EasyDiagnosis: An Accurate Feature Selection Framework for Automated Diagnosis in Smart Healthcare

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Abstract

The rapid advancements in artificial intelligence (AI) have revolutionized smart healthcare, driving innovations in wearable technologies, continuous monitoring devices, and intelligent diagnostic systems. However, security, explainability, robustness, and performance optimization challenges remain critical barriers to widespread adoption in clinical environments. This research presents an innovative algorithmic method using the proposed EasyDiagnosis algorithm to improve feature selection in healthcare datasets and overcome problems. EasyDiagnosis integrating Genetic Algorithms (GA), Explainable Artificial Intelligence (XAI), and Permutation and Combination Techniques (PCT), the algorithm optimizes Clinical Decision Support Systems (CDSS), thereby enhancing predictive accuracy and interpretability. The proposed method is validated across three diverse healthcare datasets using six distinct machine learning algorithms, demonstrating its robustness and superiority over conventional feature selection techniques.

The results underscore the transformative potential of EasyDiagnosis in smart healthcare, enabling personalized and transparent patient care. Notably, the proposed algorithm, when combined with a Multi-layer Perceptron (MLP), achieved an accuracy of up to 98.79%, highlighting its capability to improve clinical decision-making processes in real-world healthcare applications.

Keywords: Smart Healthcare, Healthcare Cyber-Physical System (H-CPS), Machine Learning, Genetic Algorithm, Explainable Artificial Intelligence (XAI), Automatic Health Diagnosis

1 Introduction

Today's world has made medical illness analysis more and more critical [19], leading to increased research and development efforts in this area. Advances in technology, such as deep learning and machine learning [41], have enabled researchers to leverage the potential of healthcare data to create novel approaches that enhance human health outcomes. The algorithms can anticipate outcomes reasonably. However, the algorithms frequently need to explain the performance forecasts clearly, which reduces the effectiveness and reliability [32]. "Black Box" is the term or issue discussed about the reliability problem in [16]. Furthermore, the said algorithms' lack of interpretability presents severe difficulties in clinical contexts where medical personnel need lucid explanations to comprehend and rely on the advice these models provide [25]. The urgent need for specific procedures in medical illness analysis is highlighted by this opacity, which not only makes adoption difficult and also raises questions about accountability and ethical issues [17] [38]. In response to the difficulty, Explainable AI (XAI) has surfaced to clarify the decision-making procedure of machine learning models, thereby offering discernment into the how and why of a given prediction [6]. In medicine, XAI is essential for improving the dependability and comprehensibility of disease analysis models [9].

The process starts with selecting an extensive healthcare dataset to guarantee data quality and integrity. Following, detailed data analysis and preprocessing procedures are performed. The dataset is optimized for precise model training by researchers through data cleaning, normalization, and transformation. Following data preprocessing, various deep learning and machine learning methods are employed to develop the model, including neural networks, decision trees, random forests, support vector machines, and ensemble techniques. Employing a range of algorithms allows researchers to examine each method's unique strengths and limitations, thereby increasing the likelihood of identifying the optimal model for disease prediction. The main concern shifts to model explainability once the models are trained. Researchers implement several explainable AI strategies to clarify the models' decision-making process. Implemented methods include attention mechanisms in deep learning models, SHAP values, feature importance analysis, and LIME [21]. Inspired by natural selection, genetic algorithms are widely used to iteratively identify optimal feature subsets

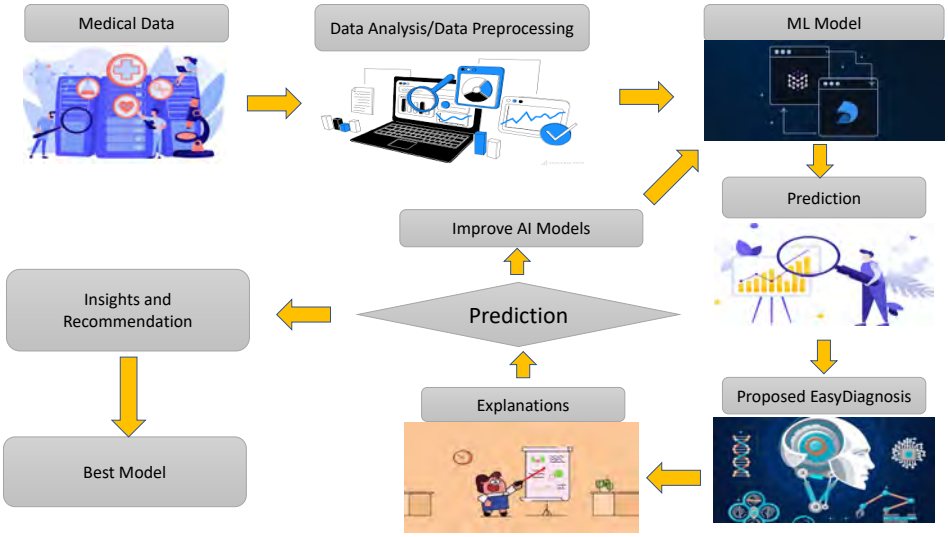

Fig. 1 System Model for Integrating Explainable AI in Clinical Decision Support Systems

that improve machine learning model performance. Likewise, permutation and combination techniques provide a thorough method for feature selection by evaluating all possible feature subsets using a fitness function. Using such techniques, researchers can obtain essential insights into the fundamental principles underlying the predictions, improving comprehension and confidence in the model's results. Integrating XAI, GA, and PCT improves model robustness by identifying biases and outliers, enhancing disease analysis and advancing reliable, transparent healthcare analytics.

The proposed EasyDiagnosis is a novel algorithm designed to assess feature significance across various datasets. Through rigorous testing on diverse datasets using both machine learning and deep learning algorithms, the EasyDiagnosis has consistently outperformed existing feature selection methods. One of the critical strengths of EasyDiagnosis is its adaptability, making it compatible with any algorithm and dataset. Our approach integrates three popular and highly effective feature selection strategies: XAI, PCT, and GA. By combining the techniques, the work computes accuracy scores for each method individually, consistently demonstrating superior performance compared to traditional feature selection algorithms.

The initial phase in the proposed paradigm is the gathering and preparation of medical data. After processing, a machine learning (ML) model is trained using the data to produce predictions. By integrating XAI, GA, and PCT, valuable insights and recommendations can be generated. The EasyDiagnosis algorithm is subsequently applied to determine the most appropriate approach for clinical decision support. Fig. 1 illustrates a system model which integrates an explanatory model in clinical decision support. The workflow begins with Medical Data Analysis and Data Preprocessing, followed by building ML Models for prediction. The Proposed EasyDiagnosis algorithm is then applied to improve model accuracy and interpretability. The proposed approach provides insights and recommendations by identifying the Best Model for

robust clinical decision-making. The salient contributions of the proposed work are as follows:

- Development of the EasyDiagnosis: The study presents an innovative algorithm that combines XAI, GA, and PCT to enhance feature selection, particularly in Clinical Decision Support Systems (CDSS).
- Superiority in Performance: EasyDiagnosis shows clear advantages over conventional feature selection techniques, achieving accuracy rates as high as 98.5% across a range of datasets and algorithms. This highlights its strength in both reliability and performance.
- With its inherent flexibility, the EasyDiagnosis is suitable for a broad range of algorithms and datasets, significantly expanding its applications within healthcare analytics.
- Advancing healthcare analytics, this work enhances clinical decision-making with systems that are more dependable, transparent, and interpretable, supporting improved patient care.

Overall, the contribution of this work lies in developing the EasyDiagnosis algorithm, which combines cutting-edge feature selection techniques with XAI to enhance CDSS in healthcare analytics by increasing accuracy, transparency, and robustness significantly advances the field.

