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Skewing: An Efficient Alternative to Lookahead for Decision Tree Induction

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Abstract

This paper presents a novel, promising approach that allows greedy decision tree induction algorithms to handle problematic functions such as parity functions. *Lookahead* is the standard approach to addressing difficult functions for greedy decision tree learners. Nevertheless, this approach is limited to very small problematic functions or subfunctions (2 or 3 variables), because the time complexity grows more than exponentially with the depth of lookahead. In contrast, the approach presented in this paper carries only a constant run-time penalty. Experiments indicate that the approach is effective with only modest amounts of data for problematic functions or subfunctions of up to six or seven variables, where the examples themselves may contain numerous other (irrelevant) variables as well.

1 Introduction

Algorithms for the top-down induction of decision trees (TDIDT) are among the most widely used algorithms for machine learning, data mining and statistical classification. TDIDT implementations such as ID3 [Quinlan, 1983], C4.5 [Quinlan, 1997], C5.0 (www.rulequest.com) and CART [Breiman *et al.*, 1984] are easy to use and (often) produce human-comprehensible models. Nevertheless, TDIDT algorithms are well-known to be myopic because of their greedy strategy for choosing split variables, or internal node labels. This myopia is at its worst when the data are labeled according to parity functions such as exclusive-or (2-bit odd parity, denoted by $\oplus$). These and related other problematic functions naturally arise in real-world data. For example, in fruitfly experiments, flies that are *either* male and have an active *Sxl* gene *or* that are female and have an inactive *Sxl* gene survive, while other flies die; hence survival is an exclusive-or function of gender and *Sxl* activity (Table 1).

Gender Female	Sxl active	Survival
0	0	0
0	1	1
1	0	1
1	1	0

Table 1: Truth table for *Drosophila* (fruitfly) survival based on gender and *Sxl* gene activity.

Of course, parity and parity-like functions are also problematic for other machine learning or statistical algorithms that employ (explicitly or implicitly) a linear assumption in order to gain efficiency. Such models include perceptrons, logistic regression, linear support vector machines, Fischer's linear discriminant and naive Bayes. They also include any of a variety of data analysis approaches that employ an information gain or Kullback-Leibler divergence filter to do variable selection or to control computation time, for example as in the sparse candidate algorithm for learning Bayesian networks [Friedman *et al.*, 1999]. The inability of such approaches to learn functions like $\oplus$ is frequently noted, for example, in the context of analyzing gene expression microarray data [Friedman *et al.*, 1999; Szallasi, 2001].

In TDIDT algorithms, the myopia of the search can be reduced at the cost of increased computation time. The standard approach is through depth-k lookahead [Norton, 1989], where the default for TDIDT algorithms is depth-1 lookahead. However, the time to perform a split grows exponentially with k, and problematic functions remain no matter how large a k is chosen.

The purpose of this paper is to introduce an alternative approach to problematic functions such as parity, which does not incur the high computational cost of lookahead. The approach relies on the observation that these functions are not actually problematic if the distribution over the data is significantly different from uniform. In such cases other functions may become problematic for TDIDT algorithms, but functions such as exclusive-or become relatively easy. Hence we first observe that TDIDT algorithm performance on a data set can be improved if the algorithm has access to a second, significantly different distribution over the data. Of course such a second distribution often is unavailable. Therefore, we next show how the second distribution often can be simulated by *skewing* the data from the first distribution. We note that the present paper focuses entirely on classification, ignoring regression trees, or trees that predict continuous outputs at their leaves. Furthermore, we limit our entire discussion to TDIDT algorithms that perform only binary splits, although the data may use variables that can take more than two values.

x_1	x_2	x_3	f
0	0	0	1
1	0	1	0
0	1	0	0
0	1	1	1

Table 2: For subfunctions at each of $x_2 = 0$, $x_2 = 1$, $x_3 = 0$ and $x_3 = 1$, the fraction of assignments that are positive is $\frac{1}{2}$, as for f itself. Hence x_2 and x_3 have zero gain, while x_1 has nonzero gain according to both entropy and Gini.

