Supporting Information for BARP: Improving Mister P Using Bayesian Additive Regression Trees

11,461 words

Contents

1. List of Surveys

The surveys are taken from Buttice and Highton (2013) replication materials. Table 1 summarizes all questions by year and topic. The uppercase letter refers to either the National Annenberg Election Studies (N) or the Cooperative Congressional Election Studies (C). The lowercase letter refers to the question prefix while the subscript details the particular question(s). A sub-subscript indicates where there is a series of questions on the same topic (as in the case of questions on how to use the military in 2008 asked in the CCES).

Table 1: Surveys by year and topic

Topic	**2000**	**2004**	**2006**	**2008**
Abortion	N - cb_{f02}	N - cce_{01}	C - v_{3019}, v_{3060}	N - cea_{01}, C - cc_{310}
Budget			C - $v_{4040,4044}$	C - $cc_{309,420}$
Death Penalty	N - $cbg_{01,12}$			
Defense Spend		N - $ccd_{57,67}$		C - cc_{316d}
Elections				C - $cc_{419_{1-6}}$
Environment			C - v_{3022}	N - cfd_{01}, C - $cc_{311,422}$
Gay Marriage	N - cb_{l01}	N - cce_{21}		N - cec_{01}, C - cc_{316f}
Gun Control	N - $cbg_{05,06}$	N - cce_{31}		
Health Care	N - $cbe_{02,05,08,14}$			C - cc_{316e}
Immigrants			C - v_{3069}	N - $cdd_{01,04}$
Iraq War		N - $ccd_{34,35}$	C - v_{3066}	N - cdb_{01}, C - cc_{316a}
Military Use	N - cbj_{07}	N - ccd_{03}	C - $v_{3030-3034}$	C - $cc_{418_{1-6}}$
Minimum Wage			C - $v_{2072,3072}$	C - cc_{316b}
Race Policies	N - cbl_{05}, cbm_{01}		C - v_{3027}	C - cc_{313}
Social Security	N - cbb_{05}, $cbc_{01,05}$	N - ccc_{32}	C - v_{3024}	C - cc_{312}
Stem Cell			C - v_{3063}	C - cc_{316c}
Taxes	N - cbb_{01}	N - ccb_{13}		N - cbb_{01}
Trade Policy		N - ccb_{82}	C - v_{3078}	C - cc_{316h}
Welfare	N - cbp_{01}, cbd_{02}	N - $ccc_{39,40,41}$	C - v_{3075}	C - $cc_{316_{g,i}}$

2. Alternative Measures of Performance

The main findings estimate method performance by calculating the MAE and interstate correlation ρ for each simulation and then averaging. However, Buttice and Highton (2013) use a slightly different method that takes the average prediction over the 200 simulations for each state ($\bar{y}_s = \frac{1}{200}\sum_i^{200} y_{i,s}^m$) and compares this value to the true opinion via MAE and interstate correlation. In addition, the authors divide this measure by the standard deviation of the true opinion across states. This "standardized bias" can be formally expressed as:

$$bias_s^m = \frac{abs(\bar{y}_s - y_s^{true})}{sd(y^{true})} \tag{1}$$

$$\rho^{m,state} = cor(\bar{\mathbf{y}}^m - \mathbf{y}^{true}) \tag{2}$$

Figure 1 plots the bias and ρ^* for all 89 surveys using this method. As illustrated, BARP's superior performance is even more striking when using this method. Substantively, this captures the fact that BARP's predictions are, in expectation, more accurate than MRP's.

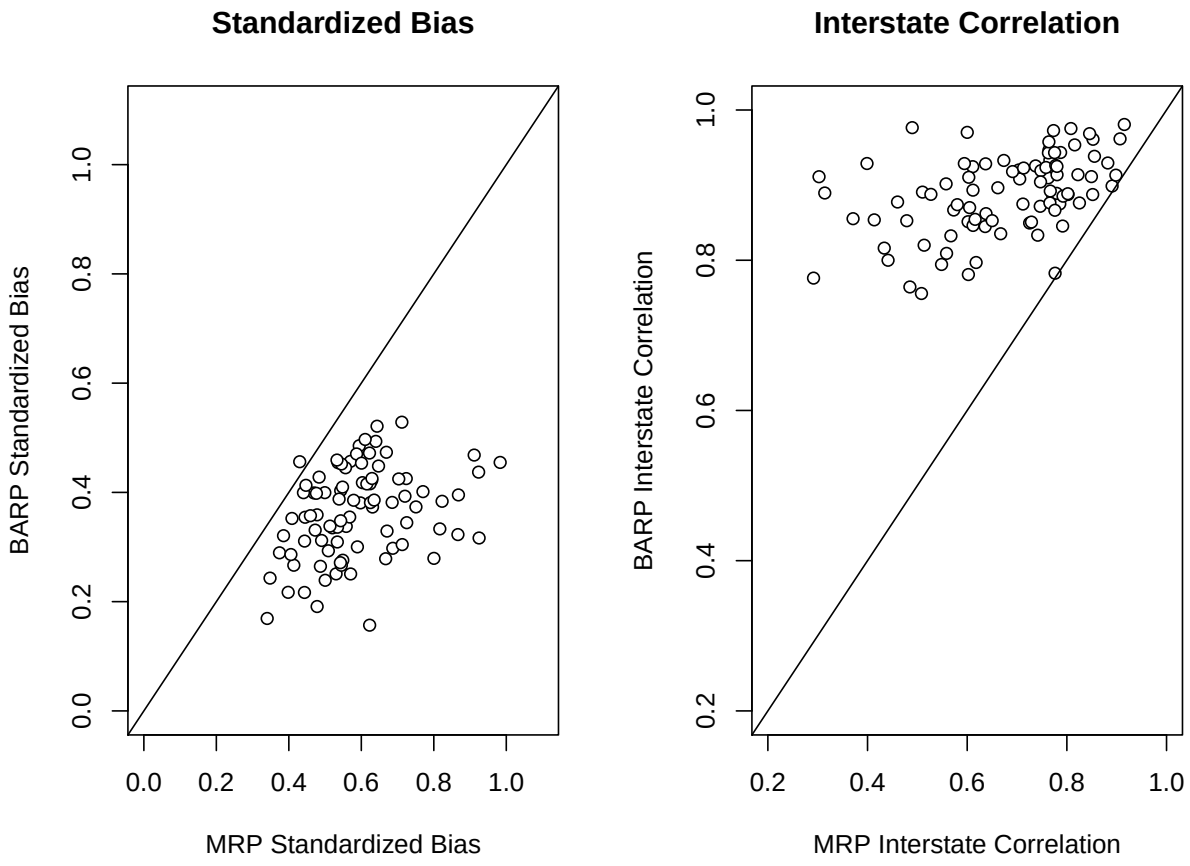


Figure 1: Standardized bias (right panel) and ρ^{state} (left panel) for all 89 surveys.

3. Data Characteristics

While BARP generally outperforms MRP across the 89 surveys, both struggle to accurately predict opinion on similar surveys. For example, both have exceptionally low interstate correlation measures for survey 3 (a question on supporting a path to citizenship for immigrants). Similarly, both BARP and MRP have high mean absolute errors on survey 65 (a question on whether voters should be able to register on election day). What is it about these surveys that is particularly challenging for extrapolating opinion to the state level?

Buttice and Highton (2013) argue that the predictive accuracy of MRP is a function of three characteristics of the data – the prognostic power of the individual-level covariates (measured by McFadden's pseudo R^2 generated by a logit regression of opinion on the individual-level covariates), the prognostic power of the geography-level covariates (the R^2 from an OLS regression of average state opinion on state-level covariates), and the degree to which individuals sort themselves geographically by opinion (measured by the intraclass correlation coefficient (ICC) of opinion by geography).

These characteristics put some structure on the intuition of garbage-in, garbage-out when it comes to how data quality affects extrapolation. In the case of the individual- and geography-level covariates, weak prognostic power means that the model is fundamentally misspecified. The researcher should consider using other explanatory variables to improve prediction. In the case of geographic preference sorting, the intraclass correlation coefficient (ICC) captures how similar units are within a group and how different they are across groups. Where this value is low it means that opinions don't differ meaningfully across the geographic unit of interest.

I calculate each of these three measures for each survey, generating a vector of 89 data quality attributes. I then regress the sensitivity of each method's predictive performance (in terms of both MAE and interstate correlation) on these different dimensions of data quality, visualized in Figure 2.

Three conclusions are worth drawing from these estimates. First, the individual-level prognostic strength does not appear to impact performance in these surveys. Second, both methods are similarly sensitive to data quality issues. The only significant difference between the methods is for how MAE is affected by the ICC (top-left panel). Third, MRP performance is competitive with BARP when the data quality measures are favorable.

One perplexing pattern that invites further analysis is the different impacts of the state R^2 on mean absolute error (no relationship) versus interstate correlation (significant positive relationship), illustrated in the center row of plots. I speculate that more prognostic state-level predictors are better able to sort states by extrapolated outcomes without necessarily bringing them any closer to the actual value of the target outcome. Since interstate correlation effectively captures how well states recover the rank ordering along each opinion, we see this discrepancy between MAE and interstate correlation.

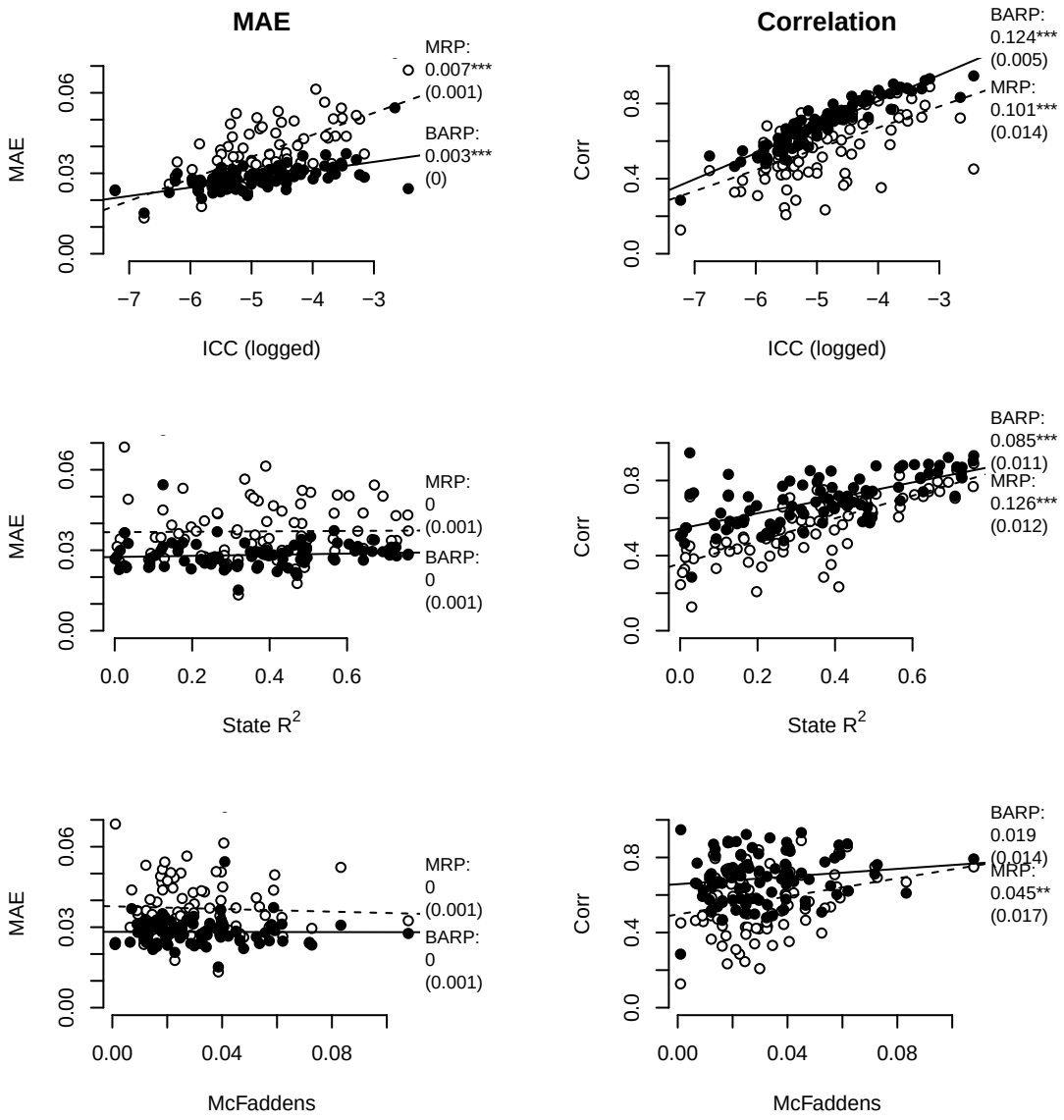


Figure 2: Relationship between method performance (MAE in left column, interstate correlation in right column) and data quality characteristic (ICC in top row, State R^2 in middle row, McFadden's pseudo R^2 in bottom row). Linear bivariate regression model overlaid as lines. $^{+} = p < 0.10$, $^{*} = p < 0.05$, $^{**} = p < 0.01$, $^{***} = p < 0.001$.

4. Replication

The main body of my paper shows that, across 89 survey items, BARP outperforms MRP in terms of both correlation and mean absolute error. But what do these improvements mean in substantive terms?

To test this, I replicate research by Hare and Monogan (2018) who replicate work by Lax and Phillips (2012). Using their publicly available data, I re-estimate opinions using BARP and then replicate their main findings with these new data. Figure 3 compares the MRP-based opinion estimates (x-axis) with the BARP-based estimates (y-axis).

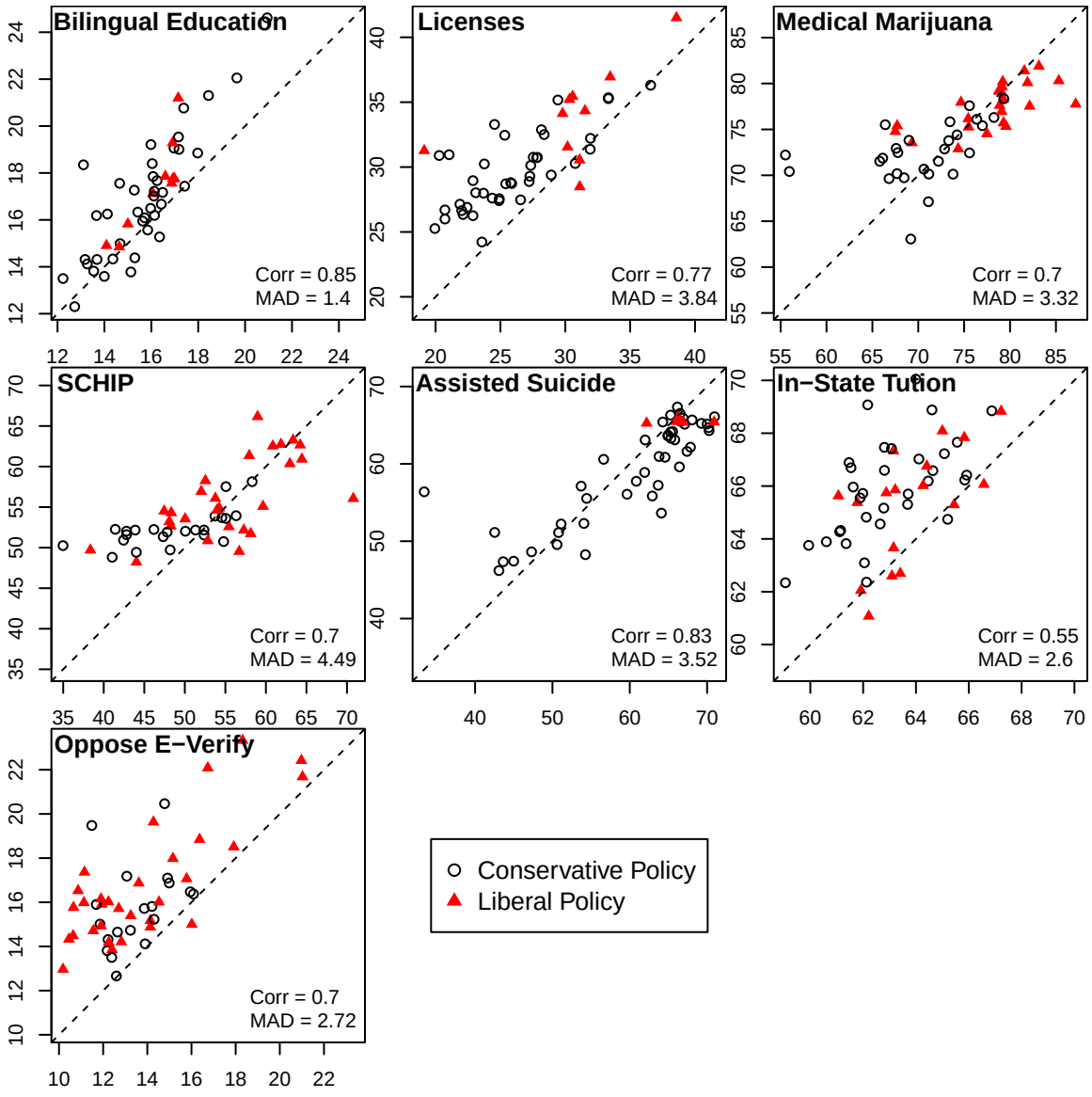


Figure 3: Hare and Monogan (2018) raw opinion estimates comparison. X-axes are MRP-based opinion estimates, y-axes are BARP-based opinion estimates.

As illustrated, the method choice matters. The mean absolute difference (MAD) ranges

from 1.6 percentage points (bilingual education) to 4.38 percentage points (State Children's Health Insurance Program – SCHIP) with some evidence that BARP returns slightly higher predictions overall (points lying above the diagonal 45° line, dashed). The correlation between each method's predicted opinions ranges from 0.54 (in-state tuition) to 0.84 (assisted suicide). From a purely descriptive perspective, the method choices appear to matter.

These differences carry substantive implications for their main analysis which tests whether state-level opinions predict state-level policies – a pattern they label congruence. Their analysis concludes that there is no significant evidence of policy congruence in 2008 or 2014 for the seven issues they identify as being highly salient. However, when controlling for the state-level 2008 policy, there is evidence that congruence has increased in 2014. They draw the substantive conclusion that, for more salient issues, the "democratic deficit" first identified in Lax and Phillips (2012) diminishes.

The authors use two distinct specifications to estimate "congruence". The first (summarized in Table 3) regresses an indicator for whether a state has a liberal policy on one of seven issue topics on state-level opinion on that topic, extrapolated using MRP. The second specification (summarized in Table 4) interrogates whether the size of the opinion majority has any impact on state policy by regressing an indicator for congruent policy on the size of the majority opinion, again extrapolated using MRP. In both cases, the results are estimated separately for 2008, 2014, and then again in 2014 using the 2008 policy as a lagged dependent variable in columns 1 through 3 respectively. The main conclusion drawn by Hare and Monogan (2018) is that there is no evidence of policy congruence in either 2008 or 2014 across these seven issues but that controlling for the 2008 policy suggests that congruence has increased.

