

AN ANALYSIS OF DECISION TREE MODELS FOR DIABETES

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Abstract – Data mining has from long been human beings friend and savior in numerous ways and one of the methods is through decision making. With increasing health concerns diabetes has a modern day scourge with millions around the world affected. Data mining is growing in relevance to solving such real world disease problems through its tools. The following study proposes to use the UCI repository Diabetes dataset and generate decision tree models for classification using LAD tree, NB tree and a Genetic J48 tree. The decision tree based classifier models study includes various parameters like computational overheads consumed, features, efficiency and accuracy and provides the results. This genetic J48 model accurately classifies the dataset when compared with the other two models in terms of accuracy and speed.

Keywords: Diabetes, Decision Tree, J48, C4.5, FB Tree, Classification,

INTRODUCTION

Data mining is increasingly applied to all walks of life as the information thus generated is applied to solve the problem. Even so it is profound in health care where the focus is on diabetes. India as a country is touted to be the global capital of the sugar – diabetes by having the largest number of people affected by this disease.

Hence the focus of this study is turned towards the application of the data mining tool namely decision tree classification to the diabetes dataset. A decision tree is a wonderful classification model. The PIMA Indian database is considered here which is taken from the UCI repository. The decision classifiers used here for the purpose are LAD [Least Absolute Deviation] Decision tree, NB [Navies Bayes] decision tree and the Genetic J48 decision tree, where using the dataset the features are extracted from the dataset to give decisions. Meanwhile parameters are analysed where the number of features generated, accuracy,

computational loads and efficiency in tree formation are recorded. Thus this study focuses on the importance of decision tree data mining structure in diabetes.

RELATED WORK

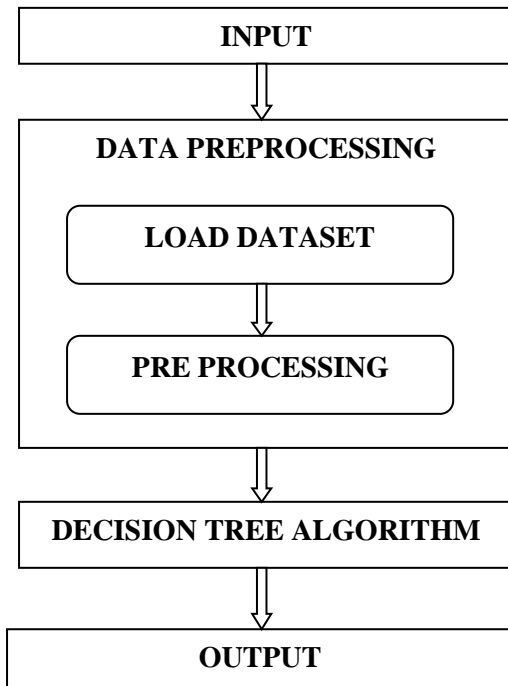
Earlier lot of works have been done in this field and to summarize a few of them have been mentioned below. **Jianchao Han** [5] used WEKA decision tree to build and predict type 2 diabetes data set which considered only the Plasma Insulin attribute as the main attribute while neglecting the other attributes given in the dataset. **Asma B.M. Patil** [7] performed different classification algorithms with varying accuracies and suggested improved prediction accuracy using weighted least squares SVM.. **A.Aljarullah** [6] also used WEKA decision tree classifier on the diabetes data set with association rule being implemented to generate a combination of attributes. **E.G.Yildirim** [8] proposed two models namely Adaptive Neuro Fuzzy Inference System – 1-Rough Set 2- ANFIS models. **Parthiban et al.** [9] in his research work proposed diabetic patient getting heart attack disease using Naive Bayes data mining classifier technique by using a minimum training dataset. **Huang Y.et al.** [10] in his work proposed decision support, prediction and estimation by extracting patterns from large data sets. **Huang, Feixiang; Wang, Shengyong**[11] studied a diabetic person having blood vessel nerves damage, eye retinopathy, heart disease, kidney disease etc. Gaganjot Kaur predicted a modified J48 Classification Algorithm for the Prediction of Diabetes [12].

