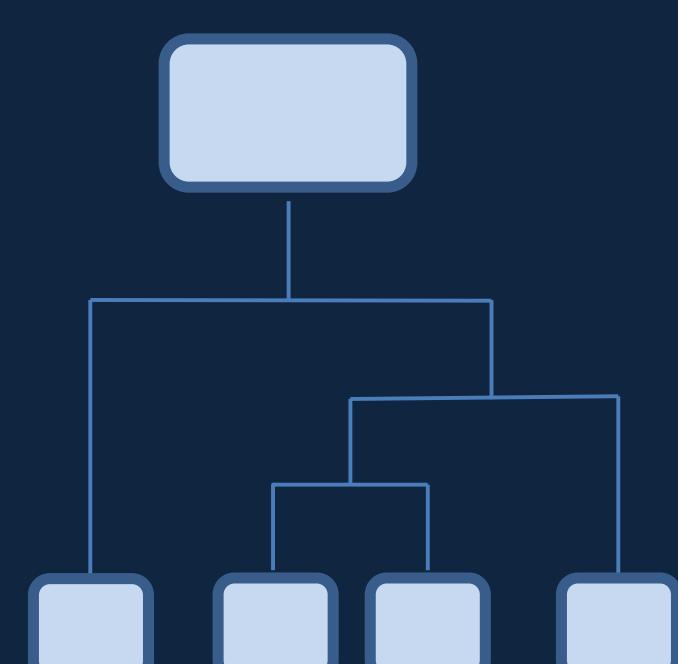


Comparison of Simulated Clinician Rankings with Semi-Automated and Automated Algorithms for Variable Selection when Conducting Anchored Matching-Adjusted Indirect Comparisons



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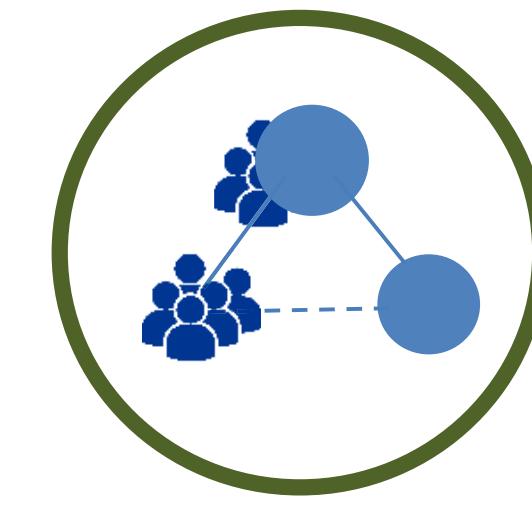
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INTRODUCTION

Anchored matching-adjusted indirect comparisons (MAICs) leverage individual patient-level data (IPD) to compare two treatments across separate trials with a common comparator arm. MAICs only require adjustments for effect modifiers, typically identified by expert clinicians a priori.



| Effect modifier | x_1 | x_2 | x_3 | ... |
|-----------------|-------|-------|-------|-----|
| Rank | 1 | 3 | 2 | ... |

Emerging semi-automated and automated variable selection algorithms may have advantages over clinician rankings in terms of considering effect modifiers on appropriate scale, reproducibility, being data driven, and ability to leverage large datasets.

OBJECTIVE

This analysis compared simulated clinician rankings with semi-automated and automated algorithms for variable selection when conducting anchored MAICs.

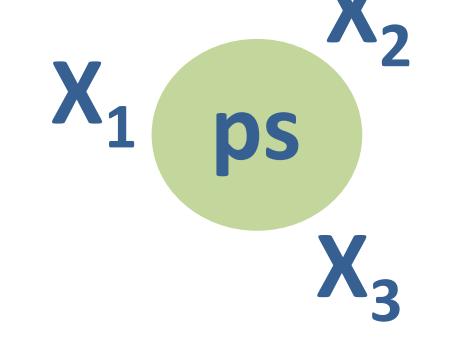
METHODS

The following variable selection algorithms were evaluated using 100 simulated trials with 2 true effect modifiers and 8 noise variables.

