Privacy-Enhanced Machine Learning Models for Heart Disease Detection Using Encrypted Patient Data

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| **How to cite this paper:** Author 1, Author 2 and Author 3 (2025) Paper Title. *\*\*\*\*\*\**, **\***, \*-\*. [https://dx.doi.org/10.4236/\*\*\*.2025.\*\*\*\*\*](https://dx.doi.org/10.4236/***.2025.*****)  **Received:** \*\*\*\* \*\*, \*\*\*  **Accepted:** \*\*\*\* \*\*, \*\*\*  **Published:** \*\*\*\* \*\*, \*\*\*  Copyright © 2025 by author(s) and Scientific Research Publishing Inc.  This work is licensed under the Creative Commons Attribution International License (CC BY 4.0).  <http://creativecommons.org/licenses/by/4.0/>  C:\Users\178\Desktop\图片1.emf |  |  | Abstract  This research presents a new framework to predict heart disease while prioritizing patient privacy. The framework involves multiple entities that come together to provide a platform for the effective collection, secured management, preprocessing, and data analysis of medical records. It introduces an implementation scheme which enforces a robust encryption policy to ensure that sensitive patient information is well-guarded throughout the entire lifecycle of the data. A comprehensive set of machine learning algorithms, such as Naïve Bayes, Decision Trees, Random Forests, K-Nearest Neighbors, Support Vector Machines, and Long Short-Term Memory networks, is applied stringently to the preprocessed data. To improve the effectiveness of predictions, dimensionality reduction techniques such as Principal Component Analysis and anomaly detection through Isolation Forest are applied. Rigorous hyperparameter optimization tuning is performed to ensure that the models are fine-tuned for optimal results. Empirical evaluation demonstrates the strong performance of the proposed framework, with Random Forest combined with Isolation Forest achieving an F1-score of 94.14%. The robust performance emanates from the well-effective combination of feature engineering, model selection, and optimization of hyperparameters. Overall, this research makes a valuable contribution to heart disease prediction by not only focusing on the high F1-score achieved through advanced machine learning techniques but also ensuring the privacy of sensitive data.  Keywords  Heart disease prediction · Data privacy · Machine learning · Isolation Forest · Long short-term memory |

1. Introduction

Heart disease remains the leading cause of deaths across the globe and one of the major public health challenges afflicting nearly 26 million people all over the world [1] and is likely to escalate prevalence in the future due to the growing populations of aged individuals [2]. Cardiovascular Disease (CVD) is becoming an increasingly important burden on health-care systems, and in the United States alone, it accounts for 17 percent of total health expenditures [3]. Innovations in diagnostic tools and medical management, however, have not improved the situation. Modern equipment patients cannot expect to have such access, especially those who are based in rural areas. Therefore, they rely on intuition from physicians to seek recommendations and treatment early [4]. Pattern recognition from high-quality datasets has recently shown promising results in machine learning (ML) in terms of the transformative capability of improving the diagnosis of diseases and prediction accuracy [5, 6]. Accordingly, the current study proposes a powerful ML system for heart disease prediction to cover the diagnostic gap with patient safety and reduced healthcare costs.

Most current diagnostic methods fall behind diagnosis, particularly at early stages, owing to accuracy, efficiency, and interpretability. Traditional models also tend to miss complex interactions of features along with temporal dependence in the data, which eventually leads to poor predictive performance. Also, privacy issues related to data poses concern about building strong models.

A hybridization model is being proposed in the present study, which includes the use of ensemble methods, dimensionality reduction, anomaly detection, and deep learning for solving the remaining issues. More robust and accurate prediction models are established, to this effect, integrating Random Forest Classifier (RF), Principal Component Analysis (PCA), Isolation Forest (iForest), and Long Short-Term Memory (LSTM). The LSTM component enables the capture of temporal patterns in patient data that might be overlooked by traditional ML models. Ensuring data security is also a focus, with encryption and privacy measures in place to safeguard patient confidentiality while supporting the development of effective models.

The hybrid method here distinguishes itself from other existing methods by multiple features (PCA and iForest); temporal dynamics (LSTM); and ensemble power (RF). Also, the data security part is fortified with ElGamal encryption, which ensures that the intermediate parties cannot change the data while it is encrypted during the application of ML techniques. All these are expected to help enhance predictive F1 score, shed more light on the underlying patterns related to heart disease, and ultimately translate to improved patient outcomes through earlier interventions. It can notably translate to reduced morbidity and mortality associated with heart disease and reduced healthcare costs. Additionally, the focus of the model on data security and privacy aligns with emerging healthcare regulations and patient expectations and, therefore, builds trust in the healthcare system. Therefore, if it succeeds in implementing the model, there is a big possibility of benefiting public health by reducing the global burden of heart diseases.

This paper attempts to assess the efficiency of various models of ML, along with their combinations, by employing the entire range of metrics like accuracy, specificity, recall, Positive Predictive Value (PPV), Negative Predictive Value (NPV), F1 score, and Area Under Curve (AUC). The strength of the aforementioned proposed approach is evaluated by viewing the effect of variation of training set size on the performance of the model.

2. Literature Review

Heart disease prediction is a primary area where a lot of research work has been done through different ML techniques and feature selection methods to enhance diagnostic accuracy. One of the studies optimized the feature selection along with classifier performance in the diagnosis of heart diseases [7].

