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# Quantum-Inspired Feature Engineering and Explainable AI for Robust Heart Disease Classification

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**Abstract** **Early and accurate prediction of cardiovascular disease is essential to improve patient outcomes and reduce healthcare costs. This research presents a hybrid classical–quantum machine learning framework for heart disease prediction using the Cleveland dataset. The proposed pipeline integrates advanced feature engineering, bio-inspired optimization, and quantum-inspired learning to improve classification performance and interpretability. The system applies multiple feature selection techniques followed by a hybrid feature fusion strategy. Orthogonal Component Analysis is then used for dimensionality transformation, while quantum-inspired feature mapping simulates quantum state coding. A feature selection mechanism based on a Genetic Algorithm optimizes the subset of features. Classical and quantum machine learning models are evaluated, including Random Forest, Gradient Boosting, K-Nearest Neighbors, Logistic Regression, Quantum Support Vector Classifier, Variational Quantum Classifier, Quantum KNN, and Quantum Neural Networks. Model performance is evaluated using accuracy metrics. To ensure transparency and trustworthiness, explainable AI techniques such as SHAP, LIME and DiCE are integrated to provide local and global interpretability of predictions. Experimental results demonstrate that the proposed hybrid framework improves predictive performance by achieving 90% accuracy compared to traditional machine learning approaches, while maintaining model explainability. The model achieved an overall accuracy of 90%, indicating strong predictive capability in cardiovascular disease risk classification. A detailed analysis of class-wise performance shows that for Class 0, the model obtained a precision of 0.85, a recall of 0.97, and an F1-score of 0.90, demonstrating excellent ability to correctly identify negative cases with minimal false negatives. For Class 1, the model achieved a precision of 0.96, a recall of 0.84, and an F1-score of 0.90, indicating high confidence in positive predictions, though with slightly lower recall compared to Class 0. This study highlights the potential of combining classical feature engineering, evolutionary optimization and quantum-inspired learning for next-generation medical decision support systems. The integration of quantum-inspired techniques also provides a promising direction for improving computational efficiency and model robustness in healthcare analytics. The findings suggest that hybrid classical–quantum learning approaches can support clinicians in making faster and more reliable diagnostic decisions.**

**Keywords** **Quantum Machine Learning, Genetic Algorithm, Explainable AI, Orthogonal Component Analysis, Heart Disease**

## I. Introduction

Cardiovascular diseases are widely recognized as one of the leading causes of mortality worldwide and represent a major burden on public health systems. In order to reduce mortality rate and improve patient outcomes, early and accurate diagnosis is needed. Conventional clinical diagnostic procedures are based more or less on human interpretation of medical information, which is subject to time consumption and may be subject to human error. Machine learning (ML) and deep learning (DL) based methods have greatly enhanced the predictive accuracy of heart disease diagnosis but feature redundancy, model interpretability, overfitting, and computational efficiency are some of the issues [1]. However, in recent years, hybrid intelligent systems combining statistical feature selection, evolutionary optimization algorithms and quantum-inspired learning paradigms have shown significant potential in biomedical prediction tasks, especially in the diagnosis of complex diseases. Statistical features selection methods, including ANOVA F-test, Mutual Information, and Recursive Feature Elimination (RFE), can be used to select the most discriminative clinical attributes through eliminating irrelevant and redundant variables [2]. It is not only a method of reducing the computational complexity, but also enhances the generalization capacity of predictive models [3].

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The evolutionary algorithm, which includes Genetic Algorithm (GA) and other evolutionary algorithms, has developed into a highly powerful optimization in biomedical prediction systems due to the capability of reaching high-dimensional feature space efficiently and complex ones [4]. Unlike traditional greedy or gradient-based optimization methods, GA is executed as a global search over populations, and this feature leads to the opportunity to overcome local optima and to obtain feature subsets having a higher ability to discriminate. The optimization problems can be solved with the help of GA, which consists of mutating candidate solutions repeatedly, crossing over candidate solutions, and selecting the best solutions, in which the fitness of a solution is typically characterized by classification accuracy and model generalization [5]. The computational dimensionality and complexity are relatively low, and the GA-based feature selection method is resistant to noise and redundancy,, which is highly prevalent in clinical data. The evolutionary feature optimization has been found to work particularly well with non-linear, multi-modal, and imbalanced biomedical data, delivering more reliable predictive performance and reduced overfitting [6].

Besides that, GA offers a high level of flexibility since it is applicable to multi-objective optimization, wherein conflicting aims such as maximizing accuracy and minimizing the number of features can be addressed simultaneously. This flexibility makes GA particularly well-suited to medical decision-support systems, where predictive performance is not of as great concern as interpretability and efficiency. GA is also compatible with other learning paradigms, such as deep learning and ensemble models, thus improving even more feature learning and classification results. Moreover, dynamic mutation and crossover rate adaptive GA variants enhance convergence rate and solution diversity. The stochasticity of GA guarantees resilience to noisy and incomplete clinical data that frequently occur in the real-life healthcare environment. Consequently, GA optimization has emerged as a foundation for the creation of powerful, scalable, and generalizable biomedical predictive models. Quantum Machine Learning (QML) is a relatively new concept; nevertheless, it offers a radically novel approach to learning high-dimensional biomedical data on the basis of quantum-inspired representations and computational principles[7], [8] . QML can be used to implicitly project classical data into exponentially large Hilbert spaces by encoding it using the simulated quantum feature maps, including ZZFeatureMap or angle encoding, and this enables it to learn complex non-linear decision boundaries. Variational quantum circuits also make the model more expressive by incorporating parameterized quantum gates with classical optimization, allowing adaptive learning of problem-specific quantum representations. Variational Quantum Classifiers (VQC), Quantum Support Vector Machines (QSVM), Quantum k-Nearest Neighbors (QKNN), and Quantum Neural Networks (QNN) are algorithms that have shown encouraging results in biomedical tasks like classification by successfully identifying complex correlations among clinical characteristics [9], [10]. Quantum-inspired models are competitive with current hardware and simulator limitations, and have the potential to be scaled, making QML an interesting addition to classical machine learning in future healthcare analytics.

