horvitz-Thompson type estimator based on weighting by the inverse of the estimated propensity scores (e.g., Dinardo, Fortin, Lemieux 1996; Hirano and Imbens 2001; Hirano, Imbens and Ridder 2003), the propensity score is used directly in the process for estimating treatment effects. Rubin (2004) notes that "[i]n such cases, the estimated probabilities can be very influential on the estimated effects of treatment versus control, and so the probabilities themselves must be very well-estimated." In this case, specification tests that can check how well the estimated propensity score is estimated would clearly be important. The graphical method discussed in this paper attempts to measure how well the propensity score is estimated by checking if there are regions of the propensity score where $X$ is unbalanced.

### 2.2 *Model Checking Diagnostics versus Propensity Score Model Diagnostics*

Little advice is currently available regarding which model or functional form (e.g., logistic models, probit models, semi-parametric models etc.) is best for estimating the propensity score, although slightly more advice is available regarding the inclusion (or exclusion) of covariates in the propensity score model (e.g., see Caliendo and Kopeinig 2008). Regardless of the method used to estimate the propensity score, as propensity scores serve only as devices to balance the observed distribution of covariates between the treated and comparison groups, many model checking diagnostics that pertain to specific model classes are arguably irrelevant. For example, in the case of logistic models, these would be tests like the Pearson $\chi^2$ goodness-of-fit test and the ROC curve. Instead, the success of propensity score estimation should be assessed by the resultant balance rather than by the fit of the models used to create the estimated propensity scores. Rubin (2004) distinguishes between: (a) diagnostics for the successful prediction of probabilities and parameter estimates underlying those probabilities, possibly estimated using logistic regression; and (b) diagnostics for the successful design of observational studies based on estimated propensity scores, possibly estimated using logistic regression. He states that "there is no doubt in my mind that (b) is a critically important activity in most observational studies, whereas I am doubtful about the importance of (a) in these." Rubin further notes that many applications of propensity score methods have not appreciated this subtle point and continue to use (a) for propensity score diagnostics. The graphical methods discussed in this paper add to the toolbox available for task (b).

2.3 *Before-matching versus After-matching Balancing Tests*

In order to understand the context in which the graphical methods discussed in this paper are relevant, it is important to make a distinction between "before-matching" and "after-matching" balancing tests. Although Caliendo and Kopeinig (2008) classify the DW algorithm as part of their step (iv) (see their Figure 1), we prefer to classify it as part of their step (i) and would only classify the other balancing tests they mention in their step (iv). This is because the DW algorithm is implemented for the full sample (in the region of common support) that is used to estimate the propensity score model *before* any matching is done (and hence is more like a specification test of the propensity score model) while other balancing tests like two sample *t*-tests and the Hotelling test are done *after* matching and use a smaller subsample of the original data (where unmatched comparison group observations in the common support region are dropped).[3]

2.4 *Choosing the Relevant Diagnostic*

Combining the three concepts discussed above – the relative importance of correctly estimating the propensity score, the difference between model checking diagnostics and propensity score model diagnostics, and the difference between before-matching and after-matching tests – this suggests that diagnostic tests for propensity score methods likely work best when closely aligned with how the estimated propensity scores are to be used.

Before-matching balance diagnostics like the DW algorithm are more relevant if the full sample (in the region of common support) that is used to estimate the propensity score is to be used for estimating average causal effects. In the case of stratification on the propensity score, as the probabilities are used only to partially order the sample, coarse estimates of the propensity score might be sufficient. However, in the case of weighting on the propensity score, since small changes in estimated probabilities can have large effects on the estimated average causal effects, more accurate estimates would be needed. Here, tests that can check for how well the propensity score is estimated would be very useful.

On the other hand, after-matching balance diagnostics such as the test of standardized differences (Rosenbaum and Rubin 1985) or two sample *t*-tests would

[3] Lee (2006) provides a more detailed discussion regarding the difference between before-matching and after-matching diagnostics.

appear to be more relevant if a smaller matched sample is used for estimating average causal effects. For example, in the case of one-to-one nearest neighbor matching, the estimated average causal effects could be rather insensitive to the estimated probabilities if the rank ordering of the estimated propensity scores remains relatively stable under different empirical specifications. However, having an accurately estimated propensity score could once again be more important if the estimated probabilities are used to create weights. For example, in kernel matching, the weight that is given to a comparison group unit is proportionate to the closeness of its characteristics to a treated unit (i.e., the further away the comparison unit is from the treated unit in terms of the estimated propensity score, the lower the weight). In particular, in using a Gaussian kernel, kernel matching uses the whole sample of comparison group units in the region of common support. It would therefore appear that tests that can check for how well the propensity score is estimated would again be helpful in this context.

In the remainder of this paper, two before-matching diagnostics are discussed: a graphical approach (sections 3 and 4) and a closely related regression test that involves the idea of non-parametric combination (section 5).

## 3. Dimension Reduction and Regression Graphics

Propensity score matching is a dimension reduction technique that attempts to avoid the problem of the curse of dimensionality when the number of covariates is large (i.e., it is difficult to match on a large number of covariates). There simultaneously exists a large literature on dimension reduction in statistics.[4] But thus far, there has been little or no connection made between the two parallel literatures of dimension reduction. As we show below, the idea of a dimension reduction subspace for the regression of *Y*

[4] Heckman, Ichimura, Smith and Todd (1998) also discuss a related notion of "index sufficiency" to characterize selection bias in matching estimators.

on $X$ (Li 1991), which represents a sufficient reduction in the dimension of the set of covariates $X$, is closely related to the balancing property of propensity scores given in Theorem 2 of Rosenbaum and Rubin (1983).

### 3.1 *Overview of Dimension Reduction Regression*

In the general regression problem, letting $n$ be the number of observations, we have a $q \times n$ response $Y$ (usually $q$ =1) and a $s \times n$ predictor $X$, and the goal is to learn about how the conditional distribution $F(Y \mid X)$ varies as $X$ varies through its sample space. In parametric regression, we specify a functional form for the conditional distribution. In non-parametric regression, no functional form assumptions are made about $F(Y \mid X)$. Dimension reduction regression is one intermediate possibility between the parametric and non-parametric extremes. Dimension reduction without loss of information is a dominant theme of regression graphics. An attempt is made to reduce the dimension of $X$ without losing information on $Y \mid X$. Although the idea of dimension reduction regression was originally introduced for continuous response variables (Cook 1994), extensions have been made for the case of binary response variables (Cook 1996, Cook and Lee 1999). These extensions are important as it is through these extensions that the ideas from regression graphics can then be related to the propensity score framework in which there is a binary treatment indicator.

In dimension reduction regression (see, for example, Cook 1998 and Cook and Weisburg 1999), it is assumed without loss of information that the conditional distribution $F(Y \mid X)$ can be indexed by $d$ linear combinations of $X$, or for some unknown $s \times d$ matrix $B$, with $d \leq s$

$$F(Y \mid X) = F(Y \mid B'X) \tag{1}$$

This statement is equivalent to saying that the distribution of $Y \mid X$ is the same as that of $Y \mid B'X$ for all values of *X*. It implies that the $s \times n$ matrix of covariates *X* can be replaced by the $d \times n$ predictor matrix $B'X$ that contains $d$ linear combinations without loss of regression information. In other words, using the conditional independence notation introduced by Dawid (1979), we can write:

$$Y \perp X \mid B'X \tag{2}$$

This represents a potentially useful reduction in the row dimension of the matrix of covariates *X* from *s* to *d*. Such a *B* always exists because (2) is trivially true when $B = I_S$, the $s \times s$ identity matrix. The relation in (2) can be viewed as a statement about a dimension reduction subspace for the regression of *Y* on *X* (see, for example, Cook 1996 and Cook and Lee 1999). The *d* linear combinations $B'X = (b_1'X, b_2'X, ..., b_d'X)$ are referred to as *sufficient predictors* in the regression graphics literature because together they contain all the regression information that *X* has about *Y*.

In the case when $d = 1$, replacing *Y* with *D* in (2) (where *D* is a binary indicator denoting treatment group membership) and the $1 \times n$ predictor vector $B'X$ with the $1 \times n$ vector *p(X)*, it is immediately obvious that (2) is the balancing property of propensity scores. Having $B = I_S$ corresponds to the propensity score being equal to the "most trivial balancing score", which is when the balancing score is *X* (see Rosenbaum and Rubin 1983, p. 42).

