

# Chapter 5.

## 5 Analysis

### 5.1 The basic algorithm

The trees created by the Genetic Algorithm were very accurate for their cost range, and the pareto front of decision trees was able to evolve to reach satisfactory levels in very short amounts of time. The structure and thresholds of the individual decision trees were shown to parallel current medical knowledge, confirming that data mining is indeed an exciting and promising field that has the possibility to reveal new and important medical knowledge when run on clinical databases.

### 5.2 Elitism

For smaller population sizes, the addition of the elite set improved the AUC measures, and for the most part ensured a steady improvement in the fitness of the population over the generations. The populations without the elite set would find improved solutions, but then lose them in later generations. As population size increased, though, the addition of the elite members eventually no longer made a significant difference.

Though genetic programming is a global search, and may avoid becoming trapped at local maximum as the way greedy heuristics do, the tradeoff is that they are computationally intensive.[35] This multi-objective tree algorithm in particular must calculate the fitness values by comparing every tree to every other tree in the population, an operation with an order of  $N^2$ . The time and resources needed will only increase when this process is applied to large medical databases. Therefore any techniques that could possibly improve the speed or lower the necessary resources are a valuable addition. The inclusion of an elite set permits the number of trees to be cut to much smaller levels, and still allows solutions with reasonable AUC to be found.

### 5.3 Mutation

Both hard and soft mutations had similar values (though soft mutation was a bit more stable, and had slightly higher AUC estimates). Adding slight amounts of mutation from the 0% starting point increased the AUC for both, and they remained stable despite increases in the amount of mutation done, until a

mutation rate of 75% was reached. At that point both strategies experienced a sharp drop as their error thresholds were reached [37]. It seems that, whether you are replacing a constant within a node's function, or replacing that entire node and its subtree, the disturbance is enough to increase the AUC to a certain extent. After that point is reached, the results stay within the same area and are not greatly affected by changes in the mutation rate until the error threshold is reached.

## 5.4 Linear Decision Trees

It was shown that it was possible to create and evolve a pareto front of linear decision trees. However, adding linear capabilities to a decision tree created in this way does not guarantee better classification of the data. It is interesting to note that adding linear capabilities to the decision trees did not improve the AUC for the populations, or decrease the number of nodes necessary to obtain the optimal solutions. In the case of the PIMA diabetes dataset, the result is slightly worse than the univariate. Longer runs for the number of generations, to allow more time for the linear nodes to find the optimal constants, did not greatly improve their performance, either.

# Chapter 6.

## 6.1 Future Work

The trees created by the genetic program at approximately the 1 to 1 cost ratio had very good accuracies, but would in general be very large, with hundreds of nodes at times. The time it takes to run the entire dataset through every tree to discover their confusion matrices (and therefore be able to determine the dominance of a particular tree or not) goes up fast with the size of the trees. Though the inclusion of multiple copies of the same decision patterns inside a single individual is actual desirable during evolution, ensuring that good patterns are not lost or destroyed during the evolution process(30), the pruning of useless nodes or branches would certainly lead to vast improvements in run time. It would be interesting to try pruning during run time, and see what performance gains it may make, how it might affect the final AUC values, and whether it would be cost effective to do so.

The addition of linear capabilities to the decision tree did not improve its capabilities on the UCI datasets used. Genetic Programming has been found to be efficient at optimizing the structure of a tree, but struggles with finding the optimum coefficients for trees, since it uses combinations of random ones.(24) To improve the performance of linear trees created with Genetic Programming, some researchers have used Quasi-Newton optimization techniques to obtain the coefficients.(23) Further study could be done by using this technique to obtain the coefficients, instead of randomly generating and mutating them.

Another possibility would be to run this algorithm on a larger more complicated dataset, that contains more attributes. In a simpler dataset, it is possible that the axis-parallel splits done by the univariate decision trees are optimal, or just as effective as the oblique splits done by the linear trees. With the addition of more attributes, some of which may have values related to and dependent on each other, the greater flexibility of the linear decision tree may make a greater difference.

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