Mine Blood Donors Information Through Fuzzy Neural Network Algorithm

Rajeswari.V [1], M. Jaikumar [2]

ABSTRACT

The growing demand within the bank sector makes it necessary to use the complete potential of hold on knowledge with efficiency. Data processing will contribute with necessary edges to the bank sector; it is often an elementary tool to research the info gathered by blood banks through their information systems. During this paper an endeavor has been created to classify and predict the amount of blood donors in line with their age and cluster blood type people. J48 algorithmic rule and weka tool are used for the entire analysis work. weka tool are used for the entire analysis work .the projected analysis work for bank sector notice the people and donor details (name, blood group, age) there we have a tendency to mistreatment classification and clump algorithmic rule k means and pca and that we projected the neurofuzzy classification algorithmic rule is show the high economical classification compared to different classification. The projected algorithmic rule is high accuracy and low price, period. finding the behavior and attitude for blood donor.

Keywords - Data mining, Blood Bank Dataset, Blood Donors, Classification Algorithm, data classification, pca, fuzzy based classification, euro fuzzy classification.

[1]M.Phil Research Scholar, Sri Ramakrishna Mission Vidyalaya College of Arts and Science, Coimbatore – 641 020, Tamil Nadu, India Email: raji_venkat2006@yahoo.com, raji.venkat2014@gmail.com

[2]Assistant Professor & Head, Dept of Computer Applications (UG), Sri Ramakrishna Mission Vidyalaya College of Arts and Science, Coimbatore – 641 020, Tamil Nadu, India Email: jai2911@gmail.com

I. INTRODUCTION

Data Mining is a technology used to describe knowledge discovery and to search for significant relationships such as patterns, association and changes among variables in databases. Medical science industry has huge amount of data. With the growth of the blood banks, enormous Blood Banks Information Systems (BBIS) and databases are produced. It creates a need and challenge for data mining. Data mining is just a step in KDD which is used to extract interesting patterns from data that are easy to perceive, interpret, and manipulate. Several major kinds of data mining techniques, including generalization, characterization, classification, clustering, association rule mining, evolution, pattern matching, data visualization and meta-rule guided mining will be reviewed. The explosive growth of databases makes the scalability of data mining techniques increasingly important. Data mining algorithms have the ability to rapidly mine vast amount of data [1].

Clustering has been used extensively as a vital tool of data mining. Data gathering has been deliberated widely, but mostly all identified usual clustering algorithms lean towards to break down in high dimensional spaces because of the essential sparsely of the data points. Present subspace clustering methods for handling high-dimensional data focus on numerical dimensions. The main idea of feature selection is to choose a subset of input variables by eliminating features

with little or no predictive information [2]. Feature selection can significantly improve the comprehensibility of the resulting classifier models and often build a model that generalizes better to unseen points. In the unsupervised clustering problem, there are no universally accepted measures of accuracy and no class labels. Another reason that many clustering algorithms struggle with high dimensional data is the curse of dimensionality. As the number of dimensions in a dataset increases, distance measures become increasingly meaningless [3]. In higher dimensional datasets this problem becomes even worse and the clusters become impossible to find, suggesting that we consider fewer dimensions.

Feature selection is an important topic in data mining, especially for high dimensional datasets. Feature selection (also known as subset selection) is a process commonly used in machine learning, wherein subsets of the features available from the data are selected for application of a learning algorithm. The best subset contains the least number of dimensions that most contribute to accuracy; we discard the remaining, unimportant dimensions [4]. This is an important stage of preprocessing and is one of two ways of avoiding the curse of dimensionality (the other is feature extraction). There are two approaches in Feature selection known as Forward selection and backward selection. Feature selection has been an active research area in pattern recognition, statistics, and data mining communities. The main idea of feature selection is to choose a subset of input variables by eliminating features with little or no predictive information [5]. Feature selection methods can be decomposed into three broad classes. The aim of our work was to investigate the performance of different Neuro-Fuzzy classification methods for the distinction of benign and malign tissue in ultrasound prostate diagnosis [6]. This study was done on segments with confirmed histology in small regions of interest within the area and it continuing to gather blood data in order to result a data base of benign and malign tissue in genes. Our results suggest that Neuro-Fuzzy classification algorithms have the potential to significantly improve common classification methods for the use in data [7].