2 Review of Lookahead for Hard Functions

We assume the reader is familiar with the approach of TDIDT algorithms. The assumed familiarity includes a knowledge of the commonly-used functions to measure node purity, such as entropy [Quinlan, 1997] or Gini index [Breiman *et al.*, 1984]. It also includes familiarity with the greedy heuristic of choosing to split on the variable that maximizes the improvement, or *gain*, in the node purity score. We now review the notions of problematic functions and lookahead. For ease of discussion, this section limits itself to two-class problems, where the classes are *positive* and *negative*.

For the various node purity functions employed by different TDIDT algorithms, splitting on a variable x_i can yield a non-zero gain only if the class distribution changes for at least one of the values (or ranges) that x_i can take. If the distribution of classes is the same for every value of x_i (or range) then x_i will have zero gain according to any node purity measure in common usage. As an example, in Table 2 the variable x_1 has non-zero gain according to either Gini or entropy, whereas the variables x_2 and x_3 have zero gain.

Consider a data set drawn from a uniform distribution over binary-valued variables $x_1, x_2 \cdots x_{100}$, labeled according to the target function $x_{99} \oplus x_{100}$. Even if we are fortunate enough to have a *complete data set*—one occurrence of each truth assignment over $x_1 \cdots x_{100}$—it is clear that for every variable x_i, the class distribution is exactly the same whether x_i is 0 or 1. So, regardless of how large a uniform sample we choose to draw, a variable will have non-zero gain only because of chance. Thus, the probability that one of the *correct* variables (x_{99} or x_{100}) will have a higher gain than every one of the *incorrect* variables is extremely low. Hence the learning task is virtually impossible for a TDIDT algorithm.

With depth-2 lookahead the preceding task becomes trivial. A depth-2 lookahead from a given node chooses not only the next split variable, but also the split variables at the next level. A TDIDT algorithm augmented in this way will consider among the possible depth-2 trees the two shown in Figure 1, each of which will have the maximum possible gain. For any reasonably large data set, with high probability all other depth-2 trees will have gain only marginally different from zero. Hence we see that with depth-2 lookahead, $\oplus$ becomes easy. Because depth-2 lookahead is repeated at every step in tree construction, many other functions that have 2-variable $\oplus$ as a subfunction become easy.

Of course, depth-2 lookahead comes with a price. Where n is the number of variables and m is the number of examples, the time to choose the split goes from $O(mn)$ to $O(mn^3)$, be-

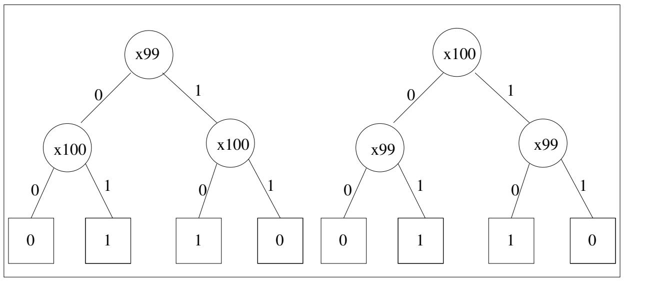


Figure 1: Two trees representing $x_{99} \oplus x_{100}$

x_1	x_2	x_3	f_1	f_2	f_3	f_4	f_5	f_6
0	0	0	0	0	0	0	1	0
0	0	1	1	1	1	0	0	0
0	1	0	1	0	1	1	0	0
0	1	1	0	0	0	0	0	1
1	0	0	0	0	1	0	0	1
1	0	1	1	0	0	1	0	0
1	1	0	1	1	0	0	0	0
1	1	1	0	0	1	0	1	0

Table 3: Six of the 12 functions over three variables that are problematic even using depth-2 lookahead. The other six problematic functions are the inverses of these.

cause labels have to be selected for three nodes from among n variables. Furthermore, there are many functions that require a higher lookahead. For example, suppose we have examples constructed from variables $x_1 \cdots x_{100}$ and the target is one of the functions in Table 3 involving x_1, x_2, and x_3. Even with depth-2 lookahead, TDIDT is highly likely to choose incorrect variables. These problems can be solved with depth-3 lookahead, but the time to choose a split becomes $O(mn^7)$, and other problematic targets remain even then.[1]

3 Motivation for Skewing

Consider the first target function discussed in the previous section, $x_{99} \oplus x_{100}$, but now suppose the data are distributed differently from uniform. For example, we might introduce dependencies not present in the uniform distribution: for every odd number i, $1 \leq i \leq 99$, if x_i is 0 then x_{i+1} has probability 0.99 of being 1. Or we might suppose all variables are independent as in the uniform distribution, but every variable has probability only $\frac{1}{4}$ of taking the value 0. In either case, with a large enough sample we expect that the class distribution among examples with $x_{99} = 0$ will differ significantly from the class distribution among examples with $x_{99} = 1$.