Moreover, Explainable Artificial Intelligence (XAI) [11] has become an indispensable part of healthcare-based machine learning. Some of these methods include SHAP (Shapley Additive Explanations), LIME (Local Interpretable Model-Agnostic Explanations), and DiCE (Diverse Counterfactual Explanations), which offer transparent and reliable explanations of complicated predictive models [12]. SHAP can perform global and local feature contribution analysis; LIME can offer instance-level interpretability by approximating complex models with local surrogate models [13]; and DiCE can produce actionable counterfactual examples, which allow clinicians to interpret why slight changes to model features can change predictions [14]. Clinical trust, regulatory compliance, and ethical utilization of AI systems in critical healthcare settings are enforced by the implementation of XAI methods. The combination of these hybrid approaches creates a strong, well-built, and transparent framework that can handle the problems of high-dimensional biomedical data, enhance the precision of diagnostic results, and facilitate the use of reliable clinical decision making.

Bataineh et al. [15] suggested and tested various intelligent systems on the machine learning algorithms to estimate the probability of heart disease using the freely available Cleveland Heart Disease dataset. The research paper proposes a different method of training a multilayer perceptron (MLP) which incorporates an algorithm from particle swarm optimization (PSO) to improve the detection of heart diseases. Ten traditional machine learning classifiers were compared to the proposed MLP-PSO hybrid model in terms of several performance evaluation measures. As shown in the experiment, the MLPPSO model is superior to any competing algorithms with 84.61 accuracy. The results suggest that the MLP PSO classifier can assist clinicians during the early diagnosis of heart disease in an accurate and efficient manner.

Azhari et al. [16] use Principal Component Analysis (PCA) to overcome multicollinearity amongst clinical characteristics. Then, the Binary Logistic Regression is applied in prediction. The PCA narrows the data to seven components explaining 72.9 per cent, and predictive accuracy is 85. This method demonstrates that dimensionality reduction may enhance the

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**Table. 1. Summary of Existing Literature on Heart Disease Prediction Using Machine Learning and Quantum Approaches**

| Reference | Dataset | Models Applied | Accuracy |
|---|---|---|---|
| [15] | Cleveland Heart Disease Dataset | Multilayer perceptron (MLP) , Particle swarm optimization (PSO) | 84.61% |
| [16] | Framingham heart | Principal Component Analysis + Binary Logistic Regression | 85% |
| [17] | Clinical Dataset | Principal Component Analysis+ Support Vector Machines | Accuracy of SVM with Principal Component Analysis (PCA) is 88.24% with 6 components. |
| [18] | Kaggle | K-Medoids clustering with Manhattan distance | 85% |
| [19] | UCI Machine Learning repository | Naïve Bayes Classifier, Federated Logistic Regression, Shapley, , Local Interpretable Model-agnostic Explanations | Naïve Bayes- 81.1%<br>Federated Logistic Regresion – 78.2% |
| [20] | Cleveland Heart Disease Dataset | Adaptive curve grey wolf optimization (ACGWO) algorithm into neural network backpropagation | 86.8% |
| [21] | Clinical | Neural Networks, Logistic Regression, Decision Trees | Artificial Neural Networks – 80.2% |
| [22] | Statlog Heart Disease Dataset | fuzzy and flower pollination neural network. | 86.7% |
| [23] | Kaggle Cardiovascular Disease Dataset | C4.5 Decision Tree algorithm | 73.25% |
| [24] | Z-Alizadeh | Firefly algorithm, Ensemble Techniques | 86.79% |
| [25] | UCI Machine Learning | Naïve Bayes Classifier | 85.24% |
| [26] | Cleveland Heart Disease Dataset | Chi Squared Test, Support Vector Machines | 85% |
| [27] | Cleveland Heart Disease Dataset | Chi-square, mutual information, ReliefF, recursive feature elimination, Lasso regression, and Ridge regression and six classification approaches, i.e., decision tree, random forest, support vector machine, K-nearest neighbor, logistic regression, and Gaussian naive Bayes | 88.52% |
| [28] | Cleveland Heart Disease Dataset | Chi-square statistical test, Light Gradient Boosting Machine (LightGBM) | 88.5% |

reliability and efficiency of the model.

Yang et al [17]paper has two dimensional reduction methodologies for heart disease prediction based on a support vector machine. The most relevant features for diagnosis are achieved by the support vector machine-recursive feature elimination (SVM-RFE) method. The best classification accuracy 88.24% is obtained by PCA-SVM via Radial Basis Function (RBF) kernel using only 6 principal components.

Wahyudi et al. [18] investigate both classical and quantum methods of predicting heart diseases based on K-Medoids clustering on Manhattan distance. The results of this study indicate that the use of quantum computing with the K-Medoids algorithm leads to the stability of the clustering accuracy at 85%. This implies that more efficient and quicker medical data analysis can be achieved with the aid of quantum-enhanced techniques.

Rodriguez M et al. [19] introduced the centralized and federated learning (FL) models of binary classification

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of heart disease with reference to the UCI dataset (920 records from four hospitals in the USA, Hungary, and Switzerland). Naive Bayes had the highest test accuracy of 81.1 in the centralized environment, and logistic regression with four client hospitals had an accuracy of 78.2 in the federated environment. The medically relevant feature importance was confirmed by the support of model interpretability with Shapley values and LIME. The research had a privacy-sensitive and explainable standard for heart disease pre-screening.

Niu et al. [20] have designed an Adaptive Gray Wolf Optimizer (ACGWO) with a sigmoid function to enhance neural network robustness and generalization. The algorithm was found to be superior to four standard test function optimizers. The model had a high potential for prediction and interpretability in the clinical heart disease diagnosis population, showing 86.8 percent accuracy when applied to the Cleveland Heart Disease dataset.

