Multi-Tier Ensemble Learning Model With Neighborhood Component Analysis to Predict Health Diseases

JOY DHAR1, (Member, IEEE), AND NIGUS ASRES AYELE2

1Department of Information Technology, Hatgobindapur M.C. High School, Hatgobindapur, West Bengal 713407, India
2Department of Information Technology, College of Computing and Informatics, Wolait University, Wolait 07, Ethiopia
Corresponding author: Nigus Asres Ayele (nigus.asres@wku.edu.et)

ABSTRACT Various well-known health diseases affect millions of people worldwide. In the early stage, the clinicians may not recognize various clinical symptoms due to lack of reflection or anything else matter. So, such diseases are not easier to identify, and there may have chances to grow these illnesses and affect millions of people worldwide. Whenever an accurate early prediction is possible, the risk factor of such diseases severity can be lessened. This study presents an innovative multi-tier weighted ensemble learning model (MTWEL) for predicting several diseases such as diabetes and hepatocellular carcinoma (HCC) and, therefore, reduces such above-said problems from the sufferers and lessens the chances of mortality. In the MTWEL model, we have utilized two lists of base classifiers in which six various machine learning (ML) classifiers are assigned in each list to develop two weighted ensemble learning (EL) models and combine them to form the proposed model by employing a weighted voting approach. In the MTWEL model, the parameters of all employed classifiers are tuned through the genetic algorithm-enabled hyperparameter optimization technique to form the optimized base models. The weight of each chosen optimized base model and generated EL model(s) is calculated using Matthews correlation coefficient value with the optimized weight value. In this study, neighborhood component analysis is employed to reduce the dimension of the given input dataset. The suggested model’s experimental outcomes are conducted on two real-world datasets to exhibit its performance. The suggested approach receives the best result in AUC values: 1.0 and 1.0, F1-score values: 0.9957 and 0.9947, and accuracy values: 0.9952 and 0.9929. Such outcomes in the form of performance exhibit that the proposed model is the best-suited model to predict several diseases than other techniques, and hence it helps clinicians make accurate decisions.

INDEX TERMS Ensemble learning, genetic algorithm, neighborhood component analysis, diabetes prediction, hepatocellular carcinoma prediction.

I. INTRODUCTION

The healthcare sector is among the early adopters and benefited greatly from artificial intelligence and machine learning (ML) technology. Machine learning is becoming an essential part of several healthcare-related solutions. It helps significantly in the early prediction of many deadly diseases such as Hepatocellular carcinoma (HCC), diabetes, to name a few. Despite the success of identifying early signs of many diseases using ML, several obvious limitations must be addressed before ML can reach its full potential. These limitations include the handling of missing entries, identification, and removal of outliers, selection of informative features, handling class imbalance, optimized inefficient hyperparameters, development of robust classifier, and ensuring that the solution is general and not data-dependent (meaning the ML solution for predicting diabetes should also work to predict HCC survival as well). Hence, such limitations may generate weaker prediction outcomes in intelligently predicting various health diseases and will be addressed in the remaining sections.

Diabetes, for example, is a very familiar word globally and a crucial challenge in developed and developing countries [1]. It is one of the most widespread and lasting diseases that affect numerous difficulties if not treated and anonymous [2]. The individual organ identified as the ‘pancreas’ is liable
to produce hormones termed insulin, liable to regulate the body’s glucose levels [3]. The causes of diabetes include obesity, improper nutrition, heredity, absence of physical activity, and many more [3]. If it delays the treatment and diagnosis of diabetes or continues anonymous and not treated, it can commence to complex difficulties: blindness, heart failure, kidney malfunction, or many more relevant or irrelevant problems [2], [3]. As living standards and lifestyles are continuously developing, it is becoming overwhelmingly common [3].

While in the case of HCC, it is the fourth most regular reason for cancer-related mortality in the world [4]. It happens mainly in chronic liver ailments, such as cirrhosis induced by hepatitis C or hepatitis B [5]. It affected 14 million people worldwide in 2012 [5]. However, liver cancer kills approximately eight lakhs of people worldwide annually [5]. If the disease is detected early, it can potentially be treated with surgery or a transplant. This type of ailment most frequently occurs in men within 30 to 50 years old and is exhibited frequently in Mongolia, China, Sub-Saharan Eastern and Western Africa, and South-East Asia [5]. Like another type of cancer, HCC cells regenerate faster and evade apoptosis [5].

The immediate diagnosis and accurate analysis of such diseases are deserving of healthcare research and may lessen medication expenses and support rescue human life [3]. In the case of diabetes disease, it is essentially diagnosed by regularly examining the sufferers’ blood glucose level and glucose endurance [3]. Research on people with diabetes exhibits that 8.5% of adults over 18 years have diabetes, quickly rising in second, especially in underdeveloped countries [6]. According to the report, diabetes was the straight reason for 16 lakh mortality in 2016, and in 2012 high blood glucose was the reason for another 22 lakh deaths. In 2017, 45.1 crores of people had diabetes, and there may be chances to grow this disease to 69.3 crores by 2045. According to the report, fifty million personalities have diabetes globally, and the estimate will grow from 25% to 51%, sequentially, from 2030 to 2045 [6]. Though there is no long-term medicine available for this disease, it can be managed and restricted if an immediate forecast is perfectly feasible [6]. While in the case of HCC disease, it is recognized with computed tomography (CT) scan and magnetic resonance imaging [5]. However, this type of liver cancer is not early detected because of the lack of indications in affected sufferers [4].

In this regard, various techniques have been adopted, either manually by physicians or by anything else, but such procedures have notable shortcomings in predicting such diseases in their beginning phases to diagnose them. Therefore, the automated investigation of healthcare data, including deep learning (DL) and ML methods, are practical strategies to predict such diseases. However, a massive quantity of healthcare data is created by each healthcare system, which can be prepared to fetch necessary data [2]. In this regard, ML algorithms’ development helps to process such data and obtain the underlying information pattern that expedites the decision-making method [2].

In recent years, several ML-based methodologies have been suggested and published for predicting such diseases, and we can categorize these methodologies based on the limitations mentioned. In the case of prediction of the HCC disease, the authors either employed class rebalancing algorithms: SMOTE and cluster-based oversampling technique included in [10], [25], [26] to solve the class balancing problems, or utilizes feature selections techniques: Linear Discriminant Analysis (LDA) and Neighborhood Component Analysis (NCA) and many more included in [27], [29], [31]–[33], [35] for the selection of informative features, or employing robust single classifiers: decision tree (DT), support vector machine (SVM), and random forest (RF) included in [5] or using methods based on ensemble models and deep learning included in [4], [50], [60], [61] to enhance the performance of their generated models after employing HCC dataset [10]. While in case of predicting diabetes disease, several previous methodologies either employed single classification models: RF, logistic regression (LR), Naive Bayes (NB), K-nearest neighbors (KNN) included [9], [13], or utilized deep learning-enabled feature selection techniques: multilayer perceptron (MLP) with adaptive particle swarm optimization with grey wolf optimization (APGWO) and GWO techniques included in [43] to select the optimum features, or utilized deep learning techniques: artificial neural network (ANN) included in [44] to classify the diabetes disease and enhancement the performance of their developed models after employing early-stage diabetes risk prediction dataset [9]. However, such above-specified methodologies have some lags due to generating inefficient and inaccurate outcomes. So, it requires several improvements in enhancing the accuracy and reliability while predicting such diseases because each machine learning researcher’s foremost objective is to give a well-built and accurate auspicious method with the best performances [7]. The main reason for doing this is that research on healthcare data is the most crucial problem due to its close relation with individuals’ lives [7]. In this regard, this paper proposes a multi-tier weighted ensemble learning model (MTWEL) to solve the above-stated problems and help physicians reduce their workload, provide the proper medication, and precise early prediction of such diseases with minimal error rate terms of treatment. In developing the proposed MTWEL model, two lists of base classification models are used to produce two weighted ensemble learning (EL) approaches and combine them to form the proposed MTWEL method after employing the weighted voting (WV) technique. In two list of base classifiers, various ML classifiers: eXtreme Gradient Boosting Machine (XGB), Light Gradient Boosting Machine (LGBM) [8], Gradient Boosting (GB), Decision Tree (DT), Random Forest (RF), Extra Trees (ET), K-nearest neighbors (KNN), Support vector machine (SVM) and its related classification model (NuSVM), Multilayer Perceptron (MLP), Bernoulli Naive Bayes (BNB), and Logistic regression (LR), are assigned for producing two weighted EL models after employing a WV procedure. However, in this study, four significant contributions are conducted.
by the proposed MTWEL model, elaborated on in the following.

1. Introduce an MTWEL approach to achieve the most reliable result after combining two generated weighted EL models by implementing a WV technique. Furthermore, this study utilizes a genetic algorithm to tune all base classifiers’ parameters, generate genetically optimized base models, and enhance the suggested approach’s performance. This study employs the positive predictive value (PPV) to choose the best-optimized base model(s) to generate the weighted EL models. The grid search (GS) strategy is employed to tune the weight of all chosen optimizing base models and generated weighted EL models, respectively, and generates an optimized weight for them. Then calculating new optimal weight for each chosen optimized base model and generated weighted EL models, respectively, after combining Matthews correlation coefficient (MCC) value with the respective optimized weights values and perform the operation for the generation of weighted EL models and the suggested MTWEL method and enhance the suggested approach’s performance.

2. KNN imputation approach employs to remove the missing entries while needed. While the isolation forest (IF) approach detects and removes the outlier(s) from the provided data to provide more desirable outcomes.

3. Neighborhood component analysis is employed for lessening the dimensions and enhancing the performance of the proposed approach.

4. The proposed approach is assessed on publicly accessible datasets: early-stage diabetes risk prediction dataset [9] and HCC dataset [10]. Comparing performances between the suggested approach and the numerous machine learning techniques represents that the suggested approach achieves the best performance to predict such diseases. Comparative research with the previous benchmark methodologies exhibits that the suggested approach achieves the best performance for predicting diabetes and HCC than the available previous approaches.

Hence, the resting part of this study is composed as follows. Part 2 represents variously related recently published earlier research works and their gaps. In part 3, it describes the proposed MTWEL model with the data employed in this study. While Part 4 demonstrates the suggested approach’s experimental results on the collected data, and Part 5 discusses the performance of our proposed approach. Part 6 describes the conclusion concerning this proposed research.

II. RELEVANT WORKS AND RESEARCH GAP
ML and DL-enabled methodologies are increasing rapidly in the health industry and may adequately early predict several diseases [7]. In this concern, to correctly and early predict people with diabetes and HCC diseases, various researchers have generated infinite ML and DL-relevant approaches to support clinical decision-making.

A. TRADITIONAL MACHINE LEARNING TECHNIQUES
In concern to traditional ML approaches, while predicting diabetes disease, Ijaz et al. [11] developed a hybrid prediction approach, which comprises density-based spatial clustering of applications with noise (DBSCAN) to identify and remove outliers, SMOTE for rebalancing the data, and RF for classification of diabetes disease after utilizing three different diabetes datasets [11, 67]. Their developed model obtained the precision values of 91.497%, 78.788%, and 83.665%, recall values of 93.403%, 70.270%, and 84.667%, specificity values of 91.749%, 82.203%, and 82.553%, F1-score values of 92.440%, 74.286%, and 84.168%, and accuracy values of 92.555%, 76.419%, and 83.644% for datasets 1, 2, and 3, respectively, for predicting diabetes disease. While Islam et al. [9] employed various ML algorithms: Naive Bayes, LR, RF to predict diabetes disease after implementing an early-stage diabetes risk prediction dataset [9]. Their used model: RF, obtained an accuracy value of 97.4% for predicting diabetes disease. In contrast, Fitrtyani et al. [12] presented a disease prediction model, which comprised isolation forest enabled outlier detection and removal approach, synthetic minority oversampling technique Tomek link (SMOTEtomek) for balancing data distribution, and the EL method for predicting diabetes disease after utilizing four datasets relevant to type 2 diabetes hypertension dataset. Their developed model achieved the performance regarding precision values: 94.49%, 93.57%, 75.6%, and 100%, recall values: 98.62%, 84.89%, 81.78%, and 100%, F-measure values: 96.32%, 88.8%, 77.12%, and 100%, accuracy values: 96.74%, 85.73%, 75.78%, and 100%, and AUC values: 99%, 87%, 76%, and 100%, for datasets 1, 2, 3, 4, respectively. However, Alpan and Ilgi [13] employed various ML models to perform an early-stage diabetes risk prediction dataset to predict diabetes. Their employed model: KNN, received an accuracy value of 98.07% while predicting diabetes disease. In contrast, Maniruzzaman et al. [14] utilized four different ML classifiers for predicting people with diabetes. In this regard, they collected data obtained from the National Health and Nutrition Examination Survey (NHNES), in which such data comprises 6561 respondents with 657 people with diabetes and 5904 healthy people [14]. The authors obtained an accuracy value: 94.25% while predicting diabetes. In comparison, Pranto et al. [15] utilized various ML classifiers: DT, KNN, RF, and NB to predict diabetes with a satisfactory result. They utilized two different diabetes datasets: PID and Kurmitola datasets, in which the Kurmitola dataset was obtained from Kurmitola General Hospital at Dhaka in Bangladesh to perform such above-said ML classifiers for predicting diabetes [15]. Their collected Kurmitola dataset comprises 181 instances to predict diabetes efficiently. The authors obtained the highest-performed model: RF and KNN for Pima Indian diabetes (PID) and Kurmitola datasets, respectively [15]. In this regard, RF and KNN models obtained the highest performance in accuracy values of 77.9% and 81.2%, precision values of 81% and 80%, F1-score values: 84% and 88%, respectively, for dataset
PID and Kurmitola. While the DT model obtained the best recall values: 90% and 100%, and RF obtained the best AUC value: 83% for the PID dataset, and NB obtained the highest AUC value: 84% for the Kurmitola dataset. In contrast, Kopitar et al. [16] utilized several ML models: Glimmet, RF, XGBoost, and LightGBM, to predict undiagnosed type 2 diabetes mellitus [16]. The authors obtained a dataset from EHR in 10 healthcare centers in Slovenia in which 3,723 participant records were applicable in their development to predict type 2 diabetes mellitus [16]. Their utilized model gained the highest performance regarding the lowest average RMSE value of 83.8% to predicting diabetes [16]. In comparison, Haq et al. [17] developed a diagnosis system after employing ML approaches to detect diabetes. In this regard, the authors implemented a filter method based on the DT algorithm for essential feature selection. They collected data relating to diabetes disease from the Kaggle ML repository to detect diabetes. Their employed approach obtained the highest accuracy value of 99.9% for detecting diabetes. Nnamoko and Korkontzelos [18] developed a selective data preprocessing technique using the IQR algorithm and synthetic minority oversampling technique (SMOTE) to predict diabetes after utilizing the PID dataset. They utilized various classifiers: Adaboost, RF, Naïve Bayes, SVM with radial basis function, RIPPER, and C4.5, with the above-said technique to predict diabetes in which C4.5 classifier with the selective data preprocessing technique obtained the highest performance regarding the accuracy of 89.5%, the precision value of 90%, recall value of 89.4%, F-score value of 89.5%, and Kappa value of 83.5% for predicting diabetes. In contrast, Shuja et al. [19] generated a two-phase classification model for predicting type 2 diabetes after utilizing 734 clinical records. In the two-phase classification model, the first phase was generally used for data preprocessing after utilizing SMOTE approach. The second phase utilized five classifiers performed on the preprocessed data for selecting the best classifier for predicting diabetes. However, they collected data from a diagnostic lab under Kashmir valley under expert supervision by physicians [19]. They obtained satisfactory outcomes regarding accuracy value: 94.7013% and ROC curve: 95.3% while utilizing the DT classifier. In contrast, Kaur and Kumari [20] utilized various ML classifiers to predict diabetes after utilizing the PID dataset. They utilized classifiers: SVM-linear and KNN models obtained the satisfactory accuracy values: 89% and 88%, recall values: 87% and 90%, precision values: 88% and 87%, F1-score values: 87% and 88%, and AUC values: 90% and 92%, respectively, for the prediction of diabetes.