I replicate the second and third columns from Tables 3 and 4 using both the authors' original MRP opinion estimates (gray) and BARP opinion estimates (black) in Figure 4. I highlight the p-values since the original authors evaluate their findings with respect to a one-sided test.

Figure 4 suggests that the choice of extrapolation method matters. In three out of the four models (columns 2 and 3 in Table 3, and column 3 in Table 4), BARP data yields significant results at the 95% level of confidence (two-tailed test) where MRP yields only marginally significant results. The original authors implement one-sided hypothesis tests, meaning that their conclusions in column 3 are bolstered with BARP-generated opinions. We are therefore more confident in their conclusion that policy congruence has increased between 2008 and 2014, and the magnitude of this increase appears larger than in their analysis using MRP.

However, their motivation to test the change in policy congruence rests on their conclusion that, in isolation, there is no evidence of congruence in 2014 alone (column 2). Yet this conclusion is undermined when using BARP-generated estimates in Table 3. Here we see a coefficient almost double that reported in the original paper and much more significant. Substantively, replacing the MRP-generated opinions with those produced by BARP suggests that:

1) in 2014, states are more likely to adopt legislation supported by a majority of their constituents (Table 3, column 2),

2) this effect increased between 2008 and 2014 (Table 3, column 3),

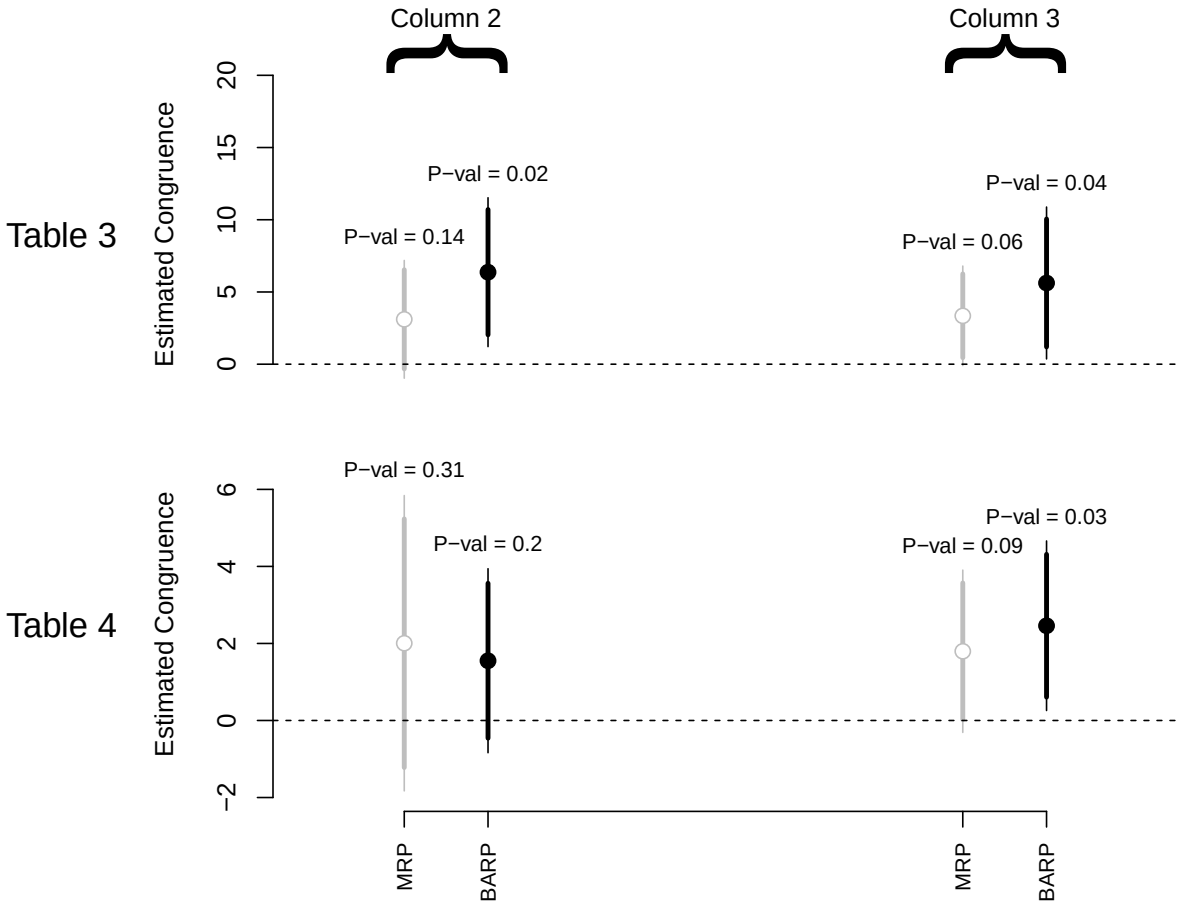


Figure 4: Hare & Monagan (2018) replication with BARP-estimated opinions. Top row replicates Table 3 and bottom row replicates Table 4. Left column replicates Column (2) and right column replicates Column (3) of each table. Original MRP results indicated with hollow circles and gray 90 and 95% confidence bars. Updated results using BARP indicated with solid black circles and confidence bars.

3) in 2014, the size of the opinion majority does not increase the probability that they get their preferred policy (Table 4, column 2),

4) but states that became more congruent between 2008 and 2014 did so thanks to having larger opinion majorities (Table 4, column 3).

Overall, replacing MRP opinions with BARP-based extrapolations provides more precise estimates, yielding a significant positive relationship between state-level opinions and state-level policies. In addition, BARP-based opinions yield both more tightly estimated zeros as well as more significant substantive results. These results suggest that a superior extrapolation method yields both more precise nulls and more striking substantive relationships.

5. Sample Sizes

The main analysis compared method performance using sample sizes ranging between 1,500 and 4,500. However, nationally representative survey sizes historically are often smaller than 1,500. And the advent of the internet has allowed for larger sample sizes than 4,500. In the following section, I compare BARP and MRP performance on small sample sizes between 700 and 1,500 observations, and large sample sizes ranging from 6,000 up to 10,500.

To test sensitivity to smaller sample sizes, I calculate MAE and interstate correlation across 200 simulations and then use a t-test to estimate the difference between $n = 700$ and $n = 1,500$. I plot the t-test coefficients as points in Figure 5, with confidence errors given by horizontal (MRP, x-axis) and vertical (BARP, y-axis). Here there is weaker evidence of BARP's relative insulation, particularly in terms of correlation where BARP appears to be *more* sensitive to sample size, recording larger benefits when moving from 700 observations to 1,500 (as illustrated by points lying closer to the vertical dashed line).

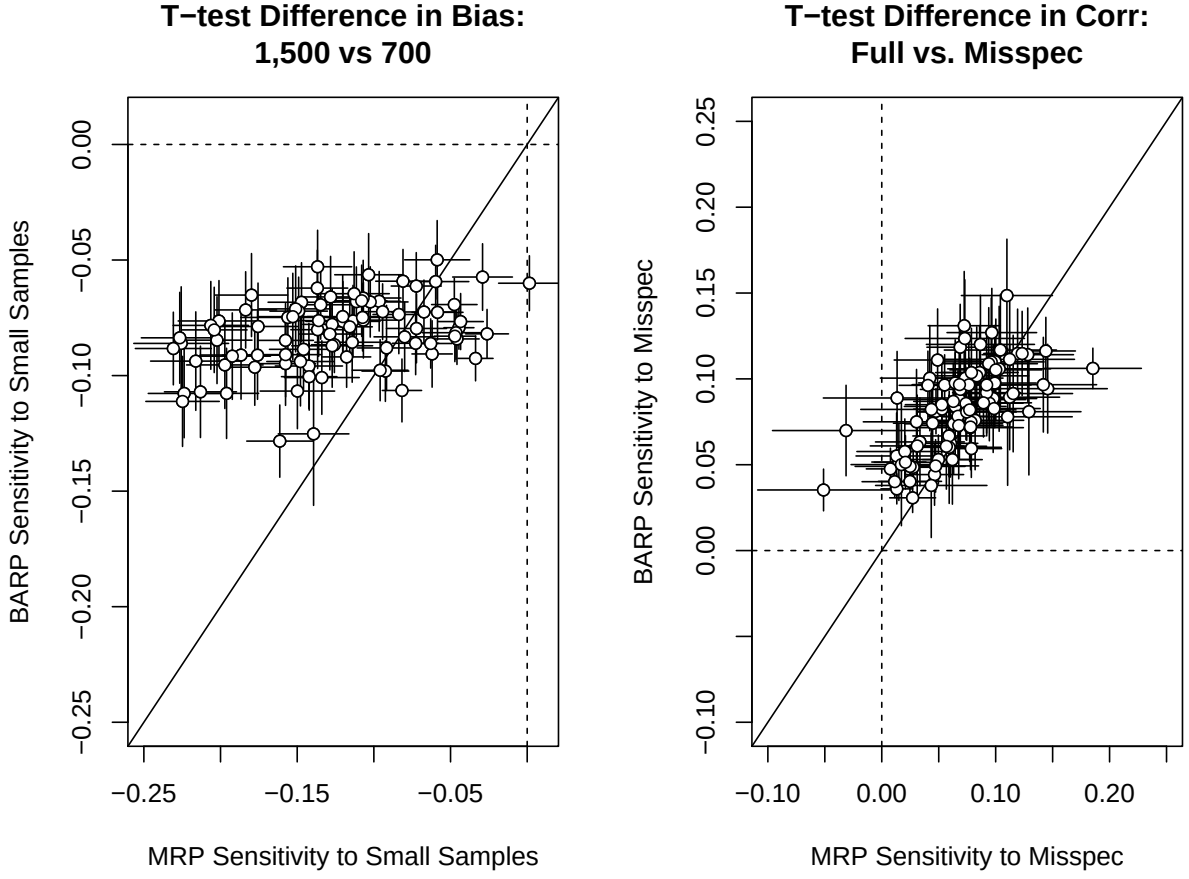


Figure 5: X-axes indicate the coefficients generated by a t-test comparing the mean absolute error (left) and correlation (right) between the full and misspecified regressions for MRP (white circles) and BARP (black circles).

How much do these methods matter when the researcher is able to obtain relatively large sample sizes? To assess this question, I re-analyze each method on sample sizes ranging from $n = 6,000$ to $n = 10,500$ and plot the average MAE and interstate correlation across all 89 surveys in Figure 6, along with the top and bottom 20^{th} percentiles (rectangles). As illustrated, MRP and a simple disaggregated mean achieve equivalence around 10,000 observations. However, BARP retains its edge across all sample sizes.

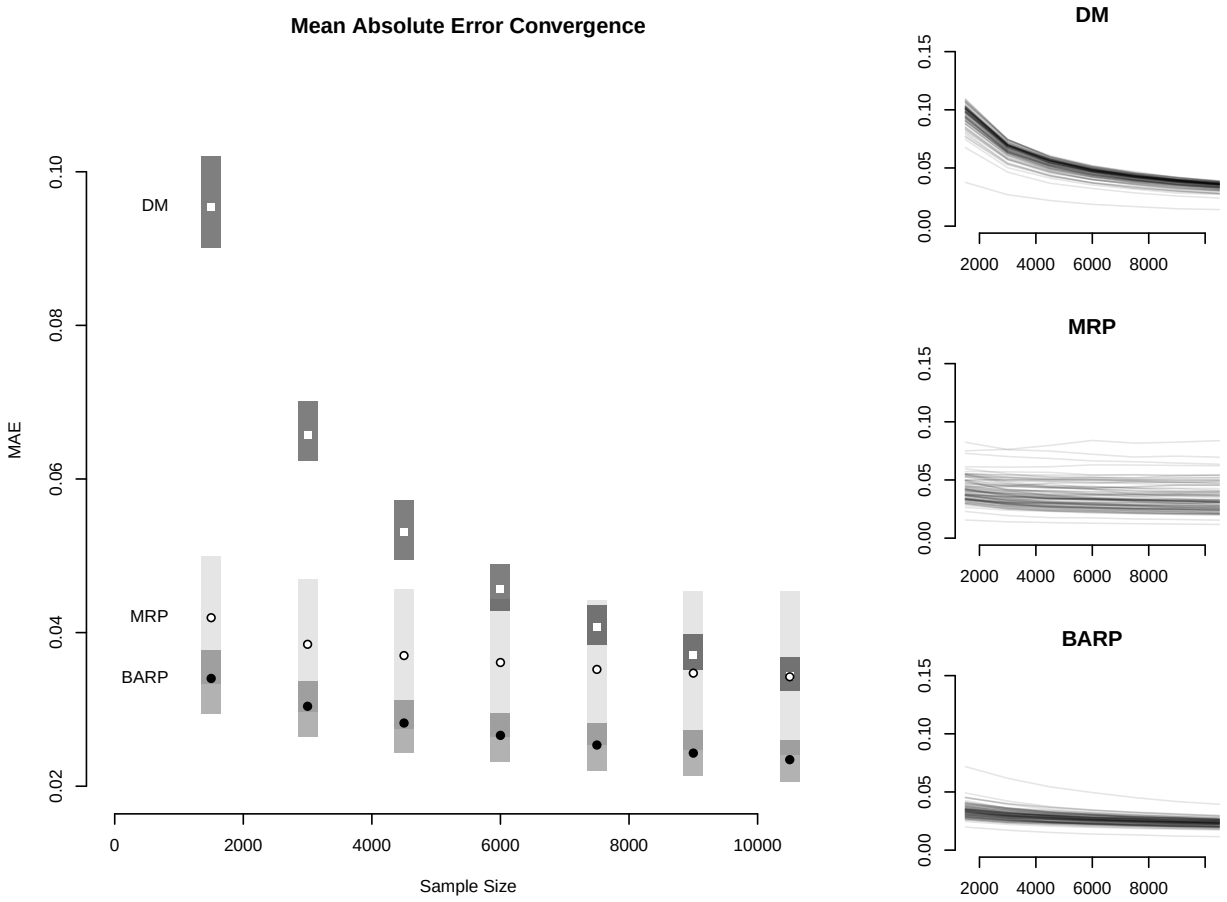


Figure 6: Left panel presents the average mean absolute error across 200 simulations and 89 surveys for different sample sizes (x-axis) for BARP, MRP, and simple disaggregated averages. Rectangles cover the top and bottom 20^{th} percentiles of these metrics. Plots in the right panel plot the average mean absolute error for each of the 89 surveys as lines.

One possible explanation for BARP's superior performance across sample sizes is the method's insulation from particularly challenging surveys. The right-column of plots in Figure 6 depict each individual survey as a single line. MRP struggles to predict opinions in the most challenging surveys regardless of sample size. Conversely, BARP is able to take the additional information provided by more observations to yield more accurate predictions. This evidence of BARP's superior regularization is also reflected in a similar analysis of correlation over sample sizes, as shown in Figure 7.

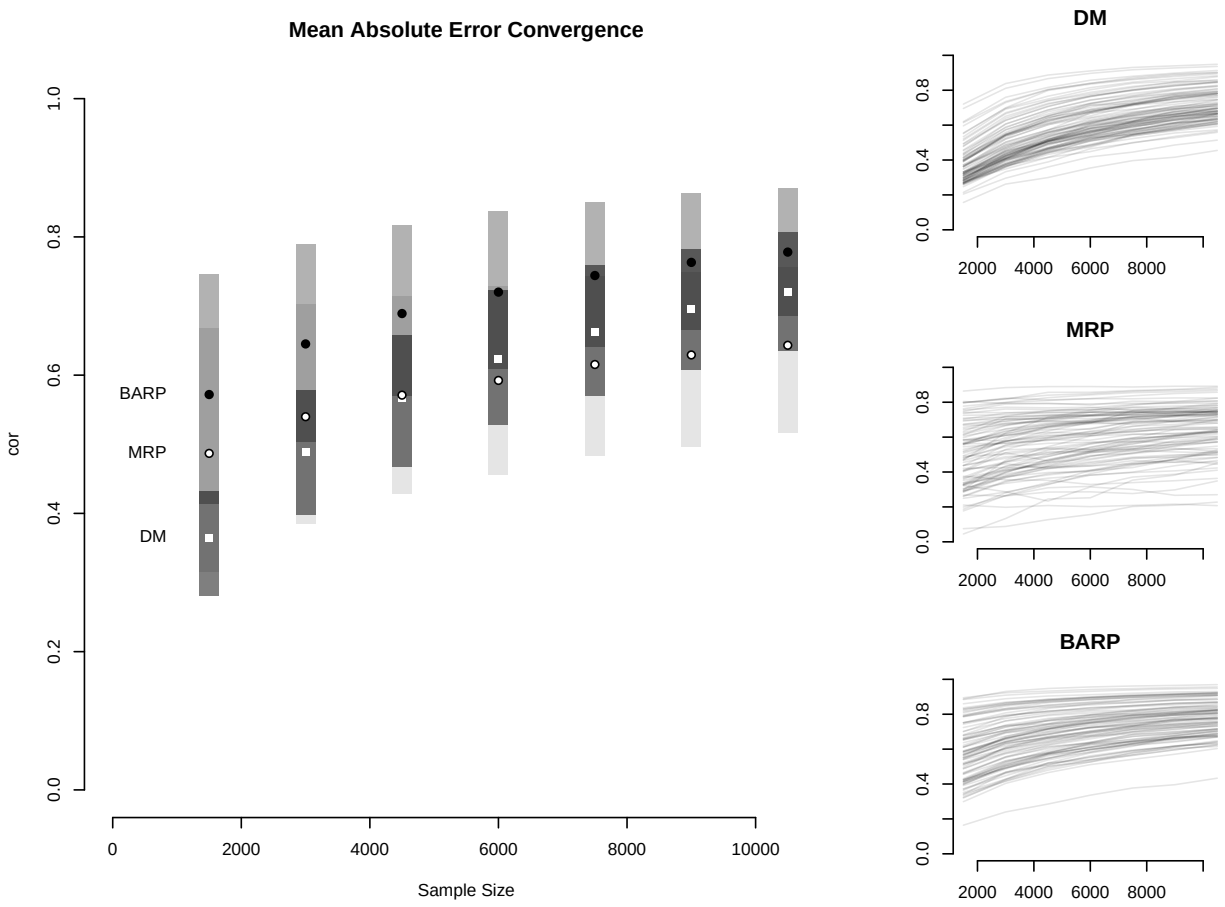


Figure 7: Left panel presents the average interstate correlation across 200 simulations and 89 surveys for different sample sizes (x-axis) for BARP, MRP, and simple disaggregated averages. Rectangles cover the top and bottom 20^{th} percentiles of these metrics. Plots in the right panel plot the average interstate correlation for each of the 89 surveys as lines.

6. Computation Time

The improvements in predictive accuracy obtained with BARP do not come with some costs. First, for applied researchers unfamiliar with Bayesian Additive Regression Trees or other machine learning methods, there is a learning curve to adoption. In section 9, I describe an `R` package I developed to aid in BARP adoption. Second, BARP is more computationally intensive, particularly in cases with larger sample sizes and / or larger numbers of trees or MCMC simulations.