Khemphilla et al. [21] compared the use of logistic regression (LR), decision trees (DT), and artificial neural networks (ANNs) in the prediction of heart disease with medical data of 303 patients. ANN attained an accuracy of 80.2, sensitivity of 81.1 and specificity of 78.7. The decision tree came up with a 79.3% accuracy, and logistic regression came up with 77.7% accuracy, where the performance was measured in terms of lift charts and error rates.

To classify heart diseases, Yazid et al.[22]suggested that a hybrid model based on fuzzy logic and flower pollination neural networks be used. The model showed a good performance with the Statlog dataset, with a classification accuracy of between 86.7 and 91.1, which showed that the hybrid neuro-fuzzy approach is robust.

Barus et al.[23] also improved the C4.5 decision tree algorithm in classifying heart diseases with clinical and lifestyle features. The model produced seven interpretable rules and had a 73.25 percent accuracy, being better than kNN and Naive Bayes, indicating its ability to be effective in clinical decision support.

Natarajan et al. [24] examined the effects of the high-level feature selection and ensemble learning methods on heart disease prediction with the Z-Alizadeh Sani dataset. The metaheuristic technique used in the study was based on the Firefly algorithm to determine the best features that were most relevant, thus dimension reduction and better efficiency were increased in the model. In order to further improve the predictive performance, the chosen features were combined with ensemble learning methods, such as stacking and voting classifiers. The experimental outcomes were that this hybrid structure delivered the highest classification accuracy of 86.79%.

Hadijah Hasanah et al. [25] came up with a decision support system of heart disease diagnosis based on Naive Bayes. The model has training accuracy of 83.21% and negative accuracy of 83.10% and testing accuracy of 83.78% and 87.50 and the AUC values stood at 83.15 (training) and 85.24 (testing), indicating its usefulness in clinical classification.

Ogundepo et al. [26] conducted a predictive analysis on the Cleveland (training) and Statlog (validation) database. A chi-square test was used to find important risk factors ($p < 0.001$). SVM, when compared to ten classifiers, had the most best performance, with an accuracy of 85 percent, a sensitivity of 82 percent, a specificity of 88 percent, a precision of 87 percent, and an AUC of 91 percent, with a tenfold cross-validation.

Dissanayake et al. [27] compared ten feature selection methods with six classifiers on the Cleveland data. Backward feature selection using a decision tree classifier resulted in the best performance with an accuracy of 88.52% and precision, sensitivity, and F measure of 91.30, 80.76, and 85.71, respectively, which demonstrates the value of optimized feature subsets.

Table. 1. represents the summary of the related research works based on Machine learning models and Quantum based Methods. The reviewed studies demonstrate the widespread use of benchmark datasets such as the Cleveland Heart Disease, UCI, Statlog, Framingham, and Z- Alizadeh datasets for evaluating heart disease prediction models. Ramalingam Sakthivelan et al. [28] developed an effective heart disease prediction model, which uses the Cleveland Heart Disease data, and implements a Light Gradient Boosting Machine (LightGBM) model alongside the chi-square feature selection model to improve predictive accuracy. They used 303 patients' records and aimed at revealing the most informative clinical features to decrease the dimensions and enhance model generalization. The authors tested several machine learning classifiers besides LightGBM; the best validation accuracy of the models was 88.5% using the random forest model. The mentioned findings prove the efficiency of ensemble-based learning in predicting clinical risks and emphasize their applicability to support the medical decision-making process.

Recent advancements in quantum computing and quantum-inspired algorithms provide new opportunities for enhancing machine learning performance. Quantum-based learning approaches can potentially improve feature representation and optimization by exploring high-dimensional solution spaces more efficiently. However, current quantum technologies are still in their early stages and may lack the computational stability and scalability required for real-world medical applications. To address these limitations, this study proposes a hybrid classical–quantum machine learning framework that combines the strengths of both paradigms. Classical machine

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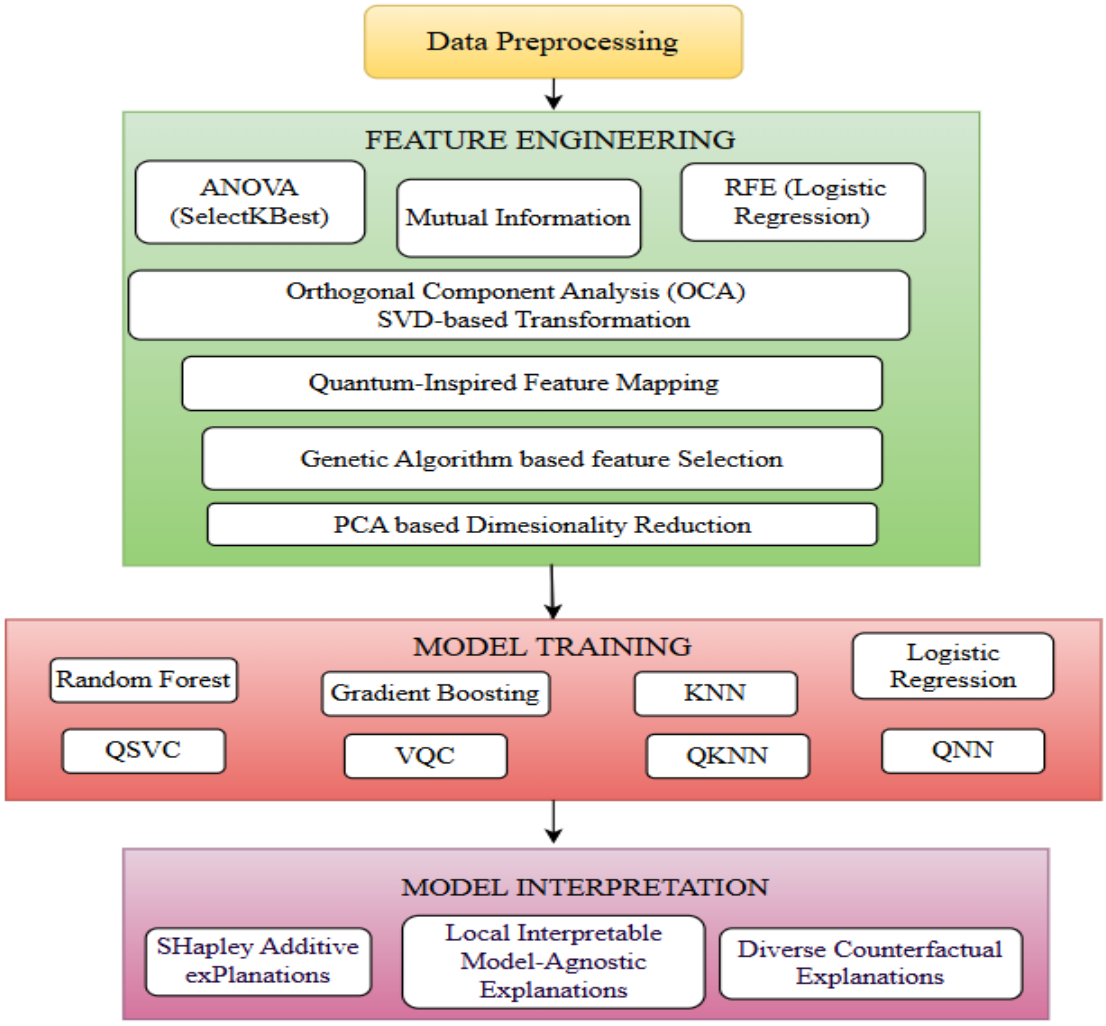


