

Genetic Algorithm Based Feature Selection Technique for Electroencephalography Data

Tariq Ali^{1*}, Asif Nawaz², Hafiza Ayesha Sadia³
¹⁻³PMAS Arid Agriculture University, Rawalpindi, Pakistan

Abstract – High dimensionality is a well-known problem that has a huge number of highlights in the data, yet none is helpful for a particular data mining task undertaking, for example, classification and grouping. Therefore, selection of features is used frequently to reduce the data set dimensionality. Feature selection is a multi-target errand, which diminishes dataset dimensionality, decreases the running time, and furthermore enhances the expected precision. In the study, our goal is to diminish the quantity of features of electroencephalography data for eye state classification and achieve the same or even better classification accuracy with the least number of features. We propose a genetic algorithm-based feature selection technique with the KNN classifier. The accuracy is improved with the selected feature subset using the proposed technique as compared to the full feature set. Results prove that the classification precision of the proposed strategy is enhanced by 3 % on average when contrasted with the accuracy without feature selection.

Keywords – Classification algorithms, evolutionary computation, feature extraction, genetic algorithms.

I. INTRODUCTION

In the revolutionary advancement era, there are many technology resources that help develop wearable devices, which are capable of safe use and improve people's life, especially of those suffering from different types of motor impairment. The emergence of these technologies with Internet of Things (IoT) can bring evolution in applications of public safety and mobile health. These applications open doors for universal ongoing testing by utilising distinctive data types, for example, Electrocardiography (ECG), Electroencephalography (EEG).

EEG is one of the most popular methods for capturing the brain waves and analysing the neurological aspects. Eighty years ago, EEG was developed by a European scientist [1], [2]. In the past, some eye tracking systems have developed through image processing techniques, which utilise eye-blink pattern, but in some applications, such as drowsiness detection, the method of eye blink pattern is not sufficient because these methods concentrate just on eye shut state, they cannot be connected to identifying sluggishness with open eyes. Due to less accuracy, the EEG based tracking system is needed [3]. Apart from the conventional use of clinical diagnosis, EEG signals are applicable in many other applications, such as computer games [4], emotion tracking [1], and stress feature identification [5]. Growing number of researchers are using EEG in the Brain-Computer Interface (BCI) [6]. The eye-tracking systems can also be used for stress feature identification [2], infant sleep-wake state

identification [7], drowsiness detection [8], Attention Deficit Hyperactivity Disorder (ADHD) patients [10] and epileptic seizure detection [9].

New research perspectives have opened due to the accessibility of economic wireless EEG devices spanning from clinical assessment of daily life activities and public safety. Wireless headsets are easy and compact to be worn during different activities. On the other hand, the ongoing intermingling of advances in wearable sensor technologies, consumer electronics, and universal figuring has prompted the requirement for gauges to deal with intercommunication among these applications and gadgets. Dealing with the physical integration of everyday objects and their unique capabilities on the Internet, Internet of Things (IoT) tackles some of these challenges. However, for excessive use of these devices on a commercial level, there should be affordable devices with reasonable accuracy. Therefore, in the paper, we focus on reducing the number of sensors of EEG devices so that combined IoMT and EEG signals give more accurate and efficient results.

II. RELATED WORK

Authors prepared a data set that is available at UCI repository and is used as a benchmark dataset by many researchers [11]. In the paper, an eye state (open or closed) predictor by using brain waves was measured by EEG. Forty-two classifiers were tested in the study and K* (K star) was considered as the best classifier with an accuracy rate of 97 %. A large number of features may reduce the overall performance. Reference [12] proposed a technique using one-channel EEG data for the detection of open and close eye state. They claimed that devices with multiple channels produced more accurate results but some operations seemed to be more time consuming and complex, such as embedding EEG device on the subject's head and selection of features. Therefore, a device with the least number of channels is needed. In this experiment, accuracy was not as high as compared to multichannel devices, but it was cost-effective and easily adapted for medical and individual use.

Another paper presented a method for eye state prediction with the algorithm C4.5 decision tree [13]. The main focus was on feature selection. Maximum classification accuracy in the paper was 91.6 % that was achieved with 13 most dominating attributes instead of 14 attributes. Reference [14] presented a method to improve the EEG, eye state data classification accuracy with the ranked order feature subsets. The effect of

* Corresponding author's e-mail: tariq.ali@uaar.edu.pk

rank order features on the accuracy of classification was analysed by applying k star classifier for original EEG data set in WEKA. Six algorithms were used for feature ordering. For unordered data set accuracy was 95.01 % and for ordered data set features accuracy was 95.09 %. A feature could be characterised as an individual quantifiable property of the procedure being watched, any machine learning algorithm could perform classification utilising an arrangement of features. In machine learning and pattern recognition, better understanding of data, reduction of computation time, and improvement of prediction accuracy are possible by the process of feature selection or feature reduction. It is a process of identifying and selecting the most relevant or most useful features of data that contribute more to the accuracy of the model. An imperative issue in the feature selection is the advancement of a strategy, which can choose amazing feature subsets and wipe out both repetitive and irrelevant features from the dataset. Methods used for feature selection are Filter method, Wrapper method and embedded method [15]. Recently, for optimal feature subset selection, wrapper method-based feature selection techniques have been showing better results to solve a feature selection problem. Among these, Genetic Algorithm (GA) is a promising way to deal with the combinational optimisation problem and it is extensively used in feature selection.

