Classification of Headache types using Modified ANN with Customized Genetic Algorithm

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Abstract-

Headache is a common disease that occurs in almost all kinds of people due to tension, changing lifestyle, and symptoms of other serious issues in the human body. The correct diagnosis of this lacks due to complex test procedures, irregular monitoring, visiting the physicians as an outpatient, and inexperience of physicians. To assist the specialists in detecting the accurate types of headaches, the proposed system is developed to classify the types of headaches using Modified Neural Network.

The Introduction of the Brilliant Binary Chromosome Algorithm (BBCA) will generate brilliant chromosomes with the filter-based method that will give the most relevant features. The optimization of resource handling and reduced computational time is achieved by using the Fitness Based Crossover Algorithm (FBCA). The public Migbase dataset is taken for the study. Migbase contains collective information on headache attacks from 849 patient data from three different hospitals in Turkey. This Customized approach of the Genetic Algorithm is proposed to extract the elite features with a significant effect. The well designed modified Artificial Neural network model is implemented as the classifying model. The entire implementation of the proposed work is performed in Python 3.7 environment from which it is confirmed that the suggested novel combined methodology (CGA & MANN) will give optimal results compared with other current research methodologies concerning the proposed method.

The proposed customized feature selection method improved the performance of the migraine classifier, producing a robust system that achieved over 98% accuracy. The results suggest that the proposed methods can be used to support specialists in the classification of migraines in patients undergoing treatment.

Keywords-Migraine; Brillian Binary Chromosome; Fitness Based Crossover; Artificial Neural Network; Feature Selection

I. INTRODUCTION

One of the commonly prevalent illnesses headaches is considered in this study for classification which makes use of the significance of biomedical data. Mostly due to focusing on complex test procedures, improper monitoring, lack of time for making a correct diagnosis if the patient attained as an outpatient, and the inexperience of the physicians, migraines are wrongly classified or the severity is underestimated. So these reasons will lead to inappropriate or imprecise remedies that will take place which results in damage to the patient's health. Hence, we need a methodology that handles tolerance for haziness, uncertainty, approximate reasoning, and inequitable truth to achieve tractability, robustness, reduced solution cost, and close similarity with human-like decision-making, unlike traditional hard computing. An artificial **neural network, a soft computing technique is** an attempt to emulate an arrangement of neurons that make a human brain like architecture so that computers can be able to learn things and humanly make decisions. **Genetic algorithms** (GA) take all their stimulation from nature, and there are no genetic algorithms based on search-based algorithms that find their roots in natural choice and concepts of genetics. The genetic algorithm is also a subset of a large branch of computation also called evolutionary computation in soft computing.

This article seeks to contribute to the identification of different types of migraines through the use of the supervised learning technique Artificial Neural Network. The purpose of this study is to develop a classification model that allows the determination of the type of migraine a patient suffers based on the

analysis of the optimum features selected by the Binary genetic algorithm. The freshness, implication, and importance of this study are outlined as follows:

a) An effective method aimed at classifying the type of migraine experienced by a patient, which, unlike existing methodologies, does not use procedures requiring brain wave measurement or the use of sensors.

b) A new Customized GA (CGA) is proposed as the FS algorithm. In CGA, a filter-based FS algorithm is merged into initialization, and the feature combination information is utilized in crossover operations to improve the efficiency of the optimization process.

c) The systematic migraine classification process used includes the stages of data collection based on symptoms and diagnosis by the treating physicians, selection of the optimum features, use of Modified Artificial neural network classification model with the best accuracy of diagnosis.

The combination of BBCA & FBCA features selection algorithm will produce the optimized features. While classifying the headache classes, the best features are identified using the customized feature selection method. Using this approach, the accuracy of classification using modified Artificial Neural Network MANN is improved. The improved performance of this combination of techniques will contribute to the biomedicine field for accurate classification of headache types by supporting the physicians in diagnosis.

The paper is organized as follows: Section 2 presents the literature review and briefly summarizes related works. Section 3 describes the problem statement. Section 4 explains the proposed CGA-based FS algorithm in detail and presents the configuration of the Modified ANN model. Section 5 concludes the paper.

II. LITERATURE REVIEW

Headache is a serious and increasingly recognized issue in society making a remarkable impact and on both the social and personal life of a person [1]. Headaches are classified as two major types called primary and secondary headaches [2]. Among these, the primary headache occurs without underlying pathology such as viral or bacterial infections.

