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Preface

This is an example of a thesis setup to use the reed thesis document class (for LaTeX) and the R bookdown package, in general.

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Abstract

The preface pretty much says it all.

Second paragraph of abstract starts here.

Dedication

You can have a dedication here if you wish.

Introduction

Chapter 1

Introduction to Trees, Random Forests, and the Bootstrap

This thesis is about understanding the variance in variable importance measures of random forests. Random Forests are a statistical learning algorithm developed by Leo Breiman and his collaborators in the early 2000's that leverages bagging and CART (Classification and Regression Trees) methodology to produce quite good predictions of an underlying classification or regression surface. The predictive capability of random forests is quite impressive and much random forest literature centers on exploring why random forests are effective. For this thesis we are interested in the use of random forests for statistical inference. More specifically we are interested in the use of random forest variable importance measures for statistical inference.

Machine learning approaches to regression can often produce models with good predictive accuracy compared to parametric modelling approaches. However, these machine learning algorithms often lack in the interpretability and inferential capabilities of more traditional statistical modelling. While predictive questions are indeed important in science and other applications, many scientific and statistical questions are concerned with description and inference. These questions could be about a causal mechanism, which hypothesis is correct concerning some phenomenon, and which are the important factors. The mechanisms that machine learning techniques use to form predictions on the data are often complicated and not easily amenable to mathematical analysis, but we believe one of Breiman's points in his 2001 paper "Statistical Modelling: Two Cultures" is that statisticians ought to work to develop inferential tools for machine learning techniques. Predictive accuracy is a good metric to measure how a model fits to the data, and without a method that can produce predictively accurate estimates of the underlying data mechanism, inferential conclusions seem less justifiable. Throughout this thesis we will be interested in both the regression and classification settings as random forests can handle response variables of both types. When the need arises to delineate between the setting we are working in, we will be explicit. Furthermore, we will be assuming that for the data at hand, there exists an underlying regression function $Y = f(X) + \varepsilon$ where $f(X)$ is the function and ε is generally assumed to be Gaussian error, but may have some other error structure.

1.1 CART

We begin our discussion of CART (Classification and Regression Trees) trees by considering the following problem. Suppose we have data generated from the piecewise function $Y = f(X) + \varepsilon$ where [at this point insert a very non-linear piecewise function.] with Gaussian error ε . One approach to fitting a model to this data would be to fit a linear regression model. However, the particular form of the data is not well suited for linear regression due to the non-linearity of the data. Another approach we might try to take is as follows. We might try to find a method that can fit a regression line to each piecewise component of the data. One such method is to fit CART trees. We fit a CART tree to the data and perform cost-complexity pruning to output the model shown in figure [figure not yet made]. In this example, we produced a regression surface which was able to take into account the piecewise, non-linear nature of the data and produce a reasonable estimate of the underlying data generating mechanism.

The CART methodology allows us to fit a model that can take into account non-linear regression or classification surfaces. The basic idea of CART is that if we can split the predictors into roughly homogenous partitions, or into partitions which minimize predictive error, then we can fit a simple model to predict the response of each partition. CART trees were first introduced by Breiman et al. in 1984 and are a flexible method, capable of handling classification and regression settings. CART is a product of computational statistics, its development influenced by a data-centric algorithmic approach distinct from the models of classical statistics influenced by the contingency of small samples.

More formally, suppose we have a training data set $Z = \{Z_1, \dots, Z_n\}$, where $Z_i = (X_i, Y_i)$ is an $p + 1$ dimensional vector in \mathbb{R}^{p+1} . Here we have X_i is a d -dimensional predictor variable and Y_i is the response. In particular, we can consider Z to be a $n \times (p + 1)$ array where the rows are observations and the columns are the response and predictor variables. CART works by partitioning the data through binary recursive splits via optimizing some loss function. CART trees are called trees because partitioning the data through binary recursive splits forms a tree-like structure. We adopt notation evocative of this tree structure. Any subset of the training data Z is called a node while the entire data set Z is called the root node. Nodes are of two kinds: they are either terminal (sometimes called leaves) or not terminal. Non-terminal nodes are nodes that are split on in the tree growing process, while terminal nodes are nodes which are not split on. Generally, a node is a terminal node if some stopping rule is reached. Note that terminal nodes form a partition of the training data Z .

We aim to grow a tree with roughly homogenous terminal nodes. As Breiman et al. (1984) note, there are several factors that we need to consider:

1. How to select splits of the data.
2. When to stop splitting the data.
3. How to assign classes or values to terminal nodes.

CART constructs trees by decreasing the nodal impurity of a node t . Nodal impurity is defined through some nodal impurity measure $i(s, t)$, usually the GINI index in the classification setting and the residual sum of squares in the regression setting. We present the regression setting and then the classification setting. If we have a continuous response Y , then we could try to predict Y by partitioning the data using the decision tree structure and predicting that points that fall within a particular partition will take on the average response on that partition. To choose the best binary split on the data, we need to search across the splitting variables and splitting points for the split which maximizes the reduction in the RSS between the parent node and daughter nodes. In particular, we want to find the split which maximizes $RSS_l(j, s) + RSS_r(j, s)$ where j is the proposed splitting variable and s is the proposed splitting point, and RSS_l is the RSS of the proposed left node and RSS_r is the RSS of the proposed right node. The assignment of response within a node is given by the average of the response. We present the following algorithm. The construction of

Algorithm 1 Construction of Regression tree

- 1: **while** minimum node size not reached **do**
 - 2: **for** each node t **do**
 - 3: **for** $j = 1, \dots, p$ and $s = 1, \dots, n$ **do**
 - 4: Compute $RSS_l(j, s) + RSS_r(j, s)$.
 - 5: Pick the (j, s) which maximizes $RSS_l(j, s) + RSS_r(j, s)$.
 - 6: Split the current node into left and right nodes according to (j, s) .
 - 7: Compute left and right averages, $\text{ave}(y_i | x_i \in t_l)$ and $\text{ave}(y_i | x_i \in t_r)$, respectively.
 - 8: Output the tree T .
-

classification trees is similar to the construction of regression trees except a different impurity measure must be used. For the node t containing N_t observations, let

$$\hat{p}_{tk} = \frac{1}{N_t} \sum_{x_i \in t} \mathbb{I}(y_i = k)$$

where $k = 0$ or $k = 1$. Then \hat{p}_{tk} measures the proportion of observations of class k in node t . Using the two-class example, there are several impurity measures available in the classification setting. The most common measure is perhaps the Gini index defined by

$$2p(1 - p).$$

Other options include misclassification error

$$1 - \max(p, 1 - p),$$

and cross-entropy

$$-p \log(p) - (1 - p) \log(1 - p).$$

If t_L and t_R are left and right nodes proposed under the split, let \hat{p}_{t_L} and \hat{p}_{t_R} be proportion of observations falling into t_L and t_R , respectively. Denote the Gini index

of the left node t_L by G_L and denote the Gini index of the right node t_R by G_R . Then our splitting criterion is to seek the splitting variable and splitting point which minimizes

$$\hat{p}_{tL}G_L + \hat{p}_{tR}G_R.$$

The case for misclassification rate and cross-entropy as the impurity measures is similar.

Some issues with CART trees include overfitting and variability. While there is a stopping criterion for growing the CART trees, often times naively growing a tree can result in overfitting to the data. One method of alleviating overfitting is to employ cost-complexity pruning, which searches for an optimal tree that balances fitting a good tree model with overfitting to the data. We do not go into details here, but the point the reader to Friedman et al. (2009). A larger issue with trees is their variability to small perturbations in the data. [Provide computational example.] Allowing the data to vary even a bit can result in a different tree structure upon refitting. As a statistical learning method, this means that CART trees are not robust and suffer from high variance, even when constructed using cost-complexity pruning. To get around this issue of variability the best solution is to employ bagging and use the random forest algorithm.

1.2 Bootstrap

We feel it is worth introducing some notation and theory for the bootstrap. In this line, for the most part we follow notation from Efron and Tibshirani (1993). As is well-known, the bootstrap is a resampling method first introduced by Efron in 1979 with links to earlier work of Tukey and Quenouille on the jackknife. It goes something like this. If we have a dataset D of size n , then it is generally infeasible to obtain more data from the underlying data generating mechanism. Assuming that the data set is not too heavily distributed in the tails and that the sample we have is representative of the population, we can independently resample n points from D to form the bootstrap resampled dataset D^* . We repeat this procedure B many times with B generally quite large. We can then proceed to use the many D^* we generated to obtain estimates, standard errors, and confidence intervals of whichever parameter is of interest. [Note: the bootstrap discussed here is called the non-parametric bootstrap. There is also the parametric bootstrap, but we do not go into that method here].

What is going on? If we obtain an i.i.d. random sample of size n from a probability distribution F , then we can form the empirical distribution function \hat{F} which places a probability of equal mass $\frac{1}{n}$ of seeing any value of x_i for $i = 1, \dots, n$. We do not want to go too deeply into bootstrap theory in this introduction, but we would like to mention the plug-in principle underlying applications of the bootstrap, as well as variance estimation.

In statistics, we are interested in obtaining information about parameters defined on a probability distribution F by dealing with statistics defined on the EDF \hat{F} . Often

a parameter is a function of the probability distribution:

$$\theta = t(F)$$

where in this context t denotes the functional form of the parameter. Often the probability distribution F is unknown or too complex to deal with directly, so we try to form estimates. One estimate we could form of the parameter $\theta = t(F)$ is the plug-in estimate (or plug-in statistic, or functional statistic), which is defined to be

$$\hat{\theta} = t(\hat{F}).$$

It can be shown under suitable conditions, that the functional statistic $t(\hat{F})$ is the nonparametric maximum likelihood estimate of $t(F)$ (Efron and Tibshirani). Therefore there is good theoretical ground for proceeding with estimating parameters using the bootstrap.

The usefulness of the bootstrap extends beyond estimating functional statistics. Using the bootstrap, we can estimate the variance of the functional statistic using several methods. The most ubiquitous is perhaps the bootstrap estimate of the standard error. Say we have drawn B many bootstrap samples of a dataset Z to obtain Z_b^* for $b = 1, \dots, B$. We compute an estimate $\hat{\theta} = s(Z)$ of $\theta = t(F)$, where Efron and Tibshirani emphasize that $s(Z)$ is not necessarily the plug-in estimate $t(\hat{F})$. To emphasize that the estimates computed from Z_b^* are bootstrap replicates of $\hat{\theta}$, we write

$$\hat{\theta}_b^* = s(Z_b^*).$$

In some settings we write $\hat{\theta}^* = s(Z^*)$ when we do not care as much about the actual subscripting from the bootstrap and just want to emphasize the fact we are estimating $\hat{\theta}$ using bootstrap replicate.

Denote the standard error of the statistic $\hat{\theta}$ by $se_F(\hat{\theta})$. Following Efron and Tibshirani, the bootstrap estimate of the $se_F(\hat{\theta})$ is a plug-in estimate of the standard error of $\hat{\theta}$ replacing the distribution F in the subscript by the corresponding empirical distribution \hat{F} and is given by $se_{\hat{F}}(\hat{\theta}^*)$. Efron and Tibshirani call $se_{\hat{F}}(\hat{\theta}^*)$ the ideal bootstrap estimate of the standard error of $\hat{\theta}$. Beyond simple examples like the mean, the exact form of $se_{\hat{F}}$ is often too difficult to compute exactly, but the bootstrap can be used to compute a good estimate of $se_{\hat{F}}$. Namely, once we have drawn Z_1^*, \dots, Z_B^* independent bootstrap samples from Z and compute the B many bootstrap replicates $\hat{\theta}_b^* = s(Z_b^*)$, then the estimate of the standard error $se_F(\hat{\theta})$ is given by

$$\widehat{se}_B = \left(\frac{1}{B-1} \sum_{b=1}^B (\hat{\theta}_b^* - \bar{\theta}^*) \right)^{1/2},$$

where $\bar{\theta}^* = \frac{1}{B} \sum_{b=1}^B \hat{\theta}_b^*$ is the sample mean of the bootstrap replicates. Note \widehat{se}_B is the familiar formula for the standard deviation of a sample.

There are several other estimates of the standard error commonly used when exact forms of the standard error are unavailable or infeasible. The first of these is the jackknife. As a computational tool, the jackknife takes a different approach from the

bootstrap. Say for the parameter θ , we have an estimate $\hat{\theta} = s(Z)$. Define the i -th “leave one out” sample $Z_{(i)} = (Z_1, \dots, Z_{i-1}, Z_{i+1}, \dots, Z_n)$. Corresponding to $Z_{(i)}$ we can form $\hat{\theta}_{(i)} = s(Z_{(i)})$, the i th jackknife replicate of the estimator $\hat{\theta}$. Define

$$\hat{\theta}_{(\cdot)} = \frac{1}{n} \sum_{i=1}^n \hat{\theta}_{(i)}$$

which is akin to the mean of the jackknife replications. From here we can obtain the jackknife estimate of the standard error, which is defined by

$$\widehat{se}_{\text{jack}} = \left(\frac{n-1}{n} \sum_{i=1}^n (\hat{\theta}_{(i)} - \hat{\theta}_{(\cdot)})^2 \right)^{1/2}.$$

The idea of the jackknife is that absent new realizations of the data, a simple procedure we can undertake is to see the effect on the accuracy of the estimator when we remove each observation sequentially. In particular, we could consider the jackknife as forming n many datasets of size $n - 1$ with the i th observation removed. The jackknife may be easier to compute than the bootstrap, but as the jackknife only uses limited information about the n observations and does not simulate additional full datasets like the bootstrap, overall it is less efficient than the bootstrap. The jackknife is related to the bootstrap in the sense that the jackknife is a linear approximation to the bootstrap. As Efron and Tibshirani explain, for linear statistics the jackknife is as efficient as the bootstrap. However, for highly non-linear statistics (of which it turns out random forests are), it turns out that jackknife estimation is very inefficient compared to the bootstrap. There are other methods of estimating the standard error such as the Infinitesimal Jackknife and Non-parametric delta method, but we will address those methods in later chapters.