**Fig. 1. Proposed Methodology for Heart Disease Prediction using Hybrid Approach**

learning techniques provide robust data preprocessing, feature engineering, and model stability, while quantum-inspired methods enhance feature mapping and optimization capabilities. By integrating these complementary approaches, the proposed framework aims to improve prediction accuracy, computational efficiency, and interpretability in heart disease diagnosis. This hybrid strategy provides a promising direction for developing advanced and explainable decision-support systems in healthcare. The key contributions are as follows:

(i) the development of a hybrid classical–quantum machine learning framework for heart disease prediction, (ii) the integration of advanced feature engineering techniques with bio-inspired optimization for improved feature selection (iii) the application of quantum-inspired feature mapping to enhance classification performance, and (iv) the incorporation of explainable AI methods such as SHAP, LIME, and DiCE to ensure model interpretability.

This paper is structured as follows: Part II details the design and implementation of the proposed methodology. Part III discusses the performance of the proposed model with state-of-the-art models. Part IV provides the conclusion and scope for future work.

## II. Design and Implementation

The learning pipeline proposed in Fig. 1. in the form of a hybrid Classical-Quantum inspired design, is used to increase the prediction accuracy and enhance the interpretability of heart diseases. The first step involves the use of tools to preprocess the data, such as standardization and noise elimination, to enhance the quality of the data and stability of the model. ANOVA F-test, Mutual Information (MI); Recursive Feature Elimination (RFE) are statistical feature selection techniques that help in selecting the most pertinent clinical features and these features are combined to

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create a powerful hybrid set of features. It is followed by Orthogonal Component Analysis (OCA), which is done using Singular Value Decomposition (SVD) to convert the correlated features into independent components and thus reduce redundancy and multicollinearity. Afterwards, a quantum-inspired feature mapping step is proposed, in which trigonometric encoding and a simulated ZZFeatureMap both transform the transformed data into a higher-dimensional space, as a feature space. The ZZFeatureMap further introduces pairwise feature interactions through nonlinear transformations, which conceptually resemble entanglement operations used in quantum circuits. By applying these transformations, the feature space is expanded into a higher-dimensional representation where complex relationships among clinical attributes can be captured more effectively. This mapping improves the separability of data points that may not be linearly separable in the original feature space, thereby enabling machine learning models to better distinguish the diseased and non-diseased.

GA was selected for this research because of its strong capability to perform global optimization and avoid local minima, which is particularly important when dealing with high-dimensional healthcare data. Unlike traditional deterministic feature selection methods, GA evaluates multiple candidate solutions simultaneously and iteratively improves them through operations such as selection, crossover, and mutation. This process allows the algorithm to discover optimal or near-optimal feature combinations that significantly enhance classification performance.

In turn, a Genetic Algorithm (GA) is used to optimize the set of features with the help of evolutionary schemes to fit the models better, so that the risk of overfitting is minimized, and the generalization of the results becomes more effective. The next method is Principal Component Analysis (PCA), which is utilized to minimize the dimensions and also to match the size of the feature space to the number of qubits needed by the quantum models. Both classical and quantum-inspired learning models are trained on the optimized feature representations. Classical machine learning models are the Random Forest, which uses ensemble decision trees to build a strong nonlinear classifier; the Gradient Boosting, which uses additive weak learners to reduce the prediction error; the K-Nearest Neighbors (KNN), which is an instance-based learner that builds the similarity between samples; and the Logistic Regression, which is a strong interpretable baseline model. Simultaneously, there are quantum-inspired models that are trained, such as the Quantum Support Vector Classifier. (QSVC) which utilizes quantum kernel methods to achieve higher class separability, the Variational Quantum Classifier, which uses parametrized quantum circuits that are optimized by classical algorithms, Quantum K-Nearest Neighbor (QKNN), which approximates similarity quantum distance measures, and the Quantum Neural Network (QNN), which models highly nonlinear decision boundaries using parameterized quantum circuits. Lastly, all the models are compared using the common performance statistics of accuracy. To provide transparency and clinical trust, Explainable Artificial Intelligence (XAI) methods, such as SHAP, LIME, and DiCE, are combined to offer both global and local explanations of model predictions. The full framework allows prediction of heart diseases to be accurate, robust, and interpretable, which makes it possible to apply it in real-life clinical decision-making.

**A. Data Preprocessing**

The initial dataset is represented as a feature matrix as stated in Eq.(1)[2].

$$X = [x_{ij}] \in \mathbb{R}^{n \times m} \quad (1)$$

where $n$ is the number of samples and $m$ is the number of features.

