Utilization of Data Mining Techniques for Prediction and Diagnosis of Major Life Threatening Diseases Survivability-Review

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Abstract—Data mining is defined as shifting through very large amounts of data for useful information. Some of the most important and popular data mining techniques are association rules, classification, clustering, prediction and sequential patterns. Data mining techniques are used for variety of applications. In health care industry, data mining plays an important role for predicting diseases. For detecting a disease number of tests should be required from the patient. But using data mining technique the number of test should be reduced. This reduced test plays an important role in time and performance. This technique has an advantages and disadvantages. This research paper analyzes how data mining techniques are used for predicting different types of major life threatening diseases. It reviewed the research papers which mainly concentrated on predicting heart disease, Diabetes, Breast cancer, HIV/AIDS and Tuberculosis.

Index Terms—Breast Cancer, Data mining techniques, Diabetes, Heart disease, HIV/AIDS and Tuberculosis.

1 INTRODUCTION

Data mining is a broad area that integrates techniques from several fields including machine learning, statistics, pattern recognition, artificial intelligence, and database systems, for the analysis of large volumes of data. There have been a large number of data mining algorithms rooted in these fields to perform different data analysis tasks. Data Mining is the process of extracting hidden knowledge from large volumes of raw data. The knowledge must be new, not obvious, and one must be able to use it. Data mining has been defined as “the nontrivial extraction of previously unknown, implicit and potentially useful information from data. It is “the science of extracting useful information from large databases”. It is one of the tasks in the process of knowledge discovery from the database. Data Mining is used to discover knowledge out of data and presenting it in a form that is easily understood to humans. It is a process to examine large amounts of data routinely collected. Data mining is most useful in an exploratory analysis because of nontrivial information in large volumes of data. It is a cooperative effort of humans and computers. Best results are achieved by balancing the knowledge of human experts in describing problems and goals with the search capabilities of computers. There are two primary goals of data mining tend to be prediction and description. Prediction involves some variables or fields in the data set to predict unknown or future values of other variables of interest. On the other hand Description focuses on finding patterns describing the data that can be interpreted by humans. The Disease Prediction plays an important role in data mining. There are different types of diseases predicted in data mining namely Hepatitis, Lung Cancer, Liver disorder, Breast cancer, Thyroid disease, Diabetes, HIV/AIDS and Tuberculosis etc...

2 REVIEW OF THE RELATED LITERATURE

2.1 Heart Disease Prediction

Medical data mining has high potential for exploring the hidden patterns in the data sets of the medical domain. These patterns can be utilized for clinical diagnosis for widely distributed in raw medical data which is heterogeneous in nature and voluminous. These data should be collected in an organized form. This collected data can be integrated to form a hospital information system. Data mining technology provides a user oriented approach to novel and hidden patterns in the data. From the analysis of World Health Organization, they estimated 12 million deaths occur worldwide, every year due to the Heart diseases. Half the deaths occur in United States and other developed countries due to cardio vascular diseases. On the above discussion, it is regarded as the primary reason behind deaths in adults. Heart disease kills one person every 34 seconds in the United States. The following paper reviewed about predicting of heart disease using data mining technique. Jyoti Soni et. al [3] proposed three different supervised machine learning algorithms. They are Naïve Bayes, k-NN, and Decision List algorithm. These algorithms have been used for analyzing the heart disease dataset [14]. Tanagra data mining tool is used for classifying these data. These classified data is evaluated using 10 fold cross validation and the results are compared. Decision tree is one of the popular and important classifier which is easy and simple to implement. It doesn’t have domain knowledge or parameter setting. It handle huge amount of dimensional data. It is more suitable for exploratory knowledge discovery. The results attained from Decision Tree are easier to interpret and read [1]. Naïve Bayes is a statistical classifier which assigns no dependency between attributes. To
determine the class the posterior probability should be maximized. The advantages are one can work with the naïve bayes model without using any Bayesian methods. Here Naïve Bayes Classifiers performs well. [1] k-nearest neighbor’s algorithm (k-NN) is the one of the important method for classifying objects based on closest training data in the feature space. It is simplest among all machines learning algorithm but, the accuracy of k-NN algorithm can be degraded by presence of noisy features. This observation is performed using training to consist 3000 instances with 14 different attributes. The dataset is divided into two testing and training i.e. 70% of data are used for training and 30 % is used for testing. The authors concluded that Naïve Bayes algorithm performs well when compared to other algorithms.