3.2 *Binary Response Plots*

For the purposes of this paper, we are interested in using a particular interpretation of an auxiliary plot used in regression graphics for binary variables.[5] In

[5] The regression graphics literature focuses on estimating *d* and the subspace $B'X$. An overview of regression graphics is given in Appendix A.

particular, these auxiliary plots are the *binary response plots* in Cook (1996, Figure 1), Cook (1998, Figure 5.3) and Cook and Weisburg (1999, Figure 22.6). Here, we integrate the interpretation of binary response plots with a suggested graphical diagnostic of Rubin (1984) for logistic regression models in order to create a diagnostic for the specification of the propensity score. By viewing Rubin's diagnostic using Cook's insights, a graphical method can be used as a diagnostic to check balance for any continuous $X$ variable, *regardless of the method used to estimate p(X)*. Rather than trying to estimate $B'X$ and the dimension $d$ in a data set, the graphical diagnostic proposed in this section focuses on the $d = 1$ scenario and on using binary response plots to check if $D \perp X \mid B'X$ holds for each $X$ in the data set.[6] In other words, we are attempting to verify if the $s$-dimensional vector $X$ can be replaced by an exogenously given 1-dimensional vector *p(X)* without loss of regression information.

The exposition of how binary response plots can be used to assess balance in the context of propensity score matching is best developed using an example that appears in the literature. Although the context of the original discussion of the example in Landwehr, Pregibon, and Shoemaker (1984) is the specification of the fit of a logistic model or what Rubin (2004) terms "diagnostics for the successful prediction of probabilities and parameter estimates," we illustrate how a slight change in interpreting a graph that arose from the discussion of the paper allows for an assessment of balance to be made or what Rubin (2004) refers to as "diagnostics for the successful design of observational studies based on estimated propensity scores."

[6] Given the balancing property of propensity scores, it is true by definition that $d = 1$. Hence, the only source of a failure of a test of the balancing property is a misspecification of the propensity score, which could be due to an incorrect link function, an incorrect index function, or both.

3.3 *Example from Landwehr, Pregibon, and Shoemaker (1984)*

This section continues a discussion between Landwehr, Pregibon, and Shoemaker (1984) and Rubin (1984). In Example 4 of Landwehr, Pregibon, and Shoemaker (1984, p. 67), one hundred observations are generated according to the model: $\text{logit}(D) = -1 + X_5 + X_6 + 2X_6^2$. Presuming that the particular functional form or nature of the dependence on $X_5$ and $X_6$ is unknown, they start by fitting a model linear in $X_5$ and $X_6$ and calculate their suggested *partial residual plots* (which is discussed in more detail in their paper but not relevant to the present discussion) for $X_6$. They find that dependence on $X_6$ is non-linear and that an additional term such as $X_6^2$ or $|X_6|$ should be included in the model.

In commenting on Landwehr, Pregibon, and Shoemaker (1984), Rubin (1984) suggested that one alternative way of assessing the fit of the logistic regression model is to plot *X* versus the predicted values of the dependent variable (i.e., the propensity score) using different symbols for the *D* = 1 and *D* = 0 points (see Rubin 1984, example 1).[7] But in his written comments, Rubin (1984) did not further discuss how the plot should be interpreted. He also did not make the distinction between diagnostics for the successful prediction of probabilities and parameter estimates underlying those probabilities, and diagnostics for the successful design of observational studies based on estimated propensity scores, which he does more recently in Rubin (2004).

The discussion continued with Landwehr, Pregibon, and Shoemaker (1984a) responding to Rubin (1984). They used the generated data from the model described above, created the plot Rubin suggested based on estimating the misspecified model that

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[7] Incidentally, another suggestion of Rubin for assessing the fit of a logistic regression model (Rubin 1984, example 3), where he suggested categorizing the fitted probabilities and comparing the distributions of *X* for the *D* = 1 and *D* = 0 units within categories of the fitted probabilities, is a precursor and an informal version of the specification test described in more detail in Dehejia and Wahba (1999, 2002).

is linear in $X_5$ and $X_6$ but found that "[this] plot does not reveal to us anything about the inadequate fit of the model nor the need to transform $X_6$." Moreover, they state that the standard test for comparing two regression lines (the conditional distribution of $X_6$ given the fitted probabilities for $D = 1$ and $D = 0$) is not significant whereas their partial residual plot clearly demonstrates the basic model inadequacy.

Figure 1 below reproduces Figure 1 from Landwehr, Pregibon, and Shoemaker (1984a). Their focus is on the two regression lines which they highlight are not significantly different.

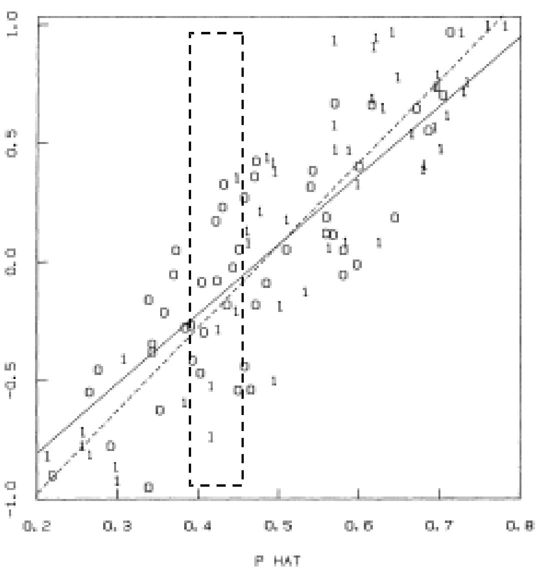



Figure 1: From Landwehr, Pregibon, and Shoemaker (1984a, Figure 1). The plot is a scatter plot of $X_6$ against the fitted probabilities. Plotted characters show the values of $D$. The solid diagonal line is the least squares regression of $X_6$ on the fitted probabilities for $D = 0$, the dashed diagonal line for $D = 1$. The meaning of the rectangular window (or vertical slice) is discussed in the text.

However, Rubin's suggestion of plotting $X$ versus the fitted probabilities using different symbols for the $D = 1$ and $D = 0$ points has a subtle interpretation that was not noted by Landwehr, Pregibon, and Shoemaker (1984a). This interpretation is similar to how binary response plots are interpreted in Cook (1996, Figure 1), Cook (1998, Figure 5.3) and Cook and Weisburg (1999, Figure 22.6).

Instead of focusing on the two regression lines, imagine viewing Figure 1 as a small rectangular window is moved horizontally across the plot (like the one over the value of PHAT = 0.4). To assess whether $D \perp X_6$ given the fitted probabilities (i.e., whether there is balance in $X_6$), Cook suggests looking for non-uniform intraslice densities within slices of the fitted probabilities, which effectively holds the fitted probabilities constant. Slices with only one type of symbol are consistent with the conditional independence statement, and so are any slices that have a roughly constant fraction of each type of symbol as one moves from the bottom to the top of the slice. Symbol density does not need to be similar from slice to slice, as long as it is constant within each slice. However, conditional independence (i.e., balance) is violated if in any slice, there is non-random variation in symbol density as one moves from the bottom to the top of the slice.

More formally, following Cook (1996), let the small rectangular window $\Delta$ for the *j*th predictor be:

$$\Delta = \{X \mid a_j \le X_j \le b_j,\ j = 1, \dots, p\}$$

where $a_j$ and $b_j$ are the left and right boundaries of the window. The ratio of the counts in each window can be expressed in terms of the fraction of one symbol in $\Delta$:

$$\frac{\Pr(X \in \Delta, D = 1)}{\Pr(X \in \Delta)} = E(D \mid B'X \in \Delta_B)$$

where $\Delta_B = \{B'X \mid X \in \Delta\}$. If $D \perp X \mid B'X$ then the fraction of each symbol should be roughly constant within each $\Delta$. Although one could technically count the ratio of one symbol relative to the total, Cook suggests that "[w]ith a little practice, it seems possible to assess relative symbol density visually without actually counting" (Cook 1996, p. 985).

The rectangular window depicted in Figure 1 (over the value of PHAT = 0.4) shows that within that slice, it is more likely for group '1' to have lower values of $X_6$ than group '0'. In other words, if we were assessing whether $D \perp X_6 \mid p(X)$ for this chosen model specification, it would be possible to conclude that the conditional independence relation is not supported by the data. Contrary to the conclusion reached by Landwehr, Pregibon, and Shoemaker (1984a), by focusing on rectangular windows instead of the two regression lines in Figure 1, it would therefore be possible to conclude that the model specification that is linear in $X_5$ and $X_6$ is inappropriate.