The structure of this paper is as follows: Section II outlines the unique contributions of our research, and Section III reviews related literature. Section IV explores the challenges faced in implementing Explainable AI (XAI). Section V provides the foundational for understanding our work along with the proposed framework.Section VI details the experimental procedures and presents the results. Lastly, Section VII offers concluding remarks on our study.

2 Contribution of the Work

2.1 Problems Addressed in the Current Work

A comprehensive investigation and comparative analysis of various algorithms are necessary. Many existing studies rely on a limited number of algorithms and must thoroughly validate their effectiveness. The approach raises concerns regarding the suitability of the algorithms for the task at hand. The current work addresses the gaps by introducing the EasyDiagnosis, which incorporates multiple effective feature selection techniques and enhances model interpretability. The proposed approach provides a more robust and transparent methodology for medical data analysis.

2.2 Solution Proposed

The proposed study addresses the explainability issue by integrating GA, XAI, and PCT. This approach aims to enhance understanding of the prediction processes by leveraging the methodologies to provide insights into the inner workings of deep learning and machine learning algorithms. By combining, the study improves

model transparency and simplifies modifications, impacting the healthcare sector significantly.

Additionally, the study tackles the problem of limited algorithm exploration by introducing a novel algorithm which leverages feature-based techniques. The new method utilizes various feature set algorithms to generate predictions for the same objectives. It identifies the most suitable model for a given dataset through hyperparameter tuning and comprehensive analysis, ensuring a thorough evaluation of algorithmic performance and enhancing healthcare applications' accuracy and predictive efficacy.

2.3 Novelty of the Work

In order to maximize feature selection in clinical decision support systems, the work presents EasyDiagnosis, a novel approach that combines genetic algorithms, permutation and combination techniques, and explainable artificial intelligence. EasyDiagnosis shows remarkable resilience and efficacy, with an accuracy of up to 98.5% across a variety of datasets and models. Because of its adaptable nature, it may be used with a variety of datasets and algorithms, which increases its usefulness in healthcare analytics.

Additionally, the study presents a novel approach to predictive modeling by employing six distinct machine learning methods and neural networks rather than limiting the investigation to a few algorithms. The diverse methodological approach provides multiple perspectives on the same dataset, offering subtle insights that can enhance the efficacy of treatment plans and diagnostics. The proposed strategy advances healthcare analytics and allows improved predictive modeling through algorithmic diversity, contributing to better patient care.

3 Related Prior Research

The study employed post-hoc and agnostic models, namely Local Interpretable Model-Agnostic Explanations (LIME) and SHapley Additive exPlanations (SHAP), to determine the most significant genes for classifying lung cancer types and subtypes [36], as well as the most crucial features for predicting lung cancer survival [42]. In recent times, the researchers discussed, for instance, and suggested utilizing SHAP and LIME in conjunction with iAFPs-EnC-GA for fungal infection [1]. The paper introduces a deep ensemble method that uses uncertainty in relevance scores to improve the reliability and trustworthiness of predictions for clinical time series data with explainable AI [45].

Recent advancements in federated learning for medical image analysis integrate explainable AI and blockchain techniques to address challenges of communication overhead and data heterogeneity, enhancing efficiency, accuracy, and interpretability [30]. Mediastinal Cysts and Tumors have also been detected using the Ensemble of Extreme Gradient Boosting (XGBoost) and SHAP [44]. Recently, bloodstream infections with SHAP(XAI) have been found in [34] using XGBoost, RF, SVM, and MLP. An SVM-based model for predicting lung cancer from an image dataset is proposed by Kumar et al. in [24]. Preprocessing is applied to a UC online dataset, and an SVM model,

trained and tested on this data, achieved 98.8% accuracy, outperforming KNN, Naive Bayes, and J48 models.Machine learning techniques have been extensively used for feature selection and categorization in many different fields. The authors used a feature selection method based on Random Forest (RF), XAI which they found effective in high-dimensional datasets [22]. They achieved better classification accuracy in [13] using 1D and 2D Deep CNN with LSTM and DeepTD. The researchers also propose using histopathology images from the LC25000 dataset to develop a CAD system for lung and colon cancer analysis. [14]. The study introduces a scalable ML model using minimal cognitive tests for accurate and explainable dementia risk prediction in aging populations. [11].The study employs DNN and XAI (SHAP) to predict postprandial glucose levels in Type 1 diabetes, enhancing artificial pancreas systems and decision-making tools. [7]. A technique for early-stage lung cancer with segmentation method is diagnosis using three picture datasets and with CNN and U-Net, and obtained an AUC of 0.6459 [23].The researchers' presented a classification technique based on choice bireducts, which produced a high F1-score [33]. Furthermore, the investigation considers LightGBM and RF classifiers with intersection strategy based feature selection, which achieved good classification task accuracy [40].

Table 1 Review of the literature in reference to the proposed study

Work	Dataset Name	Algorithm Used	Accuracy
Y. Li et al. (2020) [26]	LUNA16 Lung Cancer	CNN with ResNet-18	82.15%
Ansari et al. (2011) [8]	UCI Heart Disease	Bayes Net Based Approach	87%
Beyene et al. (2018) [12]	UCI Heart Disease	ANN and SVM	81.82%, 80.38%
Riaz et al. (2018) [39]	UCI Heart Disease	KNN and Decision Tree	78%, 80%
Guleria et al. (2022) [18]	Cardiovascular Disease	LR, SVM, KNN with XAI	81.2%, 82.5%, 75.9%
Patro et al. (2018) [35]	Heart Disease	RF with XAI (SHAP and LIME)	87%
Batista et al. (2020) [10]	COVID-19 Pandemic	LR, Random Forest, SVM	85%
Mahdy et al. (2020) [28]	COVID-19 Pandemic	Multi-level Thresholding with SVM	95%
Ahmad et al. (2023) [2]	Lung Cancer Dataset	DT, LR, RF, Naïve Bayes with XAI	95%, 97%, 97%, 92%
Malafaia et al. (2021) [29]	LIDC-IDRI Lung Cancer	CNN with XAI	89.60%
Cao et al. (2025) [13]	HIV, RNA-Seq Data	DCNN ,LSTM, DeepTD	77.64%

4 Challenges in Deploying XAI for Healthcare Applications

The development of AI systems that can provide clear, understandable justifications for their choices and actions is known as Explainable Artificial Intelligence (XAI). Incorporating XAI in the healthcare setting presents many obstacles [4].

Healthcare data is inherently complex, multifaceted, and sourced from various origins, making it challenging to integrate and interpret effectively for developing transparent AI models. [3].

Because of the complex structures, advanced artificial intelligence models based on deep learning frequently serve as "black boxes." One major challenge is explaining

the decision-making procedures of these models in a way that medical professionals can comprehend [15].

A key component of interpretability is to recognize and display the most important factors affecting a choice. Understanding which patient characteristics the AI model considers and how it affects the predictions is critical in the healthcare industry [27].

The healthcare industry, governed by strict regulations like HIPAA, faces challenges in applying XAI systems while meeting regulatory criteria and ensuring model accuracy and interpretability [37]. Creating interfaces that efficiently convey AI-generated insights to healthcare professionals involves balancing comprehensive explanations with simplicity, avoiding data overload while ensuring effective human-AI engagement [46].