Jyoti Soni et.al [3] proposed for predicting the heart diseases using the association rule data mining technique. In their work, unfortunately they have produced a large number of rules when association rules are applied to medical dataset. Most of the rules are medically irrelevant to the data. In [15], the authors proposed four constraints to reduce the number of rules i.e., item filtering, attribute grouping, maximum item set size and antecedent/consequent rule filtering. The important issue is without validation, the association rules are mined on the entire dataset. To solve these limitations, the author introduced an algorithm that uses search constraints to decrease the number of rules. The training set searches association rules and test set to check the validation. Here, a new parameter “lift” is used instead of support and confidence. Lift has been used as the metrics to evaluate the reliability and medical significance of association rules. To validate the results the two basic statistics sensitivity and specificity are used by medical doctors. The chance of correctly identifying sick patients are defined by sensitivity and chance of correctly identifying healthy individuals is defined by specificity. To find predictive association rules in medical dataset the algorithm has three steps: [15]

1. In medical dataset both the categorical and numeric attribute are transformed into transaction dataset.
2. To find the predictive association rules with medically relevant attributes the search process should be incorporate with the above mentioned four constraints.
3. To validate the association rules the train and test approach should be used.

Genetic algorithm have been used in [5], to reduce the actual data size to get the optimal subset of attributed sufficient for heart disease prediction. Classification is one of the supervised learning methods to extract models describing important classes of data. Three classifiers e.g. Decision Tree, Naïve Bayes and Classification via clustering have been used to diagnose the Presence of heart disease in patients. Classification via clustering: Clustering is the process of grouping same elements. This technique may be used as a preprocessing step before feeding the data to the classifying model. The attribute values need to be normalized before clustering to avoid high value attributes dominating the low value attributes. Further, classification is performed based on clustering. Experiments were conducted with Weka 3.6.0 tool [13]. Data set of 909 records with 13 attributes. All attributes are made categorical and inconsistencies are resolved for simplicity. To enhance the prediction of classifiers, genetic search is incorporated. Observations exhibit that the Decision Tree data mining technique outperforms other two data mining techniques after incorporating feature subset selection but with high model construction time. Naïve Bayes performs consistently before and after reduction of attributes with the same model construction time. Classification via clustering is not performing well when compared to other two methods.

In the survey of [6] Naïve bayes have been used to predict attributes such as age, sex, blood pressure and blood sugar and the chances of a diabetic patient getting a heart disease. The clinical dataset is having been collected from one of the leading diabetic research institute in Chennai. The records of 500 patients are taken. The data is analyzed and implemented in WEKA ("Waikato Environment for Knowledge Analysis") tool. Data mining finds out the valuable information hidden in huge volumes of data. Weka tool is a collection of machine learning algorithms for data mining techniques, written in Java. It consists of data pre-processing, classification, regression, association rules, clustering and visualization tools. We have used Naïve bayes method to perform the mining and classification process. We have used 10 folds cross validation to minimize any bias in the process and improve the efficiency of the process. From the experiment the result of bayes model was able to classify 74% of the input instances correctly. It exhibited a precision of 71% in average, recall of 74% in average, and F-measure of 71.2% in average. The results show clearly that the proposed method performs well compared to other similar methods in the literature, taking into the fact that the attributes taken for analysis are not direct indicators of heart disease.

Applying data mining in the medical field is a very challenging task in medical profession. In medical research the data mining begins with a hypothesis and results are adjusted to fit the hypothesis. This differs from standard data mining practice, which simply starts with datasets without an apparent hypothesis. [11]Patterns and trends in dataset are mainly concerned with traditional data mining, but in medical data mining they are not conformed. According to the doctor intuition the clinical decision are often made. The quality of service provided to patients is affected due to unwanted bias, errors and excessive medical cost. Data mining have the capacity to generate a knowledge-rich environment. It can help to improve the significant quality of clinical decision. [5] In the survey of [3] the three supervised machine learning algorithms are used. These algorithms have been used for analyzing the heart disease dataset. The Classification Accuracy should be compared for this algorithm. This work should be extended to predict the heart disease with reduced number of attributes. In
the survey of [3] the heart disease is predicted by using association rule data mining technique. The author introduced an algorithm that uses search constraint to decrease the number of rules. In future this work should be extended by using fuzzy learning models to find the accuracy of time to decrease the number of rules. In the survey of [4] the author proposed a new concept that uses weighted association rule for classification. In future this work can be extended by using association rule hiding technique in data mining. In the survey of [5] the author proposed the minimal subset of attributes for predicting heart disease. In future this work can be expanded and enhanced for the automation of heart disease prediction. Real data should be collected from health care organizations and agencies are taken to compare the optimum accuracy with all data mining technique. In the survey of [6] the author predicts attributes of a diabetic patient getting a heart disease. Weka tool is performed as a result bayes model was able to classify 74% of the input instances correctly. In future this work is extended by using other data mining techniques.