Headache disorders' not only causing a significant impact on a patients' personal life, but it is making a burden both in the working environment and in-home environment [3]. The earlier studies of migraine classification mainly focus on complex tests of brain wave analysis. Mostly due to improper monitoring, lack of time for making the correct diagnosis, the inexperience of the physicians, migraines are wrongly classified or the severity is underestimated [4]. So these reasons will lead to inappropriate or imprecise remedies that will take place which results in damage to a patient's health [5].

Migraines are said as a chronic disorder of the nervous system and are characterized by the onset of recurrent symptoms or episodes associated with headache, which can range from moderate to severe pain and includes throbbing or vibrating pain; furthermore, migraines can be experienced unilaterally or bilaterally and can generate other symptoms, such as nausea, vomiting, weakness, and light and sound sensitivity [6].

Headache disorders are the most prevalent of all the neurological conditions and they are among the most frequent medical complaints seen in general practice [7]. Almost 50 % of the common population get occurrences of a headache throughout any given year, and more than 90% report a lifetime history of head pain [8, 9].

Working people are the backbone of every family and society. The common practice is to pay attention to the health of these people when it comes to risky occupations and perform regular medical checkups. They care about employees who suffer from a primary headache begins only when they go to see a doctor [10].

Women diagnosed with migraine were more likely to have high blood pressure, high cholesterol, and a family history of heart attacks [11]. An analysis shows that women with migraines had a bigger possibility of a heart attack. Women affected with migraines were having 50 percent more likely to develop cardiovascular disease than women without severe headaches, [12]. A study which describes Women are highly affected with Migraine [13].

To manage the primary headache disorder properly requires a correct diagnosis. The occurrences of headaches have to be keeping tracked often by the patients in some form of headache journal. The gold standard for headache classification is the International Classification of Headache Disorders (ICHD) [14].

The need for systems enabling correct decision-making has led to high interest in the development of data classification models in recent decades, among which artificial neural networks have established high probable compliance, generalizability, and learning capacity and because of the possibility of representing nonlinear relationships [15].

The accuracy of the model not only depends on the model structure and related training algorithm but also on the feature space, which is constructed through the original feature set and feature selection (FS) algorithm [16]. FS is commonly used in machine learning models as part of the pre-processing step, in which a part of features (i.e. independent variables) is generated by removing features with minimal relevance [17] [18].

Advantages of FS are typically decreasing training and implementation time, facilitating data understanding, and reducing storage requirement [19]. The feature space may include several features that are less relevant to the expected prediction. Based on model parameters, several types of research quantify the relative importance of individual features after fitting the model, to explore implications of different features. These results might not be reliable with bias introduced by limited model capacity [20] [21].

Artificial neural networks and their current structures, such as deep neural networks, have been used efficiently in data classification tasks and display better results than other traditional techniques; their strength lies in their high capacity to vigorously create complex prediction functions and imitate human learning [22].

A feature reduction method that integrates a combined method of machine learning models that uses information gain and genetic algorithm as feature reduction techniques are evaluated and experimental results show better performance in terms of various measures for multi-domain review and movie reviews [23].

III. PROBLEM IDENTIFICATION

Migraines are often misdiagnosed due to focus on the analysis of brain waves, complex test procedures, and lack of timely identification and continuous monitoring of the patient. The misdiagnosis is experienced because of the imprecise classification or underestimation of the severity of the illness as it is the main pathology for several other serious diseases. The existing researches are lacking in the performance level of detecting Migraines. The general feature selection algorithms require a larger computational overhead to obtain optimum features.

IV. METHODOLOY

A. Dataset Description

The proposed work starts with Data acquisition, pre-processing. The public Migbase dataset is taken for the study.   Migbase contains collective information on headache occurrences from 849 patient data from three different hospitals in Turkey. Each record is labeled with one of the three possible primary headache disorders (Migraine, Tension, and Cluster). The independent variables are duration, location of pain, and several symptoms of headache.

