Using Pairs of Data-Points to Define Splits for Decision Trees

Geoffrey E. Hinton and Michael Revow
Department of Computer Science
University of Toronto
Toronto, Ontario, M5S 1A4, Canada
hinton@cs.toronto.edu, revow@cs.toronto.edu

Abstract

Conventional binary classification trees such as CART either split the data using axis-aligned hyperplanes or they perform a computationally expensive search in the continuous space of completely unrestricted hyperplanes. We show that the limitations of the former can be overcome without resorting to the latter. For every pair of training data-points, there is one hyperplane that is orthogonal to the line joining the data-points and bisects this line. In a comparison on a suite of 12 datasets we found that this method of generating candidate splits outperformed axis-aligned splits, particularly when the training sets are data limited.

1 Introduction

Binary decision trees come in many flavours, but they all rely on splitting the set of k-dimensional data-points at each internal node into two disjoint sets. Each split is usually performed by projecting the data onto some direction in the k-dimensional space and then thresholding the scalar value of the projection. There are two commonly used methods of picking a projection direction. The simplest method is to restrict the allowable directions to the k axes defined by the data. This is the default method used in CART [1]. If this set of directions is too restrictive, the usual alternative is to search general directions in the full k-dimensional space or general directions in a space defined by a subset of the k axes.

Projections onto one of the k axes defined by the the data have many advantages over projections onto a more general direction:

1. It is very efficient to perform the projection for each of the data-points. We simply ignore the values of the data-point on the other axes.
2. For N data-points, it is feasible to consider all possible axis-aligned projections and thresholds because there are only k possible projections and for each of these there are at most $N-1$ threshold values that yield different splits. Selecting from a fixed set of projections and thresholds is simpler than searching the k-dimensional continuous space of hyperplanes that correspond to unrestricted projections and thresholds.
3. Since a split is selected from only about Nk candidates, it takes only about $\log_2 N + \log_2 k$ bits to define the split. So it is possible to use many more of these axis-aligned splits before overfitting occurs than if we use more general hyperplanes. If the data-points are in general position, each subset of size k defines a different hyperplane so there are $N!/k!(N-k)!$ distinctly different hyperplanes and if $k << N$ it takes approximately $k \log_2 N$ bits to specify one of them.

For some data sets, the restriction to axis-aligned projections is too limiting. This is especially true for high-dimensional data, like images, in which there are strong correlations between the intensities of neighboring pixels. In such cases, many axis-aligned boundaries may be required to approximate a planar boundary that is not axis-aligned, so it is natural to consider unrestricted projections and some versions of the CART program allow this. Unfortunately this greatly increases the computational burden and the search may get trapped in local minima. Also significant care must be exercised to avoid overfitting. There is, however, an intermediate approach which allows the projections to be non-axis-aligned but preserves all three of the attractive properties of axis-aligned projections: It is trivial to decide which side of the resulting hyperplane a given data-point lies on; the hyperplanes can be selected from a modest-sized set of sensible candidates; and hence many splits can be used before overfitting occurs because only a few bits are required to specify each split.

2 Using two data-points to define a projection

Each pair of data-points defines a direction in the data space. This direction is a plausible candidate for a projection to be used in splitting the data, especially if it is a classification task and the two data-points are in different classes. For each such direction, we could consider all of the $N-1$ possible thresholds that would give different splits, or, to save time and reduce complexity, we could only consider the threshold value that is halfway between the two data-points that define the projection. If we use this threshold value, each pair of data-points defines exactly one hyperplane and we call the two data-points the "poles" of this hyperplane.

For a general k-dimensional hyperplane it requires $O(k)$ operations to decide whether a data-point, C, is on one side or the other. But we can save a factor of k by using hyperplanes defined by pairs of data-points. If we already know the distances of C from each of the two poles, A, B then we only need to compare these two distances (see figure 1). [1] So if we are willing to do $O(kN^2)$ operations to

---

[1] If the threshold value is not midway between the poles, we can still save a factor of k but we need to compute $(d_{AC}^2 - d_{BC}^2)/2d_{AB}$ instead of just the sign of this expression.

