# **Comparative analysis of Predicting Diabetes Using Machine Learning Techniques**

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**Abstract**: Diabetes is a chronic disease caused due to the expanded level of sugar addiction in the blood. Various automated information systems were outlined utilizing various classifiers for anticipate and diagnose the diabetes. Data mining approach helps to diagnose patient's diseases. Diabetes Mellitus is a chronic disease to affect various organs of the human body. Early prediction can save human life and can take control over the diseases. Selecting legitimate classifiers clearly expands the correctness and adeptness of the system. Due to its continuously increasing rate, more and more families are unfair by diabetes mellitus. Most diabetics know little about their risk factor they face prior to diagnosis. This paper explores the early prediction of diabetes using data mining techniques. The dataset has taken 768 instances from PIMA Indian Diabetes Dataset to determine the accuracy of the data mining techniques in prediction. Then we developed five predictive models using 9 input variables and one output variable from the Dataset information; we evaluated the five models in terms of their accuracy, precision, sensitivity, specificity and F1 Score measures. The purpose of this study is to compare the performance analysis of Naïve Bayes, Logistic Regression, C5.0 Decision Tree and Support Vector Machine (SVM) models for predicting diabetes using common risk factors. The decision tree model (C5.0) had given the best classification accuracy, followed by the logistic regression model, Naïve Bayes and the SVM gave the highest accuracy.

## Index Terms – Machine Learning, Prediction, Naïve Bayes, Logistic Regression, C5.0 Decision Tree and Support Vector Machine (SVM).

#### I. INTRODUCTION

Diabetes is a dangerous disease with the potential to cause a worldwide Health Care crisis. According to International Diabetes confederation 382 million people are living with diabetes world wide. By 2035, this will be doubled as 592 million. Early prediction of diabetes is quite challenging task for medical practitioners due to complex interdependence on various factors. Diabetes affects human organs such as kidney, eye, heart, nerves, foot etc. Data mining is a process to extract useful information from large database. It is a multidisciplinary field of computer science which involves computational process, machine learning, statistical techniques, classification, clustering and discovering patterns.

#### **Machine Learning**

Machine Learning is the process of discovering interesting knowledge, such as patterns, associations, changes, anomalies and significant structures, from large amounts of data stored in databases, data warehouses, or other information repositories. Due to the wide availability of huge amounts of data in electronic forms, and the imminent need for turning such data into useful information and knowledge for broad applications including market analysis, business management, and decision support, data mining has attracted a great deal of attention in information industry in recent years.

#### Diabetes

Diabetes Mellitus (DM) is commonly referred as Diabetes; it is the condition in which the body does not properly process food for use as energy. The pancreas, an organ make a hormone called insulin to help glucose get into the cell of our bodies.

#### **Types of Diabetes**

Type 1 Diabetes is called insulin-dependent diabetes mellitus (IDDM) or juvenile-onset diabetes.Type1 mostly occurs in young people who are below 30 years. In Type 1 Diabetes, the beta cell of the pancreas, which are in charge for insulin production, are destroyed due to autoimmune system.

Type 2 Diabetes is called non-insulin-dependent diabetes mellitus (NIDDM) or adult-onset diabetes. In the type 2 diabetes, the pancreas usually produces some insulin the amount produced is not enough for the body's needs, or the body's cells are resistant to it.

Gestational Diabetes is the third major form and occur when pregnant women without a previous account of diabetes develop a high blood glucose level. The majority of gestational diabetes patients can control their diabetes with exercise and diet. Between 10% to 20% of them will need to take some kind of blood-glucose-controlling medications. In few cases this gestational diabetes may lead to type 2 diabetes in future. It affects on 4% of all pregnant women.

#### **Application of Data mining Techniques in Diabetes**

Medical data can be trained using data mining techniques to predict the diabetes. For this, dataset has to be preprocessed to remove noisy and fill the missing values. Pima Indian Diabetes Dataset is taken to evaluate data mining Classification. The dataset comprises 9 attributes and 768 instances.

