S&DS 265 / 565 Introductory Machine Learning

Trees

October 4

Plan for this and next week

- Notes on assignments: select pages in Gradescope, rerun notebook, limit length of output, line wrap
- Assn 2 is out decision tree problem
- Quiz 3 Thursday; classification, GD, bias-variance, trees
- Midterm exam: Tuesday October 18 (in class); practice exams posted
- Questions?

You are here

4	Sept 20, 22	Stochastic gradient descent	CO SGD examples	Sept 20: Classification (continued) Sept 22: Stochastic gradient descent	ISL Section 6.2.2 ISL Section 10.7.2	Thu: Quiz 2
5	Sept 27, 29	Bias and variance, cross-validation	co Bias- variance tradeoff co Covid trends (revisited) co California housing	Sept 27: Bias and variance Sept 29: Cross-validation	ISL Section 2.2 ISL Section 5.1	Thu: Assn 1 in
6	Oct 4, 6	Tree-based methods	Trees and forests Visualizing trees	Oct 4: Trees Oct 6: Forests	ISL Sections 8.1, 8.2	Thu: Quiz 3
7	Oct 11, 13	PCA and dimension reduction	co PCA examples co PCA revisited co Used for regression	Oct 11: PCA Oct 13: PCA and review	ISL Section 12.2	Thu: Assn 2 in CO Assn3 out
8	Oct 18	Midterm exam (in class)			On Canvas: Practice midterm / Sample soln Midterm / Sample	

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



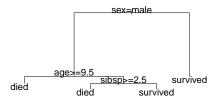
Trees



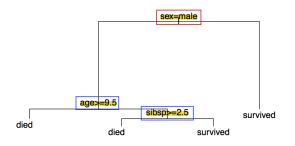
Trees



Modeling Titanic survival:

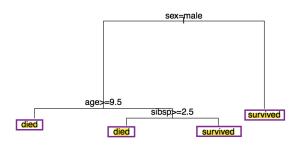


Internal nodes are points where the predictor space is split.

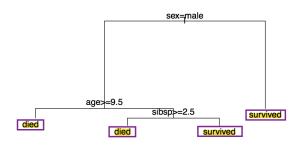


The internal node at the top is the **root** of the tree.

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

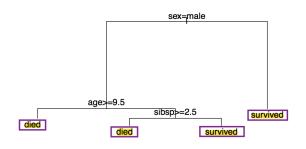


Terminal nodes (or **leaves**) are the ends of the tree where no further splitting occurs.



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

R



```
• R_1 = \{i : \text{sex}_i = \text{male} \cap \text{age}_i \ge 9.5\}

• R_2 = \{i : \text{sex}_i = \text{male} \cap \text{age}_i < 9.5 \cap \text{sibsp}_i \ge 2.5\}

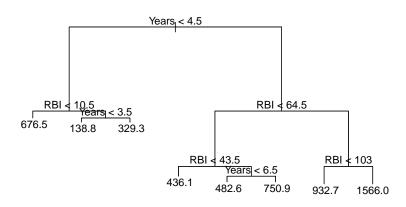
• R_3 = \{i : \text{sex}_i = \text{male} \cap \text{age}_i < 9.5 \cap \text{sibsp}_i < 2.5\}

• R_4 = \{i : \text{sex}_i \ne \text{male}\}
```

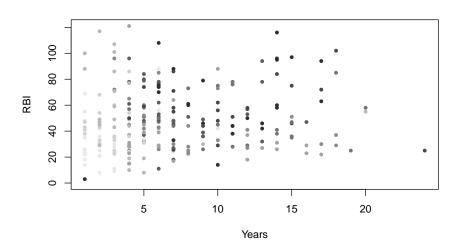
Let's go to the Titanic demo

Regression tree example

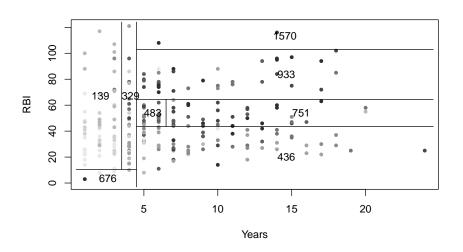
Baseball hitter salaries (in \$1,000s — old data!):



Regression tree example



Regression tree example



Trace each test observation into a leaf R_j based on the sequence of conditions. Predict \hat{y}_{R_i} for all observations in R_i .

Trace each test observation into a leaf R_j based on the sequence of conditions. Predict \hat{y}_{R_j} for all observations in R_j .

 \hat{y}_{R_j} is a function of all training observations *i* in R_j .