To examine the preceding claim more closely, consider the second distribution, where each variable has probability $\frac{1}{4}$ of being 0. If we draw a sample of 400 examples, we expect roughly 100 of these to have $x_{99} = 0$ and roughly 300 to

[1] We can reduce this super-exponential growth of lookahead to "mere" exponential growth and still address parity-like functions if we require the tree to be "leveled"—all nodes at a level are labeled by the same variable. But even this non-standard lookahead procedure imposes a high computational burden.

have $x_{99} = 1$. Of the 100 with $x_{99} = 0$, we expect roughly $\frac{3}{4}$ of these, or 75, to have $x_{100} = 1$ and hence to belong to the positive class. Of the 300 with $x_{99} = 1$, we expect only $\frac{1}{4}$ of these, or 75 again, to belong to the positive class (to have $x_{100} = 0$). Hence the fraction of positive examples is quite different for the two values of x_{99}: $\frac{3}{4}$ of the examples with $x_{99} = 0$ are positive, while $\frac{1}{4}$ of the examples with $x_{99} = 1$ are positive. As a result x_{99} (and x_{100}) will have non-zero gain; for instance, information gain is roughly 0.19 (out of maximum 1.0 possible) and Gini gain is roughly 0.06 (out of maximum 0.25 possible). On the other hand, every variable other than x_{99} or x_{100} is likely to have nearly zero gain. Hence unless a highly unlikely sample is drawn, a TDIDT algorithm will choose to split on either x_{99} or x_{100}, at which point the remainder of the learning task is trivial.

Notice that in the preceding discussion, moving to our second distribution changed the marginal distribution for *every* variable, not just for those in the target. It would have revealed the correct variables if the target function had been $x_2 \oplus x_{69}$ or even one of the problematic functions of three variables in Table 3. Notice also that the important aspect of the second distribution was that it changed the frequency distributions for the variables; the specific change for any variable could have gone the other way—to probability $\frac{3}{4}$ of taking value 0—and the second distribution still would have given non-zero gain to exactly the variables in the target.

From the preceding discussion we conclude that if we have access to two distributions that are "different enough," then choosing good variables to split on becomes relatively easy. However, in real-world problems we rarely have access to two different distributions over the data, or the ability to request data according to a second distribution that we choose. Instead, the next section discusses how in practice we can simulate a second distribution different from the first. We call this procedure *skewing*. The simulation approach tends to magnify idiosyncrasies in the data set, for example, introducing some dependencies that were not present in the original distribution. Nevertheless, our experiments indicate that, if the data set is large enough, the magnification of idiosyncrasies is not a major problem.

4 Skewing Algorithm

The desired effect of the skewing procedure is that the skewed data set should exhibit significantly different frequencies from the original data set. Because we cannot draw new examples, we change the frequency distributions for variables by attaching various weights to the existing examples. The procedure initializes the weight of every example to 1. We next present the details of the re-weighting procedure for binary-valued variables only. Nominal variables can be converted to binary variables. We discuss extensions to continuous variables in Section 7.

We may assume that every variable takes the value 0 in at least one example and takes the value 1 in at least one example—otherwise, the variable carries no information and can be removed. For each variable x_i, $1 \leq i \leq n$, we randomly, uniformly (independently for each variable) select a "favored setting" v_i of either 0 or 1. We then increase the weight of each example in which x_i takes the value v_i, by multiplying the weight by a constant; for the sake of illustration, suppose we double the weight.

