Multi Chronic Disease Prediction by Fine Tuning Random Forest using Social Group Optimization

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Abstract

Accurate disease prediction is essential for enabling preventive healthcare and reducing the burden of chronic illnesses. This study introduces an innovative multi-disease prediction framework leveraging machine learning and optimization techniques to address limitations in precision and scope present in prior research. Specifically, we focus on predicting five major diseases—diabetes, heart disease, kidney disease, liver disease, and breast cancer—by employing the Social Group Optimization (SGO) algorithm to fine-tune the Random Forest (RF) classifier's hyperparameters.The proposed SGO-optimized RF model optimizes seven critical parameters - n_estimators, max_depth, min_samples_split, min_samples_leaf, max_features, bootstrap, and criterion simultaneously, significantly enhancing the model's performance. Our approach, applied to five disease datasets, achieves notable accuracy improvements: 98.25 When tested on diverse datasets, the model achieves exceptional accuracy: 98.25% for breast cancer, 84.62% for liver disease, 93.44% for heart disease, 82.47% for diabetes, and 100% for chronic kidney disease. On average, the SGO-optimized RF outperforms existing methods with a 2.3% accuracy improvement across datasets. This research highlights the transformative potential of SGO-based optimization in advancing the accuracy and reliability of predictive models. The results demonstrate the framework's applicability in clinical scenarios, providing precise and actionable insights that support early diagnosis and improve patient outcomes.

Keywords: SGO; Random forest; Accuracy; Hyperparameters; Healthcare; Chronic disease prediction

1. Introduction

Disease is a condition that harms the body's environment and negatively influences the structure or function of the entire organism or specific parts of it. Diseases are often characterized by distinct signs and symptoms and can result from external agents like pathogens or internal dysfunctions. In humans, "illness" broadly refers to any condition that affects the patient's wellbeing, causing discomfort, dysfunction, stress, or social challenges. This broad definition sometimes includes injuries, disabilities, syndromes, infections, particular symptoms, abnormal behaviors, and unusual variations in bodily structure or function, although in some contexts, these may be classified separately. One common term in medical conversations, literature, and policy discussions is "chronic disease." A chronic disease or illness is any condition that persists for a long duration, typically defined as lasting more than three months. Chronic diseases can influence a patient's mental health, as living with such conditions may shift their outlook on life, affecting both physical and psychological wellbeing.

In this paper, we focus on predicting five chronic diseases such as Heart Disease, Liver Disease, Kidney Disease, Breast Cancer and Diabetes using machine learning techniques, which streamline the prediction process by utilizing key health characteristics. Here are brief descriptions of each of the five chronic diseases:

Heart Disease: Heart disease is a broad category of disorders that affect the anatomy and physiology of the heart. The most prevalent kind is coronary artery disease, in which the heart muscle receives less blood due to plaque accumulation in the coronary arteries. Breathlessness, angina (chest pain), and, in extreme situations, heart attacks, can result from

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this. Heart failure, heart valve disease, and arrhythmias (irregular heartbeats) are further kinds. High blood pressure, high cholesterol, smoking, obesity, and a sedentary lifestyle are risk factors. Heart disease can lead to life-threatening events and chronic complications that affect quality of life, causing fatigue, reduced physical capability, and increased risk of complications in other organs due to poor blood circulation.

Liver Disease: Liver disease refers to any condition that damages the liver and affects its ability to function properly. Common liver diseases include hepatitis (inflammation caused by viral infection or toxins), fatty liver disease (fat accumulation in liver cells), cirrhosis (scarring from long-term damage), and liver cancer. The liver is crucial for detoxifying the blood, producing bile, and processing nutrients, so liver damage can have widespread effects. Liver diseases are often caused by excessive alcohol use, viral infections, or metabolic disorders. Symptoms of liver disease include jaundice (yellowing of the skin), fatigue, abdominal pain, and swelling. Advanced liver disease can lead to liver failure, necessitating a transplant for survival.

Kidney Disease: Chronic kidney disease (CKD) is a condition in which the kidneys steadily deteriorate over time, making it more difficult for them to filter waste and extra fluid from the blood. Leading causes include high blood pressure, diabetes, and genetic disorders. CKD progresses in stages, and in advanced stages, it can lead to kidney failure, requiring dialysis or a kidney transplant. Symptoms may include swelling in the legs, fatigue, nausea, and difficulty concentrating. CKD can also lead to cardiovascular disease, as the kidneys play a role in regulating blood pressure and blood chemistry.

Breast Cancer: Women are more likely than males to develop breast cancer, a type of cancer that develops in the breast cells. It happens when breast cells change and proliferate out of control, creating a mass known as a tumor. Breast cancer has the ability to metastasize to different areas of the body via the lymphatic system or the blood. There are various forms, such as invasive ductal carcinoma (the most prevalent), invasive lobular carcinoma, and inflammatory breast cancer. Early symptoms include a lump in the breast, changes in breast shape, and skin changes. Advanced breast cancer can spread (metastasize) to bones, liver, lungs, and brain, severely affecting health. Early detection and treatment are crucial for a better prognosis.

Diabetes: Diabetes is a long-term metabolic condition marked by elevated blood sugar levels resulting from the body's incapacity to generate or properly utilize insulin. There are two primary categories: Type 1, in which the immune system targets the insulin-producing cells in the pancreas, and Type 2, which is more prevalent and generally linked to lifestyle choices and genetic factors. Uncontrolled diabetes can cause serious problems with the heart, kidneys, eyes, and nerves over time. Frequent urination, increased thirst, exhaustion, and blurred eyesight are all signs of diabetes. Complications can lead to kidney disease, cardiovascular disease, neuropathy, and vision loss, making long-term management essential for health.

Each of these diseases presents unique challenges and has significant health implications, especially as chronic conditions. To lessen problems and enhance the quality of life for those who have these disorders, early detection, lifestyle modification, and continued treatment are crucial.

In this paper, we focus on predicting above five chronic diseases using RF. Because RF uses an ensemble approach that aggregates the predictions of several decision trees, it is very effective for classification. This process reduces overfitting, making the model more generalizable and accurate. It is particularly well suited to high-dimensional datasets, as each tree is trained on a random subset of features, allowing the model to handle complex data structures without extensive feature selection. Additionally, RF can manage missing data effectively, minimizing the impact of incomplete records on accuracy. Its ability to identify feature importance is valuable for interpreting model behaviour and understanding which variables influence the predictions most.

However, RF has a large number of parameters that can be tuned, which may complicate optimization. These settings include, among other things, the minimum samples for splitting nodes, the maximum depth, and the number of trees. Adjusting these parameters can enhance performance, but it also requires careful tuning to achieve the best results without overfitting or slowing down the model.

The selection of hyperparameters is a process aimed at finding optimal values for hyperparameters-configurable settings adjusted before the execution of an algorithm to improve overall model performance [1, 2]. The number of hyperparameters to be configured varies depending on the specific selection method. Researchers may choose to configure the full set of hyperparameters [3] or focus on a targeted subset [4]. To distinguish between parameters and hyperparameters, take neural networks as an example. Here the number of hidden layers is a hyperparameter set before training, while input weights are parameters learned during training [5].

Machine learning algorithms can benefit from various hyperparameter selection methods, as relying on a single approach may not yield optimal results. The success of hyperparameter selection depends on factors such as the size of the search space, dimensionality, and characteristics of the data used in experiments [6]. Thus, it is essential to choose or adapt a selection method that is well suited to the problem's complexity [7]. Reviewing available methods for hyperparameter

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selection helps researchers identify the most effective one for specific applications [8]. Among the widely recognized methods for hyperparameter selection are grid search [9], random search [10], and Bayesian optimization [11]. Grid search can be time-intensive, especially in high-dimensional spaces, while random search is more efficient with small search spaces. Bayesian optimization, based on probabilistic modelling, is faster and generally more cost-effective, though it does not support parallel execution [12].

Natural language processing (NLP) [13], deep learning [14], cloud computing [15], and video processing [16] are just a few of the domains where hyperparameter selection has been used. There is ongoing debate about whether selection should always accompany machine-learning algorithms, as it can significantly increase computational costs and hardware resource use, such as CPU and RAM. In some cases, hyperparameter selection may not improve performance, particularly in classification tasks where the value of hyperparameter selection can be assessed by observing the effect of additional training instances [17].

In this research, we have employed the Social Group Optimization (SGO) metaheuristic technique to select hyperparameters for the RF machine-learning model. The Social Group Optimization (SGO) algorithm [18,19] offers several benefits for hyperparameter selection in machine learning models, making it an effective choice for this purpose. SGO possesses a good optimality-finding ability and is used in various fields [20-30]. Below points will explain why SGO is particularly well-suited for hyperparameter optimization:

i) Efficient Exploration and Exploitation Balance

SGO effectively balances exploration (searching broadly across the hyperparameter space) and exploitation (refining good solutions), which is crucial for finding optimal hyperparameters. By emulating social behaviors, SGO encourages both group-level knowledge sharing and individual-level exploration, which helps avoid local optima and improves the chances of finding the global optimum.

ii) Adaptability to Complex, High-Dimensional Spaces

Hyperparameter tuning can involve a complex, multi-dimensional search space, especially in models like RF or deep neural networks. SGO is adaptive to these complexities, allowing it to navigate large search spaces efficiently without requiring prior knowledge of the search space.

iii) Robust Against Local Optima

Compared to more conventional optimization techniques, SGO is less prone to become trapped in local optima. This is achieved through its social learning component, which helps particles (solutions) learn from the best solutions found by their group, making it more robust in complex, non-linear search spaces commonly found in hyperparameter tuning.

iv) Flexibility and Scalability

SGO is scalable and can handle a variety of hyperparameter types (continuous, discrete, categorical), making it applicable across a wide range of machine learning algorithms. Furthermore, it may be adapted to various tuning requirements by modifying the algorithm's parameters, enabling it to efficiently scale with the size of the data and the complexity of the model.

v) Computational Efficiency

Compared to exhaustive search methods like grid search, SGO reduces computational cost by focusing on promising regions of the search space rather than sampling all possible combinations. This is especially useful in large models or with expensive-to-evaluate metrics, as SGO can reach high-quality solutions in fewer iterations.

vi) High-Quality Solutions for Complex Models

SGO has shown effectiveness in applications where high accuracy is essential, such as multi-chronic disease prediction, by fine-tuning hyperparameters that affect model performance significantly. This adaptability helps SGO deliver high-quality solutions across various model types, including complex and non-linear models.