The bootstrap is a flexible method and applications of the bootstrap extend beyond simply sampling pairs of observations from the the data $Z = \{Z_1 = (X_1, Y_1), Z_2 = (X_2, Y_2), \dots, Z_n = (X_n, Y_n)\}$. In particular, there are model-based approaches to the bootstrap that are often useful. A particularly important example for this thesis is bootstrapping the least squares linear regression model. In least squares, we model the response Y observed at the vector X as being given by $\mathbb{E}(Y|X) = X^T \beta + \varepsilon$, where $X = (1, X_1, \dots, X_p)^T$ and $\beta = (\beta_0, \beta_1, \dots, \beta_p)$ and ε is an error term of length n . In practice, the vector of coefficients β is unknown, so we form an estimate $\hat{\beta}$ through applying least squares regression. After applying least squares. For a point X_j , the least squares estimate of Y_j is given by $\hat{Y}_j = X_j \hat{\beta}$. The raw residuals are defined by $e_j = Y_j - \hat{Y}_j$ with the estimate of the variance σ^2 is given by

$$s^2 = \frac{1}{n-2} \sum_{j=1}^n e_j^2$$

There are a couple approaches we could consider in applying the bootstrap to linear regression. The conceptually simpler method is to resample cases (X_i, Y_i) to generate bootstrap replications of Z , $Z^* = \{(X_1^*, Y_1^*), \dots, (X_n^*, Y_n^*)\}$ where the asterisks denote

Algorithm 2 Linear Regression Cases Resampling

- 1: **for** $b = 1, \dots, B$ **do**
 - 2: Draw a bootstrap sample Z_b^* of size n from the cases (X_i, Y_i) to obtain $Z_b^* = \{(X_1^*, Y_1^*), \dots, (X_n^*, Y_n^*)\}$.
 - 3: Fit least squares regression to $(X_1^*, Y_1^*), \dots, (X_n^*, Y_n^*)$ to obtain the estimates $\hat{\beta}_b^*$ and \hat{s}_b^{*2} .
-

that we have resampled from the original data. With B many such datasets Z^* , we can use the following algorithm adapted from Davison and Hinkley (1997). Another approach we could take is to resample the residuals of the linear model. To motivate this approach, note that the vector of raw residuals (e_1, \dots, e_n) approximate the error term ε . That is, assuming the bivariate distribution of (X, Y) is such that the specification of the linear model is correct, then given the true value of β , the error terms would be given by $\varepsilon_i = Y_i - X_i\beta$. As β is generally unknown, the best we can do is to form estimates of the error terms $\hat{\varepsilon}_i = Y_i - \hat{Y}_i = Y_i - X_i\hat{\beta}$. We now have a vector of estimated error terms $\hat{\varepsilon} = (\hat{\varepsilon}_1, \dots, \hat{\varepsilon}_n)$ which we could consider as being an i.i.d. sample if the cases (X_i, Y_i) were independently sampled from the distribution of (X, Y) . As Efron and Tibshirani note, we could consider obtaining any particular component of the vector $\hat{\varepsilon}$ as being from the EDF \hat{F} of the true distribution of the error terms F , where we place a probability mass of $\frac{1}{n}$ to drawing any one of the $\hat{\varepsilon}_i$. Taking this conceptual approach, we could then draw bootstrap samples of the residuals $\hat{\varepsilon}_1, \dots, \hat{\varepsilon}_n$. Consider the X_i component of the cases (X_i, Y_i) fixed and the estimate $\hat{\beta}$ as fixed. Resample with replacement the vector $\hat{\varepsilon}$ to obtain the bootstrapped vector of residuals, $\hat{\varepsilon}^* = (\hat{\varepsilon}_1^*, \dots, \hat{\varepsilon}_n^*)$. Then for each $i = 1, \dots, n$ our bootstrapped response variable would be $Y_i^* = X_i\hat{\beta} + \hat{\varepsilon}_i^*$. Denoting $X_i^* = X_i$, we obtain the bootstrapped dataset $Z^* = \{(X_1^*, Y_1^*), \dots, (X_n^*, Y_n^*)\}$. We then run a linear regression again on Z^* to obtain estimates $\hat{\beta}^*$ and \hat{s}^{*2} . We present what was just discussed in the following algorithm. Note that the two methods of resampling the linear regression model

Algorithm 3 Bootstrapping Residuals of Linear Regression Model

- 1: Fit a linear regression model to the data $Z = \{(X_1, Y_1), \dots, (X_n, Y_n)\}$ to obtain the estimate $\hat{\beta}$.
 - 2: Compute the estimated residuals vector $\hat{\varepsilon} = (\hat{\varepsilon}_1, \dots, \hat{\varepsilon}_n)$, where $\hat{\varepsilon}_i = Y_i - X_i\hat{\beta}$.
 - 3: **for** $b = 1, \dots, B$ **do**
 - 4: Sample with replacement n times from $\hat{\varepsilon}$ to obtain the bootstrapped residuals $\hat{\varepsilon}^{*b} = (\hat{\varepsilon}_1^{*b}, \dots, \hat{\varepsilon}_n^{*b})$.
 - 5: **for** $i = 1, \dots, n$ **do**
 - 6: Set $X_i^{*b} = X_i$ and $Y_i^{*b} = X_i\hat{\beta} + \hat{\varepsilon}_i^{*b}$
 - 7: Obtain the bootstrapped dataset $Z^{*b} = \{(X_1^{*b}, Y_1^{*b}), \dots, (X_n^{*b}, Y_n^{*b})\}$.
 - 8: Fit a linear regression model on the bootstrap replicate of the data Z^{*b} to obtain the estimates $\hat{\beta}^{*b}$ and $(\hat{s}^2)^{*b}$.
-

rely on different assumptions on the data. In particular, we are assuming that the

error structure of the data does not rely on our predictors X_i . By fixing the X_i , we are assuming the distribution of the error terms F is invariant to the data we have observed. This is a fairly strong assumption. Furthermore, resampling the residuals works well only if the variance of the errors is homoskedastic. If the variance of the errors is heteroskedastic, then the modeling assumptions we made are invalid and a weighted linear regression approach or wild bootstrap approach may be necessary. The cases resampling is much less sensitive to the modeling assumptions we make as we do not generate the Y_i^* 's in the same way as with the residuals method. If either of these two methods are applicable, we could then proceed to form summary statistics such as the sample mean or sample standard deviation of the coefficients and the estimate of the variance of the model. The two methods we presented for bootstrapping the linear regression are easily adapted to other types of models. In particular, we could consider applying these methods to highly non-linear estimators, which is precisely what we do with bagged and random forests with respect to CART trees.

1.3 Random Forests

Among the limitations of CART discussed in the preceding sections, the biggest issues is perhaps the variability of the method and the issue of collinearity among predictors. While overfitting can be addressed using cost-complexity pruning, variability and collinearity are not fixed by pruning. Random forests deal with these two issues of CART by introducing a resampling and randomization mechanism. The natural order is to first discuss bagged forests before turning to random forests. One method of

Algorithm 4 Bagged Forest algorithm

- 1: **for** $b = 1, \dots, B$ **do**
 - 2: Draw a bootstrap sample Z_b^* of size N from the training data Z .
 - 3: Grow a CART tree T_b on each bootstrap sample Z_b^* .
 - 4: Output the bagged forest ensemble $\{T_b\}_{b=1}^B$.
-

improving CART trees is to bag them. Bagging, which stand for bootstrap aggregating, is a variation reduction technique particularly useful for improving the predictive power of weak learners. We are interested in bagging CART trees to reduce the variability of single trees under slight perturbations of the data. Generally bagged ensembles of learners produce robust predictions in comparison to running the learner once.

1.3.1 How Bagged Forests Work

In particular, bagged forests are an ensemble obtained by taking many bootstrap samples of the data and fitting a tree to each bootstrapped dataset. In this case, we grow the trees quite deep and do not employ cost-complexity pruning. The idea behind this decision is that we want to sufficiently explore the feature space using the tree ensemble, and since we are also taking an average of the trees, we are fine with

overfitting at least a little bit. As the algorithm above for bagged forests indicates, the output is an ensemble of trees $\{T_b\}_{b=1}^B$. Given a test data point, we form a prediction by taking the average of predictions given by the tree ensemble:

$$\hat{f}_{bf}^B(x) = \frac{1}{B} \sum_{b=1}^B T_b(x),$$

where \hat{f}_{bf}^B indicates we are taking the bagged forest estimate of the underlying regression or classification function using B many trees. Note that it is important to be consistent in the choice of splitting criterion throughout the bagging process.

It has been shown by Friedman and Hall (2000) and Chen and Hall (2003) that bagging is especially effective when used on highly non-linear models such as CART trees. Under ideal conditions, bagged estimates of non-linear estimators reduces both the bias and variance of the estimator. So bagging trees seem to be effective because of the reduction to the variance of the estimator, which produces a more robust prediction.

When we bag trees each observation in the data is not used within each individual tree. A bootstrap replicate Z_b of the data Z will likely exclude some of the observations within the data. The observations used within the bootstrap replicate Z_b is called the in-bag data while the observations not used within the bootstrap replicate Z_b is called the out-of-bag (OOB) data and is denoted by \bar{Z}_b . The OOB data allows us to approximate the test error of the ensemble as follows. For simplicity suppose we are in the regression setting (the classification setting is similar). Then the OOB estimate of the MSE of the bagged forest is given by

$$MSE_{\text{OOB}}(T; Z) = \frac{1}{B} \sum_{b=1}^B MSE(T_b; \bar{Z}_b).$$

As the number of trees in the ensemble grows, the OOB estimate of the MSE for the bagged forest converges to the LOOCV estimate of the MSE for forest (Friedman et al.).

A weakness of bagged forests is collinearity between trees (Friedman et al.). This collinearity between trees grown from the bootstrap sample can be addressed by adding a randomization mechanism in the tree growing process. When we grow a tree from a bootstrap sample, even with the randomness induced by resampling from the data, certain features may be explored at the expense of other just as interesting features. This is a particular issue with collinear predictors. If two predictors are collinear, then the bagged forest might consistently choose one predictor over another even if the predictor not chosen leads to splits that are just as informative. This is due in part to the greedy nature of the CART algorithm when searching for optimal splits over the feature space (Cite ESL or some similar textbook for this point). The algorithm does not take into account the second best or third best splits. Furthermore, it is not difficult to see that bagging will generally produce an ensemble of trees that are quite similar to one another, subject to some perturbations. These trees will be strongly correlated with other trees in the ensemble, so if there is a less explored part of the feature space, then the ensemble will struggle to produce good predictions over that part of the feature space.

1.3.2 The Random Forest Algorithm

Random Forests try to deal with this issue of correlated trees and collinearity among predictors by choosing at random only $m \leq p$ of the predictors to be considered as candidate splitting variables at each split in each tree in the ensemble. This randomness further reduces the variance of the bagged forest by decorrelating the trees in the ensemble. Furthermore, while individually the trees may perform worse than a single pruned tree, collectively the ensemble has a better chance of exploring the feature space fully. To form a prediction at a test point x , we have in the regression

Algorithm 5 Random Forest algorithm

- 1: **for** $b = 1, \dots, B$ **do**
 - 2: Draw a bootstrap sample Z_b^* of size N from the training data Z .
 - 3: Grow the CART tree T_b on Z_b^* with the following modification:
 - 4: **while** minimum node size n_{\min} not reached across T_b **do**
 - 5: Select $m \leq p$ candidate splitting variables at random.
 - 6: Pick the best splitting variable and splitting point among the m variables selected at random.
 - 7: Split the node into two daughter nodes.
 - 8: Output the random forest ensemble $\{T_b\}_{b=1}^B$.
-

setting

$$\hat{f}_{rf}^B(x) = \frac{1}{B} \sum_{b=1}^B T_b(x).$$

[Add in the classification setting].

1.3.3 Variable Importance Measures

One of the advertised outputs of random forests is the variable importance (VI) measure. There are two main variable importance measures in common use, with the choice of VI measure varying depending on the setting and splitting criterion chosen. The first choice is the Mean Decrease in Impurity (MDI) which is typically used in the classification setting where the GINI index or Shannon entropy is used as the splitting criterion. The second choice is Mean Decrease in Accuracy (MDA) which is typically used in the regression setting where RSS has been used as the splitting criterion. The idea of MDI is to find how much the nodal impurity $p(t)\Delta i(s, t)$ decreases for all nodes t in which the variable of interest X_j is used and to take that average over all trees in the ensemble. More important variables are those which are on average more often chose for splits and which also contribute most to reducing the nodal impurity of the trees. The idea of MDA is to measure for each variable X_j , on average how much the predictive accuracy of the forest as measured using RSS suffers when the X_j component is permuted across observations within the OOB dataset \bar{Z}_b of each tree T_b in the ensemble. More important variables in the random forests are those for which the variable importance is large, as those are the variables for which the predictive

Algorithm 6 MDI Variable Importance

-
- 1: Grow a random forest $\{T_b\}_{b=1}^B$.
 - 2: **for** $j = 1, \dots, p$ **do**
 - 3: **for** $b = 1, \dots, B$ **do**
 - 4: Compute the importance of X_j in T_b as $VI_b(X_j) = \sum_{t \in T_b} \mathbb{I}(j_t = j)p(t)\Delta i(s, t)$ to be the sum of the decrease in impurity over nodes where variable X_j is used .
 - 5: Compute the importance of X_j in the random forest to be $VI(X_j) = \frac{1}{B} \sum_{b=1}^B VI_b(X_j)$.
-

Algorithm 7 MDA Variable Importance

-
- 1: Grow a random forest $\{T_b\}_{b=1}^B$.
 - 2: **for** $j = 1, \dots, p$ **do**
 - 3: **for** $b = 1, \dots, B$ **do**
 - 4: Permute the X_j component of Z_b to obtain the dataset Z_b^j , where X_j has been permuted.
 - 5: Compute the importance of X_j in T_b to be $VI_b(X_j) = \frac{1}{|Z_b|} (RSS(T_b, Z_b) - RSS(T_b, Z_b^j))$.
 - 6: Compute the importance of X_j in the random forest to be $VI(X_j) = \frac{1}{B} \sum_{b=1}^B VI_b(X_j)$.
-

accuracy of the random forest suffers the most. Note that as variable importance measures currently defined and used, the threshold for importance of a variable is something which the researcher has to decide.

