Linear Model Simulations: Varying the Propensity Score

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Suppose $Y = X_1 + X_2 + \epsilon$, where X_1, X_2, and ϵ are all mutually independent, standard normal random variables. There is no effect of treatment.

Let treatment assignment T be Bernoulli conditional on X_1, so that $\mathbb{P}(T = 1 \mid X_1 >= 0) = p_1$ and $\mathbb{P}(T = 1 \mid X_1 < 0) = p_2$. We'll vary p_1 and p_2.

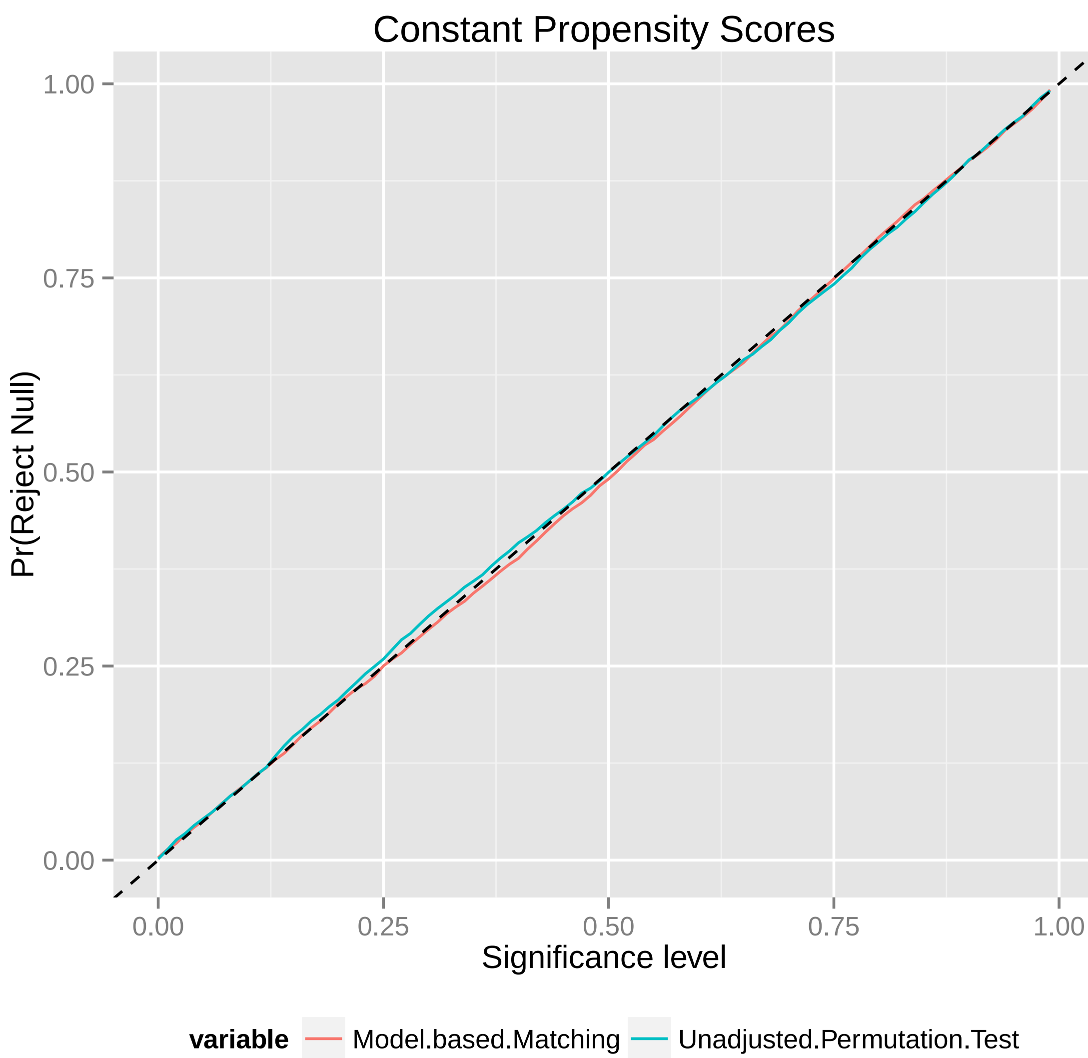
Estimate $\hat{Y}$ using OLS with X_1 and X_2 as predictors.

