A Unique approach for data classification using ANN with strengths of feature reduction techniques

Ronak Jain

Assistant Professor,
Department of Information Technology,
Acropolis Institute of Technology and Research, Indore, India

***Abstract*: Feature selection has been widely used to reduce the data dimensionality. Data reduction improves the classification performance in terms of speed, accuracy. A strategy to reduce the number of features. My basic idea is that while performing dataset classification, first we have to select attributes for inputs to the algorithm. Then algorithm would perform classification of dataset, but based on features, accuracy of classifiers would be affected. Also if there are several features in a dataset, it's not necessary that all attributes having same importance in dataset classification. Therefore, we may divide all the attributes of a dataset into two categories: significant and insignificant. Significant means attributes playing key role in data classification and also affecting accuracy significantly. Insignificant is just opposite. Based on this fact we have proposed a generic algorithm which will be able to discover the significant and non-signification list of attributes of any dataset based on results obtained after classification of given dataset. In this way we may reduce attributes of standard datasets. It will reduce complexity of classification without affecting accuracy of classifiers.The results obtained by my work in classification accuracy are superior to obtain by conventional algorithm and other recent feature selection algorithms applied to the same database. By these reasons the proposed method is an interesting alternative to reduce the data dimensionality and provide a high accuracy.**

***Keywords*: Data Reduction, Classification, Accuracy, Data Mining, Backpropagation algorithm.**

I. INTRODUCTION

Data mining is team a few of the overpower symbol croak review issues in data mining, which was introduced by Agrawal and Srikant [1] and can be designated as follows: we are disposed a traditional of data-sequences, as the input data. Eternally data combination contains a straightforward list of relationships (item sets). Given a user-specified minimum support threshold (minsup), Progressive pattern mining finds on all sides of subsequences with reference to frequencies more intelligent than minsup in a sequence database.

Various previously studies on connection critique demonstrate focus using only minsup as single prevalence threshold does not excess on the nature of as a matter of actual fact in real-life applications [2]. That is, single minsup implicitly assumes that all items in the database have similar frequency. However, some items may appear very frequently in the database while others rarely appear [3]. Under such circumstance, if we routine the reckoning of minsup counting up snotty, we firmness call for snare those order involving rare items in the database [4].
On the other hand, if we habituated wander give as well pinchbeck, it stability tote a prominent amount of meaningless patterns. Therefore, Liu et al. [3] first address this dilemma (also known as the rare item problem) and propose the concept of multiple minimum supports (MMS in short) to redefine the problem of association rule mining. The method allows users to specify different minsups for different items (MIS values) to reflect their unique natures and generate different association rules, depending on which items are in the patterns.

Some Data Mining algorithms are steadfast to the detection of such captivating subgroups [5]. Anyhow, interesting subgroups are an accepting intermediation of capturing awareness close by the database, as a remedy for by understandability they unequalled label parts of the database [6]. Most suitable algorithms will history repugnance interesting subgroups not as the end deliberation, but as mere edifice blocks for unconcealed descriptions of the genuine regularities [7]. The structures digress are the direction of such algorithms are alike as models, and the existent skirmish of in view of subgroups and zealously fib an absolute avoid of the data is therefore often referred to as modeling[8]. We can take on oneself of the database as a amassing of raw harmony with reference to a painstaking domain. Each insigne serves as a wrapper of the rules that stool this domain [9]. The hew that is induced non-native the raw data is a shortened affirmation of the action of the domain, unique the statistics of kin. Having a model allows us to convince about the domain, for example to see causes for diseases in transferable databases of patients [10-12]. Roughly evidently data Mining is often utilitarian in order to derive prophetic models [13]. If we receive that the database lower than enumeration is but a facsimile of a larger or evolvement populace of individuals, we can justify the induced model to reckon on the behavior of new individuals. We seat secure a sculpt reading in any case the answer depends on alternate categorize of the clientele, in all directions the wish of predicting despite that other patrons will respond to the offer[13]. A total of discretion and relevancy underpinning estimation be saved by desolate around customers with a predicted interest [14].

