Final_project_Bottino_Poetto_Spagliardi

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2023-06-07

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Tree-based methods partition the feature space into a set of rectangles, and then fit a simple model, say a constant, in each one. This is a simple yet powerful procedure since it is able to disentangle a model into simpler and smaller models and describe his features more accurately than global models do basically using binary conditional clustering. The geometric perspective described before can be seen as a tree where data are run and at each node a test is conducted to see what is the path a covariate should follow until reaching a leaf, which represents the final prediction explained by the constant model. For example, let's say we have p inputs and a response, for each of N observations: that is, (x_i, y_i) for $i = 1, 2, ..., N$, with $x_i = (x_{i1}, x_{i2}, ..., x_{ip})$. The algorithm has decide on the splitting variables and split points, as well as what shape the tree should have. Suppose first that we have a partition into M regions $R_1, R_2, ..., R_M$, and we model the response as a constant c_m in each region: As a criterion for optimal partitional we can minimize the sum of squares $\sum(y_i - f(x_i))^2$. In this way the best $\hat{c}_m$ is just the average of y_i in region R_m: $\hat{c}_m = av(y_i|x_i \in R_m)$. Our model will be then: $f(x) = \sum_{m=1}^{M} c_m \cdot I(x \in R_m)$.

Now finding the best binary partition in terms of minimum sum of squares is generally computationally infeasible so we can set up a CART (classification and regression tree) algorithm starting with the data, a splitting variable j, a split point s, and defining the half planes as: $R_1(j, s) = \{X \mid X_j \leq s\}$ and $R_2(j, s) = \{X \mid X_j > s\}$. Then we seek j and s that solve

$$\min_{j,s} \left[\min_{c_1} \sum_{x_i \in R_1(j,s)} (y_i - c_1)^2 + \min_{c_2} \sum_{x_i \in R_2(j,s)} (y_i - c_2)^2 \right]$$

For any choice j and s, the inner minimization is solved by:

$$\hat{c}_1 = \text{av}(y_i \,|\, x_i \in R_1(j,s)) \quad \text{and} \quad \hat{c}_2 = \text{av}(y_i \,|\, x_i \in R_2(j,s))$$

For each j, the split point s can be found very quickly and hence determination of the best pair (j, s) is feasible by brute force. Having found the best split, we partition the data into the two resulting regions and repeat the splitting process on each of the two regions. Then this process is repeated on all of the resulting regions. The question now become: how large should we grow the three? It is pretty straightforward that too many nodes (splits) may overfit the data while doing vice versa may end up not being able to capture them well, resulting in misprediction. One strategy could be to set a lower threshold for the decrease of the sum of squares and stop the splitting when this is reached. However this strategy is too short sighted since a seemingly worthless split may lead to a very good one below. A more robust strategy may be to do kind of the opposite: grow a very large tree and then use a cost-complexity pruning criterion to collapse one internal node at a time from the full tree until the single node tree so that we find a sequence. It is intuitive that the optimal tree must be somewhere in the sequence. Now, with a cross validation selection method, we can find the actual optimal tree just minimizing the cross validated sum of squares.

This is how the CART algorithm for growing decision trees basically works. Note that decision trees are divided in classification and regression trees if the response is a factor or a numerical or continous variable. Below it is proposed a very basic implementation of a CART algorithm using mean squared error cost complexity criterion. The algorithm is not implemented to prune the tree.

visuals bagging application - model setting (paragrafo 5+ fig1)

2 Data Exploratory Analysis (DEA)

This data can be used to compare with cancer genes and label these data to predict and diagnose cancers such as breast cancer and also to diagnose the stage of different cancers. Also, from the expression of these DNAs, artificial intelligence models can be obtained that can predict future mutations in any disease, or find the mechanisms of protein production and their gene ontology, and treat, diagnose and predict the disease such as cancer.

3 References

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