B. Proposed System Flow
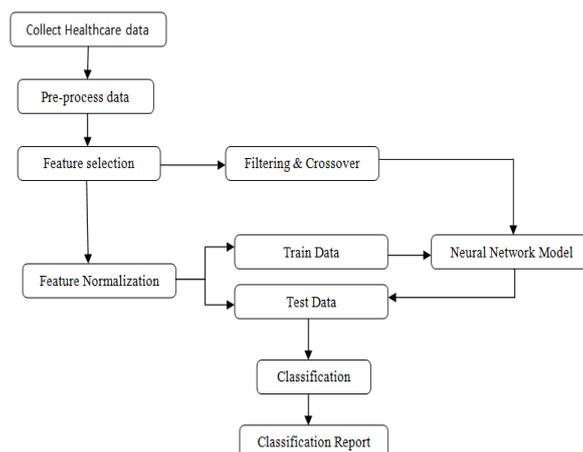
The flow of the proposed system is shown in Figure 1.

Figure 1 Proposed System Flow

C. Brilliant Binary Chromosome Algorithm (BBCA)

The generation of Brilliant Binary Chromosome is performed by categorizing the best-related variables by computing a T-test. The probability density of this result will be considered as the relative significance of the feature. The higher the value of this will be considered as good genes. The collection of these good genes generates the Brilliant Binary Chromosome. The
Algorithm – 1 shows the Brilliant Binary Chromosome Algorithm (BBCA).

Algorithm - 1
Step 1: Fit a multiple linear regression model to the training
      Set.
Step 2: Calculate T-Test for individual regression coefficient.
Step 3: Calculate $q_i \leftarrow |l_i| / \sum_{i=1}^{m} |l_i|$.
Step4: The $|l_i|$ calculated from the *t*-test will be the condition
      to compute the relative significance of feature i.
Step 5: The higher $|l_i|$ entailed that the corresponding
      features is more considerable
Step 6: Calculate fitness $c_i = MSE\ c_i + \lambda S\ c_i$.

The fitness is estimated by computing the predicted accuracy of the feature subset through the modified neural network. The fitness function will take the accuracy of the selected chromosome (**c_i**) times the Mean Square Error (MSE) added with the weight of penalty (λ) times the number of features in the subset (**Sc_i**). Here the MSE will act as the performance indicator of the NN which is modified as a restricted model by limiting the number of layers by three and the number of nodes is set as 20 in each layer to achieve less computation time of the model.

C. Fitness based Chromosome Algorithm (FBCA)

The chromosomes selected for the crossover are by applying the Tournament selection method on two tournament groups arbitrarily chosen from the population and the criteria for success is the chromosome with the lowest fitness value. The winners chosen from the tournament groups are selected for crossover operation. The offspring generation is performed by applying crossover operators based on the predetermined probability. The offspring is generated by exchanging the crossover point of the corresponding parent chromosomes.

In this FBCA, the fitness value of the parent chromosomes is exploited for selecting the individual feature from the group, if the fitness values of the parent chromosomes are different. Algorithm – 2 shows the procedure for FBCA, the fitness-based crossover algorithm for generating a new Brilliant binary chromosome E by exchanging information in two-parent chromosomes Q_1 and Q2.

Algorithm – 2

Step 1: Check $Q^i1 = Q^i2$, ($Q^{(i)}$ denotes the value of the ith gene on the chromosome Q)

Step 2:   If the $Q^i1 = Q^i2$ is true then set $E^{(i)} = Q^i1 = Q^i2$

Step 3:   Otherwise $E^{(i)} = Q^i1$ with probability of $Q1 = fit_{Q2}/(fit_{Q1} + fit_{Q2})$ or
$E^{(i)} = Q^i2$ with probability of $Q2 = fitness_{Q1}/(fit_{Q1} + fit_{Q2})$

The higher fitness value features are replaced arbitrarily by the newly created dissimilar chromosome with lower fitness values. This replacement ensures a greater enhancement in the convergence rate. The final feature combination is obtained by decoding the best chromosomes as the final feature subset to improve the robustness of the retrieval. From this, a new chromosome is created and decoded by taking the union of all the genes on these best chromosomes.

D. Modified Artificial Neural Network (MANN)

In the present investigation, the modified ANN is introduced to achieve the goal of accurate classification of Migraines. To validate the data integrity and originality of the process a hybridized BBCA and FBCA is introduced to achieve optimized features. Here, the optimization is enhanced by performing the combined use of the filtering method and a different fitness-based crossover method. Fitness is calculated for making the cross-over operation. The modified ANN is introduced to improve the performance by reducing the number of layers and the number of nodes for the training sample.

The Best Features selected from the Customized Genetic algorithm are fit with the model. The splitting of the train and test sets is performed. The size of the test sample is 20 %.