Algorithm 1 Adaptive Feature Selection Using GA

Input: Dataset D with features $\{A, B, C, D, E\}$ and target T
Output: Best subset of features S_{best}
procedure FeatureSelection(D, T)
    Initialize: Set N (population size), k (top solutions), P_c (crossover rate), P_m (mutation rate), $MaxIter$ (iterations)
    Generate population $P = \{S_1, S_2, \ldots, S_N\}$, each $S_i \subseteq \{A, B, C, D, E\}$
    for each $S_i \in P$ **do**
        Compute fitness $F(S_i)$
    end for
    Selection: Sort P by $F(S_i)$, select top k solutions $P_{selected}$
    for each $(S_i, S_j) \in P_{selected}$ **do**
        Generate random $r \in [0, 1]$
        if $r < P_c$ **then**
            Create S_{new} from crossover of S_i and S_j
        end if
    end for
    for each S_{new} **do**
        Generate random $r \in [0, 1]$
        if $r < P_m$ **then**
            Mutate S_{new} by adding/removing a feature
        end if
    end for
    Replacement: Evaluate $F(S_{new})$; replace the least fit in P with S_{new}
    Check Termination: If $MaxIter$ or satisfactory fitness reached, stop; otherwise, repeat
    Output: S_{best} with the highest $F(S)$ from final P
end procedure

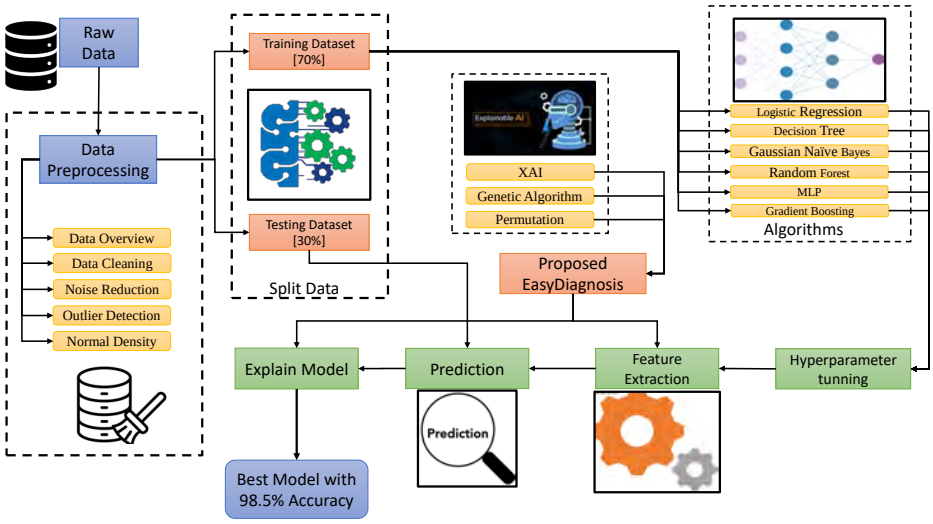

Fig. 2 Workflow framework of the proposed approach

5 The Proposed Novel EasyDiagnosis Framework

This section outlines the foundational components of our study, including the architecture of XAI, various Machine Learning (ML) frameworks, and the EasyDiagnos framework. Fig. 2 illustrates the workflow of the proposed EasyDiagnosis framework, detailing the entire implementation process. It begins with data augmentation, progresses through ML implementation and feature importance evaluation using the proposed EasyDiagnosis algorithm, and concludes with the selection of the optimal model.

5.1 What is XAI?

Explainable AI (XAI) is the term used to describe a group of artificial intelligence systems with the ability to explain their own activities, revealing the advantages, disadvantages, and possible future behaviors. XAI's main philosophy is to use a variety of approaches. The methods are meant to provide future developers with a wide range of design choices that compromise explainability and performance. Essentially, XAI aims to improve artificial intelligence system transparency by providing insights into algorithms' decision-making processes, making it easier to understand their outputs, and building user and stakeholder trust.

5.2 Genetic Algorithm and PCT for Feature Selection

A genetic algorithm for feature selection is a search heuristic using the principles of natural selection and genetics to find the optimal feature subset to improve a machine-learning model's performance. Permutation and combination algorithms are exhaustive search methods used for feature selection. It involves generating all possible

subsets of features and evaluating the performance using a fitness function. Algorithm 1 represents the working process of the GA process, and Algorithm 2 provides the approach for the PCT.

5.3 Exploration of Classification Techniques

5.3.1 Logistic Regression

Logistic regression (LR) analyzes datasets where independent variables predict an outcome by fitting data to a logistic curve, estimating event probability using $P(y = 1|x) = \frac{1}{1+e^{-z}}$ where $z = w^T x + b$.

5.3.2 Decision Tree

Decision trees (DT) are used for regression and classification by splitting data into subsets based on key attributes, forming a tree-like structure.

5.3.3 Gaussian Naive Bayes

Gaussian Naive Bayes (GNB), a probabilistic classifier, assumes feature independence and uses Bayes' theorem: $P(y|x) = \frac{P(x|y)P(y)}{P(x)}$.

5.3.4 Random Forest

Random Forest (RF) builds an ensemble of decision trees using random subsets of features and data, outputting the class mode.

5.3.5 Multi-layer Perceptron (MLP) Classifier

MLP is a feedforward neural network with multiple layers, learning non-linear relations; hidden layer activations are $h_i = \sigma\left(\sum_{j=1}^{m} w_{ij}^{(1)} x_j + b_i^{(1)}\right)$.

5.3.6 Gradient Boosting

Gradient Boosting (GB) is an ensemble technique that sequentially adds weak learners to correct previous model errors, defined as $F_m(x) = F_{m-1}(x) + \arg\min_h \sum_{i=1}^{N} L(y_i, F_{m-1}(x_i) + h(x_i))$.

5.4 Description of Interpretable Models

Contextual Importance and Utility (CIU), Gradient-Weighted Class Activation Mapping (Grad-CAM), SHAP, and LIME are fundamental approaches in XAI that enhance understanding of DL and ML algorithms. SHAP is notably recognized for improving model accuracy and clarifying model behavior. In this work, we employ SHAP as the primary part of the EasyDiagnosis. By leveraging these advanced XAI techniques, we aim to deliver precise and interpretable model outputs, foster stakeholder confidence, enable informed decision-making, and bridge the gap between complex AI models and human understanding.

Algorithm 2 Adaptive Feature Selection Using Permutations and Combinations Technique (PCT)

Input: Dataset D with features $F = \{A, B, C\}$ and target variable T
Output: Best subset of features S_{best} for predicting T

procedure FeatureSelection(D, F, T)
    Permutation Generation
    Initialize set $P \leftarrow$ all permutations of F
    Combination Generation
    Initialize set $C \leftarrow$ all combinations of F
    Fitness Evaluation
    Initialize list $FitnessScores \leftarrow [\,]$
    for $S \in P \cup C$ **do**
        Compute fitness (Accuracy) $F(S)$ using fitness function f
        Append $F(S)$ to $FitnessScores$
    end for
    Selection
    $S_{best} \leftarrow \arg\max_{S \in P \cup C} F(S)$
    Output: return S_{best}
end procedure

5.4.1 SHapley Additive exPlanations (SHAP)

SHAP is a crucial tool in XAI for interpreting machine learning models. Renowned for its adaptability, SHAP quantifies each feature's impact on model predictions using Shapley values, offering deep insights into the decision-making process. It extends the capabilities of previous XAI methods like LIME and DeepLift, making it a preferred choice for model interpretation.

In a simplified form, the SHAP value for a feature i in a prediction x can be expressed as equation 7.

$$\phi_i(x) = \sum_{S \subseteq \{1,2,\ldots,p\} \setminus \{i\}} \frac{|S|!(p - |S| - 1)!}{p!} [f_x(S \cup \{i\}) - f_x(S)] \tag{1}$$

Here, $\phi_i(x)$ represents the SHAP value for feature i in prediction x and $f_x(S)$ represents the model's output when considering only the features in subset S. p represents the total number of features. The SHAP library offers a variety of explainers, each designed to fit particular model types and data properties.

5.4.2 SHAP Value Explain By An Example

Shapley values, derived from cooperative game theory, assess each player's contribution by fairly distributing rewards based on individual input. Shapley values in machine learning assess each feature's average marginal impact by evaluating all feature combinations, offering a thorough understanding of its influence on model outcomes.