To normalize the feature scales and accelerate model convergence, standardization is applied using Z-score normalization as in Eq.(2)[10].

$$x'_{ij} = \frac{x_{ij} - \mu_j}{\sigma_j} \quad (2)$$

where: $\mu_j$ is the mean of feature $j$ , $\sigma_j$ is the standard deviation of feature $j$. This step minimizes bias caused by varying feature scales.

**B. Statistical Feature Selection**

To select the most relevant attributes, three complementary statistical techniques are applied.

1. ANOVA F-test (Select KBest)

The F-score for feature [29] $j$is computed as in Eq.(3)[3].

$$F_j = \frac{\sum_{c=1}^{C} n_c(\mu_{c,j} - \mu_j)^2}{\sum_{c=1}^{C} \sum_{i \in c}(x_{ij} - \mu_{c,j})^2} \quad (3)$$

Where $Fj$ is the F-score of the $j^{th}$ feature, $C$ is the total number of classes, $n_c$ is the number of samples in class $c$, $\mu_{c,j}$ is the mean value of feature $j$in class $c$ , $\mu_j$ is the overall mean of feature $j$, $x_{ij}$ is the value of the $j^{th}$ feature for the $i^{th}$ sample. Higher $F_j$ values indicate stronger discriminatory capability.

2. Mutual Information (MI)

Mutual information measures the dependency between feature $Xj$ and target $Y$ [30] as in Eq.(4)[3].

$$I(X_j; Y)\left(\frac{p(x,y)}{p(x)p(y)}\right) \quad (4)$$

where $I(Xj;Y)$ is mutual information between feature $j$ and target $Y$, $p(x,y)$ is the joint probability distribution of $Xj$and $Y$ , $p(x)$ is the marginal probability of $Xj$ , $p(y)$ is the marginal probability of $Y$. Features with higher MI values are retained.

3. Recursive Feature Elimination (RFE)

RFE iteratively removes features based on model coefficients derived from Logistic Regression [31] as in Eq.(5)[17].

$$w_j = | \beta_j | \quad (5)$$

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where $wj$ is the importance weight of the $j^{th}$ feature, $\beta j$ is the coefficient of the $j^{th}$ feature obtained from Logistic Regression. Low-weight features are eliminated until the optimal subset is obtained.

4. Hybrid Feature Construction

The selected features are combined to form a unified hybrid feature set as in Eq.(6)[17].

$$F_{\text{hybrid}} = F_{\text{ANOVA}} \cup F_{\text{MI}} \cup F_{\text{RFE}} \quad (6)$$

where $F_{\text{hybrid}}$ is the final hybrid feature set, $F_{\text{ANOVA}}$ a set of features selected using ANOVA, $F_{\text{MI}}$ is a set of features selected using Mutual Information, $F_{\text{RFE}}$ represents a set of features selected using Recursive Feature Elimination, ∪ isa union operation. This step improves feature diversity and robustness.

**C. Orthogonal Component Analysis (OCA)**

To eliminate feature redundancy and correlation[32], SVD-based Orthogonal Component Analysis is applied as in Eq.(7)[33].

$$X_{\text{hybrid}} = U\Sigma V^T \quad (7)$$

where $X_{\text{hybrid}}$ is the hybrid feature matrix, $U$ is a left singular matrix containing orthogonal eigenvectors, Σ is a diagonal matrix of singular values, $V_T$ is the transpose of the right singular matrix. This guarantees orthogonality among the derived components.

**D. Quantum-Inspired Feature Mapping**

Classical features are mapped into a quantum-like high-dimensional space using trigonometric encoding as stated in Eq. (8)[7].

$$\phi(x_i) = [\sin(x_{i1}), \sin(x_{i2}), \dots, \sin(x_{id})] \quad (8)$$

where $x_i$ is the i-th *input sample* (data point) from the classical dataset, $d$ is the dimensionality of the input feature space, $\phi(x_i)$ is the encoded feature vector.A simulated ZZFeatureMap operator is defined as in Eq.(9)[8]

$$U(x) \prod_{1 \le i < j \le d} \exp(i\pi\, x_i x_j Z_i Z_j) \quad (9)$$

Where $U(x)$ is the unitary feature map operator, $\prod$ is the product over all pairwise combinations of features, $x_i$, $x_j$ are elements of the classical input feature vector, $Z_i, Z_j$ is Pauli-Z operators acting on the i-th and j-th qubits, respectively. This helps capture complex nonlinear feature interactions.

**E. Genetic Algorithm (GA) Feature Selection**

Each solution (chromosome) is encoded as a binary vector [34] as in Eq.(10) [4]

$$C = [c_1, c_2, \dots, c_d], c_i \in \{0,1\} \quad (10)$$

where $C$ is a chromosome representing a feature subset, $ci$ is a binary gene indicating selection (1) or rejection (0) of the $i^{th}$ feature , $d$ is the total number of features.

The fitness function is defined as in Eq.(11) [4].

$$f(C) = \alpha \cdot Acc(C) + \beta \cdot \left(1 - \frac{|C|}{d}\right) \quad (11)$$

where $f(C)$= fitness value of chromosome $C$, Acc($C$) is classification accuracy using selected features,$|C|$ is the number of selected features, $d$ is the total number of features , $\alpha$,$\beta$ depict weighting factors controlling accuracy vs feature reduction.

**F. Dimensionality Reduction Using PCA**

The covariance matrix is computed as in Eq.(12) [16].

$$\text{Cov}(X) = \frac{1}{n-1} X^T X \quad (12)$$

where $X$ is feature matrix, n is number of samples, $X^T$ is. transpose of matrix X Eigen decomposition is computed as in Eq.(13) [16].

$$\text{Cov}(X) v_i = \lambda_i v_i \quad (13)$$

where $v_i$ is the eigenvector corresponding to the $i^{th}$principal component, $\lambda_i$ is the eigenvalue representing the variance captured, Cov($X$) is the covariance matrix.

Final reduced representation is stated in Eq.(14) [16].

$$X_{\text{PCA}} = X v_k \quad (14)$$

where $X_{\text{PCA}}$ is a transformed reduced dataset, $v_k$is matrix of top $k$ eigen vectors.