The Heart Disease Data Prediction is designed to support clinicians in their diagnosis for heart disease prediction. They typically work through an analysis of medical data and a knowledge base of clinical expertise. The quality of medical diagnostic decisions for heart disease can be increased by improvements to these Predicting systems [66]. Data mining provides a way to get the information buried in the data. Numerous experiments were conducted on linear and nonlinear characteristics of HRV (Heart Rate Variability) indices to assess several classifiers, e.g., Bayesian classifiers [67], CMAR (Classification based on Multiple Association Rules) [72], C4.5 (Decision Tree) [68] and SVM (Support Vector Machine) [64]. SVM surmounted the other classifiers. The problem of identifying constrained association rules for heart disease prediction was studied by Carlos Ordonez [63]. The assessed data set encompassed medical records of people having heart disease with attributes for risk factors, heart perfusion measurements and artery narrowing. Three constraints were introduced to decrease the number of patterns. First one necessitates the attributes to appear on only one side of the rule. The second one segregates attributes into uninteresting groups. The ultimate constraint restricts the number of attributes in a rule. Experiments illustrated that the constraints reduced the number of discovered rules remarkably besides decreasing the running time. Two groups of rules envisaged the presence or absence of heart disease in four specific heart arteries. Data mining methods may aid the clinicians in the prediction of the survival of patients and in the adaptation of the practices consequently. The work of Franck Le Duff et al. [65] might be executed for each medical procedure or medical problem and it would be feasible to build a decision tree rapidly with the data of a service or a physician. Comparison of traditional analysis and data mining analysis illustrated the contribution of the data mining method in the sorting of variables and concluded the significance or the effect of the data and variables on the condition of the study. The main drawback of the process was knowledge acquisition and the need to collect adequate data to create an appropriate model. In [70] Latha Parthiban et al. projected an approach on basis of coactive neuro-fuzzy inference system (CANFIS) for prediction of heart disease. L. Goodwin et.al [71] discussed different Data mining issues and opportunities for building nursing knowledge. In Lei Yu and Huan Liu [72] introduced a novel concept, predominant correlation, and proposed a fastfilter method which can identify relevant features as well as redundancy among relevant features without pair wise correlation analysis. The efficiency and effectiveness of their method is demonstrated through extensive comparisons with other methods using real world data of high dimensionality. A methodology for comparing classification methods through the assessment of model stability and validity in variable selection was proposed by J. Shreve et.al [69]. This study provides a systematic design for comparing the performance of six classification methods using Monte Carlo simulations and illustrates that the variable selection process is integral in comparing methodologies to ensure minimal bias, enhanced stability, and optimize performance. They quantify the variable selection bias and show that, for sufficiently large samples, this bias is minimized so that methods can be compared. Later John peter and Somasundaram [73] discussed the hybrid attribute selection method combining CFS and Filter Subset Evaluation gives better accuracy for classification. Mohammad Taha Khan [74] discussed a prototype model for the breast cancer as well as heart disease prediction using data mining techniques is presented. The data used is the Public-Use Data available on web, consisting of 909 records for heart disease and 699 for breast cancer. Two decision tree algorithms C4.5 and the C5.0 have been used on these datasets for prediction and performance of both algorithms is compared. Adithya Sundar et.al [75] discussed a prototype using data mining techniques, namely Naïve Bayes and WAC (weighted associative classifier). Srinivas et.al [76] briefly examine the potential use of classification based data mining techniques such as Rule based, Decision tree, Naïve Bayes and Artificial Neural Network to massive volume of healthcare data. Jaya Rama Krishnaiah [77] discussed how the data classification is based on supervised machine learning algorithms which result in accuracy, time taken to build the algorithm. Tanagra tool is used to classify the data and the data is evaluated using entropy based cross validations and partitioned techniques and the results are compared.

