S&DS 265 / 565
Introductory Machine Learning

Trees and Forests

October 3

Reminders

- Assn 2 out; due Thursday at midnight
- Quiz 2 last week
- Midterm in class on Tuesday, October 17
- Questions?

Trees provide ways of modeling nonlinear relationships by carving out *rectangular regions* in the feature space.

Trees provide ways of modeling nonlinear relationships by carving out *rectangular regions* in the feature space.

Response variables can be categorical or quantitative

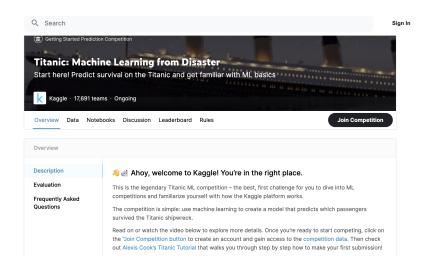
Trees provide ways of modeling nonlinear relationships by carving out *rectangular regions* in the feature space.

- Response variables can be categorical or quantitative
- Yields a set of interpretable decision rules

Trees provide ways of modeling nonlinear relationships by carving out *rectangular regions* in the feature space.

- Response variables can be categorical or quantitative
- Yields a set of interpretable decision rules
- Predictive ability is mediocre, but can be improved by combining multiple trees (resampling, ensemble methods)

Titanic data



Titanic data

- Survived: Outcome of survival (0 = No; 1 = Yes)
- Pclass: Socio-economic class (1 = Upper class; 2 = Middle class; 3 = Lower class)
- · Name: Name of passenger
- · Sex: Sex of the passenger
- . Age: Age of the passenger (Some entries contain NaN)
- · SibSp: Number of siblings and spouses of the passenger aboard
- Parch: Number of parents and children of the passenger aboard
- · Ticket: Ticket number of the passenger
- · Fare: Fare paid by the passenger
- . Cabin Cabin number of the passenger (Some entries contain NaN)
- Embarked: Port of embarkation of the passenger (C = Cherbourg; Q = Queenstown; S = Southampton)

Trees



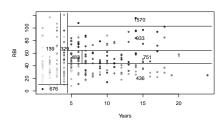
Trees



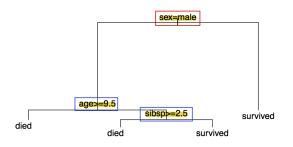
Trees



Modeling Titanic survival:

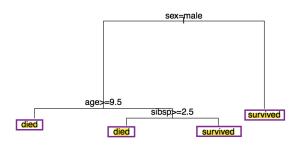


Internal nodes are points where the predictor space is split.

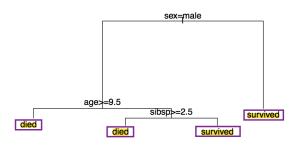


The internal node at the top is the **root** of the tree.

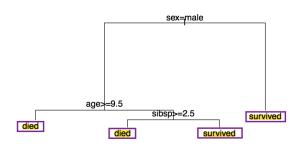
Terminal nodes (or **leaves**) are the ends of the tree where no further splitting occurs.



Terminal nodes (or **leaves**) are the ends of the tree where no further splitting occurs.



Denote these *J* regions as R_1, \ldots, R_J .



- $R_1 = \{i : sex_i = male \cap age_i \ge 9.5\}$
- $R_2 = \{i : \mathsf{sex}_i = \mathsf{male} \cap \mathsf{age}_i < 9.5 \cap \mathsf{sibsp}_i \ge 2.5\}$
- $R_3 = \{i : sex_i = male \cap age_i < 9.5 \cap sibsp_i < 2.5\}$
- $R_4 = \{i : \operatorname{sex}_i \neq \operatorname{male}\}$

Let's go to the Titanic demo

Bias-variance

- Nodes are split by greedily choosing the best question (greatest reduction in error)
- As tree is grown deeper, bias decreases
- But the variance increases
- How to choose the right size of tree?

