Investigating an Ensemble Classifier Based on Multi-Objective Genetic Algorithm for Machine Learning Applications

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Abstract—Ensemble learning in machine learning applications is crucial because it leverages the collective wisdom of multiple models to enhance predictive performance and generalization. Ensemble learning is a method to provide a better approximation of an optimal classifier. A number of basic classifiers are used in ensemble learning. In order to improve performance, it is important for the basic classifiers to possess adequate efficacy and exhibit distinct classification errors. Additionally, an appropriate technique should be employed to amalgamate the outcomes of these classifiers. Numerous methods for ensemble classification have been introduced, including voting, bagging and reinforcement methods. In this particular study, an ensemble classifier that relies on the weighted mean of the basic classifiers' outputs was proposed. To estimate the combination weights, a multi-objective genetic algorithm, considering factors such as classification error, diversity, sparsity, and density criteria, was utilized. Through implementations on UCI datasets, the proposed approach demonstrates a significant enhancement in classification accuracy compared to other conventional ensemble classifiers. In summary, the obtained results showed that genetic-based ensemble classifiers provide advantages such as enhanced capability to handle complex datasets, improved robustness and generalization, and flexible adaptability. These advantages make them a valuable tool in various domains, contributing to more accurate and reliable predictions. Future studies should test and validate this method on more and larger datasets to determine its actual performance.

Keywords—Machine learning; genetic algorithm; ensemble classification; classification error

I. INTRODUCTION

Classification is a process in which each unknown pattern is attributed to one of the known classes based on its characteristics. In other words, classification is a mapping from the n-dimensional space of features to the k-dimensional space of classes, in which the degree of belonging of the feature vector to different classes is expressed as a numerical value [1, 2]. The classifier is usually built in a learning process. Many algorithms actually perform a local search that may get stuck in a local minimum. If it is trapped in the local minimum, it is not possible to have an optimal classifier [3]. A classifier must go through at least two phases: the training phase and the testing phase [4, 5]. In the training phase, the feature vector is extracted from each sample. Feature vectors are defined according to the nature of samples and application [6]. To improve feature vectors, feature conversion, feature reduction, or feature selection can be applied to them. Genetic algorithm and principal component analysis can be mentioned from the feature reduction methods, and mutual information maximization can be mentioned from the feature selection methods. The classifier is then trained to adjust its weights, biases, and other parameters using the selected dataset. In the testing phase, features are extracted from the test dataset and samples are labeled with the help of a trained classifier [7].

Ensemble learning is a method to provide a better approximation of an optimal classifier. A number of basic classifiers are used in ensemble learning [8, 9]. Each basic learning algorithm reaches a different answer for the problem according to its parameters, and it is expected that the classification accuracy will increase by combining these answers [10]. For this reason, in recent years, using the results of multiple classifiers as an effective method in pattern recognition has attracted the attention of many researchers, and it has been used in various branches of science, especially engineering science. Diagnosing faults in gas turbines, intrusion detection in computer networks, zip code recognition, handwriting recognition, identity recognition and biomedical signal classification (such as EEG and ECG) are examples of the use of ensemble classifiers [11-14]. The classifiers whose results are combined are called basic classifiers, and the set of classifiers is called a composite or ensemble system.

Since classifiers are made in a learning process, in order to have different classifiers, their learning process should be different. It has been proven that the combination of more independent classifiers increases the recognition rate [15]. Therefore, it is tried to increase the variety of basic classifiers in different applications. Also, by using an appropriate ensemble approach to combine the outputs of the basic classifiers, the classification performance is improved. Training classifiers with various feature sets is the most effective method to create diversity in learning classifiers. The many methods of creating diversity proposed in the articles can be divided into two categories: explicit and implicit [16]. Explicit methods make classifiers different from each other by changing their learning process of them. Penalty methods and reinforcement methods are among the most important explicit methods to create diversity in basic classifiers [17]. In implicit methods, with implicit changes in the learning process of basic classifiers, an attempt is made to diversify them. In these methods, no measure of diversity is checked during learning, and therefore, there is no guarantee that the classifiers will be different, but we only hope that the errors of the created classifiers will be different from each other. The most common of these methods is random selection with replacement of samples from among all training samples, which is called the bagging method [18]. Other implicit methods include fuzzy integral [19], Dempster-Shafer [20], knowledge-behaviour space [21] and decision model [22].

