

Simulations with SITA Violation

Rachael Caelie (Rocky) Aikens

2/13/2020

Set Up with SITA violations

We compare the performance of propensity score matching, Mahalanobis distance matching, and Buffalo Matching (described in the previous section) on simulated data, varying the dimensionality of the problem, the fixed treatment to control ratio during matching, and the correlation between the true propensity and prognostic score. For this set of simulations, we also add a weak, unobserved confounder, U .

$$\begin{aligned}X_i &\sim_{iid} \text{Normal}(0, I_p), \\T_i &\sim_{iid} \text{Bernoulli}\left(\frac{1}{1 + \exp(-\phi(X_i))}\right), \\Y_i &= \tau T_i + \Psi(X_i) + \epsilon_i, \\ \epsilon_i &\sim_{iid} N(0, \sigma^2),\end{aligned}$$

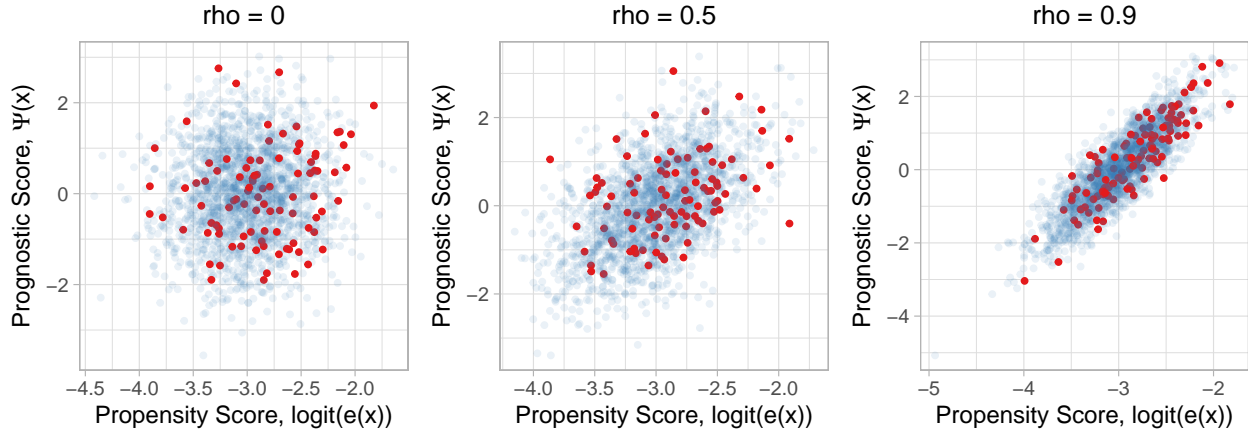
where the true propensity and prognostic scores are given by the linear combinations

$$\begin{aligned}\phi(X_i) &= X_{i1}/3 - \nu U c, \\ \Psi(X_i) &= \rho X_{i1} + \sqrt{(1 - \rho^2)} X_{i2} + \nu U,\end{aligned}$$

The constant, c in the propensity score formula was chosen such that there were approximately 100 treated observations in each dataset. For the simulations reported in the main figures of the paper, we let $c = 3$. We consider $p = 10$, $\rho = 0, 0.1, \dots, 0.9, 1.0$, and $k = 1, \dots, 10$. Each simulation consisted of a dataset of size $n = 2000$ and was repeated $N = 1000$ times. We fix the treatment effect to be constant with $\tau = 1$ and the noise to be $\sigma = 1$. For a given matching, we estimate ATT and design sensitivity $\tilde{\Gamma}$ using the permutation t -statistic from the package `sensitivtymv`