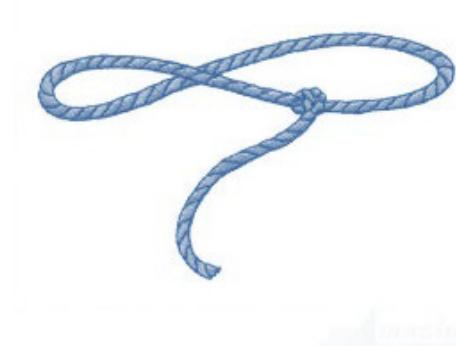


Clinician ranking

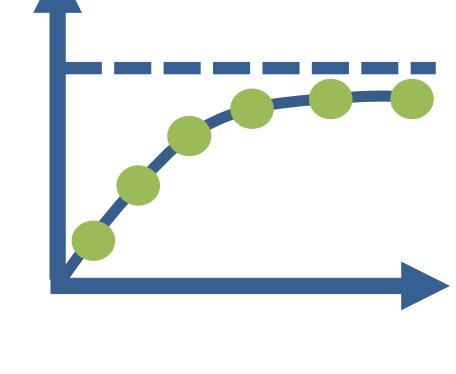
(60% chance of correct identification, which increased by 10% for every one unit increase in the log effect modifier size)



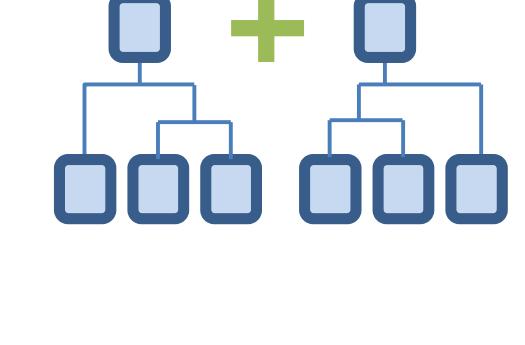
High dimensional propensity score [HDPS]



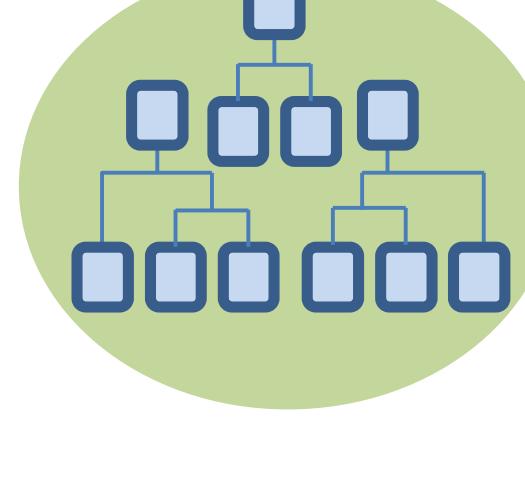
Lasso for hierarchical interactions [hierNet]



Bayesian projected prediction



Bayesian additive regression trees [BART]