II. Related Work

The vital aim of the data mining is to explore information from a data set and transform it into a meaningful structure for research in future. Mostly conventional clustering algorithms do not scale better to cluster high dimensional data sets in terms of success and proficiency, due to the natural sparsity of high dimensional data. In high dimensional data sets, there come across many problems [8]. The distance between any two data points becomes exacts the same, so it is difficult to differentiate same data points from unlike data points. Clusters are implicit in the subspaces of the high dimensional data space, and different clusters may available in various subspaces of different dimensions leads to another problem [9]. Because of these problems, almost all conventional clustering algorithms fail to work well for high dimensional data sets.

Feature selection includes classifying a subset of the most functional features that generates well-suited results as the

original entire set of features [10]. A feature selection algorithm may be compared from both the competence and success points of view. The resemblance between objects is frequently processed using distance measures over the different dimensions in the dataset [11]. Advanced Technology made data collection simple, quick, and results in larger, complex datasets with more objects and dimensions. As the datasets become larger and differs, alterations to existing algorithms are needed to hold cluster values and speed [12]. A traditional clustering algorithm predicts all of the dimensions of an input dataset help in order to learn as much as potential about each object explained. In high dimensional data, most of the dimensions are frequently irrelevant [13]. The results must be carefully analyzed to ensure they are meaningful. The algorithms must be efficient in order to scale with the increasing size of dataset [14].

K Means Algorithm

The k-means algorithm is one of the most widely used clustering algorithms and has been applied in many fields of science and technology. One of the major problems of the k-means algorithm is that it may produce empty clusters depending on initial center vectors [15]. For static execution of the k-means, this problem is considered insignificant and can be solved by executing the algorithm for a number of times. In situations, where the k-means is used as an integral part of some higher level application, this empty cluster problem may produce anomalous behavior of the system and may lead to significant performance degradation. This paper presents a modified version of the k-means algorithm that efficiently eliminates this empty cluster problem [16].

K-means clustering is a method of vector quantization, originally from signal processing, that is popular for cluster analysis in data mining. K-means clustering aims to partition n observations into k clusters in which each observation belongs to the cluster with the nearest mean, serving as prototype of the cluster. This results in a partitioning of the data space into Voronoi cells [17].

The problem is computationally difficult (NP-hard); however, there are efficient heuristic that are commonly employed and converge quickly to a local optimum. These are usually similar to the expectation-maximization algorithm for mixtures of Gaussian distribu-tions via an iterative refinement approach employed by both algorithms. Additionally, they both use cluster centers to model the data; however, k-means clustering tends to find clusters of comparable spatial extent, while the expectation-maximization mechanism allows clusters to have different shapes [18].

Given a set of observations (x1, x2, ..., xn), where each observation is a d-dimensional real vector, k-means clustering aims to partition the n observations into k ($\leq$ n) sets S = {S1, S2, ..., Sk} so as to minimize the within-cluster sum of squares (WCSS). In other words, its objective is to find:

$$\arg\min_{\mathbf{S}} \sum_{i=1}^{k} \sum_{\mathbf{x} \in S_i} \|\mathbf{x} - \boldsymbol{\mu}_i\|^2$$

Where μ_i is the mean of points in S_i.