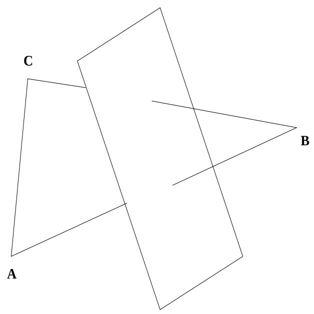

Figure 1: A hyperplane orthogonal to the line joining points A and B. We can quickly determine on which side a test point, C, lies by comparing the distances AC and BC.

compute all the pairwise distances between the data-points, we can then decide in constant time which side of the hyperplane a point lies on.

As we are building the decision tree, we need to compute the gain in performance from using each possible split at each existing terminal node. Since all the terminal nodes combined contain N data-points and there are $N(N-1)/2$ possible splits this takes time $O(N^3)$ instead of $O(kN^3)$. So the work in computing all the pairwise distances is trivial compared with the savings.

Using the Minimum Description Length framework, it is clear that pole-pair splits can be described very cheaply, so a lot of them can be used before overfitting occurs. When applying MDL to a supervised learning task we can assume that the receiver gets to see the input vectors for free. It is only the output vectors that need to be communicated. So if splits are selected from a set of $N(N-1)/2$ possibilities that is determined by the input vectors, it takes only about $2\log_2 N$ bits to communicate a split to a receiver. Even if we allow all N possible threshold values along the projection defined by two data-points, it takes only about $3\log_2 N$ bits. So the number of these splits that can be used before overfitting occurs should be greater by a factor of about $k/2$ or $k/3$ than for general hyperplanes. Assuming that $k << N$, the same line of argument suggests that even more axis-aligned planes can be used, but only by a factor of about 2 or 3.

To summarize, the hyperplanes planes defined by pairs of data-points are computationally convenient and seem like natural candidates for good splits. They overcome the major weakness of axis-aligned splits and, because they can be specified in a modest number of bits, they may be more effective than fully general hyperplanes.

3 Building the decision tree

We want to compare the “pole-pair” method of generating candidate hyperplanes with the standard axis-aligned method and the method that uses unrestricted hyperplanes. We can see no reason to expect strong interactions between the method of building the tree and the method of generating the candidate hyperplanes, but to minimize confounding effects we always use exactly the same method of building the decision tree.

We faithfully followed the method described in [1], except for a small modification where the code that was kindly supplied by Leo Breiman departed from the description in the book.

Training a decision tree involves two distinct stages. In the first stage, nodes are repeatedly split until each terminal node is "pure" which means that all of its datapoints belong to the same class. The pure tree therefore fits the training data perfectly. A node is split by considering all candidate decision planes and choosing the one that maximizes the decrease in impurity. Breiman *et. al* recommend using the *Gini* index to measure impurity. [2] If $p(j|t)$ is the probability of class j at node t, then the Gini index is $1 - \sum_j p^2(j|t)$.

Clearly the tree obtained at the end of the first stage will overfit the data and so in the second stage the tree is pruned by recombining nodes. For a tree, T_i, with $|T_i|$ terminal nodes we consider the regularized cost:

$$C = E + \alpha |T_i| \tag{1}$$

where E is the classification error and α is a pruning parameter. In "weakest-link" pruning the terminal nodes are eliminated in the order which keeps (1) minimal as α increases. This leads to a particular sequence, $T = \{T_1, T_2, ...T_k\}$ of subtrees, in which $|T_1| > |T_2| ... > |T_k|$. We call this the "main" sequence of subtrees because they are trained on *all* of the training data.

The last remaining issue to be resolved is which tree in the main sequence to use. The simplest method is to use a separate validation set and choose the tree size that gives best classification on it. Unfortunately, many of the data sets we used were too small to hold back a reserved validation set. So we always used 10-fold cross validation to pick the size of the tree. We first grew 10 different subsidiary trees until their terminal nodes were pure, using 9/10 of the data for training each of them. Then we pruned back each of these pure subsidiary trees, as above, producing 10 sequences of subsidiary subtrees. These subsidiary sequences could then be used for estimating the performance of each subtree in the main sequence. For each of the main subtrees, T_i, we found the largest tree in each subsidiary sequence that was no larger than T_i and estimated the performance of T_i to be the average of the performance achieved by each subsidiary subtree on the 1/10 of the data that was not used for training that subsidiary tree. We then chose the T_i that achieved the best performance estimate and used it on the test set. Results are expressed as the ratio of the test error rate to the baseline rate which is the error rate of a tree with only a single terminal node.