We have N =100 individuals. Suppose we use two strata, defined by whether $\hat{Y} \geq 0$ or $\hat{Y} < 0$. We'll do the model-based matching permutation test using the difference in means as our statistic 5000 times to get a distribution of p-values under the null hypothesis of no treatment effect. The simulations are done **conditionally on X and ϵ**: we draw X_1, X_2, and ϵ once to generate the potential outcomes Y, then randomly assign treatment for each simulation.

1 Constant propensity score

This is like a randomized experiment where treatment is assigned by flipping an unbiased coin for everybody.

$$\mathbb{P}(T = 1 \mid X_1 >= 0) = \mathbb{P}(T = 1 \mid X_1 < 0) = 0.5$$



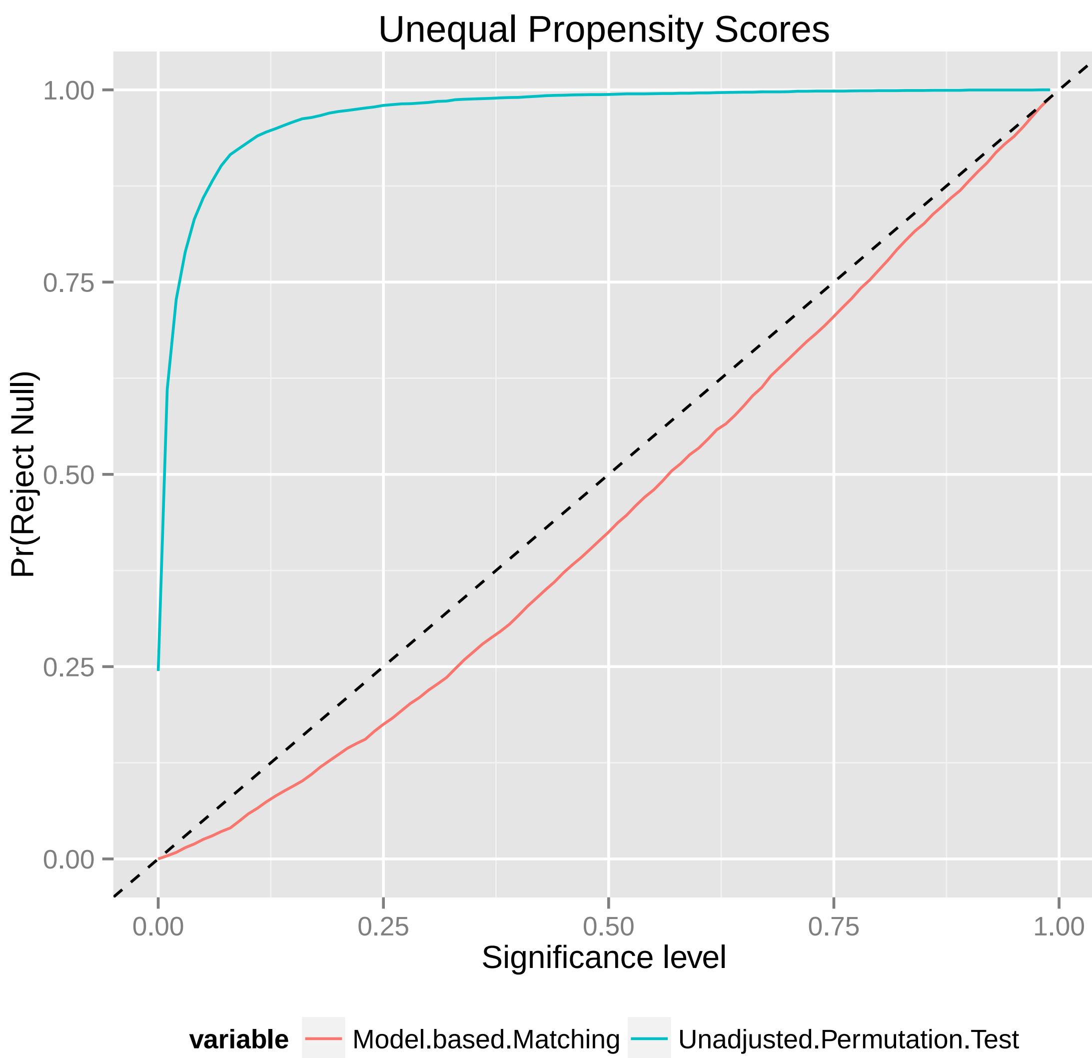
Unadjusted Permutation Test	0.053
Model-based Matching	0.051