Common methods of combining classifiers include the majority voting approach [23], weighted majority voting approach [24], methods based on Bayesian theory [25] and stacking approaches [26]. In some methods, evolutionary algorithms are used to estimate weights to combine the average weights of basic classifiers [27]. These methods are also implicit learning methods [28]. In study [29], the optimal estimation of weights has been done with the help of a genetic algorithm. In this method, the sum of error, sparsity and diversity criteria is minimized in order to obtain the best result for classification. Indeed, the genetic algorithm optimizes the sum of error, sparsity and diversity criteria, and there is no guarantee to optimize the individual fitness functions of error, sparsity and diversity. This issue can introduce an important defect into the system, and therefore, this study tries to address it. The proposed ensemble method is in the form of weighted sum of the outputs, the weights are estimated by multi-objective genetic algorithm and considering four simultaneous criteria of classification error, sparsity, diversity and density. In the proposed method, while using the criteria mentioned in study [29], the density criterion was also considered. The rest of the article is organized as follows: Section II provides an overview of different approaches for combining classifiers including reinforcement method, bagging method, voting method, evolutionary method and stacking method. Section III presents the framework and formulation of the proposed ensemble technique for combining classifiers. Section IV presents and discusses the experimental results, and Section V makes a conclusion about this study.

II. RELATED WORK

Xue et al. showed that ensemble methods can be categorized into three groups based on the type of information produced by each classifier [30]: concept-level methods, rank-level methods, and measurement-level methods. In this section, some popular ensemble methods are briefly reviewed.

1) Reinforcement method. It is a hybrid method to improve the performance of multiple weak classifiers and obtain a strong classifier. In this method, predictors are trained sequentially. The former is trained from the entire dataset, while the latter is trained from the training dataset obtained based on the performance of the previous ones. Reinforcement ensemble classifiers, also known as Reinforcement Learning with Ensemble Classifiers (RLEC), are a sophisticated approach that combines the principles of reinforcement learning and ensemble learning. In RLEC, a collection of classifiers is trained using ensemble learning techniques such as bagging or boosting, creating an ensemble that collaboratively makes predictions. The distinguishing aspect of RLEC lies in the integration of reinforcement learning, where the ensemble receives feedback in the form of rewards or penalties during training. By incorporating reinforcement learning, RLEC enables the ensemble to adapt its strategies, explore different actions, and ultimately improve its performance over time [31].

2) *Bagging method*. Bagging ensemble classifiers, short for Bootstrap Aggregating, is a powerful technique used in machine learning to improve the accuracy and stability of prediction models. In bagging, multiple classifiers are trained independently on different subsets of the training data, usually obtained through bootstrapping. Each classifier in the ensemble provides a prediction, and the final prediction is determined through voting or averaging. By combining the outputs of multiple classifiers, bagging ensemble classifiers can reduce the variance in predictions and enhance overall performance. Bagging is particularly effective when the base classifiers are diverse, as errors made by individual classifiers tend to cancel out. This technique is widely used in various machine learning algorithms, including decision trees, neural networks, and support vector machines, and it has proven to be a reliable method for reducing overfitting and improving generalization capabilities [32].

3) Voting method. Voting ensemble classifiers, also known as majority voting or democratic voting, is a popular technique in machine learning that combines the predictions from multiple individual classifiers to make final decisions. Each classifier in the ensemble independently provides a prediction, and the final prediction is determined by majority voting. This means that the class with the highest number of votes among the classifiers is chosen as the final predicted class. Voting ensemble classifiers can be applied in different ways, such as hard voting, where each classifier has an equal vote weight, or soft voting, where classifiers' votes are weighted based on their confidence levels. This ensemble method leverages the wisdom of the crowd and is effective in situations where the base classifiers are diverse and have complementary strengths. Voting ensemble classifiers have been successfully utilized in various machine learning algorithms, including decision trees, random forests, and support vector machines, to enhance prediction accuracy and improve model robustness [33].