Consider a team (A, B, C, D, E) working together to generate profit (P) for the company. To fairly distribute profits based on individual contributions, each member's

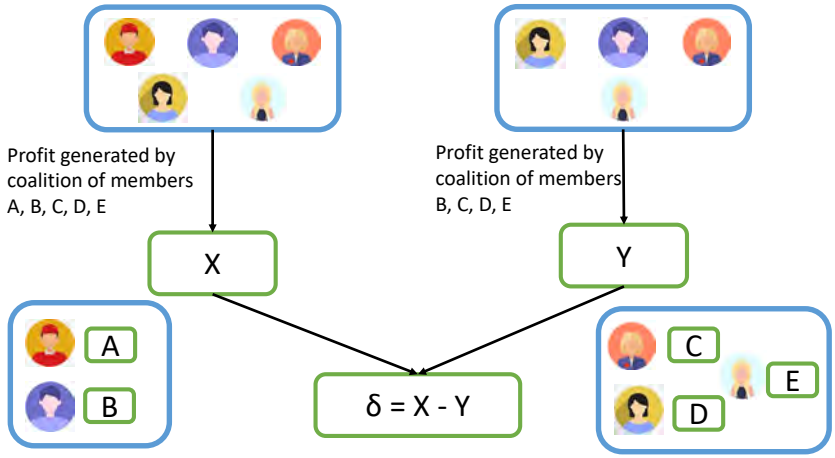

Fig. 3 Calculating the marginal distribution for a feature

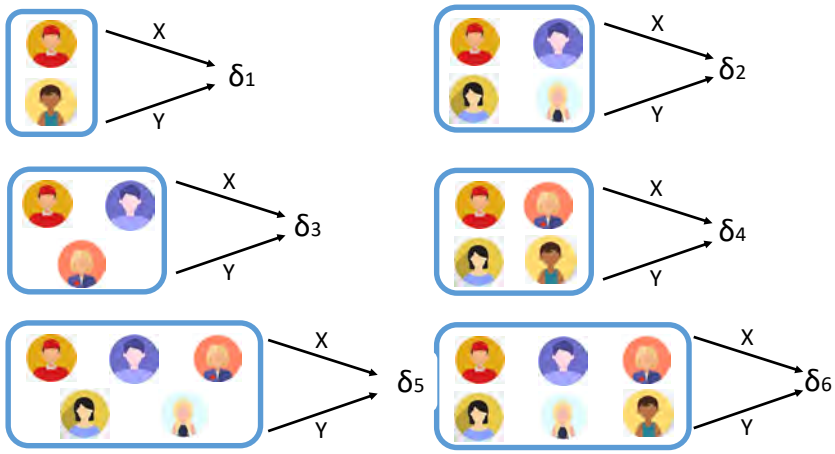

Fig. 4 Calculating the shapley value for a feature

Shapley Value is calculated by comparing the profit with and without the participation. The method quantifies each member's contribution, similar to determining Shapley values for features in a dataset. Fig. 3 shown the process clearly. Fig. 4 represents the calculation of different parameters for the Shapley values calculation. The SHAP value of member 'A' is given by mean value calculation equation, and the δ values are calculated as shown in Fig.4. The "marginal contribution" of member 'A' represents the impact of 'A' within different group configurations or coalitions. To compute the Shapley Value of 'A,' we evaluate the contribution of 'A' across all possible alliances and take the average of this assistance to quantify 'A's overall influence within the group.

Fig. 2 illustrates the complete workflow of our study, detailing the data journey from import to model evaluation. Initially, the raw data is imported to ensure accurate predictions, followed by necessary preprocessing and data cleaning. The processed data is then divided into training (70%) and testing (30%) sets. Subsequently, different models are constructed and trained using the training dataset. Hyperparameter tuning is performed to optimize model performance by iterating through various parameter values for optimal results.

After training the models, the test dataset is used to predict outcomes and assess accuracy. We introduce an XAI method, specifically SHAP, integrated with a Genetic Algorithm (GA) and a Permutation Combination Technique (PCT)-based feature importance approach, to propose a novel feature evaluator algorithm, EasyDiagnosis. EasyDiagnosis identifies key features and offers important explanations for the models. Since EasyDiagnosis is trained on testing data, it provides insights into the decision-making process of our best-performing model. Finally, the most suitable deployment model is selected based on comprehensive evaluation criteria and interpretability.

5.5 Proposed EasyDiagnosis Algorithm

The EasyDiagnosis is a novel algorithm designed to determine feature significance across various datasets. EasyDiagnosis consistently outperforms existing feature selection algorithms in comparative tests when applied to machine learning (ML) and deep learning (DL) models. Due to its global adaptability, EasyDiagnosis integrates seamlessly with any algorithm and dataset.

EasyDiagnosis combines three effective feature selection strategies: Explainable AI (XAI), Permutation & Combination Techniques (PCT), and Genetic Algorithms (GA). It computes accuracy scores independently for each methods and synthesizes all, resulting in consistently higher accuracy. The robustness of EasyDiagnosis is assessed using six different algorithms, including GB, MLP Classifier, GNB, DT, and LR, and validated on three healthcare datasets: Covid-19, Heart Disease, and Lung Cancer. EasyDiagnosis demonstrated superior performance and flexibility in all cases compared to state-of-the-art methods. Through rigorous testing and validation, EasyDiagnosis establishes itself as a highly adaptive and accurate feature selection system, surpassing conventional techniques. Fig. 5 and Algorithm 3 clearly discuss the proposed EasyDiagnosis algorithm through flowchart and algorithm consecutively.

6 Experimental Results

In this work, we propose and investigate the critical role of feature explainers using Explainable AI (XAI), in conjunction with the well-known Genetic Algorithm (GA) and Permutation Combination Technique (PCT), to enhance the performance and interpretability of machine learning algorithms. The evaluation is conducted across three distinct healthcare datasets—COVID-19, heart disease, and lung cancer, representing various medical conditions. This comprehensive assessment demonstrates the efficacy of the proposed EasyDiagnosis across various healthcare domains.

Algorithm 3 Proposed EasyDiagnosis Algorithm

Input: Dataset X with features and target variable y
Output: Sorted feature importance C_{imp}

procedure FEATURESELECTION(X, y)
  $(X_{train}, y_{train}), (X_{test}, y_{test}) \leftarrow$ SPLIT(X, y)
  $PCT_{acc}, PCT_{imp} \leftarrow$ PCT(X_{test}, y_{test})
  $SHAP_{acc}, SHAP_{imp} \leftarrow$ SHAP(X_{train}, X_{test})
  $GA_{acc}, GA_{imp} \leftarrow$ GA($X_{train}, y_{train}, X_{test}$)
  $T_{acc}, W \leftarrow$ CALCWEIGHTS($PCT_{acc}, SHAP_{acc}, GA_{acc}$)
  $C_{imp} \leftarrow$ COMBINE($PCT_{imp}, SHAP_{imp}, GA_{imp}, W$)
  DISPLAY(C_{imp})
end procedure
procedure SPLIT(X, y)
  return Split X, y into $(X_{train}, y_{train}), (X_{test}, y_{test})$
end procedure
procedure PCT(X_{test}, y_{test})
  Compute permutation importance on (X_{test}, y_{test})
  Select features where importance > median
  Train classifier; calculate PCT_{acc} on X_{test}
  return PCT_{acc}, PCT_{imp}
end procedure
procedure SHAP(X_{train}, X_{test})
  Compute SHAP values for X_{train}
  Select features where SHAP value > median
  Train classifier; calculate $SHAP_{acc}$ on X_{test}
  return $SHAP_{acc}, SHAP_{imp}$
end procedure
procedure GA($X_{train}, y_{train}, X_{test}$)
  Apply GA for feature selection on (X_{train}, y_{train})
  Select features based on GA output
  Train classifier; calculate GA_{acc} on X_{test}
  return GA_{acc}, GA_{imp}
end procedure
procedure CALCWEIGHTS($PCT_{acc}, SHAP_{acc}, GA_{acc}$)
  $T_{acc} \leftarrow PCT_{acc} + SHAP_{acc} + GA_{acc}$
  $W_{PCT} \leftarrow \frac{PCT_{acc}}{T_{acc}}, W_{SHAP} \leftarrow \frac{SHAP_{acc}}{T_{acc}}, W_{GA} \leftarrow \frac{GA_{acc}}{T_{acc}}$
  return $T_{acc}, (W_{PCT}, W_{SHAP}, W_{GA})$
end procedure
procedure COMBINE($PCT_{imp}, SHAP_{imp}, GA_{imp}, W$)
  $C_{imp} \leftarrow (W_{PCT} \times PCT_{imp}) + (W_{SHAP} \times SHAP_{imp}) + (W_{GA} \times GA_{imp})$
  return C_{imp}
end procedure
procedure DISPLAY(C_{imp})
  Sort and display features by C_{imp} in descending order
end procedure

