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ENSEMBLE LEARNING FOR HEART DISEASE PREDICTION: A NOVEL APPROACH USING ACCURACY-BASED WEIGHTED AGING CLASSIFIER ENSEMBLE

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KEYWORDS	ABSTRACT
Heart Disease, CART model, ICIT2F	The early detection of the risk for heart disease is crucial for the prevention of cardiovascular diseases which is still the leading cause of death globally. This paper introduces an ICIT2F mean partitioning-based CART model for heart disease classification if integrated with four others models. In this method, the entire dataset is divided into smaller chunks, and a CART classifier is trained on each chunk. Then, an Accuracy Based Weighted Aging Classifiers Ensemble (AB-WAE) is used to combine the classifiers, individually, creating a homogeneous ensemble with high prediction power. Proposed approach is tested on the Cleveland and Framingham heart disease databases with 93% and 91% classification accuracy respectively. A comparison with other state-of-art popular machine learning algorithms such as random forest, gradient boosting, and support vector machine shows that the proposed method outperforms existing classical methods. Further ROC curve analysis confirms its robust discriminative ability. In conclusion, the present work provides a solid and accurate tool for heart disease risk prediction which could assist clinicians in early diagnosis, timely intervention and better patient management.
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Introduction

Cardiovascular diseases (CVDs) are considered by the World Health Organization (WHO) as the principal cause of mortality globally. Of all the types of CVD, coronary heart disease (CHD) is the most prevalent and accounts for over 80% of deaths related to cardiovascular diseases worldwide [1]. Thus, it is crucial to identify potential future patients with CVD early in order to reduce premature death and to provide these individuals with timely clinical services. Along with classical clinical methods, informatics approaches, particularly machine learning (ML), have been increasingly considered for enhancing the prediction of the risk of HD. ML techniques are now widely used in laboratory diagnostics to support disease detection, clinical decision-making, and outcome prediction from complex biomedical data [24]. Furthermore, ML-based models have shown promising results in the prediction and diagnosis of liver diseases by identifying hidden patterns in clinical, biochemical, and imaging datasets [25]. Various ML-based models have been proposed and tested against different heart disease datasets, demonstrating varying levels of predictive performance and accuracy [2–6].

ML-based methods have recently attracted considerable attention in agriculture, health, and medicine, particularly in diagnostics. They have been successfully applied to forecasting pesticide usage [26], assessing and monitoring child health outcomes [27], featuring method in molecular ML [30,31] and other data-driven decision-making processes across diverse domains. Although they perform well, further studies are in progress to improve the models so that higher accuracy and reliability can be obtained. For example, ensemble learning has been shown as a powerful method for enhancing the result of ML [7]. An ensemble classifier has more than one individual classifier and the predictions made by each one are concatenated using majority voting and other mechanisms. Research has demonstrated that ensemble methods generally perform better than traditional classifiers in both accuracy and robustness [8]. Ensemble learning can be either homogeneous, in which all the members use the same base learner, or heterogeneous, where the classifiers are instantiated using different base learners. Because of the flexible nature of ensemble methods, it is possible to drastically improve the performance of the model, therefore, these methods continue to be researched in the area of medical diagnosis.

Inspired by advances in learning heart disease risk from data, this work introduces a new homogeneous ensemble learning paradigm to further enhance classification performance. The proposed approach adopts a mean-based splitting rule to partition the original data into a number of smaller subsets randomly. For each such subset, train a Classification and Regression Tree (CART) model. These separate classifiers are then combined by an Accuracy-Based Weighted Aging Classifier Ensemble (AB-WAE), which is the classical Weighted Aging Classifier Ensemble (WAE) with enhancements in computational efficiency. By weighing between accuracy of classifier and an aging factor, the proposed ensemble framework yields a more reliable prediction model for heart disease risk evaluation.

Contrary to standard random decision forests [9], which produce multiple decision trees and combine outputs by averaging for regression or through majority voting for classification [27], the

proposed solution operates differently. Rather than building trees on the entire data with traditional random sampling, the data is partitioned into blocks using the mean-based splitting strategy. On these partitions, a group of decision tree classifiers is then trained, which captures different characteristics of the data. Adaptability effect to different data distributions is enhanced and hence predictive reliability of dynamic observing environments is promoted, which thereby differentiates the proposed scheme from traditional ensemble learning approaches.