### **II. LITERATURE REVIEW**

Design of prediction models for diabetes diagnosis has been an active research area for the past decade. Most of the models found in literature are based on Classification Algorithms and artificial neural Networks (ANNs). Some of the research papers that reviewed for this research are given below: AiswaryaIyer, et al. [1] have employed Decision tree (J48), Naïve Bayes algorithms for predicting diabetes. They used Pima Indian Diabetes dataset; it was implemented using WEKA tool. They found Naive Bayes algorithm gave 79.56% accuracy than another for predicting diabetes. V.AnujaKumari, R.Chitra, [12] used SVM with Radial Basis Function Kernal for classification of diabetes disease. They used PYTHON, R2010a for implementation. They found the accuracy rate as 78%.

N. Sarma, et al. [2] used Bayesian net classifier and decision tree for Predicting Diabetes Type 2. They used PIMA indian diabetic dataset. They used WEKA tool for their implementation in that they found bayes net classifier gives the accuracy level of 71-74% depending upon the number of cross validation applied on the dataset when performing the test. and decision tree gives the accuracy level of 78-80% Which is the best accuracy without implementing any neural network structure. P.Padmaja et al. [3] used clustering concepts for character evaluation of diabetes. They evaluated 5 different clusters by using 4 algorithms, namely 1) K-means, 2) Partitioning Around Medoids(PAM), 3) Minimum spanning tree (MST), 4) Nearest Neighbours used to identify good quality clusters. The result they found was, PAM provides cluster of good quality.

G.Parthiban, S.K.Srivatsa [4] used Naïve Bayes, SVM Techniques for Diagnosing Heart Disease for Diabetic Patients. They used WEKA tool and got the result as 94.6% of accuracy for SVM. Dr. M. Renuka Devi and J. Maria Shyla[8] explored various Data mining techniques such as Naïve Bayes, MLP, Bayesian Network, C4.5, ANN, Modified J48, etc...They used PYTHON and WEKA tool. In that paper, Modified J48 classifier gave 99.87% of highest accuracy. RupaBagdi et al. [5] compared ID3 and C4.5 decision tree algorithm results. Finally they found C4.5 was more precise than ID3. Sadri sa'di et al.[6] used Naive Bayes, RBF Network and J48 datamining algorithms for diagnosing type II diabetes. They used WEKA tool. Finally they found Naive Bayes, having the accuracy rate of 76.96% than other algorithms. Sankaranarayanan.S et al. [7] intended to discover the hidden knowledge from a particular dataset to improve the quality of health care for diabetic patients.

Satheeskumar.B, Gayathri.P, [9] used Data mining Classification Algorithms such as CART, J48, NBTree for Analysis of Adult - Onset Diabetes. They used WEKA tool for implementing these algorithms. They found the accuracy rate as 80% for J48 algorithm when compared to other algorithms. Tahani Daghistani and RiyadAlshammari, [10] used MNGHA, saudhi Arabia dataset to predict diabetic patients using 18 risk factors. They found RandomForest achieved the best performance when compared to other data mining classifiers. V. Kumar and L. Velide,[11] used Data mining Approach for Prediction and Treatment Of diabetes Disease. The techniques they used as Naïve Bayes, JRip, J48 (4.5), DT, NN .They used WEKA tool for implementation. They got 68.5% of accuracy level for J48 algorithm.

Ananthapadmanaban et al., [13] developed the SVM and Naïve Bayes classification algorithms for speculating diabetic retinopathy and found out that the Naive Bayes algorithm has got the accuracy rate of 84%. Ferreira et al., [14] used different classification algorithms like SimpleCart, J48, Simple Logistics, SMO, NaiveBayes and BayesNet for diagnosing neonatal jaundice in type1 diabetes. Among all algorithms, it was found that Simple Logistics as the best algorithm. The paper [15] approached the aim of diagnoses by using ANNs and demonstrated the need for preprocessing and replacing missing values in the dataset being considered. Through the Modified training set, a better accuracy was achieved with lesser time required for training the set Mukesh kumari and Dr. Rajan Vohra [16] worked on the concept of data mining is to extract knowledge from information stored in dataset and generate clear and understandable description of patterns. The techniques are attributes selection, data normalization and then classifier is applied on data set to construct Bayesian model. Bayesian network classifier was proposed for the prediction of person whether diabetic or not.