Figure 8 illustrates these timing differences between MRP and BARP across different sample sizes and hyper-parameter settings.[1] While the differences are non-trivial, BARP is hardly prohibitively slow. Furthermore, speed improvements can be obtained by exploiting parallelization for systems with multiple CPU cores. The right panel summarizes computation time for BARP in the extreme with 500 trees and 1,000 MCMC iterations after the burn-in.

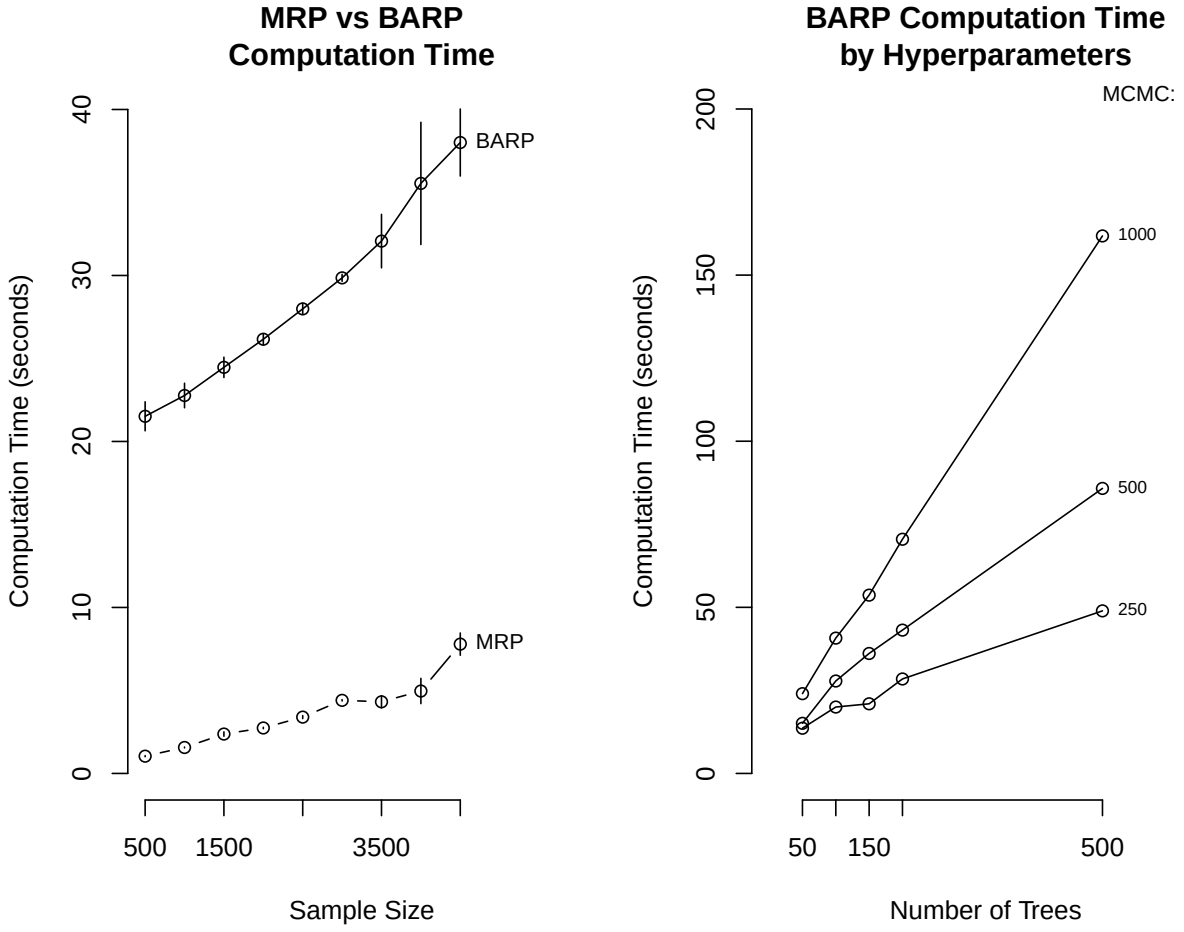


Figure 8: Computation time by method (left plot) and by BARP hyperparameter values (right plot, with trees on x-axis and MCMC iterations after the burn-in as series).

[1]Results generated using a Dell Inspiron i7559-7512GRY laptop with a 6th generation Intel Core i7 2.6 GHz processor and 16gb of RAM using a 1TB hard drive.

7. Other Machine Learning Regularization Methods

The main analysis focuses on a particular machine learning method – Bayesian Additive Regression Trees (BART). However, there are many non-linear methods that tout similar regularization benefits. To compare method performance, I re-run the main analysis with a selection of other non-parametric regularization methods, including:

- Gradient Boosting Machines (GBM)
- Kernel k-Nearest Neighbor (kNN)
- Neural Networks (NNET)
- Support Vector Machines (SVM)
- Elastic-net regularization (LASSO)

In the following section, I describe each method briefly and then compare method performance to BARP.

GBM

GBM builds new models ($h(\cdot)$) on top of weak initial models ($F(\cdot)$) in an attempt to reduce the magnitude of the residuals via gradient descent. For an initial model that predicts an outcome y as a function of some covariate(s) $F(\cdot)$, calculate the gradient $g(\cdot)$ associated with a specific loss function $L(\cdot)$. Then fit a new model $h(\cdot)$ to the gradient and add it to the initial model with some weight ρ. The process repeats until a stopping rule is reached.

1. Start with an initial model $F(X_1)$
2. Calculate the negative gradients $-g(X_1)$
3. Fit a regression tree to the negative gradients $h(X_1)$
4. Update the model $F_1(X_1) = F(X_1) + \rho h(X_1)$

GBM is conceptually similar to BART in the use of regression trees that are fit to the residuals. A more detailed description of GBM can be found in [CITE].

Kernel-kNN

A k-nearest neighbors algorithm assigns an outcome for an observational unit using the average outcome found among the k most similar observations units for which the outcome is observed where 'similarity' is defined as distance in covariate space. In the context of predicting public opinion, we feed the algorithm survey data containing both the opinion recorded (Y) for each respondent (i) as well as their individual-level and geography-level covariates of interest (X).

For a new individual for which we have covariate information X but no outcome information Y, kNN predicts their opinion by selecting some number (k) of individuals from the training data who are closest in covariate space. In both cases, I implement a kernel weight to privilege closer comparisons over those further away.

Kernel-kNN has three important hyper-parameters: the number of nearest neighbors k, the kernel function that defines how distance is penalized, and the algorithm used to measure distance. For the purposes of my analysis, I use cross validation to determine the optimal k, distance measure, and kernel from among the defaults provided in the `KernelKnn` package for `R`. However, applied researchers are encouraged to do their own cross validation tests using more sophisticated kernels, such as a gamma kernel with a free hyper-parameter for the shape α.

NNET

A neural net applies weights to a vector of information commonly referred to as the 'input layer' of neurons. In the context of predicting opinions from a survey, the input layer can be thought of as the covariate information we have on each survey respondent. A set of weights connects each neuron in the input layer to all neurons in a second hidden layer.

The values that each neuron in the hidden layer takes on are simply the weighted sum of all input layer neurons, plus some bias value. Depending on the complexity of the neural net, there can be several hidden layers of neurons. But the final set of weights transforms the last hidden layer into predictions for all possible outcome values. In the context under consideration, these outcome values are the opinions held by each survey respondent.

A loss function measures the difference between each true outcome and the prediction generated by a particular combination of weights and biases. These weights and biases are then updated via gradient descent down the surface of the loss function and assigned via back-propagation. Typically, the weights, antecedent node values, and biases are transformed via a sigmoid function to yield values on the support of $[0, 1]$.

The field of neural networks has developed substantially beyond the description provided above. However, for the applied purpose of predicting opinions based on observed covariates, I use a simple neural net with only one hidden layer. I use cross validation to determine the optimal number of nodes in this hidden layer, along with the decay parameter used to avoid overfitting via the `nnet` package for `R`.

SVM

Support Vector Machines attempt to draw a linear hyperplane through data to such that the observations are perfectly separated by the outcome data. The hyperplane is chosen such that the 'margin' – the distance between the hyperplane and the closest data point – is maximized. The margin can be expressed as $\frac{2}{||W||}$ when the binary outcome is redefined as -1

and 1 and the optimization problem can be re-expressed as minimizing $\frac{1}{2}||W||^2$, allowing it to be solved via the quadratic programming solution:

$$W(\alpha) = \sum_i \alpha_i - \frac{1}{2} \sum_{ij} \alpha_i \alpha_j y_i y_j x_i^T x_j$$
$$\text{s.t. } \alpha_i \geq 0, \sum_i \alpha_i y_i = 0$$

The method takes its name from the fact that many of the α parameters are zero, implying that only a few of the vectors matter. These are the support vectors and are similar to the nearest neighbors method except that the proximate points of interest are determined not by an arbitrary distance / number of closest matches but rather by defining the separating hyperplane.

For data that are well ordered in covariate space, the hyperplane is easily understood as a line. However, for more complicated combinations, one must project the data onto higher dimensional space. To save on computation time, one can apply a kernel function $K(\cdot)$ to the $x_i^T x_j$ part of the quadratic programming solution, avoiding calculating the projection. This kernel function must be chosen by the researcher and represents the substantive intuition behind how to define similarity.

There are a few decisions that need to be made by the researcher, the most important being the choice of kernel.

Elastic-Net

Finally, I compare these machine learning methods with an alternative linear predictor that uses an elastic-net penalty for regularization. To implement, I use the `glmnet` package for `R` which implements a more flexible elastic-net penalty of the form:

$$\min_{\beta_0, \beta} \frac{1}{N} \sum_{i=1}^{N} w_i l(y_i, \beta_0 + \beta^T x_i) + \lambda \left[(1-\alpha)||\beta||_2^2 \right]$$

Method Performance

I implement each method via the `SuperLearner` package for `R` which estimates both individual predictions as well as an ensemble that combines all methods in a weighted prediction. The weights are generated by determining how well each method performs in predicting the outcome on a validation dataset, where performance targets the maximized AUC (area under an ROC curve) criteria. For a detailed introduction to ensemble machine learning methods, see Alpaydin (2010).

Figure 9 summarizes the ensemble weights from 200 simulations for each of the 89 surveys. The left panel plots the average percent of simulations in which the weight assigned to BARP

in the ensemble is larger than the weight assigned to each of the competing five methods by survey. The right panel combines all simulations and surveys to yield the total share that BARP is more prognostic than the competing methods. Overall, BARP is assigned the largest weight in the ensemble in 61% of simulations across 89 surveys.

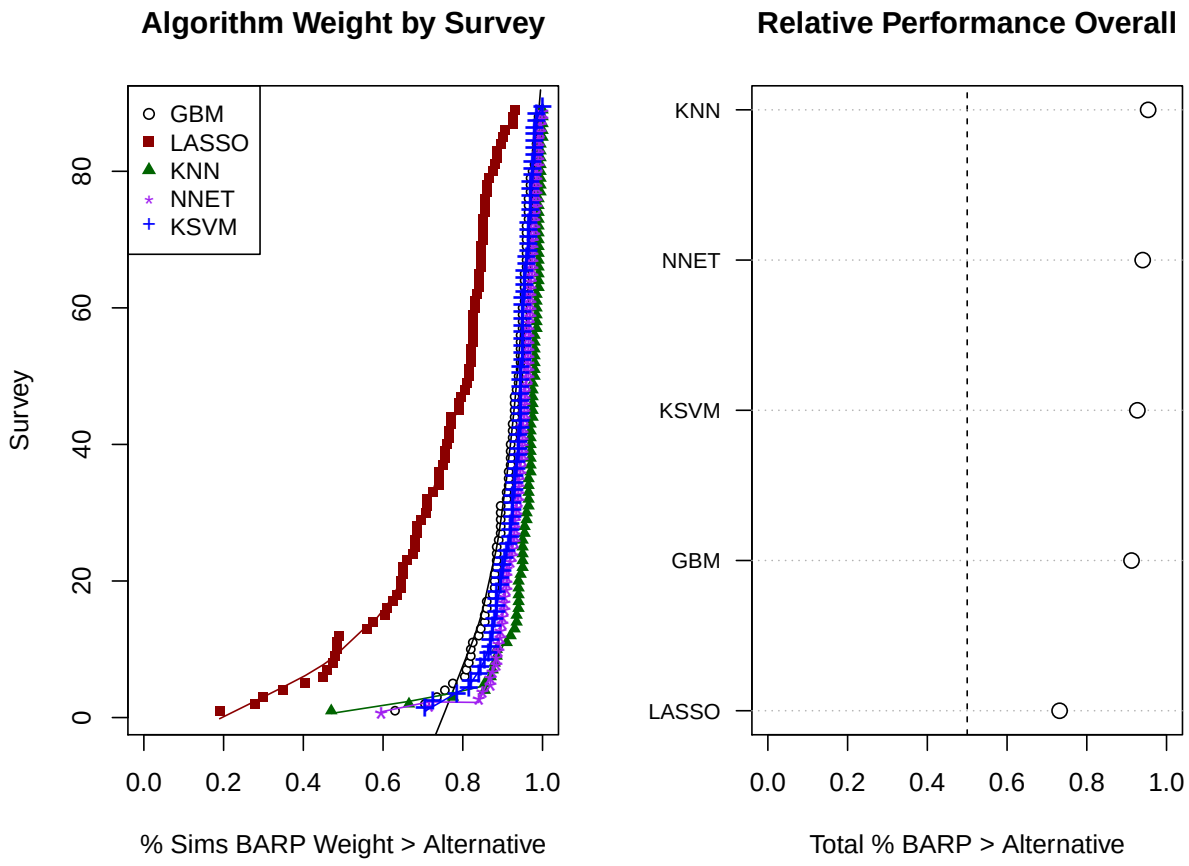


Figure 9: These plots summarize the share of simulations in which BART is given the more weight in the ensemble SuperLearner than alternative regularization methods. The left plot breaks out these comparisons by survey (y-axis) and comparison method (points). The right plot aggregates over both surveys and competing methods, yielding a single percent of all surveys and simulations in which BARP is given the most weight in the ensemble.

However, the weights used to determine method performance are optimized for classification which does not necessarily mean they are good for interstate correlation. To assess method performance in the context of the motivating interest in mean absolute error and interstate correlation, I re-estimate performance for all 89 surveys across 200 simulations randomly sampling 1,500 observations from each survey. I compare each method's performance against the true state opinion (again, calculated as the state average using the full survey data) in terms of both mean absolute error (MAE) and inter-state correlation. To visualize these results, I subtract the average MAE for each method from the average MAE for BARP, and rank these differences by survey. I do the same for correlation. These results are summarized

in the left and right panels of Figure 10 respectively.

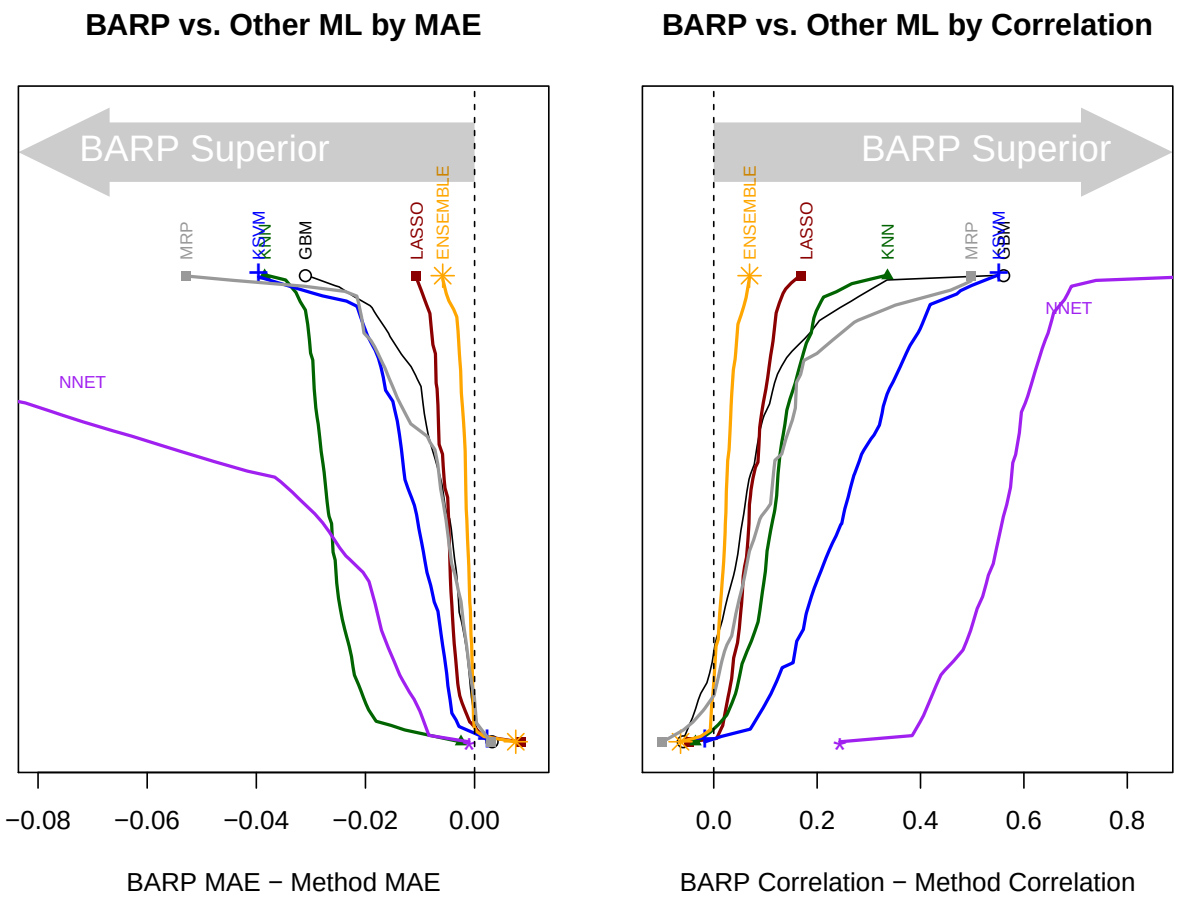


Figure 10: Machine learning method performance relative to BARP across 89 surveys (y-axis). The left plot summarizes the difference between each method's mean absolute error (MAE) and BARP, with positive values indicating larger errors on the part of the ML method. The right plot summarizes the difference between BARP's interstate correlation and each method, with positive values indicating lower interstate correlation on the part of the ML method.

As illustrated, BARP generally outperforms all other machine learning methods in terms of MAE, including the ensemble. However, there is consistent evidence that it is not as good in terms of interstate correlation, particularly when compared to the ensemble predictions which are higher than BARP across all 89 surveys. These findings are confirmed when averaging over surveys for different sample sizes, as visualized in Figure 11. While all methods improve with more data, BARP retains the predictive edge in terms of MAE although it is more in the middle of the pack in terms of interstate correlation.