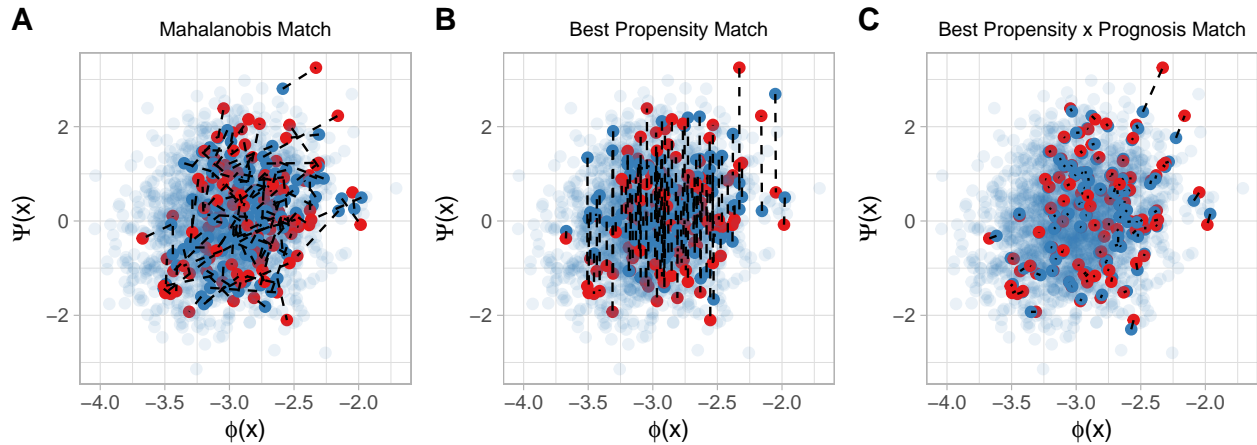
Fisher-Mill Visualizations

This set-up is a little weird. Here are some Fisher-Mill plots of the resulting data:

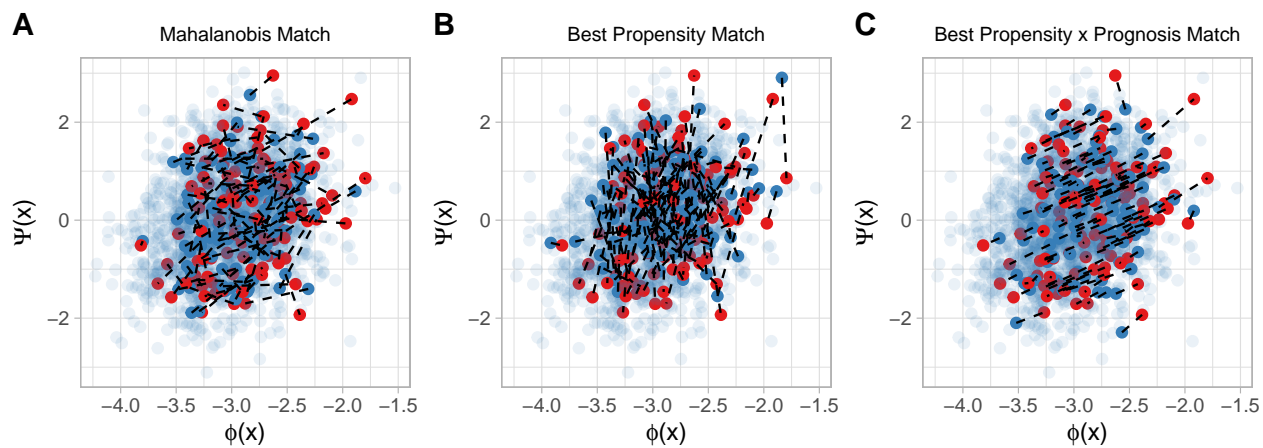


But there's something sinister going on here. Suppose we fit the best possible model for propensity and prognostic score. That is, our coefficients for X_1 and X_2 in our propensity and prognostic models are exactly correct, but we leave out U in the model because we never observed it. The plots below show the matches we might choose in this scenario under Mahalanobis, Propensity, and Joint Propensity and Prognostic score matching. As you can see, we are missing some amount of variation between matched individuals.