III. Proposed Algorithm Approach

Enhanced k means algorithm

The aim of the proposed algorithm is to improve the computational efficiency of the K Means algorithm. The algorithm involves initial centroid selection, which is done randomly in existing Algorithm [19]. Hence we propose an algorithm which selects initial centroids based on the distances calculated from the origin. One of the most popular clustering algorithms is k-means clustering algorithm, but in this method the quality of the final clusters relay heavily on the initial centroids, which are selected randomly. Moreover, the k-means algorithm is computationally very expensive also. The proposed algorithm is found to be more accurate and efficient compared to the original k-means algorithm [20]. This proposed method finding the better initial centroids and provides an efficient way of assigning the data points to the suitable clusters. This method ensures the total mechanism of clustering in O(nlogn) time without loss the correctness of clusters. This approach does not require any additional inputs like threshold values [21]. The proposed algorithm produces the more accurate unique clustering results. The value of k, desired number of clusters is still required.

Step 1: In the given data set D, if the data points contain the both positive and negative.

Step 2: Find the minimum attribute value in the given data set D.

Step 3: For each data point attribute, subtract with the minimum attribute value.

Step 4: For each data point calculate the distance from origin.

Step 5: Sort the distances obtained in step 4. Sort the data point's accordance with the distances.

Step 6: Partition the sorted data points into k equal sets.

Step 7: In each set, take the middle point as the initial centroid.

Step 8: Compute the distance between each data point di ($1 <= i <= n$) to all the initial centroids cj ($1 <= j <= k$).

Step 9: For each data point di, find the closest centroid cj and assign di to cluster j.

Step 10: Set Clustered[i]=j. // j:Id of the closest cluster.

Step 11: Set Nearest Dist[i]= d(di, cj).

Step 12: For each cluster j ($1 <= j <= k$), recalculate the centroids.

Step 13: For each data point di.

Step 14: Compute its distance from the centroid of the present nearest cluster.

In cluster analysis, the k-means algorithm can be used to partition the input data set into k partitions (clusters). However, the pure k-means algorithm is not very flexible, and as such of limited use (except for when vector quantization as above is actually the desired use case!) [22]. In particular, the parameter k is known to be hard to choose (as discussed below) when not given by external constraints. In contrast to other algorithms, k-means can also not be used with arbitrary distance functions or be use on non-numerical data.

The basic k-means algorithm is commonly measured by any of intra-cluster or inter-cluster criterion. A typical intra-cluster criterion is the squared-error criterion (Equation 1). It is the most commonly used and a good measure of the within-cluster variation across all the partitions. For the current work, we consider intra-cluster squared-error function to evaluate the present scheme of clustering. In basic k-means algorithm, a set D of d dimensional data is partitioned into K clusters, starting with a set of K randomly generated initial center vectors [23].

The process iterates through the following steps:

- Assignment of data to representative centers upon minimum distance, and
- Computation of the new cluster centers.

The process stops when cluster centers (or the metric M) become stable for two consecutive iterations. The basic k-means algorithm is greedy in nature.

K-means is the most popular and easy-to-understand clustering algorithm. The main idea of K-means is summarized in the following steps:

Arbitrarily choose k objects to be the initial cluster centers/centroids;

Assign each object to the cluster associated with the closest centroid;

Compute the new position of each centroid by the mean value of the objects in a cluster; and Repeat Steps 2 and 3 until the means are fixed.

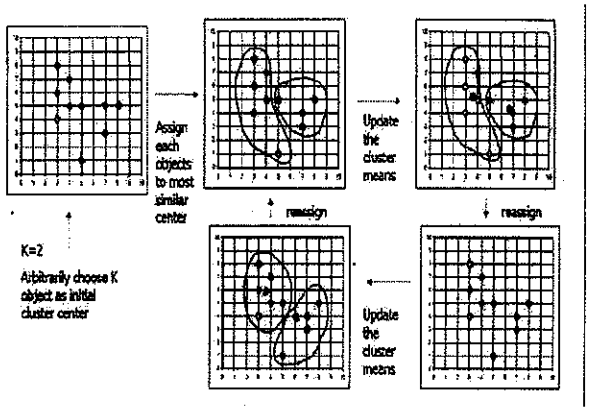


Figure 1: The process of K-means clustering algorithm.

