Clinical Decision Support System for Intensity of Heart Diseases

Kulkarni Rashmi Ravindranath
Department of Computer
P.E.S Modern College of Engineering
Pune, India

***Abstract*— Clinical Decision Support System (CDSS) is a tool constructed for evaluating the intensity of Heart Diseases. There are five types of intensities present. Each intensity type is denoted with the help of range of values associated with each attribute. To diagnose these intensities ID3 and Extended Sub Tree algorithm is implemented. Comparison of results for these algorithm is been done in this paper. Experiments are done to evaluate the performance of both algorithms and result analysis concludes with, better performance of Extended Sub Tree as compared to ID3 in respect of complexity, accuracy, specificity, sensitivity, precision, recall, f measure etc.**

Keywords*— Patient Health Information (PHI), Electronic Medical Record (EMR), Extended Sub Tree (EST), Decision Tree, Clinical Decision Support System (CDSS).

I. INTRODUCTION

Clinical Decision Support System is constructed for Heart Diseases to diagnose the intensity of Disease level. For construction of CDSS decision tree is the algorithmic aspect been considered. Decision trees classify instances by sorting them down the tree from the root to some leaf node, which provides the classification of the instance. Each node in the tree specifies a test of some attribute of the instance and each branch descending from that node corresponds to one of the possible values for this attribute.

II. DIFFERENT APPROACHES FOR DIAGNOSING HEART DISEASES

There is large amount of heart related data present, which is in unstructured format. Hence by analyzing the data and formatting it into structured manner helps for making the decision. For diagnosing the disease there are many ways in which heart related diseases can be diagnosed and treatment can be provided.

Different approaches have different aspects in diagnosing the diseases. By using the Neural network approach the accuracy secured was around 80- 90% but the hidden layers description cannot be evaluated [5]. In fuzzy logic approach the weighted rules are generated initially and then the fuzzy rule decision is provided [5][6] and the accuracy obtained id around 79.05%. In naive bayes classification approach helps in predicting whether the patient is prone to heart disease or not and depicting the risk factor for heart attack [7]. The accuracy observed for naive bayes approach was around 90% [8]. Similarly by using Support vector machines concept the accuracy was achieved around 84.12%. While as by using decision tree approach the accuracy increased up to 96% [8].

TABLE I. ANALYSIS OF METHODS

Parameters	Neural Network	Fuzzy Logic	SVM	Naïve Bayes	Decision Tree
Example Algorithms	Back propagation	Thresholds and weights applied on IF – THEN rules	Maximum & optimal margins by Gaussian theorem	Posterior Probability – Bayes Theorem	C4.5 , CART, J48 using splitting attribute entropy,
Formula	Input Layer $w_{ij} = w_{ij} + \Delta w_{ij}$ Hidden Layer $w_{jk} = w_{jk} + \Delta w_{jk}$	Fuzzy Set $\mu : X \to [0,1]$	Margins Equations $\mathbf{w} \cdot \mathbf{x} - b = 1$ $\mathbf{w} \cdot \mathbf{x} - b = -1.$	$P(A\|B) = \frac{P(B\|A)P(A)}{P(B)}$	Information Gain $i(t) = -\sum_j p(j\|t)\log(p(j\|t))$ Gini Index $i(t) = \sum_j p(j\|t)(1 - p(j\|t))$
Advantages	Minimizes error in each level	Specification is obtained	Large data set is analyzed	Minimum error occurs	No domain knowledge is required
Disadvantage	Very slow working	Comparison increases	Range should be precise else outliers are observed	Multiple symptoms cannot handle and dependency in attributes	Selection of splitting attribute & over fitting
Approximate Accuracy	80 - 90 %	78 – 85 %	85 – 90 %	90 – 95 %	94 – 96 %

III. ALGORITHMIC APPROACH

A. ID3 Algorithm

ID3 is a simple decision learning algorithm developed by J. Ross Quinlan (1986). ID3 constructs decision tree by employing a top-down, greedy search through the given sets of training data to test each attribute at every node. It uses statistical property call information gain to select which attribute to test at each node in the tree. Information gain measures how well a given attribute separates the training examples according to their target classification[4].