Trace each test observation into a leaf R_j based on the sequence of conditions. Predict \hat{y}_{R_j} for all observations in R_j .

 \hat{y}_{R_i} is a function of all training observations *i* in R_j .

• Regression: $\hat{y}_{R_j} = \bar{y}_{i:i \in R_j}$

Trace each test observation into a leaf R_j based on the sequence of conditions. Predict \hat{y}_{R_i} for all observations in R_i .

 \hat{y}_{R_i} is a function of all training observations i in R_j .

- Regression: $\hat{y}_{R_j} = \bar{y}_{i:i \in R_j}$
- Classification: $\widehat{y}_{R_j} = \text{most frequently occurring class } y_i \text{ for } i \in R_j$

Trace each test observation into a leaf R_j based on the sequence of conditions. Predict \hat{y}_{R_i} for all observations in R_i .

 \hat{y}_{R_i} is a function of all training observations i in R_j .

- Regression: $\hat{y}_{R_j} = \bar{y}_{i:i \in R_j}$
- Classification: $\widehat{y}_{R_j} = \text{most frequently occurring class } y_i \text{ for } i \in R_j$

Trace each test observation into a leaf R_j based on the sequence of conditions. Predict \hat{y}_{R_i} for all observations in R_i .

 \hat{y}_{R_i} is a function of all training observations i in R_j .

- Regression: $\hat{y}_{R_j} = \bar{y}_{i:i \in R_j}$
- Classification: $\hat{y}_{R_j} = \text{most frequently occurring class } y_i \text{ for } i \in R_j$

Fitting a tree boils down to identifying the appropriate set of regions R_1, \ldots, R_J that "best" describes the relationship between X and y.

Tree building

We want to choose R_1, \ldots, R_J to minimize error:

$$\textit{RSS} = \sum_{j=1}^J \sum_{i \in R_j} (y_i - \bar{y}_{R_j})^2$$

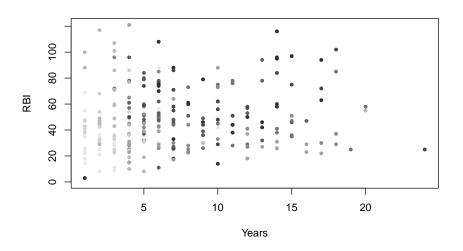
Tree building

We want to choose R_1, \ldots, R_J to minimize error:

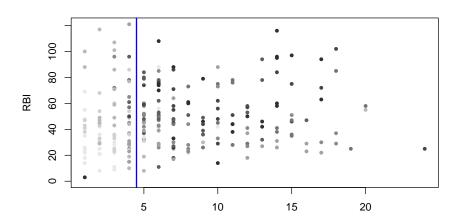
$$RSS = \sum_{j=1}^{J} \sum_{i \in R_j} (y_i - \bar{y}_{R_j})^2$$

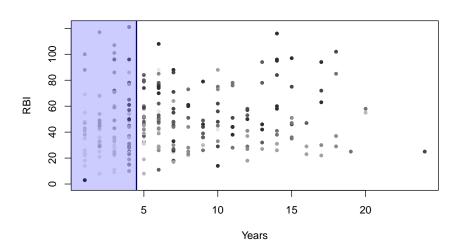
Tree building takes a *greedy* approach.

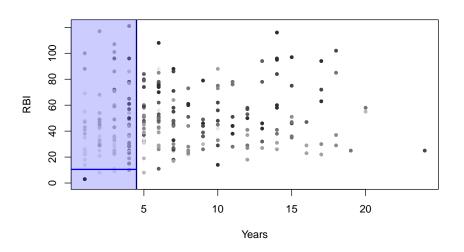
- Grow the tree by recursive binary splitting
- Prune back the tree

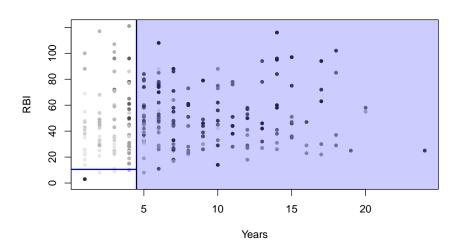


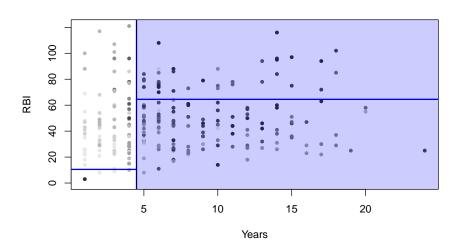
Where can we draw a horizontal or vertical line that best splits the data into two homogeneous parts?

