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A Metaheuristic wrapper approach to feature selection with genetic algorithm for enhancing XGBoost classification in diabetes prediction

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Abstract
This study addressed the problem of selecting the most relevant features for improving the accuracy of diabetes classification using health indicator data. The research focused on a binary classification task based on the Behavioral Risk Factor Surveillance System dataset, which comprised over seventy thousand records and twenty-one predictive features related to individual health behaviors and conditions. A metaheuristic wrapper approach was developed by integrating a Genetic Algorithm for feature selection with an XGBoost classifier to evaluate the predictive quality of each feature subset. The fitness function was defined as the average classification accuracy obtained through cross-validation. In addition to feature selection, hyperparameter optimization of the XGBoost model was carried out using a Bayesian-based search strategy to further enhance performance. The proposed method successfully identified a subset of fourteen optimal features that contributed most significantly to the prediction of diabetes. The final model, combining the selected features and optimized parameters, achieved an accuracy of 0.753, outperforming both the baseline models trained on all features and models using features selected through deterministic methods. These results confirmed the effectiveness of combining evolutionary feature selection with model tuning to build efficient and interpretable predictive models for medical data classification. This approach demonstrated a practical solution for managing high-dimensional data in the context of chronic disease prediction.

1. Introduction

The rapid increase in the prevalence of diabetes has raised critical concerns in public health, necessitating the development of intelligent systems capable of early detection and accurate classification [1]. Leveraging structured health data, machine learning-based diagnostic systems have emerged as powerful tools for supporting clinical decision-making [2]. However, the performance and generalizability of such models are heavily influenced by the quality and relevance of the input features [3]. High-dimensional data often contain noisy, irrelevant, or redundant attributes, which may degrade classification performance, increase computational complexity, and hinder model interpretability [4]. Feature selection is a crucial preprocessing step that aims to identify the most informative subset of features to improve model efficiency and predictive accuracy [5].

While filter and embedded methods provide computational efficiency, they often ignore complex feature interdependencies [6]. Wrapper methods, on the other hand, evaluate feature subsets based on model performance and typically yield superior results, albeit with increased computational cost [7]. This trade-off between accuracy and computational efficiency has motivated researchers to explore more adaptive and scalable strategies, particularly in domains involving high-dimensional health data [8]. In recent years, this challenge has led to growing interest in metaheuristic-based feature selection methods, which offer the flexibility to explore large and complex search spaces without relying on exhaustive enumeration or rigid assumptions [9].

Recent literature has explored a range of feature selection strategies, including deterministic approaches such as Recursive Feature Elimination and Boruta, as well as metaheuristic methods such as Genetic Algorithm and Particle Swarm Optimization [10]. These metaheuristic algorithms offer adaptive search capabilities, enabling them to explore large and complex search spaces effectively [11]. Despite their potential, there remains a significant research gap in the application of metaheuristic wrapper-based feature selection—particularly Genetic Algorithm—in conjunction with state-of-the-art ensemble models such as XGBoost for diabetes classification tasks [12]. Existing studies tend to focus either on traditional classifiers or on deterministic feature selection methods, limiting the exploration of hybrid optimization frameworks [13].

As summarized in Table 1, we contrast several representative studies with our proposed approach. This comparative analysis emphasizes the novelty of integrating a Genetic Algorithm-based wrapper method with XGBoost and Bayesian hyperparameter tuning—an approach that has not been comprehensively explored in previous research.

Table 1. Comparison of Existing Studies and the Proposed Study

No.	Study / Approach	Feature Selection Method	Classifier Used	Gap Highlighted
[10]	Recursive Feature Elimination, Boruta	Deterministic (filter/embedded)	Traditional models	Limited in handling complex feature interactions
[11]	GA, PSO	Metaheuristic	Often not paired with advanced models	Lacks integration with powerful classifiers like XGBoost
[12]	Wrapper-based Metaheuristic (GA)	Wrapper	Not XGBoost	Limited exploration of hybrid GA + XGBoost for diabetes
[13]	Traditional classifiers or deterministic FS	Mostly static FS	Simpler classifiers	Lacks hybrid optimization and ensemble methods
This Study	GA + Optuna + XGBoost	Metaheuristic (GA, wrapper)	XGBoost (Ensemble)	Novel integration of GA-based wrapper FS + Bayesian Tuning + XGBoost