The k-means is possibly the most commonly-used clustering algorithm. It is most effective for relatively smaller data sets. The k-means finds a locally optimal solution by minimizing a distance measure between each data and its nearest cluster center [24]. Many parallel versions of the k-means algorithm use the basic serial k-means at their core. Besides, a number of stochastic clustering algorithms make use of the basic k-means or some of its variations. Very often these algorithms are based on Simulated FNN dealing or Genetic Algorithms.

The k-means clustering algorithm faces two major problems. One is the problem of obtaining non-optimal solutions. As the algorithm is greedy in nature, it is expected to converge to a locally optimal solution only and not to the global optimal solution, in general. This problem is partially solved by applying the k-means in a stochastic framework like simulated FNN and genetic algorithm (GA) etc. The second problem is that of empty cluster generation [25]. This problem is also referred to as the singularity problem in literature. Singularity in clustering is obtained when one or more clusters become empty. Both the problems are caused by bad

initialization. Algorithms that use the k-means at their core suffer from the empty cluster problem too.

A very common practice to solve these problems is to repeat the initialization until we receive a set of good initial center vectors. In practice, after center initialization, we assign elements to the concerned clusters. If an empty cluster is found, at this early stage, a re-initialization takes place [26]. This process is repeated until all non-empty initial clusters are formed. This is, however, an ad-hoc technique. Several other methodical approach are also found, a refinement approach is proposed, where starting with a number of initial samples of the data set we can obtain a number of sets of center vectors. These center vectors then pass through a refinement stage to generate a set of so called good starting vectors. In [21], a genetically guided k-means has been proposed where possibility of generation of empty clusters is treated in the mutation stage. Several k-d-tree based methods are found in [17] and [18]. Another approach to initialize cluster centers based on values for each attribute of the data set has been proposed in [19]. These methods are time costly and may not be applicable by keeping the k mean's inherently simple structure.

IV. Result and Analysis

FUZZY NEURAL NETWORK AND PCA

In this research work a new approach for process monitoring was proposed. This approach was a kind of Principal component analysis based on EFNN. The reason for using fuzzy system was the Power of this system in approximating nonlinearity with arbitrary accuracy. We proposed PCA-FNN method to optimize the parameters. The PCA-FNN is proposed to categorize the blood and through the analysis, the improved method arises the recognition rate in some dimension. In this paper, only binary classification problems were considered for the experiments but multiclass problems will be investigated in the future.

Classification results of the disorder data set are collected to measure is study with respect to classification accuracy [27]. The proposed algorithm PCA-FNN was applied. Randomly half of the samples were selected for training and all samples for testing. Results are depicted in Table 2 showing the average training accuracy and the corresponding best test accuracy for gene subset of 2 and 3 genes. Best results were achieved with gene sets are shown in Table 1.

Table-1: Best Results with gene set

Name	Number of Samples	
	Blood Donors	Normal cell
PCA	36	26
CART	39	11
PCA+FNN	41	32

Blood Type O

Type O's are outgoing, and very social. They are initiators, although they don't always finish what they start. Creative and popular, they love to be the center of attention and appear very self confident.

Blood Type A

While outwardly calm, they have such high standards (perfectionists) that they tend to be balls of nerves on the inside. Type A's are the most artistic of the blood groups. They can be shy, are conscientious, trustworthy, and sensitive.

Blood Type B

Goal oriented and strong minded, type B's will start a task and continue it until completed, and completed well. Type B's are the individualists of the blood group categories and find their own way in life.

Blood Type AB

Type AB's are the split personalities of the blood groups. They can be outgoing and shy, confident and timid. While responsible, too much responsibility will cause a problem. They are trustworthy and like to help others.

Different blood data sets generated from the hospital using two different samples for experimental study. The details of the data sets, e.g., their availability, number of samples, number of genes, and partition for the experiment, are given [28].