While Ahmad et al. [21] used five various ML classification models: LR, SVM, DT, RF, ensemble learning model, and attribute elimination using attribute permutation and hierarchical clustering approach to predict diabetes mellitus after acquiring electronic health records from five variant Saudi hospitals across three regions [21]. The authors collected 3000 sufferers from 2016 to 2018 to predict diabetes precisely. In this regard, the SVM classifier obtained the highest accuracy value: 82.10%, precision value: 82.30%, recall value: 82.10%, and F1-score value: 82.05%, respectively for the HbA1c-labeled dataset. While in the case of other classification models: RF achieved the highest performance in accuracy value: 87.65%, precision value: 87.90%, recall value: 87.65%, and F1-score value: 87.72%, respectively, for the FPG-labeled dataset. In contrast, after employing the LR model, Kwon et al. [22] developed a diabetes prediction score that predicted postoperative type 2 diabetes remissions. Their employed model obtained an AUC value of 95% to predict diabetes disease [22]. In contrast, Azad et al. [23] developed a prediction model after employing the synthetic minority oversampling technique (SMOTE), GA, and DT to classify diabetes mellitus after employing the PID dataset [23]. Their developed model obtained an accuracy of 82.1256% while predicting diabetes mellitus after employing the PID dataset. In comparison, Wang et al. [24] developed various supervised ML classifiers with SVM-SMOTE, stepwise logistic regression, and LASSO dimension reduction approaches for classifying diabetes disease after employing a diabetes survey dataset obtained from China National chronic disease survey [24]. Their developed model: RF with SVM-SMOTE obtained an accuracy of 89%, the precision value of 86.9%, recall value of 91.9%, F1-score of 89.3%, and AUC value of 94.8% while classifying diabetes.

Regarding traditional ML approaches, while predicting HCC disease, Santos et al. [10] used logistic regression and neural networks to detect HCC after utilizing the HCC dataset gathered from Coimbra Hospital and University Centre (CHUC) [10]. In this regard, the authors introduced a cluster-based oversampling technique, which relies on the K-means clustering approach and the SMOTE-based approach for developing representative data [10]. The method gained performance regarding accuracy values: 75.2% and 73% for neural networks and logistic regression. While Hattab et al. [25] utilized an instance selection linked with the SMOTE oversampling approach to detect HCC after utilizing the CHUC database. The authors generated an accuracy of 84.90% to predict HCC survival [25], [26]. In contrast, Sawhney et al. [27] produced a binary firefly algorithm with a random forest classification model to diagnose cancer; after utilizing the CHUC database, the authors gained an accuracy value of 83.5% to detect HCC. In contrast, Ksiazek et al. [28] introduced a 2level genetic optimizer with a C-type support vector machine to detect HCC after utilizing 165 HCC records given by the CHUC database [28]. Their generated methodology gained performance regarding an accuracy value: 88.49% for the detection of HCC. In comparison, Christo et al. [29] used a Clinical Decision Support System that depends on the cooperative coevolution technique that operates feature selection and instance selection as independent subproblems to detect HCC; after utilizing the CHUC database, they obtained an accuracy value of 72.2% for the detection of HCC [30]. While Ali et al. [31] developed a hybrid model using LDA for dimension reduction, SVM for classification, and a genetic algorithm to
optimize the SVM’s hyperparameters after utilizing the CHUC database [31]. They reported the performance in terms of an accuracy value: 90.30%, specificity value: 96.07%, and sensitivity value: 82.25% for detecting HCC. In contrast, Tuncer and Ertam [32] utilized neighborhood component analysis and reliefF to lessen the features after utilizing the CHUC database. They reported accuracy values of 92.12% and 83.03% for neighborhood component analysis and reliefF, respectively. While Demir et al. [33] exhibited a classification method that comprised average-based supervised missing feature completion and chaotic Darcy optimization-based feature selection approach to detect HCC after utilizing the CHUC database [33]; after performing their utilized feature selection approach, there are 31 features selected for detecting HCC. Their implemented approach obtained an excellent performance in terms of an accuracy value of 98.79% to detect HCC. On the other hand, Chiico and Oneto [5] applied various ML algorithms: DT, SVM, RF, and multilayer perceptron (MLP) for predicting HCC after utilizing the CHUC database. They obtained the accuracy values of 77.2%, 77.1%, 72.7%, 68.9%, and 65.9% for RF, linear SVM, MLP, radial SVM, and DT, respectively, to detect HCC. While Islam et al. [26] applied ML calculations to anticipate the 1-year endurance of patients and discover the feature importance [26]. They also utilized the synthetic minority oversampling technique to adjust the CHUC database to enhance the model’s performance. Their utilized model XGB received an accuracy of 87% to predict HCC survival. In contrast, Ksiazek et al. [34] developed LR with GA to predict HCC survival after employing the CHUC database [34]. Their progressive approach received an accuracy of 94.55% and an F1-score of 93.56%, respectively, to predict HCC survival. In comparison, Murugesan et al. [35] employed three bio-inspired approaches: cat swarm optimization (CSO), krill herd (KH), and bacterial foraging optimization (BFO) along with the SVM classifier to classify seven UCI repository-based clinical datasets [35]. Their developed model generated a prediction accuracy of 94.74% while predicting HCC disease after utilizing the CHUC database.

B. DEEP LEARNING TECHNIQUES

On the other hand, concerning DL techniques while predicting diabetes disease, Sierra-Sosa et al. [36] utilized the deep learning technique to efficiently analyze healthcare data to predict Type 2 Diabetic Mellitus (T2DM) after utilizing 156 patients records. The Basque Health Service, Spain, provided their utilized data for the development of their research. Their employed model achieved an accuracy value of 94.6% to predict T2DM. In comparison, Massaro et al. [37] applied the Long short-term memory with artificial records to predict diabetes after employing a PID dataset. Their applied model obtained an accuracy value of 84% and an AUC of 89% for predicting diabetes. In contrast, after utilizing the PID dataset, Pradhan et al. [38] utilized an artificial neural network (ANN) approach to detect diabetes. The authors achieved an accuracy of 85.09% for detecting diabetes [38]. While Ryu et al. [39] developed a DL model for undiagnosed diabetes mellitus after utilizing Korean NHNES datasets, collected data from 2013 to 2016 were combined, and the consistency of variables was explored [40]. The authors obtained a satisfactory performance in terms of AUC value: 80.11% to predict diabetes. In contrast, Gadekallu et al. [40] implemented principal component analysis (PCA) and firefly algorithm (FA) to reduce the dimension of the given data, and a deep neural network (DNN) approach is employed to classify diabetic retinopathy Debrecen dataset [40]. The authors gathered this dataset from the UCI ML repository. Their developed model, DNN-PCA-FA, obtained the highest accuracy value: 97%, precision value: 96%, recall value: 96%, sensitivity value: 92%, and specificity value: 95% for the classification of diabetic retinopathy Debrecen dataset. While Rahman et al. [2] developed a Convolutional Long Short-term Memory (Conv-LSTM) for classifying diabetes patients with satisfactory results [2]. The authors utilized the PID data containing 768 female patients; 268 are diabetic, and the rest are healthy controls [2]. Their progressive approach: Conv-LSTM obtained an accuracy of 97.26%, a specificity value of 97.09%, and a sensitivity value of 97.28% for predicting diabetes with excellent results. In comparison, Rehman et al. [3] formed a deep extreme learning machine model to recognize diabetes disease type II after utilizing 15 thousand data instances relating to diabetes. The authors obtained the highest accuracy rate of 92.8% while predicting diabetes. In contrast, Xie and Wang [41] implemented a classic Autoregression with Exogenous inputs (ARX) approach; DL techniques: a vanilla LSTM Network and a Temporal Convolution Network (TCN) for predicting type 1 diabetes after employing the OhioT1DM dataset [41]. Their published research work examined various ML-enabled regression models, and the two above-specified DL approaches by comparing their performance while foretelling blood glucose levels of the six sufferers from the OhioT1DM data to that of an ARX model [41]. While Naz and Ahuja [42] implemented several classifications approach: ANN, Naïve Bayes, DT, and DL after employing the PID dataset in which the deep learning technique generated the best result in terms of accuracy 98.07%. However, Le et al. [43] developed a wrapper-enabled attribute selection approach after employing the Grey Wolf Optimization (GWO) and Adaptive Particle Swarm Optimization (AP) techniques for selecting optimal features from a given dataset for predicting diabetes [43]. Furthermore, they utilized various classification models for classifying and predicting the outcomes. Their model was conducted on the early-stage diabetes risk prediction dataset collected from Sylhet diabetes hospital. In this regard, their developed models, namely, AP with GWO and multilayer perceptron (MLP) classifier, and GWO with MLP, obtained satisfactory performances in terms of accuracy values: 97% and 96%, precision values: 99% and 100%, recall values: 97% and 93%, and F1-score values: 98% and 97%, respectively, for predicting diabetes. In comparison, Chaves and Marques [44] employed an ANN model for diagnosing and
predicting diabetes disease. This ANN model was conducted on an early-stage diabetes risk prediction dataset to effectively predicting diabetes. In this regard, their developed model: ANN, received an accuracy value of 98.08%.

To concern DL techniques while predicting HCC disease, Kunz et al. [45] implemented an artificial neural network to predict HCC after utilizing 282 patient records from January 2005 to December 2017 [45]. Their implemented model gained performance regarding an AUC value: 77%, a negative predictive value: 68.0%, and a PPV: 87.5% for predicting HCC [45]. While He et al. [46] implemented a convergent artificial intelligence model after utilizing 109 patients records to predict HCC. Their implemented model obtained an accuracy value of 82%, a precision value of 89%, and a recall value of 80% to predict HCC. On the other hand, Bousabarah et al. [47] employed a deep convolutional neural network with a U-Net architecture to detect HCC after utilizing 174 patients records [47]. Their developed model: deep neural network and RF with radiomic features and thresholding (TR) of the mean neural activation, obtained an average false positive rate of 64% and 68% while validation and testing data for manual segmentations and 91% and 91% while validation and testing data for liver segmentation, respectively [47]. While Chen et al. [48] developed a DL-based approach known as successive encoder-decoder performed on 4300 CT images and LiTS dataset to recognize HCC [48]. The utilized images were collected from the Kaohsiung Chang Gung Memorial Hospital to recognize HCC [48]. Their developed model obtained a satisfactory accuracy value of 99.2% and an AUC of 95% for recognizing HCC. In comparison, Wei et al. [49] designed Variational autoencoders (VAE) based survival models to predict HCC after analyzing 167 patients’ records [49]. The authors utilized radiomics, clinical features, and raw CT images to combine and form their model [49]. Their developed model achieved more reliable performance than the Cox survival models for risk assessment of HCC prognosis [49]. In contrast, Shobha and Savarimuthu [50] developed a cluster-based imputation approach (CLUSTIMP) after utilizing an unsupervised neural network adaptive resonance theory 2 to improve the quality of healthcare data and detect HCC after utilizing the CHUC database [50]. Their developed model obtained the lowest root mean squared error among 2% and 11% for each utilized classifier: DT, RF, Adaboost (AB), and GB, respectively.

C. ENSEMBLE LEARNING TECHNIQUES

While concerning EL techniques in the case of predicting diabetes disease, Hasan et al. [6] formed a weighted ensemble learning method to predict diabetes after utilizing the PID dataset. Their developed weighted ensemble learning model achieved the specificity value of 93.4%, sensitivity value of 78.9%, false omission rate of 9.2%, a diagnostic odds ratio of 66.234%, and an AUC value of 95% for prediction of diabetes [6]. In contrast, Nguyen et al. [1] applied a wide and DL method that merges the power of a generalized linear model with numerous attributes and a deep feed-forward neural network for predicting type 2 diabetes mellitus after utilizing 1904 patients’ health records out of 9948 patients’ records [51]. Their progressive ensemble approach obtained the performance in the form of an accuracy value of 84.28%, AUC value: 84.13%, sensitivity value: 31.17%, and specificity value: 96.85% for predicting diabetes. While Kumari et al. [52] formed an EL approach using the soft voting technique to predict diabetes after utilizing the PID dataset. Their ensemble learning approach satisfactorily performance regarding the accuracy of 79.04%, precision of 73.13%, recall of 70%, F1-score of 71.56%, AUC of 80.98% to predict diabetes. In contrast, El-Sappag et al. [53] developed an ensemble classification model to predict diabetes mellitus after utilizing 60 patient records collected from Mansoura University hospitals from 2010 to 2013. Their generated approach obtained an accuracy value of 90%, a recall value of 90.2%, and a precision value of 94.9% for predicting diabetes.