These comparisons produce three general conclusions.

- First, MRP is competitive with more sophisticated methods in terms of mean absolute error in larger sample sizes.

Figure 11: Machine learning method performance in terms of mean absolute error (MAE - left plot) and interstate correlation (right plot) across different sample sizes (y-axis).

- Second, BARP is among the best-in-class in terms of mean absolute error but is more in the middle of the pack in terms of interstate correlation.
- Third, the best methods evaluated in terms of mean absolute error are not the same as the best methods judged by interstate correlation. Across both metrics, LASSO regularization is competitive.

I focus the letter on BARP for it's overall strength along both dimensions but include many alternative regularization methods including the six summarized here in the R package. Applied researchers are encouraged to use different methods to test the robustness of their findings, with particular care given to whether their substantive interest is in assessing congruence (in which case mean absolute error performance is especially important) or responsiveness (in which case interstate correlation is especially important).

8 A BART primer

This section introduces Bayesian Additive Regression Trees. Users are encouraged to refer to Chipman, George, and McCulloch (2010) for a more detailed discussion.

A single regression tree $\mathcal{T}$ approximates an unknown function f by recursively partitioning the covariate space ($\mathbf{X}$) to best organize observations (i) according to some outcome Y. The resulting bins (commonly referred to as "nodes" or "leafs") proceed until a stopping criteria is met. Each terminal node b is associated with a parameter value μ_b which combine to form the set $\mathcal{M}$. Observed values of $x \in \mathcal{X}$ are assigned to a $\mu_i \in \mathcal{M}$ by a function $g(x; \mathcal{T}, \mathcal{M})$ which is an approximation of the unknown function f. Armed with many such trees indexed by t, the researcher can predict Y via

$$Y = \sum_{t=1}^{T} g(\mathbf{X}; \mathcal{T}_t, \mathcal{M}_t) + \epsilon, \qquad \epsilon \sim \mathcal{N}(0, \sigma^2)$$

The Bayesian aspect of BART imposes priors on the parameters $(\mathcal{T}_t, \mathcal{M}_t)$ and σ^2, the details of which can be found in Chipman, George, and McCulloch (2010).

Consider a simplified example where y_i is an individual's (i) opinion on gay marriage and $\mathbf{X}$ includes information on respondent age, educational attainment, and state of residence. A regression tree might first divide the data into one group (known as a "node" or a "leaf") over 35 years of age, and the other group younger if this division most cleanly separates supports of gay marriage from opponents. The algorithm might then divide the data based on gender, then back again on age, then on state of residence, each time further separating sub-groups of respondents into supporters and opponents. Each division is called a "splitting rule" where the "splitting variable" x_j is divided at a "splitting value" c.

When the tree stops growing (based on a pre-specified depth or a minimum limit on the number of observations in each terminal node), the terminal nodes each contain a fraction of the original observations characterized by observed opinions and a particular sequence of splitting rules. So for example, a terminal node containing 10 survey respondents, 9 of whom oppose gay marriage, may have been created by selecting those over 35, those without a college degree, those living in the Northeast, those *under* 50, and those living in Massachusetts. This particular sequence of splitting rules is then assigned a parameter μ capturing the aggregate opposition to gay marriage in this group. Armed with these terminal nodes and set of parameters $\mu_i \in \mathcal{M}$, the researcher can then predict opinions using new data or use the estimated functions g to evaluate the partial dependence between a given covariate and the outcome.

Repeating this process many times using the regularization priors on $(\mathcal{T}_t, \mathcal{M}_t)$ and σ^2 yields a rich characterization of the unobservable function f. Draws from the posterior distribution of $Pr(\mathcal{T}_t, \mathcal{M}_t, \sigma^2|Y)$ leverage a Metropolis-within-Gibbs sampler which first proposes a change to the structure of $\mathcal{T}_\infty$, either by growing a terminal node, pruning two child nodes, or changing one of the splitting rules. Samples of $\mathcal{M}_1$ are then drawn from this new structure and this process repeats for each tree in $\mathcal{T}$. Finally, a new draw of σ^2 completes the sampler, providing

an estimate of f.

The discussion above deals with continuous outcome variables. In applications to binary opinion data, BART can be fruitfully implemented as a linear probability method. However, if Y is coded as a factor, BART can instead be used for classification with a probit model $Pr(Y = 1|\mathbf{X} = \Phi(\sum_{t=1}^{T} g(\mathbf{X}; \mathcal{T}_t, \mathcal{M}_t))$. (Naturally, no prior is needed for σ_2 since the probit assumes $\sigma^2 = 1$.) The latent variable Z is added to the sampler, replacing Y after the additional step:

$$Z_i|y_i = 1 \sim max\left\{\mathcal{N}\left(\sum_{t=1}^{T} g(\mathbf{X}; \mathcal{T}_t, \mathcal{M}_t)\right), 0\right\} Z_i|y_i = 0 \sim min\left\{\mathcal{N}\left(\sum_{t=1}^{T} g(\mathbf{X}; \mathcal{T}_t, \mathcal{M}_t)\right), 0\right\}$$

From this brief introduction, it should be clear that BART possesses two attractive qualities. First, it allows for deep interactions that grow exponentially in the number of covariates as well as the allowed tree depth. Second, the ensemble character of the method can capture additive effects. These qualities allow for superior estimation of the unknown function f relative to multilevel models and relax the requirement that the research define the functional form correctly *a priori*. In the context of extrapolating public opinion through post-stratification, BART's superior predictive performance is particularly attractive, as discussed in detail in Bisbee (2019). In the ensuing sections, I demonstrate how to easily leverage BART's predictive power with the **BARP** package for **R**.

9 The BARP Package

In this vignette, I walk through an applied example using the **BARP** package for **R**. I use the data included with the **BARP** package which consists of:

1. A nationally representative survey of support for gay marriage fielded in 2006.
2. Census data giving the share of the population falling into different covariate bins (i.e. the share that is a black female with a college degree between the ages of 31 and 50) for the geographic unit of interest (in this example, US states).

This vignette is designed to demonstrate the functions associated with the **BARP** package. The vignette proceeds as follows: In **Section 9.1** I demonstrate how to implement the basic `barp` function to generate state-level opinions from nationally representative data. I show how to estimate upper and lower bounds of these values through either Bayesian credible intervals or through bootstrapping over random samples of the data.

In **Section 9.2** I demonstrate how to explore the partial depedencies generated by the model using the `barp_partial_dependence` function. This function allows the researcher to evaluate which covariates are most strongly associated with support of, or opposition to, a given topic. The function allows for up to three-way interaction estimation, permitting rich characterizations of how the supplied covariates predict the opinion of interest.

Section 9.3 evaluates the prognostic power of the covariates by examining the number of times they are used as a "splitting rule" (see section 3.1 for more details). The number of times the covariates are used is known as the "variable inclusion proportion". Following Bleich et al. (2014), I permute the outcome variable to break any connection with the covariates and re-estimate the variable inclusion proportions to generate a null distribution. Against that null distribution I evaluate the significance of variable inclusion. I also discuss methods for dealing with missing data, introduced in Kapelner and Bleich (2015).

Section 9.4 describes how to implement alternative prediction algorithms. Users can instantiate any one of the 43 different algorithms included in the `SuperLearner` package (Polley and Van der Laan 2015), the full list of which is viewable with a call to the `listWrappers()` function. These functions can be run in isolation or in combination, in which case the package will return both the predictions associated with each algorithm as well as those predictions generated by a weighted ensemble of all algorithms, with weights calculated with 10-fold cross validation.

Section 9.5 concludes.

9.1.0 Predicting opinions with `barp`

`barp` is the main function in the **BARP** package and produces objects of class `barp` which then can be used in other functions. A `barp` object is a list containing two components. The first is a `data.frame` that gives the predicted opinion, and the lower and upper bounds for

each geographic unit of interest. The second is the `bartMachine` object (Kapelner and Bleich 2013). I demonstrate the function below.

While the package was originally built with the intention of implementing Bayesian Additive Regression Trees, it has since been expanded to accommodate a number of alternative regularization algorithms via the `SuperLearner` package. These alternative algorithms will return predicted opinions in the same `data.frame` object but users will not be able to examine partial dependencies or prognostic covariate strength. I return to a brief discussion of how to run **BARP** with alternative regularization algorithms at the end of this vignette.

9.1.1 Installing BARP and setting available memory

BARP implements Bayesian Additive Regression Trees using the **bartMachine** package developed by Adam Kapelner and Justin Bleich (Kapelner and Bleich 2013). This requires `rJava`; installing `rJava` on a Windows PC can be tricky because some machines require users to manually set the `PATH` to their Java bin. For users confronting errors, a good start can be found here. (But Googling the specific error is always the best method.)

Once `rJava` is installed, **BARP** can be installed as follows:

```
require(devtools)
install_github('jbisbee1/BARP')
```

With **BARP** installed, the first thing to do *before* loading the package is set the memory available to Java with `options(java.parameters = "-Xmx[NUM]g")` where `[NUM]` refers to the number of gigabytes of memory to use. For common opinion datasets (i.e. $<$ 5,000 rows and $<$ 20 covariates), 3 GB should suffice.

```
options(java.parameters = "-Xmx5g")
require(BARP)
```

9.1.2 Loading the data and predicting opinions

We can now proceed to extrapolating opinions on gay marriage to the state level. Following Buttice and Highton (2013), I will use four individual-level covariates (age, education, and the interaction of gender and race), two state-level covariates (Republican presidential vote-share in the preceding election, and the share of the population identifying as a "religious conservative"), and two geographic indicators (state, and region). *Note* that the geographic unit of interest to the user (`geo.unit`) **must** be included in the vector of covariates. The outcome opinion in this example is opposition to gay marriage, surveyed in 2006.

The main parameters used by the `barp` function include:

1. the survey data `dat`
2. the census data `census`
3. variable names for the outcome `y` and covariates `x`

4. variable name of the geographic unit of interest `geo.unit`

The user should also specify the name of the column in the census data that lists the proportions or shares that fall into each covariate category (`proportion`). If left to the default "None", `barp` assumes that the census data is raw and calculates the proportions by counting the number of rows for each covariate bin over the total rows per geographic unit.

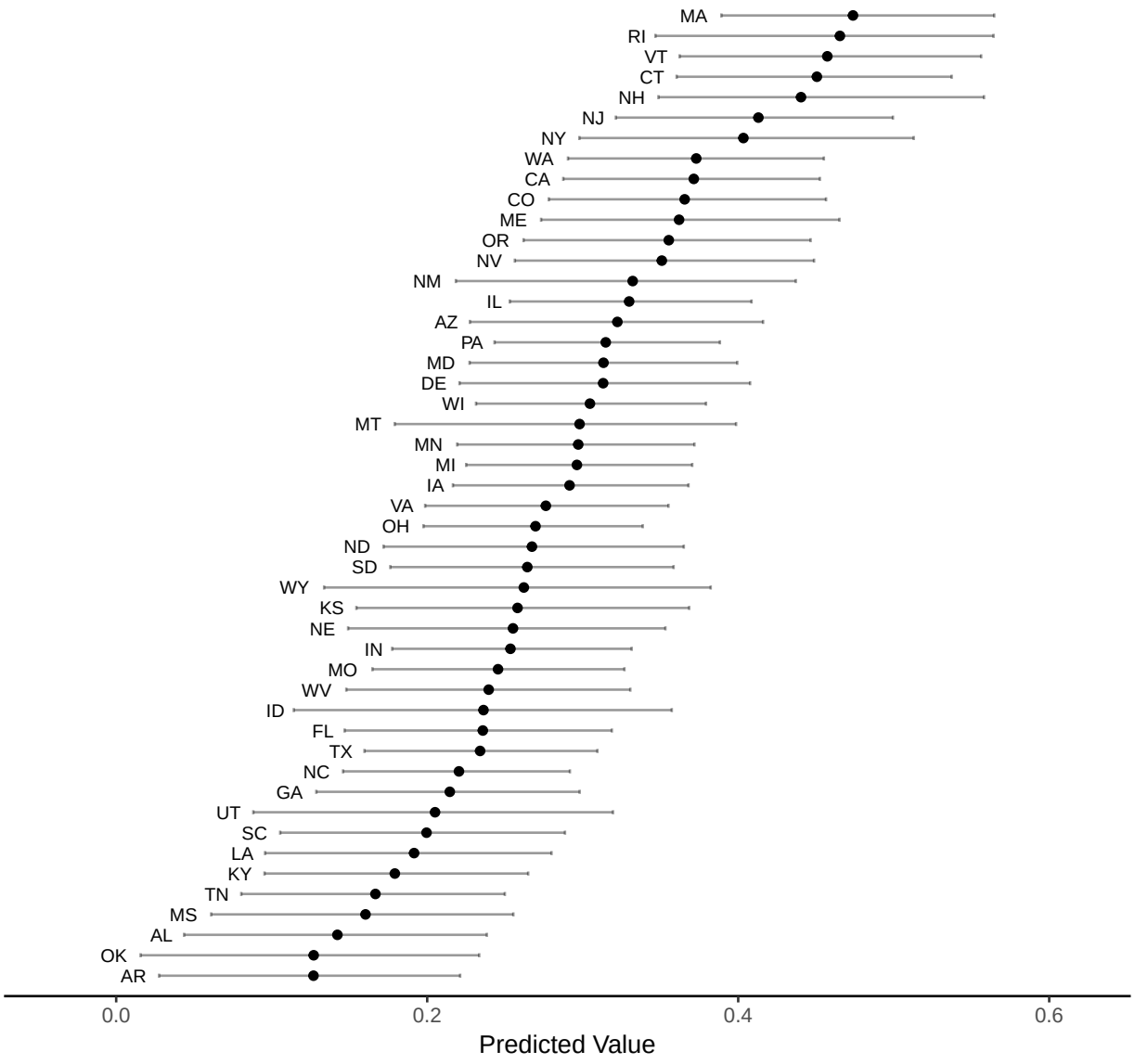
```
data("gaymar")
census06 <- census06 %>% merge(svy %>% dplyr::select(state,stateid) %>% distinct())
factors <- c("region","gXr","state")
census06[factors] <- lapply(census06[factors],factor)
svy[c(factors)] <- lapply(svy[c(factors)],factor)
barp.obj <- barp(y = "supp_gaymar",
                 x = c("age","educ","gXr",
                       "pvote","religcon",
                       "state","region"),
                 dat = svy,census = census06,
                 geo.unit = "state",
                 proportion = "n",
                 seed = 1021,
                 serialize = TRUE)
```

The resulting `barp` object summarizes the predicted opinions and bounds as a `data.frame`. Plotting the `barp` object will return either a simple plot of the predicted values and credible intervals (`evaluate_model = FALSE`, the default), or a set of convergence diagnostic plots (`evaluate_model = TRUE`). The latter plot should exhibit relative stability across the post-burn-in Markov Chain Monte Carlo (MCMC) simulations in terms of percent acceptance, number of leafs and terminal nodes, and tree depth (and σ^2 when y is not a factor).

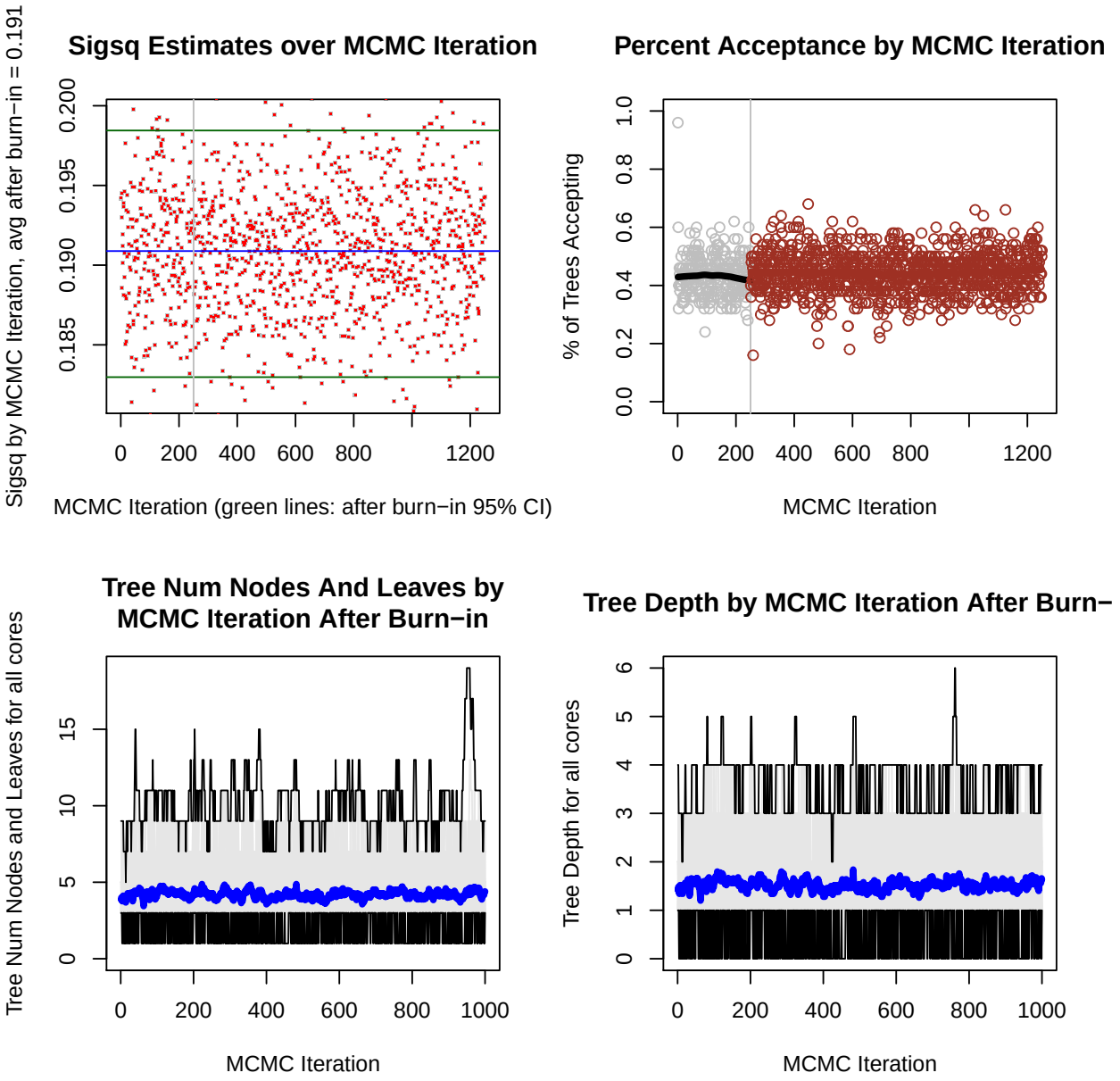
```
barp.obj$pred.opn %>% head()
```

```
##   state SL.bartMachine_1_All     opn.lb    opn.ub
## 1    AL            0.1422521 0.04367446 0.2383575
## 2    AR            0.1268787 0.02760524 0.2212013
## 3    AZ            0.3222951 0.22747162 0.4159995
## 4    CA            0.3714351 0.28748739 0.4525278
## 5    CO            0.3655661 0.27821291 0.4564940
## 6    CT            0.4506066 0.36040250 0.5372730
```

```
plot(barp.obj,algorithm = "BARP")
```




```
plot(barp.obj,evaluate_model = T)
```

