SF2930 Regression Analysis

Alexandre Chotard

Tree-based regression and classification

15 February 2018





Overview

Regression trees

Pruning

Bagging, random forests

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Let Y be a real-valued random variable. Given x ∈ X ⊂ R^d, we want to predict the value of Y.

▶ To understand how different values of x influence Y, we have $N \in \mathbb{N}^*$ examples $(x_i, y_i)_{i \in [1..N]}$.

Given ${\mathcal F}$ a family of functions and Q a cost function, solve

$$\min_{f\in\mathcal{F}}\sum_{i=1}^{N}Q(f(\boldsymbol{x}_{i}),y_{i})$$

The variable Y can have discrete or continuous values, corresponding respectively to classification and regression problems.



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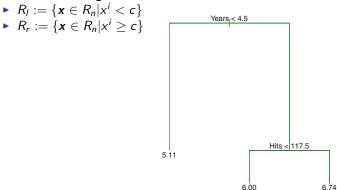
- ► We consider here binary decision trees. A decision tree partitions X into simple regions (R_j)_{j∈[1...]}. For
 - $m{x} = (x^1, \dots, x^d) \in \mathbb{R}^d$ and j such that $m{x} \in R_j$, the value predicted by the tree is
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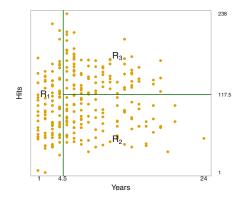
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• Each node *n* of the tree is associated to a subset R_n of \mathbb{X} , which is further split into two regions through a test comparing x^i for some $i \in [1..d]$ with a value $c \in \mathbb{R}$. Then for *I* and *r* left and right children of *n*,

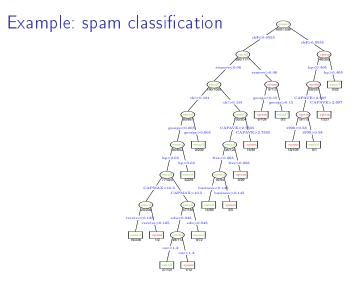


Figur: A regression tree for predicting the log salary (in 1,000\$) of a baseball player, based on the number of years played and the number of hits made in the previous year.





Figur: The three-region partition provided by the regression tree in the previous figure.



Figur: Tree for spam classification. Split variables are shown in blue. CAPMAX and CAPAVE = maximal and average length of the longest uninterrupted sequences of capital letters, respectively.



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Questions

- How do we construct such trees?
- How large should a tree be?
- What are the pros and cons of tree-based methods?



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Regression trees vs. linear regression

- We generally want to approximate a relation $Y = f(x) + \varepsilon$.
- Linear regression involves linear functions

$$f(\mathbf{x}) = \beta_0 + \sum_{j=1}^{p} \beta_j \mathbf{x}_j.$$

We will instead consider

$$f(\mathbf{x}) = \sum_{j=1}^{J} m_j \mathbb{1}_{R_j}(\mathbf{x}),$$

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Building a regression tree: cost function

We will construct the tree by minimizing

$$RSS(m_1, ..., m_J, R_1, ..., R_J) = \sum_{i=1}^N (y_i - f(\mathbf{x}_i))^2$$
$$= \sum_{j=1}^J \sum_{i: \mathbf{x}_i \in R_j} (y_i - f(\mathbf{x}_i))^2 = \sum_{j=1}^J \sum_{i: \mathbf{x}_i \in R_j} (y_i - m_j)^2.$$

► For each *j*, the m_j minimizing the sum of squares $\sum_{i:x_i \in R_j} (y_i - m_j)^2$ is always

 $m_j = \bar{y}_{R_j}$ = average over all y_i such that $x_i \in R_j$.

To find the minimizing R_j is however computationally infeasible in general.



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we proceed with a top-down, greedy approach.

In the first step, when splitting X into

 $R_1(k,s) = \{ \mathbf{x} \in \mathbb{X} : x^k < s \}$ and $R_2(k,s) = \{ \mathbf{x} \in \mathbb{X} : x^k \ge s \}$,

we minimize

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w.r.t. *k* and *s*.



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Building a regression tree: top-down minimization (cont.)