If we made Fisher Mill plots from our scores and matched on them, this what we'd see:



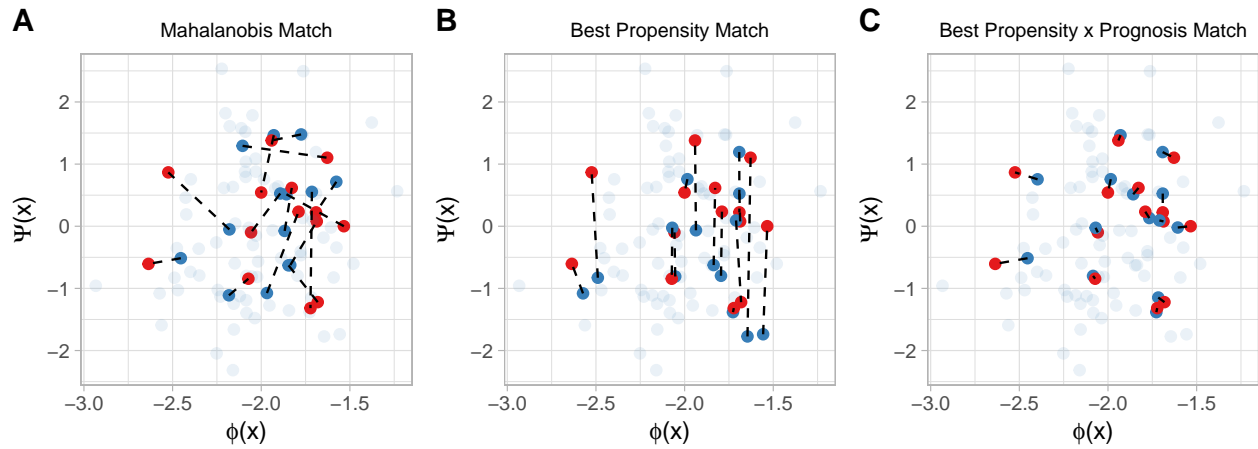
But of course, the Fisher-Mill plots we make and the matches we select are missing the unobserved confounder, U . If we made true Fisher-Mill plots based on the data generating functions, we'd see that the above matching scheme is not doing as well as we thought.



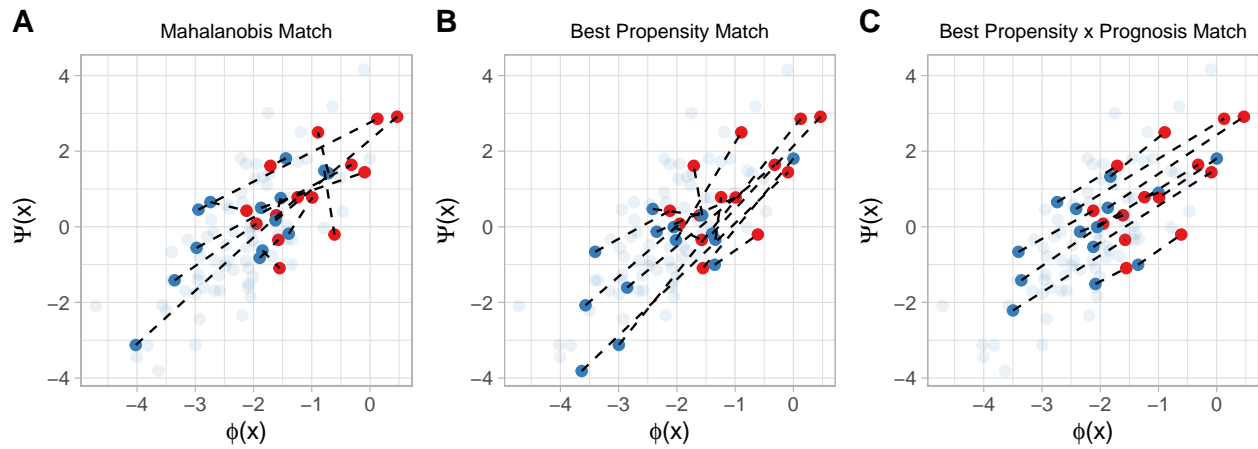
More intuition for gamma and confounding

To try and understand this better, I want to think about a smaller sample size.