This study compares established techniques like: Relief, Minimum Redundancy and Maximum Relevance (MRMR), Least Absolute Shrinkage and Selection Operator (LASSO), LLBFS to novel FCMIM algorithm for their influence on classifiers such as Logistic Regression (LR), KNN, Artificial Neural Networks (ANN), SVM, NB, and DT. The combined best results found by this study were FCMIM and SVM which achieved the maximum accuracy of 92.37% using Leave-One-Out Cross-Validation. Though the Deep Neural Networks (DNN) have practically performed well, the limited data available have made their performance poor. Another study proposed an HRFLM model which hybridizes RF and Linear Model to provide improved heart disease classification [8]. Here, the experimental results show accuracy much more elevated than traditional methods, thus proving the superiority of this method.

Another research work was conducted to achieve proper prediction regarding not just the presence or absence of CVD; it also tried to predict severity levels [9]. Here, some ML models like SVM, KNN, LR, Stochastic Gradient Descent (SGD), and tree-based ensembles were employed to overcome the problem concerning imbalanced data via Synthetic Minority Oversampling Technique (SMOTE) and hyperparameter optimization with HPO. The remarkable point here is that the tree-based ensemble models do outperform the others in terms of accuracies concerning CVD presence/absence that amounts to 99.2% and 98.52%, respectively, and for severity level predictions at 95.73%. The continuing research compared six models including Extreme Gradient Boosting (XGB), Bagging, RF, DT, KNN, and NB using a dataset of more than 300,000 cases [10]. The top scorer was scored by XGB with 91.30% accuracy and AUC of 0.83. Feature selection using sequential backward selection and KNN was also investigated, achieving a classification accuracy of 90% with six selected features [11].

Subsequent studies compared LR, KNN, SVM, and XGB classifiers, optimized with Grid Search Cross-Validation (GridSearchCV) [12, 13, 14]. RF consistently demonstrated superior performance, with accuracies reaching 99% and 98.53%. A more recent study introduced ensemble methods and a novel Quine McCluskey Binary Classifier (QMBC) classifier, along with feature selection techniques like Chi-Square and Analysis of Variance (ANOVA), further improving prediction accuracy [15].

While these studies provide valuable insights, this research distinguishes itself by introducing a novel framework prioritizing data security and privacy, encompassing a complete system lifecycle, and employing rigorous evaluation methods.

3. Preliminaries

3.1. ElGamal Cryptosystem

The ElGamal cryptosystem is a public-key encryption scheme based on the discrete logarithm problem. Given a cyclic group G of prime order p with generator g, a private key a is chosen randomly from {1, ..., p−1}. The public key is ga mod p. To encrypt a message m ∈ G, a random integer k is chosen, and the ciphertext is (c1​, c2​) = (gk mod p, m ∗ (ga)k mod p). Decryption is done by computing c2 ​/ (c1a​) mod p [16].

3.2. Naïve Bayes Classifier (NB)

NB is a simple probabilistic classifier that assumes feature independence given the class label. Despite this assumption, it often performs well due to its focus on finding the class with the highest probability. Recent research suggests that NB can be optimal even when feature independence is violated, as long as dependencies balance out across classes [17].

3.3. Decision Tree (DT)

The DT is a model for classification and regression that decides based on partitioning the data into subsets, using feature-valued attributes for this purpose. Each internal node represents a decision point, where a specific feature is selected to split the data. The terminal leaves represent the final decision or output. The tree structure allows for easy interpretation and visualization, but it can become complex with very large datasets [18].

3.4. Random Forest Classifier (RF)

RF is an ensemble method that builds multiple DTs, each trained on a random subset of features and samples. During classification, each tree votes for a class, and the majority vote determines the final output. This approach leverages bagging, where each tree is trained on a bootstrap sample, and uses the Gini Index to evaluate the impurity of nodes. By aggregating the predictions from many trees, RF improves accuracy and reduces overfitting compared to single DTs [19].

3.5. K-Nearest Neighbors (KNN)

The KNN algorithm is a simple yet effective supervised learning technique for both classification and regression tasks. Given a query point, KNN finds the k closest data points in the training set and assigns the query point to the most frequent class among those neighbors (for classification) or the mean of the neighbor values (for regression) [20].

3.6. Support Vector Machine (SVM)

SVM is a robust supervised learning technique for classification tasks. They work by identifying the optimal hyperplane that maximizes the margin between different classes. Data points nearest to the hyperplane, known as support vectors, significantly influence its placement. To handle complex, non-linearly separable datasets, SVMs employ the kernel trick. SVM employs the kernel trick for handling more complex, non-linearly separable datasets. Through this technique, data is mapped into higher dimensional space where it becomes linearly separable [21]. SVMs typically use kernel functions such as linear, polynomial, RBF, and sigmoid.

3.7. Principal Component Analysis (PCA)

This PCA is a technique that is mostly known for reducing the dimensions of data, making it recognize patterns within data and subsequently reforming it into a new coordinate system. It is made up of standardization, covariance matrix computation, eigenvalue decomposition, selection of principal components, and projection of results into the new system. PCA has many uses including dimensionality reduction, feature extraction, noise removal, visualization, and outlier detection [22].

3.8. Isolation Forest (iForest)

iForest uses a collection of isolation trees to separate abnormal observations from the distribution. Path lengths into isolation are shorter for anomalies than for normal observations. iForest has several advantages: its linear time complexities, capability to deal with high-dimensional data and tolerance against noise and outliers. It has outperformed many methods with respect to accuracy and efficiency [23].