4 The Data Sets

Eleven data sets were selected from the database of machine learning tasks maintained by the University of California at Irvine (see the appendix for a detailed description of the data sets used). Except as noted in the appendix, the data sets were used exactly in the form of the distribution as of June 1993. All data sets have

---

[2] Impurity is not an information measure but, like an information measure, it is minimized when all the nodes are pure and maximized when all classes at each node have equal probability.

only continuous attributes and there are no missing values.[3] The synthetic "waves" example [1] was added as a twelfth data set.

Table 1 gives a brief description of the data sets. The first column gives a two letter abbreviation for the dataset. The following columns give the total number of instances, number of classes and number of attributes respectively.

Database	Size (N)	Classes (c)	Attributes (k)
IR	150	3	4
TR	215	3	5
LV	345	2	6
DB	768	2	8
BC	683	2	9
GL	163	2	9
VW	990	11	10
WN	178	3	13
VH	846	4	18
WV	2100	3	21
IS	351	2	34
SN	208	2	60

Table 1: Data sets used in comparisons

A few data sets in the original distribution have designated training and testing subsets while others do not. To ensure regularity among data sets, we pooled all usable examples in a given data set, randomized the order in the pool and then divided the pool into training and testing sets. Two divisions were considered. The *large* training division had $\frac{2}{3}$ of the the pooled examples allocated data to the training set and $\frac{1}{3}$ in the testing set. The *small* training division had $\frac{1}{3}$ of the data in the training set and $\frac{2}{3}$ in the testing set.

5 Results

Table 2 give the error rates, expressed as a percentage of the base rates for both the *large* and *small* divisions of the data.

In both the *small* and *large* training divisions of the datasets, the pole pair method had lower error rates than axis aligned or linear cart in the majority of datasets tested. While these results are interesting, they do not provide any measure of confidence that one method performs better or worse than another. Since all methods were trained and tested use the same data, we can perform a two-tailed *McNemar test* [2] on the predictions for pairs of methods. The resulting P-values are given in table 3. Again the conclusion is that neither axis aligned nor linear cart significantly outperform the pole pair method in the majority of cases.

---

[3] In the BC dataset we removed the case identification number attribute and had to delete 16 cases with missing values.

Database	Small Train			Large Train		
	cart	linear	pole	cart	linear	pole
IR	14.3	14.3	4.3	5.6	5.6	5.6
TR	36.6	26.8	14.6	33.3	33.3	20.8
LV	88.9	100.0	100.0	108.7	87.0	97.8
DB	85.8	82.2	87.0	69.7	69.7	59.6
BC	12.8	14.1	8.3	15.7	12.0	9.6
GL	62.5	81.3	89.6	46.4	46.4	35.7
VW	31.8	37.7	30.0	21.4	26.2	19.2
WN	17.8	13.7	11.0	14.7	11.8	14.7
VH	42.5	46.5	44.2	36.2	43.9	40.7
WV	28.9	25.8	24.3	30.6	24.8	26.6
IS	44.0	31.0	41.7	21.4	23.8	42.9
SN	65.2	71.2	48.5	48.4	45.2	48.4

Table 2: Relative error rates expressed as a percentage of the baseline rate on the small and large training sets.

6 Discussion

In section 2, we subtly motivated the pole pair method as choosing a decision hyperplane so that the poles normal to the decision plane are *representative* of the classes that the hyperplane must differentiate. This implies that candidate hyperplanes should be generated by considering only those pairs whose poles come from *different* classes. An alternative strategy is to disregard class membership, and consider *all* possible pole pairs.

Another variant of the method arises depending on whether the inputs are scaled (for example so that all input dimensions have the same variance). Axis aligned CART is indifferent to scalings along the dimensions, but clearly the pole pair method (and linear CART) are scale dependent. We investigated both variations of the basic method, but found that the results were very similar to the basic method presented above.