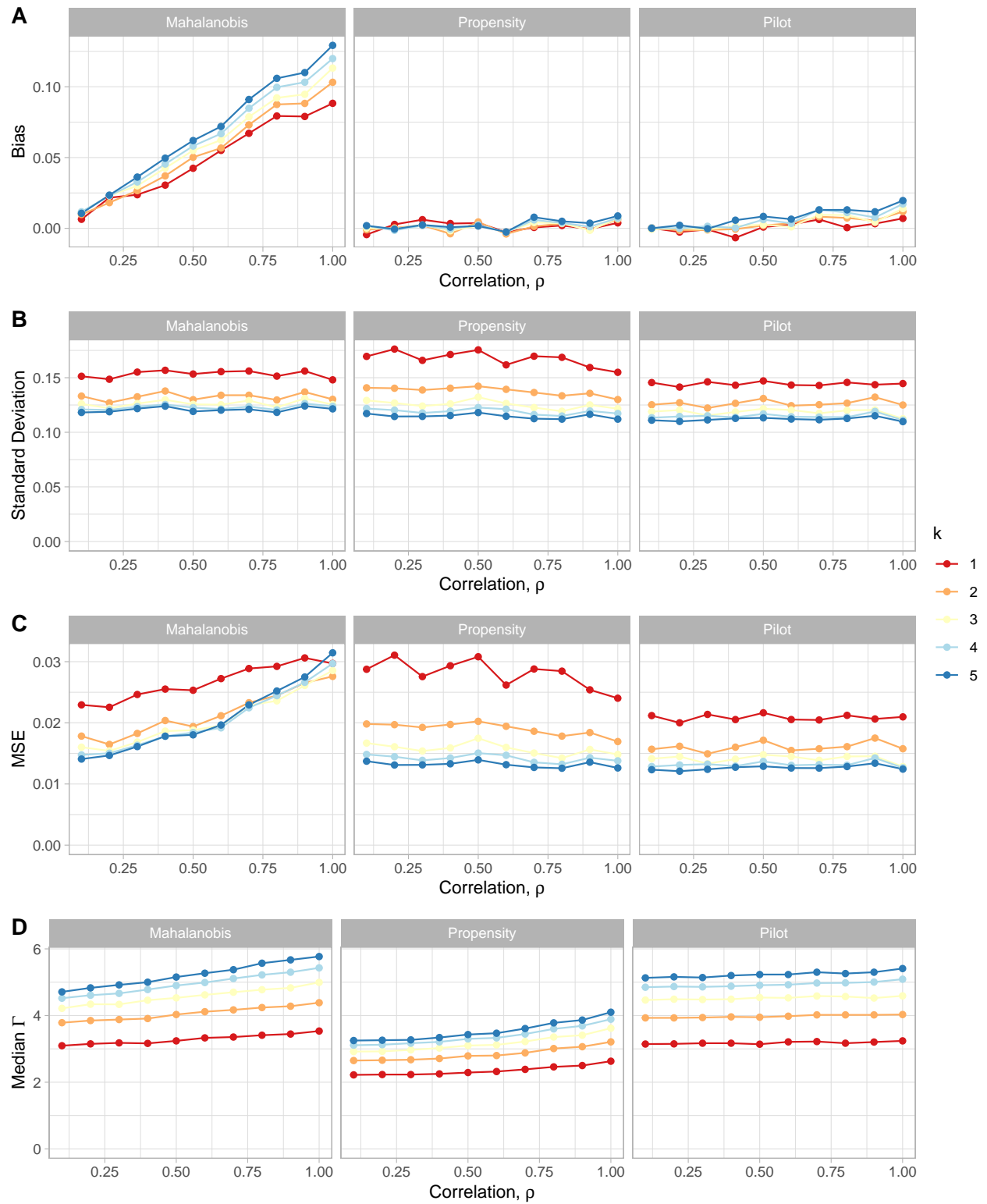
If we made Fisher Mill plots from our scores and matched on them, this what we'd see:



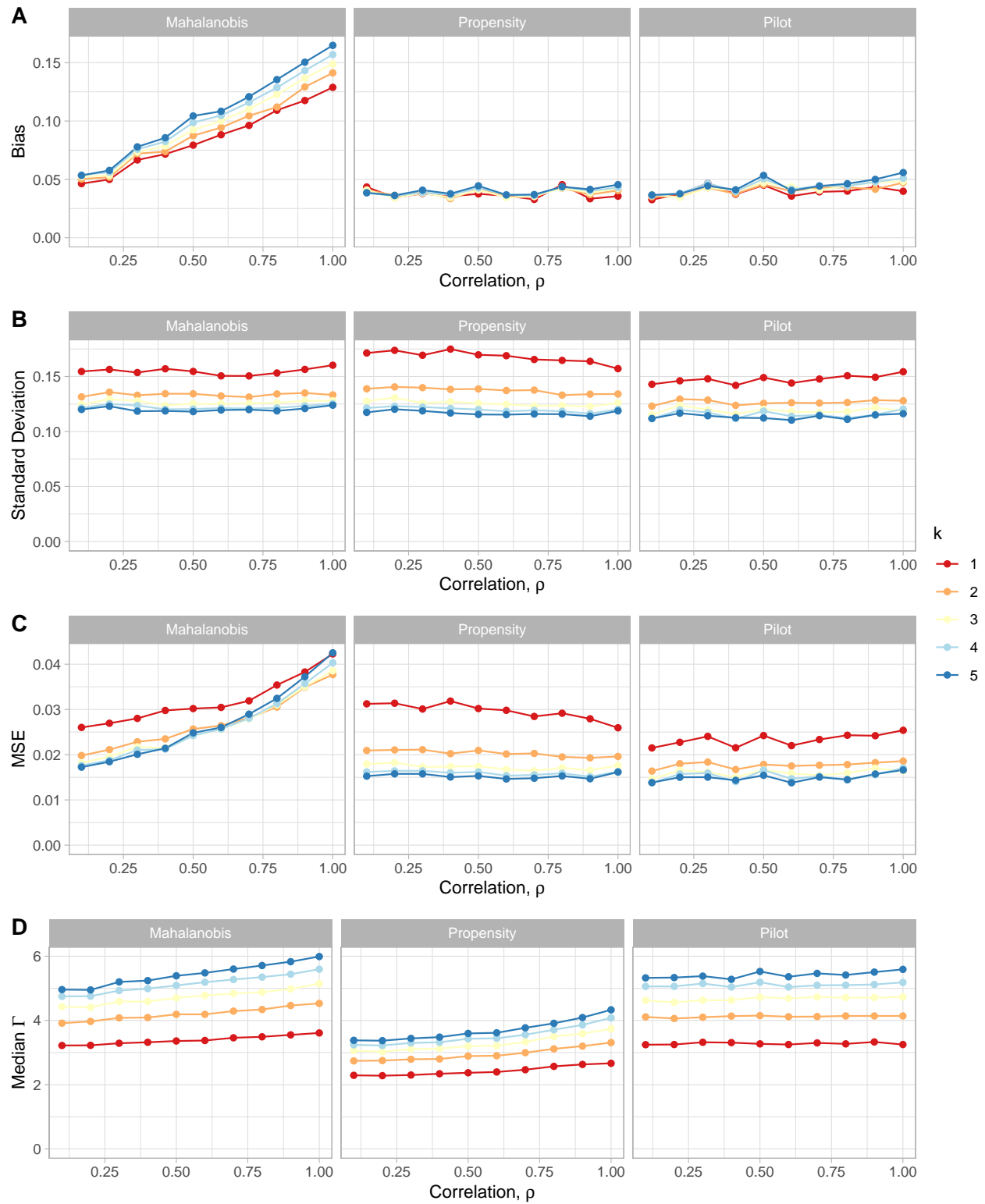
But of course, the Fisher-Mill plots we make and the matches we select are missing the unobserved confounder, U . If we made true Fisher-Mill plots based on the data generating functions, we'd see that the above matching scheme is not doing as well as we thought.



