## STAT 542: Statistical Learning <br> Tree and Random Forest

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April 3, 2022
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## Classification and regression Trees (CART)

## Tree-based methods

- Tree-based methods are nonparametric methods that recursively partition the feature space into hyper-rectangular subsets, and make prediction on each subset.
- Two main streams of models:
- Classification and regression Trees (CART): Breiman, Friedman, Olshen and Stone (1984)
- ID3/C4.5: Quinlan, 1986, 1993.
- Both are among the top algorithms in data mining (Wu et al., 2008)
- In statistical literature, CART is more popular.


## Titanic Survivals



## Classification and regression Trees

- How tree works in classification? (We will formally introduce classification problems later)
- Example: independent $x_{1}$ and $x_{2}$ from uniform [ $-1,1$ ], $90 \%$ to observed class 1 (blue) within the circle $x_{1}^{2}+x_{2}^{2}<0.6$, and $90 \%$ to observed class 2 (orange) outside the circle.
- All existing classification methods that we have introduced require either transformation of the space (SVM) or distance measure ( $k \mathrm{NN}$, kernel)
- Tree solves this by directly cutting the feature space using a binary splitting rule in the form of $1\{x \leq c\}$


## Example



## Example

## Example

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## Example



## Example

- rpart is one of the popular packages that provide CART fitting and plot
- Other choices include tree, party.
- Read the reference manual carefully!!!

```
> library(rpart)
>x1 = runif(500, -1, 1)
>x2 = runif(500, -1, 1)
>y = rbinom(500, size = 1, prob = ifelse(x1^2 + x2^2 < 0.6, 0.9, 0.1))
> cart.fit = rpart(as.factor(y)~x1+x2, data = data.frame(x1, x2, y))
> plot(cart.fit)
> text(cart.fit)
```


## Example



## Why tree-based methods?

- Tree-based methods: non-parametric, flexible model structure
- Can handel high-dimensional data without modifying the algorithm (CART may not work well in this setting)
- Single tree model - simple decision rules, interpretable
- Ensemble tree model - high prediction accuracy


## Single tree methods: recursive partitioning

- How tree-based methods work?
- Initialized the root node: all training data

Root node

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> Root node

Splitting rule $\longrightarrow 1\left\{X^{(j)} \leq c\right\}$

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- Recursively apply the procedure on each daughter node
- Predict each terminal node using within-node data



## Classification and regression Trees

- How to construct the splitting rules?
- For classification problems
- continuous predictors
- categorical predictors
- For regression problems
- Tree pruning


## Splitting rules for continuous predictors

- Splitting of continuous predictors are in the form of $1\left\{X^{(j)} \leq c\right\}$
- Consider a node $\mathcal{T}$, we want to split this node into two child nodes.
- We first evaluate the overall impurity of $\mathcal{T}$ by the Gini index (CART), assuming that there are $K$ different classes of the outcome, $1, \ldots, K$,

$$
\operatorname{Gini}(\mathcal{T})=\sum_{k=1}^{K} \widehat{p}_{k}\left(1-\widehat{p}_{k}\right)=1-\sum_{k=1}^{K} \widehat{p}_{k}^{2}
$$

where $\widehat{p}_{k}=\frac{\sum_{i} \mathbf{1}\left\{y_{i}=k\right\} \mathbf{1}\left\{x_{i} \in \mathcal{T}\right\}}{\sum_{i} \mathbf{1}\left\{x_{i} \in \mathcal{T}\right\}}$ is the within node frequency of class $k$.

## Impurity Measures

- Now propose a split: $\mathbf{1}\left\{X^{(j)} \leq c\right\}$.
- This separates all subjects in the node into two disjoint parts: $\mathcal{T}_{L}$ and $\mathcal{T}_{R}$
- For each child node, we can again evaluate $\operatorname{Impurity}\left(\mathcal{T}_{L}\right)$ and $\operatorname{Impurity}\left(\mathcal{T}_{R}\right)$
- The reduction of impurity is measured by

$$
\text { score }=\operatorname{Gini}(\mathcal{T})-\left(\frac{N_{\mathcal{T}_{L}}}{N_{\mathcal{T}}} \operatorname{Gini}\left(\mathcal{T}_{L}\right)+\frac{N_{\mathcal{T}_{R}}}{N_{\mathcal{T}}} \operatorname{Gini}\left(\mathcal{T}_{R}\right)\right),
$$

where $N_{\mathcal{T}_{L}}, N_{\mathcal{T}_{R}}$ and $N_{\mathcal{T}}$ are the sample size for the corresponding node.