1.3.4 Issues with Random Forests

While random forests are good out of the box predictors, there are situations where the random forest algorithm can fail to produce good predictions. If the underlying regression function the random forest is linear, if the predictors are highly correlated, or if the data cannot be bootstrapped, then the random forest will not perform well. Random forests are especially adept at handling highly non-linear functions, but can struggle with linear response compared to say linear regression.

If the predictors are highly correlated, then it has been shown by Strobl et al. that the trees within the forest ensemble will be biased and the variable importance measures will not be reliable due to confounding between similar looking variables. While the randomization step in random forest algorithm can alleviate the correlation between trees in the ensemble, the collinearity between predictors can cause the predictive performance of the random forest to suffer. This is an issue with the underlying CART algorithm and Hothorn, Strobl, and their collaborators developed Conditional Inference trees and forests to deal with the issue of collinearity in the data (which will be explained in the next chapter). While using random forest variable

importance for variable selection certainly seems like a good idea, the issue of collinear data makes the applicability of variable importance measures less immediate. Perhaps a proper use of random forest variable importance measures as a variable selection procedure would be to run a random forest only after some dimension reduction techniques have been applied. If the collinearity of the predictors has been dealt with, then heuristically the variable importance measures should be able to more accurately estimate the importance of predictors within the ensemble.

Finally, there are situations where the data cannot be bootstrapped. This could be due to a number of factors including that the data has a heavily-tailed distribution or if there are particularly extreme values. In this case, a different bootstrap scheme could perhaps remedy the situation where the naive bootstrap fails. One common important resampling scheme used within random forests is to use the m -out-of- n bootstrap (also referred to subsampling or subagging in the literature). The m -out-of- n bootstrap is a resampling scheme which resamples with or without replacement $m \leq n$ observations from the data to form datasets with m many data points to run the bootstrap computation. Bickel et al. have shown that in important cases, subsampling can succeed where the bootstrap fails. Of course, using less of the available data is less efficient, but in the context of random forests this loss of efficiency may not be an issue. In [Cite paper comparing CI trees to CART trees using IJ], simulation results showed that subsampling instead of using the standard nonparametric bootstrap can improve the performance of random forests. The authors suggested that subsampling further reduces the variance of the ensemble by producing trees that are even more decorrelated. Their heuristic is that there is a lower probability of duplicate data points being chosen using subsampling (this probability is zero if we are subsampling without replacement), furthermore there is a lower probability of highly correlated data points being chosen as one of the $m \leq n$ points. This certainly seems plausible, but we would like to see further simulation results or a technical result that explains why subsampling works well for forests. We would also like to note that most consistency results (Biau et al., Scornet et al., Ishwaran et al., and Wager et al.) make this subsampling assumption in their analysis of the random forest model, as subsampling constructions make the forest ensemble more amenable to mathematical analysis.

1.4 Focus of this Thesis

In the previous three sections we discussed the basics of trees, the bootstrap, and random forests. We would like to now discuss the direction we are going to take this thesis. We are interested in developing inferential tools using the random forest algorithm. The random forest often produces good predictions out of the box with little tuning required except growing a sufficient number of trees and choosing a good value of $m \leq p$ to try at each split in the tree growing process. The ease of fitting random forests is one of the advantages of the random forest compared to more complex methods like neural networks or support vector machines. Even if the random forest is easier to fit than neural nets or SVMs, the underlying random forest mechanism is quite complex. This complexity makes developing inferential tools with

random forests difficult. In the next chapter we will discuss some approaches that have been developed recently by researchers. Of particular interest for us are the variable importance measures for random forests. There is the MDI variable importance and the MDA variable importance measure. While there are concerns about the bias in the MDI and MDA VI measures with random forests using CART tree's due to how CART tree's are constructed (Strobl et al., 2008), we would like to extend the inferential capabilities of random forests using CART as this is perhaps the most popular version of the algorithm in use.

The random forest VI can be viewed as a random variable with an unknown probability distribution. While determining the distribution of random forest VI's would be ideal towards developing inference for random forests, finding the distribution of random forest VI's is difficult and unclear in general. However, note that the bootstrap provides a computational method of approximating the sampling distribution of random forest VI measures. We could then proceed to obtaining estimates of the standard error and to form approximate interval estimates. We could grow a random forest once, obtain an estimate of the VI of each variable X_j and then run a bootstrap to obtain estimates of the standard error of each variable. Inference could then proceed using the VI measures along with the estimate of standard error. Note that in this scheme there is two levels of bootstrap at play. There is the bootstrap within each random forest and then the bootstrapping to obtain the standard error estimate. The estimate we produce of the VI of a variable X_j can be erratic. Running the random forest again can produce a new estimate of the VI of variable X_j . As Efron suggests in his 2014 article "Estimation and Accuracy after Model Selection," we could remedy the erratic, non-smooth nature of the VI estimate by bagging $VI(X_j)$. However, when we bag $VI(X_j)$ we would require a third-level of bootstrapping to produce an estimate of the standard error of the bagged estimate of $VI(X_j)$. This is computationally expensive, especially considering that the computational cost of the random forest depends on the number of observations, number of tree's grown, and number of variables present. However, applying Efron's infinitesimal jackknife (IJ) technique, which we will discuss in the next chapter, we can efficiently estimate the standard error of the bagged estimate of $VI(X_j)$ only using the two levels of bootstrapping. In this thesis we will be exploring the properties of IJ estimates of the standard error of the bagged estimate $VI(X_j)$ utilizing different bootstrap schemes. Utilizing the IJ, we can then produce interval estimates and confidence intervals of the variable importance of variables in the random forest. This allows us to characterize the uncertainty of $VI(X_j)$ when using variable importance measures for description, variable selection, and inference.

1.5 Outline of Remaining Chapters

Chapter 2: Inference and variable importance for random forests. In this chapter we will discuss the various approaches to inference for random forests that have been developed by researchers. These include Ishwaran and Louppe's analysis of VI measures of RF. Ishwaran's analysis is of the variable importance scheme he devised.

Ishwaran's scheme is amenable to theoretical analysis and he produces asymptotic results for his scheme. Louppe analyzes the MDI variable importance in the context of a construction called totally randomized forests in the setting of finite sample spaces. Louppe investigates the effect of relevant and irrelevant variables to MDI VI in this setting and provides asymptotic results. These are two of the main papers investigating properties of VI.

The other schemes include Mentch and Hooker's prediction intervals which are produced by interpreting the random forest ensemble as a particular type of U-statistic and applying the U-statistics theory to produce prediction intervals. They then can produce hypothesis tests and confidence intervals in this context.

A second approach towards prediction intervals is Wager's application of the IJ to the random forest estimator to produce prediction intervals and confidence intervals. Wager has a couple of papers in this area which we will discuss. In this part we will also go into greater detail about the IJ, its properties, and why it works.

We will also discuss the conditional inference trees and conditional variable importance developed by Strobl, Hothorn, and their colleagues to deal with the biased manner in which the trees in random forests are constructed. In this part we will also discuss the Infforest variable importance measure developed by Aurora.

Chapter 3: In this chapter we will go into great detail about the bootstrap and why it works. We will discuss the technical details of different methods of estimating the standard error of functional statistics, and we will go into the construction of different bootstrap confidence intervals along with properties of these confidence intervals. We will also discuss different bootstrap schemes and in particular subsampling, and why subsampling works well, especially in the random forest context.

Chapter 4: We will present our different approaches to bootstrapping variable importance measures and provide simulation results. The first approach is the cases bootstrap, the second approach is the bootstrapping residuals of the random forest approach. Within the cases approach, there are two ways we will try to constrain the variability of bootstrap replicates. Adopting the notation from general linear models, we could fit a pruned tree predicting $Y \sim X_1, \dots, X_p$. Then we would bootstrap from the terminal nodes of this single tree to try to produce bootstrap replicates which capture the relationship between the variables. Another approach is for each predictor X_j , fit a single well pruned tree $X_j \sim X_1, \dots, X_{j-1}, X_{j+1}, \dots, X_p$. We would then draw bootstrap samples from the terminal nodes of this tree which respect the partition produced by these terminal nodes. The idea is to fix the relationship between every predictor not X_j and allow the X_j 's to be exchanged across the bootstrap samples. We would produce simulation results of each approach and compare the statistical properties of these different constructions.

Chapter 5: If all goes well there might be a chapter 5 where we explore large sample properties and distribution of VI measures. This is likely going to be a difficult mathematical problem to solve in general, so a tangible course of action might be to pick a generating mechanism and easy VI measure from which we could figure out the VI distribution under some set of strong assumptions.

Chapter 2

Variable Importance and Inference for Random Forests

2.1 Introduction

In this chapter we focus on approaches of inference for random forests involving variable importance measures of random forests. Such approaches involve using variable importance measures of random forests to evaluate the relative importance of different variables in the construction of the forest. Louppe (2014) and Ishwaran (2007) focused on theoretical properties of variable importance measures while Owens (2017), Strobl, Boulesteix, Zeileis, & Hothorn (2007), and Strobl, Boulesteix, Kneib, Augustin, & Zeileis (2008) are centered on developing less biased variable importance measures for hypothesis testing.

2.2 Theoretical Analysis of MDA Variable Importance Measures

The approach to variable importances adopted in Ishwaran (2007) differs from the original variable importance measures for random forests, so we require some additional vocabulary.

Suppose T is a binary recursive tree and suppose that T has M many terminal nodes. For each point \mathbf{x} in the feature space, T maps \mathbf{x} to one of the M -many terminal nodes. In particular, if we let \mathcal{X} denote the feature space, then T is a function $\mathcal{X} \rightarrow \{1, \dots, M\}$ defined by the equation

$$T(\mathbf{x}) = \sum_{m=1}^M m B_m(\mathbf{x}),$$

where $B_m(\mathbf{x})$ is a 0 – 1 basis function which partition the feature space \mathcal{X} .

Let $Z = \{(\mathbf{x}_i, Y_i) | i = 1, \dots, n\}$ denote the training data, where \mathbf{x}_i is a covariate in the feature space and Y_i is the response. We call T a binary regression tree if it is a binary recursive tree grown from Z using using binary recursive splits of the form

$x_j \leq c$ and $x_j > c$ where split values c are chosen based on the observed \mathbf{x}_i in the training data Z . The value a_m in the terminal node is the average response of the training observations falling in the m th node. That is,

$$a_m = \frac{\sum_{i=1}^n \mathbb{I}\{T(\mathbf{x}_i) = m\} Y_i}{\sum_{i=1}^n \mathbb{I}\{T(\mathbf{x}_i) = m\}}.$$

Note that \mathbf{x}_i denotes a row of covariates for the training data Z , while x_j denotes the j th variable along the columns of the training data.

For a binary regression tree, the basis functions $B_m(\mathbf{x})$ are product splines of the following form:

$$B_m(\mathbf{x}) = \prod_{l=1}^{L_m} [x_{l(m)} - c_{l,m}]_{s_{l,m}},$$

where L_m denotes the number of splits used to construct $B_m(\mathbf{x})$. For each split l , there is a splitting variable $\mathbf{x}_{l(m)}$ which denotes the $l(m)$ th coordinate of \mathbf{x} and a splitting value $c_{l,m}$. The $s_{l,m}$ are binary ± 1 values, where for a given scalar x , $[x]_{+1} = \mathbb{I}(x > 0)$ and $[x]_{-1} = \mathbb{I}(x \leq 0)$. Note that the basis functions satisfy an orthogonality property, which gives $B_m(\mathbf{x})B_{m'}(\mathbf{x}) = 0$ if $m \neq m'$. Note also that given a tree T , the predictor associated with the tree can be written as a linear combination of basis functions:

$$\hat{\mu}(\mathbf{x}) = \sum_{m=1}^M a_m B_m(\mathbf{x}).$$

We are now prepared to define Ishwaran's variable importance measure.

Informally, the *MDA* variable importance of a variable x_j is the difference between *MSE* of the tree T when x_j is randomly permuted and *MSE* of the tree T when x_j is not permuted. As such a scheme of variable importance is difficult to analyze, Ishwaran proposes a surrogate measure. For the variable x_j , we drop \mathbf{x} down the tree and follow the binary splits until either a terminal node is reached or a node with a split depending on x_j is reached. If a node with a split depending on x_j is reached, we then subsequently assign \mathbf{x} randomly to either the left or right daughter node, whenever there is a split, until we reach a terminal node. The difference in *MSE* between noising up x_j and not noising up x_j to be the variable importance of x_j in the tree T . Denote the tree that results from noising up x_j by T_j .