Table 3 suggest that pole pair method is only superior to the conventional forms of CART only when there is a limited amount of training data available. This conclusion may be misleading as the size of the test sets in the large training set case was much smaller than with the small training set and so the result may be simply be a consequence of the difficulty in demonstrating significant difference with limited amount of *testing* data.

To summarize, we have demonstrated that the pole pair method is a simple, effective method for choosing a projection direction at binary tree nodes. It may also be an effective way for choosing a projection direction (ie the incoming weights) for continuous valued units in a neural network.

Small Training

	IR	TR	LV	DB	BC	GL	VW	WN	VH	WV	IS	SN
Axis-**Pole**	**.02**	**.02**	.18	.46	.06	*.02*	.24	.15	.33	.07	**.00**	.44
Linear-**Pole**	**.02**	.13	1.0	.26	**.02**	.30	**.00**	.41	.27	**.02**	.17	.09
Axis-**Linear**	1.0	.06	.18	.30	.40	*.00*	*.00*	.31	.08	.32	**.03**	**.02**

Large Training

	IR	TR	LV	DB	BC	GL	VW	WN	VH	WV	IS	SN
Axis-**Pole**	.75	.23	.29	**.04**	.11	.29	.26	.69	.14	.60	.08	*.02*
Linear-**Pole**	.75	.23	.26	**.04**	.25	.30	**.01**	.50	.25	.50	.26	*.05*
Axis-**Linear**	1.0	1.0	.07	1.0	.29	.69	.06	.50	*.03*	.50	**.01**	.50

Table 3: P-Values using a two-tailed *McNemar* test on the *small* (top) and *large* (bottom) training sets. Each row gives P-values when the methods in the left most column are compared. A significant difference at the $P = 0.05$ level is indicated by printing the P-value in *italic* (**bold**) face depending on whether the first (second) mentioned method in the first column had superior performance. For example, in the top most row, the pole pair method was significantly better than the axis aligned method on the TR dataset.

A Databases used in the study

IR - Iris plant database. Predict the class of iris plant. A classical but simple domain.

TR - Thyroid gland data. Classify patient thyroids as normal, hypothyroidism or hyperthyroidism based on serum, hormonal, etc levels.

LV - BUPA liver disorders. Predict normality/abnormality of a liver from blood tests.

DB - Pima Indians Diabetes. Predict presence/absence of diabetes in adult females of Pima Indian heritage.

BC - Breast cancer database from the University of Wisconsin Hospitals, Madison from Dr. William H. Wolberg [3]. Classify as benign/malignant cases based on cell measurements. The 16 cases having missing values were removed for the experiments reported here. The sample code number attribute included in the database was not used.

GL - Glass identification database. Predict type of glass from composition and optical properties. In these experiments we only considered the classification into float/nonfloat processed glass, ignoring other types of glass.

VW - Vowel recognition. Classify 11 vowel sounds from log area parameters of the input speech waveform. The original task was to perform speaker independent vowel recognition. However the process of pooling all training and testing data resulted in the task no longer being speaker independent.

WN - Wine recognition. Predict wine class from a chemical analysis.

VH - Vehicle silhouettes. Discriminate between model cars and buses based on features extracted from silhouettes images.

WV - Waveform example. This is the only synthetic database and is taken directly from [1].

IS - Johns Hopkins University Ionosphere database. Binary classification task as to whether radar pulses encountered free electrons in the ionosphere or not based on the autocorrelation of the received signals.

SN - Sonar, Mines versus. Rocks. Classify returned sonar signals as reflected from metal or rock cylinders based on the energy of the sonar signal in different frequency bands. In these experiments we did not control for aspect-angle.

Acknowledgments

We thank Leo Breiman for kindly making his CART code available to us. This research was funded by the Institute for Robotics and Intelligent Systems and by NSERC. Hinton is the Noranda fellow of the Canadian Institute for Advanced Research.

References

References

[1] L. Breiman, J. H. Freidman, R. A. Olshen, and C. J. Stone. *Classification and regression trees*. Wadsworth international Group, Belmont, California, 1984.

[2] J. L. Fleiss. *Statistical methods for rates and proportions*. Second edition. Wiley, 1981.

[3] O. L. Mangasarian and W. H. Wolberg. Cancer diagnosis via linear programming. *SIAM News*, 23(5):1 & 18, 1990.