Authors proposed an automated feature selection method for BCI data [17]. The results of the paper showed that classification accuracy was improved by 0.9 % after feature selection as compared to the accuracy without feature selection. Reference [18] displayed a feature subset selection technique dependent on genetic algorithms for cancer dataset. The consequences of this investigation demonstrated that the proposed strategy gave preferred execution over the execution of the full feature set. Reference [9] proposed a GA based technique for feature selection of PVC arrhythmia dataset. The objective of the proposed technique was to select the optimal feature subset. Support Vector Machine (SVM), neural networks and k-Nearest Neighbor (KNN) algorithm were used for classification. The results showed that the proposed method gave better results than previously proposed techniques. This system obtained an accuracy of 99.69 %. Reference [20] proposed a genetic algorithm-based method for optimal feature subset selection for the efficient classification of Event-Related Potentials (ERPs). The proposed GA based technique selected 8 features out of 47 and achieved an accuracy of 93.8 %. From the literature review above, it is concluded that there should be an eye tracking system with the least number of attributes, which gives better classification accuracy than existing techniques. GA is the best method for selection of an optimal feature set. Therefore, we propose a GA based technique for feature subset selection. KNN classifier is used to assess the centrality of each chosen subset of features.

III. THE PROPOSED MODEL

A Feature Subset (FS) selection or simply feature selection technique is an operator, for example, FS from a k -dimensional input feature space to l -dimensional output feature space like,

$$FS: R^{rk} \rightarrow R^{xl}, \quad (1)$$

where $k, l \in \mathbb{Z}^+$ and $k \geq l$. R^{rk} are any matrix or database that has the original feature set with “ r ” observations or instances and R^{xl} contains the selected feature set with “ r ” instances. Feature selection can be described as a multi-objective technique that has two objectives; one is minimisation of the number of attributes and other is improvement of the classification accuracy. In the proposed technique, GA is used for finding of an optimal feature subset. The wrapper-based methods primarily use population-based selection of feature subset where a learning algorithm is employed to evaluate the worth of selected subsets of features [21]. The objective of the research is to select the optimal number of features in EEG eye state dataset. We have used different existing feature selection techniques and then proposed a GA based feature selection method.

As many existing techniques for eye state classification have good accuracy, but all of these use a very large feature set. In the present study, we have selected an optimal feature subset without compromising on the classification accuracy. Feature selection helps obtain a better predictive and less computationally intensive classification model by limiting the number of input features to a classifier. We have applied different existing feature selection methods and also proposed a GA based technique for EEG eye state data. Our proposed methodology combines GA and KNN for optimal feature subset selection. The proposed system consists of the following steps, as shown in Fig. 1.

Step 1: Data Set

In the research, we have used two datasets for eye state classification obtained from the UCI repository. The first data set was prepared by [11] and used as benchmark data in the existing literature. This data set consists of 14 977 instances, where 55.12 % (8255) of instances represent the eye open, and 44.88 % (6722) represent the closed eye state. The measurement duration was 117 seconds and the sampling frequency was 128 Hz during which the participants close/open their eyes at their own will. There are total 15 attributes for each instance, 14 of them represent the electrode values and 1 attribute represents the state of the eye. To be able to analyse the temporal dependencies, the instances are stored in chronological order in the corpus. The output “1” represents the eye-closed state and “0” – the eye-open state [14]. The second dataset is prepared by [22]; in this dataset “1” represents the eye-closed state and “0” represents the eye open state. This dataset is for epileptic seizure recognition and contains 5 classes and 11 500 instances; we extracted only eye state data. There are total 4600 instances of eye state, where 50.1 % (2301) instances corresponds to the eye-closed state and 49.9 % (2300) correspond to the open eye state. Of the total 179 attributes in this dataset, 178 represent the electrode values and 1 represents the state of the eye. The description of datasets is given in Table I.