For the remainder of this paper, we refer to this plot as the *Rubin-Cook plot*, as Rubin had first suggested it as a possible diagnostic for fitting logistic regression models while Cook's interpretation of such binary response plots is what makes it useful as a propensity score model diagnostic. Recall that the intuitive idea behind propensity score matching is that there are many miniature experiments at each value of the propensity score (see Zhao 2004). In other words, holding the propensity score constant, there should be no relationship between each covariate and the treatment indicator. The graphical diagnostic described in this section essentially puts into practice this intuitive idea.[8]

Although graphical tests like the Rubin-Cook plot that depend on eyeballing the data might be considered subjective and not have the rigorous flavor that statistical tests that involve the use of non-subjective and easy to interpret p-values might have, complements to statistical tests can be useful if they help researchers see different aspects of their data more clearly.

[8] From the practical perspective, Rubin-Cook plots can be created by any standard statistical software packages that can create scatter plots. Specialized software like *Arc* that are necessary for regression graphics are not needed in order for the plots to be created.

## 4. Simulated Data Example

In this section, we generate 200 observations according to the model: $\text{logit}(D) = -1 + X_1 + X_2 + 3X_1X_2$, where $X_1$ and $X_2$ are drawn from N(0, 1) distributions.[9] As we draw error terms such that they are independent of *X*, the generated data set is balanced by construction.[10] We estimate the propensity score using two specifications. In the first specification (S1), we do not correctly model the interaction term in a logistic model and instead specify a model linear in $X_1$ and $X_2$ while in the second specification (S2), we correctly include $X_1, X_2$ and the interaction term $X_1X_2$ in our logistic model. The question examined in this section is how well diagnostics for assessing the specification of *p(X)* work under S1 and S2. Will a researcher correctly choose S2 over S1 based on diagnostics performed on the estimated propensity score? As the data generated under S1 are unbalanced by construction while the data under S2 are balanced by construction, we can evaluate the ability of "diagnostics for the successful design of observational studies based on estimated propensity scores" to uncover the truth. The issue of which variables to include in *X* is not examined here as it is assumed that the researcher knows that $X_1$ and $X_2$ both need

[9] We draw values from N(0, 1) instead of U(-1, 1) distributions like in Landwehr, Pregibon, and Shoemaker (1984) because matching theory is more developed under the assumption of X having an ellipsoidal distribution (e.g., distributions such as the normal or *t*). For example, Rubin and Thomas (1992b) show that affinely invariant matching methods, such as Mahalanobis metric matching and propensity score matching (if the propensity score is estimated by logistic regression), are equal percent bias reducing if all of the covariates used have ellipsoidal distributions (note that "bias" here refers to mean differences in covariates and not bias in estimated treatment effects). The seed number used in the simulations in *Stata /SE 9.2* is 55623.

[10] Generating a balanced data set under the null in order to perform the simulations was done as follows. In the binary choice selection equation, because we assume that the error term in the selection equation is independent of the *X*s, when we use the error term, arbitrary values of and *X* to generate *D*, it is true that:

$$D \perp X \mid X\mathrm{b}$$

As only monotonic transformations are performed, it therefore follows that

$$D \perp X \mid \text{logit}(X\mathrm{b}) \quad \text{or} \quad D \perp X \mid p(X)$$

Therefore by construction, these data sets satisfy the balancing property of propensity scores: $D \perp X \mid p(X)$.

to be included in the model in order to fulfil the conditional independence assumption underlying matching estimators, but does not know the functional form they take.

4.1 *Rubin-Cook Plots for Simulated Data*

The Rubin-Cook plots for both covariates $X_1$ and $X_2$ are constructed in this section. Figure 2 plots the Rubin-Cook plots under the incorrect specification of the propensity score while Figure 3 does the same using the correct specification of the propensity score.

In the top panel of Figure 2, when assessing balance for $X_1$, checking for constant symbol density within vertical slices shows that in at least three intervals of the propensity score, there is non-constant symbol density. The findings are similar when checking for balance in $X_2$ in the bottom panel of Figure 2, where four occasions of non-constant symbol density are highlighted using rectangular windows. As the Rubin-Cook plots in Figure 2 depict that it is not the case that $X_1 \perp D \mid p(X)$ and $X_2 \perp D \mid p(X)$, this suggests that S1 is not a useful balancing score. A parallel and equivalent interpretation is that using S1 as the estimated propensity score does not lead to sufficient dimension reduction so it cannot be concluded that information in *p(X)* can be used to replace information in *X*. It is also worth noting that if the data set contains many more observations (e.g., $n$ = 10,000), the Rubin-Cook plot can still be used. The only adjustment that needs to be made is to zoom in on smaller regions of the propensity score. For example, each graph in Figure 2 could be replaced by 10 separate graphs plotting the intervals *p(x)* = 0 to 0.1, 0.1-0.2 etc.

Figure 3 repeats the same exercise for the correct specification of the propensity score. Relative to Figure 2, one immediately obvious finding from the figures is that there is more separation between the $D$ = 1 and $D$ = 0 observations, with more of the former clustered around high values of *p(X)* and more of the latter clustered around low values of *p(X)*. Recall that each slice where there are only $D = 1$ or $D = 0$ observations can be ignored when assessing balance. Assessing balance in Figure 3 therefore involves focusing on rectangular windows that start from approximately *p(X)* = 0.2 and end with *p(X)* = 0.7 where there are both $D = 1$ or $D = 0$ observations. Compared to Figure 2, it is clear that the symbols are distributed much more randomly within each vertical slice, reflecting the intuition of miniaturized experiments at each value of *p(X)*. Compare, for example, the highlighted rectangular windows in Figure 3 with the windows in Figure 2. Based on the Rubin-Cook plot for S2, a researcher would be much more likely to conclude that S2 serves as a useful balancing score.

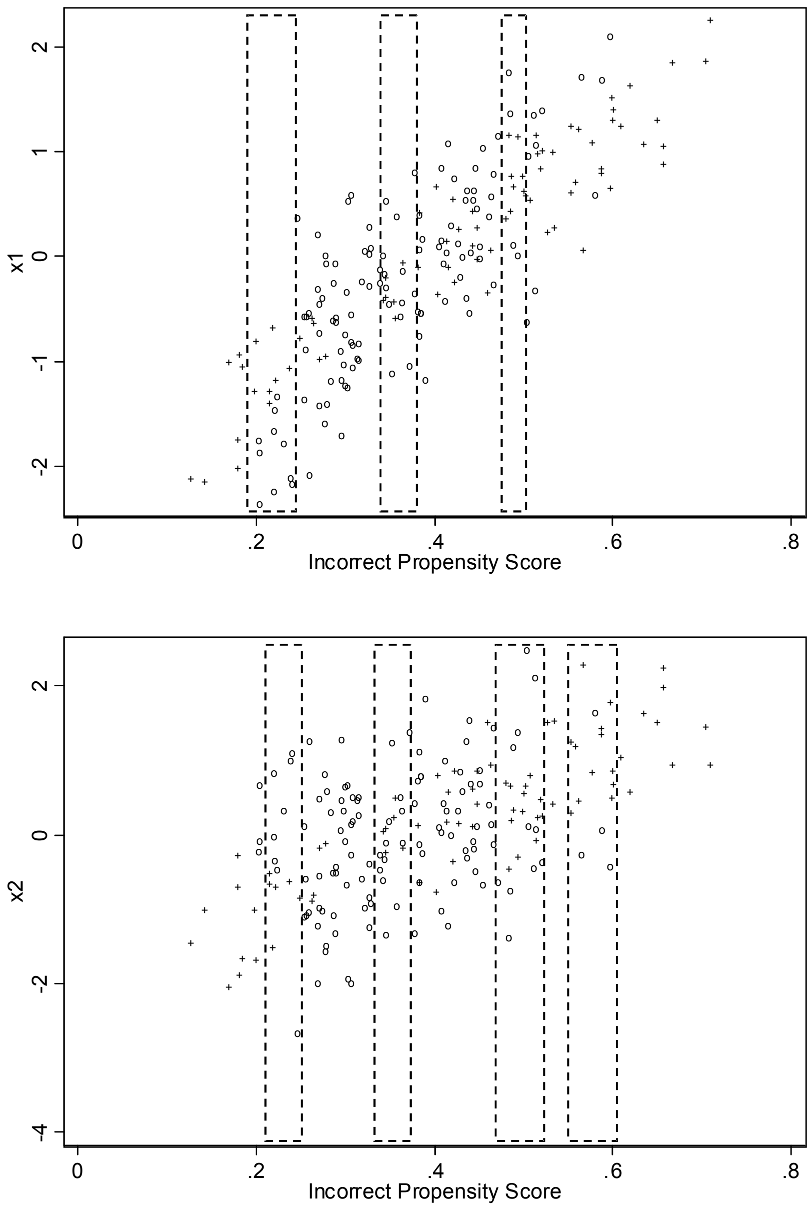
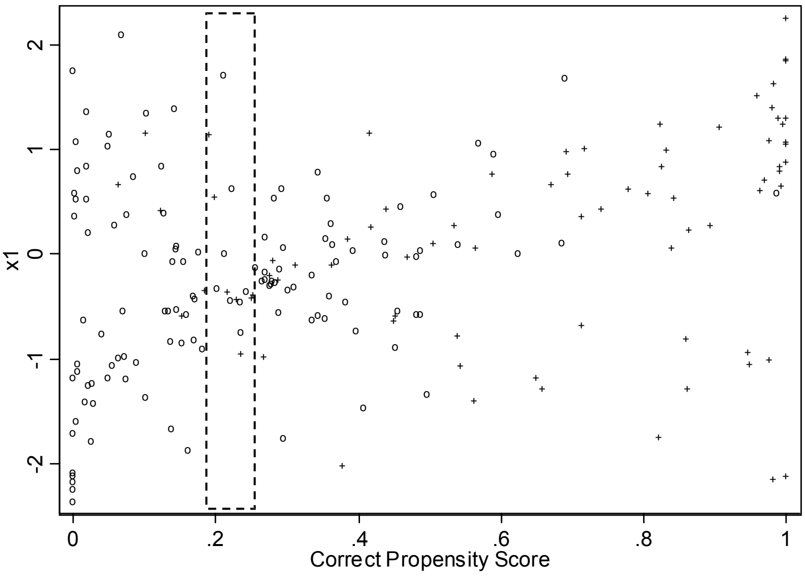