Such a scheme relies on the following heuristic: if we chose an adequate splitting rule to construct our tree, then we expect that variables that are split earlier in the tree are more important, since prediction will suffer the most from noising up a variable higher up in the tree than a variable close to a terminal node. This is a behavior observed in CART trees and random forests based on CART: splits closer to the root node are more influential than splits close to terminal nodes, so the MDA or MDI variable importance of variables split on close to the root node are expected to be higher than otherwise.

2.2.1 Maximal Subtrees and Theoretical Results

Defining a structure on binary regression trees called subtrees, we can write the predictor for the noised up tree as a deterministic component relying on terminal

nodes for no parent nodes involve a split on x_j , and a random component involving terminal nodes for which there are parent nodes involving a split on x_j . The definition of the subtree is quite intuitive. We call \tilde{T}_j a j -subtree of the tree T , if the root node of \tilde{T}_j has daughters that depend on an x_j split. A j -subtree \tilde{T}_j is a maximal j -subtree of the tree T , if there are no larger j -subtrees containing \tilde{T}_j . For a given tree T and for each variable x_j , there is a set of K_j many distinct maximal j -subtrees, which are denoted by $\tilde{T}_{1,j}, \dots, \tilde{T}_{K_j,j}$. Note each distinct $\tilde{T}_{k,j}$ maximal j -subtree contains a set of distinct terminal nodes $M_{k,j}$. Each $M_{k,j}$ is distinct for $k = 1, \dots, K_j$, since we are working with maximal j -subtrees. Define

$$M_j = \bigcup_{k=1}^{K_j} M_{k,j}$$

to be the set of terminal nodes for which there is a parent node involving a split on x_j . Ishwaran (2007) proves the following lemma about the functional form of the predictor for the tree T_j .

Lemma 2.1. *Let $\hat{\mu}_j(\mathbf{x})$ denote the predictor for T_j . Then*

$$\hat{\mu}_j(\mathbf{x}) = \sum_{m \notin M_j} a_m B_m(\mathbf{x}) + \sum_{k=1}^{K_j} \tilde{a}_{k,j} \mathbb{I}\{T(\mathbf{x}) \in M_{k,j}\},$$

where $\tilde{a}_{k,j}$ is the random terminal value assigned by $\tilde{T}_{k,j}$ under the random left right path through $\tilde{T}_{k,j}$. We write $\tilde{P}_{k,j}$ to denote the distribution of $\tilde{a}_{k,j}$.

For a proof, see Ishwaran (2007). It is a bit surprising that the functional form of $\hat{\mu}_j(\mathbf{x})$ can be separated into the two components. Given this lemma and the definition of j -subtrees, we can more formally define the variable importance of x_j in the tree T .

Let g be a loss function. Often we use the squared error to evaluate loss, which corresponds to MSE , but there is no strict requirement in the definition. Denote the test data by (Y, \mathbf{x}) . Then the prediction error of the predictor $\hat{\mu}$ is given by $\mathbb{E}(g(Y, \hat{\mu}(\mathbf{x})))$. As a reminder, we assume that there is an underlying regression function

$$Y = \mu(\mathbf{x}) + \varepsilon,$$

where ε is independent error with zero mean and variance $\sigma^2 > 0$. Similarly, we can define the prediction error of the predictor $\hat{\mu}_j$ to be $\mathbb{E}(g(Y, \hat{\mu}_j(\mathbf{x})))$. Set $g(Y, \hat{\mu}(\mathbf{x})) = (Y - \hat{\mu}(\mathbf{x}))^2$ to be the L_2 loss, which corresponds to MSE . Define the variable importance of the variable x_j to be

$$\Delta_j = \mathbb{E}((Y - \hat{\mu}_j(\mathbf{x}))^2) - \mathbb{E}((Y - \hat{\mu}(\mathbf{x}))^2).$$

Application of the lemma and some manipulation allows us to write

$$\Delta_j = \mathbb{E}(R_j(\mathbf{x})^2) - 2\mathbb{E}(R_j(\mathbf{x})[\mu(\mathbf{x}) - \hat{\mu}(\mathbf{x})]),$$

where

$$R_j(\mathbf{x}) = \sum_{k=1}^{K_j} \sum_{m \in M_{k,j}} (\tilde{a}_{k,j} - a_m) B_m(\mathbf{x}).$$

As noted in Ishwaran (2007), we make the assumption that the true regression function μ is of similar form to T . That is, assume

$$\mu(\mathbf{x}) = \sum_{m=1}^M a_{m,0} B_m(\mathbf{x}),$$

where $a_{m,0}$ are the true, but unknown, terminal values. Under this and some other large sample assumptions, Ishwaran finds that asymptotically, each maximal j -subtree will tend to contribute equally to the variable importance Δ_j . In effect, nodes closer to the root of a maximal j -subtree will have a larger effect on Δ_j than nodes closer to the terminal nodes.

2.2.2 Extension to Forest Ensembles

The framework developed in Ishwaran (2007) extends naturally to forest ensembles and his theoretical result regarding forest ensembles provides some information of the behavior of variable importance measures for random forests. First for some notation, recall that in the forest ensemble setting, we draw B many bootstrap resamples of the training data to obtain the bootstrap replicates $Z^b = \{(\mathbf{x}_i^b, Y_i^b) | i = 1, \dots, n\}$ of the training data for $b = 1, \dots, B$. We then construct a binary regression tree $T(\mathbf{x}; b)$ on each bootstrap replicate of the data and have the forest $\hat{\mu}_F$ as the average of predictions over the trees $T(\mathbf{x}; b)$:

$$\hat{\mu}_F(\mathbf{x}) = \frac{1}{B} \sum_{b=1}^B \hat{\mu}(\mathbf{x}; b),$$

where $\hat{\mu}(\mathbf{x}; b)$ denotes the predictor for the tree $T(\mathbf{x}; b)$. Given that each $\hat{\mu}(\mathbf{x}; b)$ is a linear combination of basis functions, we can write

$$\hat{\mu}_F(\mathbf{x}) = \frac{1}{B} \sum_{b=1}^B \sum_{m=1}^{M^b} a_m^b B_m(\mathbf{x}; b).$$

Again assume that the $\mu(\mathbf{x})$ has a similar structure to $\mu(\mathbf{x})$. That is, $\mu(\mathbf{x}) = \frac{1}{B} \sum_{b=1}^B \sum_{m=1}^{M^b} a_{m,0}^b B_m(\mathbf{x}; b)$, where $a_{m,0}$ are the true, but unknown, terminal values. We denote the noised up forest predictor for the variable x_j by $\hat{\mu}_{F_j}(\mathbf{x})$. As with the normal forest predictor, the noised up forest predictor is the average of the noised up predictors $\hat{\mu}_j$ over the bootstrap resamples:

$$\hat{\mu}_j(\mathbf{x}) = \sum_{b=1}^B \hat{\mu}_j(\mathbf{x}; b).$$

As forest predictors are simply the average of individual trees, we can extend the lemma to $\hat{\mu}_{F_j}$ with the use of b 's in appropriate places denoting the usage of the b th bootstrap resample. That is, we can write

$$\hat{\mu}_{F_j}(\mathbf{x}) = \frac{1}{B} \sum_{b=1}^B \left(\sum_{m \notin M_j^b} a_m^b B_m(\mathbf{x}; b) + \sum_{k=1}^{K_j^b} \tilde{a}_{k,j}^b \mathbb{I}\{T(\mathbf{x}; b) \in M_{k,j}^b\} \right).$$

The variable importance of the variable x_j is defined to be

$$\Delta_{F_j} = \mathbb{E}((Y - \hat{\mu}_{F_j}(\mathbf{x}))^2) - \mathbb{E}((Y - \hat{\mu}(\mathbf{x}))^2).$$

Similar to the single tree case, the variable importance of the variable x_j in the forest ensemble can be written as

$$\Delta_{F_j} = \mathbb{E}(R_{F_j}(\mathbf{x})^2) - 2\mathbb{E}\left(R_{F_j}(\mathbf{x})[\mu(\mathbf{x}) - \hat{\mu}_F(\mathbf{x})]\right),$$

where

$$R_{F_j}(\mathbf{x}) = \frac{1}{B} \sum_{b=1}^B \sum_{k=1}^{K_j^b} \sum_{m \in M_{k,j}^b} (\tilde{a}_{k,j}^b - a_m^b) B_m(\mathbf{x}; b).$$

We are now ready to state a result about the asymptotic form of $\Delta_{f,j}$:

Theorem 2.1. *Let $R_{F_j,0}(\mathbf{x})$ be the function $R_{F_j}(\mathbf{x})$, in which each instance of a_m^b has been replaced with $a_{m,0}^b$. Assume that Y can be written in terms of a regression model*

$$Y = \mu(\mathbf{x}) + \varepsilon$$

and that

$$\mu(\mathbf{x}) = \frac{1}{B} \sum_{b=1}^B \sum_{m=1}^{M^b} a_{m,0}^b B_m(\mathbf{x}; b).$$

If $a_m^b \rightarrow a_{m,0}^b$ for each m and b , then

$$\Delta_{F_j} \rightarrow \mathbb{E}\left(R_{F_j,0}(\mathbf{x})^2\right) \leq \mathbb{E}\left(\frac{1}{B} \sum_{b=1}^B \sum_{k=1}^{K_j^b} \theta_0(k, j, b)\right),$$

where

$$\theta_0(k, j, b) = \sum_{m \in M_{k,j}^b} \pi_{m,b} \tilde{P}_{k,j,0}^b \left(\tilde{a}_{k,j,0}^b - a_{m,0}^b \right)^2$$

is the node mean squared error for the k th maximal v -subtree of $T(\mathbf{x}; b)$ and $\pi_{m,b} = \mathbb{P}(B_m(\mathbf{x}; b) = 1 | Z)$.

For a proof, see Ishwaran (2007). As Ishwaran (2007) notes, the bound in the above theorem becomes tighter as the trees in the forest become more and more orthogonal to each other. The above theorem is applicable if the forest predictor is consistent. This suggests that forest ensemble methods which are consistent and produce trees

that are at least approximately orthogonal to each other allow for variable importance to be characterized through node mean squared error of subtrees. Variable importance as defined above differs from the *MDA* variable importance for random forests, but the two follow a similar heuristic towards measuring variable importance via the loss of predictive accuracy when the variable x_j is perturbed. Therefore this result suggests that, perhaps, so long as the random forest estimator is consistent and the trees constructed are at least approximately orthogonal, the *MDA* variable importance can be characterized via the mean squared error of some analogous structure to maximal subtrees. This is, of course, conjectural, but we are interested whether for simpler forest algorithms, results similar to the theorem can be proven. Asymptotic results for the *MDA* and also *MDI* variable importance measures are difficult to formulate and prove for several reasons. First, the *CART* tree construction process combined with the bootstrapping and randomization procedure of the random forest is difficult to mathematically analyze. Second, it is still unknown whether random forests constructed via *CART* are consistent. However, there are other random forest variants known to be consistent, so those variants may be a natural starting point to try to prove asymptotic results about *MDA* and *MDI* variable importances. Third, the definition of *MDA* variable importance involves a permutation step that is difficult to analyze mathematically. The above results are mathematically amenable due to the noising-up procedure adopted allowing for a quite elegant analysis of the variable importance. One possible approach to dealing with this issue may be to adopt the above definition of variable importance in different random forest settings and see if similar results to Ishwaran (2007) may be derived. Another approach, which is the one more or less taken by Ishwaran (2007), is to find a mathematically tractable definition of variable importance which is approximately the *MDA* variable importance measure and proceed with analysis from there.

2.3 Theoretical Analysis of MDI Variable Importance

Up to now in this chapter, we have been discussing theoretical results concerning the *MDA* variable importance. Louppe (2014) has explored some of the theory for *MDI* variable importance of forest ensembles.

In order to discuss the following theoretical results regarding *MDI* variable importance, we make some modifications to the setting we are working in. Assume that we are working in a finite probability space [this assumption is necessary primarily for technical reasons] and that observations Y, X_1, \dots, X_p in the training set Z are categorical variables. Recall that if a forest ensemble is grown by choosing splits and variables maximizing the decrease in nodal impurity where $i(s, t)$ denotes the impurity measure used, then the *MDI* variable importance of the variable X_j is defined to be

$$VI(X_j) = \frac{1}{B} \sum_{b=1}^B \sum_{t \in T_b} \mathbb{I}(j_t = j) p(t) \Delta i(s, t),$$

where $p(t)$ is the proportion of samples which reach the node t in the tree T_b . Note that MDI variable importance is the average over the bootstrap resamples of the sum of the weighted decrease in impurity over the nodes of the tree using X_j as the splitting variable.

Rather than working with random forests, we will work with an infinite ensemble of totally randomized and fully developed trees. Totally randomized and fully developed trees are a variant of forest ensembles given by the following. A totally randomized and fully developed tree is a decision tree in which each node t is partitioned using a variable X_j picked uniformly at random among those not yet used at the parent nodes of t , where each node t is split into $|X_j|$ sub-trees, i.e., one for each possible value of X_j , and where the recursive construction process halts only when all p variables have been used along the current branch.

Using an impurity measure called Shannon entropy, Louppe (2014) is able to show that only relevant variables (that is variables whose information content, conditional on the other variables, is useful towards explaining the response Y) have non-zero infinite sample size variable importance. Furthermore, this means that irrelevant variables (which are variables whose information content, conditional on the other variables, is not useful towards explaining the response Y) have a infinite sample size variable importance of zero. In fact, in this context, a variable is irrelevant if and only if it has an infinite sample size variable importance of zero. Generalizing from Shannon entropy to other impurity measures, for the GINI index (used in commonly in classification problems) and variance (used in regression via MSE), only irrelevant variables result in no decrease in nodal impurity. We would like to reiterate that these results concerning irrelevant variables are valid particularly in the setting of infinite ensembles of totally randomized and fully developed trees.