- Go through all variables $j$ and all cutting points $c$ to find the split with the best score
- Using rpart or tree, the magnitude of this score is reflected by the hight of each split (plot in page 13)


## Other Measures

- Gini index is not the only measurement
- Shannon entropy (ID3/C4.5)

$$
\operatorname{Entropy}(\mathcal{T})=-\sum_{k=1}^{K} \widehat{p}_{k} \log \left(\widehat{p}_{k}\right)
$$

- Similarly, we can use Shannon entropy to define the reduction of impurity and search for the best splitting rule
- There are other differences between C4.5 and CART, for example, C4.5 can create multiple child nodes from one node.
- Misclassification error

$$
\operatorname{Error}(\mathcal{T})=1-\max _{k=1, \ldots, K} \widehat{p}_{k}
$$

## Comparing Measures



## Comparing Measures

|  | Class 1 | Class 2 | $\widehat{p}_{1}$ | $\widehat{p}_{2}$ | Gini | Entropy | Error |
| :--- | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| $\mathcal{T}$ | 7 | 3 | $7 / 10$ | $3 / 10$ | 0.420 | 0.611 | 0.3 |
| $\mathcal{T}_{\text {left }}$ | 3 | 0 | $3 / 3$ | 0 | 0 | 0 | 0 |
| $\mathcal{T}_{\text {right }}$ | 4 | 3 | $4 / 7$ | $3 / 7$ | 0.490 | 0.683 | $3 / 7$ |

$$
\begin{aligned}
\text { score }_{\text {Gini }} & =0.420-(3 / 10 \cdot 0+7 / 10 \cdot 0.490)=0.077 \\
\text { score }_{\text {Entropy }} & =0.611-(3 / 10 \cdot 0+7 / 10 \cdot 0.683)=0.133 \\
\text { score }_{\text {Error }} & =3 / 10-(3 / 10 \cdot 0+7 / 10 \cdot 3 / 7)=0
\end{aligned}
$$

## Comparing Measures

- Gini index and Shannon Entropy are more sensitive to the changes in the node probability
- They prefer to create more "pure" nodes
- Misclassification error can be used for evaluating a tree, but may not be sensitive enough for building the tree.


## Categorical Predictors

- For categorical predictor $X^{(j)}$ talking values in $\{1, \ldots, M\}$, we search for a subset $A$ of $\{1, \ldots, M\}$, and evaluate the child nodes created by the splitting rule

$$
\mathbf{1}\left\{X^{(j)} \in A\right\}
$$

- Maximum of $2^{M-1}-1$ number of possible splits
- When $M$ is too large, this can be computationally intense.
- Some heuristic methods are used, such as randomly sample a subset of categories to one child node, and compare several random splits.


## Tree for Regressions

- When the outcomes $y_{i}$ 's are continuous, all we need is a corresponding impurity measure and score
- Consider the weighted variance reduction:

$$
\text { score }_{\operatorname{Var}}=\operatorname{Var}(\mathcal{T})-\left(\frac{N_{\mathcal{T}_{L}}}{N_{\mathcal{T}}} \operatorname{Var}\left(\mathcal{T}_{L}\right)+\frac{N_{\mathcal{T}_{R}}}{N_{\mathcal{T}}} \operatorname{Var}\left(\mathcal{T}_{R}\right)\right)
$$

where for any node $\mathcal{T}, \operatorname{Var}(\mathcal{T})$ is just the variance of the node samples:

$$
\operatorname{Var}(\mathcal{T})=\frac{1}{N_{\mathcal{T}}} \sum_{i \in \mathcal{T}}\left(y_{i}-\bar{y}_{\mathcal{T}}\right)^{2}
$$

## Overfitting and Tree Pruning

- A large tree (with many splits) can easily overfit the data
- Small tree may not capture important structures
- Tree size is measured by the number of splits
- Balancing tree size and accuracy is the same as the "loss + penalty" framework
- One possible approach is to split tree nodes only if the decrease in the loss exceed certain threshold, however this can be short-sighted
- A better approach is to grow a large tree, then prune it


## Cost-Complexity Pruning

- Fit the entire tree $T_{\max }$ (possibly one observation per terminal node). Specify a complexity parameter $\alpha$.
- For any sub-tree of $T_{\text {max }}$, denoted as $T \preceq T_{\text {max }}$, calculate

$$
\begin{aligned}
C_{\alpha}(T) & =\sum_{\text {all terminal nodes } t \text { in } T} N_{t} \cdot \operatorname{Impurity}(t)+\alpha|T| \\
& =C(T)+\alpha|T|
\end{aligned}
$$

where $N_{t}$ is the number of observations in $t,|T|$ is the size of $T$, i.e., the number of terminal nodes

- Find $T$ that minimize the $C_{\alpha}(T)$
- Large $\alpha$ results in small trees
- Choose $\alpha$ using CV