Figure 2: Rubin-Cook Plots for $X_1$ versus the Incorrect Propensity Score (top panel) and $X_2$ versus the Incorrect Propensity Score (bottom panel)

Notes: The '+' symbol denotes treatment group members while the 'o' symbol denotes comparison group members.



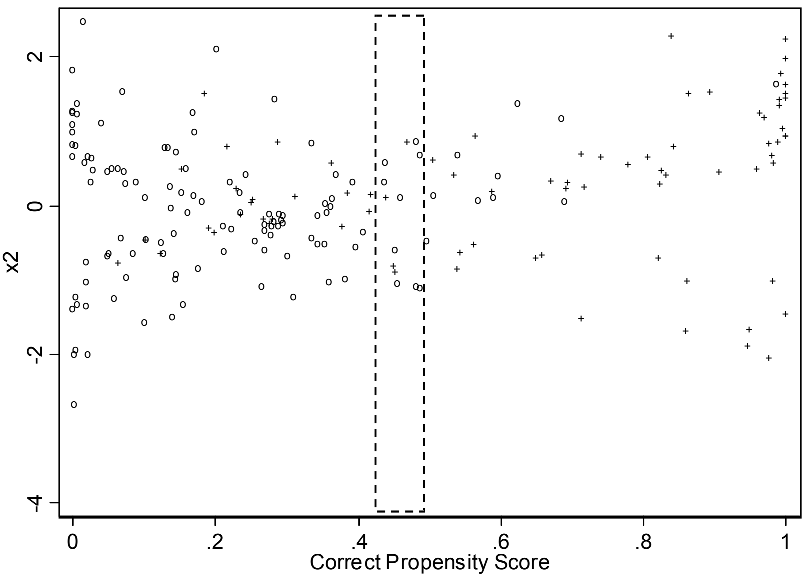




Figure 3: Rubin-Cook Plots for $X_1$ versus the Correct Propensity Score (top panel) and $X_2$ versus the Correct Propensity Score (bottom panel)

Notes: The '+' symbol denotes treatment group members while the 'o' symbol denotes comparison group members.

## 5. A Regression Test Interpretation of the Rubin-Cook Plot

Although Rubin-Cook plots can be informative, their use is rather limited when the number of covariates in $X$ is large (as there is one plot per regressor and it is not clear what the implications are if conflicting results for different regressors show up) or when there are categorical variables. For example, in the simulated example in section 4, if $X_1$ were binary instead of continuous, then a Rubin-Cook plot of $X_1$ versus $p(X)$ would have values of $X_1$ lined up along $X_1 = 1$ and $X_1 = 0$, making any kind of graphical interpretation impossible, even if the points are "jittered" (i.e., introducing controlled amount of noise to plots to prevent overprinting in the same spot). One possible way around this would be to have different Rubin-Cook plots for each value of the categorical variable. For example, in a model with $X_1$ binary and $X_2$ continuous, instead of plotting the two graphs of $X_1$ versus $p(X)$ and $X_2$ versus $p(X)$, one could plot two graphs of $X_2$ versus $p(X)$, one each for $X_1 = 1$ and $X_1 = 0$. However, if there are many categorical variables in the data set, it is not difficult to see that such an approach can quickly become impractical.

In addition, it is difficult to generalize the results in section 4 from a single simulated data set. Although one might consider performing a Monte Carlo study of Rubin-Cook plots, that would require a method of summarising the information in the plots obtained from the different replications. Unfortunately, it does not appear that there is a simple automated method of summarizing information from the plots. We therefore turn to a regression test interpretation of the "eyeball" test in the Rubin-Cook plot that is more amenable to a Monte Carlo study.

The balancing property of propensity scores contends that when the regression vector $X$ is augmented by the propensity score, the $(s+1)$-dimensional vector ($X$, $p(X)$) can be reduced to $p(X)$ for the conditioning set. This hypothesis suggests a natural localized regression test. After *p(X)* is estimated, within local rectangular windows of *p(X)*, one can estimate the following regression:

$$D = \alpha + \sum X\beta \qquad (3)$$

A permutation version of the standard *F*-test can then be conducted to test that all the $\beta$ coefficients are jointly equal to zero. In other words, under the null that *p(X)* is a balancing score, within small rectangular windows of *p(X)*, information from the vector *X* would no longer provide useful information on *D*. This test is a literal multivariate interpretation of the Rubin-Cook plot seen in Figures 2 and 3. The test combines features of both the DW algorithm (in that it requires suitable intervals or windows of *p(X)* to be defined) and the regression test described in Smith and Todd (2005b) (who suggest using an F-test in a regression as a test for balance, but in a different way).

Once the results of the permutation version of the *F*-test for each window of *p(X)* have been tabulated, following Pesarin (2001), a non-parametric combination of univariate tests is then performed using Fisher's combining function in order to obtain an omnibus statistic that will allow us to determine if the propensity score serves as a useful balancing score. Fisher's combining function is based on the statistic:

$$T_F = -2\sum_{i=1}^{k} \log(\lambda_i)$$

It is well known in the statistics literature that if the *k* partial test statistics are independent and continuous, then in the null hypothesis $T_F$ follows a central $\chi^2$ distribution with 2*k* degrees of freedom.[11]

A Monte Carlo simulation is conducted in the next section in order to better understand the statistical properties of the proposed test.

[11] A good illustrative example involving propensity score strata and non-parametric combination is given in section 12.7 of Pesarin (2001).