2.2 Breast Cancer Prediction

Breast cancer has become a common cancer in women. For instance, it affects one in every seven women in the United...
Moreover, Elmore indicated that 90% of radiologists recognize considerable variability in how they interpret a mammogram. However, the radiologists show considerable variability in breast cancer diagnosis. In [8] the author discussed and resolved the algorithms, issues and techniques for the problem of breast cancer prediction. This analysis does not include records with missing data so in future this work is enhanced by including the missing data. In [9] by analyzing the artificial neural network, trained on a number of clinic pathological variables of patients with breast cancer, predicted survival with high accuracy. The author concluded that the consistent accuracy over time and the good predictive performance of a network trained without information on nodal status. It shows that neural networks are valuable tools in cancer survival prediction. In future the study should concentrate on collecting data from a more recent time period and find new potential prognostic factors to be included in a neural network model. In the survey [10], the study is based on multiple prediction models for breast cancer survivability using large datasets along with 10 fold cross validation method. It provides a relative prediction ability of different data mining methods. In future this work is extended by collecting real dataset in the clinical laboratory. Recently Dursun Delen [78] et.al discussed the comparative study of multiple prediction models for breast cancer survivability using a large dataset along with a 10-fold cross-validation provided us with an insight into the relative prediction ability of different data mining methods. Shweta Kharya [79] discussed various data mining approaches that have been utilized for breast cancer diagnosis and prognosis. Breast Cancer Diagnosis is distinguishing of benign from malignant breast lumps and Breast Cancer Prognosis predicts when Breast Cancer is to recur in patients that have had their cancers excised. Ramachandran [80] has evolved from an experimental analysis to a predicting methodology due to highly precise algorithms and high performance data mining tools. Knowledge discovery in database has been used to predict survivability and diagnosis of diseases in the field of medicine. This can prove helpful for prevention of epidemics.

### 2.3 Diabetes Prediction

Insulin is one of the most important hormones in the body. It aids the body in converting sugar, starches and other food items into the energy needed for daily life. However, if the body does not produce or properly use insulin, the redundant amount of sugar will be driven out by urination. This disease is referred to diabetes. The cause of diabetes is a mystery, although obesity and lack of exercise appear to possibly play significant roles. Based on the American Diabetes Association in November 2007, 20.8 million children and adults in the United States (i.e., approximately 7% of the population) were diagnosed with diabetes. In early the ability to diagnose diabetes plays an important role for the patient’s treatment process.
In [18] the author predicts whether a new patient would test positive for diabetes. This paper studied a new approach, called the Homogeneity-Based Algorithm (or HBA) to determine optimally control the over fitting and overgeneralization behaviors of classification on this dataset (Pima Indian diabetes data set). The HBA is used in conjunction with classification approaches (such as Support Vector Machines (SVMs), Artificial Neural Networks (ANNs), or Decision Trees (DTs)) to enhance their classification accuracy. Some experimental results seem to indicate that the proposed approach significantly outperforms current approaches. From the experiment the author concluded that it is very important both for accurately predicting diabetes and also for the data mining community, in general. In [19] Data mining algorithm is used for testing the accuracy in predicting diabetic status. Fuzzy Systems are been used for solving a wide range of problems in different application domain Genetic Algorithm for designing. Fuzzy systems allows in introducing the learning and adaptation capabilities. Neural Networks are efficiently used for learning membership functions. Diabetes occurs throughout the world, but Type 2 is more common in the most developed countries. The author implemented in Genetic Algorithm. The steps involved in this algorithm namely selection, crossover, mutation, fitness and population statistics. As a result the author concluded that the optimization of chromosome using GA is obtained and it is based on the rate of old population diabetes can be restricted in new population to get chromosomal accuracy. Recently Karthikeyani et.al [57 & 58] discussed comparison a performance of data mining algorithms for diabetes disease based on computing time, precision value , the data evaluated using 10 fold Cross Validation error rate, error rate focuses True Positive, True Negative, False Positive and False Negative, bootstrap validation and accuracy. In [18] the author proposed a new algorithm Homogeneity-Based Algorithm to determine over fittting and over generalization behavior of classification. The algorithms used in this paper are Support Vector Machine, Decision Tree and Artificial Neural Networks. In future this work is enhanced by using any optimization techniques. In [19] for predicting diabetic status the author uses data mining algorithm for testing the accuracy. The author implemented using genetic algorithm. In future this work is extended by using other optimization technique.