The Steps followed for classifying the classes with the modified ANN model using the best features selected after applying the Customized Genetic algorithm procedure:

1) The splitting of train and test sets is performed. The size of the test sample is 20 %.

2) Scaling the features.

3) Weight Initialization.

4) Takes in the weighted sum of the inputs and normalizes them through between 0 and 1 through a sigmoid function

5) The derivative of the sigmoid function is used to calculate necessary weight adjustments.

6) Find loss between the predicted and ground-truth value

7) Training the model by trial and error method, adjusting the synaptic weights each time to get a better result

8) Pass training set through the neural network

9) Calculate the error rate

10) Multiply error by input and gradient of the sigmoid function. The weights which are Less confident are adjusted more through the nature of the function.

11) Adjust synaptic weights.

12) Pass inputs through the neural network to get output. Calculate output.

13) Initialize ANN and add input, hidden (10 % node dropped out), and output layers.

14) Compiling the ANN - apply stochastic gradient descent

15) Fitting the ANN to the Training set

16) Print Classification report and Kappa scores.

E. Experimental Result & Discussion

The Customized genetic algorithm generates only highly related features for detecting the classes. The features selected by the proposed algorithm are denoted as 1 and the features which are not selected are denoted as 0 in Table I. The total number of features selected is 29. Table I shows the features selected in binary form after applying the Customized genetic algorithm for feature selection.

TABLE I.   BEST FEATURES

Features selected (Best Features)	Best Value	Dimension
0111111101100111011111111011100011111011	0.98235	29

Sensitivity is a metric used to measure the proportion of the definite positive cases predicted as positive (True Positive). The higher sensitivity value would mean the high true positive and low false-negative values. Specificity is the measure used to give the proportion of the actual negatives predicted as negatives. The higher specificity describes that the model predicts the true negative as negative and low false positive

Table-II displays the sensitivity and specificity scores with corresponding standard deviations for each class in the Migbase dataset for the existing training set and the changed datasets.

TABLE II.   SENSITIVITY & SPECIFICITY SCORE OF MIGRAINE, TENSION & CLUSTER HEADACHES

Migraine		Tension		Cluster	
Sensitivity	0.9984 ± 0.004	Sensitivity	0.9895 ± 0.009	Sensitivity	0.9836 ± 0.022
Specificity	0.9834 ± 0.006	Specificity	0.9980 ± 0.006	Specificity	0.9994 ± 0.002

Precision is the rate not to classify a positive as a negative instance. Here the high Precision shows that the proposed MANN model is not classifying the negative case as positive.
The actual positive cases which are predicted as positive are called Recall. This means for example that the Migraine cases are predicted as Migraine and the corresponding cases as it is respectively. The high Recall value depicts that the greater number of positive predictions that are correctly identified.
F1 score is the weighted harmonic mean of Precision and Recall, used to compare the model. Support is the fraction that gives the number of occurrences in the corresponding class.
Table III displays the classification report of the Modified ANN model for the classes Migraine, Tension, and Cluster.

TABLE – III CLASSIFICATION REPORT OF MANN

Class	Precision	Recall	f1-score	Support

0	1.00	0.86	0.92	7
1	0.99	1.00	1.00	124
2	1.00	1.00	1.00	39

Table IV shows the accuracy and κ-score on the Migbase dataset, for classifying the headache types using the proposed algorithm.

TABLE – Iv ACCURACY & COHEN SCORE

Algorithm	Accuracy	Cohen κ
Proposed	0.9979013 ±0.0196	0.986013 ±0.01231

Thus in the proposed study the implementation of the Customized Genetic Algorithm (BBCA & FBCA) and the Modified ANN gives the improved performance and accuracy level over 98 % of classification.

V.   CONCLUSION

The healthcare data is acquired, pre-processed, and analyzed for best-fit values. By utilizing the Brilliant Binary Chromosome Algorithm and Fitness Based Crossover Algorithm the optimized features are ensured for assisting the Modified ANN model. This Customized approach of the Genetic Algorithm is proposed to extract the elite features with a significant effect. The well designed modified Artificial Neural network model is implemented as the classifying model to increase the classification accuracy. The entire implementation of the proposed work is performed in Python 3.7 environment from which it is confirmed that the suggested novel combined methodology (CGA & MANN) will leads to give optimal results compared with other current research methodologies concerning the proposed method.

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