5.1 *Monte Carlo Simulation*

The Monte Carlo simulations in this section are based on the NSW-PSID data used in Dehejia and Wahba (1999, 2002) and many other papers in the labor economics literature. In particular, we examine the size of the test and if the power of the proposed balancing tests increases as the degree of misspecification of the propensity score systematically increases. For the power simulations, in our data generating process (DGP), we generate the true propensity score using a heterogeneous probit model. Assume the true DGP for treatment assignment is:

$$\begin{aligned} D = 1\{&-4.5001 + 0.1931\text{age} - 0.0036\text{age}^2 + 0.4188\text{educ} - 0.0239\text{educ}^2 + 0.1152\text{nodegree} \\ &- 0.9599\text{married} + 0.6594\text{black} + 1.084\text{hisp} - 0.00005\text{re74} - 0.00009\text{re75} \\ &- 0.00000000116\text{re74}^2 - 0.0000000000281\text{re75}^2 + 1.228\text{black*U74} + u > 0\} \end{aligned}$$

where $u$ is independent of the covariates and has a standard normal distribution (i.e., the true model is a probit). Similarly, assume the true DGP for the outcome variable is given by:

$$\begin{aligned} Y = &-2872.058 + 1000D + 106.30\text{age} - 2.62\text{age}^2 + 586.52\text{educ} + 629.18\text{nodegree} \\ &+ 975.46\text{married} - 518.28\text{black} + 2248.67\text{hisp} + 0.2757\text{RE74} + 0.5659\text{RE75} + e \end{aligned}$$

where $e$ is N(0, 1000). The coefficients for these equations are based on the actual coefficients from the NSW-PSID data set, using the originally assigned treatment group values and earnings in 1978 (*RE78*) as the outcome. The true treatment effect is set at \$1,000.

The heteroskedastic probit model generalizes the standard probit model by assuming that the variance of the error term is no longer fixed at one but allowed to vary as a function of the independent variables. Following Harvey (1976), assume that the variance of $\upsilon$ has a multiplicative functional form

$$Var(\upsilon) = \sigma^2 = \exp(z\gamma)^2$$

where $z$ is a vector of covariates that define groups with different error variances in the underlying latent variable, and $\gamma$ is a vector of parameters to be estimated. This is a convenient functional form because if all the elements of $\gamma$ are equal to zero, then $e^0 = 1$ and the heteroskedastic probit model is reduced to a standard probit model.

Seven different DGPs are used to determine how results of balance and imbalance in covariates from permutation tests relate to bias in the estimated average treatment effect on the treated (ATT). In particular, suppose that:

$$\begin{aligned} z\gamma = c[&0.1931\text{age} - 0.0036\text{age}^2 + 0.4188\text{educ} - 0.0239\text{educ}^2 + 0.1152\text{nodegree} - 0.9599\text{married} \\ &+ 0.6594\text{black} + 1.084\text{hisp} - 0.00005\text{re74} - 0.00009\text{re75} - 0.00000000116\text{re74}^2 \\ &- 0.0000000000281\text{re75}^2 + 1.228\text{black*U74}] \end{aligned}$$

and that we use values of $c = \{0, 0.1, 0.2, 0.5, 1, 2, 4\}$.

Define <u>Specification 1</u> as the case where the correct index function is used but the incorrect link function is used (logistic instead of probit). Figure B.1 in Appendix B shows how heteroskedasticity can lead to substantial misspecification in the estimated propensity score. Based on a single simulation, the figures in the left panel of Figure B.1 compares the densities of the true propensity score versus the estimated propensity score, while the figures in the right panel of Figure B.1 show in an alternative way the extent in which the propensity score is estimated incorrectly (they should be on a 45 degree line if the estimated propensity score equals the true propensity score). Note that when c = 0, the model is a standard probit model. As the graphs for the standard probit and standard logistic models are rather similar, the extent to which the graph with c = 0 is different from the graphs when c ≠ 0 can be used as an indication of the severity of model misspecification. The simulations under specification 1 involve generating the data assuming that the true DGP is a heterogeneous probit model (while varying a parameter that captures the degree of heterogeneity) but estimating the propensity score using a logistic model.

In order to reflect choices that a researcher might make in estimating the propensity score using the same data, four additional scenarios are considered in addition to the case where the correct index function but incorrect link function is used. Scenarios 2 to 5 differ in the index function used and are defined below. In all cases, the (incorrect) logistic link function is used.

<u>Specification 2</u>: Omit the squared terms $age^2$, $educ^2$, $re74^2$, and $re75^2$ .

<u>Specification 3</u>: Omit the race variables *black*, *hisp*, and *black*U74*.

<u>Specification 4</u>: Omit terms involving *re74* in the index function but overspecify the model using higher order terms and interactions for the other variables.[12]

<u>Specification 5</u>: Over-specify the model using higher order terms and interactions.[13]

Specification 2 is the case when the propensity score is under-specified. Specification 3 reflects the case when there are omitted variables. Specification 4 likewise is an omitted variables case, but it adopts a suggestion put forth by Millimet and Tchernis (2007) and over-specifies the propensity score. Finally, specification 5

[12] The variables in the index function are: age $age^2$ $age^3$ educ $educ^2$ $educ^3$ married nodegree black hisp re75 $re75^2$ married*U75 nodegree*U75 black*U75 hisp*U75 age*educ age*married age*re75 educ*re75.
[13] The variables in the index function are: *age* $age^2$ $age^3$ *educ* $educ^2$ $educ^3$ *married nodegree black hisp re74* $re74^2$ *re75* $re75^2$ *married*U74 nodegree*U74 black*U74 hisp*U74 married*U75 nodegree*U75 black*U75 hisp*U75 age*educ age*married age*re74 educ*re74 age*re75 educ*re75.*

includes the set of variables that fulfills the CIA and like scenario 3 over-specifies the propensity score.

The regression test in equation (3) requires the definition of suitable windows or propensity score strata so that localized regressions can be run. The implementation of the test in this paper uses a variation of the method described in the appendix of Dehejia and Wahba (2002) to choose the 'optimal' number of intervals. First, the sample is split into $k$ equally spaced intervals of the propensity score. Next, using a standard $t$-test, a test is conducted at the Bonferroni adjusted level $(\alpha / k)$ that the mean values of $p(X)$ for the treated and comparison units do not differ. If the test fails, the sample is split in half and the test is repeated again. The 'optimal' number of intervals is found when the values of $p(X)$ for the treated and comparison units do not differ in all intervals. After experimenting with the choice of the number of initial intervals to use, we decided to use $k = 5$ as our initial starting point. Larger choices of $k$ (e.g., $k = 20$) led to similar results but also tended to produce very sparse regions of the propensity score where an $F$-test would arguably have little power. For the permutation versions of the $F$-tests conducted within each interval of the propensity score, 1,000 random permutations were used.[14]

### 5.2 *Monte Carlo Simulation Results*

The results of the Monte Carlo simulations are given in Tables 1 to 3. The estimated ATT is obtained by taking the mean difference $(Y \mid D = 1) - (Y \mid D = 0)$ averaged over 500 replications. The bias is then defined as 1,000 (the true treatment

[14] Although a permutation version of the $t$-test can be used to choose the optimal number of intervals, in practice, we found that it made little difference here in the overall results. The standard $t$-test here is used as it lowers the run time for the simulations considerably. However, permutation versions of the $F$-test are essential for applying the non-parametric combination approach described in section 5.

effect) minus the estimated ATT. In addition to bias, estimates of the root mean square error (RMSE) – the square root of the squared bias – are also presented.

Table 1 reports the simulation results of how often the non-parametric combination test approach rejects the null. The size of the test is reported in the first row in Table 1. The test sizes appear to be very reasonable especially when the CIA is fulfilled (specifications 1 and 5).

As far as power is concerned, in all five specifications considered, it is clear that as the degree of heteroskedasticity increases (i.e., as c increases), the test has higher power to detect the misspecification in the link function. However, as highlighted by Smith and Todd (2005a), balancing tests do not provide any guidance regarding which variables to include in the propensity score model. This point is illustrated in Table 1, where it is shown that the test has little or no ability to detect the omission of variables that are required to satisfy the CIA (specifications 2 to 4). In other words, positive results from this test (or any other balancing test for that matter) should not be used to support the case the CIA is fulfilled. However, in the case when the CIA is plausible (specifications 1 and 5), the proposed test can be useful in detecting misspecified link functions.