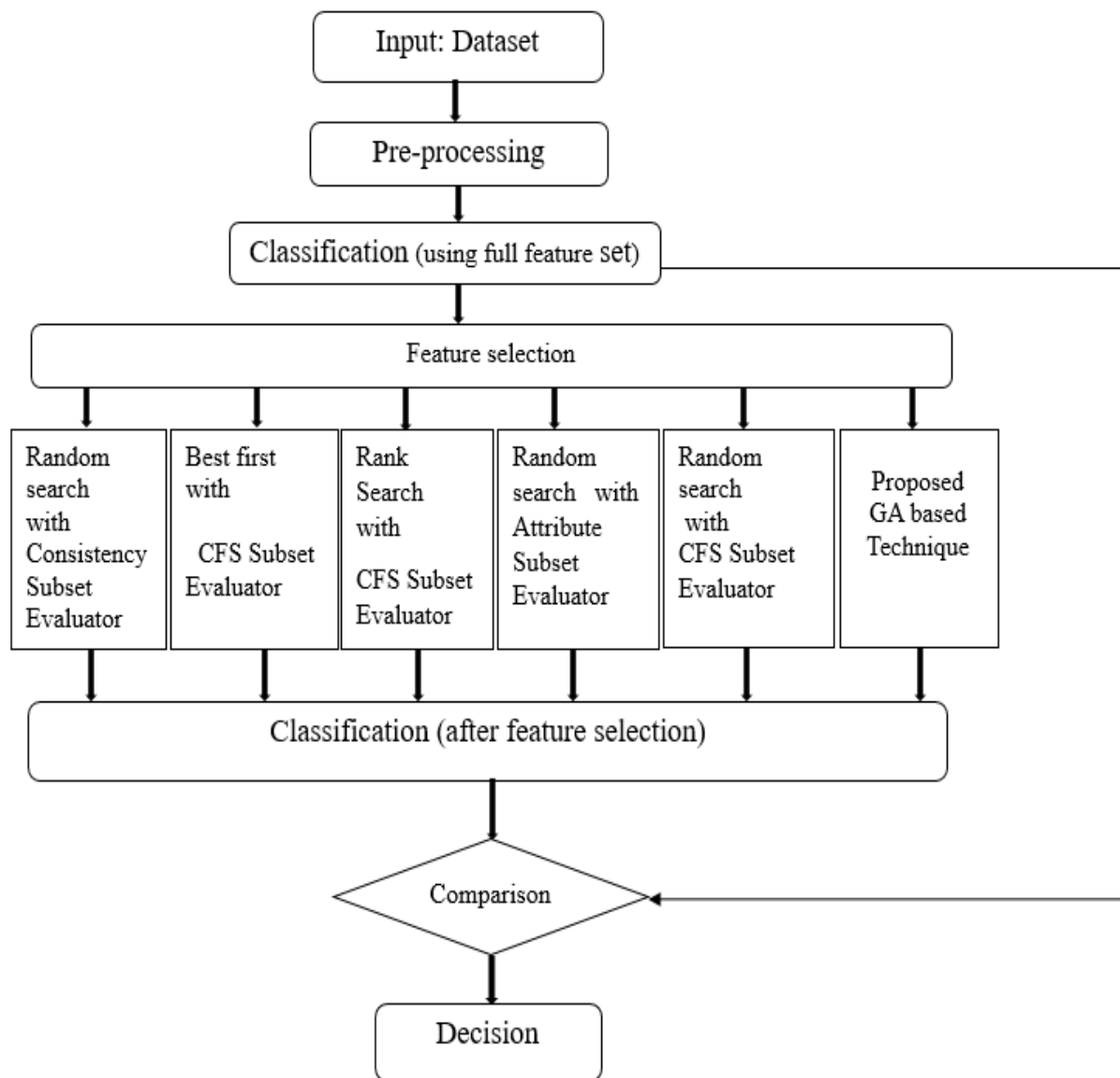


Fig. 1. Steps of the proposed framework.

TABLE I
DATASETS

No		Datasets	No of attributes	No of instances	No of classes
1	Rosler et al. 2013	EEG eyes	14	14977	2
2	Wu and Ernest 2017	Eye data from Epileptic seizure Recognition	178	4601	2

Step 2: Pre-Processing

During the pre-processing step, missing values are handled using the “Remove with Values” method in Weka tool. It removes instances that contain missing values.

Step 3: Classification

During the third step, classification of data without feature subset selection is performed. For this experiment, dataset1 contains 14 features and dataset2 contains 178 features. The classification step is repeated again after performing feature selection. Although there are many reliable classifiers, such as Bayesian, SVM and ANN, we prefer a KNN classifier. KNN is a very simple, highly effective and efficient classifier introduced by Fix and Hodges in 1951. It is a conventional classification algorithm, where classification is performed on the basis of the nearest neighbour class [23]. The KNN algorithm is an instance based classifier. It is a very convenient algorithm, which stores all the available instances and classifies a new arrived instance by measuring the similarity between them (e.g., using a distance function). In the proposed approach for classification, we use the KNN algorithm. KNN is also known as a lazy learner, such classifiers are the best approach for a dataset like EEG, because these classifiers best perform on data with a fewer number of attributes and larger instances. Even being simple and easy, this algorithm can give much better results than other classifiers. There are many distance functions, such as Cosine Eq. 2, Euclidean distance Eq. 3, Manhattan distance Eq. 4, Minkowsky Eq. 5, Standardised Distance and Chi-square etc. [24].