II. LITERATURE REVIEW

In 2010, Marcano-Cedeño et al. [15] suggested that the feature selection has been widely used to reduce the data dimensionality. Information lessening enhances the grouping execution, the estimation capacity, and example acknowledgment frameworks as far as rate, exactness and straightforwardness. A technique to lessen the quantity of components in neighborhood pursuit is the consecutive look calculations. They have exhibited a component choice method based on Sequential Forward Selection (SFS) and Feed Forward Neural Network (FFNN) to estimate the prediction error as a selection criterion. Three well-known database have been used to test the SFS-FFNN with Artificial Metaplasticity on Perceptron Multilayer (AMMLP). The AMMLP is another technique connected for arrangement of examples. The outcomes acquired by SFS-FFNN with AMMLP in arrangement exactness are predominant than got by routine BP calculation and other later highlight choice calculations connected to the same database. By these reasons the proposed technique SFS-FFNN with AMMLP is a fascinating contrasting option to decrease the information dimensionality and give a high exactness.

In 2013, Naseriparsa et al. [16] proposed a hybrid feature selection method which takes advantages of wrapper subset evaluation with a lower cost and improves the performance of a group of classifiers. The technique utilizes mix of test area sifting and resampling to refine the example space and two component subset assessment strategies to choose solid elements. This strategy uses both element space and test area in two stages. The principal stage channels and resamples the specimen area and the second stage receives a half breed strategy by data pick up, wrapper subset assessment and hereditary hunt to locate the ideal component space. Tests completed on various sorts of datasets from UCI Repository of Machine Learning databases and the outcomes demonstrate an ascent in the normal execution of five classifiers (Naïve Bayes, Logistic, Multilayer Perceptron, Best First Decision Tree and JRIP) all the while and the arrangement mistake for these classifiers diminishes significantly. The trials likewise demonstrate that this strategy outflanks other element determination strategies with a lower cost.

In 2013, Ozarkar et al. [17] suggested that the spam is a key problem in electronic communication, including large-scale email systems and the growing number of blogs. According to the author there are several research work are going in the automatic detection of spam emails using classification techniques such as SVM, NB, MLP, KNN, ID3, J48,Random Tree, etc. For spam dataset it is conceivable to have substantial number of preparing occasions. Based on this, they have made utilization of Random Forest and Partial Decision Trees calculations to arrange spam versus non-spam messages. These calculations outflanked the already executed calculations as far as precision and time many-sided quality. As a preprocessing step we have utilized element choice strategies, for example, Chi-square, Information pick up, Gain proportion, Symmetrical instability and Correlation. This permitted us to choose subset of important, non-excess and generally contributing components to have an additional advantage as far as impromptu creation in precision and decreased time unpredictability.

In 2014, Murthy et al. [18] suggested Microarray Gene Profile for assessing the global patterns of thousands of genes under different varying conditions. It provides important insights about the underlying genetic causes for diseases, ultimately allowing the development of modern chemical entities as medical-kit drug candidates. The informatics analysis and integration of microarray gene expression pattern are difficult for understanding or interpretation of gene array features. In this paper, we discuss the deterministic computational analysis of: the identification of differentially expressed genes using statistical methods, the discovery of gene clusters, and the classification of biological samples using standard clustering and classification approaches.

In 2014, Kumar et al. [19] suggested that the data mining provides an automatic extraction of useful and relevant content, often previously unknown information from large databases or data sets. Many data mining applications contain high dimensional data. The High dimensionality diminishes the execution of the mining calculations and builds the time and space required for preparing the information. The high dimensionality issue is determined utilizing the Dimensionality Reduction (DR) system. The DR is partitioned into two: component determination and highlight extraction. They have used a subtle element study has been done to know how the dimensionality issue has settled by utilizing the two diverse systems. Furthermore different factual measures are disclosed to choose the most significant components and diverse measurable procedures are broke down to remove the new arrangement of highlights frame the first components.

In 2015, Vaska et al. [20] suggested that the E-Health has grown popular due to a wide range of services provided. The part of a patient has likewise changed in today's social insurance as they are relied upon to utilize ICT administrations to pick up data and information to think about their prosperity. In the field of information mining grouping is a broadly utilized system for finding designs as a part of hidden information. Customary grouping calculations are ordinarily constrained to taking care of datasets that contain either numeric or unmitigated properties. Nonetheless, datasets with blended sorts of qualities are likewise normal, in actuality, information mining applications. They have presented a cluster feature based incremental clustering algorithm; MCIFA (Cluster Feature-Based Incremental Clustering Approach to mixed data) is applied on the diabetes dataset to check its suitability in the medical domain. The accomplished grouping precision in results area demonstrates this is in fact reasonable for medicinal space and can be utilized for 'e-endorsing'. However, it should be adjusted in order to expand the bunching precision as the rate of permitted mistake rate in therapeutic area ought to be as little as could reasonably be expected.