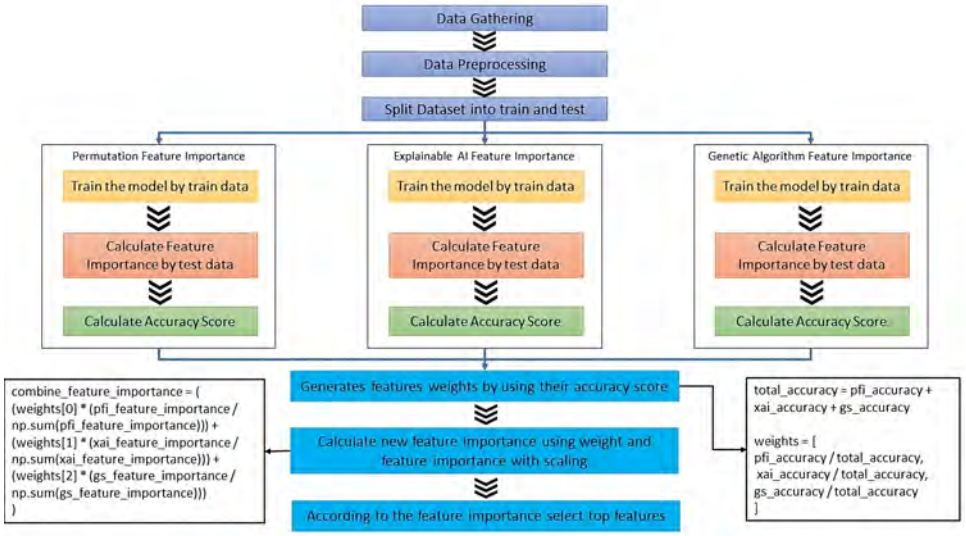

Fig. 5 Diagram of the EasyDiagnosis Algorithm for Enhanced Feature Selection

6.1 Simulation Setup

The data visualization and manipulation experiment is in a Python 3.12 environment using packages like matplotlib, pandas, numpy, and seaborn.

The implementation utilizes the scikit-learn (SKLearn) toolkit for predictive modeling, employing six distinct algorithms to enhance prediction accuracy. The proposed study investigates various methods by implementing each algorithm and importing custom libraries customized to meet specific requirements. We use the Stable-Baselines3 library with Proximal Policy Optimization (PPO) to train an RL agent for feature selection.

We utilize the SHAP libraries along with GA and PCT methods to enhance the interpretability and insights of our models. The libraries help clarify the predictions made by our models, shedding light on the underlying factors driving the results and improving the transparency of our research.

6.2 Dataset Overview

The proposed work use three different types of datasets for this investigation. The Lung Cancer online repository from the University of California, Irvine [20]. The entire dataset consists of one class attribute, 32 instances, and 57 characteristics. There are one label feature and fifteen input features in this dataset. Total 16 features and 309 data samples are available in the dataset.

The UCI Machine Learning Repository provided one of the datasets use in our study, which is centered on heart disease [5]. The output features in the dataset indicate several kinds of cardiac disorders. Total 12 features and 918 samples are available in the dataset.

One of the most extensive compilations of current COVID-19-related data is the Google Health COVID-19 Open Data Repository [43]. Including information from over 20,000 sites globally, it offers a wide range of data formats to support researchers, policymakers, public health experts, and others in understanding and managing the virus. Total 11 features and 278848 samples are available in the dataset.

6.3 Detailed Discussion

This paper explores the role of feature importance in enhancing the performance and interpretability of machine learning algorithms across three diverse healthcare datasets—COVID-19, heart disease, and lung cancer. The datasets represent a broad spectrum of medical conditions, allowing for a comprehensive evaluation of the effectiveness of Explainable Artificial Intelligence (XAI) across different healthcare domains.

We employed six distinct classification algorithms: Logistic Regression (LR), Decision Tree (DT), Gaussian Naive Bayes (GNB), Random Forest (RF), Multi-layer Perceptron Classifier (MLP), Gradient Boosting (GB). By leveraging the diverse set of algorithms, we aim to capture the variation in model performance across different healthcare datasets and conditions. Each algorithm offers unique strengths and weaknesses. The comprehensive approach is essential for thoroughly evaluating the models' performance and interpretability.

The proposed model ensemble consists of six algorithms, where the LR is with random_state=0 (default parameters otherwise), Decision Tree with entropy criterion and random_state=0, Gaussian Naive Bayes, Random Forest are using default configurations. Additionally, we include an MLP Classified with a hidden layer size of 100, ReLU activation (f(x) = max(0, x)), Adam optimizer, and a learning rate of 0.001. Finally, the ensemble incorporates Gradient Boosting with log_loss function, a learning rate of 0.1, and the friedman_mse criterion.

The result matrices for COVID-19, heart disease, and lung cancer datasets are presented in Table 2, where only data preprocessing are applied, without any feature importance techniques. The tables provide a baseline performance metric, enabling us to evaluate the impact of feature importance strategies in subsequent analyses. Comparing initial results with outcomes after applying feature selection methods aims to demonstrate improvements in model accuracy, robustness, and interpretability. Performance is measured using accuracy and F1 score, with accuracy reflecting overall performance and F1 score balancing recall and precision as its harmonic mean.

The accuracy metrics after applying Permutation Feature Importance, Explainable AI (XAI) techniques, and the Genetic Algorithm (GA) feature importance technique are presented in Table 3 using lung cancer data. A reinforcement learning-based method, a Deep Q-Learning algorithm that dynamically chooses the most relevant features to improve feature selection, is also implemented for comparison with the proposed EasyDiagnosis. The observation we found with an F1 score of 92. 12% and a mean accuracy of 91. 71% shows that the EasyDiagnosis method significantly increases the accuracy of the model. Although the methods improved the accuracy of specific models, they did not enhance the performance across all algorithms. We introduced our proposed EasyDiagnosis algorithm to address the limitation, consistently improving

Table 2 Performance prediction metrics without features importance consideration

Sl No	Algo	Lung Cancer		Heart Disease		Covid-19 Data	
		Accuracy	F1 Score	Accuracy	F1 Score	Accuracy	F1 Score
1	LR	89.855	94.117	83.478	86.619	92.363	92.526
2	DT	91.304	94.915	80.869	83.823	93.395	94.452
3	GNB	91.304	94.827	83.478	86.713	90.452	91.352
4	RF	91.304	94.915	83.043	85.920	93.399	94.459
5	MLP	88.405	93.333	84.782	87.632	92.396	94.452
6	GB	89.855	94.117	88.043	86.021	93.399	94.457

Table 3 Performance prediction metrics with feature importance consideration for Lung Cancer

Sl No	Algorithm	PCT		XAI		GA		Deep Q-learning		EasyDiagnosis	
		Acc	F1	Acc	F1	Acc	F1	Acc	F1	Acc	F1
1	LR	89.96	94.31	89.86	94.21	89.86	94.31	90.65	91.23	94.16	95.46
2	DT	91.80	95.92	89.86	94.02	92.75	95.80	89.19	91.01	96.76	96.76
3	GNB	86.96	92.31	86.96	92.31	86.96	92.31	90.76	92.75	94.18	94.73
4	RF	89.86	94.12	92.75	95.87	92.75	95.80	91.19	92.24	98.79	99.42
5	MLP	89.86	94.12	91.30	95.08	88.41	93.55	88.40	93.75	96.19	96.76
6	GB	89.86	94.12	89.86	94.02	92.75	95.80	91.71	92.12	99.19	99.79