$$\text{Similarity} = \cos \theta = \frac{(A, B)}{|A||B|}; \quad (2)$$

$$d(A, B) = d(B, A) = \sqrt{\sum_{i=1}^n (B_i - A_i)^2}. \quad (3)$$

Manhattan distance: The Manhattan distance formula between points $A = (A_1, A_2, \dots, A_n)$ and $B = (B_1, B_2, \dots, B_n)$ is given as Eq. 4.

$$\text{Distance} = \sum_{i=1}^n |A_i - B_i|; \quad (4)$$

$$d(i, j) = \sqrt[q]{|x_{i1} - x_{j1}|^q + |x_{i2} - x_{j2}|^q + \dots + |x_{ip} - x_{jp}|^q}. \quad (5)$$

Step 4: Feature Selection

For feature selection, five different types of FS techniques that are available in WEKA are applied and one GA based technique is proposed. GA is one of the best optimisation problem-solving methods. It is a useful tool for feature reduction, especially for high dimensional data. GA uses a heuristic search technique, it selects random chromosomes and at each step tries to select the best individuals. These chromosomes then undergo mutation and crossover process to create a succeeding generation. This procedure continues till an optimal subset of features is formed [26]. Criteria to stop the GA, chromosome encoding, selection mechanisms, fitness evaluation and genetic operators are the five important issues in

GA. Figure 2 shows the proposed genetic algorithm for feature selection.

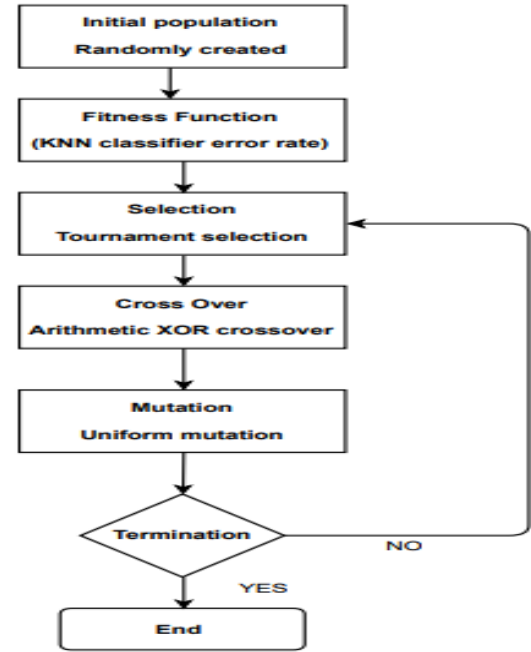


Fig. 2. The proposed genetic algorithm for feature selection.

A. GA Search Space

Genetic Algorithm works on binary search space (0 or 1) as a chromosome. First, initial population is produced, which is usually random and evaluated using a fitness function. In case of chromosomes which are binary, we use 1 for selected feature and 0 for not selected feature. Figure 3 shows features indexed using 1's, ranked chromosomes are selected for next generation.

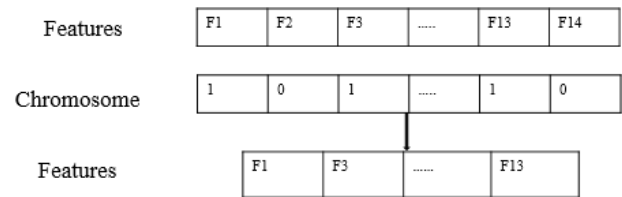


Fig. 3. Search space of GA.

B. Initial Population

After encoding the initial population is defined. For the present study, the initial population (stating population 0) is a matrix of chromosome length and population size that consists of only irregular binary (i.e., 0 or 1) digits. Size of population represents the number of individuals (chromosomes) in initial population. Each chromosome is shown in Fig. 4. To make it sure that each population chromosome spans the search space, the population size must be equal to at least the value of chromosome length.

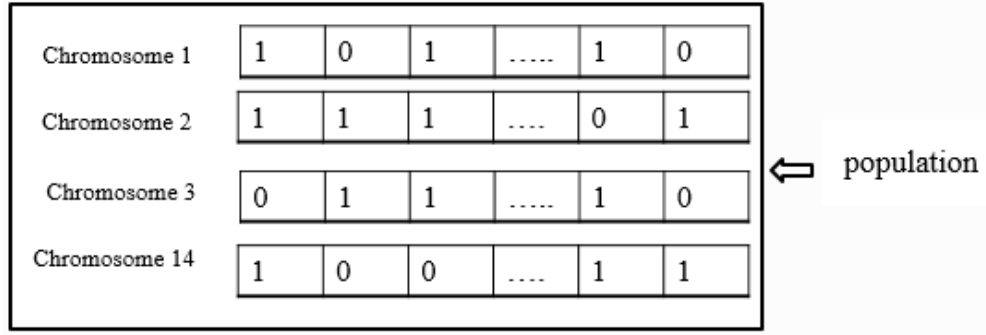


Fig. 4. The initial population of GA.