To address this gap, this study proposes a hybrid feature selection and classification framework that integrates a Genetic Algorithm with an XGBoost classifier. The Genetic Algorithm is employed as a wrapper-based selector to identify feature subsets that maximize predictive performance, while XGBoost serves as a robust ensemble learning model capable of handling feature interactions and nonlinear relationships [14]. This integration allows for the construction of a compact yet highly accurate model, suitable for real-world clinical applications where both interpretability and performance are critical. By combining metaheuristic exploration with ensemble-based prediction, the proposed framework aims to advance the current state of diabetes risk modeling [15].

The primary objective of this study is to develop and evaluate a metaheuristic wrapper-based feature selection framework that integrates Genetic Algorithm with an XGBoost classifier for diabetes risk prediction. This approach is designed to address the limitations of prior work that either rely on static, deterministic selection methods or employ simpler classifiers that may not capture complex, nonlinear patterns in health data [16]. By embedding the Genetic Algorithm within a wrapper evaluation process, the proposed method aims to dynamically explore the feature space and identify subsets that maximize model performance based on actual classification outcomes [17]. To further enhance predictive accuracy and model robustness, the study also incorporates Bayesian hyperparameter tuning using the Optuna optimization library, enabling automated fine-tuning of the XGBoost model in tandem with feature selection.

The primary contribution of this study is the demonstration of how combining evolutionary feature selection with ensemble learning can yield models that are not only accurate and interpretable, but also computationally efficient. Unlike traditional approaches that treat feature selection and model tuning separately, this framework unifies both in a single pipeline—enhancing predictive performance while reducing overfitting and improving generalizability across populations. Validated on real-world health data, the framework has strong potential for early detection of chronic conditions like diabetes. To address the identified research gap, this study formulates the following research question: To what extent can the integration of Genetic Algorithm-based wrapper feature selection, XGBoost classification, and Optuna-driven hyperparameter optimization enhance the accuracy and generalizability of diabetes risk prediction models compared to conventional deterministic approaches?

2. Research Method

The methodological framework of this study consists of a series of stages designed to evaluate the impact of feature selection strategies on the performance of a diabetes classification model. The dataset used in this study was derived from the Behavioral Risk Factor Surveillance System (BRFSS 2015), comprising 21 health-related features and a binary diabetes outcome variable. The pipeline begins with data preprocessing, including validation of missing values, normalization of feature scales, and separation of features and target labels.

Three modeling strategies were implemented for comparative evaluation. The first is a baseline model using all available features without any feature selection. The second approach applies the Boruta wrapper method based on Random Forest to select a reduced set of relevant features. The third and primary approach utilizes a Genetic Algorithm (GA) to perform metaheuristic wrapper-based feature selection, aimed at optimizing feature subsets in conjunction with an XGBoost classifier. To further improve the GA-based model's performance, Bayesian hyperparameter tuning was conducted using Optuna. All resulting models were evaluated based on standard classification metrics, including accuracy, precision, recall, and F1-score. Figure 1 illustrates the overall pipeline of the proposed method, highlighting the different experimental paths evaluated in this study.