4) Evolutionary method. Evolutionary ensemble classifiers, also known as evolutionary ensembles, are a popular technique in machine learning that harnesses the principles of evolution to create robust and accurate prediction models. In this approach, a population of diverse classifiers is initially generated, each with its own set of parameters or configurations. The classifiers are assessed on their individual performance using evaluation metrics such as accuracy or error rate. Through a process of selection, crossover, and mutation inspired by natural selection, the genetic makeup of the classifiers evolves over multiple generations. The fittest classifiers, those with superior performance, are selected to reproduce and pass on their traits to the next generation while lesser-performing classifiers are either eliminated or undergo random modifications. This evolutionary cycle continues until a termination criterion, such as reaching a desired level of accuracy or a predefined number of generations, is met. By leveraging the diversity and complementarity of ensemble members through evolutionary search, evolutionary

ensemble classifiers can improve prediction accuracy and generalization ability. They have proven to be effective in various domains, including classification, regression, and feature selection, providing a powerful tool for solving complex machine-learning problems [34].

5) Stacking method. Stacking ensemble classifiers, also referred to as stacked generalization, is a powerful technique in machine learning that combines the predictions of multiple individual classifiers to make more accurate and robust predictions. In this approach, a diverse set of base classifiers are trained on the same dataset. Each base classifier learns different aspects of the data and produces its predictions. Instead of treating these predictions equally, a meta-classifier is then used to learn how to combine them into a final prediction. The metaclassifier takes the outputs of the base classifiers as input features and learns to make a higher-level prediction based on this information. This meta-learning step allows the ensemble to capture complex relationships and patterns within the data that may not be apparent to individual classifiers. The stacking ensemble approach can lead to improved predictive performance by leveraging the strengths of different classifiers and reducing the weaknesses of individual models through the combined decision-making process [35].

III. THE PROPOSED ENSEMBLE TECHNIQUE

In this research, we proposed an ensemble evolutionary technique for improving the efficiency of each classifier based on the multi-objective genetic algorithm by considering the criteria of classification error, diversity, sparsity and density. In combining classifiers, each sample S is associated with a label y. In order to classify each sample S into k classes, it is assumed that there are N classifiers, $h_1, h_2, ..., h_N$, and each of them uses a certain feature vector for the sample S. For an input sample S, the classifiers recognize the values $X^n = h_n(S)$. $X = [X^1, ..., X^N]^T$ can be obtained through all classifiers. In other words, the final result is obtained from the output combination of all classifiers in the form of the following relationship.

$$H(S)=F\bigl(h_1(S)\ldots,h_N(S)\bigr)=F(x)=f\bigl(x^1\ldots,x^N\bigr)\ (1)$$

In this article, the weighted average of the output of the classifiers is used to make the final decision. The following relation is used for the weighted sum of the output of the classifiers:

$$H(S) = \sum_{n=1}^{N} W_n x_n = W^T \tag{2}$$

where, W_n is the weight of nth classifier, and $W = [w_1, ..., w_n]^T$. Consider $\{(S_m, y_m)\}_{m=1}^M$ with M sample and N classifiers, where S_m is the mth sample and y_m denotes its label. $\{(x_m, y_m)\}_{m=1}^M$ denotes the classifier output for mth sample, where x_m indicates the vector $x_m = [x_m^1, x_m^2 \dots x_m^N]^T$. Fig. 1 shows the scheme of the suggested algorithm. As shown, the samples are given to N basic classifiers and the output of these classifiers are combined with each other in the combiner in a weighted sum and create the final output. In the proposed method, a multi-objective genetic algorithm is used to estimate the weights. As shown, in this method, four fitness functions of classification error, diversity, sparsity and density are used. Each of these fitness functions, as well as the details of the multi-objective genetic algorithm and its structure, are explained below.