C. Fitness Function

In the proposed algorithm, the fitness of every chromosome of the current population is checked using KNN-based classifier error rate. The k -nearest neighbours algorithm works on the base of the shortest distance between a training set and a test set. Euclidean distance is computed between test data x_{test} and the training sets x_i and then the shortest distance (closest point) is found from a training set to a test set as given in Eq. 6.

$$D(x_{\text{test}}, x_i) = \sqrt{\sum_{m=1}^M (x_{\text{test}}, x_i)^2}. \quad (6)$$

Fitness function is applied to population in order to evaluate the results, and, on the basis of fitness function, fitness of population is ranked. Those lower in rank have more chance to go to next generation. Iterations are run in order to reduce the error rate and pick the individual with a lower rank value. The fitness of each individual is calculated using Eq. 7.

$$fit = \frac{\alpha}{N_f} + \exp\left(\frac{-1}{N_f}\right), \quad (7)$$

where

α – the classification error based on k -nearest neighbours Algorithm;

N_f – the number of the selected features.

D. Phenomena for the Creation of New Child

After fitness evaluation, new population is formed from three different children. Crossover and mutation are used in order to create new population.

Elite Children

These children are the individuals with the best fitness values and are pushed automatically into the next generation. The proposed method selects the top two best chromosomes and pushes them to the next generation automatically.

Crossover Children

In GA, the crossover operator combines two chromosomes to form a new child (chromosome) for the next generations. In crossover, two individuals (chromosomes) are needed and these are taken from the tournament selection. In the present study, the arithmetic type crossover function is used, the probability of crossover children is 0.8 and XOR operation is performed on two parent chromosomes (because they are binary strings) to create a child for the next generation as shown in Fig. 5. The XOR operation is given in Eq. 8.

$$\text{Crossover Kid} = P1 \oplus P2, \quad (8)$$

where

$P1$ – the chromosome used as the first parent in the crossover operation;

\oplus – the XOR operation that operates on binary values;

$P2$ – the chromosome used as the second parent in the crossover operation.

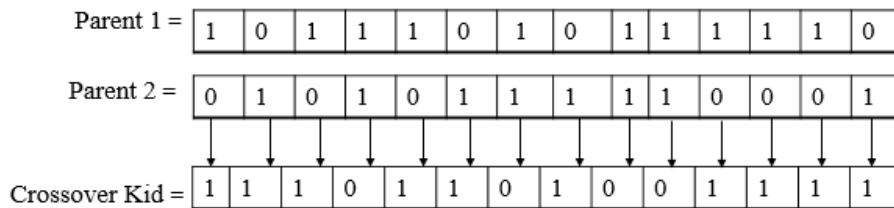


Fig. 5. Arithmetic crossover.

Mutation Children

Mutation operator in GA just alters one or more gene values in a chromosome from its initial state to create a child for the next generation. In mutation, the solution may change entirely from the previous solution. Mutation is used in different forms, like inversion mutation, uniform mutation, swap mutation, insert mutation etc. [27]. In our experiments, we use uniform mutation, where a set of random numbers (RD) is generated for

uniform distribution. Position of each gene bit is attached with a random number in a chromosome. Then, the chromosomes are checked from left side to right side. For each bit, mutation probability (mp) is compared with the value of each RD. If the RD at position '*i*' is less than pm, then gene (a bit) at position '*i*' is spun (0 to 1, 1 to 0). Otherwise, the gene is left the same. It is shown in Fig. 6.

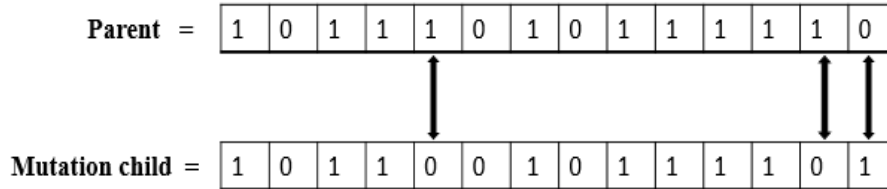


Fig. 6. Mutation child.

E. Termination

Once the GA reaches the optimal solution, it stops. Termination conditions are as follows:

- For *X* iterations, GA shows no progress;
- Reaches an absolute number of generations;
- Value of objective function reaches a certain pre-defined value.

Usually, the GA checks difference in values of fitness of generations. If the difference in average of hundred generations is equal or less than 0.000001, the GA terminates.