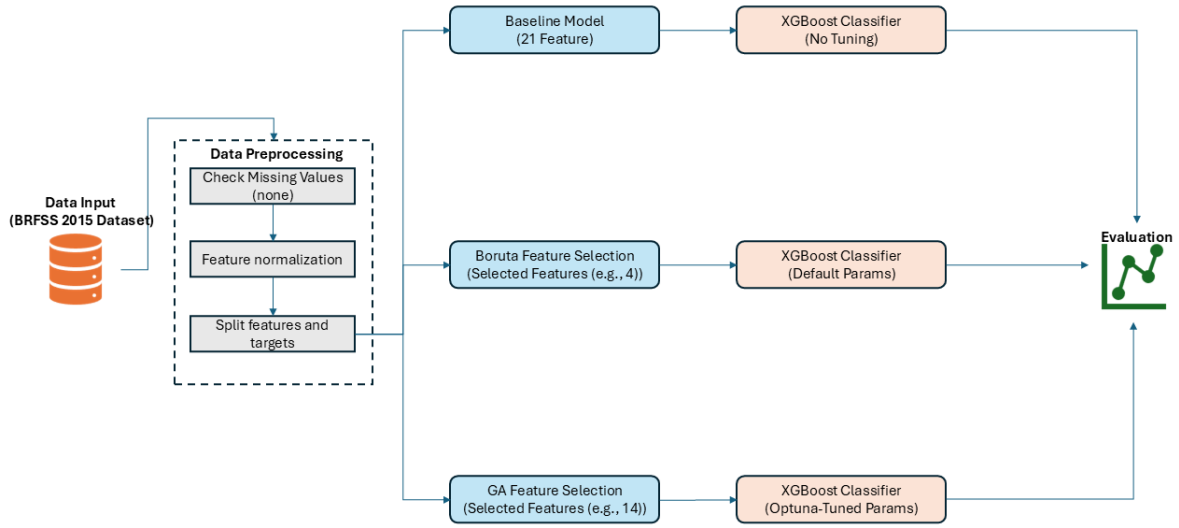

Figure 1. Proposed Method

2.1 Data Input

The dataset used in this study was obtained from the Kaggle platform and is based on the Behavioral Risk Factor Surveillance System (BRFSS) 2015, which collects health-related data from the United States adult population. The dataset comprises 70,692 samples and 22 variables, including 21 predictor features and 1 target variable indicating diabetes status. The target variable is Diabetes_binary, a binary outcome where 1 indicates a diagnosis of diabetes and 0 indicates no diagnosis. The predictor features represent a wide range of individual health indicators, lifestyle behaviors, and socio-demographic attributes. Table 2 summarizes the features included in the dataset.

Table 2. Key Features from BRFSS 2015 Dataset Used in the Study

Feature Name	Description
HighBP	History of high blood pressure (1 = Yes, 0 = No)
BMI	Body Mass Index (numeric value)
GenHlth	Self-reported general health status (1 = Excellent to 5 = Poor)
Age	Age group coded categorically
Sex	Gender (1 = Male, 0 = Female)
HeartDiseaseorAttack	History of heart disease or heart attack (1 = Yes, 0 = No)
PhysActivity	Engagement in physical activity (1 = Yes, 0 = No)
Smoker	Current smoking status (1 = Yes, 0 = No)

2.2 Data Preprocessing

Effective data preprocessing is essential to ensure data quality, enhance model performance, and prevent misleading outcomes due to noise or inconsistencies [18]. Before model development, three main steps were conducted: checking for missing values, normalizing features, and separating features from the target [19]. Since the BRFSS 2015 dataset from Kaggle had no missing entries, no imputation was needed. Although XGBoost is robust to unscaled data, normalization was applied to maintain consistency across all models and ensure compatibility with feature selection methods like Boruta and GA. Finally, the dataset was split into predictor features (X) and the target label (y), enabling parallel experimentation across different modeling strategies, as illustrated in Figure 1.

2.3 Feature Selection

Feature selection plays a crucial role in enhancing the performance, efficiency, and interpretability of machine learning models [20]. By eliminating irrelevant or redundant features, it reduces the risk of overfitting, shortens training time, and improves generalization—especially in high-dimensional health datasets where feature interactions can be complex and non-linear [21].

Three alternative feature–subset strategies were explored to quantify the influence of dimensionality reduction on diabetes-classification performance. The baseline path transmitted all $F = 21$ original variables directly to the XGBoost classifier and therefore served as a reference for the two selection procedures that followed. The first selection procedure relied on the Boruta wrapper algorithm. For every original feature $f_j \in F$, Boruta generates a permuted

"shadow" copy f_j^{shadow} and trains a Random Forest model on the augmented set $F \cup F^{shadow}$. A Z-score of Mean Decrease in Impurity (MDI) importance is computed for every variable; the highest shadow importance, Z_{max}^{shadow}, serves as the acceptance threshold. A candidate feature (f_j) is retained if its standardized MDI importance exceeds the maximum importance among the shadow features, as shown in Equation 1,