At the end of this process, each example has a weight between 1 and 2^n. It is likely that each variable has a significantly different weighted frequency distribution than previously, as desired. But this is not guaranteed. For example, suppose the original data set consists of 100 truth assignments over variables x_1 and x_2. Suppose further that in half of these examples $x_1 = 0$ and $x_2 = 1$, and in the other half $x_1 = 1$ and $x_2 = 0$. If the favored setting for each variable happens to be 1, then all examples get assigned weight 2, so the new frequency distribution for each variable is the same as the original frequency distribution. In addition to this potential difficulty, a second difficulty is that this process can magnify idiosyncrasies in the original data. For instance, suppose we have a data set over $x_1, ..., x_n$, and (for simplicity) the favored setting for each variable is 1. If we happen to have one example with many variables set to 1, it will get an inordinately high weight compared with other examples, potentially giving some insignificant variable a high gain. Can we mitigate these potential problems with the skewing procedure?

The difficulties in the preceding paragraph occur with some data sets combined with some choices of favored settings. Other selections of favored settings for the same data set may leave other variables' frequencies unchanged, but it is relatively unlikely they will leave the same variables' frequencies unchanged. Furthermore, while other selections of favored settings may magnify other idiosyncrasies in the data, it is unlikely they will magnify the same idiosyncrasies. Therefore, instead of using skewing to create only a second distribution, we use it to create k additional distributions, for small k such as 9 to give a total of 10 distributions. The k different distributions come about from randomly (without replacement) selecting k different combinations of favored settings for the n variables according to a uniform distribution. To ensure that tree construction is not thrown off course by any single bad distribution (either original or skewed), the tree construction process is modified as described in the following paragraph.

Suppose we have $k + 1$ weightings of the data (the original data set plus k reweighted versions of this data set), and we are considering a split. We score each of the n variables against each of the $k + 1$ weightings of the data. A variable that is not part of the target function should have nearly zero gain on every weighting, although as already noted, it may occur that on some weightings some of these variables can achieve high gain. But only variables that appear in the target should have significantly non-zero gain on *most* of the weightings (though not necessarily on all). Therefore, we set a *gain threshold*, and the variable that exceeds the gain threshold for the greatest number of weightings is selected as the split variable. Our expectation is that the selected variable is highly likely to be *correct* in the sense that it actually is a part of the target function. Yet the time for choosing the split remains $O(mn)$, in contrast to lookahead. We have increased the run-time only by a small constant.

Pseudocode for the algorithm is shown in Algorithm 1. Rather than actually doubling or tripling weights, the algorithm takes a parameter $\frac{1}{2} < s < 1$. The weight of an ex-

Algorithm 1 Skewing Algorithm

Input: A matrix D of m data points over n boolean variables, gain fraction G, number of trials T, skew $\frac{1}{2} < s < 1$
Output: A variable x_i to split on, or -1 if no variable with sufficient gain could be found

```
N ⇐ Entropy of class variable in D
v ⇐ Variable with max gain in D
g ⇐ Gain of v in D
if g < G × N then
    v ⇐ −1
for i = 1 to n do
    F(i) ⇐ 0
{begin skewing loop}
for t = 1 to T do
    for i = 1 to n do
        V(i) ⇐ Randomly chosen favored value for x_i
    for e = 1 to m do
        W(e) = 1
        for i = 1 to n do
            if t > 1 then
                if D(e,i) = V(i) then
                    W(e) ⇐ W(e) × s
                else
                    W(e) ⇐ W(e) × (1 − s)
    N ⇐ Entropy of class variable in D under W
    for i = 1 to n do
        E ⇐ Gain of x_i under distribution W
        if E ≥ G × N then
            F(i) ⇐ F(i) + 1
{end skewing loop}
j ⇐ arg max F(i)
if F(j) > 0 then
    return x_j
else
    return v
```

ample is multiplied by s if x_i takes preferred value v_i in the example, and is multiplied by $1 - s$ otherwise. Hence for illustration, if s is $\frac{2}{3}$, the weight of every example in which x_i takes value v_i is effectively doubled relative to examples in which x_i does not take value v_i.

Our conjecture is that in practical experiments the new algorithm will run somewhat slower than an ordinary TDIDT algorithm, only by a constant factor. It will rarely produce trees with lower accuracy than those of an ordinary TDIDT algorithm. It will often produce trees with slightly to moderately higher accuracy—when the target contains one or more problematic subfunctions. And it will sometimes produce trees with much higher accuracy—when the target is itself a problematic function. When the target is a problematic function over many variables, even after skewing the gain of any individual variable in the target is likely to be small. Therefore, we also conjecture that unless the data set is large, the benefits of the skewing approach will not apply to problematic target functions of five or more variables. Note that while a large number of variables in the *target* reduces the potential gain, the number of variables in the *examples* does not. The following section describes the experiments designed to test the preceding conjectures.