However, Syed and Khan [54] developed utilized the Chi-Squared analysis and binary LR for analyzing and screening the most crucial diabetes uncertainty circumstance for T2DM risk prediction after utilizing the PID and NHNES datasets [54]. Furthermore, they also implemented a two-class decision forest model based on ensemble learning [54]. Their implemented model: decision forest obtained a satisfactory accuracy value of 82.1%, the precision value of 77.6%, recall value of 89%, F1-score value of 82.9%, and AUC value of 86.7%, respectively, for predicting T2DM. In this context, Singh et al. [55] developed an ensemble-based framework, namely, eDiaPredict, after employing various ML classifiers: XGB, RF, SVM, neural network, and DT for predicting diabetes status among sufferers after employing PID dataset [55]. Their developed model obtained an accuracy of 95% while predicting diabetes disease. While Fazakis et al. [56] developed an EL model: WeightedVotingLRRF’s after employing Naïve Bayes (NB), DT, RF, ANN, deep neural network for type 2 diabetes risk prediction [56]. Their developed stacking-based, voting-based and weighted voting-based EL models: StackingLRRF’s, VotingLRRF’s, and WeightedVotingLRRF’s generated AUC values: 83.3%, 88.1%, and 88.4%, sensitivity values: 77.3%, 79.4%, and 85.6%, and specificity values: 79.2%, 84%, and 79.8%, respectively for predicting diabetes [56]. Kaushik et al. [57] implemented a stacked deep learning technique: stacked generalization of the convolutional neural network to predict diabetic retinopathy data [57]. Their developed model obtained a precision value of 100%, recall value of 96%, and F1-score of 97.9% while predicting diabetic retinopathy. However, Muneeb and Henschel [58] developed a hybrid approach which included statistical techniques and ML approaches in which stacked ensembles of the LSTM model beat other models with an accuracy of 96% and AUC value of 98% after employing 107 samples of people belong to diabetes patients and remaining 74 samples of people belong to healthy controls [58]. In contrast,
Lu et al. [59] developed an EL model after employing LR, KNN, SVM, NB, DT, RF, XGB, ANN to predict diabetes with the AUC value range from 79% to 91% [59]. Their developed model employed 1028 T2DM sufferers and 1208 non-T2DM sufferers records [59].

Regarding EL techniques while predicting HCC disease, Wang et al. [60] developed an ensemble feature selection that depends on a sort aggregation approach to detect HCC after utilizing the CHUC database [60]. After utilizing various feature selection techniques, they first developed their approach to obtaining candidate sets of multiple optimal feature subsets [60]. The learning outcomes of multiple optimum attribute subset candidate sets are aggregated for achieving the optimum attribute subsets [30], [60]. Then, three classifiers: KNN, RF, and XGB, with excellent performance, are employed to verify the suggested approach. While Ksiaez et al. [4] developed a stacking ensemble learning technique with genetic optimization methodology to select each classification model’s features to achieve excellent performance for detecting HCC after utilizing the HCC dataset, in this case, they gained an accuracy: 90.30% and an F1-score: 88.57%, respectively, to detect HCC [4]. On the other hand, Sharma and Kumar [61] presented an ensemble learning model to predict HCC survival. They employed fifteen various models that were presented for evaluating the prediction. Their developed model: random forest with Gradient Boosting Ensemble Learning (RFGBEL) model received the performance regarding an accuracy value of 93.2%, sensitivity value: 94.73%, log-loss score: 5.89%, Jaccard score: 72%, AUC value: 93.2% while predicting HCC disease after employing CHUC database [61]. While Rehman et al. [62] implemented an EL model using stacking learning that works on the iris and physiological features, of which 453 samples belong to chronic liver disease, and the remaining 426 samples belong to healthy control [62]. Their developed model generated an accuracy of 98% while predicting chronic liver disease.

After examining the prior investigations, it has been revealed that various past studies included either for generating various dimension reduction approaches: attribute permutation and hierarchical clustering approach, binary firefly algorithm, cooperative coevolution technique, LDA, NCA, ReliefF, Chaotic Darcy optimization, CSO, KH, BFO included in [21], [27], [29], [31]–[33], [35], or employing various single ML classifiers: DT, SVM, RF, MLP, NB, LR, KNN, XGB, LGBM, SVM-linear included in [5], [9], [13], [14], [15]–[17], [20], [22], or developing several combined approaches consisting of various outlier detection and removal approaches along with the imbalance learning algorithms: cluster-based oversampling technique, DBSCAN with SMOTE, Isolation forest with SMOTE, Tomek, IQR algorithm with SMOTE, Instance selection with SMOTE included in [10]–[12], [18], [25], or utilizing only single imbalance learning algorithms: SMOTE, SVM-SMOTE included in [19], [23], [24], [26], or implementing hyperparameter optimization strategies: 2-level genetic optimizer with c-type SVM, LR with GA optimization strategy included in [28], [34], or implementing several DL-enabled techniques: Conv-LSTM, deep extreme learning model, LSTM, ANN, deep neural network, MLP, convergent artificial intelligence model, deep convolutional neural network, successive encoder-decoder approach, VAE, CLUSTIMP included in [2], [3], [36]–[41], [42]–[47], [48]–[50], or utilizing ensemble learning approaches: weighted EL model, two-class decision forest model, eDiaPredict, WeightedVotingLRRF’s model, stacked generalization of CNN model, stacked ensembles of LSTM model, ensemble feature selection model, stacking based EL model, RFGBEL model included in [1], [4], [6], [52]–[62], to exhibit and enhance their developed model’s performance after employing various diabetes and HCC disease relevant datasets. However, in respect of employing early-stage diabetes risk prediction dataset and HCC dataset (CHUC database), several past researchers performed various ML or DL techniques either employing single powerful ML classifiers: NB, LR, RF, KNN, DT, SVM, MLP included in [9], [13] (for early-stage diabetes risk prediction dataset), [5], (for HCC dataset), or employing various DL techniques: MLP with AP and GWO, ANN, CLUSTIMP included in [43], [44] (for early-stage diabetes risk prediction dataset), [50] (for HCC dataset), or implementing various dimension reduction techniques: binary firefly algorithm, cooperative coevolution technique, LDA, NCA, ReliefF, Chaotic Darcy optimization, CSO, KH, BFO, included in [27], [29], [31]–[33], [35] (for HCC dataset), or utilizing various hyperparameter optimization strategies: 2-level genetic optimizer with c-type SVM, genetically optimized LR model included in [28], [34] (for HCC dataset), or implementing several imbalanced learning approaches: cluster-based oversampling technique, SMOTE included in [10], [25], [26] (for HCC dataset), or utilizing several EL techniques: Stacking based EL, ensemble feature selection, RFGBEL models included in [4], [60], [61] (for HCC dataset), on these datasets, respectively. Thus, in this case, most of the above-specified researchers did not focus on developing an innovative EL model to predict diabetes and HCC diseases and achieve the best accuracy. Although, few researchers include [4], [60], [61], were involved in developing the EL model after employing the HCC dataset but they did not involve in developing an innovative EL approach like our suggested method. In addition, those researchers who developed EL approaches after employing various diabetes disease-relevant datasets do not involve in predicting diabetes after employing early-stage diabetes risk prediction dataset [9]. Hence, there is no single past research available that implemented a multi-tier EL approach like our proposed model to predict diabetes and HCC diseases, as per our understanding. Therefore, this proposed research fulfills these research gaps and develops an innovative EL model: a novel multi-tier weighted EL model that relies on a WV strategy to enhance the performance for predicting diabetes and HCC diseases more reliable and efficient way and achieve
the most beneficial outcomes and beats prior benchmark procedures.

III. MATERIALS AND METHODS
This segment is employed in our study, which is tested. Furthermore, we also tested diabetes and HCC datasets applied to deliver in this suggested approach.

A. DATASETS USED
In this study, our suggested MTWEL model is performed on two real-world publicly accessible datasets available in the UCI repository: early-stage diabetes risk prediction dataset [9] and HCC dataset [10] described below to validate the performance of our suggested approach.

1) DIABETES DATASET
In the early-stage diabetes risk prediction dataset [9], 520 sufferers’ records were gathered from the sufferers of Sylhet Diabetes Hospital in Sylhet, Bangladesh using direct surveys [9]. This dataset contains 16 features, 15 dependent on categorical values, and the remaining variable belongs to continuous data, as represented in Appendix 1 of the supplemental files. Moreover, this dataset consists of a binary classification problem in which 320 patients’ records belong to the Positive class and the remaining 200 patients’ records belong to the Negative class.

2) HCC DATASET
In the HCC dataset [10], 165 patient records diagnosed with HCC were collected from the CHUC in Portugal. This dataset contains 49 features selected that are being utilized by physicians to make the precious diagnosis. Such features are further partitioned into two groups: a quantitative group with 23 features and a qualitative group with 26 features. HCC dataset is exhibited in Appendix 1 of the supplemental files. This dataset comprises 10.22% of missing data of the whole dataset [7]. This dataset comprises 0 for the dead class, and 1 for the alive class, in which 63 sufferers belong to the dead class and 102 sufferers belong to the alive class.

B. METHODOLOGY
This segment has several steps of the suggested model presented in Figure 1. These steps comprise the data preprocessing steps: the missing data imputation approach (while needed), outlier detection and removal technique, data normalization process, dimension reduction step, multi-tier weighted ensemble learning (MTWEL) approach, and model assessment step. The fundamental parts of individual steps are detailed below.

1) DATA PREPROCESSING TECHNIQUES
In the data preprocessing step, various subsequent steps are performed in this study to improve the intended MTWEL model’s performance. These steps are represented as follows.

a: MISSING DATA IMPUTATION USING KNN IMPUTATION TECHNIQUE
In this paper, the KNN imputation technique is employed on the HCC dataset, in which forty-four features comprise missing data presented in Appendix 1 of the supplemental files. Regarding this matter, filling the missing value in the HCC dataset, we implemented the KNN missing data imputation technique [4], [7]. This approach can preserve the actual data distribution after determining the fittest K value [4], [7], [10]. The nearest neighbor’s approach executes it worthwhile to decide the missing data that depends on numerous familiar examples [4], [7]. This approach is a comparatively more stable, correct evaluation than the conventional strategy to fulfill the missing data [7]. Hence, delivering more stable quality values conducts the construction of a significant classifier [7].

b: OUTLIERS DETECTION AND REMOVAL
In the research world of machine learning, the outlier(s) are the occurrence point(s) considerably apart from the number of occurrences. In this regard, outliers detection is determined to recognize and eliminate outliers from the given data. The significant benefit of reducing outliers is to improve accuracy. An outlier can degrade any ML methods’ performance; hence, this study applies isolation forest (IF), an unsupervised outlier detection approach, which serves rather than profiling anticipated points on isolating outliers. The IF distinguishes outliers after forming isolation tress and maintaining outliers as short average length inside isolation tress. The IF can be viable and beneficial to discover the outliers [67]. It employs the point that outliers are more exposed to isolation; hence, it is possible to distinguish outliers as observations with short predicted track lengths throughout the forest [67]. The hyperparameters applied in isolation forests are further displayed in Table 1 for discarding outlier(s) from the provided occurrences.

| Parameters List | Values |
|-----------------|--------|
| contamination   | 0.2    |
| n_estimators    | 1000   |

c: DATA NORMALIZATION
Following the performing of the afore-specified sub-steps, we are implementing normalizing the data. During this step, the data is rearranged to employ for further investigation [7]. The fundamental aspiration of normalizing the data is to group the data and discard irrelevant and unnecessary data that may appear within the data [7]. The conventional normalization procedures occur min-max, z-score, and several techniques [7]. In this regard, we have employed the min-max scalar strategy, which is the most robust strategy for the diabetes risk prediction dataset and HCC dataset. Therefore, this study utilizes the min-max scalar normalization technique, and the data is reorganized to either value: 0 or 1 [7].
Neighborhood Component Analysis for Dimension Reduction

The unnecessary appearance of attributes is one of the most significant reasons to overfit issues in an ML classifier. Hence, the attribute selection should be performed while commencing for training the classifiers. Hence, the attribute selection procedure may enhance various classifiers’ performance, commanding fast creating a more cost-efficient approach. Therefore, this study employs the neighborhood component analysis (NCA) to lessen the preprocessed dataset features. In this study, the discriminative attributes are chosen using the NCA from the diabetes early risk prediction dataset or the HCC dataset provided input features. NCA is a non-parametric supervised embedded dimensionality reduction approach to classify the multivariate data into distinct classes. It sorts the attributes with regularization for determining the attribute weights to lessen a cost function that estimates the mean leave-one-out (LOO) classification loss on the labeled train data [63]. It increases the LOO severance result with the optimized regularization parameter(s) using attribute weights over the training dataset [64]. Assume the train data be $X = \{x_1, x_2, \ldots, x_n\} \in \mathbb{R}^d$ and their respective class labels $C = \{c_1, c_2, \ldots, c_n\} \in \{0, 1\}$ to find a QDM that maximizes classification performance [64]. The distance function

**FIGURE 1.** Framework of the suggested Multi-Tier Ensemble Learning Model (MTWEL) to predict diabetes disease and HCC survival.
between two samples \((x_i, x_j)\) is estimated by the equation as follows.

\[
D_w(x_i, x_j) = \sum_{l=1}^{D} w_l^2 |x_{il} - x_{jl}|
\]

(1)

where \(w_l\) denotes as a weight associate with the \(l\)th attribute [63].

The LOO procedure is analyzed to enhance the correctness of the train data [63]. The possibility distribution is an efficient premise to choose any reference point from the train data [63]. The possibility distribution is an efficient premise to choose any reference point from the train data [63]. Thus, a point \(x_i\) may choose another point \(x_j\) as its reference point, defined as follows [63].

\[
p_{ij} = \frac{\eta(D_w(x_i, x_j))}{\sum_{k \neq i} \eta(D_w(x_i, x_k))}
\]

while \((i \neq j)\)

\[
or p_{ij} = 0
\]

while \((i = j)\)

(2)

where \(\eta(x) = e^{\beta x}\) denotes a kernel function and \(\beta\) denotes the kernel function width, which acts as an input parameter [63]. In this way, it influences the possibility to be selected as the reference point.