The SGO algorithm's ability to explore large, multi-dimensional spaces efficiently while avoiding local optima and handling diverse hyperparameter types makes it a powerful tool for hyperparameter selection. These advantages allow SGO to optimize model performance effectively and adapt to the unique challenges of each machine-learning problem.

This paper is organized as follows: In Section 2, relevant work is reviewed; in Section 3, the SGO algorithm is explained; in Section 4, methodology is introduced; in Section 5, the suggested SGO-optimized RF algorithm is described; in Section 6, Experimental Design, Results Analysis, and Discussions are presented; and in Section 7, conclusions and future research directions are presented.

2. Literature Review

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Over the past 20 years, the number of cases of breast cancer has almost doubled, making it one of the most prevalent malignancies identified in women globally. The International Agency for Research on Cancer (IARC) estimates that by 2040, the number of new cancer diagnoses may rise by about 50%, underscoring the necessity of improvements in diagnosis and detection to lower death rates [31]. The use of information and communication technology (ICT) for data mining and machine learning (ML) in early disease diagnosis is a significant breakthrough. ML algorithms offer substantial diagnostic support, which not only enhances efficiency but also has the potential to save lives through cost-effective and timely decision-making.

Numerous machine-learning algorithms have been evaluated for breast cancer prediction, with a focus on optimizing classification accuracy. Among the most promising are Support Vector Machie(SVM), RF, Logistic Regression (LR), Decision Tree (DT), and k-Nearest Neighbours (KNN). Each of these methods has shown substantial results on various datasets, including the SEER dataset, mammogram images, and the Wisconsin Breast Cancer Dataset (WBCD). For instance, SVM has been widely regarded as a top performer due to its high diagnostic accuracy across various studies. Sudarshan Nayak [32] found SVM to be superior for breast cancer classification, while Hiba Asri [33] reported 97.13% accuracy with SVM, displaying its precision and low error rate.

Other studies have highlighted the strength of the Relevance Vector Machine (RVM), with B.M. Gayathri [34] noting its low computational cost and impressive 97% diagnostic accuracy. More recent research by Youness Khoudfi and Mohamed Bahaj [35] revealed that SVM achieved a 97.9% accuracy using a Multilayer Perceptron (MLP) model with five layers and ten-fold cross-validation, outperforming other algorithms like KNN, RF, and Naïve Bayes. Comparative analyses also show strong results for other algorithms. Bazazeh and Shubair [36] achieved 97% accuracy with SVM, RF, and Bayesian networks using the WBCD, while SVM and KNN-based models reached 98.57% and 97.14% accuracy, respectively [37]. Naji et al. [38] explored a hybrid approach combining SVM, RF, LR, DT, and KNN, achieving an accuracy of 97.2%. Sharma et al. [39] validated the effectiveness of SVM, RF, and NB in breast cancer detection, reporting accuracies of 94.7%, 95.9%, and 94.47%, respectively. Similarly, Sengar et al. [40] presented a detection model with LR and DT, obtaining accuracies of 94.40% and 95.10%.

In summary, the SVM algorithm consistently demonstrates high accuracy for breast cancer prediction, often outperforming other models. However, RF and hybrid approaches combining multiple classifiers also provide competitive results, indicating that diverse ML techniques may be effective for early diagnosis in varied clinical settings. These findings underscore the role of ML in improving breast cancer detection accuracy and support its potential in clinical applications.

i) Heart disease

Research into heart disease prediction increasingly emphasizes the role of ML algorithms for enhancing diagnostic accuracy. Studies utilizing the UCI Heart Disease dataset, which contains 303 instances and 14 features, have demonstrated promising results across several ML methods. Logistic Regression (LR), while straightforward, remains effective for binary classification, achieving an accuracy of 85% according to Mohan et al. [41]. However, due to its linear nature, LR may struggle with complex, non-linear relationships within data. KNN, another commonly used technique, reached 86% accuracy in heart disease prediction, though it can be computationally intensive for larger datasets [42]. Artificial Neural Networks (ANNs) have also been highlighted for their predictive accuracy in medical applications, with backpropagation and multilayer perceptron (MLP) architectures improving upon existing models [43]. Studies using ANN in conjunction with UCI data have compared its performance to other methods, such as Decision Trees (DT), SVM, and Naive Bayes, with hybrid models achieving an F-measure of 86.8% [44]. Additionally, Convolutional Neural Networks (CNN) have been applied to ECG signal data for heart disease prediction without segmentation, using heart cycles from various start positions to extract features during both training and testing [45,46]. This CNN approach demonstrates that advanced feature extraction methods can improve accuracy significantly.

The breadth of machine learning techniques-ranging from Naïve Bayes, Generalized Linear Models, Logistic Regression, and RF to Gradient Boosted Trees, SVM, and hybrid approaches like HRFLM (hybrid RF with a linear model)-underscores the robust potential of ML and deep learning (DL) in accurately predicting heart disease [47,48]. The application of these diverse methods has helped reduce prediction costs and improved the reliability of diagnoses, displaying how ML innovations can make heart disease detection both effective and accessible.

ii) Diabetes

Numerous studies have used the Pima Indian Diabetes Dataset (PIDD), which contains information on 768 female patients and 9 variables, to apply machine learning to diabetes prediction. Alam et al. [49] achieved an accuracy of 75.7% with an Artificial Neural Network (ANN) on PIDD, while Sisodia et al. [50] applied Support Vector Machine (SVM), Naive Bayes (NB), and DT, finding NB to perform best with an accuracy of 76.3%. Tigga et al. [51] applied logistic regression and identified pregnancies, BMI, and glucose as the most influential predictors for diabetes. In a different approach, Diwani et al. [52] trained models using 10-fold cross-validation, testing Naive Bayes and decision

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tree algorithms in WEKA, which indicated Naive Bayes as the most accurate (76.3%). Zou et al. [53] applied feature reduction methods, such as Principal Component Analysis (PCA) and Minimum Redundancy Maximum Relevance (mRMR), before using RF, achieving 77.2% accuracy-the highest among studies reviewed. This body of research highlights the importance of both feature selection and careful choice of classifiers for improving predictive accuracy in diabetes risk, with ensemble methods and feature reduction showing significant promise for optimized performance.

iii) Kidney

Various studies have explored ML approaches for early diagnosis and prediction of chronic kidney disease (CKD) using diverse algorithms and datasets. Polat et al. [54] examined classifiers like kNN, NB, SVM, RF, and J48, and applied the k-means and Apriori algorithms to CKD diagnosis, achieving promising results. Ani et al. [55] utilized classifiers such as DT, NB, LDA, and kNN for CKD prediction, focusing on reducing CKD-related mortality. Wickramasinghe et al. [56] developed a dietary recommendation system for CKD patients, derived from medical records.Additional research by Charleonnan et al. [57] compared kNN, SVM, LR, and DT classifiers using CKD patient data, while Qin et al. [58] processed the CKD dataset from UCI with kNN imputation for missing data, achieving 99.75% accuracy with RF. Their optimized model combining LR and RF achieved 99.83% accuracy. Almasoud and Ward [59] emphasized minimal feature selection using ANOVA, Pearson's correlation, and Cramer's V, where gradient boosting achieved 99.1% accuracy, showing hemoglobin as a critical feature. These studies collectively underscore ML's potential for early CKD diagnosis, advancing healthcare decision-making in CKD management.

Moreover, the ability of ML to handle large, complex datasets with missing values further highlights its importance in healthcare. By combining multiple techniques such as ensemble methods, feature selection, and imputation strategies, researchers have successfully enhanced the prediction accuracy for CKD. The results from these studies provide valuable insights into how different classifiers can be tailored for specific CKD diagnosis tasks, thereby improving early detection and ultimately patient outcomes.

iv) Liver disease

Several studies have explored various ML algorithms for liver disease prediction. Algorithms such as Naive Bayes, DT, RF, SVM, KNN, LR, and Multilayer Perceptron (MLP) have been widely used in these studies. The F-Tree algorithm, combined with fuzzy K-means and feature selection methods, has shown high accuracy for liver disease prediction [60]. Feature selection, such as Particle Swarm Optimization (PSO), has been effective in improving model performance, with J48 performing well when coupled with PSO [61]. In terms of performance, MLP was found to have the highest precision, while Naive Bayes excelled in execution time in some studies [62]. The J48 and DT algorithms outperformed Naive Bayes in terms of accuracy, as demonstrated in [63]. LR and KNN also achieved good accuracy in liver disease prediction, with LR showing higher sensitivity in [64]. The combination of RF with oversampling techniques yielded the best results in [65]. Further research by [66] proposed new models for liver disease prediction. These studies used various classification methods, including RF, SVM, J48, and MLP, and employed normalization techniques and feature selection methods to improve accuracy. In particular, [66] explored the effectiveness of different classifiers on a liver disease dataset, while [67] proposed a hybrid approach using feature selection and classifiers to enhance prediction results. The studies demonstrated that no single algorithm consistently outperforms others, highlighting that performance varies depending on the dataset and evaluation metrics used, with MLP, RF, and SVM generally performing better in most scenarios.