Srideivanai Nagarajan and R.M. Chandrasekaran[17] proposed a method for improvement of iagnosis of gestational diabetes with data mining techniques. Also they Analyse the performance of ID3, Naïve Bayes, C4.5, and Random tree i.e. the algorithm for supervised Learning. They used the data set of Pregnant Womens. The results they found that Random tree served to be the best one with higher accuracy and least error rate. K.Rajesh and V.Sangeetha[20] proposed that data mining relationship for efficient classification they applied data mining techniques to classify diabetes clinical data and predict the patient being affected with diabetes or not. They applied C4.5 Algorithm gave classification rate of 91%.

Dr. B .L. Shivkumar and S Thiyagarajan c et al (2016), In this work [19], an effective machine learning algorithm is proposed for the classification of type dm patients. This machine learning algorithm used for classification will find the optimal hyper-plane which divides the various classes. Nahla H. Barakat (2010), In this paper [20] support vector machines (SVMs) are recommended for the diagnosis of diabetes. In this, they used a description module, which is known as "black box" model of an SVM which we used for diagnostic (classification) decision. Results retrieved on diabetes dataset with the use "black box" proves that it is an emerging tool that is by intelligible SVM's for the prediction of diabetes, with prediction accuracy of 94%, sensitivity of 93%, and specificity of 94%.

## • METHODOLOGY

## **DECISION TREES C5.0**

Decision tree is a tree structure. It is in the form of a flowchart. It is used as a method for classification and prediction using nodes and internodes. The root and internal nodes are the test cases that are used to separate the instances with different features. Leaf nodes denote the class variable.

#### C5.0 Algorithm

| C6.0 decision true syntax   |        |  |
|---|--------|--|
| unding the ≤\$ - 0 ( ) furnition in the ≤\$0 pandage  |        |  |
| Building the oisselfler:<br>m <- c5.0(train, class, trials = 1, costs = NULL)<br>trials is a data there containing maining data<br>class is a factor sector with the class for each rate in the training data<br>to the the training data for each trial to the training data<br>to the the training data for each trial to the training data<br>build to the training data for each trial to the training data<br>build to the trial trials and the training data for each trial to the training data<br>build to the trial to the trial trials the training data for each trial<br>build to the trial trials and the trial trials to the trial trial to the trial<br>trial trials to the trial trials to the trial trials to the trial trials to the trial<br>trials the trials the trial trials to the trial trials to the trial trials to the trial<br>trials trials to the trial trials to the trial trials to the trial trials to the trial trials trials to the trial trials to the trial trials to the trial trials trials to the trial trials to the trial trials to the trial trials to the trial trials trials to the trial trials trials trials to the trials tria |        |  |
| The function will return a CD.0 model object that can be used to make predictions<br>Making predictions:  |        |  |
| <ul> <li>p = predict(e, test, type = "class")</li> <li>a be model tested by the CS D(3 hardbon)</li> <li>test is a data hame containing test data with the same features as the tides of the classifier.</li> <li>type is either "class" or "prob" and specifies whother the oredict is boother inclusion of the respective field and outlines.</li> </ul>  | one.   |  |
| The function will return a sector of predicted class values or rate predicted probab<br>depending sport the selice of the 3.550 percention.   | illien |  |
| Reample:<br>credit_model <- c5.0(credit_train, Toan_default)<br>credit_prediction <- predict(credit_model,<br>credit_test)  |        |  |

C5.0 offer a number of improvement on C4.5. They are:

- Speed C5.0 is much quicker than C4.5
- Memory usage C5.0 is added memory proficient than C4.5
- Smaller decision trees C5.0 gets alike results to C4.5 with significantly smaller decision trees.
- Support for boosting Boosting improve the trees and give them further precision.
- Weighting C5.0 allow you to weight diverse cases and misclassification types.