The likelihood \(p_i\) of correctly classifying data point \(i\) is the likelihood of classifying the point of each of its neighbors with the same class \(C_i = \{j | c_i = c_j\}\) is given by:

\[
p_i = \sum_{j \in C_i} p_{ij} = \sum_{j} c_{ij}p_{ij}
\]

(3)

where \(c_{ij} = 1\) only for \(c_i = c_j\) and 0 otherwise.

Thus, the objective function \(\psi(w)\) using leave-one-out classification is estimated as follows.

\[
\psi(w) = \sum_i p_i = \sum_i \sum_j c_{ij}p_{ij}
\]

\[
- \varphi \sum_{l=1}^{d} w_l^2 = \psi(w) - \varphi R
\]

(4)

where \(\psi(w) = \sum_i \sum_j c_{ij}p_{ij}\) is approximate leave-one-out classification accuracy \(\varphi > 0\) is a regularization parameter that can be optimized through cross-validation and \(R = \sum_{l=1}^{d} w_l^2\) signifies the regularization term enhancing dimension reduction and avoiding overfitting. However, if \(\beta = 0\), then \(\psi(w)\) becomes an accurate classification accuracy.

The gradient enabled rule is applied after utilizing the derivative to the \(\psi(w)\) that is estimated as follows.

\[
\frac{\partial \psi(w)}{\partial w_l} = 2\left(\frac{1}{\beta} \sum_i (p_i \sum_{j \neq i} p_{ij} |x_{il} - x_{jl}| - \sum_j c_{ij}p_{ij} |x_{il} - x_{jl}| - \varphi)w_l\right)
\]

(5)

Hence, the acquired weight vector is employed to choose the attributes [63]. Each attribute is sorted based on its respective weight, and the highest-ranked attributes are chosen for classification [63].

2) SUGGESTED MULTI-TIER WEIGHTED ENSEMBLE LEARNING MODEL

This part introduces a novel multi-tier weighted ensemble learning (MTWEL) model that depends on the weighted voting procedure. This proposed MTWEL model is developed to predict diabetes and HCC diseases by utilizing several approaches. In this regard, in the first tier of developing the suggested model, twelve classification models are applied to participate and form two weighted ensemble learning (EL) models through the WV technique. The parameters of all classification models are tuned using a genetic algorithm (GA) to generate genetically optimized base models. Furthermore, the weight of each chosen optimized base model is generated using two procedures: (1) producing optimized weights using grid search (GS) strategy for the individually chosen optimized base model; (2) Calculating new optimum weights after combining Matthews correlation coefficient (MCC) value with such generated optimized weights. Then, operating for generating weighted EL models for further process.

In the second tier of the suggested MTWEL model, such weighted EL models developed by the first tier are performed to combine and create the suggested MTWEL model rely on the WV strategy. Moreover, the GS strategy is employed to tune each developed weighted EL model’s weight. Next, such tuned weights are further calculated with the MCC value of each weighted EL model to produce the most optimum weight for each developed weighted EL model. The flowchart that represented the various procedures (discussed below) of the suggested MTWEL method is represented in Figure 2.

a: A HYPERPARAMETER OPTIMIZATION ALGORITHM

A genetic algorithm (GA) is a meta-heuristic hyperparameter optimization algorithm in which it chooses the most fitted chromosomes or individuals from the population [65]. In this study, GA is used to tune the hyperparameters of each base classification model to improve the suggested model’s performance. The representation used for the base classification models in the GA uses a vector of integers, as all the hyperparameters are chosen to configure where integer-valued. Each integer corresponds to the value of a hyperparameter of the base classification model that is being optimized.

GA is exhibited in Algorithm 1. In the first step of the GA, create the initial population of each model. The values of the hyperparameters for each classifier are randomly selected from the defined search spaces.

In the second step, evaluate the fitness function of each classifier. During the experiments, the AUC performance assessment metric is utilized as the fitness function of each used base classifier. The fittest classifiers are considered those with the highest accuracy. Next, to choose the two highest fitted individuals from the population. Next, choosing a random crossover point and the tails of both the individuals are swapped to generate new offsprings, and the subsequent mutation operator is getting permission to change in offsprings’ genes, making them different parents. Next, the fitness function of such produced offspring is validated. In this regard, if such offspring(s) are considered fitter, then it will replace lesser fit individuals from the population. Such
FIGURE 2. Flowchart of the proposed MTWEL model.

three operators are performed till the number of defined generations has reached its limit. Finally, the highest fitted individuals of the population are identified and exhibits as the output of the algorithm.

b: OPTIMIZED BASE MODEL GENERATION AND SELECTION
In recent years, several ML classifiers predict health diseases efficiently, and such models perform well and provide excellent results. We have utilized twelve different ML classifiers:
LR, SVM, NuSVM, KNN, RF, ET, XGB, LGBM, DT, MLP, and BNB, to build a novel proposed MTWEL model in this paper. In this regard, in this study, there are two lists of base classifiers (LoBC) assigned to develop two weighted EL models using the WV strategy. While in the first list of LoBC, LR, SVM, NUSVM, KNN, MLP, and BNB classification models are assigned as the first LoBC to develop a weighted EL model using the WV strategy. On the other hand, in the second list of LoBC, DT, RF, XGB, LGBM, ET, and GB classification models are assigned as a second LoBC and developed another weighted EL model using the WV strategy.

The optimal hyperparameters provide the most notable impact on the performance of any ML classifiers. Therefore, generating optimized base models is one of the most fundamental procedures and helps develop the suggested MTWEL model. In this case, this study employs a GA exhibited in Algorithm 1 to tune each classifier’s hyperparameters. Appendix 2 of the supplemental files describes the hyperparameters employed to implement the GA as the hyperparameter tuning approach [7]. Furthermore, Appendix 3 of the supplemental files illustrates the parameters list employed by each above-specified classifier for tuning using a genetic algorithm. Such tuned hyperparameters are employed to generate the optimized base models, which provide excellent accuracy. Algorithm 2 represents the procedure to generate the optimized base models after employing the GA for hyperparameter optimization for the above-specified ML classifiers. This algorithm implements such above-specified classification models with tuned parameters for each chosen LoBC, shown in equation (6). In the next step, such tuned base models assist in enhancing the performance of two weighted EL models.

\[
B_L(\theta_L) = \{B_1(\theta_1), B_2(\theta_2), \ldots, B_l(\theta_l)\},
\]

where \(B_L = \{B_1, B_2, \ldots, B_l\}\) is the list of base classification models such that \(L \in [1, L]\), \(\theta \in GA\) generates optimized parameters, and the lists \(\theta_L = \{\theta_1, \theta_2, \ldots, \theta_l\}\) is the optimized parameters for each base classification model.

Choosing the best-optimized classification model is necessary because it generates the functional and desirable performance for developing the proposed approach. If we select the best-optimized model(s) from the generated optimized base models list for each LoBC, then the proposed approach’s performance will enhance otherwise degrades. Hence, in this proposed research, those optimized base models are chosen that are appropriate to develop an EL model. In this context, to choose the most desirable optimized base models, we have implemented Algorithm 2. This algorithm selects the most desirable optimized base models from the generated optimized base models list for each LoBC after utilizing a positive predictive value (PPV). The optimized base models for each LoBC are further employed to develop a weighted EL model using the WV strategy with their optimum weight. In this study, Algorithm 2 demonstrates the strategy for selecting the most desirable optimized base model(s) from the list of generated optimized base models for each LoBC. In this regard, Algorithm 2 generates the probability value \(\text{Prob}_B_L(\theta_L)\) for each employed optimized base model \(B_L(\theta_L)\) of each LoBC. The generated probability value \(\text{Prob}_B_L(\theta_L)\) is exhibited in equation (7).

\[
\text{Prob}_B_L(\theta_L) = \{\text{Prob}_{B_1(\theta_1)}, \text{Prob}_{B_2(\theta_2)}, \ldots, \text{Prob}_{B_l(\theta_l)}\}
\]

In this regard, such optimized base models generate the positive predictive value for each LoBC, which is exhibited in equation (8).

\[
\text{PPV}_{B_L(\theta_L)} = \{\text{PPV}_{B_1(\theta_1)}, \text{PPV}_{B_2(\theta_2)}, \ldots, \text{PPV}_{B_l(\theta_l)}\}
\]

Next, estimate the mean value of PPV of such optimized base models \(B_L(\theta_L)\) for each LoBC exhibited in equation (9).

\[
\mu_{\text{PPV}} = \frac{1}{L} \sum_{L=1}^{L} \text{PPV}_L,
\]

where \(\text{PPV}_L\) is the PPV value for each optimized base model of each LoBC.

To select the most desirable optimized base model(s) for each LoBC, the mean PPV value of all optimized base models for each LoBC is equal to or less than each used optimized base model’s \(\text{PPV}_L\) value for each LoBC exhibited in equation (10).

\[
\mu_{\text{PPV}} \leq \text{PPV}_L.
\]

Then, such selected optimum optimized base models for each LoBC are presented in equation (11).

\[
B_S(\theta_S) = (B_1(\theta_1), B_2(\theta_2), \ldots, B_s(\theta_s))
\]

where \(S \in [1, s] \in \text{the list of selected optimized base models for each LoBC from 1 to s.}\)

c: WEIGHT OPTIMIZATION AND NEW OPTIMUM WEIGHT GENERATION

In a weighted voting strategy, each classification model’s suitable and desirable weight improves the performance. So, it is necessary to intelligently generate the optimum weight through which any classifier would get the proper and most desirable weight to develop an EL model. In this context, this study applies a grid search strategy (GS) to generate the optimized weight for all chosen optimized base models of each LoBC. In respect to this matter, Algorithm 3 specifies the procedure to generate an optimized weight for all chosen optimized base models of each LoBC. In the procedure of Algorithm 3, each chosen optimized base model’s weight is assigned using equation (12).

\[
\omega = \{S^s\},
\]

where \(S \in [1, s] \in \text{the number of chosen optimized base models for each LoBC, } S^s \in \text{the number of combinations, and } \omega \in \text{weight of individually chosen optimized base models for each LoBC.}\)

Next, applying the GS technique to tune such assigned weights and generate the effective, optimized weight for each
chosen optimized base model of each LoBC is shown in equation (13).

\[ \omega_S(\varphi_S) = \{\omega_1(\varphi_1), \omega_2(\varphi_2), \ldots, \omega_s(\varphi_s)\}. \]  

Equation (13) \( \omega_S(\varphi_S) \) denotes the optimized weights for all chosen optimized base models of each LoBC, where \( \varphi_S = \{\varphi_1, \varphi_2, \ldots, \varphi_s\} \in \) applying GS technique for weight optimization from model 1 to s of each LoBC.

Next, in this proposed research, we must find and estimate a new desirable and effective optimum weight after implementing Algorithm 3. In calculating the new optimum weight, this proposed research implements an MCC value that is the probability of patients with diabetes or HCC disease. In this proposed work, the MCC value of the individually selected optimized base model for each LoBC is achieved from the confusion matrix. The MCC value is the impactful approach to combine with the optimized weight for each chosen optimized base model of each LoBC and generate the new desirable and efficient optimum weight for each chosen optimized base model of each LoBC, represented in equation (14).

\[ \text{MCC}_S = \frac{(a \times d) - (b \times c)}{\sqrt{(a + b)(a + c)(b + d)(c + d)}}, \]  

where \( a = \) true positive, \( b = \) false positive, \( c = \) false negative, \( d = \) true negative, respectively, collected from the generated confusion matrix provided by each chosen optimized base model for each LoBC.

After calculating the MCC value for each chosen optimized base model of each LoBC, such generated MCC values are further employed to produce a new desirable optimum weight for each chosen optimized base model of each LoBC using equation (15).

\[ \omegaW_S = \text{MCC}_S \times \omega_S(\varphi_S), \]  

such that \( \omegaW_S \in \) new generated optimum weight for individually selected optimized base models \( S \) of each LoBC. Now generating new optimum weight for individually selected optimized base models of each LoBC is further employed and forming a new weighted EL model.

d: DEVELOPING THE WEIGHTED EL MODEL

This segment elaborates on developing an innovative weighted EL model employing a weighted voting procedure. The procedure for developing the weighted EL model(s) is demonstrated in Algorithm 4. This algorithm combines the chosen optimized base models for each LoBC and the generated new optimum weights for each chosen optimized base model to develop each weighted EL model. However, the combination process of all chosen optimized base models for each LoBC is done by the WV strategy, represented using equation (16).

\[ E(X_m) = \sum_{S=1}^{s} B_S(\theta_S)\omegaW_S(X_m) \]  

Here, \( E(X_m) \in \) new developed weighted EL model and \( B_S(\theta_S) \in \) all chosen optimized base models for each LoBC. Equation (16) describes the procedure to form a weighted EL model for developing the suggested MTWEL model.

e: DEVELOPING A MULTI-TIER WEIGHTED EL MODEL

This part elaborates on developing a multi-tier weighted EL model (MTWEL) using the WV technique. This study’s suggested MTWEL model combines two developed weighted EL models with the WV technique exhibited in Algorithm 5. The first tier of the suggested MTWEL model in Algorithm 5 creates two lists of base classification models that act as an input in this algorithm and develop two weighted EL models at each iteration. In this regard, one LoBC is fetched from the two LoBC at each iteration to form a weighted EL model. This process proceeds till the LoBC is available. Algorithm 5 elaborates that \( n \) number of weighted EL model(s) can be explicitly generated to develop the proposed MTWEL model. In this proposed research, the value of \( n \) is specified by 2. While in the second tier of the suggested MTWEL approach, each developed weighted EL model’s weight is first assigned employing equation (17).

\[ W_n = \{2^n\}. \]  

where \( W_n \) denotes the assigned weights for each weighted EL model, and \( n \) specifies the number of developed weighted EL models.