Fig. 1. Block diagram of the suggested algorithm for the ensemble classification.

The ensemble classifier focuses on finding the weights in such a way that the minimum classification error is obtained. The error function is defined as follows:

$$F_{error} = \frac{1}{M} \sum_{m=1}^{M} (W^T x_m - y_m)^2$$
(3)

The minimization of the error function is considered an optimization problem, and in this article, an attempt is made to reduce the classification error function from a threshold value, which is shown in Eq. (4).

$$F_{error}(W) \le t_1 \tag{4}$$

where, t_1 is a control parameter. In the proposed method, the I_1 -norm function is used to calculate the sparsity, according to Eq. (5), which should be less than a determined value (t_2).

$$F_{sparsity}(W) = \|W\|_1 \le t_2 \tag{5}$$

Using different classifiers creates diversity. Eq. (6) is used to estimate diversity.

$$F_{diversity}(W) = \frac{2}{N(N-1)} \sum_{n_1=1}^{N-1} \sum_{n_2=n_1+1}^{N} \frac{1+Q_{n_1\cdot n_2}}{2}$$
(6)

where, Q is the statistical measure introduced by Yule to estimate the degree of diversity. The smaller the Q, the more diverse the classifiers. The diversity value in the proposed method should be less than a specified threshold, which is shown in Eq. (7):

$$F_{diversity}(W) \le t_3 \tag{7}$$

The density criterion is used as the fourth criterion to estimate weights in the combination of classifiers. For this reason, to increase the correct rate of pattern recognition, the density should be maximized. $F_{density}$ is given by Eq. (8):

$$F_{density} = \frac{1}{\sum_{n=1}^{N} \sum_{m=1}^{M_n} (x_m - \mu_n) (x_m - \mu_n)^T}$$
(8)

where, μ_n is the mean of nth class, and M_n is the number of samples in the nth class. The criterion specified in Eq. (8) must be less than the threshold specified in Eq. (9):

$$F_{density}(W) \le t_4 \tag{9}$$

where, t_4 is a control parameter. Finally, the main goal in combining classifiers is to estimate the weights using the multiobjective genetic algorithm in such a way that Eq. (4), (5), (7) and (9) are established. In general, it can be said that using the proposed method reduces the destructive effects of noise and increases the distance between classes. It is also expected that the proposed method will obtain better results in the experiments due to the change in the process of estimating W_i with the multi-objective genetic algorithm and the use of various criteria.

IV. RESULTS AND DISCUSSION

In this section, the performance of the proposed method is compared to the methods of bagging, voting, stacking, boosting, and genetic algorithm-based ensemble method [29] on UCI data. The Iris, CMC, Diabetes, Vowel, Glass and Ionosphere datasets from the UCI repository database were used for the experiments, whose characteristics are shown in Table I [36]. In these experiments, the basic classifiers are of the same type with different parameters that have acceptable diversity. In the conducted experiments, the basic classifiers for all methods were chosen the same, and all of them are multilayer perceptron neural networks with different numbers of hidden layers and different number of nodes in each layer.

In the proposed method, the parameters of the multiobjective genetic algorithm are set as follows:

- Population size: 100 chromosomes
- Chromosome length: an array of length 4 of decimal numbers equivalent to the weight of each of the basic classifiers
- Mutation operator: randomly selecting a gene from a chromosome and randomly resetting that gene
- Combination operator: single-point type
- Selection operator: tournament type
- Termination criterion: if the fitness functions of the best solution do not change significantly after a certain number of iterations.

Performance evaluation was done using a random partitioning technique. The random partitioning method involves the random division of the dataset into three distinct subsets: training, validation, and testing [37]. Specifically, 70% of the data were allocated to the training subset, while 30% were assigned to the testing subset. Additionally, 15% of the training subset was designated for validation purposes. To evaluate the overall classification performance, the trained model was applied to the testing subset, and performance metric values were computed accordingly. It is worth noting that in the context of random partitioning, the early stopping method is implemented as a means to halt training when the model's performance ceases to improve on a separate validation subset. The classification performance of different ensemble methods was investigated through accuracy and F-measure indices. Tables II and III show the accuracy and F-measure obtained from different ensemble techniques in comparison with the proposed method for the mentioned dataset using the random partitioning method.