• Winnowing - a C5.0 option repeatedly winnows the attributes to eradicate those that may be unsupportive.

#### **SUPPORT VECTOR MACHINE (SVM)** (a) Introduction

Support Vector Machine is based on the concept of hyperplanes that define the decision boundaries. A hyperplane is one that separates between the set of objects that having different class members. A schematic example is given in the illustration below. In this example, the objects are belong to either class GREEN or RED. The separating line defines the boundary on the right side of which all the objects are GREEN and to the left of which all the objects are RED.



#### Fig 4. Support Vector Machine (b) Technical Notes

Support Vector Machine is a classifier method that perform classification task by constructing the decision planes in a multi-dimensional space that separates the case of diverse class labels. SVM supports regression and classification tasks, that can handle multiple continuous and the categorical variables. For the categorical variables, dummy variable is created with case values either 0 or 1. Thus, a categorical dependent variables consists of three levels, say (A, B, C), is represented as a set of three dummy variables:

#### A:{100},B:{010},C:{001}

## **CLASSIFICATION SVM TYPE1**

For this type of Classification SVM Type I, training phase involves the minimization of error function:

$$\frac{1}{2}w^Tw + C\sum_{i=1}^N \xi_i$$

subjects to the constraint:

$$y_i(w^T\phi(x_i)+b) \ge 1-\xi_i \text{ and } \xi_i \ge 0, i=1,...,N$$

where C denotes the capacity constant, w denotes the vector coefficients, b denotes the constant, and represents the

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parameter for handling non separable data (inputs). The index i labels the N training cases. Note that  $\mathcal{Y} \in \pm 1$  represent the class labels and xi represent the independent variables. The kernel  $\phi$  is used to transform the data from input (independent) to the feature space. It is ought to be noted that larger the C, the more error is penalize. Thus, C is ought to be chosen with care to avoid over fitting.

## CLASSIFICATION SVM TYPE2

In contrast to Classification SVM Type 1, the Classification SVM Type 2 model minimizes the error function:

$$\frac{1}{2}w^Tw - v\rho + \frac{1}{N}\sum_{i=1}^N \xi_i$$

subject to the constraints:

In a regression SVM, you have to estimate the functional dependence of the dependent variable y on a set of independent variables x. It assumes, like other regression problems, that the correlation between independent and dependent variables is given by a deterministic function f plus the addition of some additive noise:

Fig. 1. Regression SVM REGRESSION SVM TYPE1

For this type of Regression SVM Type1, the error function is given as

 $\frac{1}{2}w^{T}w + C\sum_{i=1}^{N}\xi_{i}^{*} + C\sum_{i=1}^{N}\xi^{*}i$ 

which we minimize the subject to:

#### **REGRESSION SVM TYPE2**

For this type of Regression SVM Type2, the error function is given by: which we minimize the subject to: There are number of kernels that can be used in Support Vector Machine models. These includes linear, polynomial, radial basis function (RBF) and sigmoid models.

 $w^{T}\phi(x_{i}) + b - y_{i} \leq \varepsilon + \xi_{i}$  $y_{i} - w^{T}\phi(x_{i}) - b_{i} \leq \varepsilon + \xi$  $\xi_{i}, \xi_{i}^{*} \geq 0, i = 1, ..., N$ 

#### (e) Kernel Functions

where  $K(\mathbf{X}_i, \mathbf{X}_j) = \phi(\mathbf{X}_i) \cdot \phi(\mathbf{X}_j)$  that is, the kernel function, that represents the dot product of input data points that is mapped into the multidimensional space by transformation.