Once we stop, we relabel the terminal nodes to be R_1, \ldots, R_J and compute \bar{y}_{R_i} (means within each region) to serve as \hat{y} values.

But when do we stop?

Once we stop, we relabel the terminal nodes to be R_1, \ldots, R_J and compute \bar{y}_{R_i} (means within each region) to serve as \hat{y} values.

But when do we stop?

Some possibilities:

number of observations in a node has reached a minimum

Once we stop, we relabel the terminal nodes to be R_1, \ldots, R_J and compute \bar{y}_{R_i} (means within each region) to serve as \hat{y} values.

But when do we stop?

Some possibilities:

- number of observations in a node has reached a minimum
- depth of tree has reached a maximum

Once we stop, we relabel the terminal nodes to be R_1, \ldots, R_J and compute \bar{y}_{R_i} (means within each region) to serve as \hat{y} values.

But when do we stop?

Some possibilities:

- number of observations in a node has reached a minimum
- depth of tree has reached a maximum
- grow until no further splits can reduce RSS by some amount

Once we stop, we relabel the terminal nodes to be R_1, \ldots, R_J and compute \bar{y}_{R_i} (means within each region) to serve as \hat{y} values.

But when do we stop?

Some possibilities:

- number of observations in a node has reached a minimum
- depth of tree has reached a maximum
- grow until no further splits can reduce RSS by some amount

Once we stop, we relabel the terminal nodes to be R_1, \ldots, R_J and compute \bar{y}_{R_i} (means within each region) to serve as \hat{y} values.

But when do we stop?

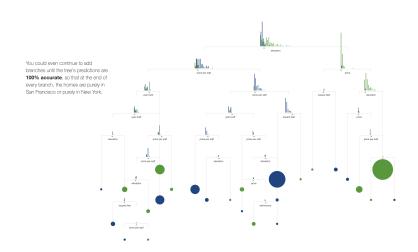
Some possibilities:

- number of observations in a node has reached a minimum
- depth of tree has reached a maximum
- grow until no further splits can reduce RSS by some amount

Many options – resulting in tuning parameters that are hard to deal with.

Another way to get around the overfitting problem is to grow a large tree and then **prune** it back.

Typically, pruning involves looking at subtrees of the fully-grown tree, and comparing how well the subtrees perform.



How do we prune?

How do we prune?

cross validation

How do we prune?

- cross validation
- cost-complexity pruning

Cost-complexity pruning

Minimize: Loss(
$$T$$
) + λ {# of nodes in T}
$$= \sum_{m=1}^{|T|} \sum_{i \in R_m} (y_i - \widehat{y}_{R_m})^2 + \lambda |T|$$

 λ is a tuning parameter that controls for the complexity of the model.

Cost-complexity pruning

Minimize: Loss(
$$T$$
) + λ {# of nodes in T}
$$= \sum_{m=1}^{|T|} \sum_{i \in R_m} (y_i - \hat{y}_{R_m})^2 + \lambda |T|$$

 λ is a tuning parameter that controls for the complexity of the model.

• $\lambda = 0$ implies the full tree

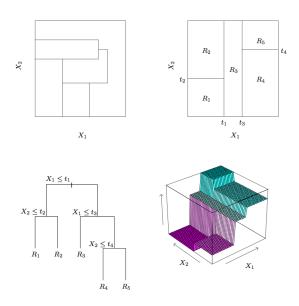
Cost-complexity pruning

Minimize: Loss(
$$T$$
) + λ {# of nodes in T}
$$= \sum_{m=1}^{|T|} \sum_{i \in R_m} (y_i - \hat{y}_{R_m})^2 + \lambda |T|$$

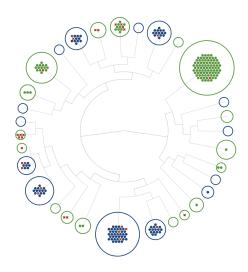
 λ is a tuning parameter that controls for the complexity of the model.