3.9. Long Short-Term Memory (LSTM)

LSTM networks are a type of recurrent neural network (RNN) specifically designed to solve the vanishing gradient problem, which prevents standard RNNs from displaying effective performance for long-term dependencies on sequential data. This is accomplished through a special cell structure that contains input, output, and forget gates. These gates allow information to flow into and out of cells, storing and making it possible to retrieve information over long-term history [24]. They can perform a task very efficiently when the length of many input sequences provides context, such as in NLP tasks and speech recognition.

3.10. Train-Test Split

Train-test split is a method of evaluation of ML models. In this approach, data is divided into a training set (to fit the model) and a test set (to measure performance). Some common ratios for the split are 70:30 or 80:20. Well-chosen ratios are important because poor ratios can lead to misinterpretation of performance metrics due to a shortage or an over-abundance of test data [25].

3.11. K-Fold Cross-Validation

K-fold cross-validation is one of the ways to evaluate the performance of models by splitting the dataset into k equal sections or folds. k−1 folds are used to train the model while the last remaining fold serves as a testing set. This process is repeated on every fold so that every data point is included for both training and validation [26].

4. System Model and Functional Roles

This section provides a detailed architectural blueprint of the system, as shown in Figure 2. It defines the system's components, their interactions, and respective functions. Additionally, it outlines the sequential flow of activities within the system.

4.1. Roles of Each Entity

The proposed system comprises six primary entities: Central Coordinator (CC), Cryptographer (CR), Service Provider (SP), System (SYS) and System User (SU), as illustrated in Figure 1.

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| **Figure 1.** Interactions between entities |

1. *CC:* The CC oversees the entire process, starting by gathering raw datasets related to heart disease from various hospitals and combining them into a unified dataset. It generates public-private key pairs, shares the public keys with the CR for data encryption, and securely stores the private keys. Once the encrypted dataset is received from the CR, the CC validates its integrity by decrypting it with the private keys and verifying the data. If the dataset is deemed valid, the CC forwards it to the SP for model training. After receiving the trained models, test datasets, preprocessing scalers, and F1-scores from the SP, the CC tests the models on its own encrypted dataset and compares the F1-scores with those reported by the SP. If the models pass validation, the CC develops the SYS using the best-performing model and preprocessing scaler. This SYS is then deployed for SUs to use.
2. *CR:* The CR receives the unified dataset from CC and encrypts it using the public keys shared by CC, ensuring the data remains confidential. Once encrypted, the dataset is sent back to CC.
3. *SP:* The SP preprocesses the encrypted dataset received from CC and trains several ML models. After evaluating these models using metrics like F1-score, the SP selects the best-performing model. The trained models, test datasets, preprocessing scalers, and F1-scores for the selected model are then shared with CC.
4. *SYS:* The SYS is the final application developed by CC, using the trained model and preprocessing scaler provided by SP. It takes input data from SUs, encrypts it with the public keys shared by CC, preprocesses the data, and then makes predictions based on the trained model.
5. *SU:* The SUs interact with the SYS to check whether they have heart disease.

4.2. Table of Notations

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
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| |  |  | | --- | --- | | **Table 1.** Notation Used | | | *Symbol* | *Description* | | *ωk* | Raw dataset from the k-th Kaggle repository, where k ∈ {1, 2, ..., 7} | | *ω* | ω1, ω2, …, ω7 | | *Φ* | Dataset features | | *d* | No. of crucial features | | *r* | No. of medical records | | *ξ* | Crucial features (ξ1,ξ2, …, ξd) | | *λ* | Label value (Categorial) | | *i ∈ d* | i-th column | | *j ∈ r* | j-th row | | *Δ* | Combined Dataset (Δ1, Δ2, …, Δd, λ) | | *∅* | Missing value | | *κ* | ​Public keys (pi, gi, hi) | | *ρ* | Private keys (pi, gi, ai) | | *E(κi, ξi)* | ElGamal encryption function | | *λ'* | Encoded label value | | *Θ* | Encrypted dataset (Θ1­,Θ2,​ …, Θd, λ’) | | *D(ρi, Θi)* | ElGamal decryption function | | *Υ* | Decrypted dataset (Υ1­,Υ2,​ …, Υd, λ’’) | | *θ* | Standardized Dataset (θ1­,θ2,​ …, θd, λ’) | | *η1, η2, η3, η4 η5* | ML models: NB, DT, RF, KNN, SVM | | *η*α | Best performing model | | *ηα1, ηα2, ηα3, ηα4* | Base model, ηα with PCA, ηα with iForest, ηα with LSTM | | *{ηαk1, ..., ηαk10} ∈ ηαk* | Models of ηαk for 10-fold cross validation, where k ∈ {1, 2, 3, 4} | | *ηβ ∈ {ηα1, ηα2, ηα3, ηα4}* | Best configuration of {ηα1, ηα2, ηα3, ηα4} | | *{ηβ1, ..., ηβ10} ∈ ηβ* | Models of ηβ for 10-fold cross validation | | *ηγ* | Best performing model | | *Π1, Π2, Π3,Π4, Π5,Π6,Π7,Π8* | Confusion Matrix, Accuracy, Specificity, Recall, PPV, NPV, F1-score, AUC | | *τ* | Train-test split ratios (0.1:0.9 to 0.9:0.1) | | *δ* | Preprocessing transformer | |

4.3. Individual Stages

The proposed framework consists of nine distinct stages. These are: (1) Data Collection, (2) Data Encryption, (3) Data Decryption and Verification, (4) Data Preprocessing, (5) Model Training, (6) Model Optimization, (7) Final Model selection, (8) Model verification and (9) System Development. These stages are detailed below, with notations referenced from Table 1:

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| Figure 2. Proposed Heart Disease Prediction System |

4.3.1. Data Collection

The CC is responsible for collecting datasets from various hospitals for heart disease prediction. Hospitals may share anonymized or de-identified medical data with the CC for research or clinical studies, under strict ethical approvals, consent from patients, and formal data-sharing agreements. For this research, data was gathered from seven publicly available Kaggle repositories [27-33]. The datasets, denoted as ω1​, ω2, ..., ω7, contain several inconsistencies. These include irrelevant features that aren't necessary for prediction. The features consist of both numerical and categorical values, and some of them are encoded differently across the ω.