Further, we separate the validation set from the training set by taking 20 percent samples from the training set. All the data set is normalized (feature wise) by subtracting the training mean and then dividing by the standard deviation of the same training Data.

Table 2: Performance comparison of PCA-FNN method with other classifiers

Method name	Accuracy in %	Speed in seconds
Combination of PCA & FNN method	96.23	186.29
Other Classifiers85.08	536.65	

Consequently, the researchers classify the microarray data sets by using the FNN algorithm and this EFNN put together essential features of fuzzy generalization. By considering the lesser amount of genes needed by the EFNN and its elevated accuracy, it is to be concluded that the EFNN classifier not only supports biological researchers to differentiate bloods that are complex to be classified using normal clinical techniques, but also helps biological researchers to focus on a minimum number of important genes to explore the relationships among those significant genes and the development of bloods [29].

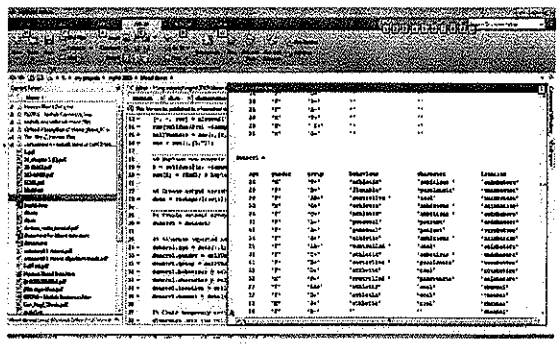


Figure 2: Blood Donors Dataset

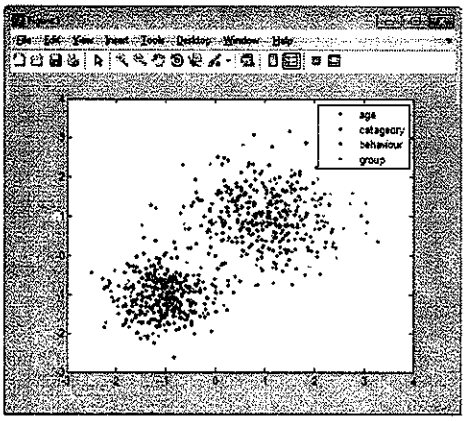


Figure 3: Classify the data using Algorithm

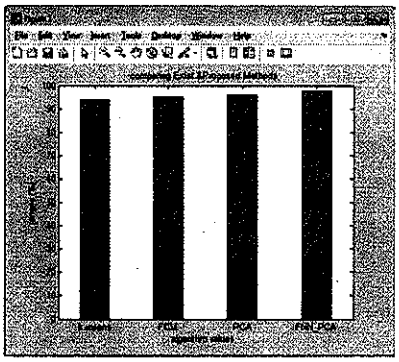


Figure 4: Accuracy comparison for classification algorithms

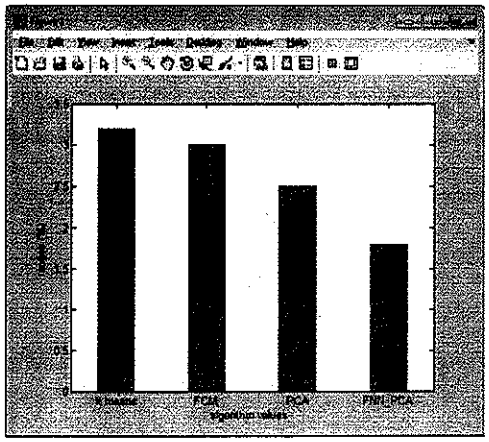


Figure 5: Time period calculation and analysis

Principal component analysis (PCA) is an essential method in the framework of the various analysis methods. It is successfully used in many areas such as pattern recognition, process monitoring, data compression, and feature extraction, image processing and signal analysis. It is due to reason of its easiness and capability in processing massive amount of process data, PCA is identified as a dominant tool of statistical process care and widely used in the area for fault detection and diagnosis. The Proposed method acts well discriminating influence in gene expression research. The PCA-EFNN [5] offers better classification accuracy than any other classifier [30]. The experimental results are presented to establish the contribution of each factor used to optimize the FNN by using PCA method. First, we already quoted the reason for using the PCA for the model selection of a FNN. The comparison between GA search and PCA-FNN based model selection method in terms of average CPU time and testing accuracy. It has been empirical that many permutations may offer with similar validation and accuracy and the final sample can be trained by any one among them. The results in all the data sets prove that the EFNN-PCA can achieve 95.8% accuracy with a much lesser amount of genes. The experimental study shows that the PCA-EFNN model is very effective in terms of both evaluation time and classification performance [31].

Neuro Fuzzy classification

In the field of artificial intelligence, **neuro-fuzzy** refers to combinations of artificial neural networks and fuzzy logic. Neuro-fuzzy was proposed by J. S. R.