In order to assess the Efficiency and robustness of the proposed approach, experiments are performed on two real heart disease datasets: Cleveland and Framingham. Then the suggested model's performance is compared with some popular machine learning classifiers such as KNN, LR, LDA, SVM, CART, gradient boosting and random forest. The key contributions of the proposed framework are as follows:

We propose a mean-based splitting strategy, which is coupled with an Accuracy-Based Weighted Aging Classifier Ensemble (AB-WAE) to enhance the performance of the prediction of heart disease risk and overcome the weaknesses of the conventional approaches.

The method proposed is thoroughly evaluated on two popular benchmarks, namely the Cleveland and Framingham datasets, and the results are compared with those of several advanced machine learning algorithms.

The proposed method shows better prediction accuracy and robustness of heart disease risk than traditional ensemble learning methods.

The paper is organized as follows: In Section 2, various ensemble learning methods are reviewed; in Section 3, the proposed method is detailed; Section 4 describes the dataset and the performance evaluation metrics. The results are discussed in Section 5, and the paper is concluded in Section 6.

Literature Review

Coronary heart disease (CHD) in particular is one of the major killers in the broader category of cardiovascular diseases (CVDs), for which the World Health Organization (WHO) estimates that it is a top cause of death globally [10]. Hence, early detection and effective treatment would be beneficial for a patient's life and for curbing mortality rate of the disease. Recently, there has been an increasing interest in machine learning (ML) based heart disease risk prediction models which enable data-driven and more accurate clinical decision making. Different ML-based classification models have also been used for the prediction of heart disease, but their results have been varying across datasets and experimental configurations [11].

The significance of machine learning as a tool for analysis in the field of health care prediction and risk evaluation for related diseases is becoming more prominent [32,33]. In contrast to traditional diagnostic methods, ML techniques are capable of analyzing multi-source, complex, and high-dimensional medical data, and discovering latent patterns that cannot be directly observed through manual clinical diagnosis. Several algorithms such as LR, LDA, SVM, KNN, RF and GB were employed for predicting heart disease [12, 28, 29].

LR and LDA are among the first algorithms used for prediction of heart disease. These are two linear models that find a linear combination of input features (such as age, cholesterol levels and blood pressure) that best predicts the risk of heart disease [13]. However, such models tend to have difficulty dealing with highly complex and non-linear relationships between data that are often found in medical data. On the other hand, Support Vector Machines (SVM) have become very popular for many years, which can describe non-linear decision boundaries. SVM classifiers are known to perform well in high dimensional spaces and have been widely used for two class classification problems in medical diagnosis [14]. It has been demonstrated that SVM is superior to simpler models such as LR and LDA in heart disease prediction task if tuned appropriately [15].

k-Nearest Neighbor (KNN) is also a popular method in medical classification problems. KNN is based on the idea of similarity, it classifies a data point based on how its neighbors are classified. Despite its simplicity, the KNN algorithm is prone to noise and suffers from high dimensionality if not regularized. More recently, methods of ensembling have gained popularity when addressing the challenges of predictive modeling in healthcare. The ensemble learning technique leverages the predictions from the sub-models to enhance predictive accuracy by minimizing the bias and variance errors. RF and GB are two popular ensemble algorithms used to predict cardiovascular disease. Two such algorithms, random forest and gradient boosting, build a collection of trees and combine their predictions to increase accuracy [16].

RF creates a forest of decision trees, where each tree is built using a random selection of samples. The predictions of the single trees are combined, usually by majority vote for classification problems. RF has been proven effective in many applications of health care, such as heart disease prediction, because it can manage missing data and it conducts feature selection automatically. In contrast, Gradient Boosting (GB) concentrates on producing an ensemble of weak learners, in which each tracer error-shift correction erroneous predictions of previous trees. Methods such as XGBoost and LightGBM have gained significant popularity owing to their efficiency and performance in large-scale data applications. GB methods are generally more accurate than RF, although they can require more tuning, and are more sensitive to noise in the data [17].