Hussein Asmaa S,Wail M [13] et al stated that presently 246 million people are having diabetes or its related variants and which will double by 2025 coming to 500 million soon touching 1billion. Decision Tree Algorithm is to find out the way the attributes and features extracted for a fixed dataset. By training datasets the classes for newly generated instances are being found [20], which in turn generates prediction for test data inputs.

METHODOLOGY

Proposed Framework

The data are collected from real time UCI repository and it conforms to Type II diabetes based on the given attributes. The data set has ten attributes which predict the onset of diabetes in adults. The attributes description are entailed below.



The attributes are given based on data types. The data set is based on both numerical and nominal data types. Here the Patient Id, Plasma insulin glucose data are given in the numeric data type and BMI, Blood Pressure, gender data are given in nominal type.

DIABETES DATASET

The variables being investigated is whether the patient shows diabetes according WHO criteria Results: The parameters used are real-valued between 0 and 1, transformed into a binary decision using a cutoff of 0.448. There are 576 training instances in the PIMA Indian data set, there are 768 instances and 9 Attributes like Number of times pregnant, Plasma glucose concentration, oral glucose test, a 2-Hour serum insulin (mu U/ml), Diastolic blood pressure (mm Hg), the Triceps [skin fold] thickness measured in mm, Diabetes pedigree function, patients Age in years and finally the Class [whether tested

positive or tested negative] and Body mass index [BMI] which is the weight in kg divided by the height in m .Class Distribution: Class value 1 means having diabetes and 0 means negative diabetes.

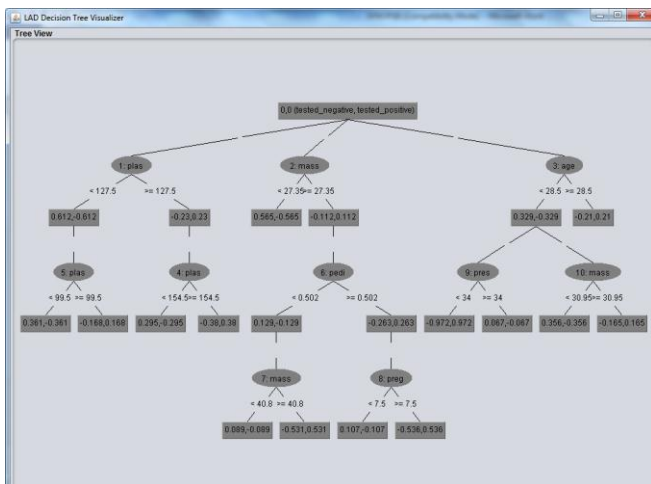
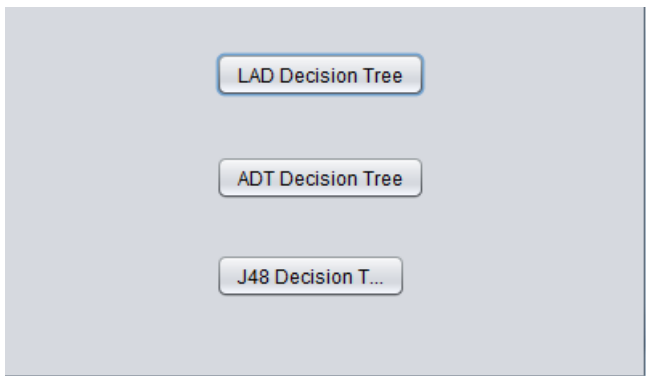
Class Value	Number of instances
0	500
1	268

GENETIC J48 TREE ALGORITHM

Procedure DecisionTreeLearner(X, Y, E)