3. SGO Algorithm

The Social Group Optimization (SGO) algorithm, proposed by Suresh Satapathy et al. [18.19], is an innovative optimization technique based on human social behavior. It simulates the learning and interaction between individuals in a group to solve complex optimization problems. SGO proceeds through two major stages: the Improving phase and the Acquiring phase.

i) Improving Phase

In this phase, each individual improves its knowledge by learning from the best individual in the population. This phase helps refine the individual's solution, promoting convergence toward better results. The mathematical model governing this stage is expressed as:

$$X_i^{new} = c.X_i^{old} + r_1.\left(X_{best} - X_i^{old}\right) \quad (1)$$

Where:

- X_i^{new} is the updated position (solution) of the i-th individual after the improvement.
- X_i^{old} is the previous position (solution) of the i-th individual.
- X_{best} refers to the best position (solution) found by any individual in the population.

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- c is a self-introspection parameter, typically a constant between 0 and 1, that influences the rate of learning.
- r_1 is a random number between 0 and 1, ensuring the algorithm introduces some randomness to avoid local optima.

This phase adjusts each individual's solution based on the best individual in the population, promoting convergence to a better solution.

ii) Acquiring Phase

In this phase, each individual interacts with another individual in the group. The interaction is designed to further refine the individual's solution by combining knowledge from the best individuals in the group. The mathematical model for this phase is given by:

- $X_i^{new} = \begin{cases} X_i^{old} + r_2.(X_i - X_k) + r_3.(X_{best} - X_i) & if\ f(X_i) < f(X_k) \\ X_i^{old} + r_2.(X_k - X_i) + r_3.(X_{best} - X_i) & otherwise \end{cases}$ ……(2)
- Where:
- X_i and X_k are the positions (solutions) of the i-th and k-th individuals, respectively.
- X_{best} is the position (solution) of the best individual in the population.
- $f(X_i)$ and $f(X_k)$ are the fitness values of the i-th and k-th individuals, respectively.
- r_2 and r_3 are random numbers between 0 and 1, which help to introduce diversity and exploration in the search process.
- In this phase, an individual's position is updated based on two factors:
- The difference between the individual and another individual in the population $(X_i - X_k)$.
- The difference between the individual and the global best solution $(X_{best} - X_i)$.

The algorithm evaluates the fitness of the two interacting individuals and adjusts their solutions accordingly. If the fitness of individual i is better than that of individual k, the update is based on the interaction between them and the best solution. If not, the update is based on the interaction between i and k with the best solution still influencing the update.

iii) Advantages of SGO

SGO is relatively simple compared to other optimization algorithms due to its clear two-phase structure. The algorithm emphasizes self-improvement and knowledge acquisition to explore the search space and converge toward a global optimum. Each solution undergoes iterative improvements, where the individual continuously learns and adapts based on the knowledge of the best-performing individuals in the group. This approach is particularly useful in avoiding local minima and improving the overall convergence rate.

The pseudo-code for SGO clarifies the detailed steps involved in each phase, highlighting its robust mechanism for optimizing complex problems. SGO is an effective optimization technique, combining social behavior modeling with individual learning and interaction, leading to efficient problem-solving capabilities.

Algorithm 1 Pseudocode of SGO

1. Initialize Parameters:

- Set function evaluations (FEs) to 0

- Define maximum function evaluations (MaxFEs)

- Define population size (N) and dimension of each individual (D)

- Set self-introspection parameter (c)

2. Initialize Population:

- Generate the initial population of search agents

- Calculate fitness of each agent and identify the best solution as gbest

3. Optimization Loop:

- While FEs < MaxFEs:

4. Improving Phase:

- For each search agent in the population:

- Update position (X_new) using Eq. (1)

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- If X_new goes out of the search space, reinitialize it within the search space
- Calculate the fitness of X_new
- If the fitness of X_new is better than the previous position (X_old), update X_old with X_new

- End for loop

5. Acquiring Phase:

- For each search agent:
- Select another random individual from the population
- Update position (X_new) using Eq. (2)
- If X_new goes out of the search space, reinitialize it within the search space
- Calculate the fitness of X_new
- If the fitness of X_new is better than X_old, update X_old with X_new

- End for loop

6. Update Global Best:

- Identify and update the best search agent in the population as gbest

- End While loop

7. Return gbest as the optimal

4. Methodology

The main objective of this experiment is to identify an effective and accurate algorithm for detecting multiple chronic diseases, with the proposed structure detailed in Figure Fig 1. To accomplish this, we utilized a machine learning classifier, RF, and optimized its hyperparameters using the Social Group Optimization (SGO) metaheuristic algorithm. This optimization is aimed at selecting an optimal parameter set to improve model accuracy for each chronic disease.

Our methodology begins with data acquisition, followed by pre-processing, which involves two key steps: data cleaning and attribute selection. We employed a heatmap to detect collinearity, enabling us to retain only essential features. The preprocessed data was then used to build RF models capable of predicting chronic diseases based on new input measurements.

Before training the RF model, we tuned its hyperparameters using the SGO algorithm to find an optimal set of parameters. To assess the model's performance, we split the dataset into 80% for training and 20% for testing using the train_test_split method. The model was trained on the training set (80%) and then evaluated on the test set (20%) to determine its predictive accuracy. After testing, we generated a confusion matrix and calculated additional performance metrics such as accuracy, precision, recall, and F1 score to thoroughly evaluate the model's effectiveness.

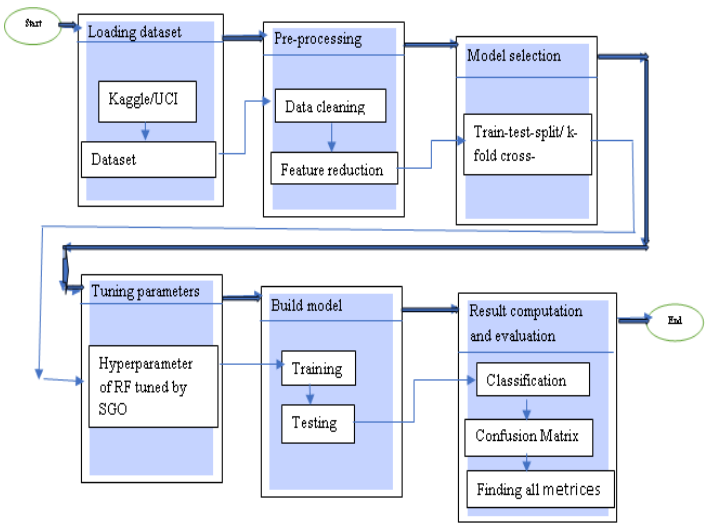

Figure 1. The proposed architecture for Multi Chronic Disease Prediction

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A. Feature selection process

One important strategy for raising any classifier's performance is feature reduction. Overall training and prediction time could be decreased with feature reduction.

Only the most important features from the original datasets were chosen in this step. These attributes were then analyzed for testing and training. The outcomes of categorization are significantly impacted by these methods [68]. Here Correlation Heatmap has been used to reduce the number of features of the dataset.

B. Correlation heatmap

Correlation helps assess how closely two or more variables move together. When two variables have a high correlation, it indicates that the independent variable has a significant impact on the dependent one. Depending on whether the variables move in tandem, in opposition to one another, or not at all, correlation values might be positive, negative, or zero. A high correlation between two independent variables is undesirable because of possible redundancy, even when a large correlation between a dependent and independent variable is beneficial.

A correlation heatmap visually displays the correlation coefficients across multiple variables in a dataset. This tool facilitates the identification of patterns, multicollinearity, and feature dependencies by indicating the direction and degree of correlations between variables. The correlation coefficient measures linear relationships, ranging from -1 to 1:

- 1 represents a perfect positive correlation (both variables increase proportionally).
- -1 indicates a perfect negative correlation (one variable increases as the other decreases).
- 0 signals no linear relationship.

Detecting multicollinearity involves identifying feature pairs with high correlation coefficients (close to 1 or -1), as multicollinearity can impact the interpretability and performance of machine learning models. Highly correlated features often convey similar information, so removing one of these features can simplify the model while maintaining its predictive strength. In this experiment, we applied a correlation threshold of 0.8, meaning that when the correlation coefficient between two features exceeds 0.8, one feature is removed. This approach reduces dataset dimensions, leaving only essential features, and thus improves model efficiency.

C. Performance metrics: Confusion matrix, and Evaluation Metrics

True Negative (TN), False Positive (FP), False Negative (FN), and True Positive (TP) are the four components of the confusion matrix, a 2x2 matrix used to assess the performance of classification models. They are positioned at (1,1), (1,2), (2,1), and (2,2), respectively. This matrix divides the predicted outcomes of a classification model into four categories:

- True Negative (TN): Negative cases that are correctly classified.
- False Positive (FP): Positive cases that are incorrectly classified.
- False Negative (FN): Negative cases that are incorrectly classified.
- True Positive (TP): Positive cases that are correctly classified.

Evaluation Metrics

Accuracy:

Accuracy measures the proportion of all correct predictions relative to the total predictions made.

Accuracy= $\frac{TP+TN}{TP+TN+FP+FN}$

Precision:

Precision, also known as positive predictive value, measures the proportion of predicted positive cases that are actually positive. It indicates the accuracy of positive predictions.

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

Recall:

Recall, also referred to as sensitivity or true positive rate, and represents the proportion of actual positive cases that are correctly predicted by the model.