III.A.I Entropy

It is a measure in the information theory, which characterizes the impurity of an arbitrary collection of samples. If the target

attribute takes on *c* different values, then the entropy S relative to this c-wise classification is defined as,

$$Entropy\ (S) = \sum_{i=1}^{c} -p_i \log_2 p_i \quad \cdots\cdots\cdots\cdots (1)$$

where P_i is the proportion/probability of S belonging to class *i*. Logarithm is base 2 because entropy is a measure of the expected encoding length measured in bits.

III.A.II Information Gain

The information gain, Gain(S, A) of an attribute A, relative to the collection of samples S, is defined as,

$$Gain\ (S, A) = Entropy\ (S) - \sum_{v \in Values\ (A)} \frac{|S_v|}{|S|} ntropy\ (S_v)$$

where *Values*(*A*) is the set of all possible values for attribute A, and S_v is the subset of S for which the attribute A has value *v*. We can use this measure to rank attributes and build the decision tree where at each node is located the attribute with the highest information gain among the attributes not yet considered in the path from the root.

III.A.III ID3 Algorithmic Steps

The ID3 algorithm is as follows: -

ID3 (Samples, Target_Attribute, Attributes)

Samples are the training examples. Target_Attribute is the attribute whose value is to be predicted by the tree. Attributes is the list of attributes which may be tested by the learned decision tree. Returns a decision tree that correctly classifies the given Examples.

- Create a root node for the tree
- IF all examples are positive, Return the single-node tree Root, with label = +
- If all examples are negative, Return the single-node tree Root, with label = -
- If number of predicting attributes is empty, then Return the single node tree Root,
- with label = most common value of the target attribute in the examples
- Otherwise Begin
    1. A ← The Attribute that best classifies examples
    2. Decision Tree attribute for Root ← A
    3. For each positive value, vi, of A,
        - Add a new tree branch below Root, corresponding to the test A = vi
        - Let Examples(vi), be the subset of examples that have the value vi for A
        - If Examples(vi) is empty
            - Then below this new branch add a leaf node with label = most common target value in the examples
            - Else below this new branch add the subtree ID3 (Examples(vi), Target_Attribute, Attributes – {A})
- End
- Return Root

B. Extended Sub Tree Algorithm

Extended Sub Tree algorithm is upliftment for decision tree algorithm. For working with Extended Sub Tree, basic tree structured format of data or constructed tree becomes input. To this tree structure below mentioned rules are applied and merging of sub trees is been done. Then to make decision classifier is applied so that decision can be made[1]. The paper prescribes about two classifiers namely SVM (Support Vector Machine) and KNN (K Nearest Neighborhood). The results are deduced with help of these classifiers.

Consider $T^P and\ T^q$, proposed system of EST. It handles to maintain tree structure by mapping subtrees of T^P to the similar subtree of T^q. Now while mapping these $T^P and\ T^q$ there are some rules to be followed:-

Rule 1 : EST mapping, not only mapping single nodes together, but also identical subtrees mapped together.

Rule 2 : No similar subtrees $T^P and\ T^q$ are allowed to mapped together, that is dissimilar trees cannot be mapped together.

Rule 3 : In one to many mapping, subtree of T^P can be mapped into different subtrees of T^q or vice versa.

Rule 4: m is the weighted as, $W(m_x) = \frac{W(T^{px}) + W(T^{qx})}{2}$ where $W(T^{px})$ and $W(T^{qx})$ are weights of subtrees in mapping. The $W(T^p)$ is calculated as

$$W(T^{px}) = \sum_{t_i^{px} \in T^{px}} W(t_i^{px}) \quad \cdots\cdots\cdots\cdots\cdots\cdots (3)$$

where $W(T^{px})$ is the scalar unit, when T^{px} is largest subtree that t_i^{px} belongs to, and zero otherwise.Then we compute $S^*(T^P, T^q)$ based on all possible mappings such as

$$S(T^P, T^q) = \alpha \sqrt{\sum_{m_k \in M} \beta_k \mathbf{X}\ \mathbf{W}(m_k)^\alpha} \quad \cdots\cdots\cdots\cdots (4)$$

where $\boldsymbol{\alpha}$, $\boldsymbol{\alpha} \geq 1$, is a coefficient to adjust the relation among different sizes of mappings. Then β_k is the unit scalar, when the root nodes of $T^{pk} and\ T^{qk}$ have same depth with