Regular machine learning algorithms have been demonstrated to predict heart disease successfully, however ensemble learning strategies are gaining traction as the next step towards increasing prediction accuracy. The principal intuition behind ensemble learning is to pool a collection of different models, and then make the best use of these differing models by combining them. Ensemble approaches can be divided into homogeneous and heterogeneous techniques, based on whether the base learners are identical or different. Homogeneous Ensemble Learning employs the same family of models as the base learners, e.g., decision trees or SVMs. A popular homogeneous ensemble technique is the Random Forest, which aggregates a number of decision trees to generate a powerful predictive model. Another common approach is bagging, an abbreviation for Bootstrap Aggregating, which fits multiple copies of the same prediction method on different bootstrapped samples of the training data, then combines them in order to reduce variance. Ensemble approaches designed using Bagging, notably Random Forests, have been used

for the prediction of heart disease, confirming their superiority over individual decision tree models.

Heterogeneous Ensemble Learning method conducts integration of various classifiers like decision trees, SVM, neural networks and so on at the same time slot. One prominent method is that of Boosting, which generates an ensemble of weak learners that successively modifies errors previously committed. Although boosting strategies (e.g., AdaBoost and Gradient Boosting) have demonstrated high predictive power, they are considered to be computationally complex and are prone to overfitting if they are not adequately regularized. In this study, ensemble methods are being optimized by utilizing recent advances in order to further enhance heart disease prediction models. Accuracy-Based Weighted Aging Classifier Ensembles (AB-WAE) are introduced as an adapted form of traditional weighted aging classifier ensembles (WAE) wherein the weight of each base classifier is modulated according to its prediction accuracy as well as its age. Such joint dynamic weighting process/scheme can better adapt for aging classifiers and can lead to improved overall/long-term performance of an ensemble model over time [18].

Mean splitting has also been investigated recently in the context of ensembling. This strategy consists of dividing the dataset randomly into smaller segments, training a classifier on each segment, and then aggregating the predictions. In addition, this technique can be used to prevent overfitting when dealing with highly variable large samples. The data with certain kernel function is divided, and each partition is trained with classifier, also named as heart disease risk prediction.

In spite of the success of ML algorithms, there exist a number of challenges when it comes to applying these techniques for prediction of heart disease. The quality and completeness of the data, was one of the major concerns. Several heart disease datasets are usually incomplete or contain missing values that may lead to ML model performance degradation. Additional effort is necessary in terms of data preprocessing and feature engineering for better results. Interpretability is another challenge when working with machine learning. Ensembler learners (i.e. Random Forest and Gradient Boosting) have proven to be very powerful predictors but they lack interpretability that is a major limitation in medical applications where we need to understand why the predictions are made in order to use them for clinical decision making. Future work would be to investigate approaches that simultaneously improve prediction accuracy and interpretability of ML models in healthcare.

Machine learning algorithms, in particular ensemble learning, have recently shown great promise for the prediction of heart disease risk. Algorithms such as Random Forest, Gradient Boosting or other ensemble algorithms have shown better results than traditional classifiers [28,29]. However, there are still issues with quality of data, interpretability of models, and overfitting. Given that new methodologies for context-based partitioning including AB-WAE and mean-based splitting approaches are continuously being proposed, it is foreseen that the performance of the prediction models for heart disease may be further improved in the future, which might ultimately lead to a revolution in the early detection and treatment of CHD.

Proposed methodology

In this work, we present a powerful machine learning model on the basis of ensemble technique to predict the risk of heart disease. The proposed methodology is systematic and sequential as depicted in Figure 1 and consists of dataset collection, preprocessing, training, ensemble creation and testing.

The methodology starts with collecting the related datasets. In this paper, we are working with publicly available heart disease datasets, namely the Cleveland and Framingham heart disease datasets. These datasets have vital features like patient demographic details, cholesterol level, blood pressure and other medical history, which influence the prediction of risk of heart disease.