IV. RESULTS AND DISCUSSION

The proposed feature selection approach is evaluated using two different datasets taken from the UCI repository. The proposed technique is implemented in MATLAB2016a. The experiments were conducted on HP (Core i5-7200U CPU @ 2.50 GHz, 4 GB RAM) running Windows 10, 64-bit. A cross validation (10 fold) method is used to evaluate the results. In this cross-validation, the datasets are divided into ten equal sized. Each subset is used for testing and rest of subsets is used for training. We have tested 60 different classifiers and selected ensemble subspace KNN because it gives higher accuracy. Table II shows the average accuracy of 15 different classifiers. Accuracy is defined as the number of properly classified instances divided by a number of total testing instances. Accuracy can also be calculated as in Eq. 9 [29].

$$\text{Accuracy} = \frac{TP + TN}{TP + TN + FP + FN}. \quad (9)$$

The average accuracy is calculated using Eq. 10.

$$\text{Avg Accuracy} = \frac{\sum_{k=1}^{10} \% \text{ Accuracy}}{K}. \quad (10)$$

TABLE II
COMPARISON OF ACCURACY OF 15 DIFFERENT CLASSIFIERS

#	Classifier	Accuracy	
		Dataset 1	Dataset2
1	Subspace KNN	96.3	82.8
2	Kstar	94.7	82.0
3	Bagged Trees	92.9	81.7
4	Random forest	92.2	80.3
5	Decorate	90.7	79.0
6	Bagging	88.6	76.8
7	Weighted KNN	86.6	74.5
8	LMT	86.5	76.0
9	Fine KNN	85.7	71.8
10	IB1	84.6	70.0
11	Ibk	84.6	71.4
12	Medium KNN	84.5	71.5
13	Cubic KNN	84.3	71.9
14	Fine Gaussian SVM	83.8	70.5
15	J48	83.5	68.0

After performing classification on a full feature set, we have used different feature selection techniques available in WEKA tool shown in Table III and also proposed a GA based feature selection technique. Parameter setting for GA is shown in Table IV.

TABLE III
DIFFERENT FEATURE SELECTION TECHNIQUES

Feature selection technique	No. feature selected for dataset1 out of 14	No. feature selected for dataset2 out of 178
Random search with Consistency Subset Evaluator	13	162
Best first with CFS Subset Evaluator	10	155
RankSearch with CFS Subset Evaluator	9	141
Random search with Attribute Subset Evaluator	7	80
Random search with CFS Subset Evaluator	5	37

TABLE IV
PARAMETERS WITH THEIR VALUES USED FOR GA

GA parameter	Value
Population size	14 178
Population type	Bit strings
Genome length	14 178
Fitness function	The error rate of KNN classifier
Number of generations	300
Probability of crossover	0.9
Crossover	Arithmetic XOR crossover
Probability of mutation	0.1
Mutation	Uniform mutation
Selection	Tournament selection
Elite Count	2

Optimal feature subset is selected using our technique and on this reduced feature subset the classification accuracy is calculated. The proposed algorithm accuracy has been compared with the feature selection techniques in WEKA. The proposed algorithm has achieved better performance on both datasets. Table V demonstrates the accuracy values of (a) – without feature subset selection; (b) – after feature subset selection using WEKA tool and (c) – feature subset selection using genetic search against each dataset.

The experimental results show that the proposed GA based feature selection technique gives better accuracy as compared to the accuracy computed without feature subset selection. We have compared the accuracy results obtained from our proposed FS technique with the accuracy of different feature subsets selected from other methods available in WEKA tool and it has been observed that the proposed technique gives the optimal feature subset. In addition to accuracy, a number of features are also reduced. Figure 7 shows the total number of features in each dataset and the number of features reduced after the experimentation.

TABLE V
ACCURACY CALCULATED WITH ALL FEATURES AND AFTER SELECTING FEATURES USING DIFFERENT FEATURE SELECTION TECHNIQUES

Data set	Accuracy without feature selection	Accuracy using feature selection techniques in WEKA					Accuracy of the proposed GA based technique
		Random search with Consistency Subset Evaluator	Best first with CFS Subset Evaluator	Rank search with CFS Subset Evaluator	Random search with Attribute Subset Evaluator	Random search with CFS Subset Evaluator	
Dataset 1	96.3 %	96.1 %	91.1 %	88.5 %	83.6 %	83.5 %	97.2 %
Dataset 2	82.8 %	82.5 %	82.1 %	81.8 %	80.3 %	77.5 %	87.2 %

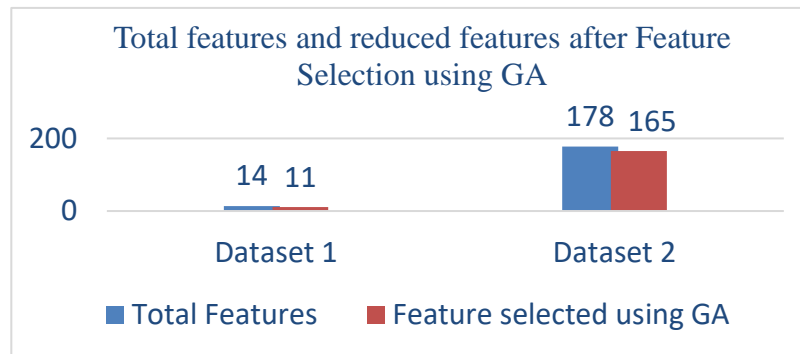


Fig. 7. Number of reduced features after applying feature selection using GA.