Next, such assigned weights \( W_n \) are tuned by the grid search strategy represented in equation (18).

\[ W_n(\varphi_n) = \{W_1(\varphi_1), \ldots, W_n(\varphi_n)\}. \]  

The above equation \( W_n(\varphi_n) \) denotes the optimized weights for all weighted EL models, where \( \varphi_n = \{\varphi_1, \ldots, \varphi_n\} \in \) applying GS technique for weight optimization for weighted EL model from 1 to \( n \).

Then such optimized weights are further calculated with the MCC value generated by each weighted EL model represented in equation (19) to produce the optimum weights for all developed weighted EL models.

\[ O_n = \text{MCC}_n \times W_n(\varphi_n), \]  

where \( O_n \in \) the new generated optimum weight for each weighted EL model.

Finally, a WV-based strategy is employed in both developed weighted EL models to combine them and generate a novel suggested multi-tier weighted EL model to predict diabetes and HCC diseases using equation (20).

\[ \text{MTWEL}(X_m) = \sum_{o=1}^{n} O_{o,q} E_{o,q}(X_m). \]  

where \( E_{o,q}(X_m) \) denotes developed weighted EL model at each iteration up to \( n \).
Algorithm 1 GA

**Input**: train data: \((X_m, Y_m)\) with \(m\) samples;
Number of generations;

**Procedure**
1. Randomly generating initial population: \(P\);
2. Encode \(P\);
3. Estimating fitness(chromosomes) = maximum(AUC/100);
4. Performing selection, crossover, and mutation operations;
5. Generating \(P_{\text{new}}\) as new population;
6. Repeat step 3 for each chromosome in \(P_{\text{new}}\);
7. if AUC(\(P_{\text{new}}(\text{chromosome})\)) > AUC(\(P(\text{chromosome})\)):
8. \(P(\text{chromosome}) \leftarrow P_{\text{new}}(\text{chromosome})\)
9. else: return to step 4;
10. if Number of generations is available:
11. return
12. else: rejected;
13. output: generating optimum parameters;

Algorithm 2 Optimized Base Model Generation and Selection

**Procedure**
1. Optimized base model generation:
2. for each iteration \(L\) from 1 to \(l\):
3. \(\theta_L \rightarrow \text{GA}(); /\ast\) To call GA */
4. Generation of base models with optimum parameters:
\(B_L(\theta_L) = \{B_1(\theta_L), B_2(\theta_L), \ldots, B_l(\theta_L)\}\);
5. end;
6. Generated optimized base model selection:
7. Generating probability values for each optimized base model:
\(\text{Prob}_{B_L}(\theta_L) = \{\text{Prob}_{B_1}(\theta_L), \text{Prob}_{B_2}(\theta_L), \ldots, \text{Prob}_{B_l}(\theta_L)\}\);
8. Estimating PPV value for each optimized base model:
\(\text{PPV}_{B_L}(\theta_L) = \{\text{PPV}_{B_1}(\theta_L), \text{PPV}_{B_2}(\theta_L), \ldots, \text{PPV}_{B_l}(\theta_L)\}\);
9. the estimating mean of all optimized base model’s PPV value:
\(\mu_{\text{PPV}} = \frac{1}{L} \sum_{L=1}^{L} \text{PPV}_L\);
10. for each optimized base model \(L\) from 1 to \(l\):
11. if \(\mu_{\text{PPV}_L} \leq \text{PPV}_L\):
12. Choosing such an optimized base model:
13. \(B_S(\theta_S) = \{B_1(\theta_1), B_2(\theta_2), \ldots, B_s(\theta_s)\}\);
14. else: rejected;
15. end;
16. return \(B_S(\theta_S)\);

Algorithm 3 Optimum Weight Generation

**Procedure**
1. Call Algorithm 2 for optimized base model generation and selection;
2. Optimized weight generation using GS technique for the individually chosen optimized model(s):
3. for each \(S\) from 1 to \(s\):
4. (a) Assign weights:
5. \(\omega = \{S\}\);
6. (b) Applying the GS technique and produce the most desirable optimized weights:
7. \(\omega_S(\phi_S) = \{\omega_1(\phi_1), \omega_2(\phi_2), \ldots, \omega_s(\phi_s)\}\);
8. end;
9. Optimum weight generation for the individually chosen optimized model(s):
10. for each \(S\) from 1 to \(s\):
11. (a) Calculating the MCC values for all selected optimized base models:
12. \(\text{MCC}_S = \frac{(a \times d) \mp (b \times c)}{\sqrt{(a + b)(a + c)(b + d)(c + d)}}\);
13. (b) Calculating a new optimum weight for each chosen Optimized base model:
14. \(\text{OW}_S = \text{MCC}_S \times \omega_S(\phi_S)\);
15. end;
16. return \(\text{OW}_S\);

Algorithm 4 Weighted_EL

**Procedure**
1. Call Algorithm 2 for optimized base model generation and selection;
2. Call Algorithm 3 for optimum weight generation;
3. Employing a voting technique to develop a weighted EL model:
4. for each \(S\) from 1 to \(s\):
5. \(E(X_m) = \sum_{S=1}^{S} B_S(\theta_S) \text{OW}_S(X_m)\);
6. end for;
7. Output a new weighted EL model: \(E(X_m)\);

\[\begin{align*}
\text{(2) F1-score} & : \text{F1-score} = 2 \times \frac{\text{PR} \times \text{REC}}{\text{PR} + \text{REC}} \\
\text{(3) Precision (PR)} & : \text{Precision (PR)} = \frac{\text{TP}}{\text{TP} + \text{FP}} \\
\text{(4) Recall (REC)} & : \text{Recall} = \frac{\text{TP}}{\text{TP} + \text{FN}}
\end{align*}\]

In the 10-fold cross-validation (CV) strategy, the given preprocessed dataset is partitioned randomly into ten separate subsets of the same size. At each validation step, 20% of the preprocessed dataset is retained as the validation dataset to test the suggested method’s performance, while the left 80% of the preprocessed data is utilized as the training dataset. This process is reapplied ten times till each subset had been utilized. The mean value of the performances of the ten test
Algorithm 5 MTWEL Model

**Input:**
List 1 = ['LR', 'SVM', 'NuSVM', 'KNN', 'MLP', 'BNB']; /* First list */
List 2 = ['DT', 'RF', 'XGB', 'LGBM', 'GB', 'ET']; /* Second list */
LoBC = [List 1, List 2]; /* Two lists of base classification models */
Number of LoBC: q = 2;

**Procedure**
/* First tier of developing the suggested EL model */
1. for each q from 1 to n: /* for generation of individual weighted EL models up to n */
2. for each p from 1 to r: /* r = 2 */
3. Fetch LoBC[p]; /* Fetch one list of base classification model at each iteration p */
4. $E_q(X_m) = $ Weighted_EL (); /* To call developed weighted EL model at each iteration q. */
5. p = p + 1;
6. q = q + 1;
7. end;
8. end;
/* Second tier of developing the suggested EL model */
9. Generate an optimum weight for each weighted EL model $E_q(X_m)$:
10. for each n:
11. (a) $W_n = (2^n)$;
12. (b) Applying the GS technique and generating optimized weights for each developed weighted EL model:
13. $W_n(\varphi_n) = \{W_1(\varphi_1), \ldots, W_n(\varphi_n)\}$;
14. (c) Calculating optimum weight with MCC value generated by the developed weighted EL model:
15. $O_n = MCC_x \times W_n(\varphi_n)$;
16. Develop an MTWEL model:
17. for each $E_q(X_m)$:
18. $MTWEL(X_m) = \sum_{o=1}^{n} O_o q E_o q(X_m)$;
19. end;
20. return $MTWEL(X_m)$;

subsets is estimated. The ultimate effect is the entire performance of the suggested model on the 10-fold CV technique.

**IV. RESULTS**
The resulting performance delivered through the proposed MTWEL model accompanied the diabetes early risk prediction dataset and HCC dataset after employing a 10-fold cross-validation procedure displayed in Table 2. The suggested approach achieves the mean AUC values: 1.0 and 1.0, mean PR values: 0.9958 and 1.0, mean REC values: 0.9957 and 0.99, mean F1-score: 0.9957 and 0.9947, and mean accuracy values: 0.9952 and 0.9929, while predicting diabetes disease and HCC survival, respectively. However, in this study, the suggested method’s ROC and PR-REC curves are presented in Figures 3 and 4. These curves illustrate the suggested model’s achievement much more trustworthy and deliver actuality and give a detailed representation concerning the suggested model’s achievement after employing the 10-fold CV procedure. Figures 5-6 exhibit the suggested model’s accuracy value and F1-score value for predicting diabetes disease and HCC survival, respectively, after using the 10-fold CV strategy [7]. While Figure 7 exhibits the confusion matrix of the proposed model on average per each fold while predicting diabetes disease and HCC survival. However, Table 3,
Figures 8 and 9 exhibit that the TN, FP, FN, and TP values of the proposed model’s confusion matrix are available on average for each fold while predicting diabetes disease and HCC survival. In this study, each hyperparameter’s optimized value for each base classification model provided by the GA is exhibited in Appendix 4 of the supplemental files.
FIGURE 6. The proposed model's performance regarding accuracy and F1-score values while predicting HCC survival after employing the 10-fold CV procedure.

FIGURE 7. Confusion matrix of the proposed MTWEL model in respect to average/folds while predicting diabetes disease and HCC survival.

FIGURE 8. TN, FP, FN, and TP values of the proposed model's confusion matrix are available on average for each fold while predicting diabetes disease.

There are two supporting approaches simultaneously performed to achieve the proposed model’s performance and enhance its performance. Such supporting approaches are described as follows. Firstly, in this study, the IF technique is implemented to detect the outlier(s), eliminate it from the provided data, and improve the suggested approach’s performance. Secondly, the neighborhood component analysis-based feature selection technique is employed for dimension reduction and improves the proposed methodology’s performance.
A. PERFORMANCE COMPARISONS OF THE PROPOSED MTWEL MODEL WITH VARIOUS DIMENSION REDUCTION TECHNIQUES

In this segment, comparing the performances of the suggested MTWEL approach with different dimension reduction strategies: Principal Component Analysis (PCA), Linear Discriminant Analysis (LDA), and NCA, in terms of AUC, precision, recall, F1-score, and accuracy based performance assessment metrics presented in Table 4 and Figures 10-13, respectively, while predicting diabetes disease and HCC survival. While Figures 14 and 15 exhibits the confusion matrix of the proposed MTWEL model with LDA and PCA-based dimension reduction techniques for predicting diabetes disease and HCC survival.

The performance of the suggested MTWEL approach with the NCA dimension reduction technique achieves the highest AUC values: 1.0 and 1.0, PR values: 0.9957 and 1.0, REC values: 0.9957 and 0.99, F1-score values: 0.9957 and 0.9947, and accuracy values: 0.9952 and 0.9929 while predicting diabetes disease and HCC survival, respectively. While the MTWEL with the PCA receives the second-most desirable AUC value of 0.9941, PR value of 0.9917, REC value: 0.9790, the accuracy of 0.9833, and F1-score: 0.9849 to predict diabetes disease [7], [67]. On the other hand, the MTWEL model with the LDA dimension reduction approach obtains the second-best AUC value of 0.9460, PR value of 0.9343, accuracy of 0.9124, and F1-score: 0.9350 to predict HCC survival [7], [67]. In comparison, the MTWEL model with LDA and PCA enabled dimension reduction techniques to receive the least AUC values: 0.9897 and 0.7465, PR values: 0.9767 and 0.7625, accuracy values: 0.9714 and 0.76, and F1-score: 0.9748 and 0.8419 to predict diabetes disease and HCC survival, respectively [7], [67]. Hence, this suggested model improves the
Figure 11. Comparing the performances of the proposed MTWEL model with three dimension reduction techniques while predicting HCC survival.

Figure 12. Comparing the performances of the proposed MTWEL approach with different dimension reduction techniques in terms of accuracy and F1-score values while predicting diabetes disease.

B. PERFORMANCE COMPARISON WITH SEVERAL ML CLASSIFIERS IN TERMS OF VARIOUS PERFORMANCE ASSESSMENT METRICS

In this segment, comparing the performances of the proposed MTWEL approach with various ML classifiers: LGBM, XGB, GB, DT, RF, ET, KNN, SVM, NuSVM, MLP, and LR in terms of various performance assessment metrics presented in Table 5 and Figures 16-19, respectively, while predicting diabetes disease and HCC survival [7]. On the other hand, Figures 20 and 21 compare performances between the suggested approach and various ML classifiers in terms of the generated confusion matrix while predicting diabetes disease and the HCC survival.

In this context, the performance of the proposed approach achieves most reliable AUC values: 1.0 and 1.0, PR values: 0.9958 and 1.0, REC values: 0.9957 and 0.99, F1-score values: 0.9957 and 0.9947, and accuracy values: 0.9952 and 0.9929 while predicting diabetes disease and HCC survival [7], [67]. While RF classifier achieves the second-best PR value: 0.9885, REC value: 0.9917, accuracy of 0.9881, and F1-score of 0.9896 for predicting diabetes disease [7], [67]. In comparison, ET classifier receives the second-best AUC value of 0.9998 for predicting diabetes disease. In comparison, LR classifier receives the...
least AUC value: 0.9757, on the other hand, DT classifier generates the least PR value: 0.9720 to predict diabetes disease. In comparison, NuSVM receives the least REC value: 0.9020, accuracy of 0.9328, and F1-score of 0.9370 to predict diabetes disease [7], [67]. In contrast, MLP, LR, and XGB models receive the second-most desirable PR value: 0.7944, accuracy value: 0.7557, and AUC value: 0.8044 while predicting HCC survival [7], [67]. While SVM classifier receives the second-most desirable REC value: 0.9078 and F1-score: 0.8297 while predicting HCC survival [7]. While DT classifier receives the least AUC value: 0.5342, PR value: 0.7090, REC value: 0.6633, F1-score of 0.6734, accuracy of 0.5790 to predict HCC survival. Hence, this suggested model improves the AUC values: 0.0026, 0.006, 0.0039, 0.0206, 0.0006, 0.0002, 0.0108, 0.0066, 0.0132, 0.0092, and 0.0243, and 0.2089, 0.1956, 0.2207, 0.4658, 0.2356, 0.1969, 0.3825, 0.2213, 0.24, 0.2069, and 0.2309, PR values: 0.0073, 0.0177, 0.0121, 0.0238, 0.0073, 0.0146, 0.0208, 0.0073, 0.0177, 0.0121, 0.0238, 0.0073, 0.0146, 0.0208,
FIGURE 16. Comparing the performances of the suggested MTWEL approach with several ML classifiers while predicting diabetes disease.