- $\lambda = 0$ implies the full tree
- Larger λ implies higher penalty for complexity of model

- Grow a big tree on a training set.
- ② Obtain a nested set of subtrees T_L ⊂ · · · ⊂ T₂ ⊂ T₁ ⊂ T₀ corresponding to a sequence of λ values.
- 3 Use (leave-one-out or k-fold) cross-validation to identify the subtree/ λ that does best.



Beautiful demo http://www.r2d3.us/



Trees vs. other methods

Decision trees are similar in spirit to *k*-nearest neighbors.

Trees vs. other methods

Decision trees are similar in spirit to *k*-nearest neighbors.

 Both produce simple predictions (averages/maximally occurring) based on "neighborhoods" in the predictor space.

Decision trees are similar in spirit to *k*-nearest neighbors.

- Both produce simple predictions (averages/maximally occurring) based on "neighborhoods" in the predictor space.
- Neighborhoods chosen very differently

Recall that linear regression fits models of the form

$$f(X) = \beta_0 + \sum_{j=1}^{p} X_j \beta_j$$

Recall that linear regression fits models of the form

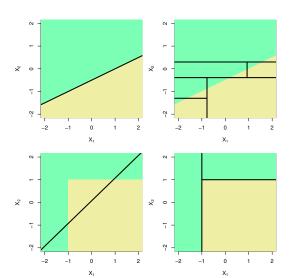
$$f(X) = \beta_0 + \sum_{j=1}^{p} X_j \beta_j$$

Regression trees are like fitting linear regression models with a bunch of indicators

$$f(X) = \sum_{j=1}^{J} \beta_j \mathbb{1} \left\{ X \in R_j \right\}$$

18

Are trees always better than linear methods?



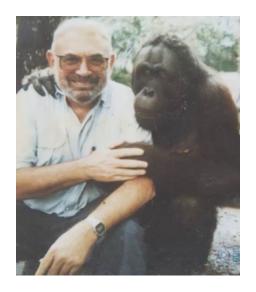
Summary so far

- Trees give interpretable, nonlinear prediction rules
- Deep trees have low bias, high variance
- Shallow trees have high bias, low variance
- Deep trees are pruned back using cross-validation to find best bias/variance tradeoff.

Random Forests

- Grow many trees and average their predictions
- Trees are grown deep, to have low bias, but high variance
- To "decorrelate" the predictors, each tree is
 - grown on a bootstrap sample of the data
 - grown with random subsets of the predictors at each split
- Tree growing can be done in parallel

Leo Breiman—"Keep it simple"



Random Forests Algorithm

- **1** For b = 1 to B:
 - (a) Draw a bootstrap sample Z^* of size n from the training data
 - (b) Grow a random-forest tree T_b to the bootstrapped data, recursively repeating following steps, until minimum node size reached:
 - i. Select *m* variables at random from the *p* variables
 - ii. Pick the best variable/split-point among the m
 - iii. Split the node into two children nodes
- 2 Output the ensemble of trees $\{T_b\}_{b=1}^B$.

Random Forests Algorithm

To make a prediction at a new point *x*:

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

Classification: Majority vote of the individual trees

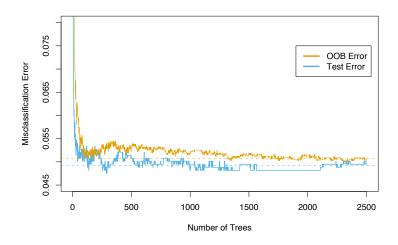
Out of bag (OOB) prediction

Each tree is grown on a random sample containing about $\frac{2}{3}$ of the original data. The remaining $\frac{1}{3}$ can be used as validation data

- For each observation $z_i = (x_i, y_i)$, construct its random forest predictor by averaging only those trees corresponding to bootstrap samples in which z_i did not appear
- Thus, cross-validation can be performed "along the way"

Chance a sample x_i does not appear in a bootstrap sample is $\left(1-\frac{1}{n}\right)^n \longrightarrow \frac{1}{e} \approx 0.37$

Out of bag (OOB) prediction



Performance on email spam task

Single tree: 8.7%

Random forests: 5.1%

(standard error of the estimates is $\approx 0.6\%$)

Random forests improve upon the predictive ability of trees, but kills off the interpretability of the model.