respect to T^P and T^q and it is equal to $\boldsymbol{\beta}$ (a constant no between zero and one) otherwise, leads to enhancement of mapping of same depth regarding subtrees. To normalize the similarity score, we divide it by its higher bound. Since $0 \leq \beta_k \leq 1$, we have $S(T^P, T^q) \leq \alpha \sqrt{\sum_{m_k \epsilon M} W(m_k)^\alpha}$ .Further, $\alpha \sqrt{\sum_{m_k \epsilon M} W(m_k)^\alpha} \leq \sum_{m_k \epsilon M} W(m_k)$ where $\boldsymbol{\alpha} \geq 1$ and $W(m_k)$ is a positive number. In addition, each node counted as one in weight calculation as, $\sum_{m_k \epsilon M} W(m_k) \leq \text{Max}(|T^p|, |T^q|)$. This evaluates to, $S(T^P, T^q) \leq \text{Max}(|T^p|, |T^q|)$ and similarity function normalizes to,

$$S^*(T^P, T^q) = \frac{S(T^P, T^q)}{\text{Max}(|T^p|, |T^q|)} \quad \ldots\ldots\ldots\ldots\ldots\ldots (5)$$

II.B.I Computational Algorithm

Hypothesis $T^p_{i,j}$ represents a subtree of T^p rooted to t^p_i is mapped to identical subtree of T^q rooted to t^q_j namely $T^q_{j,i}$. Now evaluation of $S(T^P, T^q)$ is done in four steps as follows :-

Step 1 : Identifying all mappings : We evaluate all possible mappings, whether it may be valid or invalid (i.e invalid mappings will have weight zero from step 3), and store into two lists of nodes having each list for one each subtree. T^P and T^q are the inputs, while as V^P and V^q are the outputs (inputs for next step) . V^P and V^q are the two dimensional matrices where each element is a list of nodes represented as $V^p_{[i][j]}$ and $V^q_{[j][i]}$ to the list of nodes of mapped subtrees of $T^p_{i,j}$ and $T^q_{j,i}$ respectively. In this step GetMapping(i,j) function results into two list of nodes ($V^p_{[i][j]}$ and $V^q_{[j][i]}$) for mapping. Its objective is to detect the largest mapping, which can be achieved at rooted children of t^p_i and t^q_j . Now among these t^p_i and t^q_j 's children, t^p_{ia} is the a^{th} child of t^p_i node, where $1 \leq a \leq deg(t^p_i)$, and ia denotes index of a^{th} child of t^p_i node. Similarly t^q_{jb} is the b^{th} child of t^q_j node, where $1 \leq b \leq deg(t^q_j)$, and jb denotes index of b^{th} child of t^q_j node. E is a matrix which indicates how children of t^p_i and t^q_j are matched. Also E is used to update $V^p_{[i][j]}$ and $V^q_{[j][i]}$. Therefore of $T^p_{i,j}$ and $T^q_{j,i}$ are identical so $|V^p_{[i][j]}| = |V^q_{[j][i]}|$.

Step 2 : Identifying each node's largest mapping : A node T^P or T^q may belong to many mappings, so we consider largest sub tree in mapping for each node. To evaluate this, hypothesis of two arrays namely, LS^p and LS^q of size T^P and T^q respectively. $LS^p[i]$ indicates largest subtree that t^p_i belongs to indexes of root nodes of mapping, denoted by $LS^p[i]_{mi}$ and $LS^p[i]_{mj}$ .The goal of this step is to fill LS^p and LS^q with appropriate values. Check if $|V^p_{[i][j]}|$ is larger than the subtree store it into LS^p for that node and then update it as per the upliftment. Similarly follow for rach node in $V^q_{[j][i]}$.

Step 3 : Compute the weight of each subtree : For this step, evaluate $W(T^p_{i,j})$ and $W(T^q_{j,i})$ for all subtrees in mapping, which is stored into $W^p[i][j]$ a nd $W^q[j][i]$. If largest value as compared to previous value is found then add it to LS^p and increment the weight of subtree. Similarly follow for LS^q .