FIGURE 17. Comparing the performances of the suggested MTWEL approach with several ML classifiers while predicting HCC survival.

FIGURE 18. Comparing the performances of the suggested MTWEL approach with several machine learning classifiers regarding accuracy and F1-score values while predicting diabetes disease.

0.0194, 0.0181, 0.0194, and 0.0237, and 0.1974, 0.2182, 0.2433, 0.291, 0.2463, 0.2416, 0.2714, 0.2295, 0.2193, 0.2056, and 0.2106, REC values: 0.0125, 0.0212, 0.0042, 0.0042, 0.004, 0.004, 0.0596, 0.0458, 0.0937, 0.0551, and 0.0636, and 0.1722, 0.1822, 0.1411, 0.3267, 0.0911, 0.1222, 0.0933, 0.0822, 0.1633, 0.1722, and 0.1222, F1-score values:
0.0104, 0.021, 0.0084, 0.0144, 0.0061, 0.01, 0.0413, 0.0372, 0.0587, 0.0386, and 0.0459, and 0.1881, 0.2041, 0.1979, 0.3213, 0.1786, 0.1896, 0.192, 0.165, 0.1976, 0.1912, and 0.1713 and accuracy values: 0.0119, 0.0239, 0.0095, 0.0167, 0.0071, 0.0119, 0.0454, 0.0406, 0.0624, 0.043, and 0.0502 and 0.2572, 0.2777, 0.2843, 0.4139, 0.2643, 0.2729, 0.2867, 0.2381, 0.2729, 0.2577, and 0.2372 than the LGBM, XGB, GB, DT, RF, ET, KNN, SVM, NuSVM, MLP, and LR, respectively, while predicting diabetes disease and HCC survival.

C. PERFORMANCE COMPARISONS BETWEEN DIFFERENT DIMENSION REDUCTION TECHNIQUES ENABLED VARIOUS MACHINE LEARNING MODELS AND THE SUGGESTED MODEL

In this section, the performance comparisons of the proposed MTWEL approach with the second-best dimension reduction enabled approaches such as PCA and LDA with several machine learning classifiers. The main reason for doing this is that while our proposed model was performing on diabetes and HCC datasets after employing two dimension reduction techniques: PCA and LDA for predicting diabetes disease and HCC survival, respectively, in this case, we have got two different second-best dimensions reduction techniques: PCA and LDA that are exhibited in subsection A of the result section while predicting diabetes disease and HCC survival. In this regard, PCA-enabled and LDA-enabled several
TABLE 6. Comparing the performances between the suggested MTWEL approach and several ML models with the different dimension reduction techniques.

| Model       | AUC   | PR    | REC   | F1-score | Accuracy |
|-------------|-------|-------|-------|----------|----------|
| PCA-LGBM    | 0.9955| 0.9803| 0.9705| 0.9744   | 0.9714   |
| PCA-XGB     | 0.9947| 0.9915| 0.9663| 0.9782   | 0.9761   |
| PCA-GB      | 0.9888| 0.9763| 0.9707| 0.9724   | 0.9690   |
| PCA-DT      | 0.9654| 0.9657| 0.9748| 0.9688   | 0.9642   |
| PCA-RF      | 0.9980| 0.9846| 0.9746| 0.9788   | 0.9762   |
| PCA-ET      | 0.9971| 0.9731| 0.9707| 0.9709   | 0.9667   |
| Proposed MTWEL model | 1.0 | 0.9958 | 0.9957 | 0.9957 | 0.9952 |

D. COMPARISON OF PERFORMANCES BETWEEN THE SEVERAL GENETICALLY OPTIMIZED ML MODELS WITH THE SUGGESTED MODEL

In this section, comparing the performances of the proposed MTWEL approach with several genetically optimized (GO) machine learning models: GOLGBM, GOXGB, GOGB, GODT, GORF, GOET, GOKNN, GOSVM, GONuSVM, GOMLP, and GOLR presented in Table 7 and Figures 28-31, respectively while predicting diabetes disease and HCC survival. On the other hand, Figures 32 and 33 compare performances between our suggested approach and GO with various ML models in the generated confusion matrix while predicting diabetes disease and HCC survival. The performance of the suggested approach receives the highest AUC values: 1.0 and 1.0, PR values: 0.9958 and 1.0, REC values: 0.9957 and 0.99, accuracy values: 0.9952 and 0.9929, and F1-score: 0.9957 and 0.9947 to predict diabetes disease and HCC survival. The performance of the suggested approach receives the best PR values: 0.9958 and 1.0, AUC values: 1.0 and 1.0, REC values: 0.9957 and 0.99, accuracy values: 0.9952 and 0.9929, and F1-score: 0.9957 and 0.9947 for predicting diabetes disease and HCC survival [7]. In this study, PCA-RF achieves the second-best AUC value of 0.9980, accuracy of 0.9762, and F1-score of 0.9788, respectively, for predicting diabetes disease [7], [67]. While the PCA-XGB achieves the second-best PR value: 0.9915 and the PCA-DT model receives the second-best REC value: 0.9748 to predict diabetes disease. On the other hand, the PCA-DT classifier obtains the least AUC value: 0.8886, and the PCA-KNN classifier obtains the least PR value: 0.9656, an accuracy of 0.9304, and an F1-score of 0.9359, respectively, for predicting diabetes disease [7]. In contrast, the PCA-NuSVM model receives the least REC value: 0.8978 to predict diabetes disease. In comparison, the LDA-ET model and LDA-MLP model achieve the second-best PR value of 0.9436 and AUC value of 0.9662 for predicting diabetes disease while predicting HCC survival, respectively. While LDA-XGB model achieves the second-best REC value of 0.96, F1-score of 0.9457, and an accuracy value of 0.9257 for predicting HCC survival, respectively. In contrast, the LDA-LGBM model receives the least PR value of 0.9050 and accuracy of 0.8848, the LDA-ET model receives the least AUC value of 0.9189, and the LDA-DT model receives the least REC value of 0.9189 while predicting diabetes disease. On the other hand, LDA-KNN model achieves the second-best REC value of 0.9789 and F1-score of 0.8494 to predict HCC survival, respectively. In contrast, the GOLGBM model receives the least PR value of 0.9050 and accuracy of 0.8848, the LDA-ET model receives the least AUC value of 0.9189, and the LDA-DT model receives the least REC value of 0.9189 while predicting diabetes disease. In contrast, the GOET model achieves the second-best REC value of 0.9789 and F1-score of 0.8494 to predict HCC survival, respectively [7]. In contrast, the GODT model receives the...
FIGURE 20. The various ML classifiers’ performance along with the proposed model in terms of their generated confusion matrix while predicting diabetes disease.
FIGURE 21. The various ML classifiers’ performance along with the proposed model in terms of their generated confusion matrix while predicting HCC survival.
least AUC value of 0.7284 and REC value of 0.8178, respectively, while predicting the HCC survival. While the GOXGB model receives the least F1-score of 0.8020 and accuracy of 0.7224, and the GOSVM model receives the least PR value of 0.7486, respectively, while predicting the HCC survival.

E. COMPARISON OF PERFORMANCES BETWEEN THE SUGGESTED MODEL AND WEIGHTED EL MODEL

This section compares our suggested approach with the weighted EL model after employing the early-stage diabetes risk prediction dataset and HCC dataset for predicting diabetes disease and HCC survival. Such corresponding experimental result is exhibited in Table 8 and Figures 34-35. In this case, our suggested model achieves the best AUC value: 1.0, PR value: 0.9958 for predicting diabetes disease. While our suggested model achieves the best REC values: 0.9957 and 0.99, F1-score: 0.9957 and 0.9947, and accuracy values: 0.9952 and 0.9929 while predicting diabetes disease and HCC survival, respectively, after employing the above-specified datasets. Hence, this suggested model improves the AUC value: 0.0003 and PR value: 0.004 than the weighted EL model while predicting diabetes disease. In addition, this
suggested model also improves the REC values: 0.0041 and 0.02, F1-score values: 0.0041 and 0.0105, and accuracy values: 0.0047 and 0.0134 compared to the weighted EL model while predicting diabetes disease and HCC survival.

**F. COMPARISON OF PERFORMANCES USING WILCOXON SIGNED-RANK TEST**

This section compares our suggested approach with the above-specified ML models, including the weighted EL model performed on the early-stage diabetes risk prediction dataset and HCC dataset after employing the Wilcoxon signed-rank significant test. The outcomes of such significant testing are exhibited in Tables 9 and 10.

In this study, we have employed Wilcoxon signed-rank test to investigate whether the prediction of our suggested model was statistically different or not compared to the above-specified different ML techniques, which is why we have used such a non-parametric hypothesis test. In Wilcoxon
FIGURE 26. The performance of various ML classifiers with PCA dimension reduction technique along with the proposed model in terms of their generated confusion matrix while predicting diabetes disease.
FIGURE 27. The performance of various ML classifiers with LDA dimension reduction technique along with the proposed model in terms of their generated confusion matrix while predicting HCC survival.
signed-rank test, if the threshold p-values lie lesser than 0.05, we could reject the null hypothesis that the performances of two models of interest are statistically indifferent; otherwise, we could not reject the null hypothesis in favor of the alternative hypothesis.

In this study, our suggested MTWEL model achieved fewer p-values ($p < 0.05$) while investigating the differences between the predictions of our suggested model and several ML models such as RF, ET, KNN, NuSVM, MLP, and PCA-ET while predicting diabetes disease. While in the case of predicting HCC survival patients, our suggested MTWEL model obtained fewer p-values ($p < 0.05$) while investigating the differences between the predictions of our suggested model and various ML models: LGBM, XGB, GB, DT, NuSVM, MLP, LDA-LGBM, LDA-XGB, LDA-GB, LDA-DT, LDA-ET, GOXGB, and GODT. By contrast, p-values between our suggested approach and remaining ML models are not small enough to reject the null hypothesis.

G. COMPARING THE PERFORMANCES WITH THE PREVIOUS APPROACHES

In this proposed research, the performance of the suggested MTWEL approach relies on the WV technique is compared to the previous essential works presented in Table 11 for the prediction of diabetes disease and HCC survival. Several past research works are based on either traditional ML techniques.
such as employing single powerful ML classifiers included in [5], [9], [13], implementing various dimension reduction techniques included in [27], [29], [31]–[33], [35], utilizing various hyperparameter optimization strategies included in [28], [34], implementing several imbalanced learning approaches included in [10], [25], [26], or DL approaches included in [43], [44] or EL techniques included in [4], [61] for the prediction either diabetes disease or HCC survival, respectively. In this regard, as per our understanding, this is the leading study to employ the weighted voting technique-enabled proposed MTWEL approach for intelligently predicting diabetes disease and HCC survival.

Several ML-based solutions were proposed to predict diabetes disease and HCC survival, and we can categorize these solutions based on the limitations mentioned. The proposed method is employed to solve the problems while degrading the performance conducted by the single powerful classification models, such as NB, LR, RF, KNN, DT, SVM, MLP includes [5], [9], [13], methods that employ dimension reduction techniques; namely, binary firefly algorithm, cooperative coevolution technique, LDA, NCA, ReliefF, Chaotic Darcy optimization, CSO, KH, BFO, includes [27], [29], [31]–[33], [35], methods that utilize various hyperparameter optimization strategies, such as, 2-level
FIGURE 32. The performance of various GO ML classifiers along with the proposed MTWEL model in terms of their generated confusion matrix while predicting diabetes disease.
FIGURE 33. The performance of various GO ML classifiers along with the proposed MTWEL model in terms of their generated confusion matrix while predicting HCC survival.
genetic optimizer with c-type SVM, genetically optimized LR model includes [28], [34], methods that employ several imbalanced learning approaches, namely, cluster-based oversampling technique (a neural network with Augmented sets technique), SMOTE includes [10], [25], [26], deep learning approaches such as MLP with GWO and Adaptive Particle swarm optimization with GWO (APGWO) techniques and ANN model includes [43], [44], and methods that utilize several EL techniques: Stacking based EL, RFGBEL models include [4], [61]. Hence, it has been declared that the suggested MTWEL approach achieved outstanding performance while comparing with the prior benchmark methods and provides the most desirable classification outcomes.