Recall(Sensitivity) =$\frac{TP}{TP+FN}$

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Specificity:
Specificity measures the proportion of actual negative cases that are correctly identified by the model. It is also known as the true negative rate.

$$\text{Specificity}=\frac{TN}{TN+FP}$$

F1 Score:

The F1 Score provides a single statistic that combines precision and recall by taking the harmonic mean of the two. It is particularly helpful in situations where both recall and precision are crucial, or where there is an unequal distribution of classes.

$$\text{F1 score} = 2 \times \frac{Precision \times Recall}{Precision + Recall}$$

5. Proposed SGO-optimized RF model

To employ SGO for optimizing RF model hyperparameters, it is crucial to identify the most promising ones. The performance of RF models hinges greatly on its hyperparameters like Number of Trees (n_estimators), Maximum Depth of Trees (max_depth), Minimum Samples Split (min_samples_split), Minimum Samples per Leaf (min_samples_leaf), Maximum Features (max_features), Bootstrap Sampling (bootstrap), and criterion. There are many other parameters for RF but in our research, we have considered only these seven parameters. Fig 2 displays how RF model has been converted into decision vector or population for SGO algorithm.

n_estimators	max_depth	min_samples_split	min_samples_leaf	max_features	bootstrap	criterion

Figure 2. Converting a RF model into a decision vector (population).

All hyperparameters are discrete-valued. Regarding the bootstrap and criterion, we have explored two alternatives each, encompassing True and False for bootstrap, and entropy and gini for criterion range from 0 to 1 respectively.

Number of Trees (n_estimators) count is confined between 10 and 1000. Maximum Depth of Trees (max_depth), range from 5 to 50. Minimum Samples Split (min_samples_split) ranges from 2 to 10. Minimum Samples per Leaf (min_samples_leaf) and Maximum Features (max_features) range from 0 to number of features in the dataset. When decoding this, we use the rounded-off value of the decision variable.

Algorithm 2: Decode a Decision Vector to RF Model

Input: Decision vector V = [v (1), v(2),⋯, v(d)], where d=7

Output: Optimized RF model

```
FUNCTION decode_decision_vector_to_RF_model(V):
FUNCTION get_criterion_function (v):
var = ROUND(v)
SWITCH var:
CASE 0: RETURN "entropy"
CASE 1: RETURN "gini"
FUNCTION get_bootstrap_function (v):
var = ROUND(v)
SWITCH var:
CASE 0: RETURN "True"
CASE 1: RETURN "False"
FUNCTION get_hyperpara_value(V) :
RF = RandomForestClassifier (
n_estimators=round(V[0]),
max_depth=round(V[1]),
min_samples_split=round(V[2]),
min_samples_leaf=round(V[3]),
max_features=round(V[4]),
bootstrap=get_bootstrap_function(V[5]),
criterion=get_criterion_function(V[6]),
random_state=42 )
RF.fit(X_train,y_train)
```