## Cost-Complexity Pruning

- We do not need to exhausting all possible sub-trees of $T_{\max }$ (computationally intense)
- Weakest-link cutting is used to find the best sub-tree:
- Look at an internal node $t$ of $T_{\max }$, and denote the entire branch starting from $t$ as $T_{t}$
- Compare: remove the entire branch (collapse $T_{t}$ into a single terminal node) vs. keep $T_{t}$

$$
\alpha \leq \frac{C(t)-C\left(T_{t}\right)}{\left|T_{t}\right|-1}
$$

- Cut the branch that has the smallest value on the right hand side (the smallest $\alpha$ ), then iterate
- Will provide a solution path of $\alpha$ (from smallest to largest).


## Missing Values

- If each variable has $5 \%$ chance have missing value, then with 50 variables, there are only $7.7 \%$ of the samples that has compete measures.
- Traditional approach is to discard observations with missing values, or impute them
- Tree-based method can handle them by either putting them as a separate category, or using surrogate variables whenever the splitting variable is missing.


## Remark

- Advantages of tree-based method:
- handles both categorical and continuous variables in a simple and natural way
- Invariant under all monotone transformations of variables
- Robust to outliers
- Flexible model structure, capture iterations, easy to interpret
- Limitations
- Small changes in the data can result in a very different series of splits
- Non-smooth. Some other techniques such as the multivariate adaptive regression splines (MARS, Friedman 1991) can be used to generate smoothed models.


## Random Forests

## Weak and Strong Learners

- Back in the mid-late 90's, researches started to investigate whether aggregated "weak learners" (unstable, less accurate) can be a "strong learner".
- Bagging, boosting, and random forests are all methods along this line.
- Bagging and random forests learn individual trees with some random perturbations, and "average" them.
- Boosting progressively learn models with small magnitude, then "add" them
- In general, Boosting, Random Forests $\succ$ Bagging $\succ$ Single Tree.


## Bagging Predictors

- Bagging stands for "Bootstrap aggregating"
- Draw $M$ bootstrap samples from the training dataset, fit CART to each, then average
- Motivation: CART is unstable as we discussed earlier, however, perturbing and averaging can improve stability and leads to better accuracy


## Ensemble of trees



## Bagging Predictors

- Bootstrap sample with replacement: some observations can be repeated multiple times. $\sim 63.2 \%$ unique samples
- Fit a CART model to each bootstrap sample (may require tuning using CV).
- To combine each learner, for classification problems:

$$
\widehat{f}_{\text {bag }}(x)=\text { Majority Vote }\left\{\widehat{f}_{b}(x)\right\}_{b=1}^{B},
$$

and for regression problems:

$$
\widehat{f}_{\mathrm{bag}}(x)=\frac{1}{B} \sum_{b=1}^{B} \widehat{f_{b}}(x),
$$

- Dramatically reduce the variance of individual learners
- CART can be replaced by other weak learners


## CART vs. Bagging



CART vs. Bagging on our previous example, both are pruned

## CART vs. Bagging



## Remarks about Bagging

- Bagging can dramatically reduce the variance of unstable "weak learners" like trees, leading to improved prediction
- The simple structure of trees will be lost due to bagging, hence it is not easy to interpret
- However, the performance of bagging is oftentimes not satisfactory. Why?
- Different trees have high correlation which makes averaging not very effective
- How to de-correlate trees?


## Random Forests

- Several articles came out in the late 90 's discussing the advantages of using random features.
- "The Random Subspace Method for Constructing Decision Forests" by Ho (1998) greatly influenced Breiman's idea of random forests
- In Ho's method, each tree is constructed using a randomly selected subset of features
- Random forests take a step forward: each splitting rule only consider a random subset


## Tuning parameters: mtry

- An important tuning parameter of random forests is mtry
- At each split, randomly select $m$ try variables from the entire set of features $\{1, \ldots, p\}$
- Search the best variable and splitting point out of these mtry variables
- Split and proceed to child nodes
- This procedure turns out working remarkably well, even in high-dimensional data


## Tuning parameters: $n_{\min }$

- Another important tuning parameter is $n_{\min }$ (terminal node size)
- Random forests does not perform pruning anymore
- Instead, splitting does not stop until the terminal node size is less or equal to $n_{\text {min }}$, and the entire tree is used.
- $n_{\text {min }}$ controls the trade-off between bias and variance in each tree
- In the most extreme case, $n_{\text {min }}=1$ means exactly fit each observation, but this is not 1-NN!
- Lin and Jeon (2004) formulate random forests as "potential nearest neighbor" (a much larger neighborhood than $k \mathrm{NN}$ )