In the random forest setting, the results discussed in the previous paragraph may not be valid. In the random forest setting, a key step in the construction of trees is the randomization step in which we choose at random a subset of size $m \leq p$ of the variables to choose the next split from. If $m > 1$, then it is possible for some variables to never be chosen at a node t , since there will always be other variables which have a larger decrease in nodal impurity. This results in trees in which the variables with the largest reduction in nodal impurity are centered in the trunk of the tree with variables with smaller reduction in nodal impurity are pushed to leaves, or otherwise not chosen to split on. This is an undesirable property to have since this can result in an ensemble which inadequately explores the feature space and is thus more consistently biased towards some variables over others, even if other variables can provide only slightly lower reductions in nodal impurity. As a consequence, if $m > 1$, then it is not the case that a variable is irrelevant if and only if it has a variable importance of zero. One implication is that in data sets where there are correlated variables, random forest variable importance measures may result in variable importances which do not reflect the actual importance of variables in explaining the response Y . In particular, it could be the case that if X_j and $X_{j'}$ are two correlated variables, then even if both X_j and $X_{j'}$ are important in explaining the response Y , it may be the case that X_j is consistently chosen as the splitting variable over $X_{j'}$ if the two variables are both possible splitting variables.

2.4 Dealing with Bias in Random Forest Variable Importance

In the previous two sections of this chapter we discussed theoretical results pertaining to MDA and MDI variable importance measures. For MDA variable importance, a consistent ensemble with orthogonal trees have a nice asymptotic form in the framework developed in Ishwaran (2007). On the otherhand, with MDI variable importance, if the trees are grown in the random forest setting, then there are issues of the variable importance not capturing the actual importance of the variables in the training data. This could particularly arise as an issue in data sets with correlated variables where equally important variables receive different variable importances due to bias introduced by tree construction process. In using the term ‘bias,’ we would like to emphasise that this is not bias in the sense of biased estimators, but bias in the sense of which variables are chosen to be split upon in the tree growing process. Bias in the variable importance measures of random forests is concerning as we would like to be able to use random forests for inferential statistics. A couple of methods have been proposed to construct more reliable variable importance measures, which we discuss in this section.

2.4.1 Bias in Random Forest Variable Importance Measures

Bias in random forest variable importance measures was first substantively analyzed in Strobl et al. (2007). Strobl et al. (2007) ran a simulation study comparing MDI variable importance using the GINI index, MDA variable importance, and a conditional variable importance measure in a classification setting. The conditional variable importance measure used by Strobl et al. (2007) is a variable importance method similar to MDA variable importance, but utilizing an ensemble of conditional inference trees. We will define conditional inference trees and the conditional variable importance measures below. For now, note that Strobl et al. (2007) found that MDI variable importance using the GINI index and MDA variable importance tends to be biased from the expected variable importance value within their simulation. They also found that subsampling without replacement tends to reduce the bias in variable importance in comparison to using bootstrap resampling with replacement. In their analysis, Strobl et al. (2007) claim that the GINI index tends to favor variables with more potential cutpoints. Hence the MDI variable importance measure using the GINI index is biased towards variables with more potential cutpoints. Strobl et al. (2007) also found that in using the MDA variable importance measure, since variables that are split upon closer to the root node affect the predictive accuracy of the ensemble more than variables split upon in leaves, the MDA variable importance measure will be affected by the variable selection bias of individual trees. Furthermore, Strobl et al. (2008) find that correlated variables tend to be overselected in the tree growing process. In order to utilize random forest variable importance measures as inferential tools, several methods have been proposed to deal with the issue of variable selection bias in random forests.

2.4.2 Conditional Variable Importance

The MDA variable importance measure can be viewed in the context of permutation tests and hypothesis testing. In particular, we can consider that the MDA variable importance measure operates on the null hypothesis that permuting the values of the variable X_j has no effect on the predictive accuracy of the random forest predictor. This corresponds to the null hypothesis that the variable X_j is independent of the response Y and the variables X_1, \dots, X_p . If the predictive accuracy of the random forest suffers from permuting X_j , that is if the $VI(X_j)$ is nonzero, then if also $X_j \perp X_{-j}$, it would follow that Y and X_j are not independent. However, it is important to note that the null hypothesis under which the MDA variable importance measure operates is:

$$H_0 : X_j \perp Y, X_{-j}.$$

If on the otherhand, X_j and X_{-j} are not independent, then $VI(X_j)$ will be biased by the correlation between X_j and X_{-j} . It could be that Y and X_j are not independent or that Y and X_j are independent, but in either case, if the predictor variables are correlated, we see that $VI(X_j)$ will not accurately capture the importance of X_j . Strobl et al. (2008) propose a permutation scheme corresponding to the null hypothesis

$$H_0 : (X_j \perp Y) | X_{-j},$$

that is that X_j is independent of Y conditional on the X_{-j} . Such a permutation scheme would take into account the correlation structure of the predictor variables and would allow for a less biased variable importance measure so long as the individual trees within the ensembles do not exhibit large variable selection bias.

Strobl et al. (2008) propose defining a grid within which values of X_j are permuted according to partitions of the feature space given by each tree. While Strobl et al. (2008) propose using unbiased conditional inference trees from Hothorn, Hornik, & Zeileis (2006) to determine the partition, it is possible to use partitions given by CART trees. The algorithm is presented as follows. To determine the variables X_i to be conditioned on Strobl et al. (2008) suggest including only variables whose empirical correlation with the variable X_j suggests some reasonable threshold.

2.4.3 Infforest Variable Importance

While simulation results of Strobl et al. (2008) suggest that the conditional variable importance is more effective at capturing the importance of each variable X_j compared to the marginal approach followed in MDA, they note that conditional variable importance cannot completely eliminate preference for correlated variables in random forests. Owens (2017) instead suggests a partition then permute scheme which produces a sampling distribution for the variable importance of each variable X_j . Once a sampling distribution for $VI(X_j)$ has been obtained, hypothesis testing and other sorts of statistical inference can proceed. As the Infforest variable importance is quite complicated, some explanation is needed.

After growing a forest ensemble $\{T_b\}_{b=1}^B$, infforest variable importance values are computed as follows. First, for each $b = 1, \dots, B$ and each variable X_j , grow a tree

Algorithm 8 Conditional Variable Importance

-
- 1: Grow a forest ensemble $\{T_b\}_{b=1}^B$
 - 2: **for** $j = 1, \dots, p$ **do**
 - 3: **for** $b = 1, \dots, B$ **do**
 - 4: Compute $RSS(T_b, Z_b)$.
 - 5: **for** all variables X_i to be conditioned on **do**
 - 6: Extract cutpoints that split X_i in the tree T_b and create a grid \mathcal{G} by bisecting the sample space in each cutpoint.
 - 7: Within the grid \mathcal{G} , permute the values of X_j and denote the permuted resample by Z_b^j .
 - 8: Compute $RSS(T_b, Z_b^j)$.
 - 9: Compute the conditional variable importance of X_j in the tree T_b to be $VI_b(X_j) = \frac{1}{|\bar{Z}_b|} (RSS(T_b, Z_b) - RSS(T_b, Z_b^j))$.
 - 10: Compute the conditional variable importance of X_j in the forest ensemble to be $VI(X_j) = \frac{1}{B} \sum_{b=1}^B VI_b(X_j)$.
-

$X_j \sim X_1, \dots, X_{j-1}, X_{j+1}, \dots, X_p$ using all $p - 1$ predictors using the in-bag sample used to grow T_b . Denote this tree by T_j^{b*} . The rows of \bar{Z}_b are permuted within the partitions of the feature space determined by T_j^{b*} . The difference in predictive accuracy of T_b before and after the OOB sample \bar{Z}_b has been permuted is the infforest variable importance for the variable X_j in the tree T_b . Owens (2017) suggests then using the sampling distribution of $VI(X_j)$ obtained from the infforest partition-permute scheme to test the null hypothesis that the variable importance of X_j is zero. On the other hand, if we let $VI_b(X_j)$ denote the infforest variable importance of the variable X_j in the tree T_b , then we could define the infforest variable importance of X_j in the forest ensemble $\{T_b\}_{b=1}^B$ to be

$$VI(X_j) = \frac{1}{B} \sum_{b=1}^B VI_b(X_j).$$

In particular, this corresponds to the mean of the sampling distribution of the infforest variable importances of X_j over the trees T_b .

Originally, Owens (2017) developed for random forests using CART trees as base learners. However, the infforest variable importance could certainly be used with random forest variants such as conditional inference forests used in Strobl et al. (2008). Another possible modification of the infforest variable importance algorithm is to only grow an auxiliary tree predicting $X_j \sim X_{\alpha_1}, \dots, X_{\alpha_k}$, where $X_{\alpha_1}, \dots, X_{\alpha_k}$ are variables whose correlation with X_j exceeds some reasonable threshold. This would combine the suggestion in Strobl et al. (2008) of considering the correlation structure of the predictor variables in setting up the grid for the conditional variable importance with the infforest partition-permute scheme.

One issue with infforest variable importance is the steep computational cost of the algorithm. The algorithm grows an auxiliary tree T_j^{b*} for each variable X_j and bootstrap resample b and then proceeds to permute the OOB sample with respect to

each T_j^{b*} . Even implementing the infforest variable importance algorithm on small bootstrap resamples of around several hundred is computationally intensive.

Algorithm 9 Infforest Variable Importance

- 1: Grow a forest ensemble $\{T_b\}_{b=1}^B$
 - 2: **for** $j = 1, \dots, p$ **do**
 - 3: **for** $b = 1, \dots, B$ **do**
 - 4: Compute $RSS(T_b, \bar{Z}_b)$.
 - 5: Grow a tree T_j^{b*} predicting $X_j \sim X_{-j}$ using in-bag sample.
 - 6: Permute rows of the OOB sample \bar{Z}_b with respect to the partitions of the feature space from T_j^{b*} to obtain the permuted OOB sample \bar{Z}_b^* .
 - 7: Compute $RSS(T_b, \bar{Z}_b^*)$.
 - 8: Compute the infforest variable importance of X_j in T_b to be $VI_b(X_j) = \frac{1}{\bar{Z}_b} \left(RSS(T_b, \bar{Z}_b) - RSS(T_b, \bar{Z}_b^*) \right)$.
 - 9: Test the null hypothesis that the variable importance of X_j is zero using the distribution of values $VI_b(X_j)$.
-

Chapter 3

Added Variable Plot Importance

3.1 Introduction

In the previous chapter, we discussed theoretical properties and observed behavior of random forest variable importance measures. In particular, we discussed issues of bias present in the MDA variable importance measure. Strobl et al. (2008) and Owens (2017) proposed the conditional variable importance measure and the Infforest variable importance measures, respectively, as methods of accounting for bias in variable selection among correlated predictors when measuring variable importance in a forest ensemble. Conditional variable importance and Infforest variable importance aim at measuring the conditional importance of a particular variable by conditionally permuting OOB data according to some criteria measured from the data, whether that be empirical correlation in the case of conditional variable importance, or the partitions induced by a particular tree in the case of Infforest variable importance. In any case, we are primarily interested in the conditional importance of a predictor given the information provided by other predictors. While we would like to have an exact method of computing the conditional importance of a predictor in a random forest ensemble, in practice it is unclear how to construct an exact method given the complexity of the random forest ensemble. We can, however, estimate the effect of adding a predictor to the set of predictors that the forest ensemble can split on via a type of diagnostic plot called added variable plots. Added variable plots are a diagnostic plot arising from the linear regression which estimate the effect of adding a predictor variable to the model. In this chapter we propose a method of measuring the importance of each predictor in a random forest ensemble via a quantity we call the Added Variable Importance (AVI) that depends on the added variable plot of each predictor. The AVI attempts to estimate the effect of adding a predictor as a possible candidate in the splitting step of the random forest ensemble. To understand AVI, we regress from the random forest setting to the linear regression setting and explain how added variable plots work in the linear regression setting.

3.2 Added Variable Plots in Linear Regression

Suppose that we have data $Z = \{(\mathbf{x}_i, Y_i) | i = 1, \dots, n\}$, where \mathbf{x}_i is a covariate in the feature space, and that we fit a multiple linear regression model of the form

$$\mathbf{Y}_1 = \mathbf{X}\beta_1 + \mathbf{W}\alpha + \varepsilon_1$$

where \mathbf{X} is a $n \times p$ matrix consisting of $p - 1$ predictors, $\beta = (\beta_0, \beta_1, \dots, \beta_p)^T$, $\mathbf{W} = (w_1, \dots, w_n)$ is a predictor, α is a scalar, and $\text{Var}(\varepsilon) = \sigma^2 I$.

Say we are interested in estimating the effect of the predictor \mathbf{W} in the regression model $\hat{\mathbf{Y}}_1$. We could first fit the models $\hat{\mathbf{Y}}_2 = \mathbf{X}\beta_2 + \varepsilon_2$ and $\hat{\mathbf{W}} = \mathbf{X}\delta + \varepsilon$, where β_2 and δ are coefficient vectors like β_1 and then plot the residuals $\mathbf{W} - \hat{\mathbf{W}}$ against the residuals $\mathbf{Y} - \hat{\mathbf{Y}}_2$. The plot we obtain by plotting $\mathbf{W} - \hat{\mathbf{W}}$ against $\mathbf{Y} - \hat{\mathbf{Y}}_2$ is called the added variable plot of \mathbf{W} and measures the effect of \mathbf{W} on \mathbf{Y} once we have adjusted for the effect of \mathbf{X} on \mathbf{W} and \mathbf{Y} , respectively. In particular, the residuals that we plot for the added variable plot is the portion of \mathbf{W} unexplained by \mathbf{X} on the x -axis and the portion of \mathbf{Y} unexplained by $\hat{\mathbf{Y}}_2 = \mathbf{X}\beta_2 + \varepsilon$ on the y -axis.