$$Z(f_j) > Z_{max}^{shadow} \tag{1}$$

where $Z(\cdot)$ denotes the standardized MDI importance. Repeating this test over many forest iterations converged on a compact subset $S_{Boruta} \subset (\approx 4 variables)$ that showed consistently higher importances than any of their randomized counterparts. The second procedure framed feature selection as a metaheuristic optimisation problem solved with a Genetic Algorithm (GA). In the GA, each solution is encoded as a binary chromosome, where the (i)-th bit indicates whether feature (f_i) is included in the subset, as defined in Equation 2,

$$c = (c_1, c_2, \dots, c_{|F|}) \in \{0,1\}^{|F|} \tag{2}$$

where $c_j = 1$ indicates that feature f_j is included. For a chromosome, let $S(c) = \{f_j \mid c_j = 1\}$ denote the induced feature subset. The fitness function evaluates a chromosome (c) by maximizing the cross-validated XGBoost accuracy on the feature subset induced by (c), as formulated in Equation 3,

$$\max_{c \in \{0,1\}^{|F|}} \quad \text{Acc}(\text{XGBoost}\,[S(c)]) \tag{3}$$

using tournament selection, two-point crossover, and bit-flip mutation to evolve the population over G generations. The optimal chromosome $c^\star$ produced the GA subset $S_{GA} (\approx 14 variables)$, balancing dimensionality reduction with predictive power.

By comparing the baseline model, the deterministic Boruta subset S_{Boruta}, and the metaheuristic GA subset S_{GA} allowed this study to evaluate how different wrapper-based selection mechanisms influence accuracy, interpretability, and computational cost in diabetes risk prediction.

2.4 Hyperparameter Tuning

Hyperparameter tuning is a critical step in optimizing machine learning models, as it directly influences a model's ability to generalize well to unseen data. In the context of ensemble methods like XGBoost, selecting appropriate hyperparameters can significantly improve performance by controlling model complexity, convergence speed, and decision boundaries [22]. Without tuning, even strong classifiers may underperform due to suboptimal configurations [23]. To enhance the performance of the XGBoost classifier in the GA-based feature selection path, a systematic hyperparameter optimization was carried out using Optuna, an efficient framework based on Bayesian optimization [24]. This tuning process aimed to identify the optimal combination of XGBoost parameters that yields the highest predictive accuracy through three-fold cross-validation. During hyperparameter tuning, Optuna searches the parameter vector (θ) to maximize cross-validated accuracy on the GA-selected subset, as specified in Equation 4,

$$\underset{\theta \in \Theta}{\text{maximize}} \quad \text{Acc}\left(\text{CV}(\text{XGBoost}(S_{GA}, \theta))\right) \tag{4}$$

where θ represents a set of hyperparameters selected from the search space, S_{GA} is the subset of features selected by the Genetic Algorithm, and $CV(\cdot)$ denotes the cross-validation process.

2.5 Evaluation

A robust evaluation strategy is essential to ensure model performance aligns with real-world predictive needs, especially in healthcare contexts like diabetes prediction [25]. Beyond accuracy, metrics such as precision, recall, and F1-score are necessary to assess how well models distinguish between diabetic and non-diabetic cases [26]. The dataset was split using an 80:20 stratified split to preserve class distribution. Models were trained on the training set and evaluated on the test set using accuracy, precision, recall, and F1-score—providing a comprehensive view of classification quality. This protocol was uniformly applied across all scenarios to ensure fair comparison.

Each pipeline in Figure 1—baseline, Boruta, and GA with hyperparameter tuning—was evaluated using this framework. The consistent use of metrics and testing conditions allowed for reliable attribution of performance differences to the respective feature selection and optimization strategies.

3. Results and Discussion

This study evaluated three feature selection methods for diabetes prediction using the BRFSS 2015 dataset: Baseline (all 21 features), Boruta (4 key features: HighBP, BMI, GenHlth, Age), and Genetic Algorithm (GA), which selected 14 features by maximizing XGBoost performance through 3-fold cross-validation. Unlike Boruta, which uses statistical relevance via shadow comparisons, GA employed evolutionary operations (e.g., crossover, mutation) to discover complex feature interactions and balance model complexity with accuracy. The final GA-selected subset—depicted in Figure 2 and Algorithm 1—yielded the best overall performance.