5 Experiments

In this section, we discuss experiments with synthetic and real data, designed to test the conjectures in the preceding paragraph. In addition, the question arises of whether problematic functions or subfunctions occur with high enough frequency to justify the additional work of skewing. The experiments in this section also address that question. We begin with a discussion of experiments using synthetic data, where target functions as well as examples are drawn randomly and uniformly, with replacement. In these experiments we compare simple ID3 against ID3 with skewing. We selected ID3 to eliminate issues to do with more sophisticated pruning. The parameters input to the skewing algorithm (algorithm 1) were $T = 30$, $s = \frac{3}{4}$ and $G = 0.05$. These parameters were chosen before the experiments and were held constant across all experiments. Improved results could perhaps be obtained by tuning s and G.

In the first set of experiments with synthetic data, examples are generated according to a uniform distribution over 30 binary variables. Target functions are drawn by randomly generating DNF formulae over subsets of 3 to 6 of the 30 variables. The number of terms in each target is drawn randomly, uniformly from between 1 and 25, and each term is drawn by choosing for each variable whether it will appear negated, unnegated, or not at all (all with equal probabilities). All targets are ensured to be satisfiable. Examples over the 30 variables that satisfy the target are labeled *positive*, and all other examples are labeled *negative*. Figures 2-5 show learning curves for different target sizes. Each point on each curve is the average over several runs, each with a different target and with a different sample of the specified sample size.

In general, these figures fit our expectations. Both algorithms perform well but skewing provides slightly yet consistently better results (we note that the differences are not statistically significant). Probably the difference is skewed ID3 is less likely than ordinary ID3 to include irrelevant variables, particularly when faced with problematic functions. One surprise is that the figures indicate that an ordinary TDIDT algorithm outperforms skewing on average when the sample size is small relative to target size. As sample size grows, a crossover point is reached after which skewing consistently outperforms the ordinary TDIDT algorithm. Furthermore, the sample size required for effective skewing grows with the number of variables in the target, although these results alone do not make clear the order of this growth. It may well be exponential, because target complexity can grow exponentially with the number of variables in the target. Further experiments explore the order of this growth. This observation implies a limitation of skewing—that skewing may be undesirable for learning tasks with small samples or target concepts that potentially employ many variables.

The next set of experiments focuses on the problematic functions alone. The methodology is the same as before, with the following exception. Targets are drawn randomly from functions that can be described entirely by variable co-