In the linear regression setting the added variable plot has some nice properties. In particular, let α_{AVP} denote the estimate of the slope from regressing $\mathbf{Y} - \hat{\mathbf{Y}}_2$ on $\mathbf{W} - \hat{\mathbf{W}}$. Then with some linear algebra it can be shown that α_{AVP} is equal to the least-squares estimate of α from $\hat{\mathbf{Y}}_1 = \mathbf{X}\beta_1 + \mathbf{W}\alpha + \varepsilon_1$. For full details see Sheather (2009) and Cook & Weisberg (1982). Hence if we want to estimate the linear effect of the variable \mathbf{W} on the linear regression $\hat{\mathbf{Y}}_1$, we can construct and visually inspect the trend of the added variable plot of \mathbf{W} .

[Provide example of added variable plot]

3.3 Added Variable Plots in Random Forests

While added variable plots in the linear regression setting allows us to conditionally estimate the effect of the predictor on the response, the picture for more complex regression functions such as random forests is more complicated. In particular, if the relationship between the response and predictors is non-linear, or we are using a statistical learning method such as a random forest, then we do not have the nice linear algebra that undergirds the interpretation of added variable plots of linear regression models. However, we can still construct a variant of added variable plots for random forests.

Suppose we are interested in the added variable effect of variable X_k . Let X_{-k} denote the set of predictors excluding X_k . As Rendahl (2008) notes, in general, for black box statistical learning methods such as random forests the only appropriate added variable plot we can form is to plot $Y - \mathbb{E}(Y|X_{-k})$ against $\mathbb{E}(Y|X) - \mathbb{E}(Y|X_{-k})$. That is, we can plot residuals of the model without the predictor X_k against the difference in predictions between the full model and the model with X_k removed. In the context of random forests, to obtain the added variable plot of the predictor X_k , we would plot

$$(\hat{\theta}_{RF}(Y|X) - \hat{\theta}_{RF}(Y|X_{-k}), Y - \hat{\theta}_{RF}(Y|X_{-k})).$$

[Add example here]

Depending on the relationship between the predictors and the response, there are several outputs we might expect from the added variable plots of the predictors in the random forest. If the predictor X_k is simply noise, i.e., if a predictor is uninformative with respect to the response, then we expect that $\hat{\theta}_{RF}(Y|X)$ and $\hat{\theta}_{RF}(Y|X_{-k})$ to form similar predictions of Y given $X = x$ and $X_{-k} = x_{-k}$, respectively. In this scenario then, suppose for a moment that $\hat{\theta}_{RF}(Y|X)$ and $\hat{\theta}_{RF}(Y|X_{-k})$ are consistent estimators of $\mathbb{E}(Y|X)$ and $\mathbb{E}(Y|X_{-k})$, respectively. Then by the Law of Total Expectation, we would expect that asymptotically $\mathbb{E}(\hat{\theta}_{RF}(Y|X)) = Y$ and $\mathbb{E}(\hat{\theta}_{RF}(Y|X_{-k})) = Y$. Hence in the limit, by linearity of expectation,

$$\mathbb{E}(\hat{\theta}_{RF}(Y|X) - \hat{\theta}_{RF}(Y|X_{-k})) = \mathbb{E}(\hat{\theta}_{RF}(Y|X)) - \mathbb{E}(\hat{\theta}_{RF}(Y|X_{-k})) = Y - Y = 0.$$

Similarly,

$$\mathbb{E}(Y - \hat{\theta}_{RF}(Y|X_{-k})) = Y - Y = 0.$$

Hence if a predictor X_k is uninformative, provided we have grown adequately accurate forest ensembles to predict Y given X and Y given X_{-k} , respectively, then we expect that the added variable plot of X_k to be radially centered about the origin or to otherwise be arranged in a line with a slope and y -intercept of zero.

On the other hand, suppose that the predictor X_k is informative with respect to the response. Then we would expect that when properly tuned the random forest ensemble $\hat{\theta}_{RF}(Y|X)$ would provide reasonably accurate predictions of Y . We would also expect that the forest ensemble $\hat{\theta}_{RF}(Y|X_{-k})$ would suffer in predictive performance due to the lack of information from X_k . Then in the limit, we would expect that

$$(\hat{\theta}_{RF}(Y|X) - \hat{\theta}_{RF}(Y|X_{-k})) \neq 0 \text{ and } Y - \hat{\theta}_{RF}(Y|X_{-k})) \neq 0.$$

That is, we would expect the trend of the added variable plot of X_k to be non-zero. In other words, in the case of informative predictors, we would expect to be correlation between $\hat{\theta}_{RF}(Y|X) - \hat{\theta}_{RF}(Y|X_{-k})$ and $Y - \hat{\theta}_{RF}(Y|X_{-k})$. The departure from a trend of approximately zero would depend on the relative informativeness of X_k . If X_k is strongly informative then we would expect the difference between Y and $\hat{\theta}_{RF}(Y|X_{-k})$ and the difference between $\hat{\theta}_{RF}(Y|X)$ and $\hat{\theta}_{RF}(Y|X_{-k})$ to often be large. If X_k is weakly informative we would expect the two differences to often be of smaller magnitude than when X_k is strongly informative. Hence visually the trend of the added variable plot of predictors used to grow a random forest ensemble offer a method of gauging the informativeness of different predictors. We note that in the above argument that we made an appeal to the random forest estimator $\hat{\theta}_{RF}(Y|X)$ being a consistent estimator of $\mathbb{E}(Y|X)$. As discussed earlier, the random forest algorithm as introduced and implemented by Breiman and collaborators has not yet been shown to be consistent. However, empirically the random forest algorithm often offers good predictions of the response, so we expect that the added variable plot as applied to the original random forest algorithm to have the properties discussed above. We also note that there are random forest variants such as Causal Forest as introduced by Wager & Athey (2017) which have been shown to be consistent estimators of $\mathbb{E}(Y|X)$. Hence in such settings

we expect that our discussion of added variable plots for forest ensembles to be fully valid.

One setting in which added variable plots for random forests are useful is in dealing with correlated predictors. As Strobl et al. (2008) notes, the random forest algorithm can have difficulty determining the relative importance of correlated predictors due to masking effects. Suppose X_j and X_k are correlated predictors with X_j only weakly informative to the response. Then if both X_j and X_k are candidate splitting variables, X_k could be chosen over X_j as the splitting variable since X_k may seem to be informative due to the correlation between X_k and X_j . The better split would have been found over X_j , but the greedy nature of the CART algorithm means the algorithm does not look forward at possible splits further down the tree if X_j is chosen over X_k . Note that the tree grown using X_k at that particular node would likely have lower predictive performance than the tree grown using X_j at that node. Hence WLOG suppose the subset $\{X_1, \dots, X_m\} \subseteq \{X_1, \dots, X_p\}$ of our predictors are correlated where $m \leq p$. If $X_j \in \{X_1, \dots, X_m\}$ is not informative to the response, then we would expect $\hat{\theta}_{RF}(Y|X)$ and $\hat{\theta}_{RF}(Y|X_{-j})$ to provide similar predictions, while if $X_k \in \{X_1, \dots, X_m\}$ is informative to the response, we would expect that $\hat{\theta}_{RF}(Y|X_{-k})$ will suffer a decrease in predictive performance in comparison to $\hat{\theta}_{RF}(Y|X)$. Then we would expect the added variable plot for X_j to be a mass of points centered about the origin without a trend while the added variable plot for X_k should have some sort of trend whose shape depends on the informativeness of X_k and the predictive performance of $\hat{\theta}_{RF}(Y|X)$ and $\hat{\theta}_{RF}(Y|X_{-k})$. This is of course despite the fact that, depending on the correlation structure and relative informativeness of X_k , that X_j may be chosen over X_k when X_j and X_k are both candidate splitting variables in the tree growing process. The full random forest model $\hat{\theta}_{RF}(Y|X)$ may be biased in how the splitting variables are chosen due to the correlation structure of $\{X_1, \dots, X_m\}$ as discussed in Strobl et al. (2008). However, absent the choice of X_k in the random forest model $\hat{\theta}_{RF}(Y|X_{-k})$, the less informative split on X_j has an increased probability of being chosen when growing the forest ensemble $\hat{\theta}_{RF}(Y|X_{-k})$ than in the full forest ensemble $\hat{\theta}_{RF}(Y|X)$. Hence the random forest model $\hat{\theta}_{RF}(Y|X_{-k})$ would have a decrease in predictive performance due to the loss of information in the predictor X_k , but also due to the increased probability of irrelevant predictors being chosen as the splitting variables due to exclusion of X_k .

3.4 Added Variable Plot Importance

In the previous section, we discussed the use of added variable plots for random forests including in settings where a subset of the predictors are correlated. Variable importance measures such as MDA variable importance and MDI variable importance have difficulties in dealing with correlated predictors. As discussed in the previous chapter, Strobl et al. (2008) proposed the conditional variable importance measure while Owens (2017) proposed the Infforest variable importance measure as methods that try to account for the correlation structure of the predictors when measuring

the importance of predictors in the forest ensemble. In this section we propose the Added Variable Plot Importance (AVPI) measure as an alternative variable importance measure to conditional variable importance and Infforest variable importance measures in accounting for correlated predictors when measuring variable importance.

To motivate the construction of AVPI, we return briefly to added variable plots in the linear regression setting. As mentioned earlier, when we construct an added variable plot for a predictor \mathbf{W} in the linear regression model, the linear trend of the added variable plot for \mathbf{W} corresponds to the least squares estimate of the linear effect α of \mathbf{W} in the full model $\mathbf{Y}_1 = \mathbf{X}\beta_1 + \mathbf{W}\alpha + \varepsilon_1$. Hence while we could simply visually inspect the trend of the added variable plot for \mathbf{W} , we could also run least squares regression on the added variable plot for \mathbf{W} to obtain an estimate for α in the regression model \mathbf{Y}_1 . The size and sign of the $\hat{\alpha}$ from running a regression model on the added variable plot of \mathbf{W} then indicates the relative importance and effect of \mathbf{W} on the response \mathbf{Y} .

In the random forest setting, we would like to have a similar procedure to determine the importance of the variable X_k with respect to the response Y once we have accounted for the effect of the other predictors, but as noted before, we are restricted to plotting the added variable plot of X_k using the random forest algorithm as

$$(\hat{\theta}_{RF}(Y|X) - \hat{\theta}_{RF}(Y|X_{-k}), Y - \hat{\theta}_{RF}(Y|X_{-k})).$$

As discussed in the previous section, depending on the relative informativeness of the predictor X_k there may or may not be a trend in the added variable plot for X_k which we could then attempt to model. Let $W_k = Y - \hat{\theta}_{RF}(Y|X_{-k})$ and $U_k = \hat{\theta}_{RF}(Y|X) - \hat{\theta}_{RF}(Y|X_{-k})$. We propose to train a bagged forest ensemble $\hat{\theta}_{BF}(W_k|U_k)$ and computing the MDA variable importance of U_k in the bagged forest ensemble. We call the MDA variable importance of U_k in the bagged forest ensemble $\hat{\theta}_{BF}(W_k|U_k)$ the added variable plot importance (AVPI) of X_k and denote this quantity by $VI_{AVP}(X_k)$. Our choice of using a bagged forest to predict W_k given U_k is motivated by the fact that unlike in the linear regression setting, there is not a clear parametric model with which to predict W_k given U_k . The bagged forest makes few assumptions on the form of the true regression function $W_k = f(U_k) + \varepsilon$ while also providing a metric in the form of MDA variable importance to assess the importance of U_k in predicting W_k once we have grown the ensemble $\hat{\theta}_{BF}(W_k|U_k)$. Furthermore, the AVPI of X_k should reflect the relative importance of X_k with respect to the response Y given that the trend of the added variable plot, i.e. the degree to which $Y - \hat{\theta}_{RF}(Y|X_{-k})$ and $\hat{\theta}_{RF}(Y|X) - \hat{\theta}_{RF}(Y|X_{-k})$ are correlated, visually indicates the informativeness of X_k .

The purpose of the AVPI of X_k is to provide a quantitative measure of the importance of the predictor X_k with respect to Y once we have taken into account the loss in predictive performance when X_k is removed as a possible splitting variable. In particular, given that the added variable plots for random forests should reflect the informativeness of correlated predictors, the added variable plot importance for correlated predictors should be able to more accurately reflect the importance of correlated predictors with respect to the response than the MDA variable importance ran on the predictors in the full model $\hat{\theta}_{RF}(Y|X)$.

