Pruning a tree

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- The process described above may produce good predictions on the training set, but is likely to *overfit* the data, leading to poor test set performance. Why?
- A smaller tree with fewer splits (that is, fewer regions R_1, \ldots, R_J) might lead to lower variance and better interpretation at the cost of a little bias.
- One possible alternative to the process described above is to grow the tree only so long as the decrease in the RSS due to each split exceeds some (high) threshold.
- This strategy will result in smaller trees, but is too short-sighted: a seemingly worthless split early on in the tree might be followed by a very good split that is, a split that leads to a large reduction in RSS later on.

Pruning a tree—continued

- A better strategy is to grow a very large tree T_0 , and then *prune* it back in order to obtain a *subtree*
- Cost complexity pruning also known as weakest link pruning is used to do this
- we consider a sequence of trees indexed by a nonnegative tuning parameter α . For each value of α there corresponds a subtree $T \subset T_0$ such that

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

is as small as possible. Here |T| indicates the number of terminal nodes of the tree T, R_m is the rectangle (i.e. the subset of predictor space) corresponding to the mth terminal node, and \hat{y}_{R_m} is the mean of the training observations in R_m .

Choosing the best subtree

- The tuning parameter α controls a trade-off between the subtree's complexity and its fit to the training data.
- We select an optimal value $\hat{\alpha}$ using cross-validation.
- We then return to the full data set and obtain the subtree corresponding to $\hat{\alpha}$.

Summary: tree algorithm

- 1. Use recursive binary splitting to grow a large tree on the training data, stopping only when each terminal node has fewer than some minimum number of observations.
- 2. Apply cost complexity pruning to the large tree in order to obtain a sequence of best subtrees, as a function of α .
- 3. Use K-fold cross-validation to choose α . For each $k=1,\ldots,K$:
 - 3.1 Repeat Steps 1 and 2 on the $\frac{K-1}{K}$ th fraction of the training data, excluding the kth fold.
 - 3.2 Evaluate the mean squared prediction error on the data in the left-out kth fold, as a function of α .

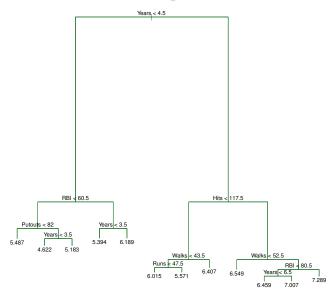
Average the results, and pick α to minimize the average error.

4. Return the subtree from Step 2 that corresponds to the chosen value of α .

Baseball example continued

- First, we randomly divided the data set in half, yielding 132 observations in the training set and 131 observations in the test set.
- We then built a large regression tree on the training data and varied α in in order to create subtrees with different numbers of terminal nodes.
- Finally, we performed six-fold cross-validation in order to estimate the cross-validated MSE of the trees as a function of α .

Baseball example continued



Baseball example continued