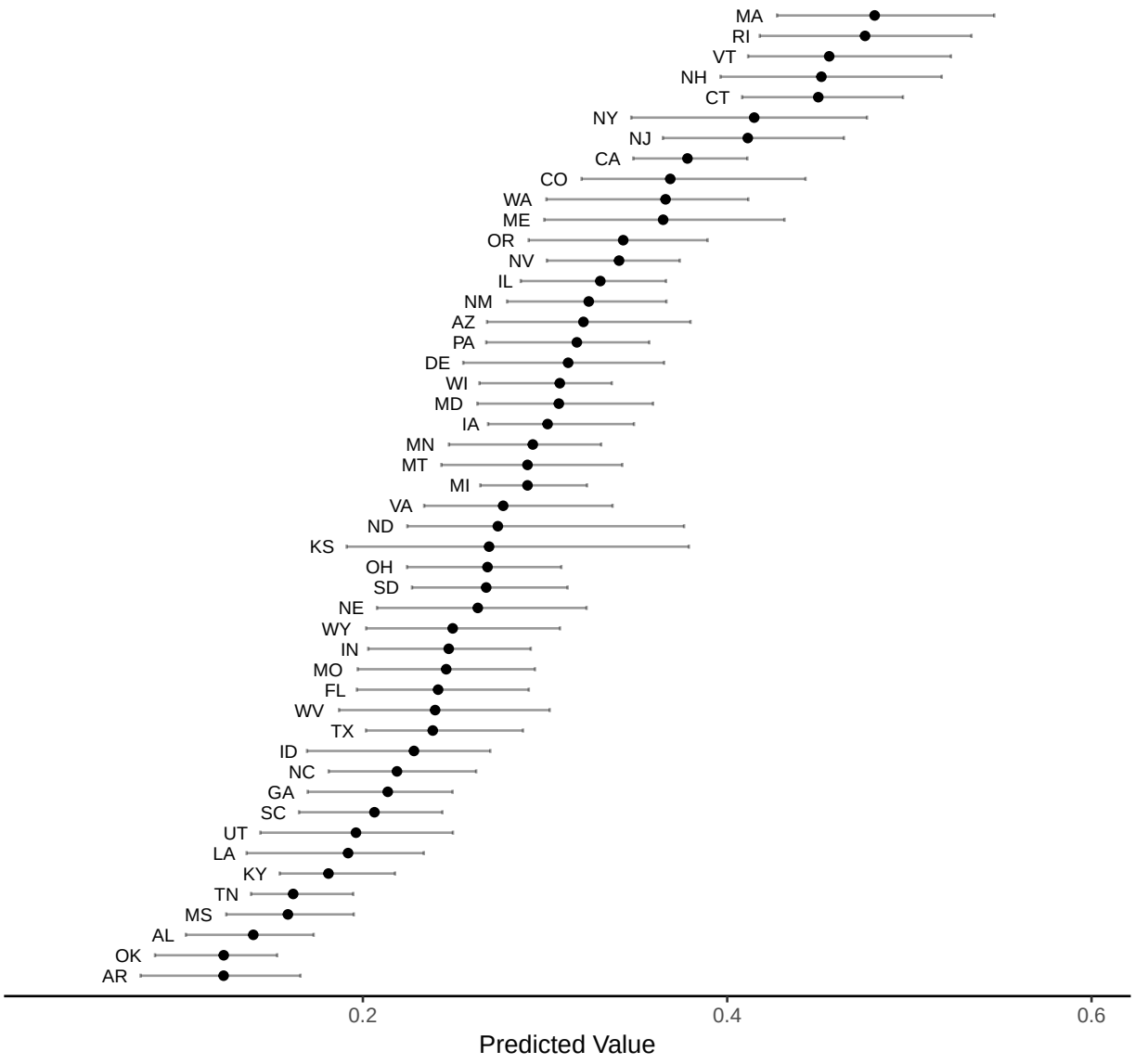


Alternatively, the user can choose to calculate the upper and lower bounds using bootstrapped simulations by setting `BSSD = TRUE` and defining the number of simulations through the `nsims` parameter. (Note that doing so will multiply the compute time accordingly). The user can set the credible intervals for the bounds with `cred_int = c(0.025,0.975)`. Lastly, additional arguments can be passed to **bartMachine** including `num_trees`, `num_burn_in`, `num_iterations_after_burn_in`, `verbose`, et cetera. These parameters are non-trivial and should be adjusted based on evaluating model performance via `evaluate_model = TRUE` in the `plot` function.

```
barp.obj2 <- barp(y = "supp_gaymar",
                  x = c("age","educ","gXr",
                        "pvote","religcon",
```

```
                    "state","region"),
                dat = svy,census = census06,
                geo.unit = "state",
                proportion = "n",
                BSSD = T,
                nsims = 50,
                num_trees = 40,
                num_burn_in = 250,
                num_iterations_after_burn_in = 250,
                setSeed = 1021)
```

```
plot(barp.obj2)
```



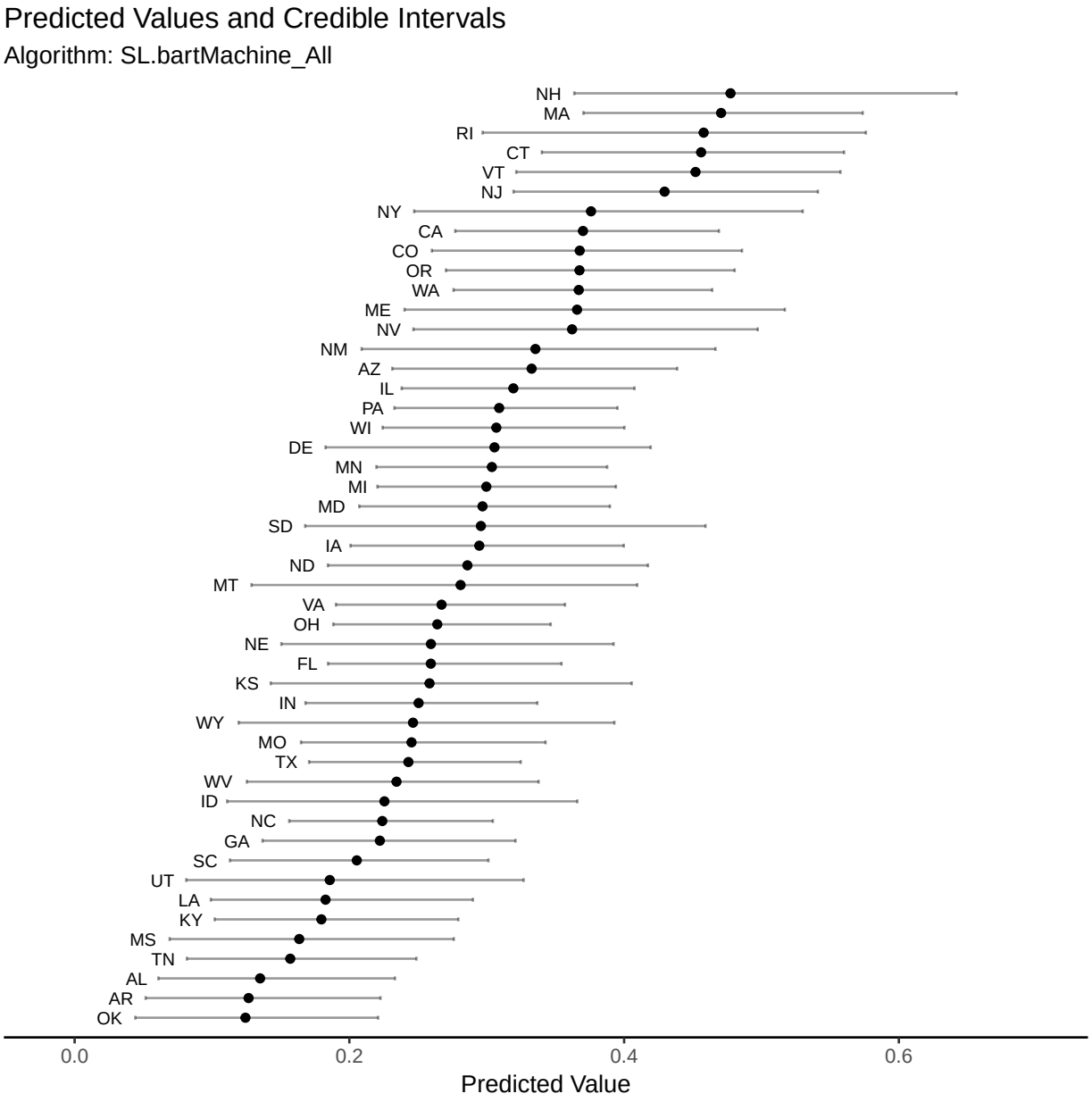
9.1.2.1 Classification vs regression

As mentioned in **Section 0.0**, `bartMachine` can handle classification tasks in addition to conventional prediction. The user can prompt `bartMachine` to execute its classification algorithm by making y a factor. However, care must be taken when ordering the factor as the predicted probabilities are based on the first value. Failing to account for this (somewhat unintuitive) nuance will result in predicted probabilities that are inverted.

```
svy$supp_gaymar <- factor(svy$supp_gaymar,levels = c("1","0"))
barp.class <- barp(y = "supp_gaymar",
                   x = c("age","educ","gXr",
```

```
                        "pvote","religcon",
                        "state","region"),
                  dat = svy,census = census06,
                  geo.unit = "state",
                  proportion = "n",
                  setSeed = 1021)
```

```
plot(barp.class)
```



While in most cases the difference between the default and classification routines is trivial, users can examine the confusion matrix of the classification object to gain further insight on

model performance and tweak the `prob_rule_class` parameter to improve the predictive power. (Note for applications of BARP to extract representative estimates of opinion at different geographic units, these changes barely influence unit-level predictions.)

```
barp.class$trees$confusion_matrix
```

```
##            predicted 1 predicted 0 model errors
## actual 1       245.000    1260.000        0.837
## actual 0       156.000    3339.000        0.045
## use errors       0.389       0.274        0.283
```

```
barp.class2 <- barp(y = "supp_gaymar",
                x = c("age","educ","gXr",
                      "pvote","religcon",
                      "state","region"),
                dat = svy,census = census06,
                geo.unit = "state",
                proportion = "n",prob_rule_class = 0.45,setSeed = 1021)
```

```
barp.class2$trees$confusion_matrix
```

```
##            predicted 1 predicted 0 model errors
## actual 1       418.000    1087.000        0.722
## actual 0       330.000    3165.000        0.094
## use errors       0.441       0.256        0.283
```

9.2.0 Partial dependencies with barp

The user may also be interested in the substantive relationships between covariates and the outcome. The **BARP** package includes tools to facilitate this type of analysis.

9.2.1 Calculating partial dependencies

The `barp_partial_dependence` function estimates partial dependence for deep interactions between the covariates using the `barp` object. The predicted values of the outcome are estimated at different values of the covariate(s) of interest and can be analyzed to make inferential statements about the relationship between the covariates and the outcome, analogous to the coefficients and standard errors of conventional regression analysis.

The `vars` parameter allows the user to indicate which covariates to explore and, if desired, define the values at which the partial dependence should be estimated. If only the variable names are entered as a character vector, the levels are automatically generated by splitting the support of the variable into quantiles at `c(0.05,seq(.1,.9,by = .1),.95)` and taking the unique values. Otherwise, the `vars` parameter must be named list where the names are the variables of interest and the contents are the custom values.

The user can also choose how much of the original data to use when calculating the partial dependence through the `prop_data` parameter, allowing for faster calculation times at the cost of less precise estimates. The value should be a numeric value between 0 and 1, corresponding to the share of the total data. Lastly, the user can stipulate the credible interval bounds through the `credible_interval` parameter.

```
bpd <- barp_partial_dependence(barp = barp.obj,
                               vars = list(age = c(1:4),educ = c(1:4)),
                               prop_data = .2,
                               credible_interval = c(0.025,0.975),
                               setSeed = 1021)
```

The resulting object of class `bpd` contains a list of two components. The first component is a summary `data.frame`, which gives the predicted outcome and the lower and upper bounds for each value of each variable. The second component is a raw `data.frame` that gives the posterior predictions (rows) for each value of each variable (columns). The user can make inferential statements using either component of the `bpd` object or can rely on default plotting methods, described below in Section 3.2.

```
round(bpd$summary %>% head(),3)
```

```
##   age educ  pred    lb    ub
## 1   1    1 0.483 0.409 0.559
## 2   2    1 0.342 0.285 0.405
## 3   3    1 0.251 0.203 0.300
## 4   4    1 0.126 0.076 0.175
## 5   1    2 0.476 0.421 0.540
## 6   2    2 0.342 0.304 0.385
```

```
round(bpd$raw[,1:4] %>% head(),3)
```

```
##   age1_educ1 age2_educ1 age3_educ1 age4_educ1
## 1      0.487      0.368      0.264      0.141
## 2      0.503      0.358      0.275      0.158
## 3      0.454      0.317      0.243      0.113
## 4      0.497      0.373      0.282      0.092
## 5      0.451      0.368      0.307      0.148
## 6      0.478      0.327      0.263      0.135
```

9.2.2 Plotting partial dependence

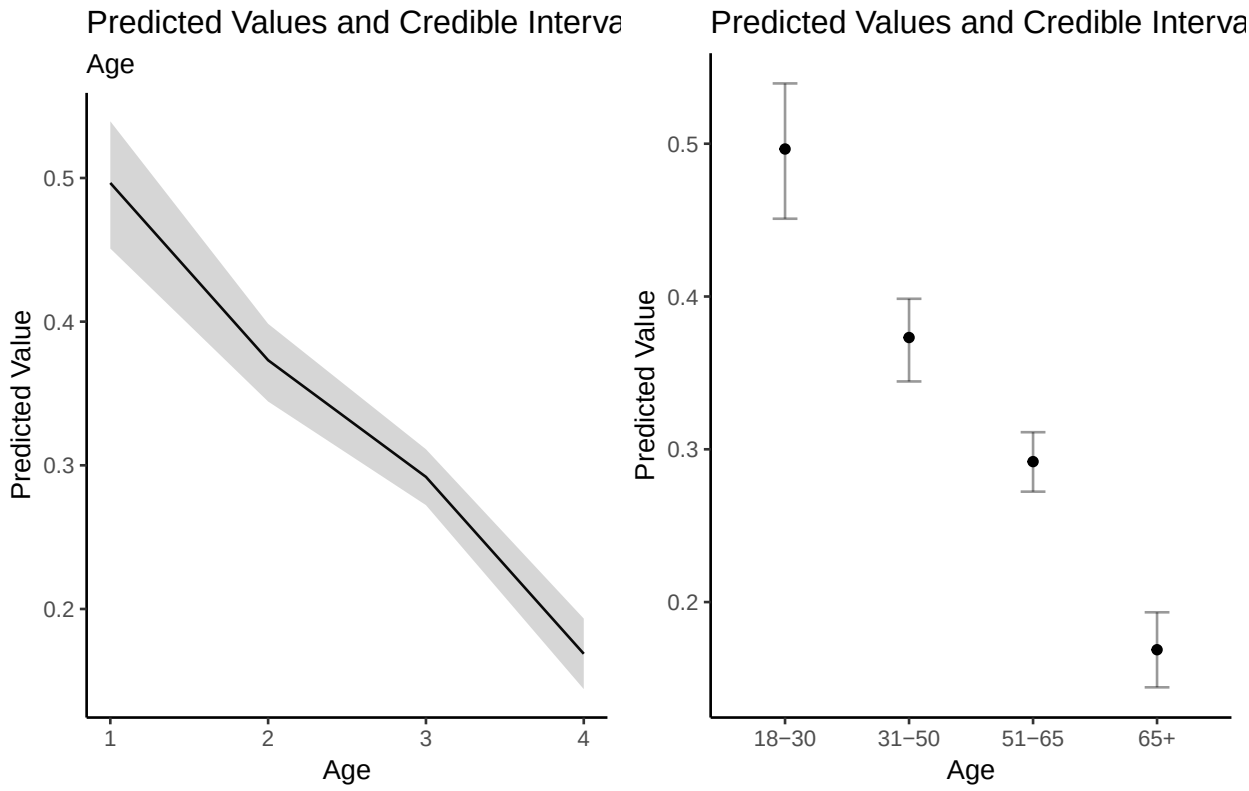
BARP provides a default plotting function to streamline the visualization of the partial dependence results up to three-way interactions. This function allows the user to provide variable names (through the `var_names` parameter) and level descriptions (through the `var_labs` parameter), as well as an indicator for which variables are categorical and which are not (`is_categorical`). The type of plot produced will depend on how many variables

are included as well as whether or not each is categorical.