Jang. Neuro-fuzzy hybridization results in a hybrid intelligent system that synergizes these two techniques by combining the human-like reasoning style of fuzzy systems with the learning and connectionist structure of neural networks. Neuro-fuzzy hybridization is widely termed as Fuzzy Neural Network (FNN) or Neuro-Fuzzy System (NFS) in the literature. Neuro-fuzzy system (the more popular term is used henceforth) incorporates the human-like reasoning style of fuzzy systems through the use of fuzzy sets and a linguistic model consisting of a set of IF-THEN fuzzy rules. The main strength of neuro-fuzzy systems is that they are universal approximates with the ability to solicit interpretable IF-THEN rules.

The strength of neuro-fuzzy systems involves two contradictory requirements in fuzzy modeling: interpretability versus accuracy. In practice, one of the two properties prevails. The neuro-fuzzy in fuzzy modeling research field is divided into two areas: linguistic fuzzy modeling that is focused on interpretability, mainly the Mamdani model; and precise fuzzy modeling that is focused on accuracy, mainly the Takagi-Sugeno-Kang (TSK) model.

Although generally assumed to be the realization of a fuzzy system through connectionist networks, this term is also used to describe some other configurations including:

- Deriving fuzzy rules from trained RBF networks.
- Fuzzy logic based tuning of neural network training parameters.
- Fuzzy logic criteria for increasing a network size.
- Realizing fuzzy membership function through clustering algorithms in unsupervised learning in SOMs and neural networks.
- Representing fuzzification, fuzzy inference and de-fuzzification through multi-layers feed-forward connectionist networks.

In this research work a new approach for process monitoring was proposed. This approach was a kind of Principal component analysis based on FNN. The reason for using fuzzy system was the Power of this system in approximating nonlinearity with arbitrary accuracy [32]. We proposed PCA-EFNN method to optimize the parameters. The PCA-EFNN is proposed to categorize the blood and through the analysis, the improved method arises the recognition rate in some dimension. In this paper, only binary classification problems were considered for the experiments but multiclass problems will be investigated in the future. Classification results of the -disorder data set are collected to measure is study with respect to classification accuracy. The proposed algorithm PCA-EFNN was applied. Randomly half of the samples were selected for training and all samples for testing. Results are depicted in showing the average training accuracy and the corresponding best test accuracy for gene subset of 2 and 3 genes are best results

V. Conclusion

Blood data research is one of the major research areas in the medical science. Accurate prediction of various blood types has maximum value in providing extended treatment and harmfulness reduction on the patients. In

the earlier, blood data categorization is generally depends on Morphological and clinical analysis. The key benefit of the creating an extended definition based on the donor definition provides a standard model to determine the donor behavior and provides the capability to build a classification model.