- For a given k, the optimal s is quite easily found by scanning though the data.
- Repeating for all $k \in [1..d]$ yields an optimal pair (k, s).
- Having found the best split, we partition the data into the two resulting regions and repeat the splitting process on each of these. And so forth.
- We stop growing the tree when some stopping criterion is reached, e.g., when no region contains more than five training data.



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Bias versus variance

- The tree size is a tuning parameter governing the model's complexity.
- A too large tree leads to overfitting (high variance on test sets), while a too small tree leads to high bias.
- The optimal tree size should be determined adaptively from the data.
- One possibility is to split a node only if the split implies an RSS reduction exceeding a certain threshold; this is however treacherous in top-down minimization, as an apparently meaningless split may imply a good split later on.



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Cost complexity pruning

- Grow a large tree T_0 while storing the different Q_{R_j} associated with each split.
- We define a subtree T ⊆ T₀ obtained by pruning T₀ in a bottom-up fashion.
- Let |T| denote the number of leaves $R_m(T)$ in T.
- Define, for some $\alpha \geq$ 0, the cost function

$$\mathsf{C}_{\alpha}(T) = \sum_{m=1}^{|T|} Q_{R_m(T)} + \alpha |T|,$$

where the $Q_{R_m(T)}$ are available from the first step. • The idea is to find a subtree T_{α} minimizing $C_{\alpha}(T)$.



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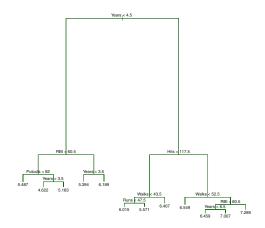
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Example: baseball player salaries (cont.)

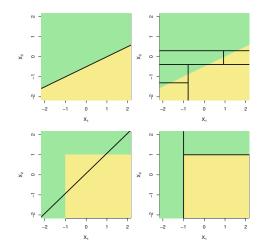


Figur: Unpruned tree for the log salary (in 1,000\$) of a baseball player.



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Trees vs. linear models



Figur: True decision boundary is indicated by the shaded regions. Linear boundary vs. decision tree (boxes).



Node impurity

- The task of growing a classification tree is very similar to that of growing a regression tree. The only difference is that the RSS is not meaningful any longer.
- ▶ We thus need to find alternative measures Q_m(T) of node impurity. For this purpose, define

$$\hat{p}_{j,k} = rac{1}{|R_j|} \sum_{i: \mathbf{x}_i \in R_j} \mathbb{1}_{\{y_i = k\}}$$
 and $k(j) = rg\max_k \hat{p}_{j,k}$

and let, e.g.,

 $Q_m(T) = \begin{cases} 1 - \hat{p}_{j,k(j)} & \text{misclassification} \\ \sum_{k=1}^{K} \hat{p}_{j,k}(1 - \hat{p}_{j,k}) & \text{Gini index,} \\ -\sum_{k=1}^{K} \hat{p}_{j,k} \log \hat{p}_{j,k} & \text{cross-entropy.} \end{cases}$



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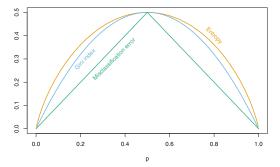
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Node impurity measures



Figur: Node impurity measures for two-class classification, as a function of the proportion p in class 2. (Cross-entropy has been scaled.)



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Pros and cons with tree-based methods

- Pros:
 - Easy to explain,
 - able to handle categorical or numerical data,
 - scales well with N
- ► Cons:
 - Do not, in their most basic form, have the same level of predictive accuracy as some other regression and classification approaches,
 - can be very non-robust (i.e., small changes in the data leads to completely different trees).
 - highly sensitive to data-representation: ill-suited to many problems
- The predictive accuracy can however be drastically improved using ideas as *bagging* and *random forests* discussed in the following.