Table 1: Rejection Rate Based on Omnibus Statistic Obtained Through Non-Parametric Combination

| | Empirical specification | | | | |
|---|---|---|---|---|---|
| | 1 | 2 | 3 | 4 | 5 |
| Logistic true *p(X)* | 3.8% | 11.8% | 9.0% | 0.6% | 2.4% |
| Heterogeneous probit true *p(X)* with c = 0 | 1.8% | 25.0% | 11.2% | 1.4% | 2.8% |
| Heterogeneous probit true *p(X)* with c = 0.1 | 6.8% | 31.2% | 5.4% | 2.2% | 0.8% |
| Heterogeneous probit true *p(X)* with c = 0.2 | 18.8% | 54.4% | 8.6% | 4.8% | 4.8% |
| Heterogeneous probit true *p(X)* with c = 0.5 | 83.2% | 87.8% | 47.2% | 35.2% | 25.2% |
| Heterogeneous probit true *p(X)* with c = 1 | 99.0% | 100% | 92.0% | 88.0% | 85.0% |
| Heterogeneous probit true *p(X)* with c = 2 | 100% | 99.8% | 99.6% | 99.6% | 98.2% |
| Heterogeneous probit true *p(X)* with c = 4 | 99.8% | 100% | 100% | 100% | 99.8% |

Notes: In scenarios 1 and 5, the CIA is fulfilled. In scenarios 2, 3, and 4, the CIA is not fulfilled due to omitted variables. See the text for details of the specifications used. The propensity score is estimated in scenarios 1 to 5 using a logistic model.

Many papers that employ propensity score matching estimators in the literature do not conduct any balancing tests and simply rely on an ad hoc specification of the propensity score. Often, either a logistic or probit link function is used, and the index function used is typically linear, with some higher order and interaction terms possibly included. In the next two tables, we report the bias and RMSE in 35 possible scenarios – these involve combinations of what the true link function is (7 possibilities) and possible specification index functions that a researcher might use (5 possibilities).

Table 2 reports the simulation results when Kernel matching (using the Gaussian kernel) and a bandwidth of 0.06 is used to obtain estimates of the ATT.[15] Table 3 reports the simulation results when propensity score stratification is done, using the same strata that the proposed test uses to conduct its specification check.[16] All tests in the simulations are conducted over the region of common support.

As is evident from Tables 1 and 2, when no balancing tests are used, bias and RMSE can be high and is highly dependent on what "world" (i.e., combination of link function and index function) one is actually in and the type of matching algorithm used. For example, suppose the true link function is a heterogeneous probit with c = 1, but the researcher incorrectly uses a logistic link and omits the race variables. Under kernel matching, the bias is -474.5, whereas with propensity score stratification, it is -138.7.[17] Combining the results of the specification test from Table 1, we see that the use of a balancing test in this case helps to restrict one to scenarios involving $0 \le c \le 0.2$ which would help limit wide variability and higher bias in the estimated ATT.

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[15] This uses the *psmatch2.ado* Stata program written by Edwin Leuven and Barbara Sianesi.
[16] This uses the *pscore.ado* and *atts.ado* Stata programs written by Sasha Becker and Andrea Ichino.
[17] Under this DGP, it appears that stratification leads to lower bias and RMSE. But this does not imply that stratification is generally superior to kernel matching in all contexts. For example, we have not experimented with varying the bandwidth or using cross-validation to find an 'optimal' bandwidth to use. In addition, Frölich (2004) has highlighted that kernel matching can outperform nearest neighbor matching in many circumstances.

Table 2: Kernel Matching (Gaussian kernel), No balancing test done

| | Empirical specification | | | | |
|---|---|---|---|---|---|
| | 1 | 2 | 3 | 4 | 5 |
| Heterogeneous probit true *p(X)* with c = 0 | | | | | |
| Bias | -195.0 | -632.6 | -427.1 | -683.7 | -133.2 |
| RMSE | 469.0 | 872.9 | 571.2 | 809.2 | 466.0 |
| Heterogeneous probit true *p(X)* with c = 0.1 | | | | | |
| Bias | -145.0 | -818.2 | -356.8 | -700.1 | -145.0 |
| RMSE | 366.5 | 1018.9 | 493.8 | 863.9 | 366.9 |
| Heterogeneous probit true *p(X)* with c = 0.2 | | | | | |
| Bias | -209.2 | -1040.1 | -353.6 | -786.7 | -181.9 |
| RMSE | 392.8 | 1216.9 | 480.2 | 945.3 | 354.9 |
| Heterogeneous probit true *p(X)* with c = 0.5 | | | | | |
| Bias | -264.8 | -782.9 | -414.0 | -639.5 | -266.8 |
| RMSE | 381.5 | 859.0 | 476.7 | 708.4 | 336.9 |
| Heterogeneous probit true *p(X)* with c = 1 | | | | | |
| Bias | -311.4 | -389.4 | -474.5 | -457.2 | -306.9 |
| RMSE | 368.9 | 429.4 | 498.5 | 488.9 | 1056.5 |
| Heterogeneous probit true *p(X)* with c = 2 | | | | | |
| Bias | -327.6 | -193.6 | -546.4 | -424.6 | -391.7 |
| RMSE | 357.7 | 233.3 | 559.1 | 463.4 | 421.8 |
| Heterogeneous probit true *p(X)* with c = 4 | | | | | |
| Bias | -347.8 | -171.0 | -580.9 | -446.4 | -440.3 |
| RMSE | 377.3 | 241.1 | 597.6 | 499.9 | 486.1 |

Table 3: Propensity Score Stratification, No balancing test done

| | Empirical specification | | | | |
|---|---|---|---|---|---|
| | 1 | 2 | 3 | 4 | 5 |
| Heterogeneous probit true *p(X)* with c = 0 | | | | | |
| Bias | -78.7 | -198.7 | -226.2 | -464.3 | -51.2 |
| RMSE | 454.9 | 446.0 | 428.4 | 627.9 | 474.7 |
| Heterogeneous probit true *p(X)* with c = 0.1 | | | | | |
| Bias | 118.9 | 18.4 | -48.7 | -244.3 | 75.8 |
| RMSE | 367.6 | 199.3 | 326.4 | 423.0 | 352.1 |
| Heterogeneous probit true *p(X)* with c = 0.2 | | | | | |
| Bias | 99.3 | 108.8 | -46.6 | -193.8 | 87.2 |
| RMSE | 337.8 | 196.8 | 258.9 | 353.3 | 318.4 |
| Heterogeneous probit true *p(X)* with c = 0.5 | | | | | |
| Bias | 60.5 | 250.8 | -22.2 | -137.0 | -12.6 |
| RMSE | 272.2 | 284.5 | 271.0 | 259.3 | 228.4 |
| Heterogeneous probit true *p(X)* with c = 1 | | | | | |
| Bias | -18.7 | 308.8 | -138.7 | -109.8 | -95.9 |
| RMSE | 228.5 | 339.8 | 259.3 | 222.7 | 201.6 |
| Heterogeneous probit true *p(X)* with c = 2 | | | | | |
| Bias | -49.3 | 319.9 | -242.3 | -206.2 | -216.4 |
| RMSE | 187.5 | 351.9 | 283.5 | 279.1 | 264.2 |
| Heterogeneous probit true *p(X)* with c = 4 | | | | | |
| Bias | -79.1 | 287.2 | -274.9 | -276.7 | -295.3 |
| RMSE | 177.1 | 326.9 | 308.4 | 350.1 | 355.3 |

Another useful point to note from Tables 2 and 3 is that the Millimet and Tchernis (2007) suggestion of over-specifying the propensity score model generally seems to work well for $c \leq 0.5$ (compare specifications 1 and 5). In other words, although the incorrect link function is used to estimate the propensity score, over-specifying the propensity score might somewhat compensate for this by allowing for more non-linearities.

## 6. Other Possible Applications

The focus of the previous section has been to justify the use of the regression test in equation (3) as a specification test for propensity score models. More generally, however, one can view the regression test as a natural extension of the ideas in Rubin (1984) and Cook (1996), and utilize it as a general specification test for a regression model where the outcome is binary.

In addition, although the simulations in this paper have focused exclusively on the case of assessing the specification of the propensity score in the case of a binary treatment, equation (3) can also be used as a more general specification test in the case of multi-valued treatments (Imbens 2000, Lechner 2001) or continuous treatments (Hirano and Imbens 2004). These papers employ the concept of a generalized propensity score (GPS) that is used to adjust for selection bias in a similar way that the propensity score does for the case of binary treatments.

In the case of a multi-valued or continuous treatment, one approach to check the balance of each covariate consists of running a regression of each covariate on the log of the treatment and the GPS (e.g., Imai and van Dijk 2004, Flores-Lagunes et al. 2007). As the GPS has a balancing property similar to that of the standard propensity score, if the covariate is balanced, then the treatment variable should have no predictive power conditional on the GPS. A comparison of the treatment variable coefficient to its corresponding value in a regression that does not include the GPS can be used to gauge the extent of balance provided by the GPS.