The research proposed an efficient approach for blood data classification based on microarray gene expression data giving out the best prediction strength using minimal gene subsets and the results have proven to be the best with the PCA-FNN method than with that of other previous methods. The method was implemented to prove the importance of gene ranking and selection prior to classification, which improves the Accuracy.

In this research work, the algorithm such as fuzzy neural network, k-means clustering principal component analysis are used to find number of blood donors in the sample data set. The sample dataset has been taken for research work.

While comparing to those algorithms is better Fuzzy neural network algorithm the merits of time concern and correct identification algorithm. The performance is also evaluated effectively by using the result of the specified algorithms.

The Research is focused on promising accuracy results with very few number of gene subsets enabling the doctors to predict the type of blood data. In general the Principal Component Analysis and the Fuzzy Neural Network handles the level of blood data that data as good as than other classification systems. This supports our earlier findings using Fuzzy neural networks. The results on datasets shows the importance of the same classifier used for both the gene selection and classification can improve the strength of the model.

References

[1] Badgett RG: How to search for and evaluate medical evidence. Seminars in Medical. Practice 1999, 2:8-14, 28.

[2] Jaiwei Han and Micheline Kamber, *'Data Mining Concepts and Techniques'*, Second Edition, Morgan Kaufmann Publishers.

[3] *'Data Mining Introductory and Advanced Topics'* by Margaret H. Dunham

[4] Heatley S. I need to know about fresh frozen plasma. Australian Red Cross Blood Service, 2009.

[5] B.G. Prema Sudha et al., *'An Application to find spatial distribution of Blood Donors from Blood Bank Information'*, Vol. II, Issue No.2, July-December 2009.

[6] Jian Mu et al., *'Segmentation, Reconstruction, and analysis of blood thrombus formation in 3 D-2photon microscopy images'*, EURASIP Journal on Advances in Signal Processing, 10 July 2009.

[7] Abdur Rashid Khan et al., *'Web based Information System for Blood Donation'*, International Journal of digital content Technology and its applications, Vol. 3, Issue No.2, July 2009.

[8] G. Satyanaryana Reddy et al; *'Management Information System to help Managers for providing decision making in any organization'.*

[9] T. Santhanam and Shyam Sunderam: *'Application of Cart Algorithm in Blood donor's classification'*, Journal of computer Science Vol. 6, Issue 5.

[10] Zhangetal. *'PP Look: an automated data mining tool for protein–protein interaction'*, BMC Bio-informatics, 2010.

[11] Dr. Varun Kumar, Luxmiverma; *'Binary classifiers for Health Care databases - A comparative study of data mining classification algorithms in the diagnosis of Breast cancer'*, IJCST, Vol. I, Issue 2, December 2010.

[12] Vikram Singh and Sapna Nagpal; *'Interactive Knowledge discovery in Blood Transfusion Data Set'*; VSRD International Journal of Computer Science and Information Technology; Vol. I, Issue 8, 2011.

[13] Wen-Chan Lee and Bor-Wen Cheng; *'An Intelligent system for improving performance of blood donation'*, Journal of Quality, Vol. 18, Issue No. II, 2011.

[14] P. Ramachandran et al. *'Classifying blood donors using data mining techniques'*; IJCST, Vol. I, Issue 1, February 2011.

[15] F. Zabihi et al. *'Rule Extraction for Blood donators with fuzzy sequential pattern mining'*; The Journal of mathematics and Computer Science; Vol. II, Issue No. I, 2011.

[16] Shyam Sundaram and Santhanam T: *'A comparison of Blood donor classification data mining models'*, Journal of Theoretical and Applied Information Technology, Vol. 30, No. 2, 31 August 2011.

[17] Shyam Sundaram and Santhanam T; *'Real Time Blood donor management using Dash boards based on Data mining models'*, International Journal of Computing issues, Vol.8, Issue5, No.2, September 2011.

[18] Prof. Dr. P.K. Srimani et al. *'Outlier data mining in medical databases by using statistical methods'*, Vol. 4, No. 1, January 2012.