In both cases, the proposed GA based technique performance was better. However, the proposed technique shows more promising results than other techniques. Comparison of the proposed technique with existing methods shows that it gives better results in terms of classification accuracy with the reduced number of features. In 2013, Rosler and Suendermann classified the same data set with an accuracy of 97 % but used complete data set without feature reduction. In [28], the number of sensors was reduced up to 10 but accuracy decreased to 83.5 %. However, the proposed technique classifies the same dataset with an accuracy of 97.2 % using only 11 sensors.

V. CONCLUSION

In the paper, for searching and selecting the most optimal attribute set from the original set of attributes, we have proposed the GA based technique, and KNN is used for fitness evaluation. Experiments are performed on standard datasets to demonstrate the proposed algorithm, which reduces the dataset dimensionality and increases the prediction accuracy by choosing significant attributes from the dataset and better accuracy is achieved on both datasets. We have compared the accuracy results obtained from the proposed FS technique with the accuracy of different feature subsets selected from other methods available in the WEKA tool. We have also compared accuracy results before applying feature selection and accuracy results after applying feature selection. The experimental results have shown that the proposed technique finds the most optimal feature sets that improve the predictive accuracy of the model.

REFERENCES

- [1] S. I. Ali and W. Shahzad, "A Feature Subset Selection Method Based on Symmetric Uncertainty and Ant Colony Optimization," in *2012 International Conference on Emerging Technologies*, Oct. 2012, pp. 1–6. <https://doi.org/10.1109/ICET.2012.6375420>
- [2] P. Asvestas, A. Korda, S. Kostopoulos, I. Karanasiou, A. Ouzounoglou, K. Sidiropoulos, and G. Matsopoulos, "Use of Genetic Algorithm for the Selection of EEG Features," in *Journal of Physics: Conference Series*, vol. 633, Sep. 2015. <https://doi.org/10.1088/1742-6596/633/1/012123>
- [3] J. Biesiada, W. Duch, A. Kachel, K. Maczka, and S. Palucha, "Feature Ranking Methods Based on Information Entropy With Parzen Windows", in *International Conference on Research in Electrotechnology and Applied Informatics*, 2004.
- [4] M. A. Jabbar, B. L. Deekshatulu, and P. Chandra, "Classification of Heart Disease Using K-Nearest Neighbor and Genetic Algorithm", *Procedia Technology*, vol. 10, pp. 85–94, 2013. <https://doi.org/10.1016/j.protcy.2013.12.340>
- [5] D. Lijuan, H. Ge, W. Ma, and J. Miao, "EEG Feature Selection Method Based on Decision Tree," *Bio-Medical Materials and Engineering*, vol. 26, iss. S1, pp. S1019–S1025, Aug. 2015. <https://doi.org/10.3233/BME-151397>
- [6] P. A. Estévez, C. M. Held, C. A. Holzmann, C. A. Perez, J. P. Pérez, J. Heiss, M. Garrido, and P. Peirano, "Polysomnographic Pattern Recognition for Automated Classification of Sleep-Waking States in Infants," *Medical and Biological Engineering and Computing*, vol. 40, iss. 1, pp. 105–113, Jan. 2002. <https://doi.org/10.1007/BF02347703>
- [7] L.-Y. Hu, M.-W. Huang, S.-W. Ke, and C.-F. Tsai, "The Distance Function Effect on k-Nearest Neighbor Classification for Medical Datasets," *SpringerPlus*, vol. 5, iss. 1, Dec. 2016. <https://doi.org/10.1186/s40064-016-2941-7>
- [8] J. P. Kandhasamy and S. Balamurali, "Performance Analysis of Classifier Models to Predict Diabetes Mellitus," *Procedia Computer Science*, vol. 47, pp. 45–51, 2015. <https://doi.org/10.1016/j.procs.2015.03.182>
- [9] S. Vachiravel, "Eye State Prediction Using EEG Signal and C4.5 Decision Tree Algorithm," *International Journal of Applied Engineering Research*, vol. 10, no. 68, Jan. 2015.
- [10] Y. Kaya and H. Pehlivan, "Feature Selection Using Genetic Algorithms for Premature Ventricular Contraction Classification," in *2015 9th International Conference on Electrical and Electronics Engineering (ELECO)*, 2015, pp. 1229–1232. <https://doi.org/10.1109/ELECO.2015.7394628>
- [11] D. Kim, H. Han, S. Cho, and U. Chong, "Detection of Drowsiness With Eyes Open Using EEG-Based Power Spectrum Analysis," in *2012 7th International Forum on Strategic Technology (IFOST)*, 2012 pp. 1–4. <https://doi.org/10.1109/IFOST.2012.6357815>
- [12] S. Li, H. Wu, D. Wan, and J. Zhu, "An Effective Feature Selection Method for Hyperspectral Image Classification Based on Genetic Algorithm and Support Vector Machine," *Knowledge-Based Systems*, vol. 24, iss. 1, pp. 40–48, Feb. 2011. <https://doi.org/10.1016/j.knosys.2010.07.003>
- [13] T. D. Pham and D. Tran, "Emotion Recognition Using The Emotiv EPOC Device," in *International Conference on Neural Information Processing*, 2012, pp. 394–399. https://doi.org/10.1007/978-3-642-34500-5_47
- [14] K. Polat and S. Güneş, "Classification of Epileptiform EEG Using a Hybrid System Based on Decision Tree Classifier and Fast Fourier Transform," *Applied Mathematics and Computation*, vol. 187, no. 2, pp. 1017–1026, Apr. 2007. <https://doi.org/10.1016/j.amc.2006.09.022>
- [15] P. P. Aghaei, T. Gulrez, O. AlZoubi, G. Gargiulo, and R. A. Calvo, "Brain-Computer Interface: Next Generation Thought Controlled Distributed Video Game Development Platform," in *2008 IEEE Symposium On Computational Intelligence and Games*, 2008, pp. 251–257.
- [16] T. Nguyen, T. H. Nguyen, K. Q. D. Truong, and Toi Van Vo, "A Mean Threshold Algorithm for Human Eye Blinking Detection Using EEG," in *4th International Conference on Biomedical Engineering in Vietnam*, 2013, pp. 275–279. https://doi.org/10.1007/978-3-642-32183-2_69