To ensure consistency, CC pre-processes the data by retaining only the relevant features (ξ, where ξ ⊂ Φ) from all available features (Φ), while discarding the irrelevant ones. CC manually transforms all the values across the datasets to ensure a uniform representation, standardizing the types of data within the entire set. To ensure consistency, CC reviews the Kaggle dataset descriptions to identify the data type for each ξi and λ in ω. A standard data type is then chosen for all features and label, and the values in each dataset are converted to this standardized format, ensuring uniformity in attribute names and value types across all datasets. Once pre-processed, ω are combined into a single, unified dataset, Δ = .

Even though the data is anonymized, sharing it with the SP in its original form could still expose sensitive patterns or correlations that may lead to the re-identification of individuals. Encrypting the dataset ensures that this risk is minimized. So, CC generates d pairs of public and private keys (κi and ρi) for d attributes following the ElGamal cryptosystem as described in section 3.1. The Δ, along with the κ, is then transferred to CR to make the dataset secure.

CC trusts CR as a reliable entity, but since CR handles the original data during encryption, there's a risk of leakage. To mitigate this, CC checks the integrity of the encrypted dataset before sending it to the SP.

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| |  | | --- | | Algorithm 1Key Generation | | 1. **function** *gen\_keys():* 2. *ρ, κ = [], []* 3. **for** *i* ∈ *d* **do**: 4. *p* ← **random prime** [1020, 1050] 5. *g* ← **random int** [2, *p*-1] 6. *a* ← **random int** [1, *p*-2] 7. *h← ga mod p* 8. *ρ.append({p, g, a})* 9. *κ.append({p, g, h})* 10. **end for** 11. **return** *κ, ρ* 12. **end function** | |

Δ has the following attributes as detailed in Table 2:

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| |  |  |  | | --- | --- | --- | | **Table 2.** Heart Disease Prediction Attributes | | | | *Attribute* | *Unit* | *Type of Data* | | Age | Numeric | In Years | | Sex | Nominal | 1. Male 2. Female | | Chest Pain Type | Nominal | 1. Typical Angina 2. Atypical Angina 3. Non-anginal Pain 4. Asymptomatic | | Resting Blood Pressure | Numeric | 94-200 (mm HG) | | Cholesterol | Numeric | 126-564 (mg/dl) | | Fasting Blood Sugar | Binary | Yes / No > 120 mg/dl | | Resting ECG | Nominal | 1. Normal 2. Abnormal ST-T Wave 3. Left Ventricular Hypertrophy | | Maximum Heart Rate | Numeric | 71-202 | | Exercise Angina | Binary | Yes / No | | Oldpeak | Numeric | 0 - 6.2 | | ST Slope | Nominal | 1. Upsloping 2. Flat 3. Downsloping | |

Figure 3 provides a visual representation of the distribution of key attributes within the dataset.

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| --- | --- | --- | --- | --- | --- |
|  |  |  |  |  |  |
| (a) | (b) | (c) | (d) | (e) | (f) |
|  |  |  |  |  |  |
| (g) | (h) | (i) | (j) | (k) |  |
| Figure 3. Distribution of Heart Disease Prediction Attributes | | | | | |

4.3.2. Data Encryption

The CR secures the dataset Δ, which contains d feature vectors (ξ1, ξ2, …, ξd​) and their associated label λ, by applying the encryption function E(κi, ξi). Each ξi is encrypted as described in section 3.1, using its corresponding public key κi, provided by CC, resulting in its encrypted form Θi. For λ, CR employs a straightforward binary encoding scheme, converting 'Yes' to 1 and 'No' to 0, producing λ′. The fully encrypted dataset Θ is then sent to CC for validation.

|  |  |  |
| --- | --- | --- |
| |  | | --- | | Algorithm 2 Data Encryption | | 1. **function** *E(κi, ξi):* 2. *p, g, h ← κi['p'], κi['g'], κi['h']* 3. *k* ← **random int** [1, *p*-2] 4. *Θi ← []* 5. **for** *j* ∈ *r* **do**: 6. **if** *ξij* *≠* *∅* **then**: 7. *ξ'ij ← datatype\_to\_int(ξij)* 8. *c1 ← gk mod p* 9. *c2 ← (ξ'ij × hk mod p) mod p* 10. *Θi.append((c1, c2))* 11. **else**: 12. *Θi.append(∅)* 13. **end if** 14. **end for** 15. **return** *Θi* 16. **end function** | |

4.3.3. Data Decryption and Verification

The CC uses the private keys ρi and the decryption function D(ρi, Θi) to decrypt Θi, obtaining the decrypted features Υi as described in section 3.1. The CC also decodes the labels λ′, converting 1 back to ‘Yes’ and 0 to ‘No,’ to produce λ′′. The CC then compares Υi and λ′′ with the original Δi and λ to ensure no data was altered during encryption or transmission by the CR. If all Δi and λ values match their corresponding Υi and λ′′ values, the CC forwards Θ to the SP for model training.

