

# Supplementary Figures

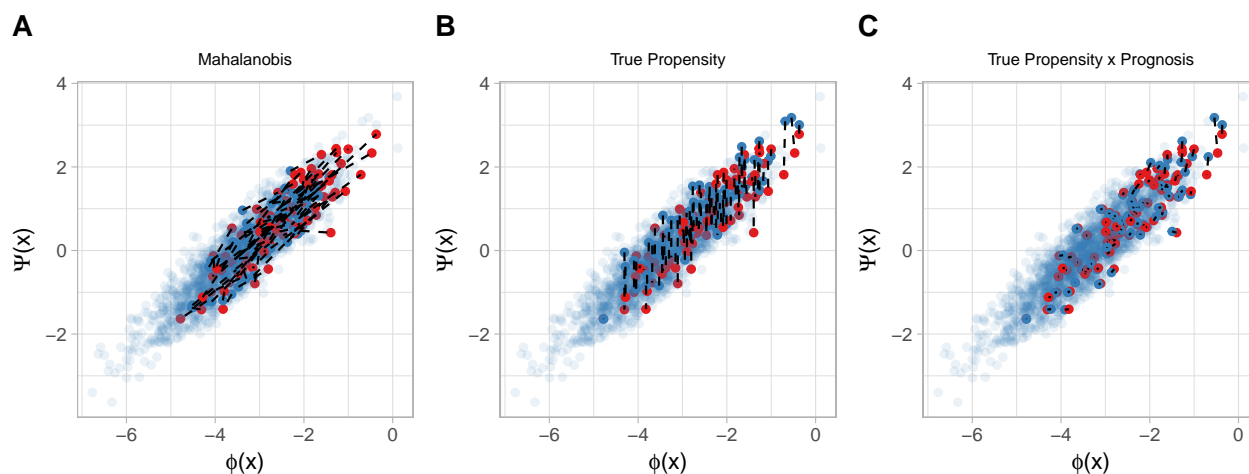
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## To do

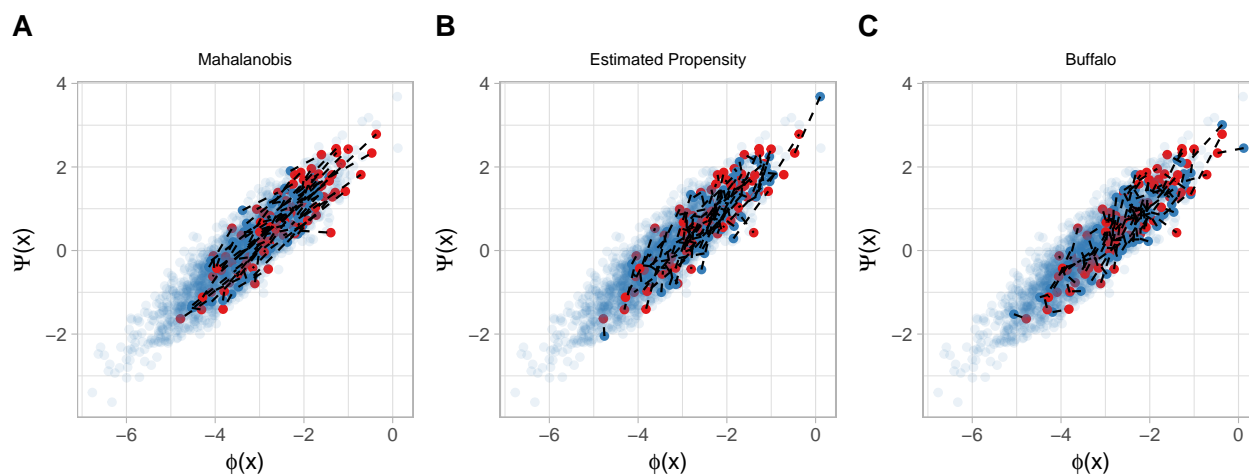
- [ ] Supplementary figure 3 ( $p = 50$ )

## Supplementary Figure 1



**Supplementary Figure 1:** Replication of Figure 1 with  $\rho = 0.9$ . This simulates the case that propensity and prognosis are highly correlated. When this occurs, matching on propensity will also achieve some prognostic balance, and vice-versa. All simulation parameters are as described in section 2.1.

## Supplementary Figure 2



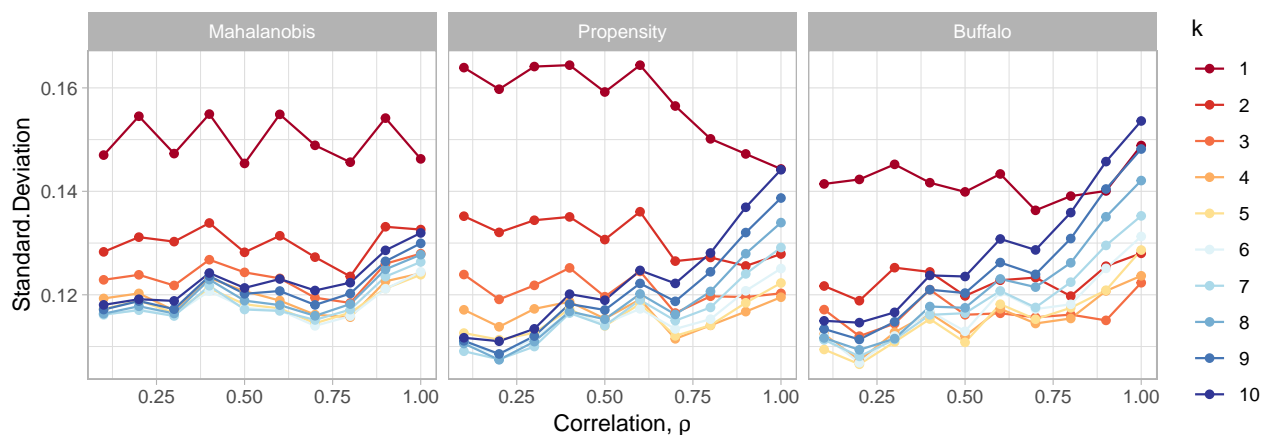
**Supplementary Figure 1:** Replication of Figure 2 with  $\rho = 0.9$ . All simulation parameters are as described in section 2.1.