In 2015, Chakraborty et al. [21] presented a feature selection method based on a multilayer perceptron (MLP) neural network, called feature selection MLP (FSMLP). They have explained how FSMLP can select essential features and discard derogatory and indifferent features. They showed the viability of the calculations utilizing a few information sets including a manufactured

information set. They additionally demonstrate that the chose elements are satisfactory to take care of the current issue. Here, they have considered a measure of direct reliance to control the repetition. The utilization of nonlinear measures of reliance, for example, shared data, is direct. Here, there are some focal points of the proposed plans. They don't require express assessment of the component subsets. Here, component choice is incorporated into outlining of the basic leadership framework. Thus, it can take a gander at all elements together and get whatever is important. Their techniques can represent conceivable nonlinear unpretentious connections between components, and also that between elements, apparatuses, and the issue being explained. They can likewise control the level of repetition in the chose highlights. Of the two learning plans, mFSMLP-CoR, enhances the execution of the framework, as well as altogether decreases the reliance of the system's conduct on the introduction of association weights.

In 2015, Senthilkumar et al. [22] suggested that the health care data are having exponential growth in volume and complexity. They have presented a correlation attribute evaluation feature selection for dimensionality reduction and t-test for comparing the performance of different classifiers before and after dimensionality reduction. Distinctive classifiers utilized as a part of this work are Naïve Bayes (NB), k- Nearest Neighbour (kNN), Classification tree (CT) and Clark and Nilbert2 (CN2). Empirical results shown that CN2 classifier is best for the multi-dimensional thyroid dataset by comparing classification accuracy of the different classifiers. There is no significant difference between before and after the dimensionality reduction in the four classifiers in the performance measure.

In 2016, Baz et al. [23] suggested that the common aim of all our daily activities is providing services to others or ourselves. They have addressed the gap in improving the quality of their customer service, and enhance the existing services by proposing a number of data analysis techniques that can be utilized to improve the quality of customer service and enhance the existing services in the Saudi government sector. They have introduced a relational database structure that can be utilized to apply the proposed data analysis techniques.

In 2016, Xu et al. [24] suggested that the dimension reduction is an important in pattern analysis and machine learning, and it has wide applications in feature representation and pattern classification. They also suggested that the, sliced inverse regression (SIR) has pulled in much research endeavors because of its viability and adequacy in measurement diminishment. Be that as it may, two downsides restrict further uses of SIR. To start with, the calculation many-sided quality of SIR is typically high in the circumstance of high-dimensional information. Second, sparsity of projection subspace is not all around dug for enhancing the component determination and model translation capacities. They have proposed to compute the SIR projection vectors in the spectral space, at that point an approximated relapse arrangement can be gotten with a quicker speed. In addition, the versatile tether is utilized to achieve a scanty and universally ideal arrangement, which is essential in variable determination. To finish the vigorous example arrangement assignment with defilements, an entropy-based and class-wise relapse model is planned in this paper. It takes a smooth punishment rather than sparsity requirement in the relapse coefficients, and it can be led in class-wise, along these lines it is more adaptable by and by. Broad tests are led by utilizing some genuine and benchmark information sets, e.g., high-dimensional facial pictures and quality microarray information, to assess the new calculations. The new recommendations accomplish focused results and are contrasted and other best in class strategies.

III. PROPOSED METHOD

A two-layer feed-forward network, with sigmoid hidden and output neurons, can classify vectors arbitrarily well; given enough neurons in its hidden layer have been proposed which is shown in figure 1. The proposed structure is used for training data with the help of scaled conjugate gradient backpropagation.

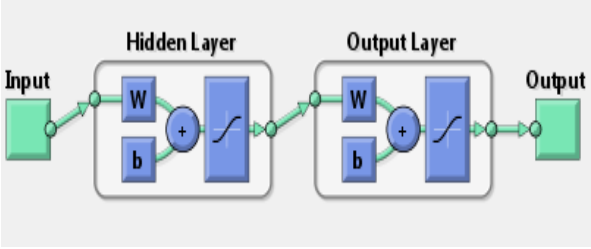

Figure 1 Two-layer feed-forward network

A classifier has been designed which is a system that assigns each data which is to be input to a class from a set of predefined classes. It can be categorized in the following ways.

- Training data: It shows the known class which is further used as a classifier design through neural network process.
- Validation data: information used to assess the conduct of the classifier amid the learning procedure; the characterization execution on the approval information is utilized to choose if the learning procedure ought to be halted or not; early ceasing of learning could be valuable to abstain from over training and upgrade the speculation capacity of the classifier.
- Testing data: It is used to check the performance of the designed classifier.