**G. Classical Machine Learning Models**

1. Random Forest (RF)

Random Forest is an ensemble learning algorithm that constructs multiple decision trees and combines their predictions using majority voting[35].The final prediction is obtained as in Eq. (15) [35]

$$\hat{y} = \text{mode}\{h_1(x), h_2(x), \dots, h_T(x)\} \quad (15)$$

where ŷ is the predicted class label , $h_t(x)$ is the prediction of the $t^{th}$ decision tree, T is the total number of trees in the forest, x is the input feature vector.

2. Gradient Boosting (GB)

Gradient Boosting builds learners sequentially, where each new model corrects the errors of the previous model[36].The model update rule is in Eq.(16) [36]

$$F_m(x) = F_{m-1}(x) + \gamma_m h_m(x) \quad (16)$$

where $F_m(x)$ is updated model after the $m^{th}$iteration, $F_{m-1}(x)$ is previous model, $h_m(x)$ is weak learner at iteration $m$, $\gamma_m$is learning rate controlling the contribution of $h_m(x)$.

3. k-Nearest Neighbors (KNN)

kNN is a distance-based classifier that assigns a class based on the majority class among the $k$ nearest samples[37]. Prediction is stated in Eq. (17) [37].

$$\hat{y} = \text{mode}\{\, y_i \mid x_i \in \mathcal{N}_k(x) \,\} \quad (17)$$

where $\hat{y}$ is the predicted class label, $y_i$ is the label of the $i^{th}$nearest neighbor, $\mathcal{N}_k(x)$ is a set of k nearest neighbors of the sample x, x is a query sample.

4. Logistic Regression (LR)

Logistic Regression models the probability of class occurrence using the sigmoid function[38]. The sigmoid function is stated in Eq.(18) [1].

$$P(y = 1 \mid x) = \sigma(z) = \frac{1}{1+e^{-z}} \quad (18)$$

where $P(y = 1 \mid x)$ is the probability of class label 1, $\sigma(z)$ is a sigmoid function, $\beta_0$ is the bias (intercept) term, $\beta$ is a vector of model coefficients, $x$ is the input feature vector.

**H. Quantum Machine Learning Models**

1. Quantum Support Vector Classifier (QSVC)

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QSVC projects classical data to a high-dimensional quantum Hilbert space by using a quantum feature map, followed by the classification with SVM-like classification[39].

Quantum kernel is stated in Eq.(19) [8]

$$K(x_i, x_j) = |\langle \phi(x_i) | \phi(x_j) \rangle|^2 \quad (19)$$

where $K(x_i, x_j)$ is the quantum kernel between samples $x_i$and $x_j$, $|\phi(x)\rangle$ is a quantum feature-mapped state of the sample $x$, $\langle\cdot|\cdot\rangle$ is an inner product in a Hilbert space.

2. Variational Quantum Classifier (VQC)

VQC represents a parameterized quantum circuit with a classical optimizer. Quantum state is calculated in Eq.(20) [7].

$$|\psi(\theta)\rangle = U(\theta)\,|0\rangle \quad (20)$$

where$|\psi(\theta)$ is a parameterized quantum state, $U(\theta)$ is a unitary transformation with parameters , 0 is the initial qubit state.

3. Quantum K-Nearest Neighbor (QKNN)

QKNN applies quantum distance estimation as a similarity evaluation method. Quantum distance is calculated in Eq.(21) [9]

$$d_q(x_i, x_j) = \sqrt{2 - 2\,|\langle \psi(x_i) | \psi(x_j) \rangle|^2} \quad (21)$$

where $d_q(x_i, x_j)$ is the quantum distance between two states. $\psi(x)$ is a quantum-encoded feature state.

4. Quantum Neural Network (QNN)

QNN applies variational quantum circuits to simulate neural networks. In Eq.(22) a parameterized quantum is formulated [7].

$$|\psi(\theta)\rangle = U(\theta)\,|0\rangle \quad (22)$$

The cost function is calculated in Eq.(23) [8].

$$C(\theta) = \sum_{i=1}^{n} (y_i - \langle Z \rangle)^2 \quad (23)$$

Where $C(\theta)$ is the cost (objective) function, $n$ is number of training samples, Z is the expectation value of the Pauli-$Z$. where $\psi(\theta)$ is the output quantum state, $U(\theta)$is a parameterized (variational) unitary operator.

## I. Interpretation Models

1. Shapley

SHAP is an explainability approach that relies on Cooperative game theory Shapley values. It reasonably blames a prediction of a model to individual predictive contributions. SHAP offers a local and global explanation that has high theoretical guarantees, like consistency. It is model-agnostic and has many applications for interpreting complex models, such as ensembles and neural networks.

2. LIME (Local Interpretable Model-agnostic Explanations)

The individual prediction using LIME approximates the black-box model locally using an interpretable surrogate model. It perturbs input samples around the instance of interest and monitors the resultant prediction changes. These coefficients of the surrogate model give feature importance. LIME is also model-agnostic, but it only pays attention to local and instance-level explanations.

3.DiCE (Diverse Counterfactual Explanations)

DiCE produces counterfactual samples demonstrating that small changes in features can change the prediction of a model. It puts a lot of emphasis on diversity amongst counterfactuals in order to offer several actionable options. DiCE assists users in knowing decision limits and enhances transparency and equity. The approach is model-agnostic and complies with real-life decision-making.

## III. Results

### A. Data Collection

The Cleveland Heart Disease dataset [19], [40], obtained from the UCI Machine Learning Repository, is a widely recognized benchmark dataset for the development and evaluation of heart disease prediction models. The dataset consists of 303 patient records with 14 clinically relevant attributes, demographic, that capture physiological, and a range of diagnostic information. The target variable is discrete and indicates whether one has heart disease. The input features are demographic parameters like age and sex, clinical parameters like resting blood pressure (transtrestbps), serum cholesterol level (chol), fasting blood sugar (fbs), and maximum heart rate achieved (thalach), diagnostic features such as the type of chest pains (cp), resting electrocardiographic parameters (restecg), angina caused by exercises (exang), ST-segment depression caused by exercises (oldpeak), slope of the ST-segment (slope), number of major vessels stained by fluoroscopy (ca), and thalassemia condition.