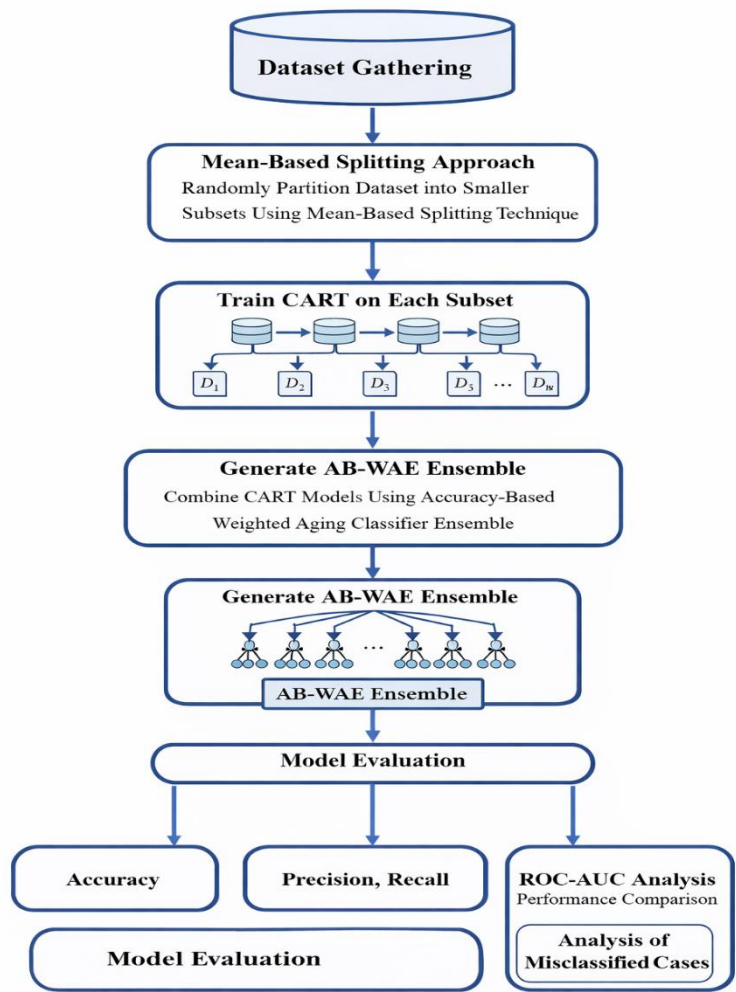


Figure 1: Proposed methodology

Preprocessing of collected data to turn it clean and ready for model training is the next stage. There are multiple subagents associated with this phase: Data cleansing to eliminate duplicated, missing, or erroneous data points from dataset and to assure dataset quality; Text preprocessing if needed on clinical notes or patient records (tokenization, stop word removal, stemming); Labels preprocessing: The target variable representing the risk of developing heart disease is converted into two classes (for example “No Disease” or “Disease”).

At a later stage, the data matrix is transformed to extract informative features that can potentially enhance the accuracy of the predictive model. Features are classified into a number of types: lexical, which consist of simple numeric features (word count, average word length, article length, numbers count); sentiment, by carrying out sentiment analysis on text to obtain positive, negative, neutral sentiments, which could be related to patient risk (twitter, facebook); n-gram, by extracting the sequence of words (unigrams, bigrams and trigrams) to discover common phrases and word association in the text.

Datasets and Performance Metrics

This work is based on two publicly available datasets of heart disease that is analyzed experimentally. The first is the Cleveland dataset [19] which is taken from UCI (University of California, Irvine) machine learning repository, the second one is the Framingham dataset from Kaggle [20]. The Cleveland dataset includes 303 patient cases with 14 attributes, while the Framingham dataset comprises 4,238 cases with 16 attributes. As there are some missing values in some variables of the Framingham dataset, the preprocessing is done to enable the data to be used in training and testing the model. The data sets offer a variety of demographic and clinical risk factors associated with age, gender, cholesterol level, blood pressure, alcohol use, diabetes status, and other health parameters. To evaluate the model, the data are split into training and testing sets with a 70:30 holdout which is popularly used in similar works and it can be easily compared with the reported results.

The effectiveness of the proposed approach is analyzed in terms of accuracy, precision, sensitivity, and F1 score. Accuracy represents the number of true predicted cases over all considered cases. Precision tells us what proportion of samples that were predicted positive, are actually positive. Sensitivity (recall) assesses how well the model is well to identify true positive instances. Incorporating precision and sensitivity into a single score, F1score is a go to measure when discussing the trade-off between correctly predicted positive and missing positive cases. The equation form of these evaluation measures are given as follows:

$$\text{classification accuracy} = \frac{TP + TN}{TP + TN + FP + FN}$$

$$\text{Precision} = \frac{TP}{TP + FP}$$

$$\text{Sensitivity} = \frac{TP}{TP + FN}$$

$$F1 = \frac{2 * \text{Precision} * \text{Sensitivity}}{\text{Precision} + \text{Sensitivity}} = \frac{2TP}{2TP + FP + FN}$$

For TP, TN, FP and FN, it corresponds to the number of true positives, true negatives, false positives and false negatives. In all, these evaluation measures provide a good overall analysis predicting heart disease risk of the model.