The classification used by our approach is also called pattern recognition. Our proposed framework of neural network architecture appropriate to solve classification problems is the feed forward one characterized by:

- There is an input layer which having several attributes along with the same number of input.
- One or several hidden layers (as the quantity of concealed units is bigger the model separated by the neural system is more perplexing–yet this is not inexorably gainful for the issue to be tackled).
- An output layer having the same number of units as classes.

The nature of a classifier (intended to distinguish two classes) is normally measured by figuring the perplexity framework and by speaking to the diagram of the receiver operating characteristic curve (ROC). The confusion matrix contains data about the percent of information which were accurately/mistakenly ordered.

The whole process is better understood from figure 2. First the data is loaded in our framework. Different data like breast cancer, thyroid and wine vintage are used for the experimentation and simulation. A feed-forward network has been used with the default tan-sigmoid transfer function for the use in the hidden layer. For the output layer linear transfer function is used. It is used for regression problems. Different neurons can be used in one hidden layer. For example 20, 10 can be used. The created network has the configuration of one neuron as an output, as there is only one target vector coordinated with each input vector. More neurons require more calculation; however they permit the system to take care of more confused issues. More layers require more calculation, yet their utilization may bring about the system tackling complex issues all the more proficiently. Be careful however that adding an excessive number of neurons contrasted with the dataset size may bring about over fitting wonders.