For a single variable, the plot type is a function of whether the variable is categorical or continuous, as illustrated.

```
bpd1 <- barp_partial_dependence(barp = barp.obj,
                                vars = list(age = 1:4),
                                prop_data = .2,
                                setSeed = 1021)
```

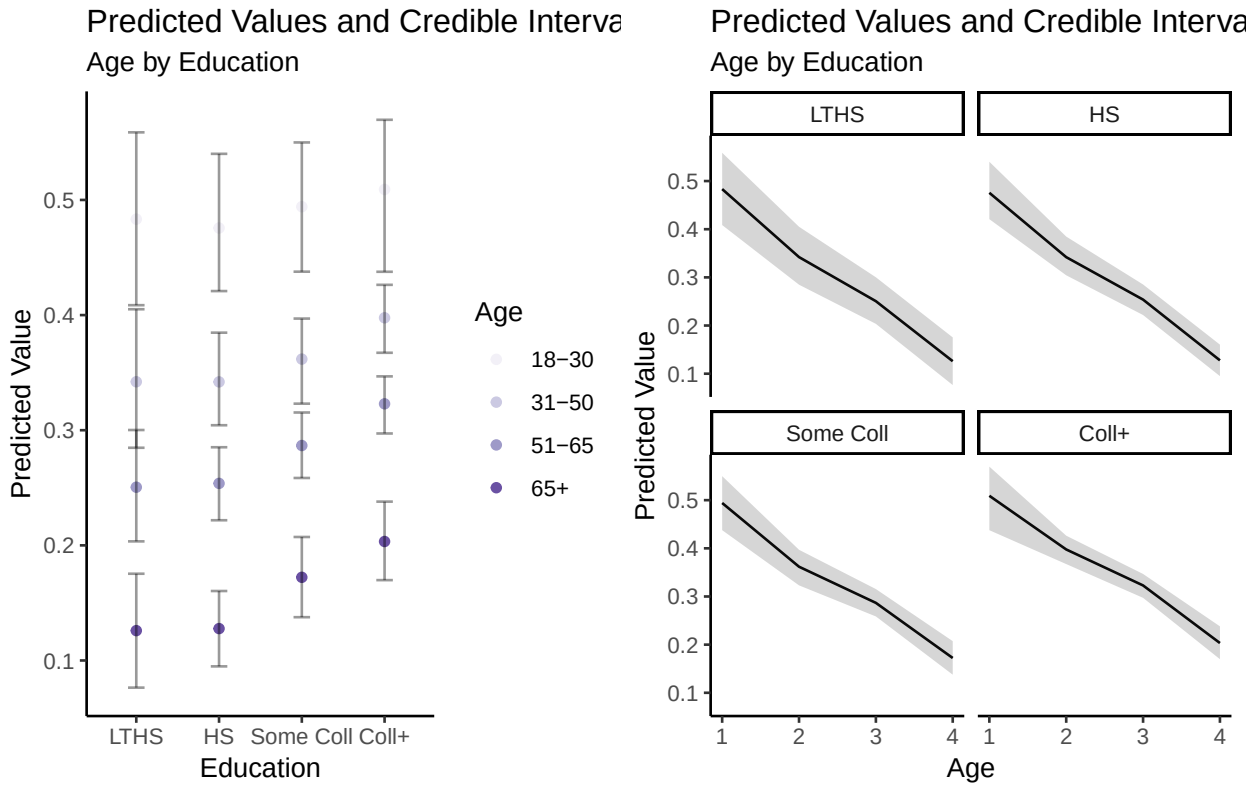
```
p1 <- plot(bpd1,var_names = "Age",
           is_categorical = F)
p2 <- plot(bpd1,var_names = "Age",
           var_labs = list(c("18-30","31-50","51-65","65+")),
           is_categorical = T)
grid.arrange(p1,p2,ncol = 2)
```



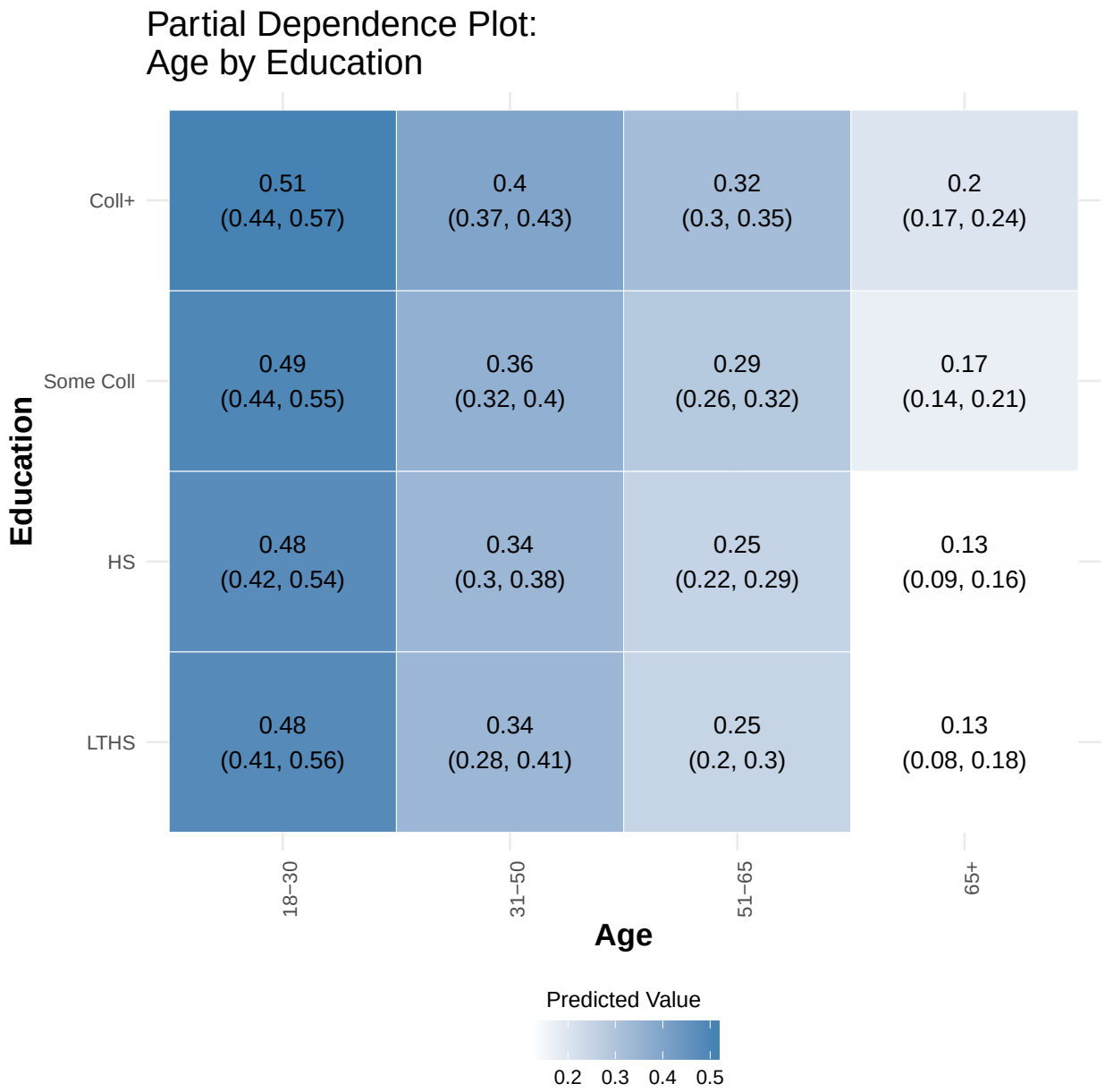
For an interaction analysis of two variables, there may be one of three different plots produced.

```
p1 <- plot(bpd,
     var_names = c("Age","Education"),
     var_labs = list(c("18-30","31-50","51-65","65+"),
                     c("LTHS","HS","Some Coll","Coll+")),
     is_categorical = c(T,T))
```

```
p2 <- plot(bpd,
     var_names = c("Age","Education"),
     var_labs = list(c("18-30","31-50","51-65","65+"),
                     c("LTHS","HS","Some Coll","Coll+")),
     is_categorical = c(F,T))
grid.arrange(p1,p2,ncol = 2)
```



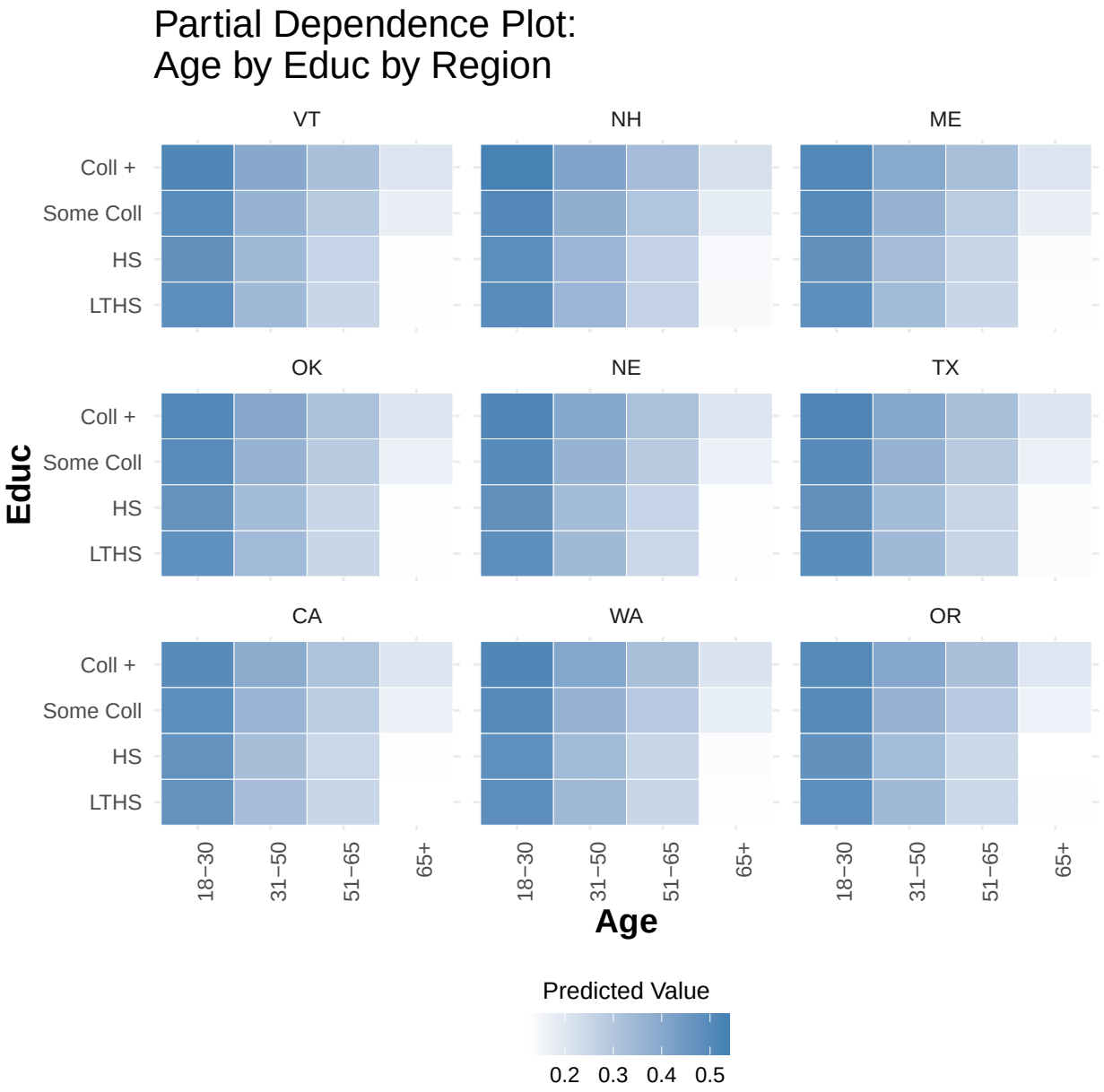

```
plot(bpd,
     var_names = c("Age","Education"),
     var_labs = list(c("18-30","31-50","51-65","65+"),
                     c("LTHS","HS","Some Coll","Coll+")),
     is_categorical = c(F,F))
```



Finally, for a three-way interaction, the plot will be a grid of heatmaps, regardless of variable type. The third variable will always be the one used to organize the grid while the first and second variables will be the x- and y-axes respectively. Users should limit the number of levels in the `barp_partial_dependence` function for visual clarity.

```
bpd3 <- barp_partial_dependence(barp.obj = barp.obj,
                                vars = list(age = 1:4,educ = 1:4,
                                            state = c("VT","NH","ME",
                                                      "OK","NE","TX",
                                                      "CA","WA","OR")),
                                prop_data = .2,
                                setSeed = 1021)
```

```
plot(bpd3,
     var_names = c("Age","Educ","Region"),
     var_labs = list(c("18-30","31-50","51-65","65+"),
                     c("LTHS","HS","Some Coll","Coll + "),
                     c("VT","NH","ME",
                       "OK","NE","TX",
                       "CA","WA","OR")))
```



9.3.0 Covariate importance using `barp`

The partial dependence analysis informs the user of different covariates' relationships to the opinion of interest. Instead, however, researchers may be interested in which covariates matter most to the BART model. One method of assessing covariate importance is through examination of how often a covariate is used, either in a tree or as a splitting rule.

As BART proceeds, it attempts to divide the data to most cleanly separate observations along the outcome variable. For example, the fastest way to separate subjects who support gay marriage from those who oppose it is likely to be to divide the data into two groups – those under 50 years of age and those over. This splitting rule may then be applied to educational attainment and then to gender. Alternatively, counting the number of times a variable appears in the trees across posterior samples yields a similar measure. **BARP's** `barp_prognostic_covs` function defaults to the splitting rule (through the `type = 'splits'` parameter).

Over the course of post-burn-in Markov Chain Monte Carlo (MCMC) iterations and over the branches of a decision tree, a variable may be chosen as a splitting rule or included in a tree a certain number of times. The Variable Inclusion Proportion (VIP) of a given covariate is the share of total splitting rules (or total trees) in which the covariate is chosen. This proportion is a measure of covariate importance in the model. For more information, please refer to Bleich et al. (2014).

9.3.1 Average variable inclusion proportions

To assess the relative covariate importance, **BARP** includes a `barp_prognostic_covs` function. This function will return the observed VIPs for all covariates averaged over a number of runs set by the user through the `num_reps` parameter. The user can also set the number of trees through the `num_trees` parameter which may differ from the number of trees used in the original `barp` command. If the user's goal is predictive accuracy, more trees allow for more flexibility. When evaluating covariate importance, however, limiting the number of trees can improve estimation because each covariate must compete with all others to be included (Chipman, George, and McCulloch 2010). If not specified by the user, `num_trees` defaults to 20.

```
barpcov <- barp_prognostic_covs(barp.obj,
                                perm_test = F,
                                interactions = F,
                                num_reps = 30,
                                num_trees = 20,
                                type = "splits",
                                setSeed = 1021)
```

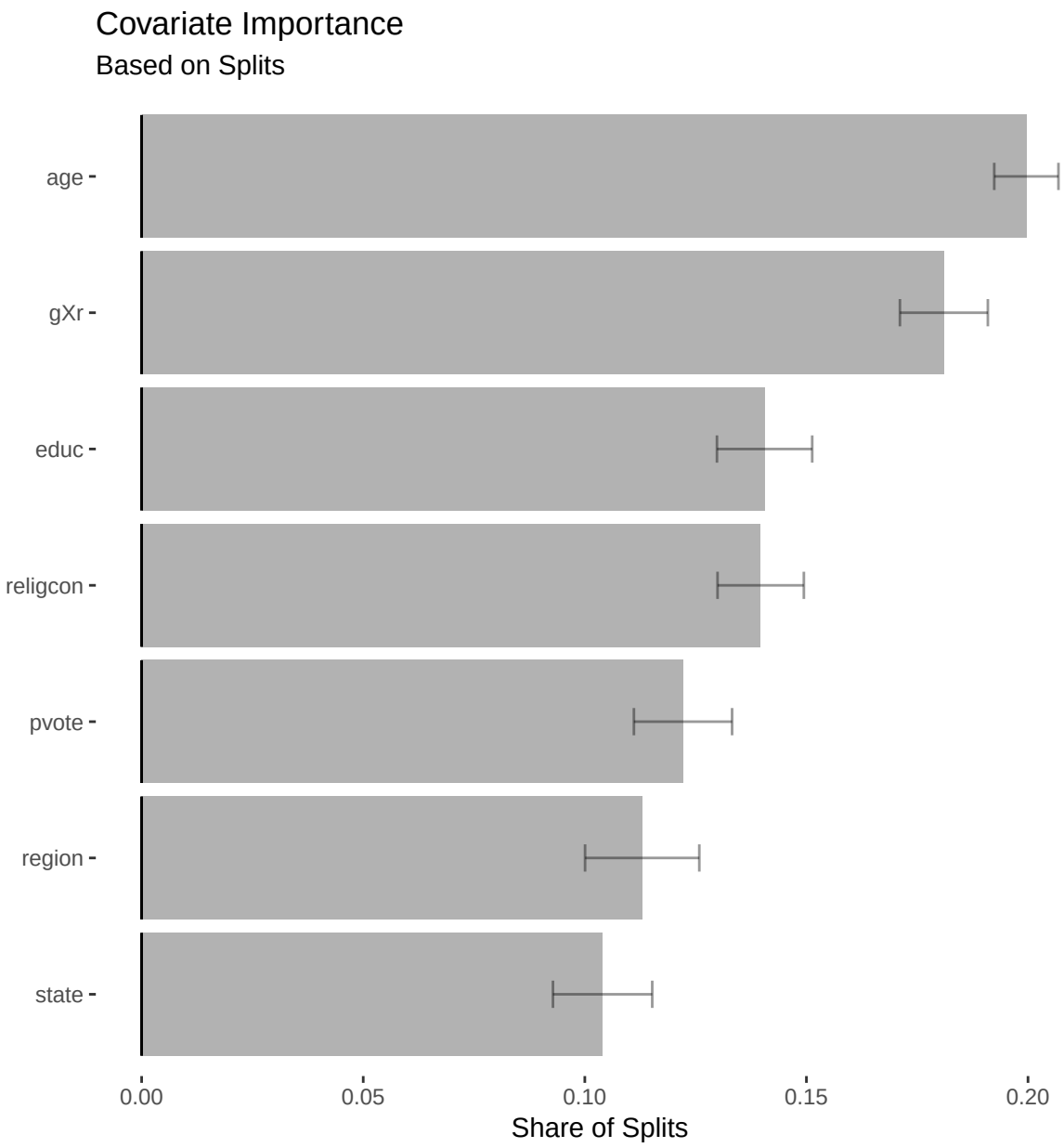
```
round(barpcov$covariate_importance %>% head(),3)
```

```
##        age  educ pvote religcon   gXr region state
```

```
## [1,] 0.204 0.129 0.126    0.132 0.189  0.126 0.094
## [2,] 0.196 0.137 0.126    0.150 0.175  0.118 0.098
## [3,] 0.215 0.133 0.106    0.134 0.192  0.098 0.123
## [4,] 0.199 0.138 0.137    0.132 0.163  0.144 0.086
## [5,] 0.203 0.140 0.141    0.143 0.166  0.117 0.090
## [6,] 0.199 0.161 0.115    0.144 0.168  0.098 0.115
```

The `barp_prognostic_covs` function returns an object of class `barpcov` which, if run without a permutation test, contains a single matrix with the number of rows equal to the `num_reps` parameter and the number of columns equal to the number of variables. Plotting this object will produce a horizontal bar chart ordered by variable importance as measured by VIPs. An optional parameter `var_names` allows the user to replace the default variable names with more descriptive labels.

```
plot(barpcov)
```



9.3.2 Permutation tests

Although the average of the VIPs for all covariates can give the user an idea of which covariates are most important, it does not allow for statistical inference. By randomly permuting y a permutation test breaks the relationship between all covariates and the outcome variable. The newly permuted VIPs represent a null distribution to compare with the observed VIPs. The user can estimate each variable's statistical significance by setting `perm_test = TRUE` and defining the number of permutation simulations to run though the `num_permute` parameter.

```
barpcov_perm <- barp_prognostic_covs(barp.obj,
                                     perm_test = T,
```

```
                                    num_permute = 30,
                                    interactions = F,
                                    num_reps = 30,
                                    num_trees = 20,
                                    type = "splits")
```

```
round(barpcov_perm$permutation_test %>% head(),3)
```