Results and discussion

In this paper, we conduct two groups of experiments to demonstrate the efficacy of our method. In the first experiment, the proposed approach is tested on two benchmark datasets for heart disease.. The parameter values are set as ($H_{\text{max}} = 3$), ($N_{\text{min}} = 40$), and ($T_{\text{max}} = 20$) as this parameter setting yields the best performance among different randomly simulated parameter settings. In the second experiment, to further verify its prediction performance, the proposed method is also contrasted with several well-known machine learning algorithms on both datasets.

All experiments are conducted on an Intel Core computer with 8 GB of RAM. The implementation is done in Python. The testing results of the proposed method on the two datasets in terms of accuracy, precision, sensitivity and F1 score are shown in Table 1.

Comparison with state of the art methods

In order to demonstrate the efficacy of our approach more clearly, we include a comparative analysis with the following widely used machine learning algorithms as our baselines: KNN, LR, LDA, SVM, CART, GB, and RF. The results of testing on the Framingham and Cleveland datasets are shown in Table 2 and Table 3, respectively.

The comparison results are illustrated in Tables 2 and 3 demonstrate that our method achieves the best predictive performance on all the baselines meet or surpasses the baseline. It obtains classification accuracies of 91% and 93% on the datasets of Framingham and Cleveland, respectively. The results also indicate that ensemble-based classifiers, in particular gradient boosting and random forest, achieve better performance in most cases than traditional classifiers, which further validates that predicting by combining multiple learners can hold more stable and more accurate prediction result.

In order to present a more in-depth analysis of the numerical performance, ROC curves are also plotted for the models examined. The ROC curve describes the balance between TPR and FPR for a range of different classification thresholds and has been used as a visual evaluation of the discriminative power of the models. It can be seen that the ROC curves for the ensemble further convincingly demonstrate the superiority of the proposed approach with respect to the other comparative methods in Figs. 2 and 3.

Table 1: Dataset description

Dataset	Accuracy (%)	Precision (%)	Sensitivity (%)	F1 Score (%)
Framingham	91.34	92.57	90.82	91.45
Cleveland	93.21	96.43	91.76	93.12

Table 2: algorithms comparison

Algorithm	Accuracy (%)	Precision (%)	Sensitivity (%)	F1 Score (%)
KNN	81.35	75.24	81.92	77.54
LR	83.72	84.13	83.67	83.91
LDA	83.47	81.56	83.45	82.48
SVM	82.21	78.19	82.64	80.27
CART	75.64	74.89	72.43	73.12
GB	83.57	87.23	87.16	84.11
RF	83.62	87.05	88.21	84.35
Proposed method	91.13	92.87	90.53	91.26

Table 3: Algorithm comparison with proposed method

Algorithm	Accuracy (%)	Precision (%)	Sensitivity (%)	F1 Score (%)
KNN	60.98	61.42	59.63	58.79
LR	78.56	69.43	71.19	70.32
LDA	83.15	84.29	81.57	82.36
SVM	68.87	65.79	66.21	65.12
CART	69.34	62.17	68.49	65.62
GB	86.47	89.35	83.11	86.52
RF	89.12	84.69	90.22	87.33
Proposed method	91.27	92.51	90.81	91.04