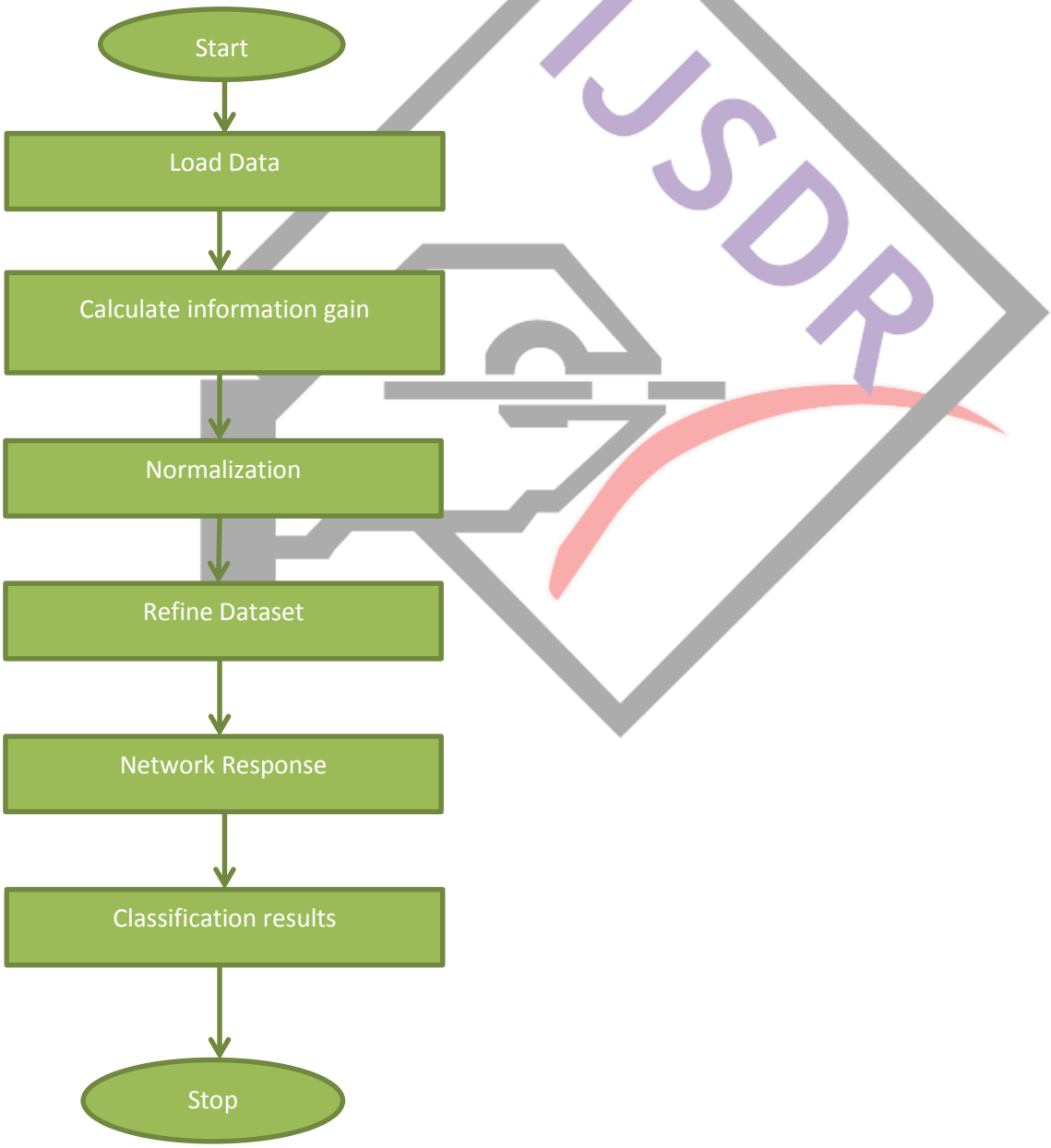

Figure 2 Proposed Flowchart

Then our proposed network uses the default Levenberg-Marquardt algorithm for training.
It is used to represent by a sum of squares for finding minimum of functions.

$F(X_0,\ldots..,X_{N-1}) = \sum_{i=0}^{M-1} f_i^2 (X_0,\ldots..,X_{N-1})$

In our approach then the framework automatically divides input vectors and target vectors into three sets which can be as follows: 70% are used for training, 15% are used to validate that the network is generalizing and to stop training before over fitting. 20% are utilized as a totally autonomous test of system speculation. To prepare the system, enter: net=train(net,houseInputs,houseTargets). Amid preparing, the preparation window (right) opens. This window shows preparing advance and permits you to intrude on preparing anytime by clicking Stop Training. The train capacity displays all the information vectors to the system on the double in a bunch. Then again, you can show the info vectors each one in turn utilizing the adjust capacity.

Second step is standardization. Since we are utilizing NNs, it just requests numerical inputs. Utilizing the accompanying recipe we have changed over the worth into fitting extent.
$x_{ij} = (x_{ij} - \min) /(\max - \min)$
Min and max are the minimum values for a single domain. x_{ij} represents the i and j row and column of the field. In this work, we have used multilayer feed forward neural network and learning algorithm as back propagation algorithm.

Back-propagation [10] training algorithm when applied to a feed forward multi-layer neural network is known as Back propagation neural network. Practical signs streams in forward bearing and mistake signals spread in reverse heading. That is the reason it is Error Back Propagation or right away Back Propagation system. The actuation work that can be separated, (for example, sigmoid enactment capacity) is decided for covered up and yield layer computational neurons. The calculation depends on blunder amendment standard. The principle for changing estimations of synaptic weights takes after summed up delta standard.

Back propagation algorithm:
Step 1: First all the weights re initialize in the network
Step 2: The input value is depends on the output of the input vector.
$Output_x = Input_x$
X is the input layer unit.
Step 3: For the hidden layer x the net input and output can be calculated by the below formula:
$Input_x = \sum_y w_{xy} Output_y$
$Output_x = 1/(1+e^{-xy})$
Step 4: The error are then back propagated for each unit of x.
$Err_x = Output_x(1- Output_x)(Test_x – Output_x)$
Step 5: For each x unit in the hidden / output layer, error to the k level
$Err_x = Output_x(1- Output_x)\sum_k Err_k w_{xk}$
Step 6: for all the weight w_{xy} in network
$\Delta w_{xy} = (\eta)\ Err_j Output_y$
Step 7: Weight can be updated by the incremented by the below formula:
$w_{xy} = w_{xy} + \Delta w_{xy}$

IV. RESULT ANALYSIS

For better under the working process of our proposed work different data like breast cancer, thyroid and wine vintage are used for the experimentation and simulation. These are presented to the network during training, and the network is adjusted according to its error.

Actually these measures are used to identify the quality. Confusion matrix is generated for designating the graphs of receiver operating characteristic curve (ROC). It shows the percentage of data correctly classified or misclassified. It is calculated based on the below formula:

- True positive (TP): It shows all the cases which are classified correctly for the first class.
- True negative cases (TN): It shows all the cases which are classified correctly for the second class.
- False positive cases (FP): It shows all the negative cases which are classified correctly for the first class.
- False negative cases (FN): It shows all the positive cases which are incorrectly classified in the second class.