2.4 HIV/AIDS Prediction

AIDS, the Acquired Immune Deficiency syndrome is a set of symptoms and infections resulting from the damage done to the human immune system caused by the Human Immunodeficiency Virus (HIV) [20]. HIV is transmitted through direct contact of mucous membrane or the blood stream with a bodily fluid containing HIV [21 & 22]. There is currently no vaccine or cure to both HIV and AIDS. However, treatment such as the antiretroviral therapy slows down the course of the disease thus reduces mortality and morbidity of HIV infection. The analysis of survival data has long been the domain of statistics as can be observed through the number of medical statistics textbooks and journals dedicated to the field [20-23]. Statistical methods such as the life-table, the Kaplan-Meier method and regression models such as the Cox Proportional Hazard are usually used to model and predict survival data with the ability to handle censored data [24 & 25]. However, these methods are usually used to explain the data and to model the progression of the disease rather than to make survival predictions for populations or individual patients. A major part of the work done in the area of survival analysis is that carried by Ohno-Machado as part of her PhD thesis. Ohno-Machado made comparisons of standard and sequential neural network models in the survival of coronary heart disease, the comparisons of neural network model with that of Cox Proportional Hazards and the use of modular neural networks to predict HIV survival [25-29]. In writing this paper, the literature review that was carried out on computer-based prognostic systems, namely, on the use of techniques of database research, AI and statistics, in prognostic systems has resulted in at least fifty different articles/papers published by international researchers. In the Malaysian scenario, the number of papers published does not even come close to this figure. A literature search in the National Library of Medicine database (PUBMED), for “Malaysia and AIDS” yielded 169 citations. A PUBMED search on “Malaysia and AIDS and prognosis” resulted in a mere 4 articles, while a search for “Malaysia and AIDS and prognosis and computer”, “Malaysia and AIDS and prognosis and artificial intelligence” and “Malaysia and AIDS and prognosis and neural network” yielded “0” (zero) articles [30-32]. Thus, there is a great potential for research in this area in the local scenario. In this paper we describe our research on using CART in the prediction of survival of AIDS in the Malaysian scenario. HIV/AIDS has emerged as one of the leading challenges for global public health. The number of reported HIV cases in Malaysia has increased from a mere three (3) cases in 1986 to 6427 cases in 2004. During the period of 1986 to 2004 the total number of HIV infections in Malaysia is a staggering 64, 439 (59,962 Male, 4477 Female) of which 9442 had developed into AIDS (8596 Male, 846 Female) with a total of 7195 cases reported to be AIDS related deaths (6661, 534 Female). The ages of these HIV/AIDS related deaths vary from as young as less than 2 years of age to that of above 50 years of age [33]. Since HIV/AIDS poses a challenge to the general development of human resource in Malaysia, any research in HIV/AIDS should thus be duly encouraged. The prediction of survival is not the only research that can be carried out in the area as researchers could also investigate the association of certain risk factors to the disease, matching patients to treatment protocols and the application of AI techniques, database research and
statistics to the follow up and management of AIDS patients [33]. One of the most challenging tasks in carrying out research in the clinical scenario is the availability of clinical data sets. This is especially so, here in Malaysia, where medical data banks do not currently exist. Medical data are usually only accessible to hospital authorities; even then, inter-hospital data accesses may not be possible. Most researchers will have to depend on the goodwill of clinicians, who may do their own medical record keeping, in order to access medical data. Furthermore, even if a researcher is able to access these data they may not be in an electronic form. For chronic illnesses in particular, clinical data sets may not contain an appreciable number of cases, some data collection may be incomplete or some attributes may not be well represented. Those that are complete may not be error-free. All these add to the difficulties of conducting research using real data sets as opposed to artificial data sets. However, recently local computer scientists are beginning to make attempts in carrying out research in medical informatics through collaborations with their medical counterparts. The various mathematical and statistical approaches have been proposed for the prediction of survival in HIV/AIDS. M. Bonarek used Kaplan-Meier method to determine prognostic factors associated with in-hospital survival in HIV-infected patients admitted to MICUs (medical intensive care units) [34]. A logistic regression model has been used in prognosis of HIV patient’s survival [35], Weibull, loglogistic, lognormal distributions has been used in formulating the prognostic model for HIV survivals [36]. Cox models are applied and STATA 7 for statistical analyses is used as well in a study to determine the survival in HIV [37]. The purpose of this study is to examine the use of CART as a tool for data mining, predictive modeling and data processing in the prognosis of AIDS. The goal of any modeling exercise is to extract as much information as possible from available data and provide an accurate representation of both the knowledge and uncertainty about the epidemic. Recently Sameem A.K. et.al [59] studied certain experiments on the application of Classification And Regression Tree (CART) to predict the survival of AIDS. CART builds classification and regression trees for predicting continuous dependent variables and categorical or predictor variables, and by predicting the most likely value of the dependent variable. A total of 998 patients who had been diagnosed with AIDS were grouped according to prognosis by CART. We found that CART were able to predict the survival of AIDS with an accuracy of 60-93% based on selected dependent variables, validated using Receiver Operating Characteristics (ROC). Rosma mohd dom et.al [60] was to describe the feasibility of applying a predictive data mining technique to predict the survival of AIDS. An adaptive fuzzy regression technique, FuReA, was used to predict the length of survival of AIDS patients based on their CD4, CD8 and viral load counts. Predictive ability of FuReA was measured and compared with fuzzy neural network prediction models. We found that both FuReA and fuzzy neural network models were able to predict the survival of AIDS with an accuracy of 60% to 100% based on selected dependent variables. Saravanan. A.M. et.al [61] was used Dempster Shafer (DS) theory and focused to identify the hidden information from the data set using the concept theory of evidence. Later Santhosh Kumar and Ramraj [62] discussed several classifier approaches are used to classify the HIV1 and HIV2. For implementation of the work a real time patient database is taken and the patient records are experimented and the final best classifier is identified with quick response time and least error rate.