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```
23. y_pred=RF.predict(X_test)
24. # Evaluate the model
25. accuracy = accuracy_score(y_test, y_pred)
26. return 1 – accuracy, RF
```

Algorithm 2 details the process of decoding a decision vector V into a RF model. The decision vector V utilizes real encoding, as exemplified in Fig 3, to represent the RF structure within the SGO algorithm. Based on the provided specifications and the encoding scheme outlined in Algorithm 2, let's break down the configuration of the encoded RF model with its hyperparameter value:

RF:

n_estimators=276,

max_depth=17,

min_samples_split=2,

min_samples_leaf=1,

max_features=1,

bootstrap='True'

criterion='entropy'

276.45	16.80	2.00	1.00	1.00	0.1878	0.089

Figure 3. An instance of an actual RF model encoded with its hyperparameters.

Algorithm 3: Procedure for SGO-optimized RF Model

Input: Input ((*X*), and Target (*y*).

Output: Optimized RF model with near-optimal hyperparameters.

Initialization:

Set up the parameters of the SGO algorithm: population size, self-introspection parameter c-0.2. decision variable count in each decision vector (dim), maximum generations (max_gen), and the upper and lower bounds of decision variables.

Partition the input and target patterns into train, and test sets.

Population Initialization:

Randomly initialize the population size and decision vector count from a uniform distribution within the upper and lower bounds of decision variables.

Each decision vector represents a RF model with associated hyperparameters.

Set the dimension (*dim*) in a decision vector to 7, where 7 hyperparameters correspond to n_estimators, max_depth, min_samples_split, min_samples_leaf, max_features, bootstrap, criterion for RF model.

Fitness Calculation:

Decode each decision vector to obtain corresponding RF model using Algorithm 2.

Calculate the fitness of each RF model, measured by accuracy and then find error as 1- accuracy

Global Best Determination:

Determine the decision vector (person) with the best error (gbest).

Iteration:

While termination criteria (e.g., reaching max_gen) are not satisfied, repeat the following steps:

For each decision vector (person) in the population:

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Perform the Improving phase to compute a new decision vector.

Conduct selection between the old and new decision vectors based on fitness.

Move the better decision vectors selected in the Improving phase to the Acquisition phase.

For each decision vector (person) in the population:

Execute the Acquiring phase to compute a new decision vector.

Perform selection between the old and new decision vectors based on fitness.

Next Generation:

Advance the better vector between the old and new decision vectors to the next generation.

Global Best Update:

Update gbest person.

Termination:

End the while loop when termination criteria are met.

Final Model Decoding:

Employ Algorithm 2 to interpret the decision vector from the last generation with the highest fitness, obtaining the optimized RF model with its corresponding hyperparameters.

Use this optimized RF model to make predictions on the test set and assess its performance.

Algorithm 3 outlines the methodology of the proposed SGO-optimized RF model, leveraging the SGO algorithm to optimize the hyperparameters of a RF model for supervised tasks. The algorithm accepts inputs such input data (X), and target data (y), and outputs the near-optimal hyperparameters of the RF model together with its performance outcomes on the test set. It consists of three main steps: Initialization, Iteration, and Final step. During the Initialization step, the SGO decision vector and the upper and lower bounds of decision variables are initialized. The input and output patterns are divided as train, and test sets. The initial population is created randomly, where (P_size) decision vector count are created from a uniform distribution, with the values falling within the limits of the respective decision variables. Each decision vector represents a RF model with associated hyperparameters. This includes 7 hyperparameters. Each decision vector is decoded using Algorithm 2 to obtain the RF model, and its fitness is evaluated by training on the train set and assessing performance on the test set.

The aim of the fitness function $f(V_i)$ (as described in Eq.

(5)) is to reduce it utilizing decoded RF model and its corresponding hyperparameters denoted by the ith decision vector V_i. Following the generation of the initial population and the evaluation of every decision vector's fitness, the iteration step begins. During this phase, the improving and acquiring phases of the SGO algorithm are applied iteratively to produce subsequent generations. This iterative process persists until a termination criterion, such as reaching the maximum generation count, is fulfilled. Upon fulfilling the termination criterion, the last step entails identifying the optimal vector from the ultimate population, representing the RF model with the optimal structure and associated hyperparameters. This optimized model is then employed to forecast the test set, and its performance is evaluated. For clarity, the graphical abstract of the proposed SGO-optimized RF method is presented in Fig. 4. This visual depiction offers a concise overview of the iterative procedure involved in optimizing the RF hyperparameters using the SGO algorithm.

$$\min_{V_i} f(V_i) \qquad \text{……..(3)}$$

Subjected to $L_j \leq V_{i,j} \leq U_j$

where f(•) denotes the (1-accuracy) utilizing the RF Model with hyperparameters encoded in V_i, L_j and U_j denotes the lower and upper bounds of the jth hyper-parameter.

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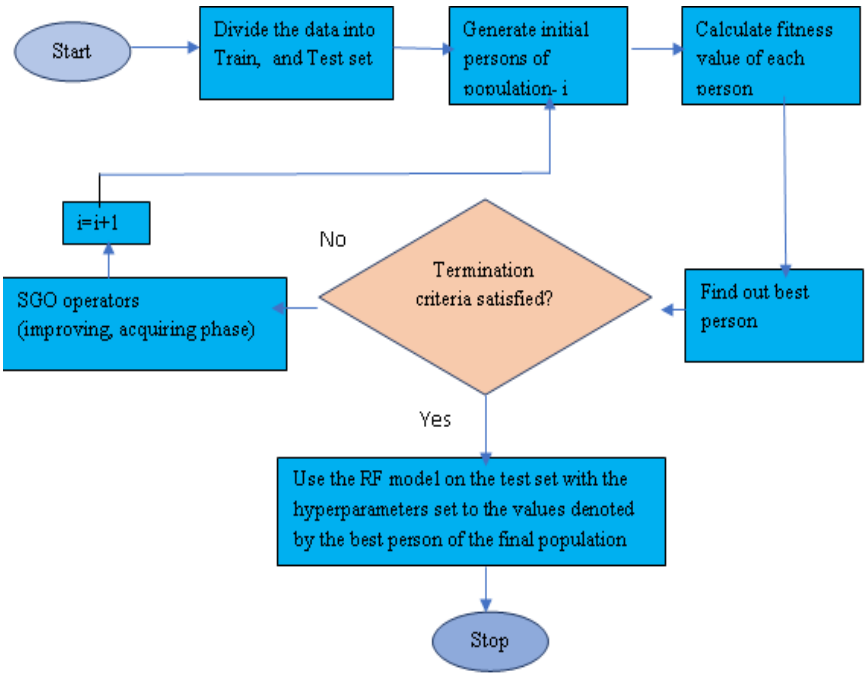

Figure 4. Graphical abstract of proposed SGO-optimized RF Model

6. Proposed Experimental Design, Results Analysis, and discussions

A. Machine Learning Library

The experiments on the ML techniques discussed in this study were conducted using Python, and the Scikit-learn library, commonly known as sklearn, which is a free package for machine learning [69]. This study also utilized various scientific computing libraries, including Scikit-learn [70], NumPy [71], matplotlib [72], pandas [73], and seaborn [74], to support the analysis and implementation.

B. Datasets

In this section, we assess the classification performance of the proposed SGO-optimized RF model using five Chronic Disease datasets and compare it against state-of-the-art classifiers. The datasets include Breast Cancer Wisconsin Diagnostic dataset, Liver disease dataset, Heart disease dataset, Diabetes dataset, and Kidney disease dataset. The Table 1 presents a summary of the characteristics of these five datasets in terms of number of instances, number of features, number of classes, class information and dataset url.

Table 1: Overview of the chronic disease datasets used for performance evaluation of SGO-optimized RF model

S. no.	Datasets	No of instances	No of features	No of classes	Class information	Resources
1	Breast Cancer Wisconsin Diagnostic dataset	69	31	2	Benign: 357 Malignant: 212	https://www.kaggle.com/datasets/uciml/breast-cancer-wisconsin-data
2	Indian Liver Patient dataset	83	10	2	1: 416 2: 167	https://archive.ics.uci.edu/dataset/225/ilpd+indian+liver+pati
3	Heart disease	303	13	2	1: 165 0:138	https://archive.ics.uci.edu/dataset/45/heart+disease
4	Pime Indian Diabates dataset	768	8	2	0: 500 1: 268	https://www.kaggle.com/datasets/uciml/pima-indians-
5	Kidney diseases	400	25	2	Ckd: 250 Notckd: 150	https://www.kaggle.com/datasets/mansoordaku/ckdisease

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C. Confusion matrix obtained by SGO- optimized RF