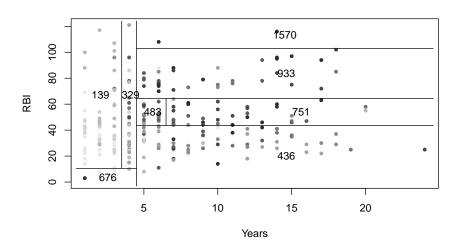












Tree growth (Regression)

① Cycle through predictors X_k for k = 1, ..., p. For each X_k ,

Tree growth (Regression)

- ① Cycle through predictors X_k for k = 1, ..., p. For each X_k ,
 - (Quantitative X_k) Consider cutpoints s (unique values of X_k) that divide up the region into two parts:

$$R_1(k, s) = \{i | X_{ik} < s\}$$
 and $R_2(k, s) = \{i | X_{ik} \ge s\}$

Tree growth (Regression)

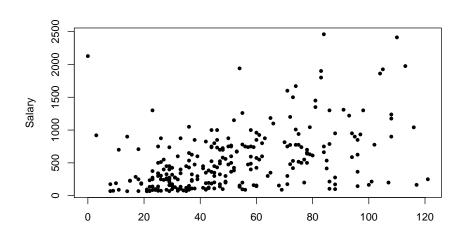
- ① Cycle through predictors X_k for k = 1, ..., p. For each X_k ,
 - (Quantitative X_k) Consider cutpoints s (unique values of X_k) that divide up the region into two parts:

$$R_1(k,s) = \{i | X_{ik} < s\}$$
 and $R_2(k,s) = \{i | X_{ik} \ge s\}$

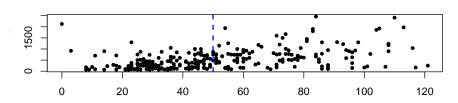
Evaluate (for regression trees):

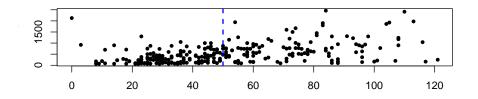
$$Q_k(s) = \sum_{i:i \in R_1(k,s)} (y_i - \bar{y}_{R_1})^2 + \sum_{i:i \in R_2(k,s)} (y_i - \bar{y}_{R_2})^2$$

$$Q_k(s) = \sum_{i:i \in R_1(k,s)} (y_i - ar{y}_{R_1})^2 + \sum_{i:i \in R_2(k,s)} (y_i - ar{y}_{R_2})^2$$



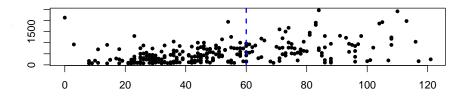
$$Q_k(s) = \sum_{i:i \in R_1(k,s)} (y_i - ar{y}_{R_1})^2 + \sum_{i:i \in R_2(k,s)} (y_i - ar{y}_{R_2})^2$$





- $R_1(RBI, 50)$: $\bar{y}_{R_1} = 359$
- $R_2(RBI, 50)$: $\bar{y}_{R_2} = 753$

$$Q_{RBI}(50) = \sum_{i:i \in R_1} (y_i - 359)^2 + \sum_{i:i \in R_2} (y_i - 753)^2$$
$$= 13015000 + 30186039$$
$$= 43201039$$



•
$$R_1(RBI, 60)$$
: $\bar{y}_{R_1} = 405$

•
$$R_2(RBI, 60)$$
: $\bar{y}_{R_2} = 802$

$$Q_{RBI}(60) = \sum_{i:i \in R_1} (y_i - 405)^2 + \sum_{i:i \in R_2} (y_i - 805)^2$$
$$= 19186489 + 24943383$$
$$= 44129872$$

Compute $Q_{RBI}(s)$ for all distinct values of RBI s.

Categorical predictors

If a predictor X_k is categorical, then cut points are modified.

Categorical predictors

If a predictor X_k is categorical, then cut points are modified.

Suppose X_k has unique values in $\{A, B, C, D, E\}$. Then, the possible splits include:

```
• {D} vs. {A, B, C, E}
```

- {*D*, *B*} vs. {*A*, *C*, *E*}
- ..

Categorical predictors

If a predictor X_k is categorical, then cut points are modified.

Suppose X_k has unique values in $\{A, B, C, D, E\}$. Then, the possible splits include:

- {*D*} vs. {*A*, *B*, *C*, *E*}
- {*D*, *B*} vs. {*A*, *C*, *E*}
- ..

Every possible partition of the set of unique values into 2 subsets is considered, and again we identify the split producing the lowest resulting RSS.