Algorithm 10 Added Variable Plot Importance (AVPI)

-
- 1: Grow the random forest ensemble $\hat{\theta}_{RF}(Y|X)$ predicting Y using the full set of predictors.
 - 2: **for** $k = 1, \dots, p$ **do**
 - 3: Grow the random forest ensemble $\hat{\theta}_{RF}(Y|X_{-k})$ predicting Y using the full set of predictors minus the predictor X_k .
 - 4: Compute $U_k = \hat{\theta}_{RF}(Y|X) - \hat{\theta}_{RF}(Y|X_{-k})$ and $W_k = Y - \hat{\theta}_{RF}(Y|X_{-k})$.
 - 5: Grow the bagged forest ensemble $\hat{\theta}_{BF}(W_k|U_k)$ predicting W_k using U_k .
 - 6: Compute the added variable plot importance of X_k to be the MDA variable importance of U_k : $VI_{AVP}(X_k) = VI_{MDA}(U_k)$.
-

3.5 Extensions of Added Variable Plot Importance

Once we have obtained added variable plot importance values there are couple directions we can extend our framework. Once again suppose we have grown our full random forest ensemble $\hat{\theta}_{RF}(Y|X)$ and also the random forest ensemble $\hat{\theta}_{RF}(Y|X_{-k})$. Let $U_k = \hat{\theta}_{RF}(Y|X) - \hat{\theta}_{RF}(Y|X_{-k})$ and $W_k = Y - \hat{\theta}_{RF}(Y|X_{-k})$.

Once we have computed the AVPI of X_k , $VI_{AVP}(X_k)$, we can take a simulation approach to generating a sampling distribution for $VI_{AVP}(X_k)$. In particular, to generate a sampling distribution for the AVPI of X_k , permute U_k to obtain U_k^* . Then grow the bagged forest ensemble $\hat{\theta}_{BF}(W_k|U_k^*)$ predicting W_k using U_k^* , and compute the MDA variable importance of U_k^* to obtain $VI_{AVP}^*(X_k)$ as the permuted AVPI for X_k . After having permuted U_k and computed $VI_{AVP}^*(X_k)$ for enough iterations to generate a sampling distribution for $VI_{AVP}(X_k)$. We can then compute a two-sided p-value using the original $VI_{AVP}(X_k)$ as the observed test statistic. If we compute p-values for each predictor, then we could proceed to a hypothesis testing framework if we believe that the simulation to generate a sampling distribution for the AVPI of each predictor was successful. Of course depending on the number of predictors in the dataset and the relationship between the predictors, it may be necessary to control for multiple comparisons. In our opinion, as simulations in the next chapter will indicate, hypothesis testing using the AVPI is likely more sensitive to type-I errors than type-II errors, so an adjustment such as the Bonferroni correction may be appropriate.

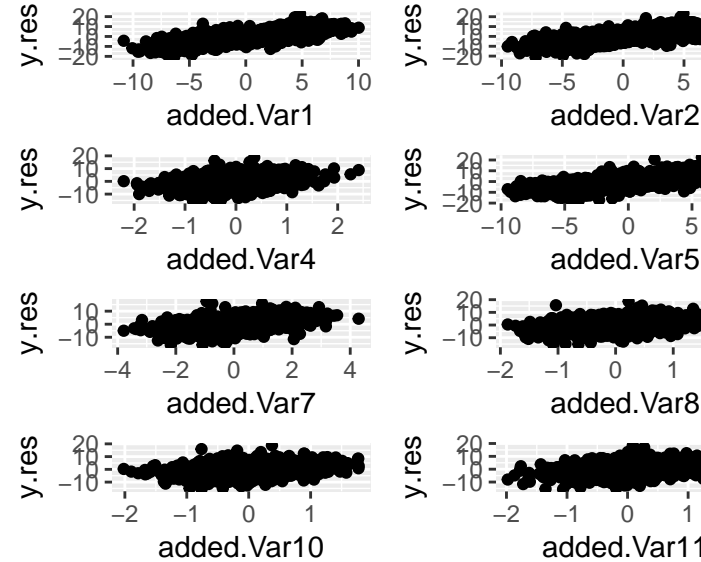
We also note that while generating adequate sampling distributions of $VI_{AVP}(X_k)$ for each predictor X_k is computationally expensive, each step of the process from growing the full ensemble $\hat{\theta}_{RF}(Y|X)$ to growing each $\hat{\theta}_{RF}(Y|X_{-k})$ to permuting U_k and growing $\hat{\theta}_{BF}(W_k|U_k^*)$ to compute $VI_{AVP}^*(X_k)$ can be coded to run in parallel. So performance gains in generating good sampling distributions of $VI_{AVP}(X_k)$ for each predictor X_k are easily attainable.

Chapter 4

Simulation and Results

4.1 Introduction

In this chapter, we present simulation results of the random forest added variable plot



and added variable plot importance methods.

Table 4.1: Simulation Results for Added Variable Plot Importances for Sampling with Replacement

	Simulation 1	Simulation 2	Simulation 3	Simulation 4	Simulation 5	Simulation 6	Simulation 7	Simulation 8
Variable 1	452.93528	209.19947	184.29378	115.75481	348.0641	110.911944	200.25310	60.67242
Variable 2	436.50160	200.30775	164.79733	49.30234	355.2946	121.012598	90.09198	33.95596
Variable 3	176.15493	76.12612	141.20267	127.73681	186.0916	4.438317	68.25077	47.94023
Variable 4	69.71643	14.09013	62.70999	44.32338	190.2879	29.697785	60.86136	52.56689
Variable 5	453.05254	479.75299	160.85322	196.06473	324.4524	245.731616	92.18312	124.80432
Variable 6	437.09922	479.78513	44.56070	39.21142	325.6628	239.388844	60.91802	32.09565
Variable 7	214.78673	270.27051	70.79758	30.53213	171.8441	32.679916	41.70790	38.16311
Variable 8	94.67066	127.68758	63.23303	53.12418	182.5039	46.141387	46.65001	41.45022
Variable 9	69.99713	104.23646	56.13219	39.10399	215.7042	22.064169	53.65208	41.27242
Variable 10	70.13127	80.45368	70.77256	54.45881	152.4064	21.740682	44.84663	34.90679
Variable 11	70.51321	91.39784	65.78904	44.82417	185.0719	17.999310	60.45611	50.53217
Variable 12	68.49742	88.75896	75.87031	26.68245	200.3480	39.174289	53.36817	41.62424

Table 4.2: Simulation Results for MDA Variable Importances for Sampling with Replacement

	Simulation 1	Simulation 2	Simulation 3	Simulation 4	Simulation 5	Simulation 6	Simulation 7	Simulation 8
Variable 1	205.7751162	43.5875638	87.9694096	39.6267348	51.3775666	68.0344640	45.2615577	16.5658513
Variable 2	182.7953452	45.3203038	47.4985731	22.9426251	51.3756589	59.7224401	6.6095155	13.8717953
Variable 3	43.3705524	31.7206332	88.2067658	46.1139125	-1.8420809	19.5960032	-0.6160646	10.7902908
Variable 4	-0.8467650	22.5345613	-1.5190519	21.3672088	0.7655721	31.1151525	0.7265404	7.7755666
Variable 5	179.2816368	210.5278772	42.5696986	52.9141820	54.3017177	44.2205811	73.4474491	90.0099288
Variable 6	190.1979559	199.6886106	3.2962175	-1.8198516	50.3953957	49.1162744	-0.1722575	0.2080882
Variable 7	49.7942892	54.4672557	-1.4994542	-1.9087069	0.1191700	-2.0071842	-0.2548386	-2.8897482
Variable 8	1.8630745	-0.4211499	-1.9256818	-2.5463545	-0.2674365	0.4980884	-0.2709784	0.7483121
Variable 9	-1.7072270	-0.3489273	1.0810682	0.9995826	4.1857040	-2.7534240	0.6012231	-0.3862685
Variable 10	0.1434588	0.0824640	1.8700646	2.1839565	-0.9314400	-2.0090863	1.0238239	0.6847400
Variable 11	0.2220114	-1.1905073	-0.2861896	-1.3776237	1.6749594	-3.2776029	0.9792522	-1.9566093
Variable 12	0.2826006	1.1815968	-0.4752267	-0.8640204	1.6851063	-0.2720373	1.7977126	-2.4189332

Table 4.3: Simulation Results for Added Variable Plot Importances for Sampling without Replacement

	Simulation 1	Simulation 2	Simulation 3	Simulation 4	Simulation 5	Simulation 6	Simulation 7	Simulation 8
Variable 1	457.02513	212.352368	213.84990	110.83360	348.6451	110.453492	167.41957	89.34318
Variable 2	457.77972	214.188658	199.28552	69.19798	356.4324	105.020452	52.91816	48.21518
Variable 3	189.22857	98.922942	134.35239	129.33500	209.8724	17.446615	51.80081	59.05998
Variable 4	80.11575	5.013828	77.20821	50.00432	214.4154	-3.569032	50.94663	44.88170
Variable 5	453.78943	492.412633	131.13573	158.58779	320.5315	237.079037	97.21665	114.92600
Variable 6	443.55902	489.822741	84.87764	44.53580	334.8463	251.124465	36.56998	41.09561
Variable 7	201.05497	275.682102	66.14043	43.32284	259.2078	73.023361	47.50904	48.39331
Variable 8	68.14961	106.313016	66.00254	54.50657	198.7929	70.151875	47.72055	56.38571
Variable 9	78.26486	77.371760	92.99772	50.10961	235.0376	49.483426	51.44996	32.54249
Variable 10	68.90864	83.184212	80.70935	60.96954	206.1605	42.379239	49.53081	48.48468
Variable 11	88.57084	90.243103	79.04303	41.84311	176.4355	39.551375	49.41950	63.93243
Variable 12	80.23029	64.317099	76.45756	61.39489	195.9230	39.499604	62.14501	54.62036

Table 4.4: Simulation Results for MDA Variable Importances for Sampling without Replacement

	Simulation 1	Simulation 2	Simulation 3	Simulation 4	Simulation 5	Simulation 6	Simulation 7	Simulation 8
Variable 1	203.8974116	43.2217090	86.6974491	38.6782561	47.7410796	67.0884007	47.9127054	18.8238892
Variable 2	184.7896642	44.8711037	48.5145679	22.8629478	47.0771667	60.8648352	11.1373919	14.1609495
Variable 3	47.5925671	31.5300753	97.4263019	48.4838317	-2.4682257	19.4952466	-2.4124545	10.9352715
Variable 4	-1.5370464	23.4295635	-2.4456640	20.0982113	1.9451710	34.5067380	0.2163598	10.1516919
Variable 5	184.7704998	204.5983543	54.0176344	57.6470636	52.0030374	39.3199135	76.8657131	93.1538797
Variable 6	188.1526981	205.5292797	2.0321326	-0.6121418	48.3237316	43.7043053	0.3913965	1.8169532
Variable 7	51.9308522	51.0196417	-1.4260717	-2.1457808	-1.4728311	-1.0650397	1.8925123	-1.5395390
Variable 8	-0.1434761	-0.4393610	-0.1664074	-3.3893701	-0.3444081	0.2141649	-0.5496865	-0.6005596
Variable 9	-1.7221738	-0.1948834	0.8563617	0.7584246	2.9144231	-1.0565879	0.7799837	-0.7651692
Variable 10	-1.3463022	0.3026227	1.1876820	2.7230832	1.4493889	-2.0950498	0.2778606	2.8284927
Variable 11	0.1626804	-1.3699901	-0.3369013	0.6452085	1.8235057	-2.8213151	-1.2349051	-1.4908094
Variable 12	-0.5193238	2.0094494	-1.0121098	0.4916756	3.0198114	1.3935243	-0.1840246	1.7284960

Table 4.5: Added Variable Importance P-values for Sampling with Replacement

	Simulation 1	Simulation 2	Simulation 3	Simulation 4	Simulation 5	Simulation 6	Simulation 7	Simulation 8
Variable 1 P-Value	0.001998	0.0019980	0.001998	0.001998	0.001998	0.0019980	0.001998	0.001998
Variable 2 P-Value	0.001998	0.0019980	0.001998	0.001998	0.001998	0.0019980	0.001998	0.001998
Variable 3 P-Value	0.001998	0.0019980	0.001998	0.001998	0.001998	0.6573427	0.001998	0.001998
Variable 4 P-Value	0.001998	0.1398601	0.001998	0.001998	0.001998	0.0059940	0.001998	0.001998
Variable 5 P-Value	0.001998	0.0019980	0.001998	0.001998	0.001998	0.0019980	0.001998	0.001998
Variable 6 P-Value	0.001998	0.0019980	0.001998	0.001998	0.001998	0.0019980	0.001998	0.001998
Variable 7 P-Value	0.001998	0.0019980	0.001998	0.001998	0.001998	0.0019980	0.001998	0.001998
Variable 8 P-Value	0.001998	0.0019980	0.001998	0.001998	0.001998	0.0019980	0.001998	0.001998
Variable 9 P-Value	0.001998	0.0019980	0.001998	0.001998	0.001998	0.0279720	0.001998	0.001998
Variable 10 P-Value	0.001998	0.0019980	0.001998	0.001998	0.001998	0.0219780	0.001998	0.001998
Variable 11 P-Value	0.001998	0.0019980	0.001998	0.001998	0.001998	0.0439560	0.001998	0.001998
Variable 12 P-Value	0.001998	0.0019980	0.001998	0.001998	0.001998	0.0019980	0.001998	0.001998

Table 4.6: Added Variable Importance P-values for Sampling without Replacement

	Simulation 1	Simulation 2	Simulation 3	Simulation 4	Simulation 5	Simulation 6	Simulation 7	Simulation 8
Variable 1 P-Value	0.001998	0.0019980	0.001998	0.001998	0.001998	0.0019980	0.001998	0.001998
Variable 2 P-Value	0.001998	0.0019980	0.001998	0.001998	0.001998	0.0019980	0.001998	0.001998
Variable 3 P-Value	0.001998	0.0019980	0.001998	0.001998	0.001998	0.6573427	0.001998	0.001998
Variable 4 P-Value	0.001998	0.1398601	0.001998	0.001998	0.001998	0.0059940	0.001998	0.001998
Variable 5 P-Value	0.001998	0.0019980	0.001998	0.001998	0.001998	0.0019980	0.001998	0.001998
Variable 6 P-Value	0.001998	0.0019980	0.001998	0.001998	0.001998	0.0019980	0.001998	0.001998
Variable 7 P-Value	0.001998	0.0019980	0.001998	0.001998	0.001998	0.0019980	0.001998	0.001998
Variable 8 P-Value	0.001998	0.0019980	0.001998	0.001998	0.001998	0.0019980	0.001998	0.001998
Variable 9 P-Value	0.001998	0.0019980	0.001998	0.001998	0.001998	0.0279720	0.001998	0.001998
Variable 10 P-Value	0.001998	0.0019980	0.001998	0.001998	0.001998	0.0219780	0.001998	0.001998
Variable 11 P-Value	0.001998	0.0019980	0.001998	0.001998	0.001998	0.0439560	0.001998	0.001998
Variable 12 P-Value	0.001998	0.0019980	0.001998	0.001998	0.001998	0.0019980	0.001998	0.001998

Chapter 5

Joint Added Variable Plot Importance

5.1 Introduction

In the previous chapters, we introduced the added variable plot importance (AVPI) of a predictor in the random forest ensemble. Simulation results showed..