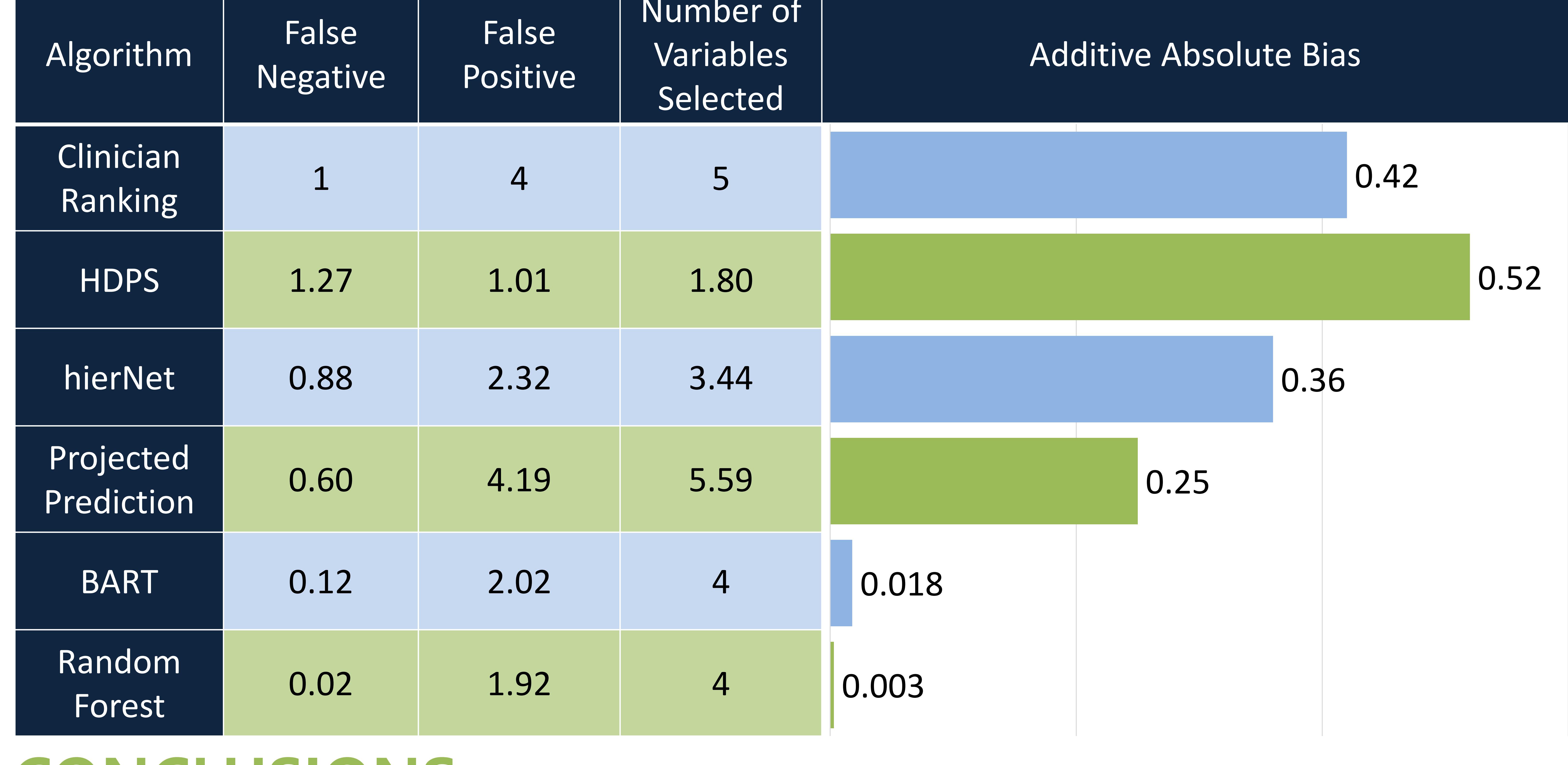
Random forest

SIMULATED
SEMI
AUTOMATED

Effect modifiers added were 50% of the size of the treatment effect. Success was measured by the mean number of false positives and negatives, and additive absolute bias of missed effect modifiers.

RESULTS

- **Clinician ranking** identified one false negative and four false positive variables with an absolute bias of 0.42.
- **HDPS, hierNet, and Bayesian projected prediction** had similar results 1.27, 0.88, and 0.60 false negatives, 1.01, 2.32, and 4.19 false positives, and absolute biases of 0.52, 0.36, and 0.25, respectively.
- Tree-based algorithms had the lowest absolute bias; **BART** and **random forest** had 0.12 and 0.02 false negatives, 2.02 and 1.92 false positives, with absolute biases of 0.018 and 0.003, respectively.



CONCLUSIONS

Based on the simulations performed, tree-based algorithms were best at variable selection in MAIC. These findings suggest that semi-automated and automated variable selection algorithms should also be considered to augment analyses based on clinician rankings when undertaking anchored MAICs.

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