#### **DECISION TREE ALGORITHM**

A decision tree is a flowchart-like tree structure where an internal node represents feature(or attribute), the branch represents a decision rule, and each leaf node represents the outcome. The topmost node in a decision tree is known as the root node. It learns to partition on the basis of the attribute value. It partitions the tree in recursively manner call recursive partitioning. This flowchart-like structure helps you in decision making. It's visualization like a flowchart diagram which easily mimics the human level thinking. That is why decision trees are easy to understand and interpret.



Decision Tree is a white box type of ML algorithm. It shares internal decision-making logic, which is not available in the black box type of algorithms such as Neural Network. Its training time is faster compared to the neural network algorithm. The time complexity of decision trees is a function of the number of records and number of attributes in the given data. The decision tree is a distribution-free or non-parametric method, which does not depend upon probability distribution assumptions. Decision trees can handle high dimensional data with good accuracy.

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#### How does the Decision Tree algorithm work?

The basic idea behind any decision tree algorithm is as follows:

- 1. Select the best attribute using Attribute Selection Measures(ASM) to split the records.
- 2. Make that attribute a decision node and breaks the dataset into smaller subsets.
- 3. Starts tree building by repeating this process recursively for each child until one of the condition will match:
- All the tuples belong to the same attribute value.
- There are no more remaining attributes.
- There are no more instances.



#### Attribute Selection Measures

Attribute selection measure is a heuristic for selecting the splitting criterion that partition data into the best possible manner. It is also known as splitting rules because it helps us to determine breakpoints for tuples on a given node. ASM provides a rank to each feature(or attribute) by explaining the given dataset. Best score attribute will be selected as a splitting attribute (<u>Source</u>). In the case of a continuous-valued attribute, split points for branches also need to define. Most popular selection measures are Information Gain, Gain Ratio, and Gini Index.

#### **Information Gain**

Shannon invented the concept of entropy, which measures the impurity of the input set. In physics and mathematics, entropy referred as the randomness or the impurity in the system. In information theory, it refers to the impurity in a group of examples. Information gain is the decrease in entropy. Information gain computes the difference between entropy before split and average entropy after split of the dataset based on given attribute values. ID3 (Iterative Dichotomiser) decision tree algorithm uses information gain.

Info(D)= - 
$$\sum_{i=1}^{m} pi \log_2 pi$$

Where, Pi is the probability that an arbitrary tuple in D belongs to class Ci.

$$Info_{A}(D) = \sum_{j=1}^{V} \frac{|Dj|}{|D|} \quad X Info(D_{j})$$

 $Gain(A)=Info(D)-Info_A(D)$ 

Where,

- Info(D) is the average amount of information needed to identify the class label of a tuple in D.
- |Dj|/|D| acts as the weight of the jth partition.
- InfoA(D) is the expected informa-tion required to classify a tuple from D based on the partitioning by A.

The attribute A with the highest information gain, Gain(A), is chosen as the splitting attribute at node N().

#### **Gain Ratio**

Information gain is biased for the attribute with many outcomes. It means it prefers the attribute with a large number of distinct values. For instance, consider an attribute with a unique identifier such as customer\_ID has zero info(D) because of pure partition. This maximizes the information gain and creates useless partitioning.

C4.5, an improvement of ID3, uses an extension to information gain known as the gain ratio. Gain ratio handles the issue of bias by normalizing the information gain using Split Info. Java implementation of the C4.5 algorithm is known as J48, which is available in WEKA data mining tool.

$$SplitInfo_A(D) = -\sum_{j=1}^{\nu} \frac{|D_j|}{|D|} \times \log_2\left(\frac{|D_j|}{|D|}\right)$$

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Where,

- |Dj|/|D| acts as the weight of the jth partition.
- v is the number of discrete values in attribute A.