Table 4 Performance prediction metrics with EasyDiagnosis feature importance consideration

Sl No	Algo.	Heart Disease		Covid-19 Data	
		Accuracy	F1 Score	Accuracy	F1 Score
1	LR	92.76	92.21	96.34	96.23
2	DT	94.10	93.72	97.95	98.58
3	GNB	91.85	91.32	94.78	95.71
4	RF	96.95	96.50	98.65	99.15
5	MLP	96.12	95.80	98.51	99.14
6	GB	97.50	96.73	97.15	98.97

accuracy across all models, and delivering more reliable and precise outcomes. Using the strengths of multiple feature importance techniques, the EasyDiagnosis algorithm ensures robust performance and enhanced interpretability in diverse healthcare applications. Comparing the results obtained using the EasyDiagnosis technique, as shown in the final column of Table 3, with the baseline metrics in Table 2, it is evident that the EasyDiagnosis algorithm outperforms the other six models.

The EasyDiagnosis is validated using two additional datasets: Heart disease and COVID-19. The accuracy metrics for the datasets are shown in Table 4. In both

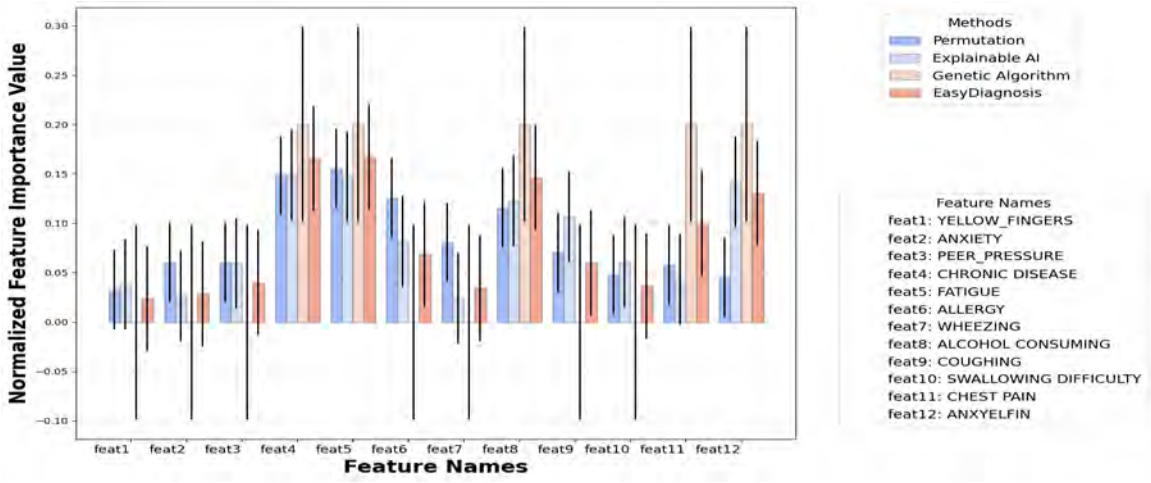

Fig. 6 EasyDiagnosis feature explanation for Lung Cancer Data

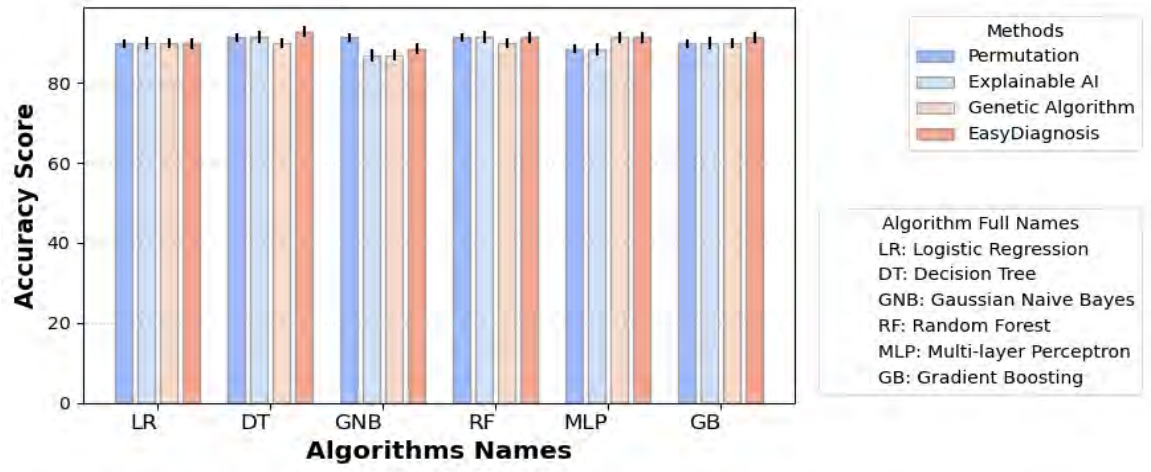

Fig. 7 Accuracy score comparison for Lung Cancer with EasyDiagnosis features

cases, EasyDiagnosis consistently outperformed other feature significance techniques. The comprehensive evaluation demonstrates that EasyDiagnosis is a valuable tool to enhance the performance of machine learning models in healthcare applications. It maintains robustness across diverse datasets and methods and significantly improves accuracy.

The feature selection process of the EasyDiagnosis algorithm provides a relevance score for each feature, ranked in descending order, as shown in Table 6. The feature importance scores are expressed as probabilities ranging from 0 to 1. The table

Table 5 Performance Comparison of EasyDiagnosis Model and Baseline with Statistical Analysis (95% CI)

SI No	Algo	Accuracy	F1 Score	Precision	Recall
1	LR	93.85% ± 0.5%	93.42% ± 0.4%	93.10% ± 0.4%	93.85% ± 0.5%
2	DT	95.30% ± 0.6%	94.89% ± 0.5%	96.15% ± 0.5%	94.64% ± 0.6%
3	GNB	94.65% ± 0.6%	94.21% ± 0.5%	92.85% ± 0.5%	96.43% ± 0.6%
4	RF	97.15% ± 0.4%	96.82% ± 0.4%	97.10% ± 0.4%	97.15% ± 0.5%
5	MLP	96.84% ± 0.5%	96.43% ± 0.4%	95.90% ± 0.4%	96.84% ± 0.5%
6	GB	97.54% ± 0.4%	97.22% ± 0.4%	97.10% ± 0.4%	97.54% ± 0.5%

Table 6 Features important of Lung Cancer Dataset

Sl. No	Features Name	Feature weight
1	ANXYELFIN	0.203482
2	COUGHING	0.135953
3	CHRONIC DISEASE	0.129164
4	FATIGUE	0.103765
5	ALCOHOL CONSUMING	0.099770
6	PEER_PRESSURE	0.072191
7	YELLOW_FINGERS	0.064810
8	ANXIETY	0.064340
9	CHEST PAIN	0.050378
10	ALLERGY	0.031955
11	SWALLOWING DIFFICULTY	0.027210
12	WHEEZING	0.016981

ranks features by importance based on the EasyDiagnosis algorithm. ANXYELFIN is the most significant feature (weight: 0.203), followed by COUGHING (0.136) and CHRONIC DISEASE (0.129). Features like FATIGUE (0.104) and ALCOHOL CONSUMING (0.100) are moderately important, while WHEEZING (0.017) is the least influential. This probabilistic representation offers an intuitive and straightforward understanding of each feature's relative importance, facilitating informed decision-making during model development. Figure 6 shows the feature importance overview of lung cancer data. By highlighting the most critical features, the EasyDiagnosis algorithm enhances the interpretability and performance of machine learning models across various healthcare applications.