|  |  |  |
| --- | --- | --- |
| |  | | --- | | Algorithm 3 Data Verification | | 1. **function** *D(ρi, Θi):* 2. *p, g, a ← ρi['p'], ρi['g'], ρi['a']* 3. *dec, miss ← [], []* 4. **for** *j* ∈ *r*: 5. **if** *ξij ≠ ∅:* 6. *c1, c2 ← split(Θij)* 7. *temp* ← *(c1a mod p)-1 mod p* 8. *val* ← *int\_to\_datatype((c2 \* temp) mod p)* 9. *dec.append(val)* 10. **if** *val ≠ ξij*: 11. *miss.append(j)* 12. **end if** 13. **end if** 14. **end for** 15. **return** "Valid" **if** *miss.len*= 0 **else** "Invalid" 16. **end function** | |

4.3.4. Data Preprocessing

The SP addresses missing values ∅ in Θ by imputing the mean value for each Θi. Missing values in Θij are replaced with the mean of all non-missing values in Θi, calculated as:

|  |  |  |
| --- | --- | --- |
| |  |  | | --- | --- | |  | (1) | |

After imputation, Θij is standardized using the StandardScaler technique, denoted as δ. Standardization ensures all features have a mean of zero and a variance of one, transforming Θij into θij:

|  |  |  |
| --- | --- | --- |
| |  |  | | --- | --- | |  | (2) | |

where, Mean,

|  |  |  |
| --- | --- | --- |
| |  |  | | --- | --- | |  | (3) | |

and, Standard Deviation,

|  |  |  |
| --- | --- | --- |
| |  |  | | --- | --- | |  | (4) | |

The entire process, handling missing values through mean imputation and scaling the data via standardization, is denoted as δ for reference.

4.3.5. Model Training

The SP partitions θ into training (θtrain) and testing (θtrain) and testing (θtest) subsets. It then evaluates a selection of ML models, including NB (η1), DT(η2), RF(η3), KNN(η4), and SVM(η5), chosen for their ability to handle categorical data without requiring decrypted features. For each model, the SP computes various performance metrics: Confusion Matrix (Π1), Accuracy(Π2), Specificity(Π3), Recall(Π4), PPV(Π5), NPV(Π6), F1-score(Π7) and AUC(Π8).

Additionally, the SP performs hyperparameter optimization to maximize the Π7 for each model, as the rationale for selecting Π7 is explained in section 6. To further refine the analysis, the SP explores the impact of different train-test split ratios (τ) on model performance, evaluating Π7 for τ values ranging from 0.1:0.9 to 0.9:0.1 across all models. Based on the highest Π7 values, the SP selects the best-performing model (ηα) for further evaluation and potential hyperparameter tuning.

4.3.6. Model Optimization

The SP conducts a thorough evaluation of ηα, the model with the best hyperparameters that produced the highest Π7. SP applies 10-fold cross-validation, splitting the θ into 10 parts. Each part is used once as a validation set, while the others are used for training, ensuring an accurate and unbiased assessment. SP also uses three advanced techniques: PCA, iForest, and LSTM, for deeper analysis.

The following hyperparameters are fine-tuned for the models:

1. RF: The number of trees (n\_estimators), maximum tree depth (max\_depth), minimum samples required to split nodes (min\_samples\_split), and split criterion (Gini).
2. PCA: The number of principal components to retain (n\_components) to balance dimensionality reduction and variance.
3. iForest: The number of trees (n\_estimators), contamination rate (the proportion of outliers expected in the data), and sample size (max\_samples) for anomaly detection.
4. LSTM: The number of LSTM units, learning rate, dropout rate, number of epochs, and batch size for sequential tasks.

4.3.7. Final Model Selection

The SP conducts a comprehensive evaluation of four configurations of the best-performing model ηα: the base model (ηα1), ηα with PCA (ηα2), ηα with iForest (ηα3), and ηα with LSTM (ηα4). For each configuration, SP applies 10-fold cross-validation, generating 10 sets of θtrain and θtest, where each set includes the randomly selected rows along with their corresponding serial numbers. Additionally, 10 trained models (ηαk1, ..., ηαk10, where k ∈ {1, 2, 3, 4}), and 10 corresponding Π7 scores. The average Π7 score across the 10 folds, denoted as Π7’, is calculated for each configuration.

The SP selects the configuration with the highest average Π7’ and identifies it as ηβ from {ηα1, ηα2, ηα3, ηα4}. All 10 models of ηβ, i.e., {ηβ1, ..., ηβ10}, along with their corresponding θtest, Π7, and δ, are then delivered to the CC for further validation.

4.3.8. Model Verification

The CC validates the models ηβ trained by the SP. For this, the CC randomly selects some or all of the θtest and retrieves the corresponding serial numbers from θ. Using these serial numbers, the CC extracts the corresponding rows from its own Θ. This subset of Θ is preprocessed using δ to produce θ and is then trained using the corresponding ηβk.

The CC then calculates the performance metric Π7 and compares it with the Π7 provided by the SP. If the calculated Π7 match exactly with those from the SP, the CC proceeds to develop the SYS. The ηβk with the highest Π7 will be selected as the best-performing model, ηγ.