V. DISCUSSION

This study developed an innovative MTWEL approach to perform the best result after combining two lists of ML classifiers by implementing a WV technique. There are six ML base classifiers available in each list to form each weighted EL model. The GA optimization procedure intelligently tunes each base classifier’s hyperparameters to generate the optimized base models in each list. Next, a suitable approach must be taken to choose the most suitable optimized base model from each list. Then generating optimized weight for all chosen optimized base models using GS strategy and such tuned weights are further employed to combine with generated MCC value to form new optimum weight for each chosen optimized base model. The WV technique is employed for each list to combine those chosen optimized base models and their respective generated new optimum weight and form each weighted EL model. Next, producing optimized weight for each developed weighted EL model using GS strategy and such tuned weights are again further employed to combine with generated MCC value (generated by each weighted EL
TABLE 7. Comparing the performances of the proposed MTWEL approach with several genetically optimized machine learning models.

| Model       | AUC  | PR   | REC  | F1-score | Accuracy |
|-------------|------|------|------|----------|----------|
| GOLGBM      | 0.9970 | 0.9920 | 0.9873 | 0.9894 | 0.9881 |
| GOXGB       | 0.9796 | 0.9755 | 0.9701 | 0.9704 | 0.9664 |
| GOGB        | 0.9993 | 0.9917 | 0.9871 | 0.9893 | 0.9880 |
| GDT         | 0.8958 | 0.9238 | 0.8636 | 0.8856 | 0.8822 |
| GORF        | 0.9995 | 0.9920 | 0.9915 | 0.9915 | 0.9905 |
| GOET        | 0.9993 | 0.9852 | 0.9915 | 0.9877 | 0.9857 |
| GOKNN       | 0.9882 | 0.9880 | 0.9790 | 0.9831 | 0.9810 |
| GOSVM       | 0.9695 | 0.9639 | 0.9745 | 0.9672 | 0.9616 |
| GOGNSVM     | 0.9900 | 0.9778 | 0.9915 | 0.9837 | 0.9810 |
| GOMLP       | 0.9772 | 0.9527 | 0.9493 | 0.9427 | 0.9426 |
| GOLR        | 0.9808 | 0.9721 | 0.9491 | 0.9592 | 0.9546 |
| Proposed MTWEL model | **1.0** | **0.9958** | **0.9957** | **0.9957** | **0.9952** |

TABLE 8. Comparison of performances between our suggested model and weighted EL model while predicting diabetes disease and HCC survival.

| Model       | AUC  | PR   | REC  | F1-score | Accuracy |
|-------------|------|------|------|----------|----------|
| GOLGBM      | 0.7973 | 0.7998 | 0.8867 | 0.8364 | 0.7686 |
| GOXGB       | 0.7677 | 0.7727 | 0.8389 | 0.8020 | 0.7224 |
| GOGB        | 0.8214 | 0.7625 | 0.9289 | 0.8332 | 0.7486 |
| GDT         | 0.7284 | 0.8255 | 0.8178 | 0.8122 | 0.7562 |
| GORF        | 0.8140 | 0.7599 | 0.9389 | 0.8374 | 0.7557 |
| GOET        | 0.8210 | 0.7570 | 0.9278 | 0.8308 | 0.7476 |
| GOKNN       | 0.7785 | 0.7532 | 0.9789 | 0.8494 | 0.7681 |
| GOSVM       | 0.8023 | 0.7486 | 0.9689 | 0.8421 | 0.7552 |
| GOGNSVM     | 0.7700 | 0.7844 | 0.8778 | 0.8268 | 0.7548 |
| GOMLP       | 0.7954 | 0.7604 | 0.9489 | 0.8422 | 0.7619 |
| GOLR        | 0.7691 | 0.7894 | 0.8678 | 0.8234 | 0.7557 |
| Proposed MTWEL model | **1.0** | **1.0** | **0.99** | **0.9947** | **0.9929** |

TABLE 9. Comparison of performances between our suggested model and several ML classifiers using the Wilcoxon signed-rank significant test.

| Model       | p-value | Model       | p-value | Model       | p-value |
|-------------|---------|-------------|---------|-------------|---------|
| LGBM        | 0.2942  | PCA-LGBM    | 0.2354  | GOLGBM      | 0.2178  |
| XGB          | 0.2942  | PCA-XGB     | 0.2354  | GOXGB       | 0.2178  |
| GB           | 0.2850  | PCA-GB      | 0.2942  | GGB         | 0.2354  |
| DT           | 0.2942  | PCA-DT      | 0.2354  | GDT         | 0.2178  |
| RF           | 0.3446  | PCA-RF      | 0.2354  | GRF         | 0.2178  |
| ET           | 0.2942  | PCA-ET      | 0.2354  | GET         | 0.2178  |
| KNN          | 0.2942  | PCA-KNN     | 0.2354  | GOKNN       | 0.2178  |
| SVM          | 0.2354  | PCA-SVM     | 0.2178  | GOSVM       | 0.2942  |
| NaSVM        | 0.2942  | PCA-NaSVM   | 0.2354  | GONaSVM     | 0.2178  |
| MLP          | 0.2354  | PCA-MLP     | 0.2942  | GOLR        | 0.2354  |
| LR           | 0.2354  | PCA-LR      | 0.2942  | GOLR        | 0.2354  |

TABLE 10. Comparison of performances between our suggested model and weighted EL model using the Wilcoxon signed-rank significant test.

| Dataset      | Model       | p-value | Dataset      | Model       | p-value |
|--------------|-------------|---------|--------------|-------------|---------|
| Diabetes     | Early-stage diabetes risk prediction dataset [9] | **0.864** | HCC dataset [10] | Weighted EL model | 0.317 |
| HCC          | Weighted EL model | **0.864** | HCC dataset [10] | Weighted EL model | 0.317 |

model) to form new optimum weight for each weighted EL model. Finally, the WV technique is employed to combine those weighted EL models and their respective generated new optimum weights and forms our proposed MTWEL model.

However, two supporting approaches are performed to obtain a better result, such as the IF for detecting and removing outliers from diabetes and HCC datasets and the NCA approach to reduce the dimension of such datasets and generate excellent outcomes.

However, identifying the outliers from the dataset is necessary because it may indicate insufficient data and impact the performance. In this study, the utilized datasets have some outliers for degrading the performance of our proposed approach. Therefore, we have employed the IF outlier detection and removal technique for detecting and removing the outliers from diabetes and HCC datasets and enhance the performance of our suggested approach.

The optimal feature selection technique is one of the significant essential components for enhancing the performance of our proposed MTWEL approach. The main reason for selecting the optimum features from the preprocessed data is to overcome degrading the performance and provide an excellent outcome. In this regard, we have implemented NCA enabled feature selection approach to reduce the dimension from the given dataset and form a reduced optimal dataset for further utilization by our proposed model. This study also exhibited the performance comparison of our suggested approach performed on several dimension reduction techniques: NCA, LDA, and PCA shown in Figures 10-15, and our proposed MTWEL model with NCA dimension reduction technique outperformed remaining above-specified dimension reduction techniques. In this case, we can understand how much NCA dimension reduction technique is needed.
to enhance the performance of our suggested MTWEL approach.

While implementing GA in this study is so much crucial for enhancing the performance of the suggested approach. The main reason is that the optimal hyperparameters provide an impact to raise any ML classification model(s) performance. According to our understanding, without using optimal hyperparameter, that may have a chance to degrade the performance of any machine learning classifiers. This paper employed a GA hyperparameter optimization strategy to diminish such drawbacks and improve the proposed model’s performance. In this study, the GA was implemented to tune the parameters of each classifier and generate GO base models and improve their performances. This study also compared our suggested method’s performance with GO machine learning classifiers shown in Figures 28-33. In this concern, we can understand how much GA is needed to enhance the performance of our suggested MTWEL approach.

In this paper, the performance gained by the suggested MTWEL approach is exhibited in Figures 3-9 after employing diabetes and HCC datasets. Furthermore, we can also compare the performance of the suggested approach with various ML techniques, including the weighted EL model exhibited in Figures 10-35. Regarding this issue, the suggested approach achieves the best performance in terms of various performance evaluation metrics compared to the above-specified ML techniques, including the weighted EL model. However, the proposed model also outclasses the prior benchmark techniques in Table 11 while predicting diabetes disease and HCC survival.

While in predicting diabetes disease and HCC survival, the proposed method to solve the problems with the highest outcomes while degrading the performance conducted by the single powerful classification models such as NB, LR, RF, KNN, DT, SVM, MLP, methods that employ dimension reduction techniques; namely, binary firefly algorithm, cooperative coevolution technique, LDA, NCA, ReliefF, Chaotic Darcy optimization, CSO, KH, BFO, GWO and APGWO techniques, hyperparameter optimization strategies, such as, 2-level genetic optimizer with c-type SVM, genetically optimized LR, deep learning approaches such as ANN and MLP classifiers, imbalanced learning approaches, namely, cluster-based oversampling technique, SMOTE, and EL techniques: Stacking based EL, RFGBEL models, respectively.

Hence, it has been declared that the suggested MTWEL approach successfully addressed all the limitations specified in the Introduction and related study and research gap sections and achieved outstanding performances to predict diabetes disease and HCC survival while comparing with the above-specified various ML techniques along with the previous benchmark methods, and provide the most desirable classification outcomes.

### VI. CONCLUSION

This proposed research presents a new MTWEL model for predicting diabetes disease and HCC survival and supports doctors in providing precise and up-to-date medicine and, hence, protecting many individual lives. In the MTWEL model, two lists of base classifiers are available to generate each weighted EL model, respectively. While in each list of base classifiers, six base models are performed to form a weighted EL model. In this regard, parameters of all base classifiers are tuned by the GA approach to generate optimal hyperparameters and produced GO base models. For
each list of base classifiers, generate a new optimum weight for each chosen optimized base model after combining the optimized weight value and the MCC value of each chosen optimized base model and generate a weighted EL model. Employ the WV technique to generate a weighted EL model for each list of base classifiers and generate our proposed MTWEL model after combining such generated weighted EL models. The IF is employed for detecting and removing outliers from the data, and the NCA approach is employed to reduce the dimension for enhancing the proposed model’s performance. The conducted examinations completely confirm the effectiveness of the suggested MTWEL approach after employing diabetes and HCC datasets. The primary outcomes of this proposed research are concluded in the following.

1. The proposed approach is precisely tailored for predicting diabetes disease and HCC survival and achieving the best performances regarding the AUC values: 1.0 and 1.0, PR values: 0.9958 and 1.0, REC values: 0.9957 and 0.99, F1-score values of 0.9957 and 0.9947, and accuracy values: 0.9952 and 0.9929, respectively.

2. The proposed MTWEL approach beats the various ML techniques, including the weighted EL model, and delivers outstanding performances.

3. The proposed MTWEL model defeats the previous benchmark techniques and validates itself as the most desirable approach for predicting diabetes disease and HCC survival.

However, this suggested MTWEL model can be improved by combining the latest boosting classifiers, improving the current proposed MTWEL model, or utilizing a deep neural network to predict diabetes disease and HCC survival. The suggested approach’s forthcoming task is to join the methodologies above and increase the performance in predicting diabetes and HCC diseases and advancing our suggested approach’s performance.

REFERENCES

[1] B. P. Nguyen, H. N. Pham, H. Tran, N. Nghiem, Q. H. Nguyen, T. T. T. Do, C. T. Tran, and C. R. Simpson, “Predicting the onset of type 2 diabetes using wide and deep learning with electronic health records,” Comput. Methods Programs Biomed., vol. 182, Dec. 2019, Art. no. 105055.

[2] M. Rahman, D. Islam, R. J. Mukti, and J. Saha, “A deep learning approach based on convolutional LSTM for detecting diabetes,” Comput. Biol. Chem., vol. 88, Oct. 2020, Art. no. 107329.

[3] A. Rehman, A. Athar, M. A. Khan, S. Abbas, A. Fatima, and A. Saeed, “Modelling, simulation, and optimization of diabetes type II prediction using deep extreme learning machine,” J. Ambient Intell. Smart Environ., vol. 12, no. 2, pp. 125–138, Mar. 2020.

[4] W. Ksiezek, M. Hammad, P. Plawiak, U. R. Acharya, and R. Tadeusiewicz, “Development of novel ensemble model using stacking learning and evolutionary computation techniques for automated hepatocellular carcinoma detection,” Biocybern. Biomed. Eng., vol. 40, no. 4, pp. 1512–1524, 2020.

[5] D. Chiccio and L. Oneto, “Computational intelligence identifies alkaline phosphatase (ALP), alpha-fetoprotein (AFP), and hemoglobin levels as most predictive survival factors for hepatocellular carcinoma,” Health Informat. J., vol. 27, no. 1, Jan. 2021, Art. no. 146045822098420.

[6] M. K. Hasan, M. A. Alam, D. Das, E. Hossain, and M. Hasan, “Diabetes prediction using ensembling of different machine learning classifiers,” IEEE Access, vol. 8, pp. 76516–76531, 2020.

[7] J. Dhar, “Multistage ensemble learning model with weighted voting and genetic algorithm optimization strategy for detecting chronic obstructive pulmonary disease,” IEEE Access, vol. 9, pp. 48640–48657, 2021.

[8] M. Massaoudi, S. S. Refaat, I. Chihhi, M. Trabelsi, F. S. Oueslati, and H. Abu-Rub, “A novel stacked generalization ensemble-based hybrid LGBM-XGB-MLP model for short-term load forecasting,” Energy, vol. 214, Jan. 2021, Art. no. 118874.

[9] M. M. Islam, R. Ferdousi, S. Rahman, and H. Y. Bushra, “Likelihood prediction of diabetes at early stage using data mining techniques,” in Computer Vision and Machine Intelligence in Medical Image Analysis, 2021, pp. 113–125.

[10] M. S. Santos, P. H. Abreu, P. J. García-Lacencina, A. Simão, and A. Carvalho, “A new cluster-based oversampling method for improving survival prediction of hepatocellular carcinoma patients,” J. Biomed. Inform., vol. 58, pp. 49–59, Dec. 2015.

[11] M. F. Ijaz, G. Alfian, M. Syafrudin, and J. Rhee, “Hybrid prediction model for type 2 diabetes and hypertension using DBSCAN-based outlier detection, synthetic minority over sampling technique (SMOTE), and random forest,” Appl. Sci., vol. 8, no. 8, p. 1325, Aug. 2018.

[12] N. L. Fitriyani, M. Syafrudin, G. Alfian, and J. Rhee, “Development of disease prediction model based on ensemble learning approach for diabetes and hypertension,” IEEE Access, vol. 7, pp. 144777–144789, 2019.

[13] K. Alpan and G. S. Ilgi, “Classification of diabetes dataset with data mining techniques by using WEKA approach,” in Proc. 4th Int. Symp. Multidisciplinary Stud. Innov. Technol. (ISMSIT), Oct. 2020, pp. 1–7.

[14] M. Maniruzzaman, M. J. Rahman, B. Ahmed, and M. M. Abedin, “Classification and prediction of diabetes disease using machine learning paradigm,” Health Inf. Sci. Syst., vol. 8, no. 1, pp. 1–14, Dec. 2020.

[15] B. Pranto, S. M. Mehnaz, E. B. Mahid, I. M. Sadman, A. Rahman, and S. Momen, “Evaluating machine learning methods for predicting diabetes among female patients in Bangladesh,” Information, vol. 11, no. 8, p. 374, Jul. 2020.

[16] L. Kopitar, P. Kocbek, L. Cilar, A. Sheikh, and G. Stiglic, “Early detection of type 2 diabetes mellitus using machine learning-based prediction models,” Sci. Rep., vol. 10, no. 1, pp. 1–12, Dec. 2020.