Table 7 Performance comparison of proposed and previous research

Work	Dataset	Algorithm	Accuracy
Ahmad et al. (2023) [2]	Lung Cancer Dataset	Random Forest	97%
Naseer et al. (2019) [31]	Lung Cancer Dataset	ANN	96.67%
Riaz et al. (2018) [39]	UCI Heart Disease Dataset	KNN, DT	78%, 80%
Wickstrøm et al. (2020) [45]	ECG Data	Ensemble Learning	93.8%
Batista et al. (2020) [10]	Covid-19 Pandemic Dataset	SVM	84.85%
Mahdy et al. (2020) [28]	Covid-19 Pandemic Dataset	SVM	95%
Nfissi et al. (2024) [33]	TESS, EMO-DB	DCNN, XAI	79.5%
Sharma et al. (2024) [40]	WSC, CAP ECG data	DWSN,TNN, XAI	98%
Proposed Work	Lung Cancer Dataset	Random Forest	98.79%
	UCI Heart Disease Dataset	GB	97.05%
	Covid-19 Pandemic Dataset	MLP	98.65%

6.4 Statistical Analysis of the Models Performance

This study applies confidence intervals (CIs) and hypothesis testing methods to validate the statistical significance of model performance improvements. A 95% confidence interval (CI) is used to verify the degree of uncertainty in model predictions is computed for each evaluation metric, including accuracy, F1-score, precision, and recall. The CIs provide an estimated range within which the actual performance metrics are expected to fall, ensuring a more reliable assessment of model effectiveness. A paired t-test is also performed to compare each model against the baseline model. This test evaluates whether the observed improvements in accuracy and other metrics are statistically significant, confirming that the enhancements are not due to random variations in the dataset.

The proposed models performed consistently in several runs using the EasyDiagnosis technique. We obtained an accuracy of 97.54% $\pm$ 0.4% (95% CI: 97.14, 97.94) using 5-fold cross-validation. On the other hand, the accuracy of the baseline model (Decision Tree) with EasyDiagnosis is 95.30% $\pm$ 0.6% (95% CI: 94.70, 95.90). The outcomes show that the proposed EasyDiagnosis model performs noticeably better than the baseline model. A paired t-test comparing the multiple models demonstrates the model's superiority, which confirmed a statistically significant difference with $t = 17.01$, $p < 0.0001$. Furthermore, the statistical significance of the observed accuracy gains is further supported by an ANOVA test with $F = 351.73$, $p < 0.0001$. Table V represents the performance comparison of proposed EasyDiagnosis Model and Baseline using 5-Fold cross-validation and statistical significance analysis

6.5 Comparative Analysis with Existing Research

The model proposed in the work achieves a prediction accuracy of 98.5% on the Covid-19 Dataset using the MLP, outperforming the other models. Similarly, on the UCI Heart Disease Dataset, our model achieves an accuracy of 90.52% using the GB

algorithm, matching the performance of previous models. Using the RF approach, the suggested model achieves an accuracy of 95.5% for the Lung Cancer Dataset, showing competitive performance in comparison to earlier research. Fig. 7 represents the effect of EasyDiagnosis features on others regarding accuracy. The comparison between the prediction accuracy of our proposed model and other existing models is shown in Table 7. The table presents a performance comparison between the proposed work and previous research across different datasets and algorithms. The proposed work demonstrates notable improvements in accuracy for each dataset and algorithm combination.

7 Conclusion

The work underscores the vital role of feature importance in improving the performance and interpretability of machine learning algorithms within the healthcare sector by evaluating various feature selection techniques in three distinct datasets: lung cancer, heart disease, and COVID-19. We identified the strengths and limitations of each method. The proposed EasyDiagnosis consistently surpasses traditional techniques, offering superior accuracy and robustness across diverse algorithms and datasets. The algorithm identifies key features with probabilistic importance and ensures their interpretability and relevance. The comprehensive evaluation validates the EasyDiagnosis as a transformative tool for advancing machine learning applications in healthcare, leading to more accurate, reliable, and actionable insights.

The algorithm ensures thorough and objective feature selection by combining PCT, SHAP, and GA. Its adaptive weighing method improves stability and robustness, which dynamically allocates importance based on accuracy contribution. It enhances model interpretability and generalization by capturing both linear and non-linear dependencies, which makes it appropriate for complex datasets. The algorithm employs various feature selection strategies, increasing its capacity to find the most relevant characteristics for better prediction performance. While this adds computing complexity, it guarantees a complete and robust feature examination. Furthermore, the model performs well with massive datasets, making it ideal for detailed analysis. The accuracy-based weighing mechanism is flexible and can be further adjusted to improve consistency across multiple applications. As healthcare data grows in complexity, the EasyDiagnosis presents a promising solution for refining predictive models and enhancing clinical decision making.

References

[1] Ahmad, A., et al.: iafps-enc-ga: identifying antifungal peptides using sequential and evolutionary descriptors based multi-information fusion and ensemble learning approach. Chemometr Intell Lab Syst **222**, 104516 (2022)

[2] Ahmed, M.S., Iqbal, N., Alam, M.G.R.: Interpretable lung cancer detection using explainable ai methods. In: 10.1109/ICONAT57137.2023.10080480 (2023)

[3] Ali, S., Abdullah, Armand, T.P.T., Athar, A., Hussain, A., Ali, M., Yaseen, M., Joo, M.i., Kim, H.C.: Metaverse in healthcare integrated with explainable ai and

blockchain: Enabling immersiveness, ensuring trust, and providing patient data security. Sensors **23**(2) (2023)
[4] Allen, B.: Discovering themes in deep brain stimulation research using explainable artificial intelligence. Biomedicines **11**(3) (2023)
[5] Andras, J., William, S., Matthias, P., Robert, D.: Heart Disease. UCI Machine Learning Repository (1988), DOI: https://doi.org/10.24432/C52P4X
[6] Angelov, P., Soares, E.: Towards explainable deep neural networks (xdnn). Neural Netw. **130**, 185–194 (2020)
[7] Annuzzi, G., et al.: Exploring nutritional influence on blood glucose forecasting for type 1 diabetes using explainable ai. IEEE Journal of Biomedical and Health Informatics **28**(5), 3123–3133 (May 2024). https://doi.org/10.1109/JBHI.2023.3348334
[8] Ansari, U., Soni, J., Sharma, D., Soni, S.: Predictive data mining for medical diagnosis: An overview of heart disease prediction. Data Mining in Healthcare for Heart Diseases (March 2011)
[9] Arrieta, A., Díaz-Rodríguez, N., Del Ser, J., Bennetot, A., Tabik, S., Barbado, A., García, S., Gil López, S., Molina, D., Benjamins, R., et al.: Explainable artificial intelligence (xai): Concepts, taxonomies, opportunities and challenges toward responsible ai. Inf. Fusion **58**, 82–115 (2020)
[10] Batista, A.d.M., Miraglia, J., Donato, T., Chiavegatto Filho, A.: Covid-19 diagnosis prediction in emergency care patients: a machine learning approach. MedRxiv (2020)
[11] Beebe-Wang, N., Okeson, A., Althoff, T., Lee, S.I.: Efficient and explainable risk assessments for imminent dementia in an aging cohort study. IEEE Journal of Biomedical and Health Informatics **25**(7), 2409–2420 (July 2021). https://doi.org/10.1109/JBHI.2021.3059563, epub 2021 Jul 27
[12] Beyene, C., Kamat, P.: Survey on prediction and analysis the occurrence of heart disease using data mining techniques. 118(8):165-173 (January 2018)
[13] Cao, Z., Sun, X., Fu, Y.: Deep neural network-based feature selection with local false discovery rate estimation. Applied Intelligence **55**, 32 (2025). https://doi.org/10.1007/s10489-024-05944-7
[14] Chehade, A.H., Abdallah, N., Marion, J.M., et al.: Lung and colon cancer classification using medical imaging: a feature engineering approach. Phys Eng Sci Med **45**, 729–746 (2022). https://doi.org/10.1007/s13246-022-01139-x, https://doi.org/10.1007/s13246-022-01139-x
[15] Ding, R., Yin, W., Cheng, G., Chen, Y., Wang, J., Wang, R., Rui, Z., Li, J., Liu, J.: Boosting the optimization of membrane electrode assembly in proton exchange membrane fuel cells guided by explainable artificial intelligence. Energy and AI **5** (2021)
[16] von Eschenbach, W.: Transparency and the black box problem: Why we do not trust ai. Philos. Technol. **34**, 1607–1622 (2021)
[17] Gerke, S., Minssen, T., Cohen, G.: Chapter 12 - ethical and legal challenges of artificial intelligence-driven healthcare. In: Bohr, A., Memarzadeh, K. (eds.) Artificial Intelligence in Healthcare, pp. 295–336. Academic Press (2020). https://doi.org/https://doi.org/10.1016/B978-0-12-818438-7.00012-5,

