Bayesian Approaches to Predicting Individual Treatment Effects in Precision Medicine

Pamela Solano¹ and Tomas Jaki^{1,2}

¹University of Regensburg, ²Cambridge University

April 11, 2025

Motivation

- Not all participants will react equally to an intervention
- Characterizing this heterogeneity in intervention effects is key to improving patients outcomes

Goal

To assess the performance of Bayesian inference across diverse data conditions, with an emphasis on their capacity to handle heterogeneity, non-linearity, and high-dimensionality in the estimation of individual treatment effects.

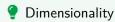
The predicted individual treatment effects (PITE) framework

- PITE estimates individual treatment effects.
- PITE consists of the difference between experimental(E) and control
 (C) prediction for each individual (Jaki et al. 2024).

$$\label{eq:pitch} \mathsf{PITE}_i = f_E(X_i) - f_C(X_i), \qquad f(\cdot) \text{ is a predictor}$$

- Challenge
 - PITE is unobserved.
 - The best method to estimate the PITE is not necessarily the best fitted model.

Bayesian approches



Bayesian Ridge Regression ("bridge"), Spike and Slab Regression ("spikeslab"), The Bayesian Lasso ("blasso").

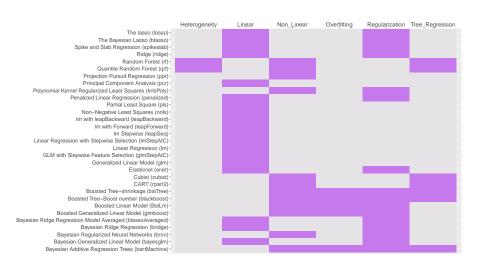
Complex outcomes

Bayesian Generalized Linear Model ("bayesglm"), Bayesian Regularized Neural Networks ("brnn").

Tree Regression

Bayesian Additive Regression Trees ("bartMachine") (Lamont et al. 2016)

Regressions approches applied



Metrics

• The risk (% Expected Prediction Squared Error)

$$\frac{1}{n}\sum_{i=1}^{i=n}(\mathsf{tPITE}_i-\mathsf{PITE}_i)^2$$

Sensitivity (Detect PITE direction)

Same
$$\mathsf{Direction}_i = 1$$
, if $\mathsf{tPITE}_i \times \mathsf{PITE}_i > 0$

 $\mathsf{true}\ \mathsf{tPITE}_i\ \mathsf{and}\ \mathsf{estimate}\ \mathsf{PITE}_i.$

Data generation mechanism 1

• Sample size n=40, 70, 100, 300, 400, **500**, **1000**,1200,1500 with allocation ratio 1:1 $(n_C=n_T=n/2)$.

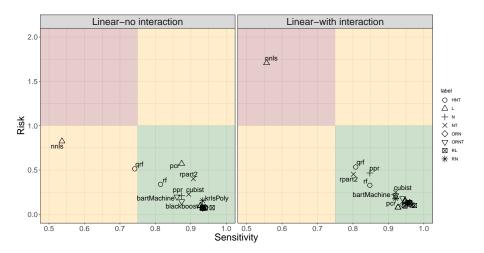
$$y = X\beta + tZ\gamma + \epsilon, \quad \epsilon \sim N(0, 1)$$

• $t \in (0,1) \Rightarrow \text{benefit } Z\gamma$

Leave-one-out cross-validation for validation

- Normal, Linear, Independent
- Normal, Linear, Interactions

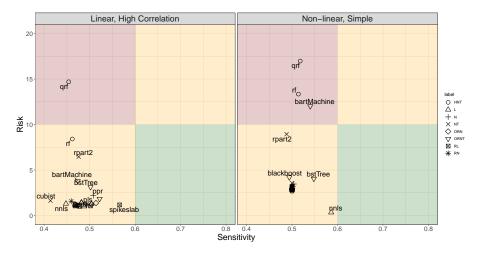
n = 500



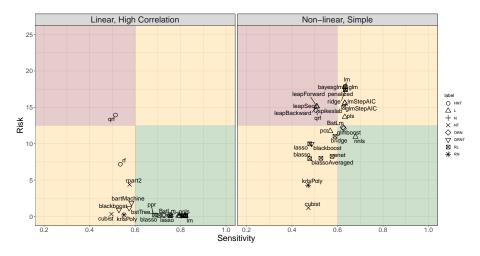
Data generation mechanism 2

- Z Normal, Linear, High correlations (up to 0.5)
- Z Normal, Linear, Low correlations (up to 0.3)
- $Z \sim U[0.1, 0.5]$, Non-linear. Benefit: $Z_1 \gamma_1/(Z_2 + \gamma_2)$
- $Z \sim U[0.1, 0.5]$, Non-linear. Benefit: $\frac{\log(Z_1)\gamma_0}{{Z_1}^{\gamma_2}-\gamma_3\sqrt{Z_2+2}}$

n = 500



n = 1000



Conclusions

- This work evidences potential approaches for different contexts.
- An analyst should know what characteristics their dataset presents.
- For each situation sensitivity varies little for different methods.
- Risk is more variable.
- Some methods benefit more from smaller sample size.
- Leave complex methods for large sample size.

References

- Jaki, Thomas, Chi Chang, Alena Kuhlemeier, and M. Lee Van Horn. 2024. Predicting Individual Treatment Effects: Challenges and Opportunities for Machine Learning and Artificial Intelligence. KünstlicheIntelligenz, January. https://doi.org/10.1007/s13218-023-00827-4.
- Lamont, Andrea, Michael D Lyons, Thomas Jaki, Elizabeth Stuart, Daniel J Feaster, Kukatharmini Tharmaratnam, Daniel Oberski, Hemantlshwaran, Dawn K Wilson, and M Lee Van Horn. 2016.
 "Identification of Predicted Individual Treatment Effects in Randomized Clinical Trials." Statistical Methods in Medical Research 27 (1): 142–57. https://doi.org/10.1177/0962280215623981.

Contact: pchiroque@gmail.com - pamela.chiroque-solano@ur.de