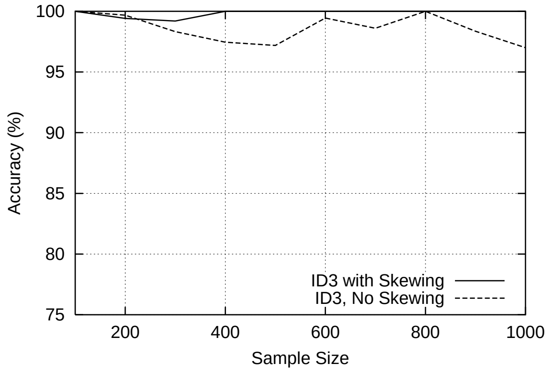


Figure 2: Three-Variable Targets

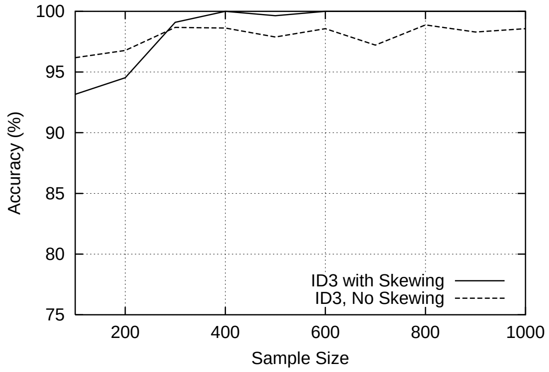


Figure 3: Four-Variable Targets

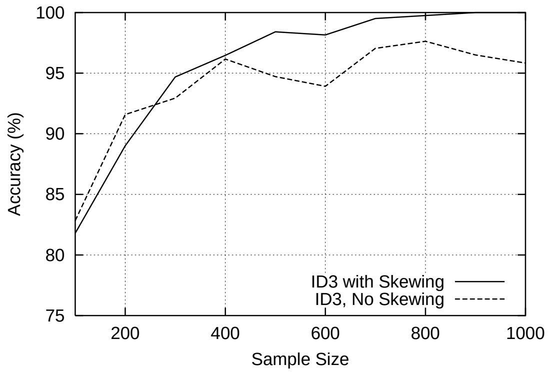


Figure 4: Five-Variable Targets

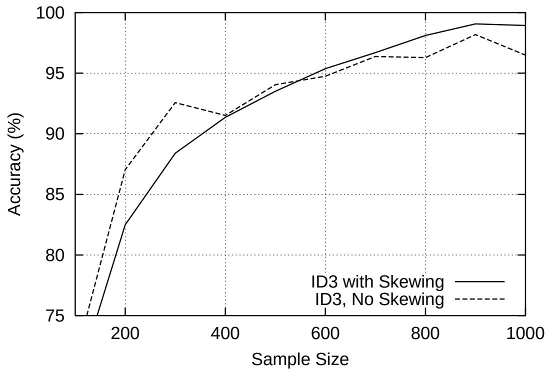


Figure 5: Six-Variable Targets

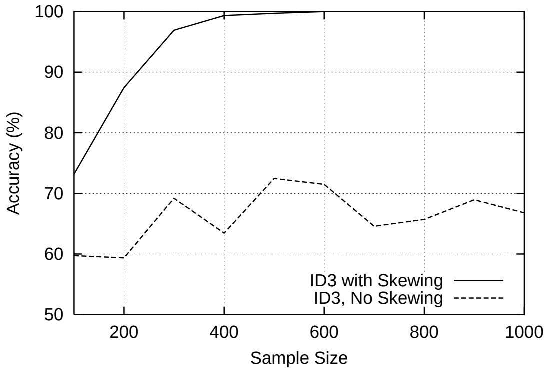


Figure 6: Three-Variable Hard Targets

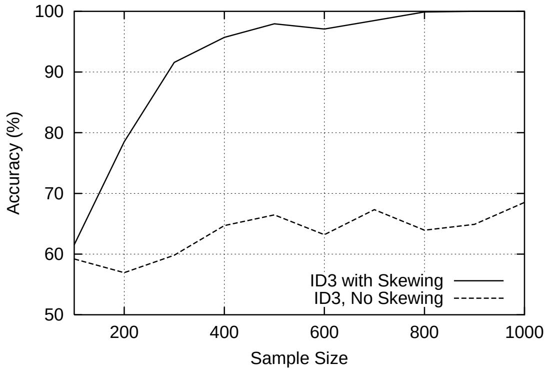


Figure 7: Four-Variable Hard Targets

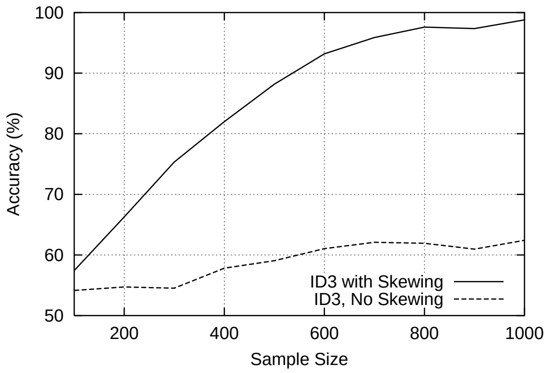


Figure 8: Five-Variable Hard Targets

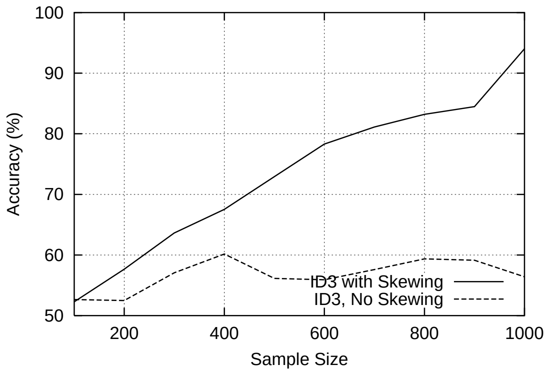


Figure 9: Six-Variable Hard Targets

Data Set	Standard ID3	ID3 with Skewing
Heart	71.9	74.5
Voting	94.0	94.2
Voting-2	87.4	88.6
Contra	60.4	61.5
Monks-1	92.6	100.0
Monks-2	86.5	89.3
Monks-3	89.8	91.7