https://www.sciencedirect.com/science/article/pii/B9780128184387000125
[18] Guleria, P., Naga Srinivasu, P., Ahmed, S., Almusallam, N., Alarfaj, F.: Xai framework for cardiovascular disease prediction using classification techniques. Electronics **11**, 4086 (2022), https://doi.org/10.3390/electronics11244086
[19] Higgins, D., Madai, V.: From bit to bedside: a practical framework for artificial intelligence product development in healthcare. Adv Intell Syst **2**, 2000052 (2020)
[20] Hong, Z., Yang, J.: Lung Cancer. UCI Machine Learning Repository (1992), DOI: https://doi.org/10.24432/C57596
[21] Hrnjica, B., Softic, S.: Explainable ai in manufacturing: a predictive maintenance case study. In: IFIP international conference on advances in production management systems. Springer (2020)
[22] Huang, Y., Chen, G., Gou, J., et al.: A hybrid feature selection and aggregation strategy-based stacking ensemble technique for network intrusion detection. Applied Intelligence **55**, 28 (2025). https://doi.org/10.1007/s10489-024-06015-7
[23] Ismail, M.B.S.: Lung cancer detection and classification using machine learning algorithm. Turkish Journal of Computer and Mathematics Education (TURCOMAT) **12**(13), 7048–7054 (2021)
[24] Kumar, C.A., Harish, S., Ravi, P., Svn, M., Kumar, B., Mohanavel, V., Alyami, N., Priya, S., Asfaw, A.: Lung cancer prediction from text datasets using machine learning. BioMed Research International **2022** (2022)
[25] Kühn, S., Rieger, U.: Health is a state of complete physical, mental and social wellbeing and not merely absence of disease or infirmity. Surg Obes Relat Dis **13**(5), 887 (2017)
[26] Li, Y., Gu, D., Wen, Z., Jiang, F., Liu, S.: Classify and explain: An interpretable convolutional neural network for lung cancer diagnosis. In: ICASSP 2020-2020 IEEE International Conference on Acoustics, Speech and Signal Processing (ICASSP). pp. 1065–1069. IEEE (2020)
[27] Linardatos, P., Papastefanopoulos, V., Kotsiantis, S.: Explainable ai: A review of machine learning interpretability methods. Entropy **23**(1) (2021)
[28] Mahdy, L., Ezzat, K., Elmousalami, H., Ella, H., Hassanien, A.: Automatic x-ray covid-19 lung image classification system based on multi-level thresholding and support vector machine. MedRxiv (2020)
[29] Malafaia, M., Silva, F., Neves, I., Pereira, T., Oliveira, H.: Robustness analysis of deep learning-based lung cancer classification using explainable methods. IEEE Access **9**, 1–1 (2021)
[30] Mu, J., Kadoch, M., Yuan, T., Lv, W., Liu, Q., Li, B.: Explainable federated medical image analysis through causal learning and blockchain. IEEE Journal of Biomedical and Health Informatics **28**(6), 3206–3218 (June 2024). https://doi.org/10.1109/JBHI.2024.3375894, epub 2024 Jun 6, PMID: 38470597
[31] Nasser, I.M., Abu-Naser, S.S.: Lung cancer detection using artificial neural network. International Journal of Engineering and Information Systems (IJEAIS) **3**(3), 17–23 (2019)
[32] Nazar, M., Alam, M., Yafi, E., Mazliham, M.: A systematic review of human-computer interaction and explainable artificial intelligence in healthcare with artificial intelligence techniques. IEEE Access **9**, 153316–153348 (2021)

[33] Nfissi, A., Bouachir, W., Bouguila, N., et al.: Unveiling hidden factors: explainable ai for feature boosting in speech emotion recognition. Applied Intelligence **54**, 7046–7069 (2024). https://doi.org/10.1007/s10489-024-05536-5
[34] Pai, K.C., et al.: An artificial intelligence approach to bloodstream infections prediction. J Clin Med **10**(13), 2901 (2021)
[35] Patro, S., Padhy, N.: A secure remote health monitoring for heart disease prediction using machine learning and deep learning techniques in explainable artificial intelligence framework. Eng. Proc. **58**, 78 (2023), https://doi.org/10.3390/ecsa-10-16237
[36] Ramos, B., Pereira, T., Moranguinho, J., Morgado, J., Costa, J., Oliveira, H.: An interpretable approach for lung cancer prediction and subtype classification using gene expression. In: Proc. 43rd Annu. Int. Conf. IEEE Eng. Med. Biol. Soc. (EMBC). pp. 1707–1710 (2021)
[37] Rane, N.: 3d, 4d, and 5d printing in architecture, engineering, and construction (aec) industry: Applications, challenges, and future scope. Available at SSRN (September 28 2023), https://ssrn.com/abstract=4609912, accessed: 2024-06-30
[38] Reddy, S., et al.: A governance model for the application of ai in health care. J Am Med Inf Assoc **27**(3), 491–497 (2020)
[39] Riaz, M.U., Awan, S.M., Khan, A.G.: Prediction of heart disease using artificial neural network. VFAST Transactions on Software Engineering **13**(3), 102–112 (2018)
[40] Sharma, N., Sharma, M., Telangore, H., et al.: Automated accurate insomnia detection system using wavelet scattering method using ecg signals. Applied Intelligence **54**, 3464–3481 (2024). https://doi.org/10.1007/s10489-024-05284-6
[41] Shortliffe, E., Sepúlveda, M.: Clinical decision support in the era of artificial intelligence. JAMA **320**, 2199–2200 (2018)
[42] Siddhartha, M., Maity, P., Nath, R.: Explanatory artificial intelligence (xai) in the prediction of post-operative life expectancy in lung cancer patients. Int. J. Sci. Res. **8**(12), 2328 (2019)
[43] Wahltinez, O., et al.: Covid-19 open-data: curating a fine-grained, global-scale data repository for sars-cov-2 (2020), https://goo.gle/covid-19-open-data
[44] Wang, X., et al.: A radiomics model combined with xgboost may improve the accuracy of distinguishing between mediastinal cysts and tumors: a multicenter validation analysis. Ann Transl Med **9**(23) (2021)
[45] Wickstrøm, K., Mikalsen, K., Kampffmeyer, M., Revhaug, A., Jenssen, R.: Uncertainty-aware deep ensembles for reliable and explainable predictions of clinical time series. IEEE Journal of Biomedical and Health Informatics **25**(7), 2435–2444 (July 2021). https://doi.org/10.1109/JBHI.2020.3042637
[46] Zhang, Z., Hamadi, H.a., Damiani, E., Yeun, C.Y., Taher, F.: Explainable artificial intelligence applications in cyber security: State-of-the-art in research. IEEE Access (2022)