Step 4 : Calculate $S(T^P, T^q)$: In this step we have all subtree weights (W^p and W^q) available. Then simply evaluate $S(T^P, T^q)$ [1].

```
Begin
Step 1
  for i = 1 to |T^p| do
    for j = 1 to |T^q| do
      if label(t_i^p) == label(t_j^q) then
        GetMapping(i, j)
      end of if
    end of for
  end of for
Step 2
  for i = 1 to |T^p| do
    for j = 1 to |T^q| do
      for k = 1 to |V^p[i][j]| do
        i' ← V^p[i][j]_k, j' ← V^q[j][i]_k
        if |V^p[i][j]| > |V^p[LS^p[i']_mi][LS^p[i']_mj]| then
          LS^p[i']_mi = i, LS^p[i']_mj = j
        end of if
        if |V^q[j][i]| > |V^q[LS^q[j']_mj][LS^q[j']_mi]| then
          LS^q[j']_mi = i, LS^q[j']_mj = j
        end of if
      end of for
    end of for
  end of for
Step 3
  for i = 1 to |LS^p| do
    W^p[LS^p[i]_mi][LS^p[i]_mj] + +
  end of for
  for j = 1 to |LS^q| do
    W^q[LS^q[j]_mj][LS^q[i]_mi] + +
  end of for
Step 4
  for i = 1 to |T^p| do
    for j = 1 to |T^q| do
      temp = ((W^p[i][j] + W^q[j][i]) / 2)^α
      if depth(t_i^p) ≠ depth(t_j^q) then
        temp = temp × β
      end of if
      S = S + temp
    end of for
  end of for
  S = ∜S
End
```

Fig.1. Pseudo code: ref [1].

IV. IMPLEMENTATION & EVALUATION

These algorithms are implemented for diagnosing the heart disease intensity or level. The diagnosis conclude with the stage in which the disease is residing. The data is in continuous form, i.e range of values for every parameters is to be considered. There were 13 parameters to be considered for diagnosing the data. The description of parameters can be given as follows:-

TABLE II. ATTRIBUTES FOR CLASSIFICATION

Sr No.	Parameter	Description
1.	Age	
2.	Gender	0 – Female 1- Male
3.	Chest Pain	1- Typical Angina 2 – Atypical Angina 3- Non Angina Pain 4 – Asymptomatic
4.	Trestbps	Resting Blood Pressure
5.	Cholesterol	
6.	FBS – Fasting Blood Sugar	1- True 0 - False
7.	RestECG – Resting Cardio graphic Results	0 – normal 1 – having ST-T abnormality 2- probable or definite left ventricular hypertrophy.
8.	Thalach – Maximum Heart Rate Achieved.	
9.	Exang – Exercise Induced Angina	0 – Yes 1 - No
10.	Oldpeak – exercise related to rest	
11.	Slope – slope of peak exercise	0 – up sloping 1- flat 2- down sloping
12.	Cardiac arest - no.of major vessels by fluoroscopy	
13.	Thal	3- normal 6 – fixed Defect 7 – reversible defect

By using these attributes the data is been classified to diagnose the level of disease of the patient. In ID3 algorithm, it cannot handle continuous data. Hence to implement ID3 algorithm, initially the data has to be converted into nominal form ie from continuous to non continuous form. After conversion it will evaluate the dataset to generate results. For evaluation purpose for each attribute, information gain is calculated with the following formula:-

$$Attribute\ Gain = \frac{\mathbf{max}\ limit - \mathbf{min}\ limit}{no.\ of\ levels\ (types)} \ldots\ldots\ldots\ldots\ldots\ldots (6)$$

In this accuracy formula, Value is the attribute gain value, max and min limits are range values for every type or level of disease. The accuracy can be evaluated with the following formula as follows:-

$$Accuracy = \frac{measured\ value - accepted\ value}{accepted\ value} \ldots\ldots (7)$$

Sensitivity measures the proportion of actual positives which are correctly identified and Specificity measures the proportion of negatives which are correctly identified. Specificity and sensitivity can be calculated with the standard formulae as follows:-

$$Specificity = \frac{TN}{(TN + FP)} \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots (8)$$

$$Sensitivty = \frac{TP}{(TP + FN)} \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots (9)$$