Table 4: Accuracies of ID3 and ID3 with skewing on 4 UCI data sets. Heart is Cleveland Heart Disease, Voting is Congressional Voting, Contra is Contraceptive Method Choice, and Monks-*x* are the Monk's problems. Voting-2 is the same as Voting, with one feature (`physician-fee-freeze`) removed to make the problem more difficult.

references together with the standard logical connectives *and*, *or*, and *not*. Many such functions exist, and for all such functions, even given a complete data set, no variable has gain. Examples of such functions are exclusive-or and exclusive-nor, and all those in Table 3. Figures 6-9 show the results for these experiments.

We observe that if the target is a problematic function, skewing outperforms standard ID3 by a wide margin. The difference in accuracy was statistically significant — the 95% confidence intervals around each sample point in these graphs do not overlap once the sample sizes become moderately large. We repeated the experiment with 6-variable hard targets with 5000 examples to verify that skewing did indeed achieve 100% accuracy (in our noise-free setting) in this case. We also verified this behavior for 7 and 8 variable targets.

In addition to the preceding experiments, we also compared ID3 against ID3 with skewing on several data sets in the UCI machine learning repository [Blake and Merz, 1998] using 5-fold cross validation. For these data sets, we discretized continuous variables by binning. Further, nominal variables were binarized using the standard 1-of-N representation. The results of these experiments appear in Table 5. In this case, we do not know whether the target concepts involve problematic subfunctions except for the concepts in the Monk's problems, where the first two involve problematic subfunctions. The only task for which there is a significant difference in accuracy is the first Monk's problem, which has an exclusive-or subfunction. We believe the reason ID3 with skewing does not dramatically outperform ID3 on the second Monk's problem is that the number of training instances is small (169) relative to the target function. We verified this by constructing a larger data set of 2000 examples using the concept that generated this data. In this case, skewing achieves an accuracy of 95%, while standard ID3 achieves 80%.

In the experiments reported in Figures 2-5, the run-time for ID3 with skewing was on average a constant times the run-time for ordinary ID3, regardless of sample size or target size. This constant was (roughly) equal to our value for T in Algorithm 1, 30. In the experiments involving hard targets, we observed that as sample size increased, ID3 with skewing became more efficient relative to ID3. This can be explained by the fact that though it takes more time to choose a split, ID3 with skewing chooses many fewer splits when the target

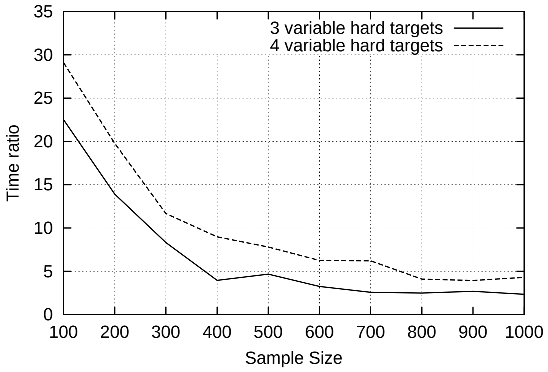


Figure 10: Time complexity of ID3 with skewing relative to standard ID3 for hard targets. The y axis represents the ratio of the average time taken by ID3 with skewing to induce a tree against the same quantity for standard ID3 for hard targets. Observe that, though the ratio is close to our value for T for small samples, it drops rapidly as the sample size increases, and the final value is much smaller.

is a hard function. In this case, the constant-factor overhead for skewing is significantly smaller than T. This behavior is shown in Figure 10. Thus in all cases, provided the sample is sufficiently large, skewing provides benefits similar to lookahead, but with only a constant increase in run-time. This is the primary result of the paper.