As shown in Table II, the proposed method has a higher classification accuracy rate than other methods for all classification problems. In fact, both ensemble techniques based on genetic algorithms perform better than other methods. However, the proposed method also improves the performance of the ensemble technique introduced in study [29], which is due to the use of four measures of classification error, dispersion, diversity and density in estimating the weights of the combination of classifiers. For example, the proposed method improves classification accuracy by 3.05% for the CMC dataset and 6.56% for the Vowel dataset compared to the genetic algorithm-based method.

TABLE I.	UCI DATA SPECI	FICATIONS [36]
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Dataset	Number of classes	Number of features	Number of samples
Iris	3	4	150
CMC	3	9	1473
Diabetes	2	8	768
Vowel	11	13	990
Glass	7	9	214
Ionosphere	2	34	351

TABLE II. CLASSIFICATION ACCURACIES OF DIFFERENT ENSEMBLE CLASSIFIERS FOR DIFFERENT DATASETS USING RANDOM PARTITIONING METHOD

	Stacking	Bagging	Boosting	Voting	Genetic	Multi-objective genetic
Iris	54.16	97.50	98.12	96.08	100.00	100.00
CMC	41.98	49.52	52.11	51.88	52.14	55.19
Diabetes	67.92	71.90	73.89	73.78	75.66	77.51
Vowel	63.39	63.45	75.86	88.11	91.94	98.50
Glass	42.21	61.82	62.48	61.20	56.36	73.09
Ionosphere	63.91	86.21	73.77	87.22	87.22	88.30

As shown in Table III, the proposed method has a higher Fmeasure value than other methods for all classification problems. In fact, both ensemble techniques based on genetic algorithms perform better than other methods. However, the proposed method also improves the performance of the ensemble technique introduced in [29], which is due to the use of four measures of classification error, dispersion, diversity and density in estimating the weights of the combination of classifiers.

In addition to the random partitioning technique, the current research employed a K-fold cross-validation approach to

evaluate the classification effectiveness of the suggested method. In this procedure, the dataset was initially divided into K folds. Out of these, K-1 folds were randomly assigned as the training set, while the remaining fold was designated as the testing set. This process was iterated K times to ensure that each fold was utilized as a testing set. In each iteration, the trained model was applied to the testing set, yielding K distinct evaluation metric values [38, 39]. In this study, K = 5 was considered. Tables IV and V show the accuracy and F-measure obtained from different ensemble techniques in comparison with the proposed method for the mentioned dataset using the 5-fold cross-validation method.

TABLE III. F-MEASURE VALUES OF DIFFERENT ENSEMBLE CLASSIFIERS FOR DIFFERENT DATASETS USING RANDOM PARTITIONING METHOD

	Stacking	Bagging	Boosting	Voting	Genetic	Multi-objective genetic
Iris	50.74	97.10	97.10	94.42	100.00	100.00
CMC	35.81	31.46	38.91	45.82	48.22	51.68
Diabetes	64.49	65.89	62.25	62.29	78.19	82.61
Vowel	59.53	44.91	63.55	66.70	71.45	92.32
Glass	49.72	59.77	52.69	48.31	50.77	64.33
Ionosphere	65.10	89.59	56.74	90.73	80.00	91.07

TABLE IV.	CLASSIFICATION ACCURACIES OF DIFFERENT ENSEMBLE CLASSIFIERS FOR DIFFERENT DATASETS USING A	5-FOLD CROSS-VALIDATION METHOD
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	Stacking	Bagging	Boosting	Voting	Genetic	Multi-objective genetic
Iris	52.39	93.88	95.18	92.51	97.78	98.05
CMC	40.28	49.13	47.96	48.70	50.68	53.31
Diabetes	63.31	70.02	70.87	71.06	73.15	74.97
Vowel	58.70	60.84	73.32	85.42	88.70	95.47
Glass	40.07	59.23	60.11	60.00	55.17	70.20
Ionosphere	61.12	83.41	70.69	84.10	86.03	86.63