4.3.9. System Development

The CC develops a user-friendly interface for SU interaction. This interface includes input fields for each of the model's d features (ξi), allowing SUs to input their data directly. The system encrypts each ξi using its corresponding public key κi, producing Θi. These encrypted values are then processed using δ to generate θi, which is fed into the ηγ to predict λi'. This prediction will inform the SUs whether they have heart disease or not. Once finalized, the CC makes the SYS publicly available for SUs.

5. Security Threats and Solutions

In our proposed heart system, several potential security threats were identified, and corresponding measures were implemented to address these threats. This section outlines the primary threats and the solutions incorporated in our methodology to ensure data integrity and system security.

5.1. Data Confidentiality Breach

*Threat:* The CR could tamper with the dataset during encryption, or the SP could potentially learn confidential information from the encrypted dataset during the model training process, compromising the data’s confidentiality and integrity.

*Solution:* In section 4.3.1, the CC generates a pair of keys and shares only the public ones along with the dataset to CR for encryption and decryption which excludes others from decrypting. Then, CC uses the private keys in section 4.3.3 to verify the integrity of the encrypted dataset to confirm that the CR has not tampered with it. The CC forwards the encrypted dataset to the SP for model training, with the data remaining confidential and unchanged as it flows.

5.2. Predictable Encrypted Data

*Threat:* When the same encryption key is applied to many different features, the identical values in various features may generate the same encrypted result. This could allow an attacker to recognize patterns between features and infer that they might be related. If such an attacker were able to predict or decrypt one feature, personal values on some of the related ones could be compromised.

*Solution:* By using distinct encryption keys for every feature this matter is taken care of in section 4.3.2. In that case, if two features have the same value, their encodings will be different, so no attacker can identify any correlation between them. This will keep each feature independently secure, even if one of them is compromised.

5.3. Model Manipulation

*Threat:* The SP could sway the model or generate false performance measures thereby invalidating the model.

*Solution:* In section 4.3.8, CC validates the models by randomly selecting test data, extracting corresponding encrypted data, and comparing the performance metrics calculated by CC with those provided by the SP to ensure accuracy and integrity.

5.4. Corruption Risk

*Threat:* Corruption of CC, CR, or SP may result into manipulated data or wrong models or violation of privacy that will finally shake the accuracy and credibility of the heart disease prediction system.

*Solution:* CC has a strong incentive to maintain the integrity of the system because if it doesn't work correctly, SUs will reject it, leading to the company's loss. CC ensures data integrity by decrypting and verifying the models and data. If corruption is detected, CC can take corrective actions, such as penalizing or replacing the corrupted parties (CR or SP), ensuring the system remains functional and trustworthy.

6. Results

The performance of ML models was evaluated using several key metrics. To comprehensively assess model accuracy, a confusion matrix was employed, offering a tabular representation of the model's predictions compared to the actual ground truth values.

A confusion matrix, as detailed in [15], is a table that summarizes the performance of a classification model by comparing its predicted values with actual values. Predictions are grouped into one of four possible outcomes: true positive (TP), true negative (TN), false positive (FP), or false negative (FN).

Based on the confusion matrix, the following performance metrics were calculated:

*Accuracy* is the number of correct predictions (both positive and negative) divided by the total number of instances.

|  |  |  |
| --- | --- | --- |
| |  |  | | --- | --- | |  | (5) | |

*Recall or Sensitivity* is the number of true positives correctly identified by the classifier model.

|  |  |  |
| --- | --- | --- |
| |  |  | | --- | --- | |  | (6) | |

*Specificity* indicates how many true negatives were correctly identified divided by all false negatives.

|  |  |  |
| --- | --- | --- |
| |  |  | | --- | --- | |  | (7) | |

*Precision or Positive Predictive Value (PPV)* indicates the proportion of correct predictions over all positive predicted instances.

|  |  |  |
| --- | --- | --- |
| |  |  | | --- | --- | |  | (8) | |

*Negative Predictive Value (NPV)* measures the proportion of actual negative cases that are correctly predicted as negative out of all predicted negative cases.

|  |  |  |
| --- | --- | --- |
| |  |  | | --- | --- | |  | (9) | |

*F1-Score* combines precision and recall into a single metric by calculating their harmonic mean, balancing both aspects of model performance.

|  |  |  |
| --- | --- | --- |
| |  |  | | --- | --- | |  | (10) | |

*Area Under the Curve (AUC)* represents the overall performance of a classification model across all possible classification thresholds. A higher AUC value indicates better model discriminative power.

Training ML models on encrypted data is challenging due to the loss of interpretability. Traditional models rely on specific features, which are obscured by encryption. However, the consistent nature of encryption can be exploited to identify relationships within the data.

While challenging, some ML algorithms like NB, DT, RF, SVM, and KNN can be adapted to encrypted data. NB leverages feature independence, DT and RF utilize relative feature ordering, SVM compares relative features, and KNN exploits distance relationships between data points.

Model robustness and generalization were assessed by employing various train-test splits, as described in section 3.10, with the training-to-testing data ratio ranging from 1:9 to 9:1. Models were trained on the training data and evaluated on the corresponding test data using metrics such as accuracy, specificity, recall, PPV, NPV, F1-score, and AUC.

|  |
| --- |
| Figure 4. Performance Metrics of Classification Algorithms with Varying Train-Test Split |

Figure 4 illustrates how the performance of different ML models on test data varies with changes in the train-test split. The evaluated models are NB, DT, RF, KNN, and SVM.