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Prelude: the bootstrap

► Given an i.i.d. sample {x_i}^N_{i=1} from a probability density p, the bootstrap algorithm is based on the approximation

$$\hat{\rho}(\boldsymbol{x}) = \frac{1}{N} \sum_{i=1}^{N} \delta_{\boldsymbol{x}_i}(\boldsymbol{x})$$

of p

- ▶ Given p̂, a new sample set {x_i^{*}}_{i=1}^N with approximately the same distribution as {x_i}_{i=1}^N can be formed by sampling from p̂, i.e., by drawing repeatedly N times among {x_i}_{i=1}^N with replacement.
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Bagging

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$$f(\mathbf{x}) = \sum_{j=1}^{J} \bar{y}_{R_j} \mathbb{1}_{R_j}(\mathbf{x}),$$

where the partition $\{R_j\}_{j=1}^N$ is formed using a decision tree.

- The decision trees discussed above suffer generally from high variance, i.e., building the tree using a different training set may lead to a quite different f.
- Better would be to use B independent training sets of similar size, each yielding a tree f_b, and use the model

$$f_{\text{avg}}(\mathbf{x}) = \frac{1}{B} \sum_{b=1}^{B} f_b(\mathbf{x}).$$



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 We use bootstrap sampling for creating artificially B such training sets, each yielding a tree f^{*}_b, and use the model

$$f_{\text{bag}}(\boldsymbol{x}) = rac{1}{B}\sum_{b=1}^{B}f_{b}^{*}(\boldsymbol{x}).$$

- The trees f^{*}_b are grown deep without pruning, implying that each tree has high variance but low bias.
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- The number of trees B is not a critical parameter with bagging; using a very large value of B will not lead to overfitting.
- ► The reason is that the probability of making an error converges as B → ∞.
- The probability of making an error depends also on the expected correlation between errors of different trees f_b(x) and f_{b'}(x) when (x, Y) varies.



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Some theory

▶ Indeed, in the classification case, let the margin function be

$$m(\mathbf{x}, y) = \frac{1}{B} \sum_{b=1}^{B} \mathbb{1}_{\{f_b(\mathbf{x})=y\}} - \max_{k \neq y} \frac{1}{B} \sum_{b=1}^{B} \mathbb{1}_{\{f_b(\mathbf{x})=k\}}$$

Moreover, define the generalization error by

$$\mathsf{PE} = \mathbb{P}(m(\mathbf{x}, Y) < 0).$$

▶ breiman:2001 (breiman:2001) shows that PE converges as $B \rightarrow \infty$. In addition, the PE can be bounded as

$$\mathsf{PE} \leq (1-s^2)
ho/s^2$$
,

where, roughly, *s* is the limiting margin function—the *strength*—and ρ describes the expected *correlation* between the trees' errors as (x, Y) varies.



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Some theory

▶ Indeed, in the classification case, let the margin function be

$$m(\mathbf{x}, y) = \frac{1}{B} \sum_{b=1}^{B} \mathbb{1}_{\{f_b(\mathbf{x})=y\}} - \max_{k \neq y} \frac{1}{B} \sum_{b=1}^{B} \mathbb{1}_{\{f_b(\mathbf{x})=k\}}$$

Moreover, define the generalization error by

$$\mathsf{PE} = \mathbb{P}(m(\mathbf{x}, Y) < 0).$$

▶ breiman:2001 (breiman:2001) shows that PE converges as $B \rightarrow \infty$. In addition, the PE can be bounded as

$$\mathsf{PE} \leq (1-s^2)
ho/s^2$$
,

where, roughly, s is the limiting margin function—the strength—and ρ describes the expected correlation between the trees' errors as (x, Y) varies.



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- In order to *decorrelate* the trees, it is desirable so build them different.
- Say that there is one strong predictor xⁱ along with a number of other moderately strong predictors ⇒ most or all of the trees will use this strong predictor in the top split ⇒ all trees will look quite similar ⇒ highly correlated predictions.
- ► Thus, at each split, consider only splitting of a randomly chosen subset of m ≤ d predictors.
- ► Therefore, on average (d m)/d of the splits will not even consider the strong predictor, and so other predictors will have more of a chance.
- ▶ Typically, one uses $m \approx \sqrt{d}$; m = d corresponds to standard bagging.



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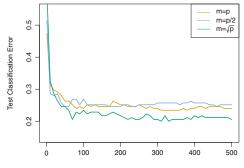
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Example: cancer-type prediction



Number of Trees

Figur: Here p = 500. The test error as a function of the number of trees. Each colored line corresponds to a different value of m. A single classification tree has an error rate of 45.7%.



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