TABLE V. F-MEASURE VALUES OF DIFFERENT ENSEMBLE CLASSIFIERS FOR DIFFERENT DATASETS USING A 5-FOLD CROSS-VALIDATION METHOD

	Stacking	Bagging	Boosting	Voting	Genetic	Multi-objective genetic
Iris	31.69	96.11	93.39	93.77	95.57	96.52
CMC	35.72	37.60	37.89	35.70	36.93	52.74
Diabetes	51.36	76.50	60.32	61.19	64.75	81.99
Vowel	36.96	96.41	94.28	74.63	77.86	96.50
Glass	37.75	65.82	60.28	58.00	60.97	72.17
Ionosphere	78.20	93.21	93.39	80.42	79.60	94.49

As shown in Tables IV and V, again, the proposed algorithm produces the best classification results for all datasets. Again, both genetic algorithm-based methods provided better performance than other methods. Genetic-based ensemble classifiers offer several advantages in the field of machine learning [40]. These classifiers utilize genetic algorithms, which mimic the process of natural selection, to train and optimize ensemble models [41]. One key advantage of genetic-based ensemble classifiers is their ability to handle complex and highdimensional datasets [42]. The genetic algorithms excel in searching through a large space of possible feature combinations, weights, or architectures, enabling the classifier to capture subtle patterns and relationships in the data [43]. This makes them particularly effective in solving problems where traditional classifiers may struggle. Another advantage is their robustness and generalization abilities. The genetic algorithms help in overcoming overfitting by finding a diverse set of base classifiers that have complementary strengths and weaknesses [44]. This diversity enhances the overall performance of the ensemble by reducing errors and increasing the reliability of predictions on unseen data [45]. Since the genetic algorithms can automatically adjust and optimize the ensemble composition, they can readily adapt to changing data distributions or incorporate new data without requiring the entire model to be retrained. This adaptability makes them suitable for real-time and dynamic environments [46, 47].

V. CONCLUSION

The combination of classifiers is an approach to improve classification performance in complex problems. For the combination of classifiers to be effective, the base classifiers must have acceptable performance and be different from each other. Also, an appropriate combination rule is required to combine their results effectively. The combination rule should be chosen in such a way that the classifiers cover each other's weaknesses. In this article, while reviewing different ensemble classifiers, a new ensemble technique was proposed to combine the results of the basic classifiers. The proposed ensemble method was based on the weighted averaging rule of the outputs of the basic classifiers, where the weights were estimated by the multi-objective genetic algorithm through the criteria of classification error, diversity, sparsity and density as fitness functions. The proposed method showed better performance by using the density criterion in the classes than other methods and using the multi-objective genetic algorithm to optimize each of the fitting functions in the experiments. However, the proposed framework in this study has some limitations like many previous studies. The performance of the proposed ensemble algorithm is highly dependent on threshold values t_1 to t_4 . In the current proposed framework, optimization methods were not used to determine these thresholds, which is one of the limitations of the study. In addition, the lack of dynamic determination of the parameters of the proposed model for different datasets is another limitation of this study.

In summary, the obtained results showed that genetic-based ensemble classifiers provide advantages such as enhanced capability to handle complex datasets, improved robustness and generalization, and flexible adaptability. These advantages make them a valuable tool in various domains, contributing to more accurate and reliable predictions. Future studies should test and validate this method on more and larger datasets to determine its actual performance. Moreover, future studies must expand the proposed framework by incorporating dynamic combinations and engaging in more intricate applications. Alongside the introduction of a mathematical model for classifier ensemble featuring density, diversity and sparsity learning, an optimization process through a heuristic and iterative approach leveraging the genetic algorithm was implemented. Therefore, achieving an optimized mathematical solution like convex optimization becomes essential for further analysis.

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