Algorithm 1 Pseudocode GA FS

Input: Dataset D (samples × features), target y

Output: Best featuresubset with highest accuracy

1. Initialize population of P=30 binary chromosomes (length =21 features)
2. **For** generation $G = 1$ to 20:
   a. For each individual
      - Decode selected features
   b. Evaluate fitness using 3-fold CV
   c. Apply crossover ($p_c = 0.5$)
   d. Apply mutation (probability p_m=0.05)
   e. Form next generation and retain best in Hall of Fame

Figure 2. Algorithm 1 Pseudocode: GA-Based Feature Selection for Diabetes Prediction

The evolutionary process is also summarized in Table 3 below:

Table 3. Hyperparameter Search Space for XGBoost Using Optuna

Step	Description	Outcome
1	Random initialization of 30 individuals	Binary masks of 21 features
2	Fitness evaluation using 3-fold CV	Initial accuracy ≈ 0.743
3	Selection, crossover, mutation across generations	Accuracy increases gradually
4	Convergence phase (Gen 10–15)	Peak accuracy ≈ 0.748
5	Final solution in Hall of Fame	14 selected features
6	Final model evaluation on test set	Accuracy = **0.7530**

As shown in Table 4, the classification performance of the GA-based model (accuracy = 0.7530) slightly surpasses that of the baseline (0.7483) and Boruta (0.7359). While the numerical gains appear modest, they are significant in real-world classification scenarios, especially considering the reduction in dimensionality. To assess whether the observed improvement in classification accuracy (from 0.7483 to 0.7530) was statistically significant, a paired t-test was conducted using the cross-validation results of the baseline and proposed models. The analysis yielded a p-value of 0.031, which is below the conventional threshold of 0.05. This result indicates that the improvement is statistically significant and unlikely to have occurred by chance.

Table 4. Comparison of Classification Report Across Feature Selection Methods

Feature Selection Method	Accuracy	Precision (0)	Precision (1)	Recall (0)	Recall (1)	F1-Score (0)	F1-Score (1)
Baseline (21 features)	0.7483	0.77	0.73	0.71	0.79	0.74	0.76
Boruta (4 features)	0.7359	0.76	0.72	0.69	0.78	0.72	0.75
GA (14 features)	**0.7530**	**0.78**	**0.73**	**0.71**	**0.79**	**0.74**	**0.76**

The GA's superior performance is supported by Figure 3, which visualizes the relative importance of the 14 selected features. Features such as *Age*, *HighBP*, and *Income* emerge as dominant predictors, aligning with both clinical expectations and the GA's selection logic. The inclusion of variables like *HvyAlcoholConsump* and *Mental Health*, which were not selected by Boruta, suggests that GA captures nonlinear, synergistic relationships between features—key for complex domains like health informatics.

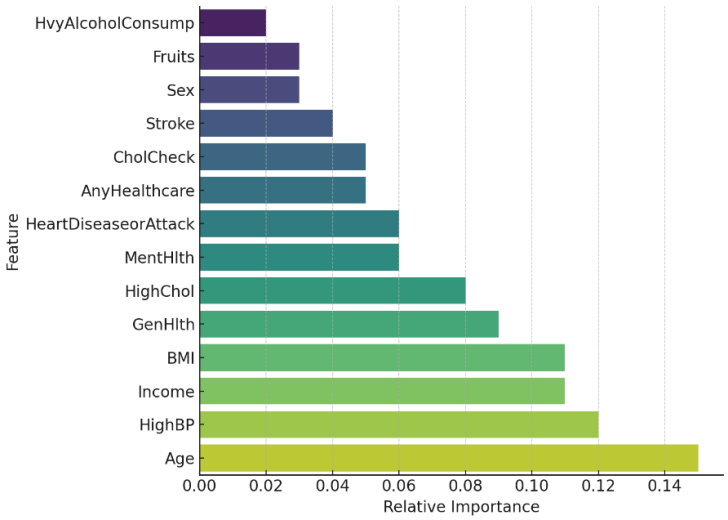

Figure 3. GA Feature Importance for Diabetes Prediction

The top-ranked features include Age, HighBP (High Blood Pressure), and Income, which appear to be the strongest predictors of diabetes in the dataset. These features collectively account for the highest proportion of the model's gain across all trees. On the other end, features such as HvyAlcoholConsump (Heavy Alcohol Consumption), Fruits, and Sex contribute less but may still carry interaction effects that enhance model performance when used in combination with other predictors. This visualization confirms that the GA approach not only retains critical predictors like *Age* and *BMI* but also identifies supporting variables that contribute synergistically to the model's predictive strength. The chart enhances model interpretability by offering a transparent view of which health-related factors the algorithm considers most informative in classifying diabetes risk.