Table 2 provides the confusion matrix for SGO- optimized RF on Breast Cancer Wisconsin Diagnostic dataset, Indian Liver Patient dataset, Heart Disease dataset, Pime Indian Diabates dataset, and Kidney Diseases dataset.

Table 2: Confusion matrix

Sl. no	Dataset	True Negative (TN)	False Positive (FP)	False Negative (FN)	True Positive (TP)
1	Breast Cancer Wisconsin Diagnostic dataset	69	0	2	43
2	Indian Liver Patient Dataset	81	6	12	18
3	Heart Disease dataset	29	0	4	28
4	Pime Indian Diabates dataset	88	11	16	39
5	Kidney diseases dataset	52	0	0	28

D. Optimized set of hyperparameters obtained by SGO-optimized RF

Table 3 provides the Optimized set of hyperparameters obtained by SGO-optimized RF method on the Breast Cancer Wisconsin Diagnostic dataset, Indian Liver Patient dataset, Heart Disease dataset, Pime Indian Diabetes dataset, and Kidney Diseases dataset.

Table 3: Optimized set of hyperparameters obtained by SGO-optimized RF method

Hyperparameters	Breast Cancer Wisconsin Diagnostic dataset	Indian Liver Patient dataset	Heart Disease dataset	Pime Indian Diabetes dataset	Kidney Diseases dataset
n_estimators	63	15	10	10	195
max_depth	8	17	8	18	5
min_samples_split	2	10	2	6	2
min_samples_leaf	7	1	2	11	8
max_features	1	1	1	1	1
bootstrap	True	True	True	True	True
criterion	Gini	Entropy	Gini	Entropy	Entropy

E. Simulation Results: Performance Comparisons in Predicting Five Chronic Diseases

a) Breast Cancer Wisconsin Diagnostic Dataset

Table 4 displays the accuracy, precision, recall and F1score achieved by proposed SGO- optimized RF and various peer methods such as SVM[75], RF[75],LR[75], DT[75], KNN[75], RF[76],NB[76] on Breast Cancer Wisconsin Diagnostic dataset. Fig 5 illustrates the performance analysis provided by them.

Table 4: Comparison of various methods with the proposed methods on Breast Cancer Wisconsin Diagnostic dataset

ML methods	Accuracy	Precision	Recall	F1-measure
RF[76]	0.947	–	–	–
NB[76]	0.825	–	–	–

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SVM[75]	0.972	0.98	0.94	0.96
RF [75]	0.965	0.96	0.94	0.95
LR [75]	0.958	0.98	0.91	0.94
DT [75]	0.951	0.94	0.92	0.93
KNN [75]	0.937	0.92	0.91	0.91
SGO-optimized RF	0.983	1.0	0.956	0.977

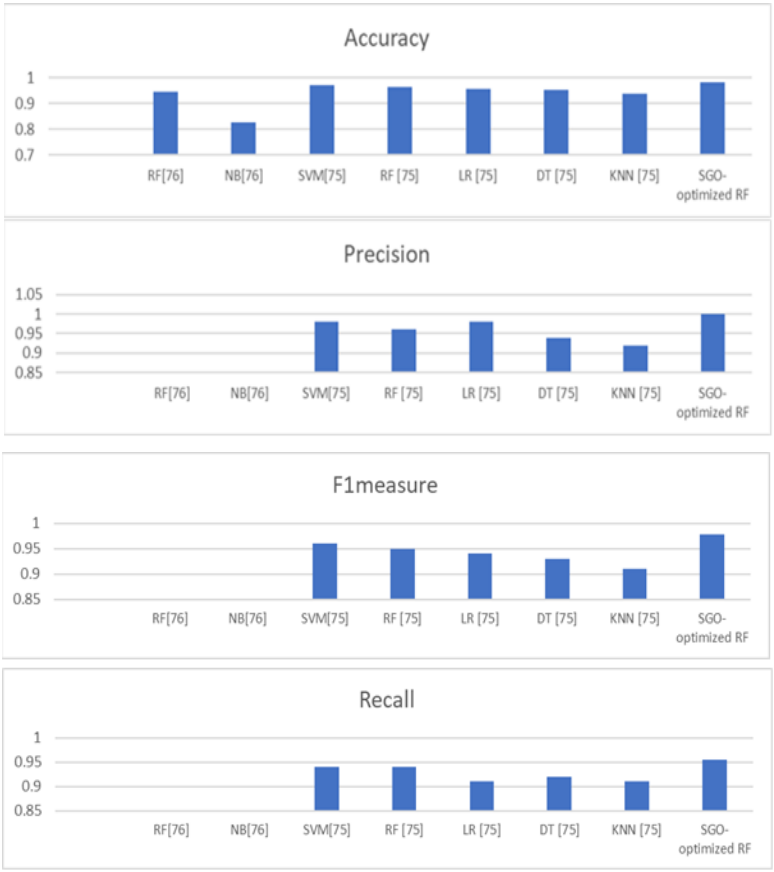

Figure 5: Graphical presentation of the performance provided by various methods on Breast Cancer Wisconsin Diagnostic dataset

Discussion

The analysis table shows the effectiveness of several ML methods for classifying breast cancer cases using the Wisconsin Diagnostic dataset. It includes traditional ML methods, ensemble methods, and an SGO-optimized RF algorithm, assessing them based on accuracy, precision, sensitivity, and F1-measure.

RF [76] achieved an accuracy of 0.947, but precision, sensitivity, and F1-measure were not provided, which limits a complete performance comparison. RF [75], with a more comprehensive metric profile, reached an accuracy of 0.965, with 0.96 precision, 0.94 sensitivity, and an F1-measure of 0.95. This combination suggests RF is highly effective at distinguishing between malignant and benign cases. NB [76] scored the lowest in accuracy at 0.825, which suggests limited performance for this dataset. Its simpler probabilistic model may struggle with complex patterns often present in medical data, which could explain its lower performance compared to other methods. SVM [75] performed exceptionally well, achieving an accuracy of 0.972. It also maintained a high precision of 0.98 and sensitivity of 0.94,

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resulting in an F1-measure of 0.96. This balance highlights SVM's robustness in classifying breast cancer cases effectively, making it one of the most reliable methods after the SGO-optimized RF. LR [75] showed a balanced performance with 0.958 accuracy, 0.98 precision, 0.91 sensitivity, and an F1-measure of 0.94. The high precision indicates fewer false positives, while its slightly lower sensitivity could miss some positive cases. This trade-off makes LR suitable for diagnostic support, although it may underperform compared to SVM and RF for datasets requiring higher sensitivity. DT [75] achieved an accuracy of 0.951, with precision at 0.94 and sensitivity at 0.92. These results are competitive, but DT's tendency to overfit can lead to limitations in generalizability. Nonetheless, it provides a valuable benchmark in interpretability, making it useful in scenarios where model transparency is essential. KNN [75] showed moderate performance with an accuracy of 0.937, precision of 0.92, and sensitivity of 0.91. While KNN is simpler and often intuitive, it requires careful tuning, and its performance may drop with high-dimensional datasets like those in medical diagnosis. The SGO-optimized RF achieved the highest accuracy at 0.9825, with a perfect precision of 1.0, a sensitivity of 0.9556, and an F1-measure of 0.9773. This indicates not only a near-perfect classification rate but also a balance between detecting all positive cases (sensitivity) and minimizing false positives (precision). These results affirm the advantage of integrating SGO, which optimizes RF's parameters, thus enhancing its predictive performance.

b) Indian Liver Patient dataset

Table 5 displays the accuracy, precision, recall and F1 score achieved by proposed SGO- optimized RF and accuracy provided by various peer methods such as SVM [77], RF [76], LR [77], and KNN [77] on Indian Liver Patient Dataset. Fig 6 illustrates the performance analysis provided by them.

Table 5: Comparison of various methods with the proposed methods on Indian Liver Patient dataset

ML methods	Accuracy	Precision	Sensitivity	F1measure
RF[76]	0.79	–	–	–
LR [77]	0.76	–	–	–
SVM [77]	0.72	–	–	–
KNN[77]	0.80	–	–	–
SGO-optimized RF	0.85	0.75	0.6	0.67

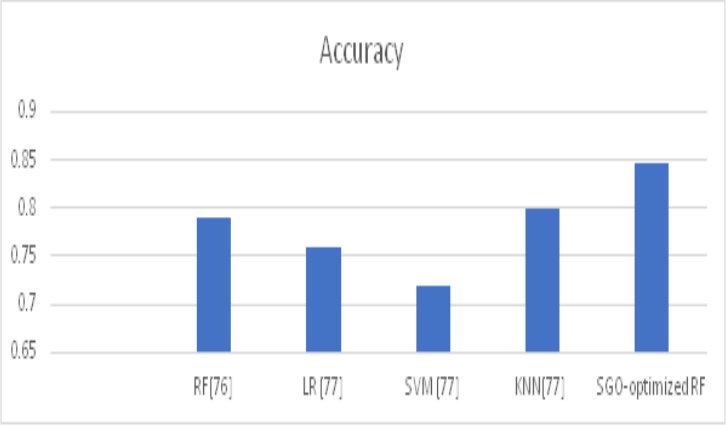

Figure 6. Graphical presentation of the performance provided by various methods on Indian Liver Patient dataset

Discussion

The presented table compares various ML methods applied to the Indian Liver Patient dataset. The comparison highlights the strengths and weaknesses of traditional ML algorithms and an SGO-optimized RF model, which is proposed for improved performance. Key observations from the results are as follow:

RF [76] achieved an accuracy of 0.7897 but lacked specific metrics such as precision, sensitivity, and F1-measure. While RF generally performs well in handling imbalanced datasets, the lack of complete evaluation limits its comparative analysis. LR [77] obtained an accuracy of 0.76, slightly below RF. This indicates LR's potential for linear decision

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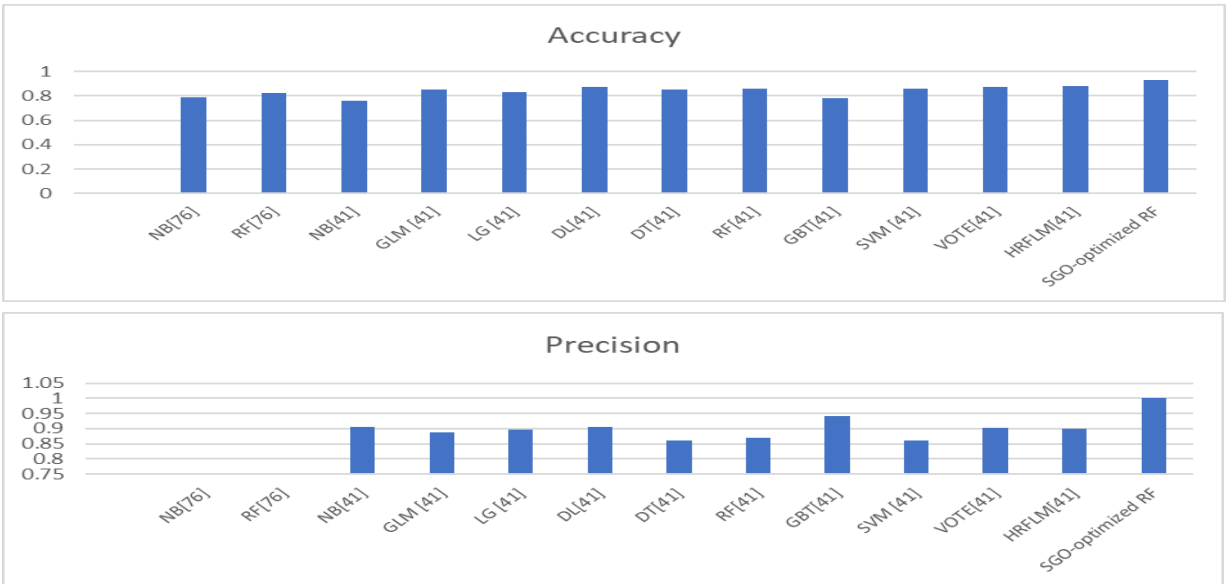
boundaries, but its performance may degrade in datasets with complex patterns, such as liver disease cases. SVM[77] performed with an accuracy of 0.72, the lowest among the evaluated methods. While SVM is robust for small datasets and can handle non-linear relationships with kernel tricks, its performance on this dataset suggests potential challenges in capturing the patterns necessary for liver disease classification. KNN [77] outperformed traditional methods with an accuracy of 0.80, indicating its suitability for this dataset. Its instance-based approach might have allowed it to effectively capture localized decision boundaries. The proposed SGO-optimized RF achieved the highest accuracy of 0.8462. Its additional metrics - 0.75 precision, 0.6 sensitivity, and 0.6667 F1-measure - further emphasize its balanced performance in identifying both true positives and minimizing false positives. The use of SGO for parameter optimization likely improved RF's ability to generalize and adapt to the dataset's characteristics, making it the most effective method.

c) Heart Disease dataset