[19] Alaa Hamouda et al; *'Automated Red Blood Cells counting'*, International Journal of Computing Science, Vol. 1, No. 2, February 2012.

[20] Ivana D. Radojevic et al. *'Total coliforms and data mining as a tool in water quality monitoring'*, African Journal of Microbiology Research, Vol. 6(10), 16 March 2012.

[21] Larose, D. T., *'Discovering Knowledge in Data: An Introduction to Data Mining'*, ISBN 0-471-66657-2, John Wiley & Sons, Inc., 2005.

[22] Qadeer, M.A., Imran, A., *"Asterisk Voice Exchange: An Alternative to Conventional EPBX"*, International Conference on Computer and Electrical Engineering, 2008. ICCEE 2008.

[23] Kapicak, L., Nevlud, P., Zdralek, J., Dubec, P., Plucar, J. *"Remote control of Asterisk via Web Services"*, 34th International Conference on

Telecommunications and Signal Processing (TSP), 2011.

[24] M. Voznak, L. Kapicak, J. Zdralek, P. Nevlud and J. Plucar, *"Multimedia services in Asterisk based on Voice XML"*, International journal of mathematical models and methods in applied sciences.

[25] Peter Marbach, Oliver Mihatsch, and John N. Tsitsiklis, *"Call Admission Control and Routing in Integrated Services Networks Using Neuro-Dynamic Programming"*, IEEE Journal on selected areas in communications, Vol. 18, No. 2, February 2000.

[26] Sripanidkulchai, K., Shu Tao, Zon-Yin Shae, *"DA VINCI: A tool to improve VoIP call routing configurations"*, IEEE Network Operations and Management Symposiwn (NOMS), 2010.

[27] Bing-Nan Li, Taipa Ming-Chui Dong, Vai, M.I. *"From Codabar to ISBT 128: Implementing Barcode Technology in Blood Bank Automation System"*, 27th Annual International Conference of the Engineering in Medicine and Biology Society, 2005.IEEE-EMBS 2005.

[28] Spyropoulos, B., Botsivaly, M., Tzavaras, A., Spyropoulou, P. Towards *"Digital blood-banking"*, ITU-T Kaleidoscope: Innovations for Digital Inclusions, 2009. K-IDI 2009.

[29] Adetunj I, A., Larij Ani, H., "Routing with a bandwidth based algorithm in virtual call centres", IEEE Network Operations and Management Symposium, 2008. NOMS 2008

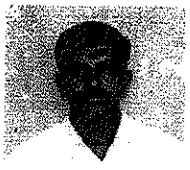
[30] Meza, M., Tasic, J.F., *"Support of the blood transfusion diagnostic process with tele medicine"*. The International Conference on Computer as a Tool, 2005. EUROCON, 2005.

[31] Soo-Jung Kim, Sun K. Yoo, Hyun-Ok Kim, HaSuk Bae, Jung-Jin Park, Kuk-Jin Seo and Byung Chul Chang, *"Smart Blood Bag Management System in a Hospital Environment"*, International Federation for Information Processing 2006 -017.

[32] Blood Safe. Flippin Blood – an administration guide. Australia, 2006.

AUTHORS PROFILE

Rajeswari completed M.Sc Computer Science and currently pursuing M.Phil in Computer Science at Sri Ramakrishna Mission Vidyalaya College of Arts and Science, Coimbatore-20. Her teaching experience is 3 years. Her area of interest is Data Mining



M. JaiKumar completed MCA at Bharathiar University, M.Phil at Bharathiar University and currently pursuing Ph.D in Sri Ramakrishna Mission Vidyalaya College of Arts and Science. He working as Assistant Professor & Head of the Dept. of Computer Applications Department (UG) in Sri Ramakrishna Mission Vidyalaya College of Arts and Science, Coimbatore-20. His teaching experience is 10 years. His area of interest is Software Engineering and Data Mining.