The gain ratio can be defined as

$$GainRatio(A) = \frac{Gain(A)}{SplitInfo_A(D)}$$

## **OPTIMIZING DECISION TREE PERFORMANCE**

- criterion : optional (default="gini") or Choose attribute selection measure: This parameter allows us to use the different different attribute selection measure. Supported criteria are "gini" for the Gini index and "entropy" for the information gain.
- **splitter : string, optional (default="best") or Split Strategy**: This parameter allows us to choose the split strategy. Supported strategies are "best" to choose the best split and "random" to choose the best random split.
- **max\_depth : int or None, optional (default=None) or Maximum Depth of a Tree**: The maximum depth of the tree. If None, then nodes are expanded until all the leaves contain less than min\_samples\_split samples. The higher value of maximum depth causes overfitting, and a lower value causes underfitting (Source). In Scikit-learn, optimization of decision tree classifier performed by only pre-pruning. Maximum depth of the tree can be used as a control variable for pre-pruning. In the following the example, you can plot a decision tree on the same data with max\_depth=3. Other than pre-pruning parameters, You can also try other attribute selection measure such as entropy.

#### **K-NEAREST NEIGHBORS (KNN)**

KNN is a non-parametric and lazy learning algorithm. Non-parametric means there is no assumption for underlying data distribution. In other words, the model structure determined from the dataset. This will be very helpful in practice where most of the real world datasets do not follow mathematical theoretical assumptions. Lazy algorithm means it does not need any training data points for model generation. All training data used in the testing phase. This makes training faster and testing phase slower and costlier. Costly testing phase means time and memory. In the worst case, KNN needs more time to scan all data points and scanning all data points will require more memory for storing training data.

#### HOW DOES THE KNN ALGORITHM WORK?

In KNN, K is the number of nearest neighbors. The number of neighbors is the core deciding factor. K is generally an odd number if the number of classes is 2. When K=1, then the algorithm is known as the nearest neighbor algorithm. This is the simplest case. Suppose P1 is the point, for which label needs to predict. First, you find the one closest point to P1 and then the label of the nearest point assigned to P1.



Suppose P1 is the point, for which label needs to predict. First, you find the k closest point to P1 and then classify points by majority vote of its k neighbors. Each object votes for their class and the class with the most votes is taken as the prediction. For finding closest similar points, you find the distance between points using distance measures such as Euclidean distance, Hamming distance, Manhattan distance and Minkowski distance. KNN has the following basic steps:

- 1. Calculate distance
- 2. Find closest neighbors
- 3. Vote for labels



#### HOW DO YOU DECIDE THE NUMBER OF NEIGHBORS IN KNN?

Now, you understand the KNN algorithm working mechanism. At this point, the question arises that How to choose the optimal number of neighbors? And what are its effects on the classifier? The number of neighbors(K) in KNN is a hyperparameter that you need choose at the time of model building. You can think of K as a controlling variable for the prediction model.Research has shown that no optimal number of neighbors suits all kind of data sets. Each dataset has it's own requirements. In the case of a small number of neighbors, the noise will have a higher influence on the result, and a large number of neighbors make it computationally expensive. Research has also shown that a small amount of neighbors are most flexible fit which will have low bias but high variance and a large number of neighbors will have a smoother decision boundary which means lower variance but higher bias.Generally, Data scientists choose as an odd number if the number of classes is even. You can also check by generating the model on different values of k and check their performance. You can also try Elbow method here.



#### IV Performance Evaluation

## 1. PERFORMANCE METRICS

## a) Dataset Description and Pre-Processing

The classification type of data mining has been applied to the Pima Indians Diabetes Dataset from UCI repositories. Table 1 shows a brief description of the dataset that is being considered.

#### Table 1 Dataset Description

| Dataset                      | No. of Attributes | No. of instances |  |
|------------------------------|-------------------|------------------|--|
| Pima Indian Diabetes Dataset | 9                 | 768              |  |

| The attributes descriptions are shown | in Table 2 below. |
|---------------------------------------|-------------------|
|---------------------------------------|-------------------|