Table 6 displays the accuracy, precision, recall and F1 score achieved by proposed SGO- optimized RF and various peer methods such as NB[76], RF[76], NB[41], Generalised linear model(GLM)[41],LG[41], Deep Learning(DL)[41], DT[41], RF[41], Gradient Boosted trees(GBT)[41], SVM[41], VOTE[41], hybrid RF with a linear model (HRFLM)[41] on Heart Disease dataset. Fig 7 illustrates the performance analysis provided by them.

Table 6: Comparison of various methods with the proposed methods on Heart Disease dataset

ML methods	Accuracy	Precision	Sensitivity	F1measure
NB[76]	0.79	–	–	–
RF[76]	0.8225	–	–	–
NB[41]	0.758	0.905	0.798	0.845
GLM [41]	0.851	0.888	0.949	0.916
LG [41]	0.829	0.896	0.911	0.902
DL[41]	0.874	0.907	0.95	0.926
DT[41]	0.85	0.86	0.988	0.918
RF[41]	0.861	0.871	0.988	0.924
GBT[41]	0.783	0.941	0.807	0.868
SVM [41]	0.861	0.861	1	0.925
VOTE[41]	0.874	0.902	–	0.844
HRFLM[41]	0.884	0.901	0.928	0.90
SGO-optimized RF	0.934	1	0.875	0.9333



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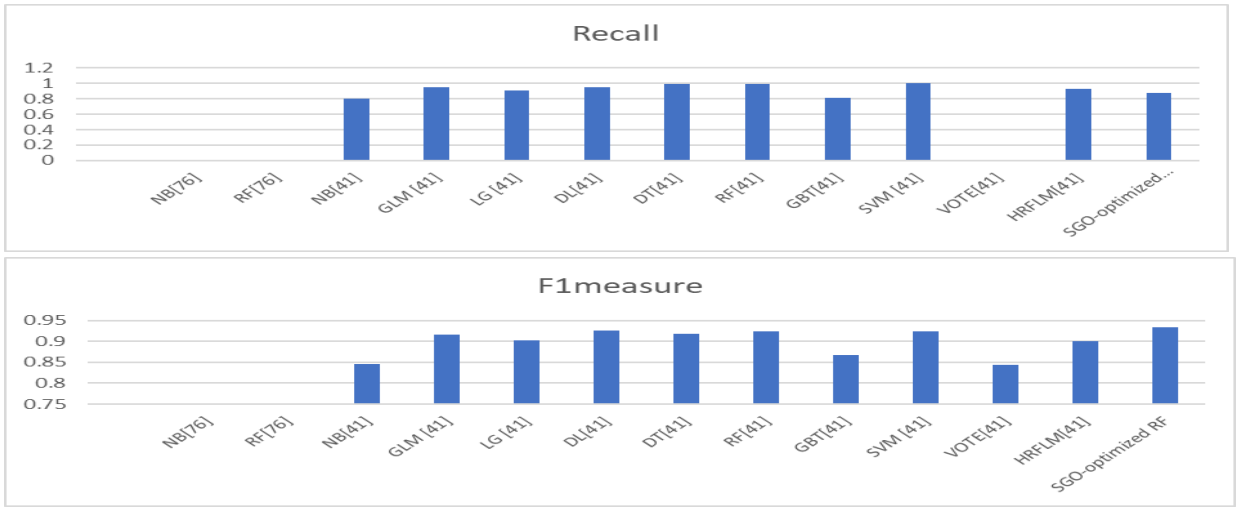

Figure 7. Graphical presentation of the performance provided by various methods on Heart Disease dataset

Discussion

The table presents a comparative analysis of accuracy, precision, recall, and F1 scores achieved by various ML methods and the proposed SGO-optimized RF model on the Heart Disease dataset. Key insights from the comparison are as follows:

Naive Bayes (NB) and RF from reference [76] achieved moderate accuracy levels of 0.79 and 0.8225, respectively, though without available precision, sensitivity, and F1 measures. These accuracies show a reliable but lower performance in comparison to more complex models, suggesting limitations in these standard methods for Heart Disease prediction. NB [28] achieved 0.758 accuracy, with good precision (0.905) but relatively lower sensitivity (0.798). The F1 score of 0.845 reflects that while NB has high predictive precision; its sensitivity is limited for this dataset. GLM [41] achieved high accuracy (0.851) and balanced performance across metrics, indicating its strong capability for linear relationships in medical prediction tasks. LG [41] showed comparable accuracy (0.829) with a strong F1 score (0.902), proving its efficiency in handling binary classification problems. DL [41] reached 0.874 accuracy and excelled in both sensitivity (0.95) and F1 measure (0.926), highlighting its ability to capture complex patterns in the data. DT [41] and RF [41] achieved similar accuracy (0.85 and 0.861, respectively), with RF slightly outperforming DT in F1 score. These methods demonstrated reliability but were outperformed by approaches that are more complex in sensitivity. GBT [41] displayed moderate accuracy (0.783) and strong precision (0.941), though with reduced sensitivity (0.807), indicating it is more conservative in positive predictions. SVM [41] reached 0.861 accuracy and achieved perfect sensitivity (1), but it was slightly lower in precision (0.861), making it highly sensitive but potentially over-predicting positives. VOTE [41] and HRFLM [41] achieved accuracies of 0.8741 and 0.884, respectively, with balanced metrics. HRFLM demonstrated high precision (0.901) and sensitivity (0.928), indicating effective ensemble learning. The proposed SGO-optimized RF achieved the highest accuracy (0.9344) among all methods, with a perfect precision score of 1. This indicates it accurately predicts positive cases with minimal false positives. With a sensitivity of 0.875, it effectively identifies true positives, and the high F1 score (0.9333) signifies an optimal balance between precision and recall. The optimization through SGO likely enhanced the RF's parameter tuning and feature selection, enabling it to better capture complex patterns in the Heart Disease dataset.

d) Pima Indian Diabetes Dataset

Table 7 displays the accuracy, precision, recall and F1 score achieved by proposed SGO- optimized RF and various peer methods such as LG[78], RF[78], SVM[78], DT[79], RF[79], NB[79], LG[79],KNN[79], SVM[79] on Pima Indian Diabetes dataset. Fig 8 illustrates the performance analysis provided by them.

Table 7: Comparison of various methods with the proposed methods on Pima Indian Diabetes dataset

ML methods	Accuracy	Precision	Recall	F1-measure
LR [78]	0.7913	0.8571	0.5455	0.6667
RF [78]	0.7739	0.8000	0.5455	0.6486
SVM [78]	0.7565	0.8077	0.4773	0.6000

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DT [79]	0.7314	0.735	0.731	0.733
RF[79]	0.7714	0.779	0.771	0.774
NB[79]	0.7828	0.787	0.783	0.785
LR [79]	0.7885	0.788	0.789	0.788
KNN[79]	0.7942	0.804	0.794	0.798
SVM[79]	0.7771	0.774	0.777	0.775
SGO-optimized RF	0.8247	0.78	0.7091	0.7427

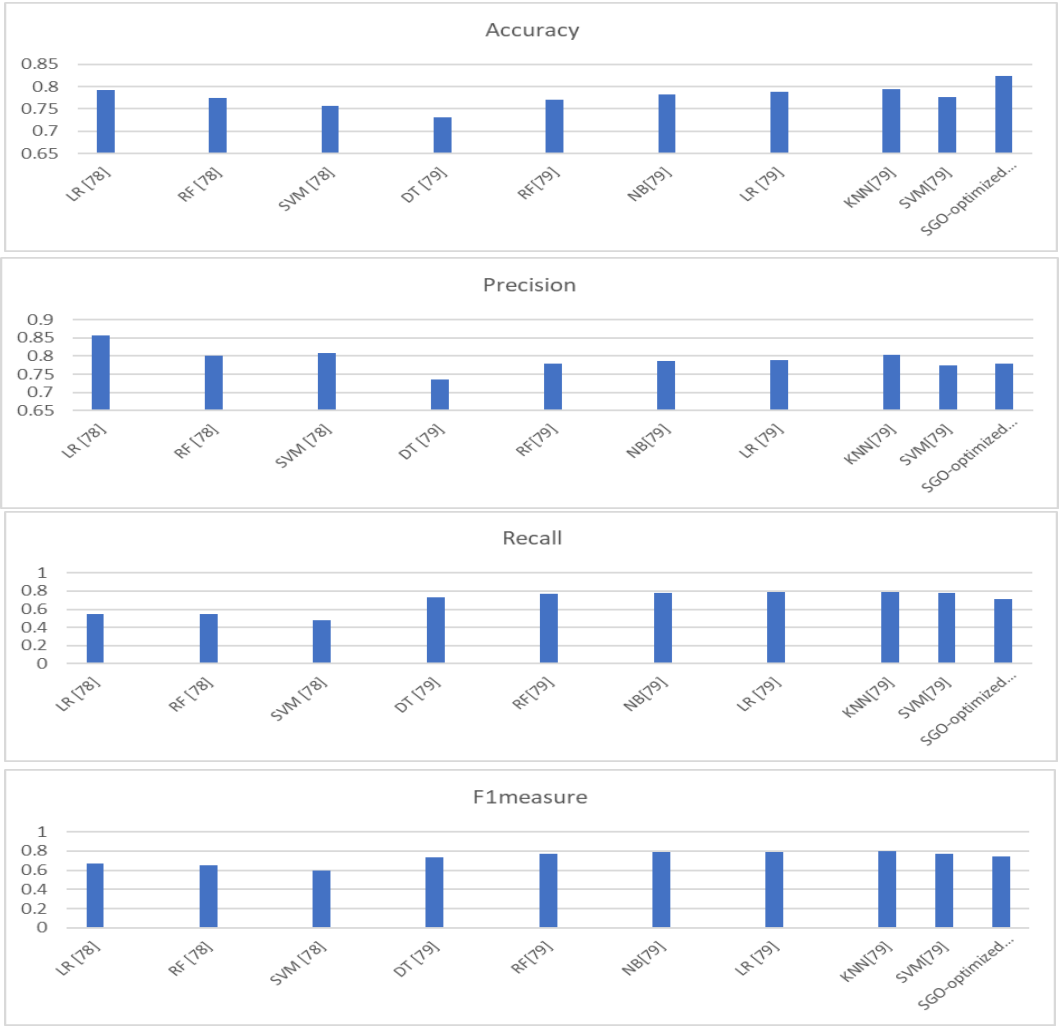

Figure 8. Graphical presentation of the performance provided by various methods on Pima Indian Diabetes dataset

Discussion

The table highlights a comparative analysis of accuracy, precision, recall, and F1 scores achieved by various machine learning methods and the proposed SGO-optimized RF model for the Pima Indian Diabetes dataset. Below are the insights derived from this data:

Logistic Regression [78] achieved an accuracy of 0.7913, with precision (0.8571) significantly higher than sensitivity (0.5455). The F1 score (0.6667) reflects an imbalance, indicating that while LR is precise in positive predictions, it misses a substantial proportion of true positives. RF [78] and SVM [78] showed slightly lower accuracies (0.7739 and 0.7565) compared to LR. RF had better F1 performance (0.6486) than SVM (0.6000), likely due to its ensemble structure enabling better generalization. DT [79] showed the lowest accuracy (0.7314), precision (0.735), sensitivity (0.731), and

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F1 measure (0.733). This result demonstrates DT's limitations in handling complex patterns without ensemble techniques. RF [68] improved upon DT, with an accuracy of 0.7714 and balanced precision (0.779), sensitivity (0.771), and F1 score (0.774), displaying RF's strength in boosting DT's individual predictions. NB [79] slightly outperformed RF in accuracy (0.7828) and F1 measure (0.785), highlighting its probabilistic nature in handling imbalanced datasets. LR [79] achieved 0.7885 accuracy, with well-aligned metrics (precision, sensitivity, F1 ≈ 0.788), reflecting its robustness for this dataset. KNN [79] achieved the highest accuracy (0.7942) among the baseline methods, with strong performance across all metrics. Its reliance on local data patterns contributed to this outcome. SVM [79] performed comparably to RF, with 0.7771 accuracy and closely aligned metrics, demonstrating its effectiveness in hyperplane-based classification. 3. Proposed SGO-Optimized RF achieved the highest accuracy (0.8247) among all methods, significantly outperforming from above methods. Precision (0.78): Indicates the model minimizes false positives effectively. Sensitivity (0.7091): Shows that the method reliably identifies true positives, although slightly lower compared to precision. F1 Score (0.7427): Demonstrates a strong balance between precision and sensitivity, suggesting a robust predictive capability for diabetes diagnosis. The SGO-optimized RF's superior accuracy reflects its enhanced ability to identify optimal feature subsets and hyperparameters using SGO. This optimization aids in capturing complex interdependencies within the dataset, which baseline methods may miss. While KNN exhibited competitive accuracy (0.7942), its lack of optimization and dependency on parameter tuning (like k) prevents it from reaching the same level of performance as the proposed method. Logistic regression's strong precision across datasets highlights its strength in linear reparability, but its lower sensitivity compared to the SGO-optimized RF underscores its limitation in capturing nonlinear patterns.

e) Chronic Kidney disease dataset