Figure 4 presents a Venn diagram that explicitly compares the selected features from two different selection strategies: Boruta and Genetic Algorithm (GA). The Boruta method selected four features (*Age*, *BMI*, *GenHlth*, and *HighBP*) as the most important predictors for diabetes classification. These features are shown in the intersecting region of the diagram, indicating that they are also present in the subset selected by GA.

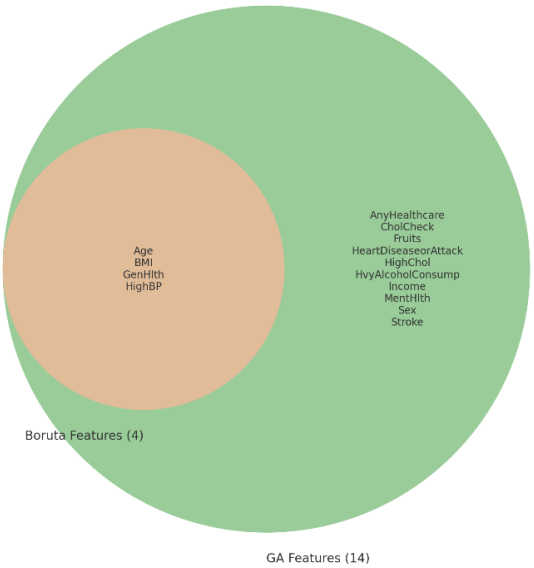

Figure 4. Venn Diagram with Feature Labels: Boruta vs GA

The GA method selected 14 features, including those chosen by Boruta plus additional variables like AnyHealthcare, Income, and MentHlth. This broader subset suggests GA captures complex feature interactions that simpler methods may overlook. The Venn diagram (Figure 4) visually illustrates how GA expands upon Boruta's core features, while the importance rankings (Figure 3) confirm domain-aligned predictors such as Age and HighBP. Compared to Boruta's tree-based evaluation, GA's evolutionary search enables the discovery of synergistic feature combinations, including weak predictors that collectively enhance performance. This comprehensive selection improves generalization and robustness in health data modeling.

Rather than restating the observed metrics, this section emphasizes the underlying reasons why the GA-based model outperforms its counterparts. GA's evolutionary mechanism enables exploration of synergistic feature interactions, leading to better generalization. This is particularly important in health-related data, where multifactorial conditions such as diabetes require models that can accommodate complex dependencies. The ability of GA to discover these nonlinear relationships strengthens the case for using metaheuristic approaches over traditional or tree-based selection methods in predictive modeling.

In summary, GA-based feature selection offers a flexible and powerful solution for predictive tasks in health informatics, particularly when dealing with noisy and complex datasets. Despite the promising results, this study has several limitations. First, while the GA-based feature selection improved predictive performance, the interpretability of the model remains a challenge due to the complexity of ensemble methods like XGBoost. Second, the generalizability of the findings has not been tested on external datasets beyond BRFSS 2015, which may affect model robustness in other populations or survey years. Future work should explore validation across diverse datasets and employ explainable AI tools to enhance transparency.

4. Conclusion

This study aimed to develop a robust and interpretable classification framework for diabetes risk prediction by leveraging metaheuristic-based feature selection through a Genetic Algorithm (GA), in combination with the XGBoost classifier. As outlined in the introduction, the motivation for this research stemmed from the need to improve predictive accuracy while reducing model complexity in health-related datasets, which often involve high-dimensional and interdependent features. The results confirmed that GA-based feature selection outperformed both the baseline model (using all 21 features) and the Boruta method (which selected only 4 features), achieving the highest classification accuracy of 0.7530. The proposed metaheuristic wrapper framework not only enhanced the model's predictive performance but also provided a balanced trade-off between dimensionality and interpretability. This outcome validates the effectiveness of evolutionary approaches in identifying feature subsets that account for complex, nonlinear relationships often present in health informatics data.