Table 1: Proportion of tests rejected at level 0.05

2 Non-constant propensity score

Now, we have vastly different propensity scores:

$$\mathbb{P}(T = 1 \mid X_1 >= 0) = 0.1$$
$$\mathbb{P}(T = 1 \mid X_1 < 0) = 0.9$$

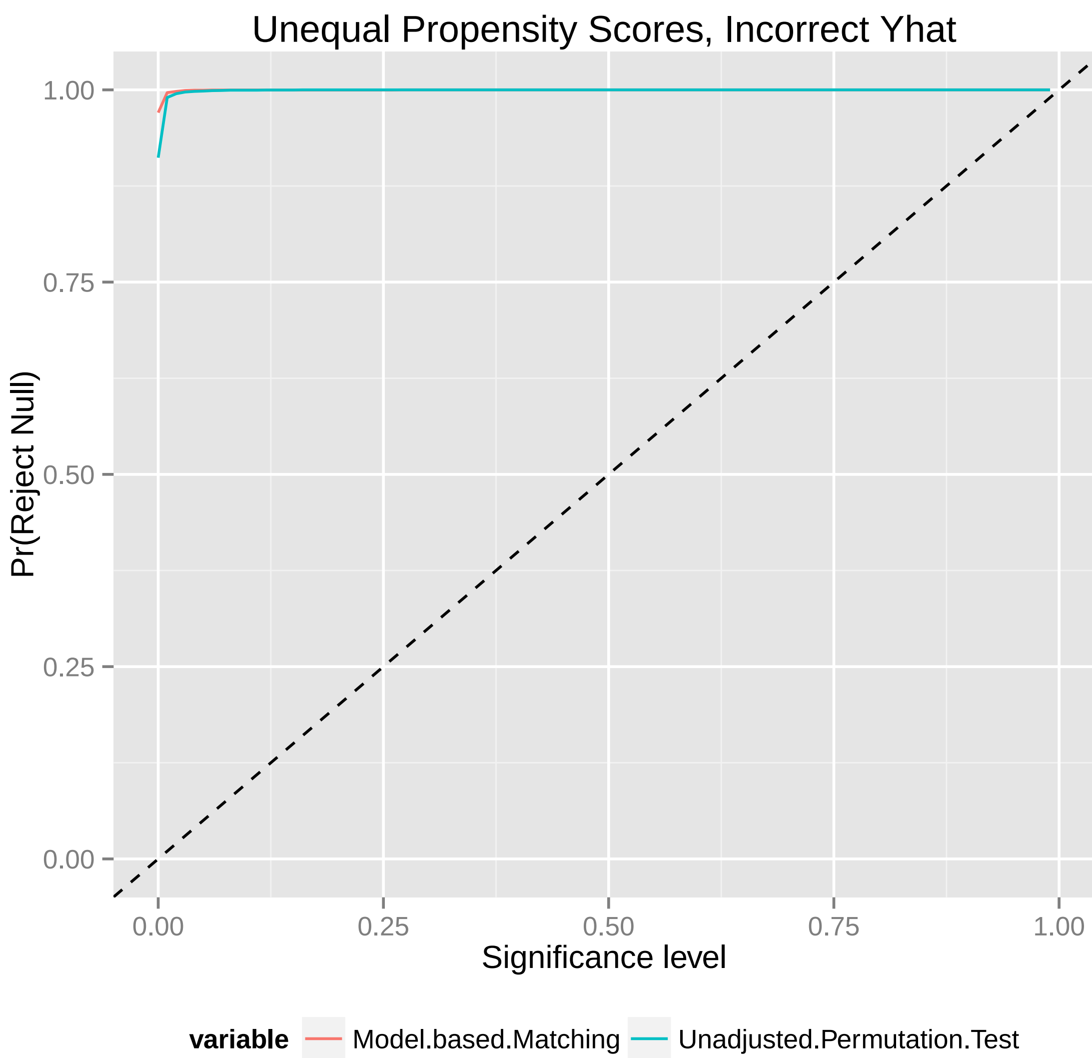


Unadjusted Permutation Test	0.860
Model-based Matching	0.025

Table 2: Proportion of tests rejected at level 0.05

3 Non-constant propensity score, inconsistent fit

Assume the propensity scores from the previous section. Now, suppose instead of fitting the correct model for Y, we estimate $\hat{Y}$ using only X_2.



Unadjusted Permutation Test	0.998
Model-based Matching	1.000

Table 3: Proportion of tests rejected at level 0.05