Now, Precision is the fraction of retrieved instances that are relevant, while recall is the fraction of relevant instances that are retrieved which can be represented as:-

$$Precision = \frac{|\{relevant\ data\}| \cap |\{retrieved\ data\}|}{|\{retireved\ data\}|} (10)$$

$$Recall = \frac{|\{relevant\ data\}| \cap |\{retrieved\ data\}|}{|\{relevant\ data\}|} \ldots\ldots (11)$$

Similarly F measure is measure of a test's accuracy. It can be interpreted as a weighted average of the precision and recall which can be given as:-

$$F\ Measure = 2.\ \frac{Precision\ .Recall}{Precision + Recall} \ldots\ldots\ldots\ldots\ldots\ldots (12)$$

In runtime measurement, its the time required for measuring the no.of tuples from dataset. Now in ID3 and Extended Sub Tree algorithm these formulae are applied to evaluate these parameters such as accuracy, specificity, sensitivity, precision, recall, f measure and runtime.

V. RESULT ANALYSIS

For evaluating these above parameters, the paper prescribes about three datasets for evaluation. The Cleveland, Statlog and Poona Hospital's live dataset is been used for analysis purpose. The metadata snapshot for the cleveland dataset can be given as follows:-

A1	A2	A3	A4	A5	A6	A7	A8	A9	A10	A11	A12	A13
63.0	1.0	1.0	145.0	233.0	1.0	2.0	150.0	0.0	2.3	3.0	0.0	6.0
67.0	1.0	4.0	160.0	286.1	0.0	2.0	108.9	1.0	1.5	2.0	3.0	3.0
68.0	1.0	4.0	120.0	229.4	0.0	2.0	129.2	1.0	2.6	2.0	2.0	7.0

TABLE III. DATA FOR CLEVELAND DATASET

Cleveland dataset contains 307 records. Similarly metadata for Statlog dataset can be given as follows:-

C1	C2	C3	C4	C5	C6	C7	C8	C9	C10	C11	C12	C13
70	1	4	130	322	0	2	109	0	2.4	2	3	3
67	0	3	115	564	0	2	160	0	1.6	2	0	7
57	1	2	124	261	0	0	141	0	0.3	1	0	7

TABLE IV. DATA FOR STATLG DATASET

Statlog dataset contains 255 records. Similarly dataset for Poona Hospital can be given as follows:-

P1	P2	P3	P4	P5	P6	P7	P8	P9	P10	P11	P12	P13
56.0	1.0	3.0	130.0	256.0	1.0	2.0	142.0	1.0	0.6	2.0	1.0	6.0
44.0	1.0	2.0	120.0	263.1	0.0	0.0	173.0	0.0	0.0	1.0	0.0	7.0
62.0	0.0	4.0	140.0	268.0	0.0	2.0	160.0	0.0	3.6	3.0	2.0	3.0

TABLE V. DATA FOR POONA HOSPITAL DATASET

With the help of these datasets results for case study in terms of accuracy, specificity, sensitivity, precision, recall, f measure and runtime is done. Now these parameters are evaluated initially for ID3 algorithm and then for Extended Sub Tree Algorithm which can be shown as follows:-

ID3 Algorithm								
Data Set	No.of Records	Accuracy (%)	Runtime (millsecs)	Specificity	Sensitivity	Precision	Recall	F Measure
Statlog	255	89.4	2964	0.88	0.88	0.82	0.89	0.88
Cleveland	307	80.14	5757	0.95	0.81	0.82	0.95	0.81
Poona Hospital	1200	98.89	12215	0.97	0.98	0.98	0.98	0.99

TABLE VI. RESULTS ANALYSIS FOR ID3

Extended Sub Tree Algorithm								
Data Set	No.of Records	Accuracy (%)	Runtime (millsecs)	Specificity	Sensitivity	Precision	Recall	F Measure
Statlog	255	98.8	2917	0.86	0.92	0.97	0.98	0.98
Cleveland	307	97.1	3993	0.99	0.98	0.96	0.99	0.97
Poona Hospital	1200	99.33	12153	0.97	0.99	0.98	0.98	0.98