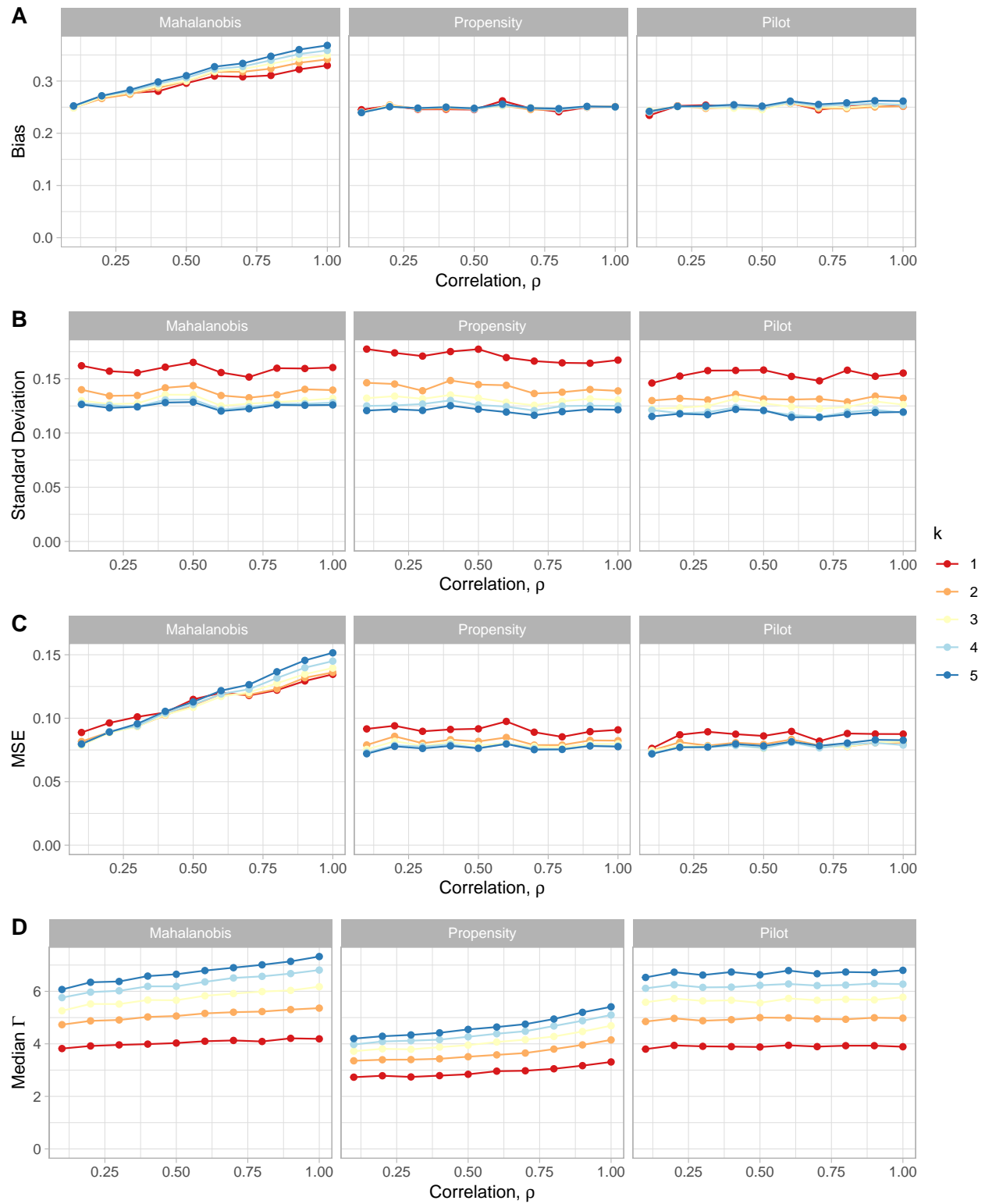
Results with no SITA violation



$\tau = 1, \nu = 0.2$

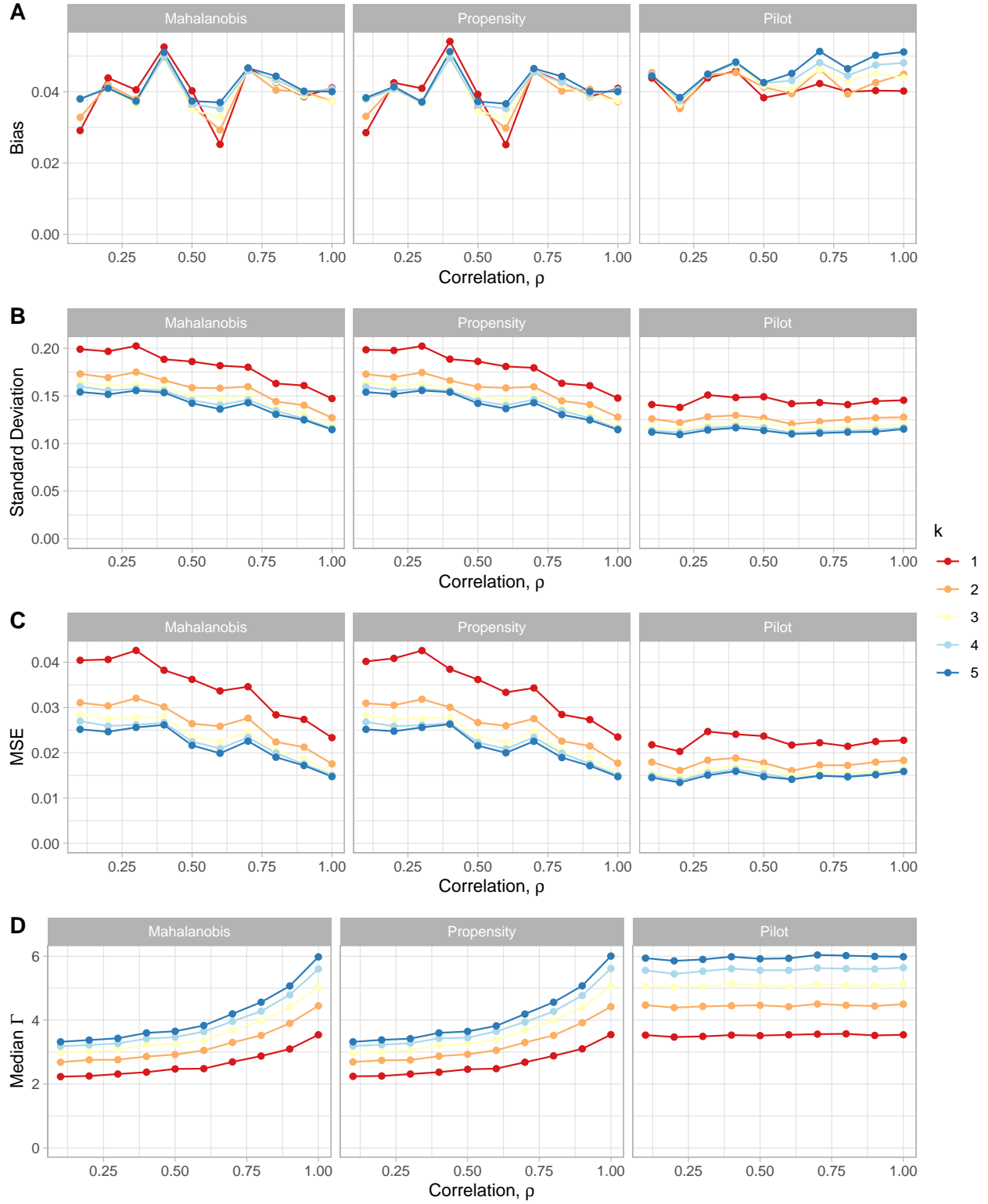


$\tau = 1, \nu = 0.5$