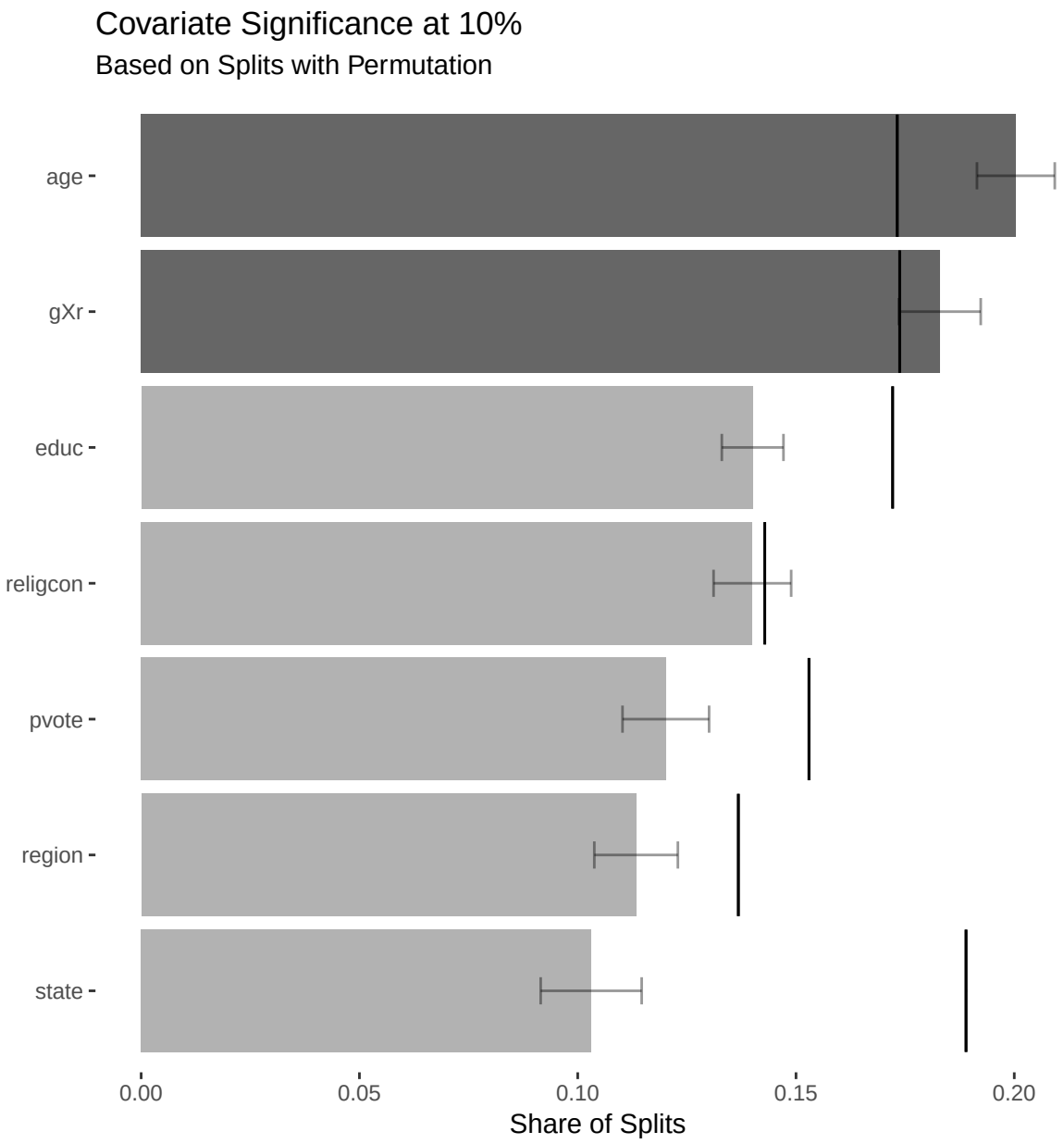
```
##        age  educ pvote religcon   gXr region state
## [1,] 0.149 0.153 0.138    0.124 0.140  0.135 0.162
## [2,] 0.134 0.153 0.148    0.133 0.143  0.121 0.168
## [3,] 0.133 0.172 0.132    0.137 0.128  0.122 0.177
## [4,] 0.164 0.119 0.120    0.123 0.165  0.128 0.181
## [5,] 0.138 0.131 0.121    0.114 0.193  0.127 0.175
## [6,] 0.146 0.146 0.101    0.180 0.173  0.105 0.148
```

```
round(barpcov_perm$p_vals[order(barpcov_perm$p_vals)],3)
```

```
##      age      gXr religcon    pvote     educ   region    state
##    0.020    0.030    0.149    0.653    0.693    0.772    1.000
```

The `barpcov`-class object now includes a matrix summarizing the permutation test results and a vector of p-values capturing the proportion of a variable's permutation test VIPs that fall below the average observed VIP. The plot command now colors the results by significance at a user-specified level through `sig_level` (defaults to 0.05), and overlays the VIP value at this level as a vertical black line.

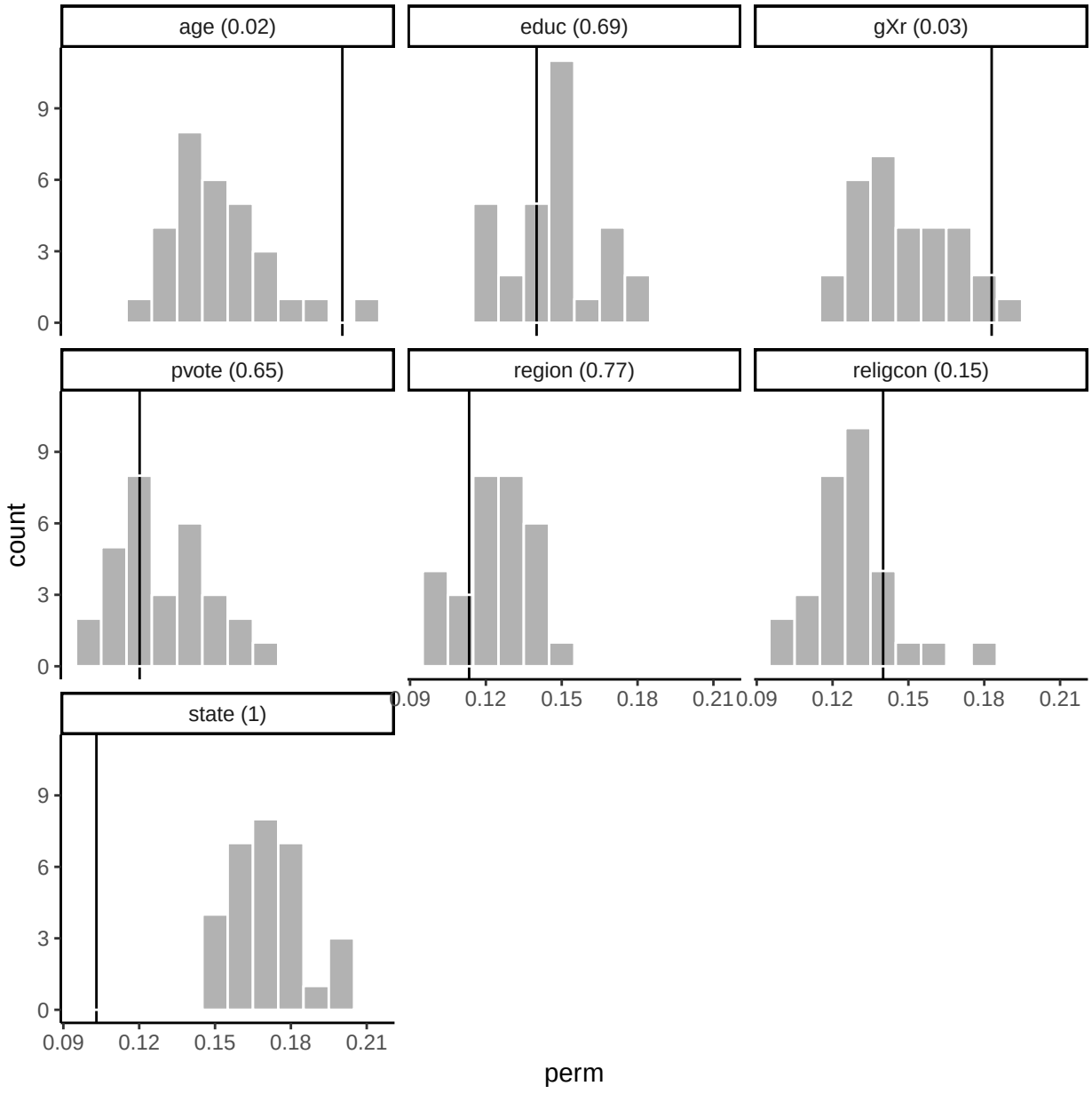
```
plot(barpcov_perm,
     sig_level = 0.10,topn = 20)
```



Alternatively, and as with all **BARP** outputs, the user may customize her own visualization using the raw data. In this example, I plot the histogram of the permutation results for each variable and overlay the average VIPs as vertical lines.

```
require(tidyr)
toplot <- gather(as_data_frame(barpcov_perm$permutation_test),variable,perm)
pvals <- data_frame(variable = names(barpcov_perm$p_vals),pvals = barpcov_perm$p_vals)
pvals <- pvals[order(pvals$pvals),]
pvals <- pvals[1:min(12,nrow(pvals)),]
avgVIPs <- apply(barpcov_perm$covariate_importance,2,mean)
avgVIPs <- data_frame(variable = names(avgVIPs),means = avgVIPs)
toplot <- pvals %>% left_join(toplot) %>% left_join(avgVIPs)
```

```r
ordered <- pvals$variable
toplot <- toplot %>% arrange(match(variable,ordered))
toplot$variable <- paste0(toplot$variable," (",round(toplot$pvals,2),")")
ggplot(toplot, aes(x=perm))+
  geom_vline(aes(xintercept = means), colour="black") +
  geom_histogram(binwidth=0.01,colour = "white",fill = rgb(0,0,0,.3)) +
  facet_wrap(~variable) +
  theme_classic()
```

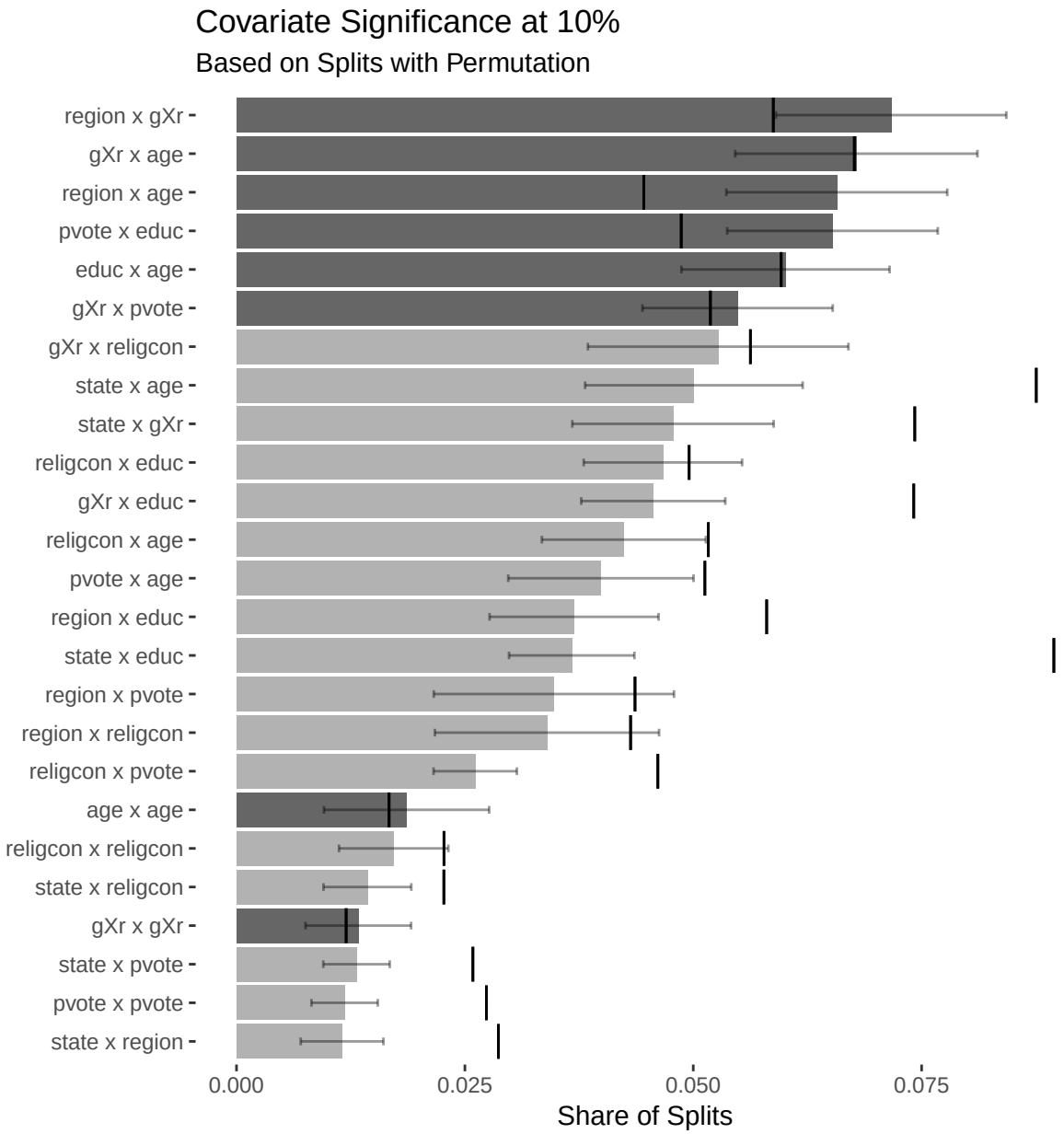


9.3.3 Interactions

These methods can also be applied to interaction terms.

```
barpcov_int <- barp_prognostic_covs(barp.obj,
                                    perm_test = T,
                                    num_permute = 30,
                                    interactions = T,
                                    num_reps = 30,
                                    num_trees = 20,
                                    type = "splits")
```

```
plot(barpcov_int,
     topn = 25,
     sig_level = 0.10)
```



9.3.4 Missing Data

The goal of extrapolating representative data from non-representative surveys is fundamentally a missing data problem where the more sparsely populated bins constitute the missing data. However, unlike well-known imputation methods such as **Amelia** (see Honaker et al. (2011) for details) which attempt to recover missing data at the unit of the original data, MRP-style methods predict opinions at the level of grouped bins of individuals where the bins are defined by observable covariates.

Nevertheless, there may be situations, particularly in panel data, where observations are missing at the individual respondent level in a survey. **BARP** allows users to implement

a variety of imputation methods via `use_missing_data`, including using the simple average of the vector of observations (`replace_missing_data_with_x_j_bar`), using a linear model (`impute_missingness_with_x_j_bar_for_lm`), or to treat the missing data as covariates (`use_missing_data_dummies_as_covars`). A future update of the **BARP** package will add in functionality for the random forest imputation method (`impute_missingness_with_rf_impute`). See Kapelner and Bleich (2015) for more details on how Bayesian Additive Regression Trees treat missing data.

```
svy$age[sample(1:nrow(svy),nrow(svy)*.01,replace = F)] <- NA
svy$educ[sample(1:nrow(svy),nrow(svy)*.01,replace = F)] <- NA

barp.covs <- barp(y = "supp_gaymar",
                  x = c("age","educ","gXr",
                        "pvote","religcon",
                        "state","region"),
                  dat = svy,census = census06,
                  geo.unit = "state",
                  proportion = "n",
                  use_missing_data = TRUE,
                  use_missing_data_dummies_as_covars = TRUE,
                  setSeed = 1021)

barp.xjbar <- barp(y = "supp_gaymar",
                  x = c("age","educ","gXr",
                        "pvote","religcon",
                        "state","region"),
                  dat = svy,census = census06,
                  geo.unit = "state",
                  proportion = "n",
                  use_missing_data = TRUE,
                  replace_missing_data_with_x_j_bar = TRUE,
                  setSeed = 1021)

barp.xjlm <- barp(y = "supp_gaymar",
                  x = c("age","educ","gXr",
                        "pvote","religcon",
                        "state","region"),
                  dat = svy,census = census06,
                  geo.unit = "state",
                  proportion = "n",
                  use_missing_data = TRUE,
                  impute_missingness_with_x_j_bar_for_lm = TRUE,
                  setSeed = 1021)
```

```
cor.mat <- cor(cbind(barp.obj$pred.opn$SL.bartMachine_1_All,
          barp.xjbar$pred.opn$SL.bartMachine_1_All,
          barp.xjlm$pred.opn$SL.bartMachine_1_All,
          barp.covs$pred.opn$SL.bartMachine_1_All))
colnames(cor.mat) <- rownames(cor.mat) <- c("No Missing",
                                            "Impute Xj Bar",
                                            "Impute Xj LM",
                                            "Missing as Covs")
round(cor.mat,3)
```

```
##                 No Missing Impute Xj Bar Impute Xj LM Missing as Covs
## No Missing           1.000         0.987        0.993           0.989
## Impute Xj Bar        0.987         1.000        0.993           0.991
## Impute Xj LM         0.993         0.993        1.000           0.993
## Missing as Covs      0.989         0.991        0.993           1.000
```

9.4.0 Alternative Regularization Methods

The updated **BARP** package allows users to replace or add additional regularization algorithms via the `method` parameter. These algorithms can be one of the 43 methods included in the `SuperLearner` package (Polley and Van der Laan 2015) although users must ensure that the associated dependencies are installed. A detailed introduction to this package can be found here.

The easiest implementation of these alternative algorithms is to include one or more as a character vector. In this case, I use the vanilla implementation of `SL.glmnet`.