2.5 Tuberculosis Prediction

Data classification process using knowledge obtained from known historical data has been one of the most intensively studied subjects in statistics, decision science and computer science. Data mining techniques have been applied to medical services in several areas, including prediction of effectiveness of surgical procedures, medical tests, medication, and the discovery of relationships among clinical and diagnosis data. In order to help the clinicians in diagnosing the type of disease computerized data mining and decision support tools are used which are able to help clinicians to process a huge amount of data available from solving previous cases and suggest the probable diagnosis based on the values of several important attributes Ensemble of classifiers has been proved to be very effective way to improve classification accuracy because uncorrelated errors made by a single classifier can be removed by voting. A classifier which utilizes a single minimal set of classification rules to classify future examples may lead to mistakes. An ensemble of classifiers is a set of classifiers whose individual decisions are combined in some way to classify new example. Many research results illustrated that such multiple classifiers, if appropriately combined during classification, can improve the classification accuracy. India has the world’s highest burden of tuberculosis (TB) with million estimated incident cases per year. It also ranks among the world’s highest HIV burden with an estimated 2.3 million persons living with HIV/AIDS. Tuberculosis is much more likely to be a fatal disease among HIV-infected persons than persons without HIV infection. It is a disease caused by mycobacterium which can affect virtually all organs, not sparing even the relatively inaccessible sites. The microorganisms usually enter the body by inhalation through the lungs. They spread from the initial location in the lungs to other parts of the body via the blood stream. They present a diagnostic dilemma even for physicians with a great deal of experience in this disease.