Measures:
Sensitivity=TP / (TP + FN)
Specificity=TN/ (TN+FP)
Precision=TP/ (TP+FP)
F=2*Precision*Recall/ (Precision + Recall)

The plotting of the Roc curves are plotted according to the specificity and sensitivity which is mainly corresponding to different classification thresholds obtained and if it is higher in the concern input it belongs to the class otherwise it not belongs to the same class. The results shown in table1 and.2 clearly reveal the fact that the features can be eliminated for classification based on low info gain and classification. It shows the total number of features reduces by the classification without affecting accuracy of classifiers.

Table 5.1: Features to be eliminated for classification based on low info gain

Feature No.	Breast Cancer Dataset	Wine Dataset	Thyroid Dataset	Spam Dataset
1.	0.9168	1.3406	0.7146	0.0873
2.	**0.4647**	1.2842	1.0640	0.131
3.	0.6843	**0.7863**	**0.7070**	0.1518
4.	0.6610	**0.7358**	**0.6008**	**0.0123**
5.	**0.4490**	**0.6362**	0.9418	0.1845
6.	0.5141	1.1813	NA	0.1116
7.	0.6060	1.4208	NA	0.2347
8.	0.5478	**0.4739**	NA	0.1261
9.	**0.4755**	1.1161	NA	0.1032
10.	**0.2101**	1.3701	NA	0.1317
11.	NA	1.0414	NA	0.1214
12.	NA	1.3471	NA	0.1284
13.	NA	1.3015	NA	0.0903
14.	NA	NA	NA	0.0541
15.	NA	NA	NA	0.0798
16.	NA	NA	NA	0.2393
17.	NA	NA	NA	0.1399
18.	NA	NA	NA	0.1212
19.	NA	NA	NA	0.2679
20.	NA	NA	NA	0.1005
21.	NA	NA	NA	0.3045
22.	NA	NA	NA	**0.0298**
23.	NA	NA	NA	0.1675
24.	NA	NA	NA	0.1975
25.	NA	NA	NA	0.1808
26.	NA	NA	NA	0.1306
27.	NA	NA	NA	0.1371
28.	NA	NA	NA	0.0655
29.	NA	NA	NA	0.0594
30.	NA	NA	NA	0.0693
31.	NA	NA	NA	**0.0476**
32.	NA	NA	NA	**0.0328**
33.	NA	NA	NA	**0.0458**
34.	NA	NA	NA	**0.0337**
35.	NA	NA	NA	0.0685
36.	NA	NA	NA	0.0549
37.	NA	NA	NA	0.0893
38.	NA	NA	NA	**0.0123**
39.	NA	NA	NA	**0.0458**
40.	NA	NA	NA	**0.0375**
41.	NA	NA	NA	**0.0233**
42.	NA	NA	NA	**0.0496**
43.	NA	NA	NA	**0.0469**
44.	NA	NA	NA	**0.0392**
45.	NA	NA	NA	0.0954
46.	NA	NA	NA	0.0746
47.	NA	NA	NA	**0.0088**
48.	NA	NA	NA	**0.0268**
49.	NA	NA	NA	0.0824

50.	NA	NA	NA	0.178
51.	NA	NA	NA	0.055
52.	NA	NA	NA	0.4605
53.	NA	NA	NA	0.3271
54.	NA	NA	NA	0.1279
55.	NA	NA	NA	0.659
56.	NA	NA	NA	0.3093
57.	NA	NA	NA	0.378

Table 2: Features to be eliminated while classification of dataset

Dataset Name	Total No. of Features (Original Dataset)	Feature No. eliminated while Classification	Total No. of Features (Reduced Dataset)
Breast Cancer	10 + 1 class label = 11	**2,5,9,10**	6 + 1 class label = 7
Wine	8 + 1 class label = 9	**3,4,5,8**	4 + 1 class label = 5
Thyroid	5 + 1 class label = 6	**3,4**	3 + 1 class label = 4
Spam	57 + 1 class label = 58	**4,22,31,32,33,34,38,39,40,41,42,43,44,47,48**	42 + 1 class label = 43

V. CONCLUSIONS

In our approach attributes have been selected for inputs to the algorithm. Then algorithm would perform classification of dataset, but based on features, accuracy of classifiers would be affected. Also if there are several features in a dataset, it's not necessary that all attributes having same importance in dataset classification. Therefore, we may divide all the attributes of a dataset into two categories: significant and insignificant. Only significant attributes are considered. A generic algorithm has been proposed for finding the significant and non-signification list of attributes. So that we are able to reduce attributes of standard datasets. It will reduce complexity of classification without affecting accuracy of classifiers. It is proved by our results as we have presented results based on varying attributes.

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