TABLE VII. RESULTS ANALYSIS FOR EXTENDED SUB TREE

The time complexity required for evaluation comes around O(n log n) for ID3. So to overcome the drawback of ID3 algorithm, extended sub tree approach is used. In this approach, continuous data can easily be handled and time required for evaluation is reduced. The time complexity of this algorithm is around $O(|T^p|,|T^q|)\,X\min|T^p|,|T^q|$. Improvement in accuracy is observed as compared to ID3 algorithm. The experimental study in graphical format for above parameters can be given as follows:-

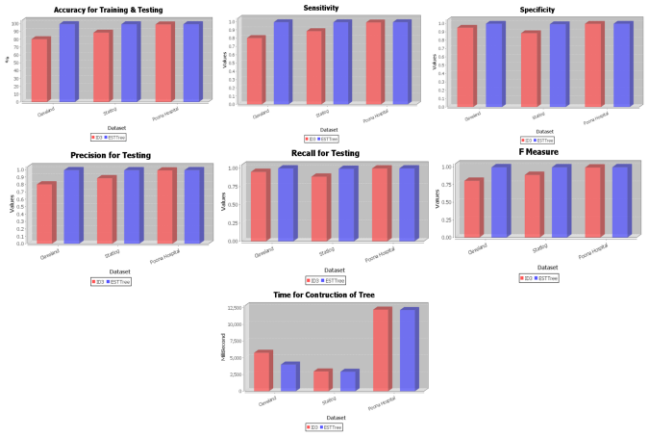

Fig.2. Graphical Representation of evaluation parameters.

So by comparing some of the tuples from dataset values for accuracy, specificity, sensitivity, precision, recall, f measure and runtimes metrics are evaluated. Accuracy measurement results are better for Extended Sub Tree as compared to ID3 algorithm while as for runtime measurement Extended Sub Tree requires more time for evaluation as compared to ID3 algorithm

Conclusion

Clinical Decision Support System for heart diseases is very effective tool for diagnosing the diseases. System will give decision of probability for patient been prone to heart diseases. Hence for implementation of such system Decision Tree technique will be an effective technique in classification. It is a simple tree like flowchart structure which helps in bifurcating the data in respective groups. The main goal of Decision Trees is in the intuitive representation that is easy to understand and comprehend. Also in decision tree construction, the nodes are constructed on splitting attribute or the flag value. Hence if continuous value is to be handled then it can prove to be fatal. So by comparing above parameters values, it proved the hypothesis that Extended Sub Tree is better approach than ID3 algorithm.

Acknowledgment

Every orientation work has an imprint of many people and it becomes the duty of author to express deep gratitude for the same. I take this opportunity to express my deep sense of gratitude towards my esteemed guide Mrs. Manisha Petare for giving me this splendid opportunity to select and present this project and also providing facilities for successful completion. I thank Prof. Suhasini Itkar , Head, Department of Computer Engineering, for opening the doors of the department towards the realization of the project report, all the staff members, for their indispensable support, priceless suggestions and for most valuable time lent as and when required. With all respect and gratitude, I would like to thank all the people, who have helped me directly or indirectly.

References

[1] Ali Shahbazi and James Miller"*Extended Subtree: A new similarity function for Tree structured Data*", IEEE Transactions on knowledge and Data Engineering, Vol 25, No 4, April 2014.

[2] Christophe Damas, Bernard Lambeau, and Axel van Lamsweerde ,"*Analyzing Critical Decision-Based Processes* ", IEEE Transcations on Software Engineering, Vol. 40, No. 4 , April 2014

[3]]Tapuria,A., Austin, T., Sun, S., Lea, N., Iliffe S., Kalra, D., Ingram, D., Patterson, D., " *Clinical Advantages of decision support tool for anti coagulation control*", 2013 IEEE Point - of - Care Healthcare Technologies (PHT), Banglore, India, 16 - 18 January 2013.

[4] Rodrigo C. Barros, M´arcio P. Basgalupp, Andr´e C. P. L. F. de Carvalho and Alex A. Freitas," *A Survey of Evolutionary Algorithms for Decision Tree Induction* ", IEEE Transcations on Systems, Man ,and Cybernetics - Part C: Applications & Reviews , Vol. X, No. X , January 2012.