Minou Rabiei et.al.[39] use tree based ensemble classifiers for the diagnosis of excess water production. Their results
demonstrate the applicability of this technique in successful
diagnosis of water production problems. Hongqi Li, Haifeng
Guo and team present[40] a comprehensive comparative study
on petroleum exploration and production using five feature
selection methods including expert judgment, CFS, LVF,
Relief-F, and SVMRFE, and fourteen algorithms from five distinct
kinds of classification methods including decision tree, artifi-
cial neural network, support vector machines(SVM), Bayesian
network and ensemble learning. Zhenzheng Ouyang, Min
Zhou, Tao Wang, Quanyuan Wu[41] propose a method, called
WEAP-I, which trains a weighted ensemble classifier on the
most n data chunks and trains an averaging ensemble classifier
on the most recent data chunk. All the base classifiers are
combined to form the WEAP-I ensemble classifier. Orhan Er.
And temuritus [42] present a study on tuberculosis diagnosis,
carried out with the help of multilayer neural networks
(MLNNs). For this purpose, an MLNN with two hidden layers
and a genetic algorithm for training algorithm has been used.
Data mining approach was adopted to classify genotype of
mycobacterium tuberculosis using c4.5 algorithm [43]. Evaluation
of the performance of two decision tree procedures and
four Bayesian network classifiers as potential decision support
systems in the cytdiagnosis of breast cancer was carried out
[44]. Paper on “Mining Several Data Bases with an Ensemble
of Classifiers”[45] analyze the two types of conflicts, one creat-
ed by data inconsistency within the area of the intersection of
the data bases and the second is created when the meta meth-
od selects different data mining methods with inconsistent
competence maps for the objects of the intersected part and
their combinations and suggest ways to handle them. Refer-
cenced paper [46] studies medical data classification methods,
comparing decision tree and system reconstruction analysis as
applied to heart disease medical data mining. Under most cir-
cumstances, single classifiers, such as neural networks, sup-
port vector machines and decision trees, exhibit worst perfor-
ance. In order to further enhance performance combination
of these methods in a multi-level combination scheme was
proposed that improves efficiency [47]. Paper [48] demonstr-
ates the use of additive network classifier committees
trained on different features for improving classification ac-
curacy in medical diagnosis. Paper on “MReC4.5: C4.5 ensemble
classification with MapReduce” [49] takes the advantages of
C4.5, ensemble learning and the MapReduce computing mod-
el, and proposes a new method MReC4.5 for parallel and dis-
tributed ensemble classification. Seppo Puuronen and team
[50] propose a similarity evaluation technique that uses a
training set consisting predicates that define relationships
within the three sets: the set of instances, the set of classes, and
the set of classifiers. Lei Chen and Mohamed S. Kamel [51]
propose the scheme of Multiple Input Representation-
Adaptive Ensemble Generation and Aggregation (MIR-AEGA)
for the classification of time series data. Kai Jiang et.al. [52]
propose a neural network ensemble model for classification
of incomplete data. In the method, the incomplete dataset is di-
vided into a group of complete sub datasets, which is then
used as the training sets for the neural networks. Recently
Asha et.al [81] discussed the comparison of classification tech-
niques for TB based on two categories namely pulmonary tu-
brerculosis (PTB) and retroviral PTB using ensemble classifiers
such as Bagging, AdaBoost and Random forest trees.

3 Conclusions

In this survey paper the problem of summarizing the differ-
tent algorithms of data mining for the major life threatening
diseases are used in the field of medical prediction are dis-
cussed. The main focus is on using different algorithm and
combination of several targets attributes for different types of
disease prediction using data mining. First we discuss about
the heart disease prediction, in that machine learning algo-
rithms namely naïve bayes, k-NN, Decision List. Of these the
classification accuracy of the naïve bayes algorithm is better
when compared to other algorithm. In Weighted Associative
Rule Classifier, the GUI has been designed to enter the patient
record and the presence of Heart Disease for a patient is pre-
dicted by using the rules stored in the rule base. Next we dis-
cuss the feature subset selection using genetic algorithm. In
this attributes are reduced using genetic search. Here the accu-
rracy is compared to the three classifiers namely Decision Tree,
Naïve bayes and classification via clustering. Association rule
discovery is mainly based on four constraints namely item
filtering, attribute grouping, maximum item set size and ante-
cedent/consequent rule filtering. To find predictive rules in
medical data set the three important steps are generated in
this algorithm. The heart disease is diagnosed for diabetic pa-
tients using Naïve Bayes technique. Of these the author co-
ncluded that naïve bayes classify 74% of input instances correct-
ly. Next we discuss about the breast cancer prediction. It is
performed by using various data mining techniques namely
C4.5, ANN and fuzzy decision trees. By using C4.5 the author
discussed and resolved the issues and algorithms of the prob-
lem. Using ANN the author concluded that the consistent ac-
ccuracy over time and good performance of the network is
trained. The fuzzy decision tree survives by using 10 fold cross
validation method. Finally we discuss about diabetes prediction,
by using homogeneity based algorithm the author find
over fitting and overgeneralization behavior of classification.
By using genetic algorithm the author predicts accuracy of the
class. In future the work can be expanded and enhanced for
the automation of various types of disease prediction. It also
extended to find other types of diseases with the uses of these
attributes. The various mathematical and statistical approach-
es have been proposed for the prediction and diagnosis of
survival in case of HIV/AIDS. An ensemble of classifiers is a
set of classifiers whose individual decisions are combined in
some way to classify new example. Many research results il-
ustrated that such multiple classifiers, if appropriately com-
bined during classification, can improve the classification accuracy. India has the world's highest burden of tuberculosis (TB) with million estimated incident cases per year.

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