### B. Experiment Results

The experiments were all conducted in Google Collaboratory, incorporating scientific and quantum computing libraries, such as NumPy, Pandas, Scikit learn, and Qiskit Machine Learning. First, the raw data was passed through Z-score normalization with StandardScaler to ensure that all features have zero mean and unit variance, which enhances numerical stability and model convergence. Multiple feature selection methods were used separately in order to increase the representational quality of the input data. These were ANOVA F-test ( SelectKBest with k = 20), Mutual Information-based feature selection ( SelectKBest with k = 20), and Recursive Feature Elimination (RFE) based on Logistic Regression as the base estimator, and 20 features are allowed. The features selected through these three methods were then combined to create a hybrid feature matrix and thus represented complementary statistical and information-theoretic properties of the data. Afterwards, Singular Value Decomposition (SVD) was used as an Orthogonal Component Analysis in order to transform the hybrid feature matrix into an orthogonal feature space. Based on this representation, the 20

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most important orthogonal components were selected to preserve the most variance and eliminate redundancy. To simulate quantum state representations that could be used in subsequent quantum learning models, these orthogonal features were then represented with a quantum-inspired sine-based trigonometric encoding scheme.

The optimization of features was further done with the help of a Genetic Algorithm (GA) to determine the most discriminative subset of features. The GA was set to 15 generations, 20 population size, and 5-fold cross-validation. This evolutionary step optimization was influenced to enhance the performance of classification by converting the feature subset before quantum processing. Principal Component Analysis (PCA) was used to eliminate the optimized feature space to six principal components. The choice of six principal components is justified based on the cumulative variance explained by the PCA transformation. preserved while eliminating redundant or less significant attributes. Retaining additional components would increase the dimensionality of the quantum feature map and the number of qubits required, leading to higher computational complexity without a substantial improvement in predictive performance. This dimensionality reduction is directly proportional to the number of qubits used in the quantum models, which means that quantum feature encoding will be efficient. The processed data was further divided into training and testing subsets at an 80:20 ratio, and the random seed was held constant at 42 to give the ability to reproduce the experimental findings. The comparison of the classical and quantum-inspired models concerning their classification accuracy is given in Fig. 2.

The performance of the quantum machine learning models was evaluated using accuracy, error rate, precision, recall, and F1-score. The Quantum Support

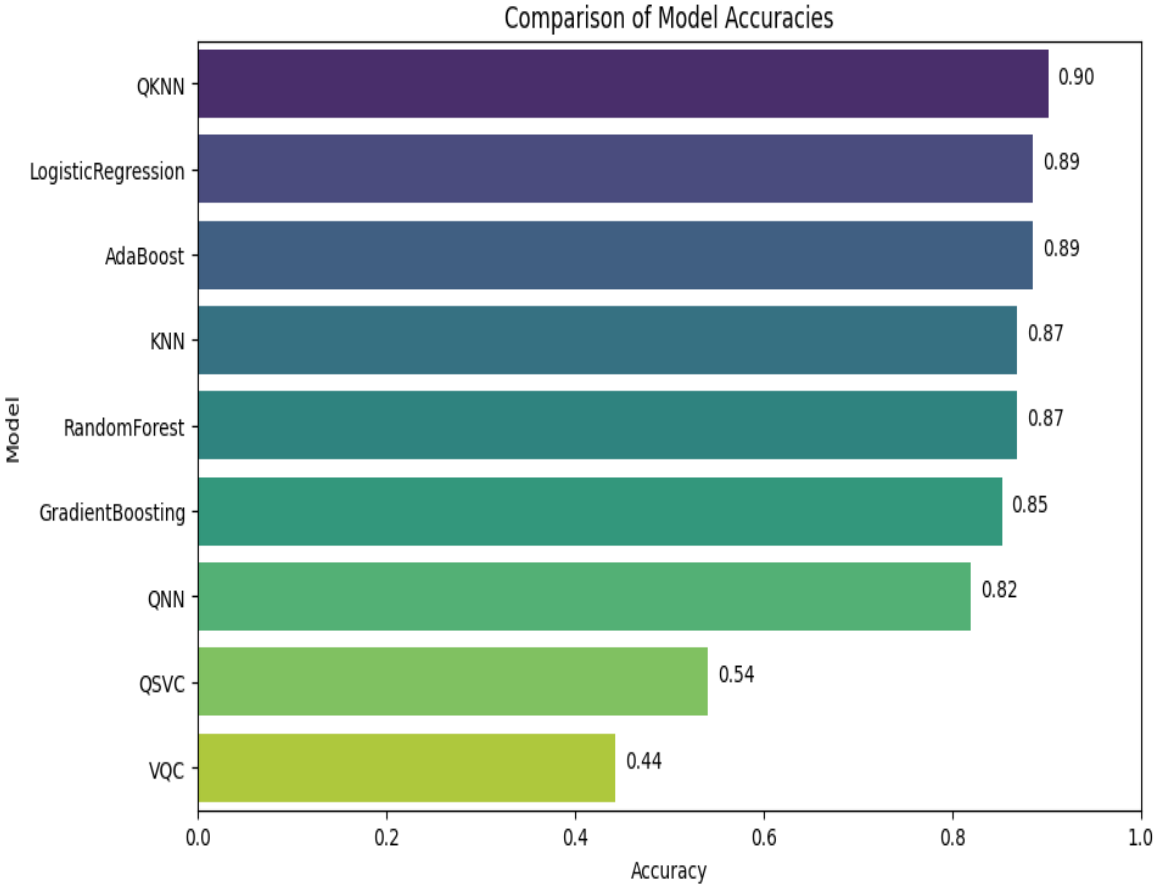


**Fig. 2. Comparative Analysis of Classification Accuracies Across Classical and Quantum-Inspired Models**

During experimentation, the first six principal components captured the majority of the variance present in the optimized feature set, ensuring that the most informative patterns in the clinical data were Vector Classifier (QSVC) achieved an overall accuracy of 0.54 (54%), corresponding to an error rate of 0.46 (46%) on the dataset of 61 samples. For Class 0, the model obtained a precision of 0.53, a recall of 0.28, and