## Supplementary Figure 3

Bias and MSE for MDM, propensity, and prognostic score matching when  $p = 50$ .

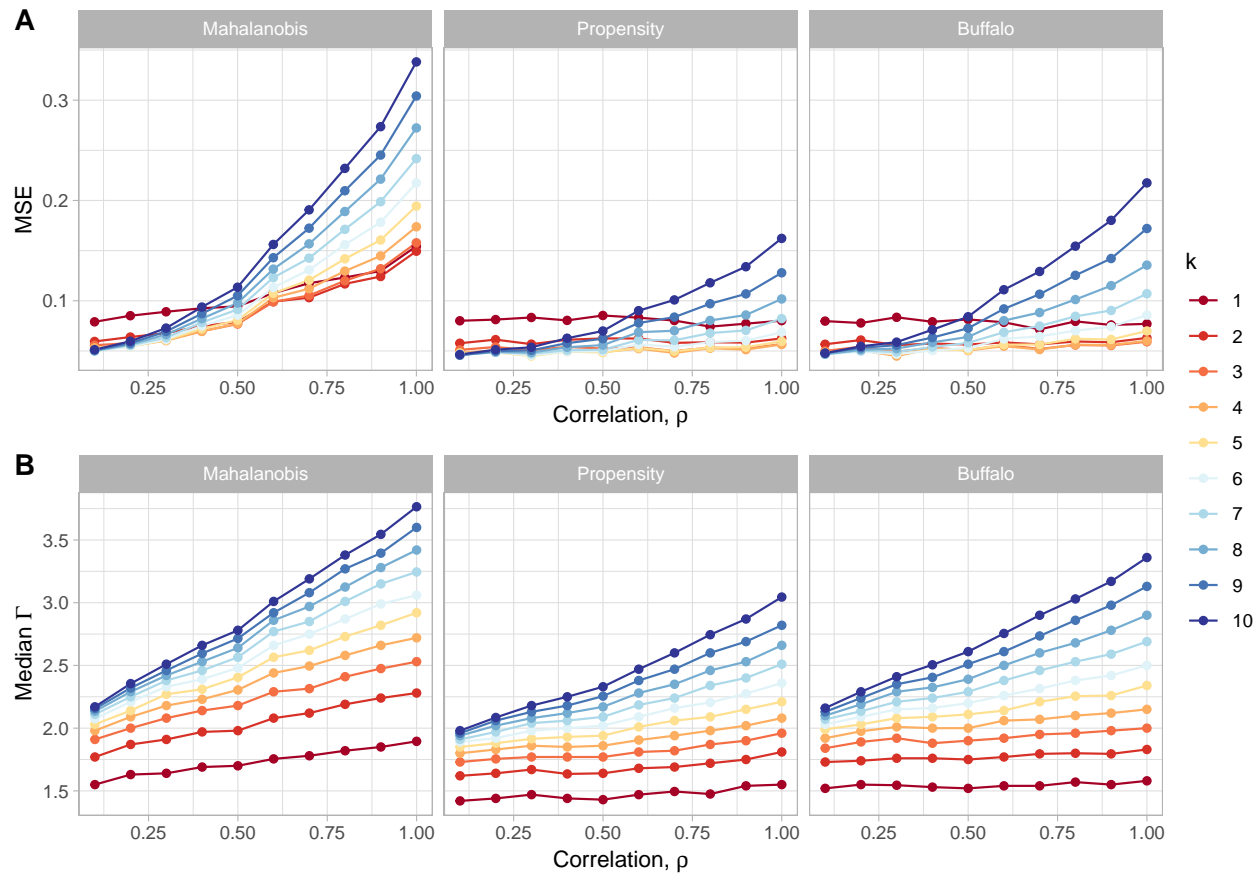
To do

## Supplementary Figure 4



**Supplementary Figure 4** Standard deviation from matching estimators when overlap between treated and control individuals is poor. Simulations were carried out as described in Section 4.1, but with  $\phi(X_i) = X_{i1} - 10/3$ . This kept the sample size and number of treated individuals constant while increasing the separation of treated and control individuals.

## Supplementary Figure 5



**Supplementary Figure 5** MSE and median gamma design sensitivity when the random noise contributing to the outcome is increased. All simulation parameters are the same as described in Section 4.1, except that  $\sigma = 2$ . This increases the difficulty of fitting the prognostic score, diminishing the performance of Buffalo matching in terms of MSE and sensitivity.