- [17] K. F. Man, K. S. Tang, and S. Kwong, "Genetic Algorithms: Concepts and Applications in Engineering Design," *IEEE transactions on Industrial Electronics*, vol. 43, iss. 5, pp. 519–534, 1996. <https://doi.org/10.1109/41.538609>
- [18] T. K. Mansoori, A. Suman, and S. K. Mishra, "Feature Selection by Genetic Algorithm and SVM Classification for Cancer Detection," *International Journal of Advanced Research in Computer Science and Software Engineering*, vol. 4, iss. 9, pp. 357–365, Sep. 2014.
- [19] M. Oner and G. Hu, "Analyzing One-Channel EEG Signals for Detection of Close and Open Eyes Activities," in *2013 IIAI International Conference on Advanced Applied Informatics (IIAIAI)*, Aug. 2013, pp. 318–323. <https://doi.org/10.1109/iiat-aa.2013.13>
- [20] O. Roesler and D. Suendermann, "A First Step Towards Eye State Prediction Using EEG," *Proc. of the AIHLS*, 2013.
- [21] S. Khadijeh, R. Boostani, and A. Ghanizadeh, "Classification of BMD and ADHD Patients Using Their EEG Signals," *Expert Systems with Applications*, vol. 38, no. 3, pp. 1956–1963, Mar. 2011. <https://doi.org/10.1016/j.eswa.2010.07.128>
- [22] M. Sahu, N. K. Nagwani, S. Verma, and S. Shirke. "Impact of Ranked Ordered Feature List (ROFL) on Classification with Visual Data Mining Techniques," in *2016 International Conference on Electrical, Electronics, and Optimization Techniques (ICEEOT)*, Mar. 2016. <https://doi.org/10.1109/ICEEOT.2016.7755289>
- [23] D. A. Singh, E. J. Leavline, R., Priyanka, and P. P. Priya, "Dimensionality Reduction Using Genetic Algorithm for Improving Accuracy in Medical Diagnosis," *International Journal of Intelligent Systems and Applications*, vol. 8, no. 1, pp. 67–73, Jan. 2016. <https://doi.org/10.5815/ijisa.2016.01.08>
- [24] S. N. Sivanandam and S. N. Deepa, *Introduction to Genetic Algorithms*. Springer Science & Business Media, 2007.
- [25] N. Sulaiman, M. Nasir T. S. Lias, Z. H. Murat, S. A. Aris, and N. H. A. Hamid, "Novel Methods for Stress Features Identification Using EEG Signals," *International Journal of Simulation: Systems, Science and Technology*, vol. 12, no. 1, pp. 27–33, Feb. 2011.
- [26] T. Michal, "Fundamentals of EEG Measurement," *Measurement Science Review*, vol. 2, no. 2, pp. 1–11, 2002.
- [27] C. F. Tsai, W. Eberle, and C. Y. Chu, "Genetic Algorithms in Feature and Instance Selection," *Knowledge-Based Systems*, vol. 39, pp. 240–247, Feb. 2013. <https://doi.org/10.1016/j.knosys.2012.11.005>
- [28] W. Qiuyi and E. Fokoue, "Epileptic Seizure Recognition Data Set," 2017. [Online]. Available: <https://archive.ics.uci.edu/ml/datasets/Epileptic+Seizure+Recognition>
- [29] M. Yeo, X. Li, K. Shen, and E. Wilder-Smith, "Can SVM be Used for Automatic EEG Detection of Drowsiness During Car Driving?," *Safety Science*, vol. 47, no. 1, pp. 115–124, Jan. 2009. <https://doi.org/10.1016/j.ssci.2008.01.007>