[17] A. U. Haq, J. P. Li, J. Khan, M. H. Memon, S. Nazir, S. Ahmad, G. A. Khan, and A. Ali, “Intelligent machine learning approach for effective recognition of diabetes in E-healthcare using clinical data,” Sensors, vol. 20, no. 9, p. 2649, May 2020.

[18] N. Nnamoko and I. Korkontzelos, “Efficient treatment of outliers and class imbalance for diabetes prediction,” Artif. Intell. Med., vol. 104, Apr. 2020, Art. no. 101815.

[19] M. Shuja, S. Mittal, and M. Zaman, “Effective prediction of type II diabetes mellitus using data mining classifiers and SMOTE,” in Advances in Computing and Intelligent Systems. Singapore: Springer, 2020, pp. 195–211, doi: 10.1007/978-981-15-0222-4_17.

[20] H. Kaur and V. Kumari, “Predictive modelling and analytics for diabetes using a machine learning approach,” Inf. Technol. Ind., vol. 9, no. 1, pp. 215–223, Feb. 2021.

[21] H. F. Ahmad, H. Mukhtar, H. Alaqiqal, M. Seliaman, and A. Alhumam, “Investigating health-related features and their impact on the prediction of diabetes using machine learning,” Appl. Sci., vol. 11, no. 3, p. 1173, Jan. 2021.

[22] Y. Kwon, J.-W. Kwon, J. Ha, D. Kim, J. Cho, S. M. Jeon, S.-H. Park, J. Hwang, N. H. Kim, and S. Park, “Remission of type 2 diabetes after gastrectomy for gastric cancer: Diabetes prediction score,” Gastric Cancer, Jul. 2021.

[23] C. Azad, B. Bhusan, R. Sharma, A. Shankar, K. K. Singh, and A. Khamparia, “Prediction model using SMOTE, genetic algorithm and decision tree (PMMSGD) for classification of diabetes mellitus,” Multimedia Syst., Jun. 2021.

[24] X. Wang, M. Zhai, Z. Ren, H. Ren, M. Li, D. Quan, L. Chen, and L. Qiu, “Exploratory study on classification of diabetes mellitus through a combined random forest classifier,” BMC Med. Inform. Decis. Making, vol. 21, no. 1, pp. 1–14, Dec. 2021.

[25] M. Hattab, A. Maalel, and H. H. Ghzala, “Towards an oversampling method to improve hepatocellular carcinoma early prediction,” in Digital Health in Focus of Predictive, Preventive and Personalized Medicine (Advances in Predictive, Preventive and Personalised Medicine), vol. 12, Springer, 2020, pp. 139–148, doi: 10.1007/978-3-030-49815-3_16.

[26] L. Akter and M. M. Islam, “Hepatocellular carcinoma patient’s survival prediction using oversampling and machine learning techniques,” in Proc. 2nd Int. Conf. Robot., Electr. Signal Process. Techn. (ICREST), Jan. 2021, pp. 445–450.
T. M. Le, T. M. Vo, T. N. Pham, and S. V. T. Dao, “A novel wrapper-based feature selection method for cancer diagnosis,” in *Proc. Int. Conf. Comput. Sci. Appl.*, 2018, pp. 438–449, 2018.

W. Książek, M. Abdar, A. F. Kocamaz, and F. Ertam, “A novel classification method for hepatocellular carcinoma patients with chaotic Darcy optimization method based feature selection,” *Med. Hypotheses*, vol. 139, Apr. 2020, pp. 109–126.

W. Książek, M. Gandor, and P. Plawiak, “A novel machine learning approach for early detection of hepatocellular carcinoma,” *Neural Comput. Appl.*, vol. 33, no. 7, pp. 2783–2792, Apr. 2021.

T. He, J. N. Fong, L. W. Moore, C. F. Ezeana, D. Victor, M. Divatia, M. Vasquez, R. M. Ghobrial, and S. T. C. Wong, “Prediction of survival risk for diabetes patients with chaotic Darcy optimization method based feature selection,” *Appl. Sci.*, vol. 11, no. 1, p. 11, Dec. 2020.

T. M. Le, T. M. Vo, T. N. Pham, and S. V. T. Dao, “A novel wrapper-based feature selection method for cancer diagnosis,” in *Proc. Int. Conf. Comput. Sci. Appl.*, 2018, pp. 438–449, 2018.

W. Książek, M. Abdar, A. F. Kocamaz, and F. Ertam, “A novel classification method for hepatocellular carcinoma patients with chaotic Darcy optimization method based feature selection,” *Med. Hypotheses*, vol. 139, Apr. 2020, pp. 109–126.

W. Książek, M. Gandor, and P. Plawiak, “A novel machine learning approach for early detection of hepatocellular carcinoma,” *Neural Comput. Appl.*, vol. 33, no. 7, pp. 2783–2792, Apr. 2021.

T. Tuncer and F. Ertam, “A comparative study of various dimensionality reduction and genetic optimization support vector machine,” *Neural Comput. Appl.*, vol. 33, no. 7, pp. 2783–2792, Apr. 2021.

T. He, J. N. Fong, L. W. Moore, C. F. Ezeana, D. Victor, M. Divatia, M. Vasquez, R. M. Ghobrial, and S. T. C. Wong, “Image recognition and multi-network based deep learning model for risk assessment of liver transplantation for hepatocellular cancer,” *Computized Med. Imag. Graph.*, vol. 89, Apr. 2021, Art. no. 101894.

T. M. Le, T. M. Vo, T. N. Pham, and S. V. T. Dao, “A novel wrapper-based feature selection method for cancer diagnosis,” in *Proc. Int. Conf. Comput. Sci. Appl.*, 2018, pp. 438–449, 2018.

W. Książek, M. Abdar, A. F. Kocamaz, and F. Ertam, “A novel classification method for hepatocellular carcinoma patients with chaotic Darcy optimization method based feature selection,” *Med. Hypotheses*, vol. 139, Apr. 2020, pp. 109–126.

W. Książek, M. Gandor, and P. Plawiak, “A novel machine learning approach for early detection of hepatocellular carcinoma,” *Neural Comput. Appl.*, vol. 33, no. 7, pp. 2783–2792, Apr. 2021.

T. Tuncer and F. Ertam, “Neighborhood component analysis and reliefF based survival recognition methods for hepatocellular carcinoma,” in *Proc. 4th Int. Conf. Comput. Sci. Appl. Eng.*, Oct. 2020, pp. 1–7.

S. Kaur, D. Kumar, and M. Mittal, “An ensemble approach for classification and prediction of diabetes mellitus using soft voting classifier,” *Int. J. Comput. J. Cognit. Eng.*, vol. 2, pp. 40–46, Jun. 2021.

S. El-Sappagh, M. Elmagy, F. Ali, T. Abuhmed, S. M. R. Islam, and K.-S. Kwak, “A comprehensive medical decision-support framework based on a heterogeneous ensemble classifier for diabetes prediction,” *Electronics*, vol. 8, no. 6, p. 635, Jun. 2019.

A. H. Syed and T. Khan, “Machine learning-based application for predicting risk of type 2 diabetes mellitus (T2DM) in Saudi Arabia: A retrospective cross-sectional study,” *IEEE Access*, vol. 8, pp. 199539–199561, 2020.

S. K. Ryu, S. W. Lee, E. Batbata, J. W. Lee, K. S. Choi, and H. S. Cha, “A deep learning model for estimation of patients with undiagnosed diabetes,” *Appl. Sci.*, vol. 10, no. 1, p. 421, Jan. 2020.

T. R. Gadekallu, N. Khare, S. Bhattacharya, S. Singh, P. K. R. Maddikunta, I.-H. Ra, and M. Alazab, “Early detection of diabetic retinopathy using PCA-firefly based deep learning model,” *Electronics*, vol. 9, no. 2, p. 274, Feb. 2020.

J. Xie and Q. Wang, “Benchmarking machine learning algorithms on blood glucose prediction for type 1 diabetes in comparison with classical time-series models,” *IEEE Trans. Biomed. Eng.*, vol. 67, no. 11, pp. 3101–3124, Nov. 2020.

H. Naz and S. Ahuja, “Deep learning approach for diabetes prediction using PIMA Indian dataset,” *J. Diabetes Metabolic Disorders*, vol. 19, no. 1, pp. 391–403, Jun. 2020.

T. M. Le, T. M. Vo, T. N. Pham, and S. V. T. Dao, “A novel wrapper-based feature selection for early diabetes prediction enhanced with a Metaheuristic,” *IEEE Access*, vol. 9, pp. 7869–7884, 2021.

L. H. Staib, M. Kocher, J. Chapiro, and M. Lin, “Automated detection and prediction of diabetes mellitus using soft voting classifier,” *Int. J. Comput. J. Cognit. Eng.*, vol. 2, pp. 40–46, Jun. 2021.

S. Fazakis, O. Kocsis, S. Alexiou, N. Fakotakis, and K. Moustakas, “Machine learning tools for long-term type 2 diabetes risk prediction,” *IEEE Access*, vol. 9, pp. 103737–103757, 2021, doi: 10.1109/ACCESS.2021.3089691.

H. Kaushik, D. Singh, M. Kaur, H. Alshazly, A. Zaguia, and H. Hamam, “Diabetic retinopathy diagnosis from fundus images using stacked generalization of deep models,” *IEEE Access*, vol. 9, pp. 108276–108292, 2021, doi: 10.1109/ACCESS.2021.3101142.

M. Muneeb and A. Hensche, “Eye-color and type-2 diabetes phenotype prediction from genotype data using deep learning methods,” *BMC Bioinf.*, vol. 21, no. 1, pp. 1–26, Feb. 2020.

H. Lu, S. Uddin, F. Hajati, M. A. M. Moni, and M. Khushi, “A patient network-based machine learning model for disease prediction: The case of type 2 diabetes mellitus,” *Appl. Intell.*, Jun. 2021.

J. Wang, J. Xu, C. Zhao, Y. Peng, and H. Wang, “An ensemble feature selection method for high-dimensional data based on sort aggregation,” *Syst. Sci. Control Eng.*, vol. 7, no. 2, pp. 32–39, Nov. 2019.

M. Sharma and N. Kumar, “Improved hepatocellular carcinoma fatality prognosis using ensemble learning approach,” *J. Ambient Intell. Humanized Comput.*, Apr. 2021.

M. U. Rehman, S. Najam, S. Khalid, A. Shafique, F. Alqatami, F. Baothman, S. Y. Shah, Q. H. Abbasi, M. A. Imran, and J. Ahmad, “Infrared sensing based non-invasive initial diagnosis of chronic liver disease using ensemble learning,” *IEEE Sensors J.*, vol. 21, no. 17, pp. 9195–9406, Sep. 2021.

M. K. I. Molla, A. A. Shiam, M. Islam, and T. Tanaka, “Discriminative feature selection-based motor imagery classification using EEG signal,” *IEEE Access*, vol. 8, pp. 98255–98265, 2020.

M. T. Sadiq, Y. Xu, and Z. Yuan, “Exploiting dimensionality reduction and neural network techniques for the development of expert brain–computer interface,” *Expert Syst. Appl.*, vol. 164, Feb 2021, Art. no. 110431.

Z. Momeni and M. S. Abadeh, “MapReduce-based parallel genetic algorithms,” *IEEE Access*, vol. 164, Feb. 2021, Art. no. 110431.

M. T. Sadiq, Y. Xu, and Z. Yuan, “Exploiting dimensionality reduction and neural network techniques for the development of expert brain–computer interface,” *Expert Syst. Appl.*, vol. 164, Feb 2021, Art. no. 110431.

Z. Momeni and M. S. Abadeh, “MapReduce-based parallel genetic algorithms,” *IEEE Access*, vol. 164, Feb. 2021, Art. no. 110431.

M. T. Sadiq, Y. Xu, and Z. Yuan, “Exploiting dimensionality reduction and neural network techniques for the development of expert brain–computer interface,” *Expert Syst. Appl.*, vol. 164, Feb 2021, Art. no. 110431.

Z. Momeni and M. S. Abadeh, “MapReduce-based parallel genetic algorithms,” *IEEE Access*, vol. 164, Feb. 2021, Art. no. 110431.

M. T. Sadiq, Y. Xu, and Z. Yuan, “Exploiting dimensionality reduction and neural network techniques for the development of expert brain–computer interface,” *Expert Syst. Appl.*, vol. 164, Feb 2021, Art. no. 110431.
[67] Y. Sakai, C. Yang, S. Kihira, N. Tsankova, F. Khan, A. Hormigo, A. Lai, T. Cloughesy, and K. Nael, “MRI radiomic features to predict IDH1 mutation status in gliomas: A machine learning approach using gradient tree boosting,” *Int. J. Mol. Sci.*, vol. 21, no. 21, p. 8004, Oct. 2020. [Online]. Available: https://www.mdpi.com/1422-0067/21/21/8004/html

**JOY DHAR** (Member, IEEE) is currently working as a Vocational Trainer at Hatgobindapur M.C. High School and a Researcher, who focuses on machine learning and deep learning-based methodologies. He has published two scientific results in reputable journals, such as IEEE Access and *Ingénierie des Systèmes d’Information*. His research interests include supervised and unsupervised machine learning techniques, various hyperparameter optimization techniques, several ensemble learning techniques (bagging, voting, and stacking), deep learning, and genetic algorithm. He is currently a Reviewer in many journals, such as the *Journal of Intelligent and Fuzzy Systems* (seven times) and IEEE Access (six times). He was qualified at the Graduate Aptitude Test in Engineering (GATE) and UGC-NATA-NTA awarded by the Ministry of Human Resource Development (MHRD) and the UGC with NTA.

**NIGUS ASRES AYELE** received the Bachelor of Science degree from Wolkite University, Ethiopia, in 2015, and the Master of Science degree from Addis Ababa Science and Technology University, in 2020. He is currently a Lecturer at Wolkite University. His research interests include artificial intelligence, machine learning, deep learning, image processing, big data analytics, data science, bioinformatics, software testing and quality assurance, network security, and software-defined networks. However, he has done the following research works: developing classification model for chickpea types using machine learning algorithms, designing time series crime prediction model using long short-term memory recurrent neural network, and the principle of architecture first in software project management minimizes the cost of software development process and telecommunication network architecture for telemedicine in Ethiopia and its applicability.

* * *