Based on the suggested specification test in this paper, rather than estimating a separate regression for each covariate, an alternative approach would be to simply estimate equation (3) for different windows of the GPS, replacing $D$ with the multi-valued or continuous treatment and $p(X)$ with the GPS, and to test if all the coefficients on $X$ are equal to zero. A single omnibus statistic can then be obtained in the same way.

## 7. Discussion

There is an unambiguous need for more options for assessing the specification of the propensity score, in particular if the propensity score is to be used for weighting. Rubin (2004) highlights the importance of distinguishing between regression model diagnostics like goodness-of-fit tests and tests for the design of observational studies. According to a recent survey by Caliendo and Kopeinig (2008), this is an area which the literature currently offers little guidance. The main contributions of this paper are that it proposes a new graphical approach for propensity score model diagnostics based on two-dimensional scatter plots which we term Rubin-Cook plots, and a closely related and more general regression test interpretation of it.

Rubin-Cook plots can help the researcher visualize clearly where regions of thin and thick support for each continuous covariate are and make it easy to assess the quality of randomisation at each small moving window of $p(X)$. Although Rubin-Cook plots can be helpful for making assessments regarding whether the estimated propensity score is a useful balancing score and is well estimated, they are not complete tests as they do not allow checks on balance to be made for categorical covariates. In addition, the problem of how best to condition on the propensity score (e.g., what interval widths to use) remains an open problem.[18]

This paper proposes a non-parametric combination approach to assessing the specification of the propensity score that is a literal multivariate interpretation of the Rubin-Cook plot. Based on Monte Carlo simulations, it is found that the test has power to detect misspecified link functions, but not omitted variables.

Based on the results in this paper, a preliminary answer can be provided to Smith and Todd's (2005b) question regarding the utility of balancing tests. Essentially, balancing tests are really only useful when the CIA is fulfilled. Furthermore, when the CIA holds, balancing tests can be useful to the extent that they can help detect a misspecified link function. As using alternate and more suitable link functions can lead to lower biases in the ATT, the ability to detect such a misspecification in the context of propensity score matching is important.[19] In the context of matching, the development of such a test parallels the line of research that explores the use of more flexible semi-parametric approaches (e.g., Kordas and Lehrer 2004) and the use of alternative link functions (e.g., Koenker and Yoon 2006) to estimate the propensity score

For applied researchers, a simple to implement strategy involves using the proposed test in this paper in conjunction with other tests that check for possible omitted variables (e.g., Rosenbaum 1987; Ichino, Mealli and Nannicini 2007). The proposed specification test in this paper can help one avoid a misspecified link function while the sensitivity analysis for omitted variables can help to ascertain if the CIA is fulfilled. In terms of Tables 2 and 3, this makes it more likely that one ends up in the first six rows of columns 1 and 5, where bias and RMSE are relatively smaller.

[18] See also a related discussion in Dahiya and Gurland (1973).

[19] The goodness of link test proposed by Pregibon (1980) is an obvious alternative to the test proposed in this paper. However, to date, Pregibon's link test has found limited application because of its poor statistical properties.

Although the Monte Carlo simulations in this paper are necessarily limited to a few DGPs given finite time constraints, they are highly suggestive of the usefulness of the proposed test. Future research could include subjecting the test to different DGPs as well as exploring in more detail the power of the proposed test when used in conjunction with the above mentioned tests for sensitivity.

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## Appendix A: Structural Dimension in Graphical Regression

The minimal number $d$ of sufficient predictors is called the *structural dimension* of the regression. A model where (2) holds for dimension $d$ is referred to as having $d$D structure. If $d < p$, then a sufficient reduction in the regression is achieved which in turn leads to *sufficient summary plots* of $Y$ versus $B'X$ as graphical displays of all the necessary modelling information for the regression of $Y$ on $X$. As discussed by Cook (1996) and Cook and Lee (1999), having binary response variables instead of continuous response variables cause no conceptual complications, but construction and interpretation of summary plots must recognize the nature of the response.

Suppose that $X$ consists of two variables. Dimension reduction to $d = 1$ would mean reducing two covariates to the single linear combination $B'X = b_1'X$ without any evidence in the data that this reduction would result in loss of information on $Y \mid X$. An example of a 1D model is the single index model:

$$
\begin{aligned}
Y &= m(\alpha + B'X) + \varepsilon \\
&= m(\alpha + b_1'X) + \varepsilon
\end{aligned}
$$

where $\varepsilon \perp X$ and $m$ is a link function (e.g., the link function is the identity function in the case of multiple linear regression). Alternatively, a regression has 2D structure if two linear combinations $B'X = (b_1'X, b_2'X)$ are needed to characterize the regression, so that $Y$ is independent of $X$ given $b_1'X$ and $b_2'X$. An example of a 2D model is:

$$Y = m(b_1'X, b_2'X) + \varepsilon$$

where $b_1$ and $b_2$ are not collinear. More generally, in a $d$D model, $B'X = (b_1'X, b_2'X, \ldots, b_d'X)$ and all the regression information is contained in the $d$ linear combinations $(b_1'X, b_2'X, \ldots, b_d'X)$.

Related to the idea that there exist many balancing scores for propensity score matching (and that controlling for any balancing score is sufficient for the theory of propensity score matching to be valid), sufficient predictors are not unique. If $B'X$ is a vector of $d$ sufficient predictors and $A$ is any $d \times d$ full rank matrix then $AB'X$ is another set of sufficient predictors. In practice, however, this non-uniqueness of sufficient predictors is not an important issue in regression graphics as the distribution of $Y \mid B'X$ and $Y \mid AB'X$ contain the same statistical information so sufficient summary plots of $Y$ versus $B'X$ and $Y$ versus $AB'X$ would be identical.

An emphasis of the literature on regression graphics has been to find the $B$ of lowest possible dimension $d$ for which the representation in (2) holds and to use sufficient summary plots as a guide to formulate appropriate models for $F(Y \mid X)$.[20] For example, if $d$ = 2 and $B$ is known, then a three-dimensional plot of $Y$ versus $(b_1'X, b_2'X)$ can be used as a sufficient summary plot for the regression. In general, both $d$ and $B$ are usually unknown and need to be estimated. In general, if non-linearities are present and not represented by the predictor variables, then the dimension of the regression cannot be 1D. Cook (1996) discusses in more detail in the context of a logistic model how a specially written *Xlisp-Stat* program *Arc* for regression graphics can be used to check the structural dimension of the regression and help assess candidate models.[21] This graphical assessment involves rotating graphical displays based on lower dimensional projections of the data in *Arc* to get the "best" visual fits. See, for example, Figure 2 in Cook (1996) where it is illustrated how the goal of the visual fit is to stop rotation at a point where the relative intraslice density is constant in any slice parallel to the stationary vertical axis. The horizontal axis in such a plot

[20] Techniques for estimating the dimension of a regression include sliced inverse regression, sliced average variance estimation and principal Hessian directions. See Cook (1998) and Cook and Weisburg (1999) for more discussion.
[21] This software is available at no cost at: http://www.stat.umn.edu/arc.

corresponds to a particular combination of the predictors $B'X$ that *Arc* can provide estimates of.

An estimate of the subspace spanned by $B$ is obtained once the dimension and directions have been estimated. Given the estimate of the subspace, the next phase involves recovering information about $F$ and identifying the best model for the reduced data, where both parametric and non-parametric models can be used. Cook (1998) and Cook and Weisburg (1999) provide more details on how graphical regression can be implemented in practice.