Table 8 displays the accuracy, precision, recall and F1score achieved by proposed SGO- optimized RF and various peer methods such as AdaBoost, DT, XgBoost, CatBoost, KNN, RF, NB, Gradient Boosting(GB), Stochastic gradient boosting(SGB), LGBM, Extra Tree, SVM, and ANN on Chronic Kidney disease dataset. All these methods are referred from [80]. Fig 9 illustrates the performance analysis provided by them.

Table 8: Comparison of various methods with the proposed methods on Chronic Kidney Disease dataset

methods	Accuracy	Precision	Sensitivity	F1-measure
AdaBoost[80]	0.983	0.98	0.98	0.98
DT [80]	0.975	0.98	0.97	0.97
XgBoost [80]	0.9916	0.99	0.99	0.99
CatBoost [80]	0.975	0.98	0.97	0.97
KNN[80]	0.59	0.58	0.59	0.59
RF [80]	0.975	0.98	0.97	0.97
NB [80]	0.8833	0.89	0.88	0.88
GB [80]	0.975	0.98	0.97	0.97
SGB [80]	0.975	0.98	0.97	0.97
LGBM [80]	0.983	0.98	0.98	0.98
Extra tree [80]	0.9833	0.98	0.98	0.98
SVM [80]	0.9666	0.97	0.97	0.97
ANN [80]	0.6	0.36	0.60	0.45
SGO-optimized RF	1	1	1	1

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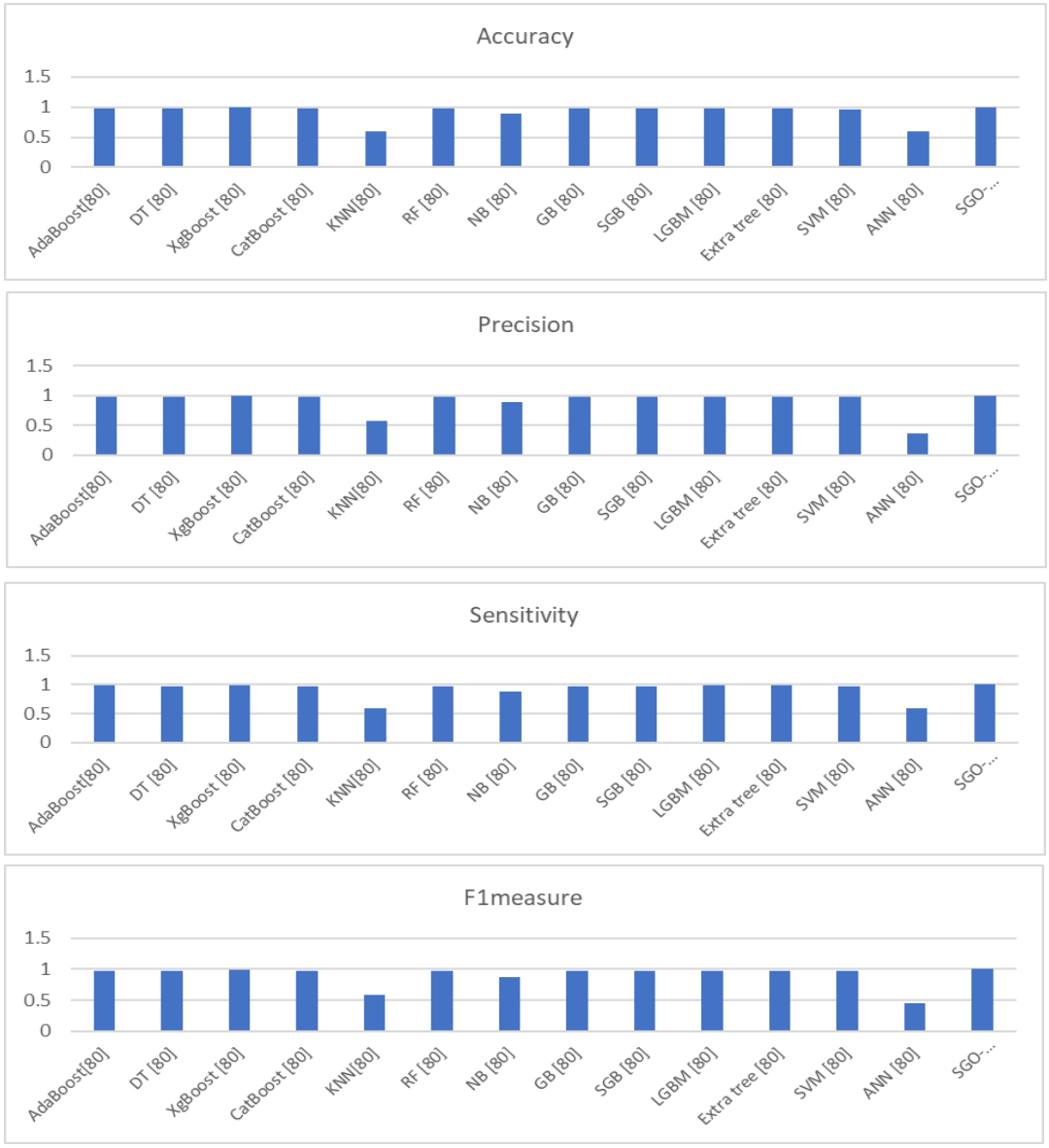

Figure 9. Graphical presentation of the performance provided by various methods on Chronic Kidney Disease dataset

Discussion

Table 6 showcases a detailed comparison of various ML methods with the proposed SGO-optimized RF model in terms of accuracy, precision, recall, and F1score on the Chronic Kidney Disease dataset. The table highlights the consistent superiority of the SGO-optimized RF over peer methods.

Methods like XgBoost achieved high accuracy (0.9916) and balanced metrics (precision, sensitivity, F1 = 0.99), reflecting its robust boosting mechanism that excels in complex datasets. AdaBoost, LGBM, and Extra Tree also demonstrated competitive results, each achieving an accuracy of 0.983 and similarly strong metrics (precision, sensitivity, F1 = 0.98). These methods leverage boosting or tree-based ensemble strategies for improved generalization. DT and its ensemble counterparts (RF, Gradient Boosting, and Stochastic Gradient Boosting) exhibited slightly lower but consistent accuracy (0.975) with balanced metrics (precision, sensitivity, F1 = 0.97). Their ensemble nature helps address the inherent overfitting of standalone decision trees. CatBoost, tailored for categorical data, performed similarly, with an accuracy of 0.975 and balanced metrics. NB achieved an accuracy of 0.8833, with precision, sensitivity, and F1 score around 0.88. While effective for probabilistic classification, it may have struggled with the dataset's complexities. SVM delivered an accuracy of 0.9666 with balanced metrics, reflecting its capability to handle non-linear separable data effectively. KNN and ANN showed subpar results, with accuracies of 0.59 and 0.6, respectively. KNN's dependency on distance metrics and ANN's need for large-scale data likely contributed to their underperformance on this dataset. The SGO-optimized RF outperformed all

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peer methods, achieving perfect scores across all metrics (Accuracy, Precision, Sensitivity, F1 = 1.0). This exceptional performance can be attributed to: Enhanced Parameter Tuning: The Social Group Optimization (SGO) algorithm identifies optimal hyperparameters for RF, maximizing its classification potential. Feature Selection and Interaction: The SGO-optimized RF efficiently handles interactions between features, crucial for complex datasets like Chronic Kidney Disease. Ensemble Strength: RF's inherent robustness against overfitting, combined with SGO's exploration and exploitation capabilities, enhances prediction accuracy. While advanced models like XgBoost and LGBM come close, the SGO-optimized RF achieves a rare perfect classification, setting it apart. Ensemble models generally dominate, as standalone models (DT, KNN, ANN) underperform due to limitations in capturing intricate data patterns. The boosting models (e.g., AdaBoost, XgBoost) and hybrid strategies (e.g., LGBM) illustrate the importance of integrating optimization or ensemble techniques for achieving competitive performance.

f) Overall Discussion

The SGO-optimized RF achieves balanced precision and sensitivity, handling complex, imbalanced datasets effectively. Its high accuracy highlights its potential for reliable clinical decision support in liver disease detection, reducing diagnostic errors. With perfect precision and strong sensitivity, the SGO-optimized RF outperforms all peer methods on Heart Disease Dataset. It displays the value of integrating metaheuristic techniques to enhance diagnostic accuracy and reduce unnecessary interventions in clinical scenarios. The SGO-optimized RF's balanced performance demonstrates its utility in predicting diabetes, minimizing both false positives and negatives, and ensuring actionable and reliable predictions. The model's perfect scores across all metrics set a benchmark for healthcare applications, emphasizing its reliability and potential to transform diagnostic workflows for Chronic Kidney Disease in chronic conditions. The SGO-optimized RF consistently outperforms state-of-the-art methods across datasets, demonstrating its robustness and transformative potential in healthcare applications.

7. Conclusion

The research conducted illustrates the transformative potential of integrating the Social Group Optimization (SGO) algorithm with machine learning models across diverse healthcare datasets. By optimizing traditional ensemble methods such as RF, the proposed SGO-optimized RF consistently achieved superior results in terms of accuracy, precision, sensitivity, and F1-score, outperforming state-of-the-art methods on datasets for chronic diseases like heart disease, diabetes, liver disease, and chronic kidney disease.

Key findings from the analysis include:

Superior Predictive Performance: The SGO-optimized RF demonstrated exceptional accuracy and balanced metrics across all datasets, achieving 100% accuracy on the Chronic Kidney Disease dataset and significant improvements on the Pima Indian Diabetes, Indian Liver Patient, and Wisconsin Breast Cancer datasets.

Balanced Metric Contributions: Its ability to maintain high sensitivity and precision ensures minimal false negatives and false positives, crucial for clinical applications where diagnostic reliability directly affects patient outcomes.

Applicability across Domains: The model's robustness in handling class imbalances and complex feature interactions across datasets highlights its versatility for medical diagnostics.

Practical Implications: The findings validate the potential of SGO-optimized RF as a decision-support tool, enabling early and accurate detection while reducing diagnostic errors, healthcare costs, and patient anxiety.

This study underscores the value of metaheuristic optimization techniques in advancing machine-learning methodologies, particularly for healthcare applications. Future research will aim to validate the generalizability of the SGO-optimized RF on larger, more diverse datasets and explore its integration with other State-of-the-art metaheuristic algorithms. The results presented here establish a strong foundation for adopting optimized ensemble models in clinical practice, offering a promising direction for precision medicine and automated healthcare diagnostics.

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Sudhirvarma Sagiraju: Writing – original draft, Methodology, Software, Validation, Investigation, Resources, Data curation.

Jnyana Ranjan Mohanty: Conceptualization, Investigation, Methodology, Software, Formal analysis, Supervision.

Anima Naik: Conceptualization, Investigation, Methodology, Software, Formal analysis, Supervision, Writing – review & editing.

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