6 Related Work

A natural question to ask of the preceding results is whether they could as easily be obtained by other techniques that effectively re-weight the data. We know of two such related techniques: boosting [Freund and Schapire, 1997] and bagging [Breiman, 1996] (sampling with replacement may be thought of as providing a re-weighting of the data).While these techniques were not developed to enable tree induction algorithms to address problematic functions, it is possible that their re-weighting schemes might nevertheless be successful in this task. Therefore, we ran ID3 with each of these re-weighting techniques on hard targets, using the same methodology as in the preceding section. We also ran ID3 with a procedure that randomly reweighted the data as in the data perturbation approaches of Elidan et al[2002]. We observed that ID3 with each of the three re-weighting schemes performed on average no better than ordinary ID3. Hence we conclude that the benefit of skewing comes from the type of re-weighting being performed, not merely from the general notion of re-weighting.

7 Conclusions and Future Work

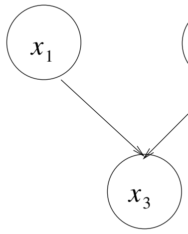
We have shown that the advantages of lookahead for decision trees can be obtained with only a constant increase in run-time, rather than a super-exponential increase, by the process of *skewing*. Nevertheless, the approach has limitations that need to be addressed in future work. It also has potential applications beyond decision trees, to be investigated in future work. The remainder of this section briefly outlines these directions.

Decision tree induction algorithms often are applied to data sets that involve some continuous variables in addition to nominal variables only. Therefore, one direction for further work is to extend the skewing algorithm to handle continuous variables. Here we briefly outline a natural such extension that we plan to test in future work. For continuous variables, the favored value is either *less* or *greater* than the split point, rather than 0 or 1. This makes skewing trickier because we do not know ahead of time what split point will be chosen. Hence for each continuous value v that a variable x takes in the data set, we compute the probability that v will be less than or greater than the split point. To do this computation, we might assume the split point is drawn from a uniform distribution over the values that x takes in the data set. We can then reweight an example with the expected weight over all possible split points. For example, suppose we have 100 examples, and the favored value for a variable x is *less*. An example that takes the tenth lowest value for x has probability 0.9 of being lower than the split point. Hence the weight of this example will get multiplied by $(0.9)(2)+(0.1)(1) = 1.9$.

Second, while we have demonstrated that skewing works for parity and other problematic functions of up to seven variables, for more variables it appears that large numbers of examples (at least several thousand) will be required. If the number of examples is too small relative to the size of the problematic portion of the target, then skewing can cause predictive accuracy to degrade somewhat, though the reason for this is unclear. Hence if a data set is small it may be desirable to try both skewed and normal versions of the tree learner. In spite of this limitation, skewing makes it possible to gain the effect of five- or six- step lookahead where only 2- or perhaps 3-step lookahead was computationally feasible previously.

The third direction for future work is to address high-dimensional data sets. The skewing approach may have trouble with such data sets for the following reason. If each data point has thousands of features, then one data point is likely to get a much higher weight than all others (to have many more variables with the preferred values), merely by chance, leading to a model that overfits this data point. One solution may be to lessen the degree of skewing. This and other approaches should be tested on high-dimensional data sets.

We would also like to apply the skewing approach to other types of learning algorithms that have trouble with similar hard functions. To focus on a specific algorithm for illustration, the introduction noted that the sparse candidate algorithm for learning Bayesian networks [Friedman *et al.*, 1999] was susceptible to functions like exclusive-or. This susceptibility is because of its use of information gain or more generally Kullback-Leibler divergence to narrow the candidate parents for any given node. For example, suppose the variables x_1 and x_2 together are highly predictive of the value of x_3 and hence would be excellent parents of x_3, as shown in the Bayesian network fragment in Figure 11. If x_1 and x_2 are independent of one another and take the value 0 roughly half of the time, then among tens or hundreds of other variables neither x_1 nor x_2 is likely to be considered as a candidate parent for x_3. Nevertheless, if several skewed versions of the data are used to select candidate parents (a variable is a potential parent if it scores well according to most of the skews), then x_1 and x_2 are likely to be selected. Modifying the sparse candidate algorithm is a direction for further work. More generally, we believe the *skewing* approach presented in this paper may be applicable to a variety of learning algorithms besides decision trees.



x_1	x_2	$\Pr(x_3)$ 0	1
0	0	0.99	0.01
0	1	0.02	0.98
1	0	0.01	0.99
1	1	0.97	0.03

Figure 11: Variable x_3 is an approximation of $x_1 \oplus x_2$

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