[5] Gwenole Quellec, Mathieu Lamard, Lynda Bekri, Guy Cazuguel; "*Medical Case Retrieval From a Committee of Decision Trees*", IEEE Transactions On Information Technology in Biomedicine , Vol. 14, No. 5, September 2011.

[6] Kittipol Wisaeng ,"*Predict the Diagnosis of Heart Disease Using Feature Selection and k-Nearest Neighbor Algorithm* ",Applied Mathematical Sciences, Vol. 8, no. 83, 4103 - 4113, 2014..

[7] Dhanashree S. Medhekar1, Mayur P. Bote2, Shruti D. Deshmukh, "*Heart Disease Prediction System using Naive Bayes*", INTERNATIONAL JOURNAL OF ENHANCED RESEARCH IN SCIENCE TECHNOLOGY & ENGINEERING VOL. 2 ISSUE 3, ISSN NO: 2319-7463, MARCH.-2013.

[8] Shamsher Bahadur Patel 1, Pramod Kumar Yadav2, Dr. D. P.Shukla," *Predict the Diagnosis of Heart Disease Patients Using Classification Mining Techniques*", IOSR Journal of Agriculture and Veterinary Science (IOSR-JAVS) e-ISSN: 2319-2380, p-ISSN: 2319-2372. Volume 4, Issue 2, PP 61-64 , July - August 2013 .

[9] Chaitrali S. Dangare Sulabha S. Apte, " *Improved Study of Heart Disease Prediction System using Data Mining Classification Techniques* ","International Journal of Computer Applications (0975 – 888) Volume 47– No.10, June 2012 .

[10] R. S. Bichkar,Dipak V. Patil,"*Issues in Optimization of Decision Tree Learning*: A Survey", International Journal of Applied Information

systems (IJAIS) – ISSN : 2249-0868 Foundation of Computer Science FCS, New York, USA Volume 3 – No.5, July 2012 .

[11] Hadi Sadoghi Yazdi,and Nima Salehi-Moghaddami," Multi *Branch Decision Tree: A New Splitting Criterion*",International Journal of Advanced Science and Technology Vol. 45, August, 2012.

[12] Miss. Chaitrali S. Dangare1, Dr. Mrs. Sulabha S. Apte, "*A DATA MINING APPROACH FOR PREDICTION OF HEART DISEASE USING NEURAL NETWORKS*", INTERNATIONAL JOURNAL OF COMPUTER ENGINEERING & TECHNOLOGY (IJCET), ISSN 0976 – 6375, Volume 3, Issue 3, pp. 30-40, October - December 2012.

[13] P.K. Anooj, "*Clinical decision support system: Risk level prediction of heart disease using weighted fuzzy rules*",Journal of King Saud University – Computer and Information Sciences , 2012.

[14] Yang Zhang,Simon Fong,Jinan Fiaidhi,and SabahMohammed, "*Real-Time Clinical Decision Support Systemwith Data StreamMining*", Hindawi Publishing Corporation Journal of Biomedicine and Biotechnology Volume 2012.

[15] Mrs.G.Subbalakshmi,Mr. K. Ramesh, Mr. M. Chinna Rao ,"*Decision Support in Heart Disease Prediction System using Naive Bayes*" Indian Journal of Computer Science and Engineering (IJCSE), ISSN : 0976-5166 Vol. 2 No. 2 , Apr-May 2011.

[16] Sunita Pachekhiya, Gwalior,"*DISEASE DIAGNOSIS OF HEART MUSCLES USING ERROR BACK PROPAGATION NEURAL NETWORK*", International Journal of Engineering Science and Technology (IJEST), ISSN : 0975-5462 Vol. 3 No. 7, July 2011.

[17] Mai Shouman, Tim Turner, Rob Stocker,"*Using Decision Tree for Diagnosing Heart Disease Patients*", Proceedings of the 9-th Australasian Data Mining Conference (AusDM'11), Ballarat, Australia, CRPIT Volume 121 - Data Mining and Analytics 2011.

[18]]M. ANBARASI,E. ANUPRIYA, N.CH.S.N.IYENGAR, "Enhanced *Prediction of Heart Disease with Feature Subset Selection using Genetic Algorithm* ",International Journal of Engineering Science and Technology Vol. 2(10), 5370-5376, ISSN: 0975-5462, 2010.