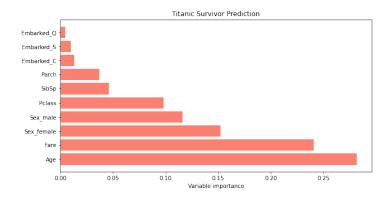
Random forests improve upon the predictive ability of trees, but kills off the interpretability of the model.

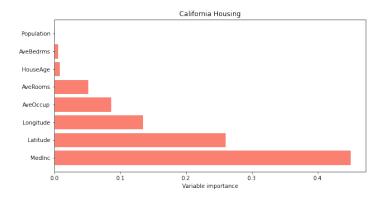
A good tool for interpreting a forest the **variable importance measure**.

Random forests improve upon the predictive ability of trees, but kills off the interpretability of the model.

A good tool for interpreting a forest the **variable importance measure**.

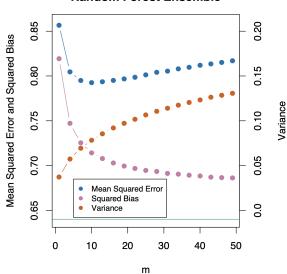
Variable importance can be measured by the amount that the RSS (or other loss) is reduced due to splits over a given predictor, averaged over all trees in the forest





Random forest MSE





Let's go to the notebook

```
In [1]: import numpy as np import matplotlib.pyplot as plt import pands as pd
```

In [2]: titanic_train = pd.read_csv('https://raw.githubusercontent.com/minsuk-heo/kaggle-titanic/master/input/train.csv')
titanic_test = pd.read_csv('https://raw.githubusercontent.com/minsuk-heo/kaggle-titanic/master/input/test.csv')
titanic_train

Out[2]:

	Passengerld	Survived	Pclass	Name	Sex	Age	SibSp	Parch	Ticket	Fare	Cabin	Embarked
0	1	0	3	Braund, Mr. Owen Harris	male	22.0	1	0	A/5 21171	7.2500	NaN	s
1	2	1	1	Curnings, Mrs. John Bradley (Florence Briggs Th	female	38.0	1	0	PC 17599	71.2833	C85	С
2	3	1	3	Heikkinen, Miss. Laina	female	26.0	0	0	STON/02. 3101282	7.9250	NaN	s
3	4	1	1	Futrelle, Mrs. Jacques Heath (Lily May Peel)	female	35.0	1	0	113803	53.1000	C123	s
4	5	0	3	Allen, Mr. William Henry	male	35.0	0	0	373450	8.0500	NaN	s
886	887	0	2	Montvila, Rev. Juozas	male	27.0	0	0	211536	13.0000	NaN	s
887	888	1	1	Graham, Miss. Margaret Edith	female	19.0	0	0	112053	30.0000	B42	s
888	889	0	3	Johnston, Miss. Catherine Helen "Carrie"	female	NaN	1	2	W./C. 6607	23.4500	NaN	s
889	890	1	1	Behr, Mr. Karl Howell	male	26.0	0	0	111369	30.0000	C148	С
890	891	0	3	Dooley, Mr. Patrick	male	32.0	0	0	370376	7.7500	NaN	Q

891 rows x 12 columns

Summary

- Trees give interpretable, nonlinear prediction rules
- Deep trees have low bias, high variance
- Random forests are a way of combining trees
- Want: Different trees should capture different aspects of the data
- How: Grow each tree on a random (bootstrap) sample of the data and choosing from a random set of questions at each split