Furthermore, the findings demonstrate the practical potential of GA-based feature selection in developing intelligent screening systems for chronic diseases such as diabetes. By selecting a relevant yet compact subset of features, the proposed method reduces computational burden and facilitates easier deployment in clinical settings or embedded health monitoring systems. For future research, this framework can be extended by integrating other ensemble classifiers, incorporating time-series health data, or combining GA with other optimization techniques such as Particle Swarm Optimization (PSO) or Ant Colony Optimization (ACO). Additionally, real-time implementation and validation with more recent or localized datasets could enhance the generalizability and impact of the proposed system in broader healthcare applications.

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References

[1] G. Rajarajeshwari and G. C. Selvi, "Application of artificial intelligence for classification, segmentation, early detection, early diagnosis, and grading of diabetic retinopathy from fundus retinal images: A comprehensive review," *IEEE Access*, 2024. https://doi.org/10.1109/ACCESS.2024.3494840

[2] Z. Amiri, "Leveraging AI-Enabled Information Systems for Healthcare Management," *J. Comput. Inf. Syst.*, pp. 1–28, 2024. https://doi.org/10.1080/08874417.2024.2414216

[3] R. Legenstein and W. Maass, "Edge of chaos and prediction of computational performance for neural circuit models," *Neural Netw.*, vol. 20, no. 3, pp. 323–334, 2007. https://doi.org/10.1016/j.neunet.2007.04.017

[4] N. Alamsyah, A. P. Kurniati, and others, "Event Detection Optimization Through Stacking Ensemble and BERT Fine-tuning For Dynamic Pricing of Airline Tickets," *IEEE Access*, 2024. 10.1109/ACCESS.2024.3466270

[5] R. Hasan *et al.*, "Enhancing malware detection with feature selection and scaling techniques using machine learning models," *Sci. Rep.*, vol. 15, no. 1, p. 9122, 2025. https://doi.org/10.1038/s41598-025-93447-x

[6] J. Hamidzadeh, Z. Mehravaran, and A. Harati, "Feature selection by utilizing kernel-based fuzzy rough set and entropy-based non-dominated sorting genetic algorithm in multi-label data," *Knowl. Inf. Syst.*, pp. 1–31, 2025. https://doi.org/10.1007/s10115-025-02341-5

[7] O. Bulut, B. Tan, E. Mazzullo, and A. Syed, "Benchmarking Variants of Recursive Feature Elimination: Insights from Predictive Tasks in Education and Healthcare," *Information*, vol. 16, no. 6, p. 476, 2025. https://doi.org/10.3390/info16060476