One direction we can extend our framework of added variable plot importances is to compute the joint added variable plot importance for a set of predictors. We would like to capture the joint effect of sets of predictors on the performance of the random forest ensemble in predicting the response. One scenario in which we might want to capture the joint effect of sets of predictors is if out of a set of correlated predictors, we believe that only a subset of the correlated predictors are informative to the response. In such a scenario, we would like a quantitative measure to compare the joint importance of the subset of correlated informative predictors with the subset of correlated uninformative predictors.

5.2 Partial F-Test

In the linear regression context, we may be interested in if a subset of predictors are informative or not towards the linear regression model. If our covariates are \mathbf{X} , then we would partition the covariates to $\mathbf{X} = (\mathbf{X}_1, \mathbf{X}_2)$, where \mathbf{X}_1 are the first $p - q$ predictors and \mathbf{X}_2 are the last q predictors. Similarly partition the coefficients from the linear model $\beta = (\beta_1, \beta_2)$, where β_1 are the coefficients for the first $p - q$ predictors and β_2 are the coefficients for the last q predictors. Then we would like to test whether β_2 should be non-zero for \mathbf{X}_2 . We are testing the hypotheses

$$\begin{aligned} H_0 : \mathbf{Y} &= \mathbf{X}_1\beta_1 + \varepsilon \\ H_1 : \mathbf{Y} &= \mathbf{X}_1\beta_1 + \mathbf{X}_2\beta_2 + \varepsilon. \end{aligned}$$

The partial F-test allows us to test the above hypotheses. First fit the model under the null hypothesis H_0 and find the residual sums of squares RSS_{H_0} and degrees of freedom

df_{H_0} of the model. Next fit the model under the alternative hypothesis H_1 and find RSS_{H_1} and df_{H_1} . As Weisberg (2005) notes, $df_{H_0} > df_{H_1}$ and $RSS_{H_0} - RSS_{H_1} > 0$. The partial F-test statistic is

$$F = \frac{(RSS_{H_0} - RSS_{H_1}) / (df_{H_0} - df_{H_1})}{RSS_{H_1} / df_{H_1}}.$$

If F is large when compared to the $F(df_{H_0} - df_{H_1}, df_{H_1})$ distribution, then there is evidence against the null hypothesis that the coefficients of β_2 should be set to zero. In particular, while we cannot compute a test statistic similar to the F-test statistic for joint added variable importance, we can take the approach of comparing models fit with and without \mathbf{X}_2 to determine the importance of \mathbf{X}_2 in the random forest context.

5.3 Joint Added Variable Plots

Suppose that out of a particular set of correlated predictors, we believe that two, X_j and X_k , are particularly informative to the response while the other correlated predictors are uninformative. Denote the set of correlated predictors by $H = \{X_{\alpha_1}, \dots, X_{\alpha_m}\}$ of which $K = \{X_j, X_k\}$ is a subset. One approach to determining the relative importance of the variables in H is to plot added variable plots and compute added variable plot importances for each variable in H . However, if based on looking at the full random forest model variable importance, or based on some other information, we think that the variables in K are more important we could instead train a random forest excluding the variables in K , a random forest excluding the variables in $H \setminus K$, and a random forest excluding the variables in H . From there we can compute and compare added variable plots and added variable plot importances for predictors in the set K , the set $H \setminus K$, and the set H , respectively, as we would in the single variable added variable plot scenario.

More generally, suppose we have a subset $J = \{X_{\alpha_1}, \dots, X_{\alpha_m}\} \subseteq \{X_1, \dots, X_p\}$, where $m < p$, for which we are interested in the joint added variable effect of the predictors in J . As in the case of the added variable plot of a single variable, we could grow the full random forest $\hat{\theta}_{RF}(Y|X)$ and the reduced model $\hat{\theta}_{RF}(Y|X_{-J})$, where X_{-J} denotes the set of predictors not in J . The joint added variable plot for the predictors in J is then given by

$$(\hat{\theta}_{RF}(Y|X) - \hat{\theta}_{RF}(Y|X_{-J}), Y - \hat{\theta}_{RF}(Y|X_{-J})).$$

The rationale for forming the joint added variable plot of the predictors in J is similar to the single variable case, although care has to be taken in describing what sort-of relationship the joint added variable plot of J provides. The joint added variable plot for J captures the aggregated informativeness of the predictors in J with respect to the response. In particular, if at least one predictor in J is informative, then we would expect that the random forest ensemble $\hat{\theta}_{RF}(Y|X_{-J})$ would have a decrease in predictive performance in comparison to the full model. If many predictors in J are informative, then we would expect that, correspondingly there would be a large decrease

in predictive performance in $\hat{\theta}_{RF}(Y|X_{-J})$. At each node split, as the predictors in J are unavailable to be chosen as one of the m_{try} variables, there is a greater chance for an uninformative variable to be chosen as the splitting variable. On the other hand, if no variable in J is informative, then we would expect $\hat{\theta}_{RF}(Y|X_{-J})$ to have similar predictive performance to the full model $\hat{\theta}_{RF}(Y|X)$. Hence for reasons similar to the single added variable plots, if at least one variable in J is an informative predictor of the response, the trend of the joint added variable plot will be strongly non-zero, while if no predictor in J is informative, we would expect the joint added variable plot to be centered about the origin and have no significant trend. If there are a mixture of informative and uninformative variables contained in J , then the joint added variable plot of J would have a non-zero trend although the magnitude and direction of the trend would depend on the composition of the variables in J .

Depending on the number of predictors in J relative to number of predictors not in J , computing the joint added variable plot for J can be quicker than computing the individual added variable plots of each variable in J . This is as once the variables in J are removed, there are fewer potential splitting variables for the tree growing algorithm to search through at each split on each node. We would also recommend when computing the joint added variable plot of J , to also compute the joint added variable plot of the predictors not in J , that is to also compute the random forest $\hat{\theta}_{RF}(Y|X_J)$. Doing so allows us to compare the predictive value of $\hat{\theta}_{RF}(Y|X_{-J})$ and $\hat{\theta}_{RF}(Y|X_J)$, while allowing us to also compare the added variable effect of J versus the complement of J .

[Have examples here. One of correlated predictors, another of uncorrelated predictors]

5.4 Joint Added Variable Plot Importance

As with the single variable case, once we have acquired the joint added variable plot for J , we would like to have a quantitative measure of the joint importance of J . As with added variable plot importance, once we have acquired the joint added variable plot of J ,

$$(\hat{\theta}_{RF}(Y|X) - \hat{\theta}_{RF}(Y|X_{-J}), Y - \hat{\theta}_{RF}(Y|X_{-J})),$$

we can try to model the trend in the joint added variable plot utilizing a bagged forest. Let $U_J = \hat{\theta}_{RF}(Y|X) - \hat{\theta}_{RF}(Y|X_{-J})$ and $W_J = Y - \hat{\theta}_{RF}(Y|X_{-J})$. To measure, the joint added variable importance, grow the bagged forest $\hat{\theta}_{BF}(W_J|U_J)$ and compute the MDA variable importance of U_J in predicting W_J . We call the MDA variable importance of U_J the joint added variable importance (JAVPI) of J and denote the quantity by $VI_{JAVP}(X_J)$. Note that the joint added variable plot importance of J provides a quantitative measure of the relative importance of U_J in predicting the trend in the added variable plot. As mentioned previously, the trend in the added variable plot of J should reflect the aggregated informativeness of the variables in J with respect to the response, so the JAVPI of J indicates the relative aggregated importance of the variables in J as predictors of the response. In particular, higher values of JAVPI for J should indicate that the variables contained in J are more

informative than lower values of JAVPI for J . That is, the value of JAVPI measures the importance of all the predictors in J to the response Y via the loss in predictive performance in the ensemble when we remove the predictors in J as potential splitting variables in the forest growing process. As in the previous section, we also recommend that $VI_{JAVP}(X_{-J})$, the JAVPI of those predictors not in J be concurrently computed to provide a comparison of joint importance between sets of predictors.

Algorithm 11 Joint Added Variable Plot Importance (JAVPI)

- 1: Grow the random forest ensemble $\hat{\theta}_{RF}(Y|X)$ predicting Y using the full set of predictors.
 - 2: Grow the random forest ensemble $\hat{\theta}_{RF}(Y|X_{-J})$ predicting Y using the full set of predictors minus the predictors in J .
 - 3: Compute $U_J = \hat{\theta}_{RF}(Y|X) - \hat{\theta}_{RF}(Y|X_{-J})$ and $W_J = Y - \hat{\theta}_{RF}(Y|X_{-J})$.
 - 4: Grow the bagged forest ensemble $\hat{\theta}_{BF}(W_J|U_J)$ predicting W_J using U_J .
 - 5: Compute the added variable plot importance of X_J to be the MDA variable importance of U_J : $VI_{JAVP}(X_J) = VI_{MDA}(U_J)$.
-

5.5 Permutation Tests Using Joint Added Variable Plot Importance

Once we have computed $VI_{JAVP}(X_J)$, we can again take a simulation approach to generating a sampling distribution for $VI_{JAVP}(X_J)$. The process is essentially analogous to computing sampling distributions of single added variable plots. To compute $VI_{JAVP}(X_J)$, we require the joint added variable plot (U_J, W_J) , where $U_J = \hat{\theta}_{RF}(Y|X) - \hat{\theta}_{RF}(Y|X_{-J})$ and $W_J = Y - \hat{\theta}_{RF}(Y|X_{-J})$. Permute U_J to obtain U_J^* and grow the bagged forest $\hat{\theta}_{BF}(W_J|U_J^*)$ using the permuted U_J^* as the predictor. We then use the resulting ensemble to compute $VI_{MDA}(U_J^*) = VI_{JAVP}^*(X_J)$ as the permuted JAVPI of J . Once we have ran enough iterations of permutations of U_J^* and computation $VI_{JAVP}^*(X_J)$, we can compute a two-sided p-value using $VI_{JAVP}(X_J)$ as our test statistic.

If we have a collection J_1, \dots, J_q of subsets of the predictors, we could simulate sampling distributions of $VI_{JAVP}(X_{J_i})$ for each $i = 1, \dots, q$ and compute two-sided p-values for each subset J_i . We could then enter into a hypothesis testing framework. We do offer some words of caution here with respect to using joint added variable plot importances in a hypothesis test framework with multiple subsets. In particular, due to sensitivity of permutation tests using JAVPI to type-I errors and due to possible overlap of predictors in the J_i , we would recommend most certainly using a multiple comparisons procedure such as the Bonferonni correction. Furthermore, we would like to emphasize the use of JAVPI and AVPI as variable selection tools and diagnostic tools for random forests, rather than tools purely of inferential statistics and hypothesis testing.

With the JAVPI, in particular, our intention in introducing the JAVPI variable importance measure was to offer a method that utilizes the random forest mechanism to measure the importance of a subset J of predictors while taking into account the effect of the predictors not in J . However, as we have noted above, if the subset J of predictors consists of a mixture of informative and uninformative predictors, then a finer analysis of the variables in J may be required if the JAVPI of J is high. Concluding that each variable in J is informative based on a high JAVPI value or low p-value from simulation would be erroneous if J is a mixture of informative and uninformative. We would also like to emphasize that it is important to check the fit and residual sum of squares of the random forest model if using the JAVPI or AVPI to see if conclusions drawn from JAVPI or AVPI are valid. Furthermore, we would like to remind the reader that inference based on residuals as we are describing with JAVPI and AVPI can be sensitive to outliers and extreme points such that statistically significant results from JAVPI or AVPI should be examined with some scrutiny.

5.6 Simulation and Results of Joint Added Variable Plot Importance

Conclusion

If we don't want Conclusion to have a chapter number next to it, we can add the `{-}` attribute.

More info

And here's some other random info: the first paragraph after a chapter title or section head *shouldn't be* indented, because indents are to tell the reader that you're starting a new paragraph. Since that's obvious after a chapter or section title, proper typesetting doesn't add an indent there.

Appendix A

The First Appendix

This first appendix includes all of the R chunks of code that were hidden throughout the document (using the `include = FALSE` chunk tag) to help with readability and/or setup.

In the main Rmd file

```
# This chunk ensures that the thesisdown package is  
# installed and loaded. This thesisdown package includes  
# the template files for the thesis.  
if(!require(devtools))  
  install.packages("devtools", repos = "http://cran.rstudio.com")  
if(!require(thesisdown))  
  devtools::install_github("ismayc/thesisdown")  
library(thesisdown)
```

In Chapter ??:

Appendix B

The Second Appendix, for Fun

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