| Table 2 Attribute Description |                          |  |  |  |
|-------------------------------|--------------------------|--|--|--|
| Attribute<br>No.              | Attribute                | Description  |  |  |
| 1                             | Pregnancies              | Number of times pregnant   |  |  |
| 2                             | Glucose                  | Plasma glucose concentration a 2 hours in an oral glucose tolerance test |  |  |
| 3                             | BloodPressure            | Diastolic blood pressure(mmHg)   |  |  |
| 4                             | SkinThickness            | Triceps skin fold thickness(mm)  |  |  |
| 5                             | Insulin                  | 2-Hour serum insulin (mu U/ml)   |  |  |
| 6                             | BMI                      | Body Mass Index(BMI)   |  |  |
| 7                             | DiabetesPedigreeFunction | Diabetes Pedigree function   |  |  |
| 8                             | Age                      | Age(in years)  |  |  |
| 9                             | Outcome                  | Class variable(0 or 1)   |  |  |

#### Table 2 Attribute Description

Pre-processing and transformation of the dataset are done using R tools. Transformation steps include:

- Replacing missing values, and
- Normalization of values.

The descriptive statistics of the dataset is presented in Table 3. Since the parameters are normalized the range of all are in the range 0 to 1.

#### **Table 3 Descriptive Statistics of Transformed Dataset**

| Parameter                | Minimum | Maximum | Mean  | Std. Deviation |
|--------------------------|---------|---------|-------|----------------|
| Glucose                  | 0       | 1       | 0.608 | 0.161          |
| BMI                      | 0       | 1       | 0.477 | 0.117          |
| DiabetesPedigreeFunction | 0       | 1       | 0.168 | 0.141          |
| Age                      | 0       | 1       | 0.204 | 0.196          |

b) Evaluation of Classifiers Performance Metrics

This paper used confusion matrix to appraise the performance of the five models for incidence of diabetes and five evaluated indices for accuracy, sensitivity, specificity, Precision and F1 Score.

- Accuracy = (TP + TN)/(TP + FP + TN + FN)
- Sensitivity = TP/(TP+FN)
- Specificity = TN/(FP+TN)
- Precision = TP/(TP+FP)
- F1 Score = (2\*Precision\*Recall)/(Precision+Recall)

where TP, TN, FP and FN denote true positives, true negatives, false positives and false negatives, respectively. The model with highest the sensitivity, specificity, and accuracy is the best predictive model.

#### c) Time Calculation

The execution time for each classifier algorithms are calcuted by using the following R Tool command:

#### PERFORMANCE ANALYSIS OF THE CLASSIFIER a) Accuracy Measures:

The Accuracy measures of Data mining Classification Algorithms, i.e., KNN, RF, Decision Tree C5.0, SVM and ANN and their analysis report is given in the following Table 4

| ALGORITHMS    | ACCURACY |
|---------------|----------|
| KNN           | 73.57%   |
| Random Forest | 74.67%   |
| C5.0          | 74.63%   |
| SVM           | 72.17%   |

#### Table 4 Accuracy Measures of Naïve Bayes, Logistic Regression, C5.0, SVM

#### V CONCLUSION AND FUTURE ENHANCEMENT

#### 1. CONCLUSION

The automatic diagnosis of diabetes is an important real-world medical problem. Detection of diabetes in its early stages is the key for treatment. This paper shows how the Data mining classification algorithms say Naïve Bayes, Logistic Regression, C5.0, SVM and ANN are used to model actual Prediction of Diabetes Mellitus and a comparative analysis are made between them by making use of their Metric Measures say Accuracy, Precision, Sensitivity, Specificity and F1 Score. As a results of the research work, the C5.0 and Logistic Regression are equally good based on their Accuracy measures, the Naïve Bayes algorithm has the Second highest accuracy, followed by ANN and the most lowest accuracy is predicted in the SVM algorithms.

#### 2. FUTURE ENHANCEMENT

In future it is planned that the work can be extended and improves for the automation of diabetes analysis. In future the diabetes can be prevented using gene analysis from the previous history of the diabetes. Future work will focuses on collecting real time dataset and discover the new potential prognostic elements that are to be incorporated. The Fuzzy Logic can be included in future to diagnoise the diabetes types automatically.

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