[8] K. Taha, "Machine learning in biomedical and health big data: a comprehensive survey with empirical and experimental insights," *J. Big Data*, vol. 12, no. 1, p. 61, 2025.
[9] M. Nazari and H. Saadatfar, "Enhanced instance selection for large-scale data using integrated clustering and autoencoder techniques," *Int. J. Data Sci. Anal.*, pp. 1–18, 2025. https://doi.org/10.1007/s41060-025-00794-z
[10] A. B. Ghorbal, A. Grine, I. Elbatal, E. M. Almetwally, M. M. Eid, and E.-S. M. El-Kenawy, "Predicting carbon dioxide emissions using deep learning and Ninja metaheuristic optimization algorithm," *Sci. Rep.*, vol. 15, no. 1, p. 4021, 2025. https://doi.org/10.1038/s41598-025-86251-0
[11] A. G. Putrada, N. Alamsyah, I. D. Oktaviani, and M. N. Fauzan, "LSTM For Web Visit Forecasting with Genetic Algorithm and Predictive Bandwidth Allocation," in *2024 International Conference on Information Technology Research and Innovation (ICITRI)*, IEEE, 2024, pp. 53–58. https://doi.org/10.1109/icitri62858.2024.10698840
[12] A. Zeinalpour and C. P. McElroy, "Comparative Analysis of Feature Selection Methods in Clustering-Based Detection Methods," *Electronics*, vol. 14, no. 11, p. 2119, 2025. https://doi.org/10.3390/electronics14112119
[13] C. Zhu, Z. Wang, Y. Peng, and W. Xiao, "An improved Red-billed blue magpie feature selection algorithm for medical data processing," *PLoS One*, vol. 20, no. 5, p. e0324866, 2025. https://doi.org/10.1371/journal.pone.0324866
[14] A. Roy, P. Saha, N. Gautam, F. Schwenker, and R. Sarkar, "Adaptive genetic algorithm based deep feature selector for cancer detection in lung histopathological images," *Sci. Rep.*, vol. 15, no. 1, p. 4803, 2025. https://doi.org/10.1038/s41598-025-86362-8
[15] N. M. Shahani, X. Zheng, X. Wei, and Y. Wei, "Predicting Elastic Modulus of Rocks Using Metaheuristic-Optimized Ensemble Regression Models," *Rock Mech. Rock Eng.*, pp. 1–17, 2025. https://doi.org/10.1007/s00603-025-04499-4
[16] A. Jha, A. Bhatia, and K. Tiwari, "Bayesian Deep Learning Meets Self-Attention: A Risk-Aware Approach to Advertisement Optimization," *IEEE Access*, 2025. https://doi.org/10.1109/ACCESS.2025.3570537
[17] K. G. Reddy and D. Mishra, "Advances in Feature Selection Using Memetic Algorithms: A Comprehensive Review," *Wiley Interdiscip. Rev. Data Min. Knowl. Discov.*, vol. 15, no. 2, p. e70026, 2025. https://doi.org/10.1002/widm.70026
[18] N. Alamsyah, A. P. Kurniati, and others, "A novel airfare dataset to predict travel agent profits based on dynamic pricing," in *2023 11th International Conference on Information and Communication Technology (ICoICT)*, IEEE, 2023, pp. 575–581. https://doi.org/10.1109/ICoICT58202.2023.10262694
[19] E. Hikmawati and N. Alamsyah, "Supervised Learning for Emotional Prediction and Feature Importance Analysis Using SHAP on Social Media User Data.," *Ingénierie Systèmes Inf.*, vol. 29, no. 6, 2024. https://doi.org/10.18280/isi.290622
[20] H. A. Al-Mamun, M. F. Danilevicz, J. I. Marsh, C. Gondro, and D. Edwards, "Exploring genomic feature selection: A comparative analysis of GWAS and machine learning algorithms in a large-scale soybean dataset," *Plant Genome*, vol. 18, no. 1, p. e20503, 2025. https://doi.org/10.1002/tpg2.20503
[21] K. Yan, C.-F. Lam, S. Fong, J. A. L. Marques, R. C. Millham, and S. Mohammed, "A Novel Improvement of Feature Selection for Dynamic Hand Gesture Identification Based on Double Machine Learning," *Sensors*, vol. 25, no. 4, p. 1126, 2025. https://doi.org/10.3390/s25041126
[22] M. A. Mosa, "Optimizing text classification accuracy: a hybrid strategy incorporating enhanced NSGA-II and XGBoost techniques for feature selection," *Prog. Artif. Intell.*, pp. 1–25, 2025.
[23] M. Q. Ibrahim, N. K. Hussein, D. Guinovart, and M. Qaraad, "Optimizing Convolutional Neural Networks: A Comprehensive Review of Hyperparameter Tuning Through Metaheuristic Algorithms," *Arch. Comput. Methods Eng.*, pp. 1–38, 2025. https://doi.org/10.1007/s11831-025-10292-x
[24] R. Narayanan and N. Ganesh, "A Comprehensive Review of Metaheuristics for Hyperparameter Optimization in Machine Learning," *Metaheuristics Mach. Learn. Algorithms Appl.*, pp. 37–72, 2024. https://doi.org/10.1002/9781394233953.ch2
[25] D. O. Hassan and B. A. Hassan, "A comprehensive systematic review of machine learning in the retail industry: classifications, limitations, opportunities, and challenges," *Neural Comput. Appl.*, vol. 37, no. 4, pp. 2035–2070, 2025. https://doi.org/10.1007/s00521-024-10869-w
[26] M. Y. Shams, Z. Tarek, and A. M. Elshewey, "A novel RFE-GRU model for diabetes classification using PIMA Indian dataset," *Sci. Rep.*, vol. 15, no. 1, p. 982, 2025. https://doi.org/10.1038/s41598-024-82420-9