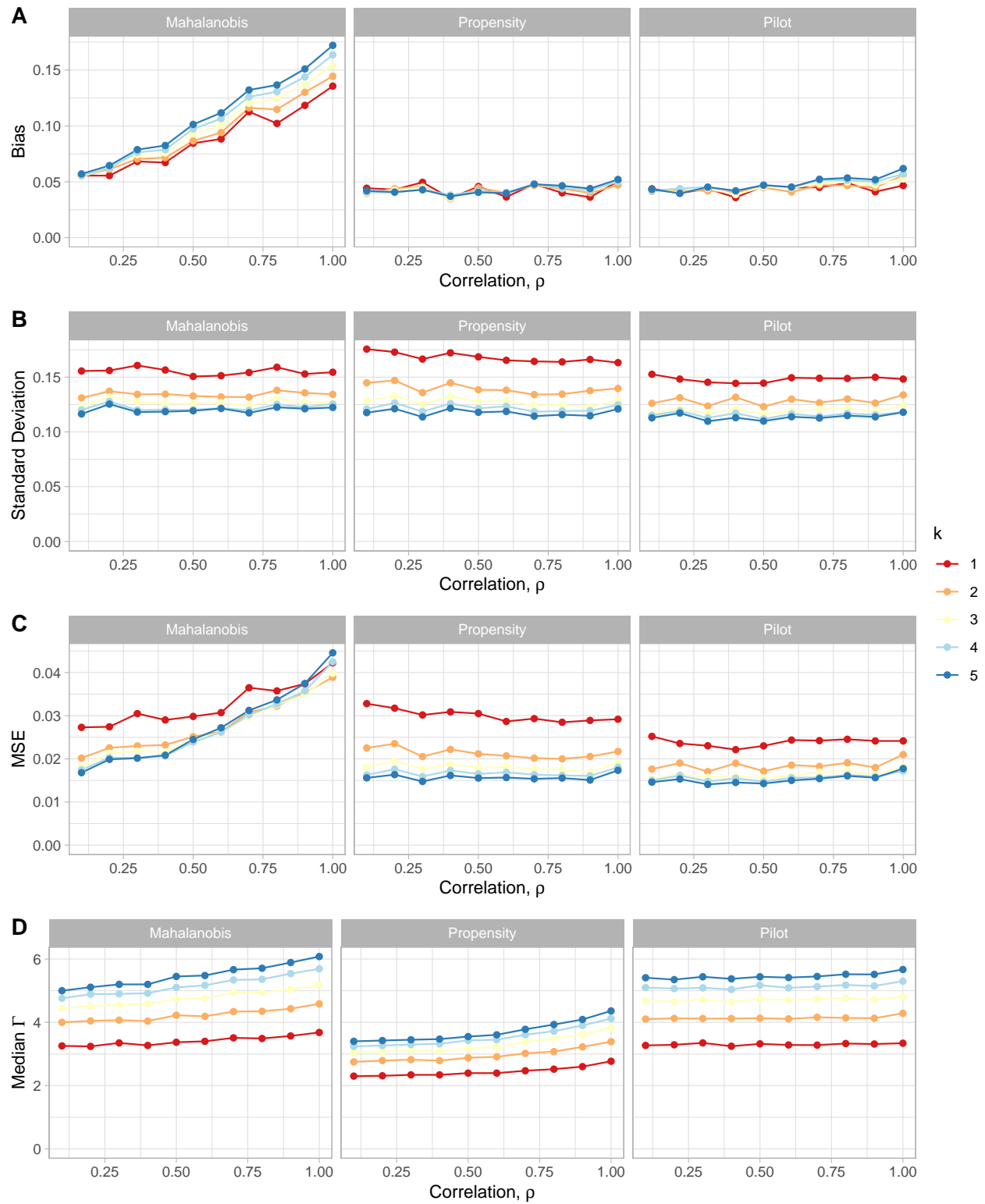


$\tau = 1$, $\nu = 0.2$, model correctly specified

Something buggy happened to the MDM results; they're almost exactly the same as propensity score.



$\tau = 1$, $\nu = 0.2$, confounder attenuates



$\tau = 0$, $\nu = 0.2$, confounder attenuates