RF consistently outperforms other algorithms across all evaluation metrics. It achieves excellent performance in accuracy (average 88.11%), specificity (average 85.82%), recall (average 89.86%), PPV (average 89.09%), NPV (86.90%), F1-score (average 89.46%), and AUC (average 94.00%). These results indicate that RF is highly effective in classifying the dataset.

SVM demonstrates strong performance, particularly in accuracy (79.35%), specificity (69.58%), recall (86.79%), PPV (78.88%), NPV (80.24%), F1-score (82.63%), and AUC (85.79%). While not surpassing RF, SVM provides robust classification results.

DT exhibits acceptable performance across most metrics, with accuracy (82.65%), specificity (80.52%), recall (84.30%), PPV (84.70%), NPV (80.06%), F1-score (84.49%), and AUC (82.41%) falling within the good performance range.

NB and KNN demonstrate similar performance patterns, with strengths in recall, PPV and AUC, but weaknesses in accuracy, specificity and NPV. Both models show room for improvement, especially in terms of specificity and NPV.

Increasing the training set size generally improves performance for all algorithms, but the rate of improvement diminishes after a certain point. Increasing the train-test split ratio from 0.1 to 0.9 helped identify trends in model behavior and provided evidence of stable generalization across varying dataset sizes.

RF is chosen as the best model due to its consistently superior performance across all metrics, indicating its robustness and generalization ability. In contrast, DT, NB, KNN and SVM perform relatively well in some metrics, but their performance is less consistent and shows weaknesses. These limitations make DT, NB, KNN and SVM less reliable for precise and consistent classification.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Table 3.** Performance Comparison of Classification Models with Varying Training-Testing Sets and Hyperparameters (F1-Score in %) | | | | | | | | | | | | | | |
| *Classifiers* | *Hyper-parameters* | | | *10-Fold Cross Validation* | | | | | | | | | | *Mean* |
| *k=1* | *k=2* | *k=3* | *k=4* | *k=5* | *k=6* | *k=7* | *k=8* | *k=9* | *K= 10* |
| *RF* | StratifiedKFold   * n\_splits: 10 * shuffle=True * random\_state: 115 | RandomForestClassifier   * random\_state: 79 |  | 94.69 | 93.96 | 94.20 | 94.17 | 92.48 | 94.20 | 94.17 | 93.06 | 94.23 | 94.79 | 94.00  ±  0.70 |
| *RF PCA* | StratifiedKFold   * n\_splits: 10 * shuffle=True * random\_state: 378 | RandomForestClassifier   * random\_state: 22 * n\_estimators: 157 | PCA   * n\_components: 0.95 * random\_state: 378 | 95.07 | 89.49 | 93.57 | 93.99 | 90.00 | 93.75 | 92.76 | 90.35 | 92.31 | 90.51 | 92.18  ±  1.86 |
| *RF iForest* | StratifiedKFold   * n\_splits: 10 * shuffle=True * random\_state: 429 | RandomForestClassifier   * random\_state: 530 * n\_estimators: 77 * criterion: gini | IsolationForest:   * n\_estimators: 100 * contamination: 0.05 * random\_state: 530 * max\_samples: 256 | 93.53 | 96.45 | 94.37 | 95.67 | 92.23 | 93.09 | 93.27 | 94.76 | 94.39 | 93.62 | 94.14  ±  1.20 |
| *RF LSTM* | StratifiedKFold   * n\_splits: 10 * shuffle=True * random\_state: 115 | Optimizer (Adam)   * learning\_rate: ~0.0526 (1/19) | Model Training  (model.fit)   * epochs: 27 * batch\_size: 10000 * verbose: 0 | 89.87 | 86.12 | 88.33 | 91.07 | 87.70 | 91.42 | 88.60 | 89.24 | 88.53 | 90.09 | 89.10  ±  1.51 |
| Sequential  Dropout   * rate: 0.05   Dense   * units: 1 * activation: sigmoid | RandomForestClassifier   * random\_state: 115   n\_estimators: 71 | Model Compilation (model.compile)   * loss: binary\_crossentropy |

