RECSM Summer School: Machine Learning for Social Sciences

Session 2.4: Boosting

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1 Boosting

Algorithm What Is the Idea Behind boosting? Tuning Parameters for Boosting Example: Gene Expression Data

Boosting

- Like bagging, boosting is a general approach that can be applied to many machine learning methods for regression or classification.
- Recall that bagging creates multiple bootstrap training sets from the original training set, fits a separate tree to each bootstrap training set, and then combines all trees to create a single prediction.
- This means that each tree is built on a bootstrap sample, independent of the other trees.

- In boosting, the trees are grown sequentially: each tree is grown using information from previously grown trees.
- Boosting does not involve bootstrap sampling. Instead, each tree is fit on a modified version of the original data set.

Algorithm: Boosting for Regression Trees

1 Set $\hat{f}(x) = 0$ and $r_i = y_i$ for all i in the training set.

- **⊘** For b = 1, 2, ..., B, repeat:
 (a) Fit a tree f^b with d splits (d + 1 terminal nodes) to the training data (X, r).
 - (b) Update \hat{f} by adding in a shrunken version of the new tree

$$\hat{f}(x) \leftarrow \hat{f}(x) + \lambda \hat{f}^b(x).$$
 (2.4.1)

(c) Update the residuals

$$r_i \leftarrow r_i - \lambda \hat{f}^b(x_i). \tag{2.4.2}$$

Output the boosted model

$$\hat{f}(x) = \sum_{b=1}^{B} \lambda \hat{f}^{b}(x).$$
 (2.4.3)

- Unlike fitting a single large decision tree, which potentially overfits the data, boosting learns slowly.
- Given the current model, we fit a new decision tree to the residuals from that model (rather than the outcome Y).
- We then add the new decision tree into the fitted function in order to update the residuals.

- Each of the trees can be rather small, with just a few terminal nodes, determined by parameter *d*.
- Fitting small trees to the residuals means that we slowly improve \hat{f} in areas where it does not perform well.
- The shrinkage parameter λ slows the process even further, allowing more and different shaped trees to attack the residuals.

$\textcircled{\ } \textbf{Number of trees } B$

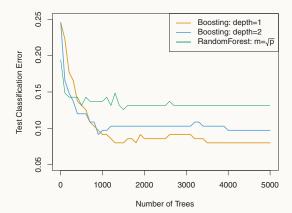
- Boosting can overfit if *B* is too large.
- Use CV to select B.
- **2** Shrinkage parameter λ
 - Controls the rate at which boosting learns.
 - A small positive number, typical values are 0.01 or 0.001.
 - Very small λ can require a very large value of B in order to achieve good performance.

3 Number of splits in each tree d

- Controls the complexity of the boosted ensemble.
- It is the interaction depth, since *d* splits can involve at most *d* variables.
- Often d = 1 works well, in which case each tree is a stump (consisting of a single split).

Example: Gene Expression Data

Boosting and Random Forests Results for the Gene Expression Data



(Boosting with stumps, if enough of them are included, outperforms the depth-two model. Both boosting models outperform a random forest. Source: James et al. 2013, 324)

For the two boosted models, $\lambda=0.01.$ Note that the test error rate for a single tree is 24%.