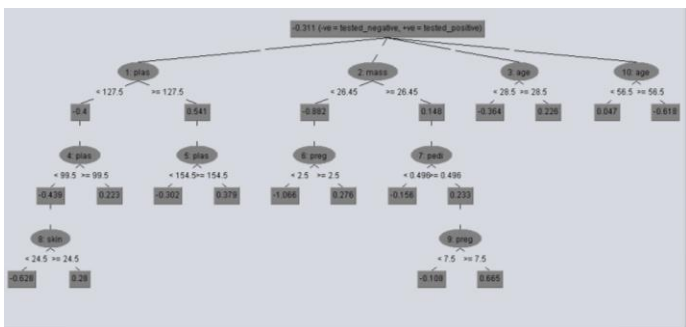
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1:   Inputs
2:      $X$ : set of input features,  $X = \{X_1, \dots, X_n\}$ 
3:
4:      $Y$ : feature boundary
5:      $E$ : set of training examples
6:   Output
7:     decision tree
8:   if stop criteria is true then
9:     return pointEstimate( $Y, E$ )
10:  else
11:    Select feature  $X_i \in X$ , with domain  $\{v_1, v_2\}$ 
12:    let  $E_1 = \{e \in E: val(e, X_i) = v_1\}$ 
13:    let  $T_1 = DecisionTreeLearner(X \setminus \{X_i\}, Y, E_1)$ 
14:    let  $E_2 = \{e \in E: val(e, X_i) = v_2\}$ 
15:    let  $T_2 = DecisionTreeLearner(X \setminus \{X_i\}, Y, E_2)$ 
16:    return  $\langle X_i = v_1, T_1, T_2 \rangle$ 
17:
18: Procedure DecisionTreeClassify( $e, X, Y, DT$ )
19:   Inputs
20:      $X$ : set of input features,  $X = \{X_1, \dots, X_n\}$ 
21:      $Y$ : target feature
22:      $e$ : example to classify
23:      $DT$ : decision tree
24:   Output
25:     prediction on  $Y$  for example  $e$ 
26:   Local
27:      $S$  sub branch of  $DT$ 
28:      $S \leftarrow DT$ 
29:     while  $S$  is an internal node of the form  $\langle X_i = v, T_1, T_2 \rangle$  do
30:       if  $val(e, X_i) = v$  then
31:          $S \leftarrow T_1$ 
32:       else
33:          $S \leftarrow T_2$ 
34:
35:
36:   return  $S$ 
  
```



ALGORITHM STEPS

1. Check for base cases - I
2. For each attribute - *a*
Find the information gain from splitting on *a*
3. Let *a_{best}* be the attribute with the highest standardized gain
4. Create a decision *node* that splits on *a_{best}*
5. Recursive on the sublists obtained by split on the best and add those nodes as children of nodes.



5.1 LOAD DATA SET

In this project, the PIMA Indians Diabetes dataset is input from the UCI repository to the algorithms.

5.2 IRRELEVANT FEATURE REMOVAL

First eliminate the irrelevant features in the data set using the feature removal algorithm and then find out relevance between each feature and the target feature which is to calculate the distance between each and every varying feature using Euclidian and Manhattan models. If the distance is found to be greater than the threshold value then it is relevant else it is irrelevant feature. Thus the irrelevant features are removed and the relevant features are obtained.

5.3 REMOVING REDUNDANT FEATURE

There are three steps.

- i. Minimum Spanning Tree Construction
- ii. Tree Partition -- Clustering