## Appendix B:

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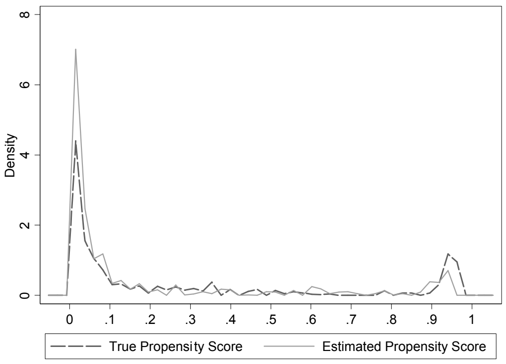


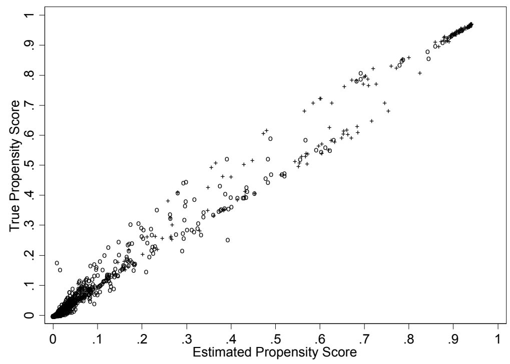


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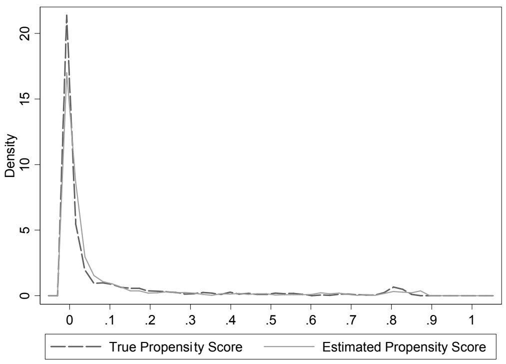


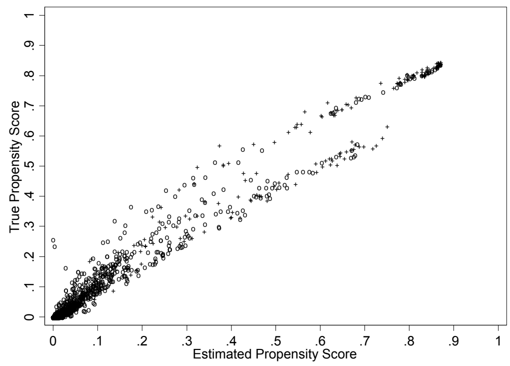


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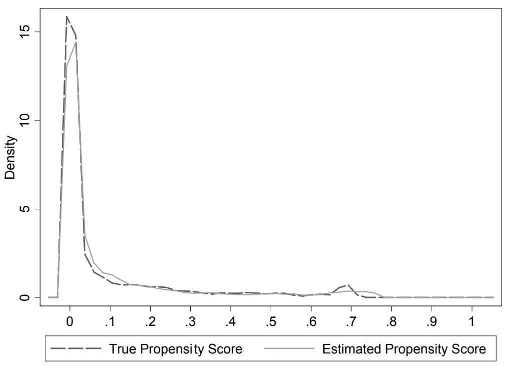


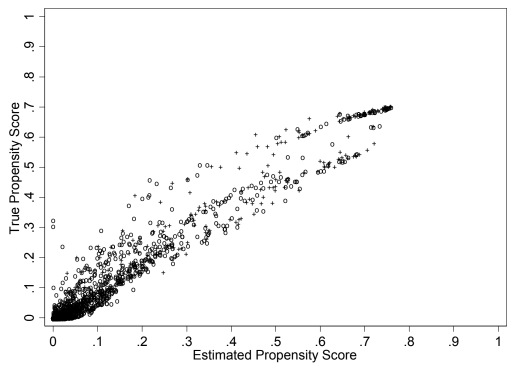


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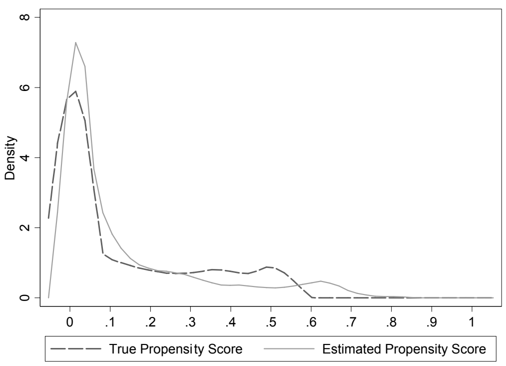


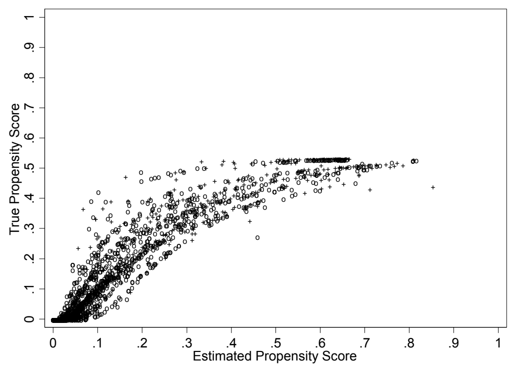

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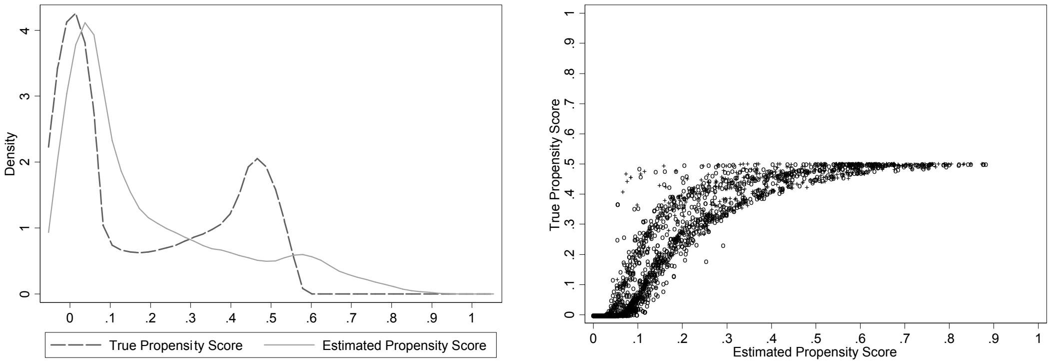


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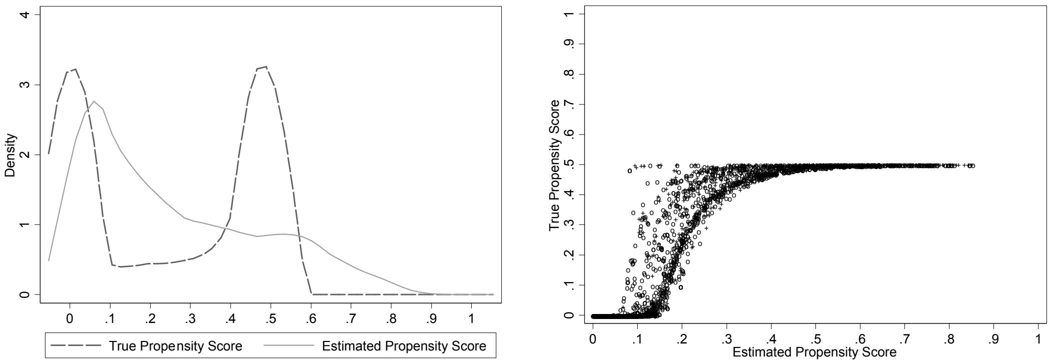


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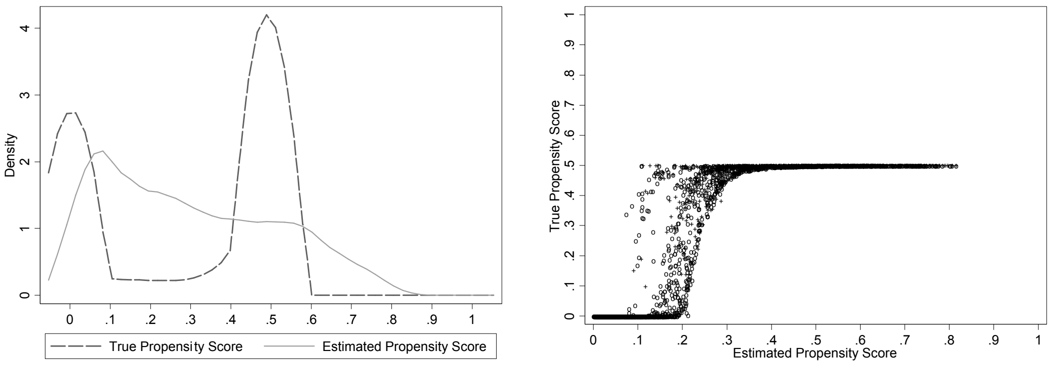


Figure B.1: DGPs for Power Simulations (Correct Index Function, Incorrect Link Function)

Notes: The figures illustrate seven DGPs for the power simulations using specification 1 (see the first column in Tables 2 and 3 for the corresponding results). In the right panel, ‘+’ denotes treatment observations; ‘o’ denotes control observations.