While all the performance metrics offer valuable insights, the F1-score is prioritized for comparing the models. This is due to its ability to balance precision and recall, both of which are critical in this context. Precision ensures that positive predictions are accurate, while recall ensures that a high proportion of actual positive cases are identified. By optimizing the F1-score, the goal is to develop a model that minimizes both false positives and false negatives.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Table 4.** Comparative Analysis of Proposed System with Existing Methods | | | | | | |
| *Attributes* | *[7]* | *[8]* | *[9]* | *[12]* | *[15]* | *Proposed System* |
| *Dataset Size and Diversity* | Cleveland dataset | Cleveland dataset | Two public datasets | Cleveland, Hungary, Switzerland, Long Beach V, UCI Kaggle | Cleveland, Comprehensive, CVD datasets | Combined hospital data |
| *Data Quality and Preprocessing Techniques* | Missing values removed, SS, Min-Max | Missing values removal, Binary conversion | SMOTE, Splitting, Balancing | Quality implication, Standard preprocessing | Data type conversion, Outliers handling, SMOTE, Under- sampling | Standardization, Scaling, Encoding, PCA, iForest, Data cleaning, Feature selection, Encryption |
| *Feature Engineering* | Relief, MRMR, LASSO | HRFLM method | Significant features | 14-attribute dataset created | Chi-Square, ANOVA, FS, FE | - |
| *ML Algorithms* | ANN, LR, K-NN, SVM, DT, NB | NB, GLM, LR, DL, DT, RF, GBT, SVM | SVM, SGD, K-NN, ET, XGB, LR | LR, K-NN, SVM, GBC | LR, DT, RF, K-NN, NB, SVM, MLP, QMBC | NB, DT, RF, KNN, SVM |
| *Hyperparameter Tuning* | Leave-one-subject-out | - | Hyperband, SMOTE | GridSearchCV | Minimal, Basic evaluation | - |
| *Evaluation Metrics* | Accuracy, Specificity, Sensitivity, MCC | Accuracy, Sensitivity, Specificity, Precision, F-Measure | Accuracy, F1-Score, MCC | Accuracy, Precision, Recall, F1-Score | Accuracy, Sensitivity, Specificity, Precision, Recall, F1-Score, AUC | Accuracy, Recall, Specificity, PPV, NPV, F1-Score, AUC |
| *ML Model,*  *Result* | SVM+ Relief + LASSO + FCMIM + LLBFS,  Accuracy (92.37%) | HRFLM (RF+LM),  Accuracy (88.7%) | HB+ SMOTE+ ET,  F1-Score (95.78%) | XGB + GridSearchCV,  Accuracy (99.03%) | Cleveland Dataset: QMBC+ Anova+ PCA,  F1-Score (98.59%) | RF+iForest,  F1-Score (94.14%) |
| CVD Dataset: QMBC+ Chi-Square+ PCA,  F1-Score (99.92%) |
| HD Dataset: QMBC+ Anova+ PCA,  F1-Score (98.42%) |
| *Novelty of Approach* | Fast mutual information | HRFLM hybrid model | Hyperband, balancing | Near-zero prediction error, unique model | Novel QMBC, improved performance | Encryption, data privacy |

Although accuracy might seem appealing, it can be misleading in imbalanced datasets, where the majority class dominates the evaluation. PPV focuses on the accuracy of positive predictions, but it might not capture the ability of the model to identify all positive cases. NPV is valuable for assessing the reliability of negative predictions, but it's less critical in our scenario. AUC provides a global measure of model performance, but it doesn't directly address the trade-off between precision and recall. Therefore, the F1-score emerges as the most suitable metric for our comparative analysis.

Table 3 presents a comparative analysis of various RF-based models, including RF, RF with dimensionality reduction (PCA), RF with anomaly detection (iForest), and RF with LSTM, evaluated using 10-fold cross-validation as described in section 3.11.

RF with Isolation Forest demonstrated the highest mean F1-score of 94.14%, outperforming other configurations. RF achieved a mean F1-score of 94.00%, while RF with PCA showed a mean F1-score of 92.18%. RF with LSTM achieved the lowest mean F1-score of 89.10%.

These results show that RF with iForest delivers the best performance, slightly outperforming RF alone. RF with PCA showed a decrease in performance due to dimensionality reduction, which led to the loss of important information. RF with LSTM had the lowest score, as the integration of LSTM’s temporal learning with the RF model caused instability and overfitting, hindering its effectiveness.

The comparative analysis between the proposed system and the existing methodologies is described in Table 4. The table consists of a systematic comparison of diverse attributes such as characteristics of datasets, preprocessing methods, types of features engineered, ML algorithms, hyper-parameter tuning, evaluation metrics, and performances over different approaches. Our proposed system adopts a combined hospital dataset that adds to the diversity and robustness of the data as opposed to previous studies' smaller datasets [7, 8]. Extensive preprocessing including standardization, scaling, and feature selection has differentiated our method from the others that utilize simple methods or techniques such as SMOTE [9, 12].

By integrating several ML algorithms and tuning hyperparameters, our system demonstrates improved scoring measures including accuracy, sensitivity, specificity, and F1-score compared to models HRFLM [8] and Hyperband [9]. Thus, the results in Table 4 are proof of the effectiveness and reliability of our proposed system, which is considered to be a big advancement in the field.

7. Conclusion and Future Works

This paper describes a heart disease prediction model that works under a comprehensive framework with data privacy and security. The approach embodies steps that span data collection, encryption, preprocessing, and model training with the use of NB, DT, RF, KNN, and SVM techniques as well as their evaluation. Improvements in model performance and robustness have been examined through the inclusion of dimensionality reduction and anomaly detection techniques, all the while being considerate of the sensitive information about patients.

Results of experiments indicate the performance of single models and their collections as well. Respectively, the distribution transformed by the DT gave it a fair average mean F1-score of 84.49%, while the SVM showed a mean F1-score of 82.63%. Even though both models performed well, their results were generally lower compared to those given by the models based on RF. Among all the RF-based models, the RF with iForest has shown the best performance with an average F1-score value of 94.14%, which exceeds the performances of all other configurations. Next for RF only is the mean F1-score of 94.00%, while that for RF with PCA is 92.18%. Lastly, RF together with LSTM had the lowest mean F1-score of 89.10%. Such results provide proof that RF with iForest is the most powerful, taking the benefits of anomaly detection to augment predictive strength.

To maintain the privacy of patients, the proposed system encrypts patient data and allows the training of models on encrypted data without exposing patient information. The system provides a suitable balance between these two competing measures of data security and prediction accuracy.

Future work could explore the integration of advanced deep learning architectures, such as CNNs and RNNs, to potentially improve prediction accuracy further. Additionally, investigating the impact of different encryption algorithms and their computational efficiency would be valuable.

By addressing the challenges of data privacy, model accuracy (achieving over 90% F1-score for RF ensembles), and computational efficiency, this research contributes to the development of reliable and secure heart disease prediction systems.

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