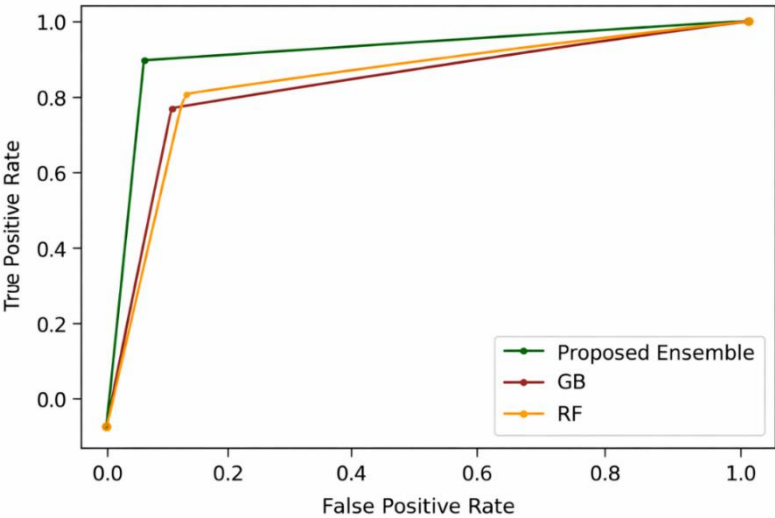


Figure 2: Proposed method ROC for Framingham dataset

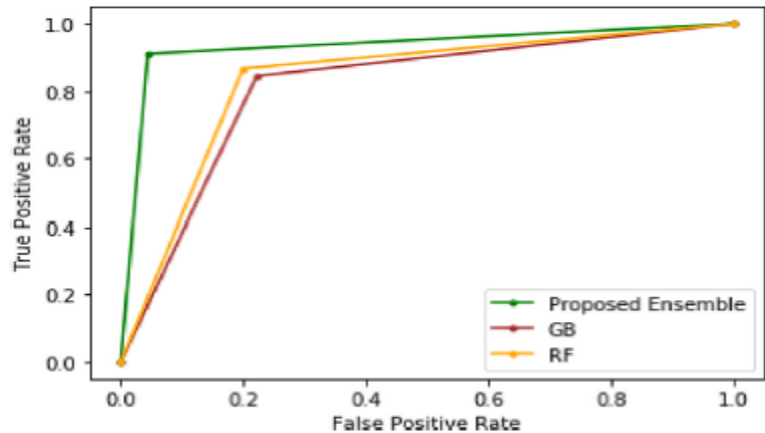


Figure 3: Proposed method ROC for Framingham dataset

Comparison with state of the art methods

In our following experiments, the results of seven conventional classifiers over the TwiMedT-HL dataset in macro-F1 measure were used as baselines. Nevertheless, the baseline algorithms comparison is not enough to well demonstrate the competitiveness of our method. Thus, we also compare with some earlier work of heart disease prediction based on the Cleveland dataset. We select this dataset since it has been extensively used in the literature and is often regarded as a benchmark dataset in studies for the classification of heart diseases [5]. The results of comparison are listed in Table 4 from which it can be observed that the proposed method yields a significant performance improvement over a few existing methods.

Table 4 also shows the comparison between the proposed method and several existing methods in the literature according to the experimental results. The chosen baseline methods include: an ensemble model of NB, BN, RF, and MLP [5]; a stacked classifier of L1-regularized linear SVM, L2-regularized linear SVM, and RBF-kernel SVM [6]; a HRFLM [24]; a smart heart disease prediction model based on NB and AES [25]; and a hybrid model based on ANN and Fuzzy Analytical Hierarchy Process [26]. The comparison results show that the proposed ensemble framework attains better or comparable performance with other popular ensemble frameworks on the well-known cleveland database.

Table 4: Proposed method comparison with SOTA

Author(s)	Method	Accuracy (%)	Precision (%)	Sensitivity (%)	F1 Score (%)
Latha and Jeeva [5]	Majority vote with NB, BN, RF, and MLP	85.46	–	–	–
Ali et al. [6]	L1 Linear SVM + L2 Linear SVM & RBF SVM	92.22	–	82.92	–
Mohan et al. [21]	HRFLM	88.40	90.10	92.80	90

Repaka et al. [22]	NB and AES	89.77	–	–	–
Samuel et al. [23]	ANN and Fuzzy_AHP	91.00	–	–	–
Proposed method	Randomized decision tree ensemble	93.00	96.00	91.00	93.00

Conclusion

In this paper, we put forward a novel and efficient machine learning methods to estimate heart disease risk, which can aid in the early prevention for long-termed development of the disease. Initially, the original dataset is split into smaller chunks via a mean-based random splitting strategy in the proposed method. A CART model is then learned on each partition, and by an Accuracy-Based Weighted Aging Classifier Ensemble the classifiers are aggregated to a homogeneous ensemble model. The experimented ensemble was able to achieve 93% and 91% correctness in classification on the test data sets, respectively.

In comparison with traditional machine learning algorithms and state-of-the-art work that have been reported in the literature, the suggested approach outperformed all of them in terms of predictive performance. ROC curve analysis also verified the enhanced power classification of the proposed ensemble. Besides, the technique can be useful to be embedded in clinical decision making systems, since it offers a reliable tool for predicting heart disease risk. In this paper, the proposed scheme is able to identify subjects at high-risk for timely medical intervention and patient's potential for improving outcomes by offering early prediction.

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