## Tuning parameters

- A summary of important tuning parameters in Random forests (using R package randomForest)
- ntree : number of trees, set it to be large. Default 500.
- mtry: number of variables considered at each split. Default $p / 3$ for regression, $\sqrt{p}$ for classification.
- nodesize : terminal node size, same as $n_{\text {min }}$. Default 5 for regression, 1 for classification
- Overall, tuning is quite crucial in random forests


## CART vs. Bagging vs. RF



## CART vs. RF in regression



Model patients' length of stay (LOS) in hospital: Diagnosis (categorical) and Age (continuous)

## Variable Importance

- There is a build-in feature called variable importance that utilize the samples not selected by bootstrapping (out-of-bag data):
- For each tree $m$, use the out-of-bag data as the testing set to obtain the prediction error: $\mathrm{Err}_{0}^{m}$
- For each variable $j$, randomly permute its value among the testing samples, and recalculate the prediction error: $\mathrm{Err}_{j}^{m}$
- calculate for each $j$

$$
\mathrm{VI}_{m j}=\frac{\mathrm{Err}_{j}^{m}}{\mathrm{Err}_{0}^{m}}-1
$$

- Average $\mathrm{VI}_{m j}$ across all trees (index $m$ ) to get the importance of each variable $\mathrm{VI}_{\text {. }}{ }$


## Variable Importance

- In many practice areas, random forests variable importance measure is used extensively
- Usually the misclassification error is used instead of Gini index
- Higher VI means larger loss of accuracy due to the loss of information on $X^{(j)}$, hence more important.


## Variable Importance in RF



Same simulation setting as the "circle" example, with additional 48 noise variables.

## Additional Developments

- Random splitting point: Instead of searching through all possible cuts, we can just generate several random cutting points and choose the best among them (extremely randomized trees, Geurts et al., 2006). This is computationally much faster, especially for large dataset.
- Linear combination split: at each split, a linear combination $\beta^{\top} X$ is created and used as the splitting rule $\mathbf{1}\left\{\boldsymbol{\beta}^{\top} X \leq c\right\}$. The $\boldsymbol{\beta}$ estimations can be searched by a ridge regression (oblique random forests, Menze et al., 2011)


## Kernel View of RF

- Denote $\mathcal{A}=\left\{A_{k}\right\}_{k \in \mathcal{K}}$ the collection of all terminal nodes in a single tree, where $\mathcal{K}$ is a set of indices.
- Then, for any target point $x_{0}$, if $x_{0}$ falls into the a terminal node $A$, we would predict its outcome by node averaging:

$$
\widehat{f}\left(x_{0}\right)=\frac{\sum_{i=1}^{n} \mathbf{1}\left\{x_{i} \in A\right\} y_{i}}{\sum_{i=1}^{n} \mathbf{1}\left\{x_{i} \in A\right\}}
$$

- Note that there is a slight difference from the traditional RF, which is to average the node first than average over trees.


## Kernel View of RF

- Instead, we can define a random forest kernel:

$$
\begin{aligned}
\mathcal{A}\left(x_{i}, x_{0}\right) & =\sum_{k \in \mathcal{K}} \mathbf{1}\left\{x_{i} \in A_{k}\right\} \mathbf{1}\left\{x_{0} \in A_{k}\right\} \\
& = \begin{cases}1 & \text { if } \exists A \in \mathcal{A} \text { s.t. } x_{i}, x_{0} \in A \\
0 & \text { o.w. }\end{cases}
\end{aligned}
$$

- Then $\widehat{f}\left(x_{0}\right)$ can be expressed in the N-W kernel estimator form:

$$
\widehat{f}\left(x_{0}\right)=\frac{\sum_{i=1}^{n} \mathcal{A}\left(x_{i}, x_{0}\right) y_{i}}{\sum_{i=1}^{n} \mathcal{A}\left(x_{i}, x_{0}\right)}
$$

- We can extend this to the forest version by stacking the kernels
- However, $\mathcal{A}(\cdot, \cdot)$ is not invariant to location shift.


## Kernel View of RF



## Adaptiveness of RF kernel

- Random Forests is a kernel method with adaptive bandwidth:
- Each tree in a forests defines a kernel: uniform within each terminal node
- Ensemble: sum of kernels is still a kernel
- A tree is "more likely" to split on important variables, making their "bandwidth" smaller
- If the splitting variables are selected wisely, the bandwidth is adaptive to the signal strength
- The cutting point is more likely to happen on the curvature of the underlying target function
- In a high-dimensional sparse model, random forests performs better (both theoretically and practically) than those non-adaptive local methods


## Theoretical Cutting Points

Theoretical cutting points on a function (Ishwaran 2015) prefer places with steepest derivative.