- iii. Representative feature selection

RESULTS AND DISCUSSION

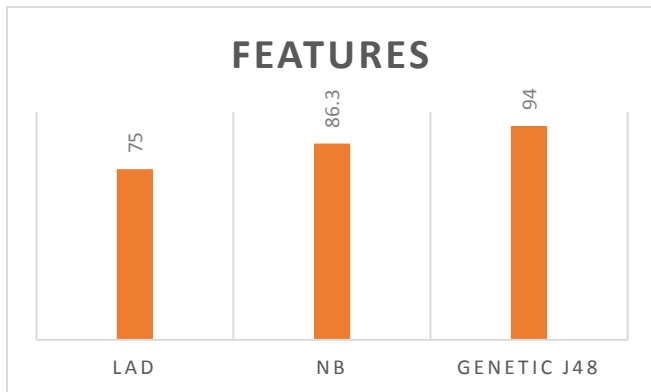
It has been found that of the three decision tree classification algorithms, (i) different values result in different classification accuracies; (ii) there is a value where corresponding classification accuracy; and (iii) the values, in which the best classification features are got, are different for both the data sets, the modified – genetic J48 Decision Tree model is found to be the best. The results and findings are tabulated below with appropriate charts

Table 1: Parameters for all three algorithms

ALGORITHMS	LAD	NB	Genetic J48	
FEATURES		80.4	86.3	90
EFFICIENCY		90.4	94.8	97.2
ACCURACY		89.6	98.6	95.8

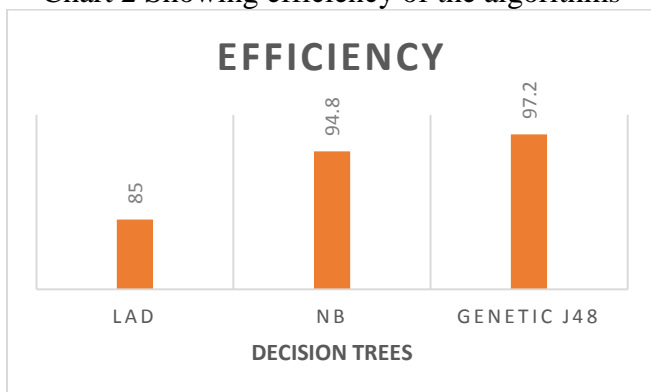
In terms of features Genetic J48 Tree shows the maximum efficiency with 94% followed by NB tree and finally LAD with 75%.

Chart 1 showing the features generated



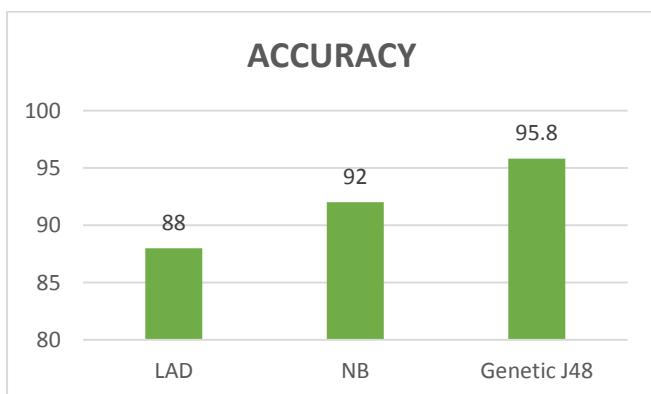
In terms of efficiency again Genetic J48 Tree shows the maximum efficiency with 97.2% followed by NB tree with 94.8% and finally LAD with 85%.

Chart 2 Showing efficiency of the algorithms



Finally when it comes to accuracy the genetic J48 is most accurate as it comes with 95.8% while NB has 92% and LAD Tree has 88% accuracy.

Chart 3 Showing Accuracy of the algorithms



This means the results are the best, and the performance is optimal for the genetic J48 tree. For each of the three decision tree algorithms,

although the values where the best classification accuracies are obtained are different for various parameter in the dataset, the genetic J48 is the preferred model because the classification accuracies are the best among the lot. When determining the value, besides classification accuracy, the proportion of the selected features are taken into account as well.

CONCLUSION

The study thus successfully shows the comparison of the three decision tree classification models for the UCI repository diabetes dataset and shows the tree structure formed enabling users to take accurate decisions based on the input parameters. Further the genetic J48 model is found to be the most efficient and accurate when compared with the other two decision models in terms of time, accuracy and features. In future the models may include other decision support systems with parameters from clinical tests aiding prediction of the diabetes.

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