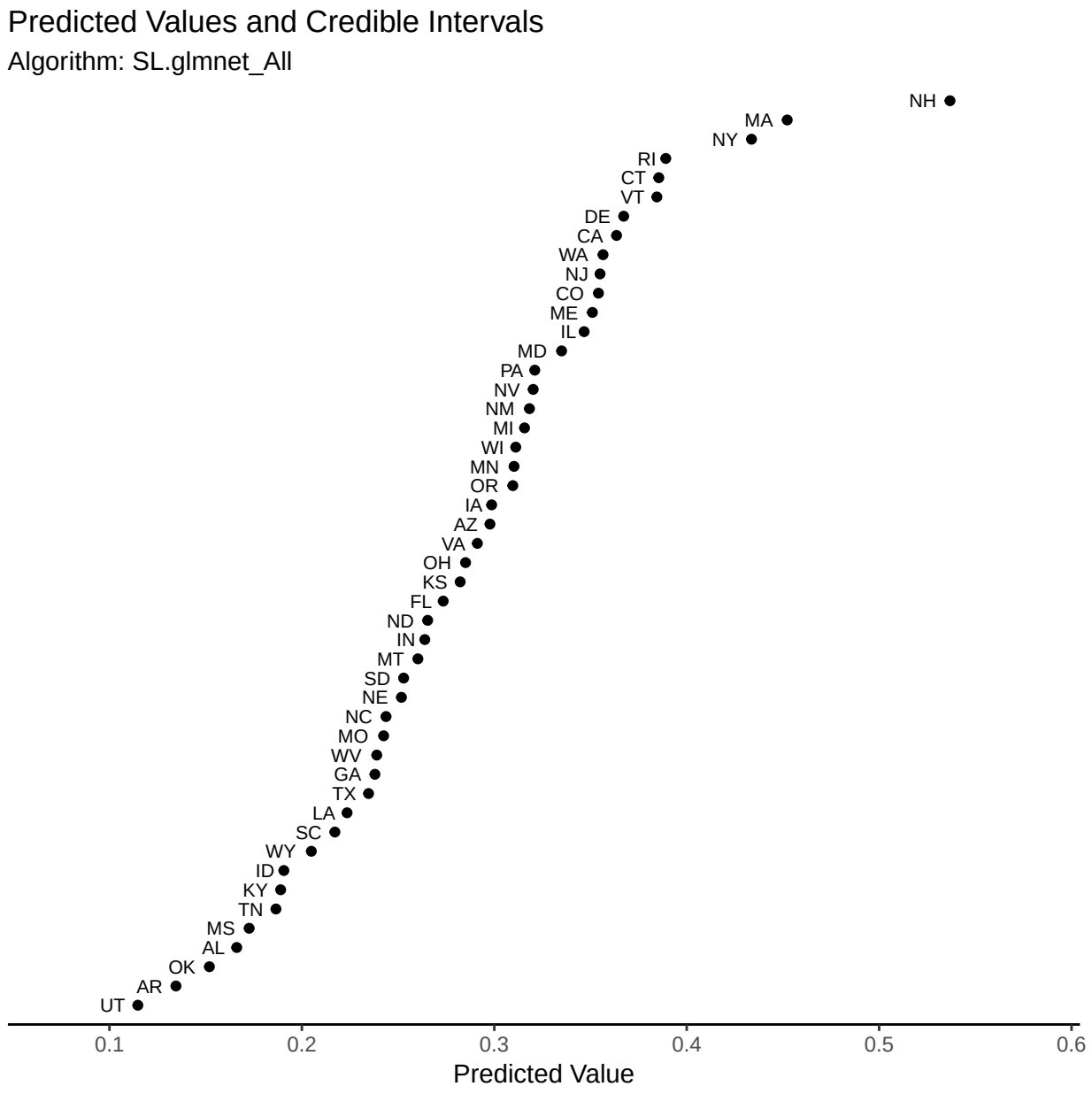
```
data("gaymar")
census06 <- census06 %>% merge(svy %>% dplyr::select(state,stateid) %>% distinct())

barp.objSL <- barp(y = "supp_gaymar",
                   x = c("age","educ","gXr",
                         "pvote","religcon",
                         "state","region"),
                   dat = svy,census = census06,
                   algorithm = c("SL.glmnet"),
                   geo.unit = "state",
                   proportion = "n",
                   setSeed = 1021)
```

```
barp.objSL$pred.opn %>% head()
```

```
##    state SL.glmnet_All opn.lb opn.ub
## AL    AL     0.1661456     NA     NA
## AR    AR     0.1345653     NA     NA
```

```
## AZ    AZ     0.2977428     NA     NA
## CA    CA     0.3635293     NA     NA
## CO    CO     0.3541205     NA     NA
## CT    CT     0.3854912     NA     NA
```

```
plot(barp.objSL,algorithm = "SL.glmnet")
```



Unlike with `barp` objects, other algorithms do not provide uncertainty estimates without turning on bootstraps with `BSSD = TRUE`.

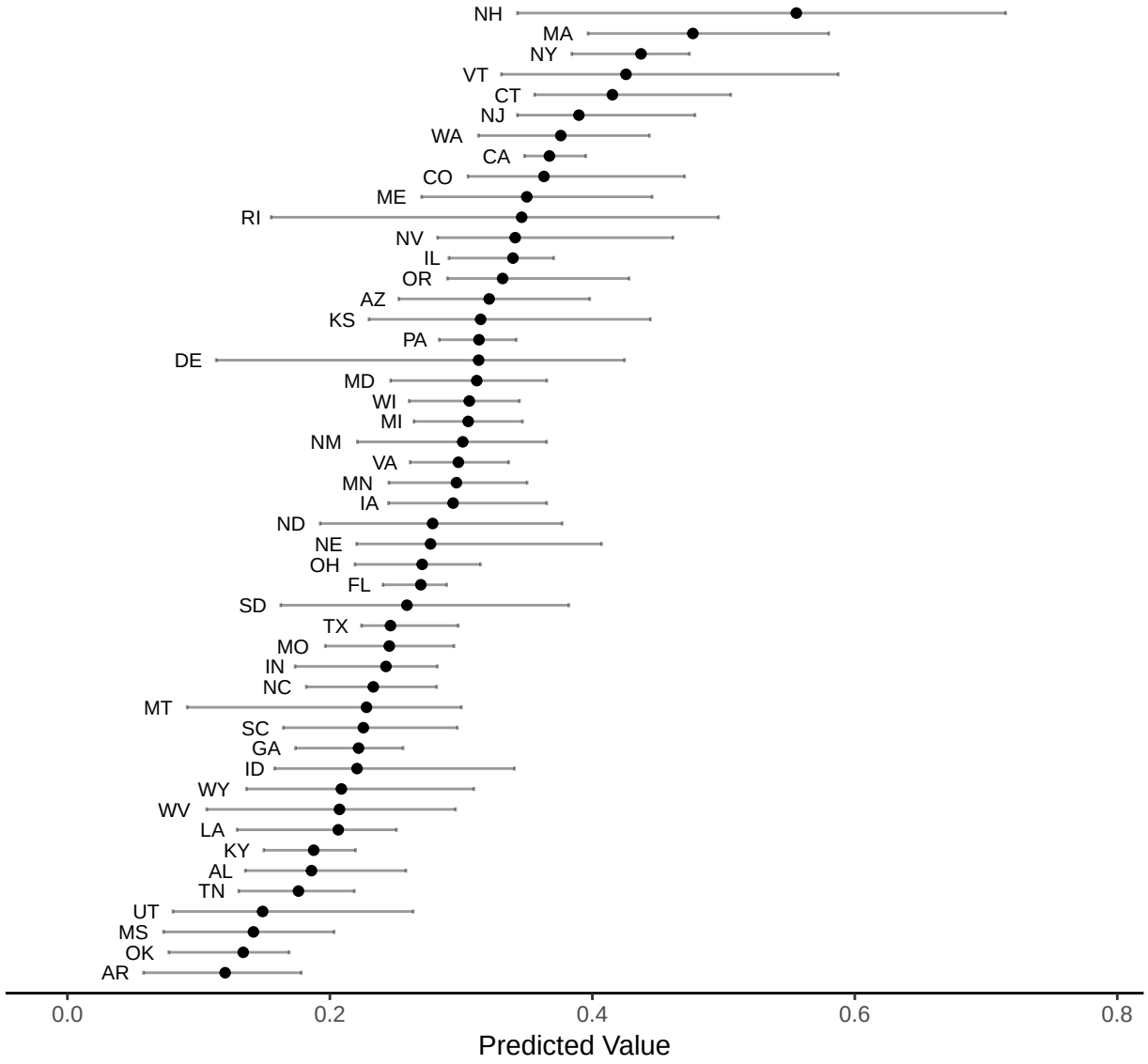
```
barp.objSLBS <- barp(y = "supp_gaymar",
                     x = c("age","educ","gXr",
                           "pvote","religcon",
```

```
                      "state","region"),
                dat = svy,census = census06,
                algorithm = c("SL.glmnet"),
                geo.unit = "state",
                proportion = "n",
                BSSD = TRUE,
                nsims = 50,
                setSeed = 1021)
```

```
barp.objSLBS$pred.opn %>% head()
```

```
##   state  pred.opn     opn.lb    opn.ub
## 1    AL 0.1860024 0.13558079 0.2579651
## 2    AR 0.1201974 0.05798779 0.1782284
## 3    AZ 0.3214124 0.25244014 0.3980291
## 4    CA 0.3672889 0.34826682 0.3950198
## 5    CO 0.3631236 0.30516150 0.4702434
## 6    CT 0.4153072 0.35595841 0.5055253
```

```
plot(barp.objSLBS)
```



These algorithms can be customized as described in the `SuperLearner` documentation. For example, if we wanted to run a random forest with 150 trees, we would do the following:

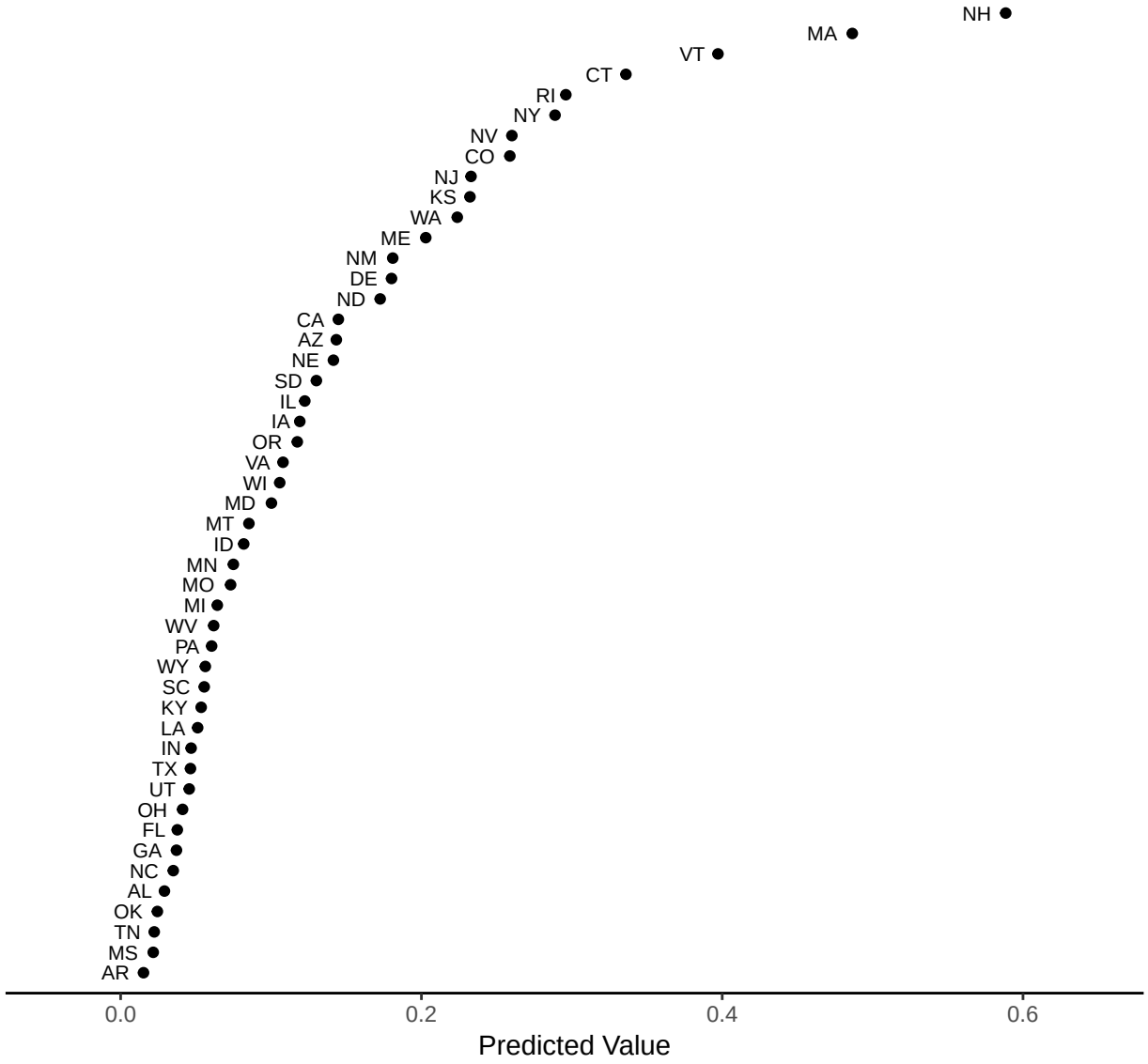
```
rf_new <- create.Learner("SL.randomForest",params = list(ntree = 150))
barp.objRF <- barp(y = "supp_gaymar",
                   x = c("age","educ","gXr",
                         "pvote","religcon",
                         "state","region"),
                   dat = svy,census = census06,
                   algorithm = c(rf_new$names),
                   geo.unit = "state",
                   proportion = "n",
```

```
                  setSeed = 1021)
```

```
barp.objRF$pred.opn %>% head()
```

```
##    state SL.randomForest_1_All opn.lb opn.ub
## AL    AL            0.02913993     NA     NA
## AR    AR            0.01521739     NA     NA
## AZ    AZ            0.14342199     NA     NA
## CA    CA            0.14478368     NA     NA
## CO    CO            0.25880952     NA     NA
## CT    CT            0.33599271     NA     NA
```

```
plot(barp.objRF)
```



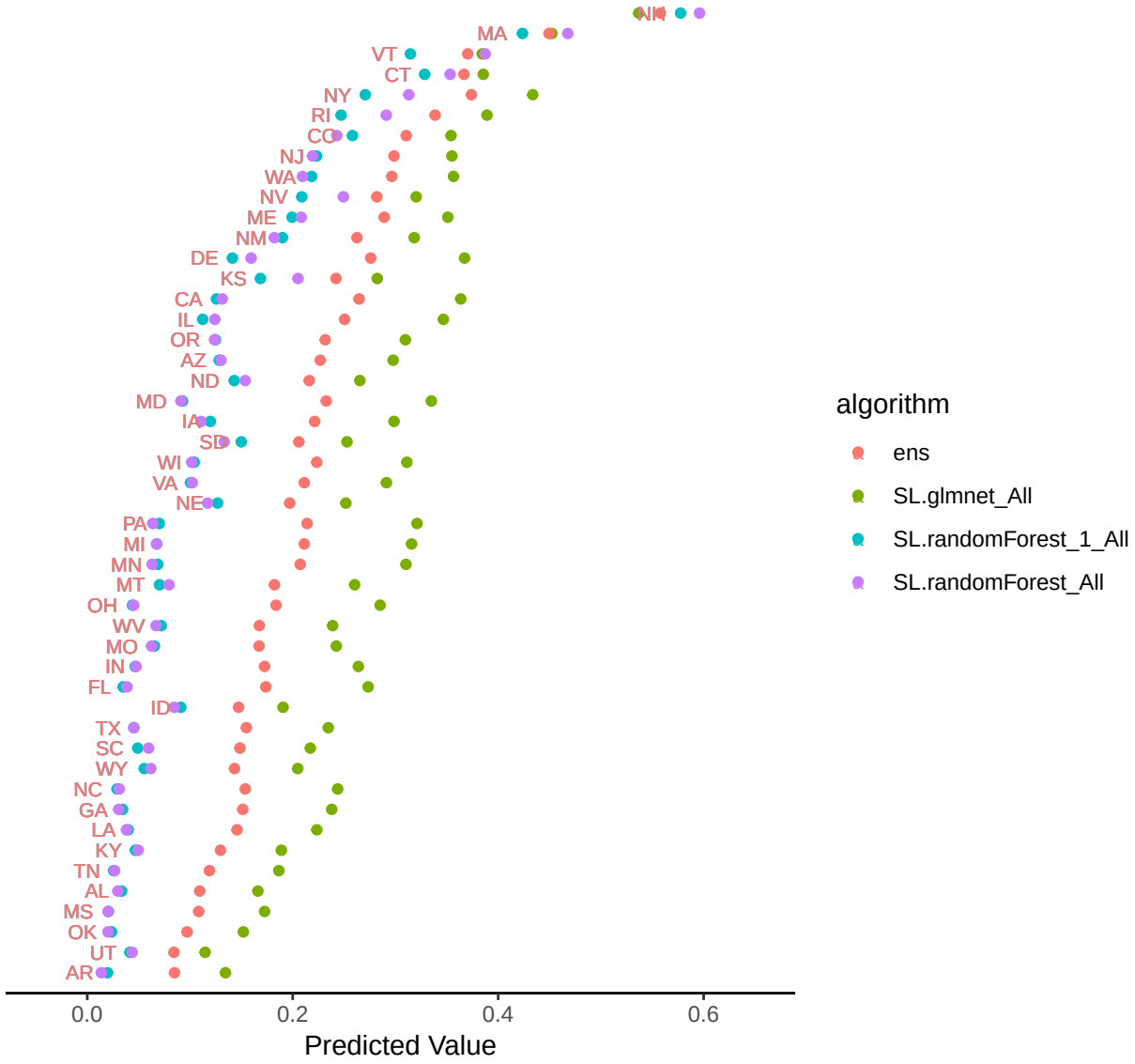
Finally, we can test multiple algorithms at once and examine which perform the best via cross validation by feeding in a vector of algorithm names to the `algorithm` parameter.

```
barp.objEns <- barp(y = "supp_gaymar",
                    x = c("age","educ","gXr",
                          "pvote","religcon",
                          "state","region"),
                    dat = svy,census = census06,
                    algorithm = c(rf_new$names,"SL.glmnet","SL.randomForest"),
                    geo.unit = "state",
                    proportion = "n",
                    setSeed = 1021)
```

```r
barp.objEns$pred.opn %>% head()
```

```
##    state SL.randomForest_1_All SL.glmnet_All SL.randomForest_All
## AL    AL            0.03346351     0.1661456          0.02982427
## AR    AR            0.01981159     0.1345653          0.01366304
## AZ    AZ            0.12843085     0.2977428          0.13021941
## CA    CA            0.12583631     0.3635293          0.13147678
## CO    CO            0.25814103     0.3541205          0.24294918
## CT    CT            0.32847602     0.3854912          0.35322040
##           ens     opn.lb    opn.ub
## AL 0.10949208 0.02681255 0.1637349
## AR 0.08493234 0.01357357 0.1308434
## AZ 0.22680901 0.12184227 0.2934351
## CA 0.26460884 0.12359648 0.3572818
## CO 0.31048271 0.23437961 0.3644853
## CT 0.36670956 0.32045860 0.3985555
```

```r
plot(barp.objEns)
```



As illustrated, the `SL.randomForest` algorithm returns very similar predictions when using the default number of trees (1,000) versus 150. We can further examine how these algorithms perform by looking at their cross-validated risk via the `risk` object in the output. The first column returns the performance metric (typically AUC for classification, NNLS for regression,although these can be adjusted by the user) and the second provides the weight associated with this algorithm in estimating the ensemble predictions.

```
barp.objEns$risk
```

```
##                              AUC      coef
## SL.randomForest_1_All 0.3560406 0.2097273
## SL.glmnet_All         0.3309479 0.5788130
```

```
## SL.randomForest_All   0.3529118 0.2114597
```

Some of these algorithms require bespoke packages which will need to be installed before running `barp`. In addition, others may only work for classification or regression and will give an error if applied to the incorrect data type.

9.5.0 Conclusion

This vignette has introduced and demonstrated the features of the **R** package **BARP**. The purpose of this package is to improve on the estimation of opinion at narrower levels of geography than originally represented in a survey. The package includes several helper functions designed to facilitate exploration of the model, both in terms of performance and in terms of covariates. I invite comments on bugs, corrections, improvements, and any other suggestions.

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