- **①** Cycle through predictors X_k for k = 1, ..., p. For each X_k :
 - (Quantitative X_k) Consider cutpoints s (unique values of X_k) that divide up the region into two parts:

$$R_1(k,s) = \{i | X_{ik} < s\}$$
 and $R_2(k,s) = \{i | X_{ik} \ge s\}$

Evaluate (for regression trees):

$$Q_k(s) = \sum_{i:i \in R_1(k,s)} (y_i - \bar{y}_{R_1})^2 + \sum_{i:i \in R_2(k,s)} (y_i - \bar{y}_{R_2})^2$$

Find the value of s that minimizes $Q_k(s)$. Call this s_k .

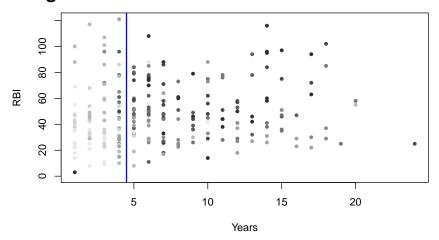
- **①** Cycle through predictors X_k for k = 1, ..., p. For each X_k :
 - (Quantitative X_k) Consider cutpoints s (unique values of X_k) that divide up the region into two parts:

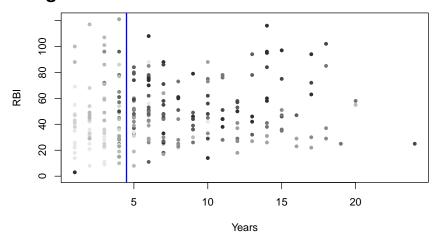
$$R_1(k,s) = \{i | X_{ik} < s\}$$
 and $R_2(k,s) = \{i | X_{ik} \ge s\}$

Evaluate (for regression trees):

$$Q_k(s) = \sum_{i:i \in R_1(k,s)} (y_i - \bar{y}_{R_1})^2 + \sum_{i:i \in R_2(k,s)} (y_i - \bar{y}_{R_2})^2$$

- ▶ Find the value of s that minimizes $Q_k(s)$. Call this s_k .
- 2 Find the predictor X_k with the minimum $Q_1(s_1), Q_2(s_2), \ldots, Q_p(s_p)$. Make the first binary partition along predictor X_k at cut point s_k .





Repeat the previous 2 steps on each of the resulting regions separately, iteratively. (Hence **recursive** binary partitioning.)

Bias-variance

Bias-variance

- 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.

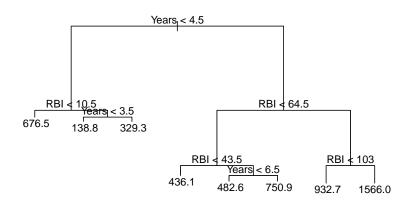
Another way to get around the overfitting problem is to grow a large tree and then **prune** it back.

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.

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

$$C(T) = \sum_{m=1}^{|T|} \sum_{i \in R_m} (y_i - \widehat{y}_{R_m})^2 + \alpha |T|$$

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

$$C(T) = \sum_{m=1}^{|T|} \sum_{i \in R_m} (y_i - \widehat{y}_{R_m})^2 + \alpha |T|$$

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

• $\alpha = 0$ implies the full tree

$$C(T) = \sum_{m=1}^{|T|} \sum_{i \in R_m} (y_i - \widehat{y}_{R_m})^2 + \alpha |T|$$

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

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

$$C(T) = \sum_{m=1}^{|T|} \sum_{i \in R_m} (y_i - \widehat{y}_{R_m})^2 + \alpha |T|$$

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

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

$$C(T) = \sum_{m=1}^{|T|} \sum_{i \in R_m} (y_i - \widehat{y}_{R_m})^2 + \alpha |T|$$

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

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

It is possible to efficiently identify a sequence of nested subtrees that are optimal for a sequence of increasing α .

- Grow a big tree on a training set.
- ② Obtain a nested set of subtrees $T_L \subset \cdots \subset T_2 \subset T_1 \subset T_0$ corresponding to a sequence of α values.
- 3 Use K-fold cross-validation to identify the subtree/ α that does best.

Issues with trees

- Instability. Trees can have high variance. As data change, tree topology can change dramatically, making interpretation difficult
- Lack of smoothness. The splits lead to a "jagged" decision boundary. More of a problem for regression than classification
- Difficulty capturing additive structure, where the regression function is a sum of terms

Demos

Some nice demonstrations of decision trees:

```
http://www.r2d3.us/
visual-intro-to-machine-learning-part-1/
http://www.r2d3.us/
visual-intro-to-machine-learning-part-2
```

Summary from today

- 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.