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an F1-score of 0.36, indicating poor sensitivity in identifying negative cases. For Class 1, the model achieved a precision of 0.54, a recall of 0.78, and an F1-score of 0.64, showing relatively better performance in detecting positive cases. The macro-average F1-score is 0.50, while the weighted-average F1-score is 0.51, indicating overall limited and imbalanced performance.

and an error rate of 0.18 (18%). For Class 0, the model achieved a precision of 0.80, a recall of 0.83, and an F1-score of 0.81, while for Class 1, it obtained a precision of 0.84, a recall of 0.81, and an F1-score of 0.83. The macro-average and weighted-average F1-scores are both 0.82, indicating balanced and consistent performance across classes.

The Quantum K-Nearest Neighbors (QKNN) model

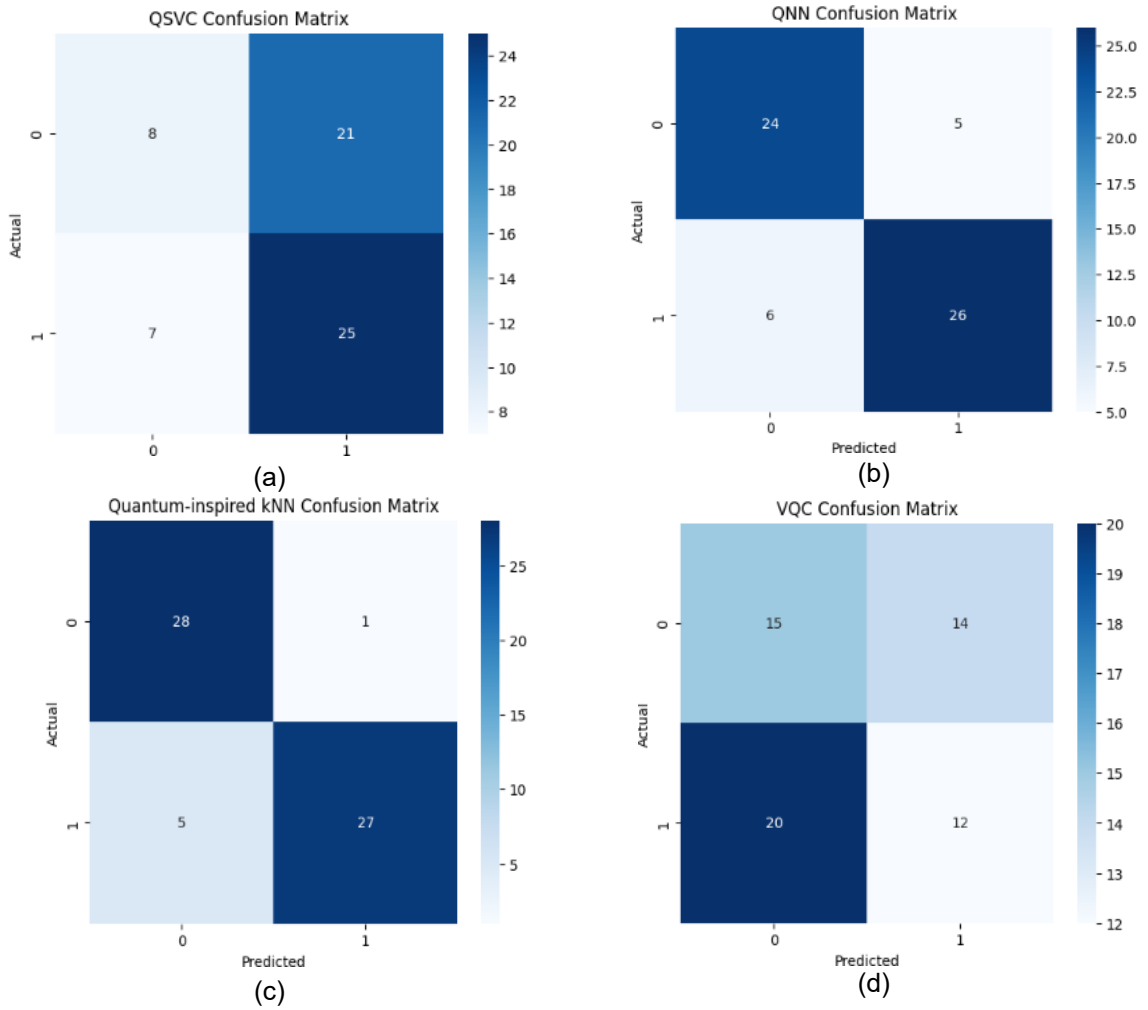


**Fig. 3. Confusion Matrices of Quantum Inspired Models (a) QSVC, (b)QNN ,(c)Quantum inspired kNN and (d) VQC respectively.**

The Variational Quantum Classifier (VQC) demonstrated lower predictive performance, with an overall accuracy of 0.44 (44%) and an error rate of 0.56 (56%). For Class 0, the model achieved a precision of 0.43, a recall of 0.52, and an F1-score of 0.47, while for Class 1, it obtained a precision of 0.46, a recall of 0.38, and an F1-score of 0.41. The macro-average F1-score is 0.44, and the weighted-average F1-score is also 0.44, reflecting consistently low performance across both classes. The Quantum Neural Network (QNN) showed significant improvement compared to QSVC and VQC, achieving an overall accuracy of 0.82 (82%)

achieved the best performance among all evaluated models, with an overall accuracy of 0.90 (90%) and an error rate of 0.10 (10%). For Class 0, the model obtained a precision of 0.85, a recall of 0.97, and an F1-score of 0.90, while for Class 1, it achieved a precision of 0.96, a recall of 0.84, and an F1-score of 0.90. The macro-average F1-score is 0.90, and the weighted-average F1-score is also 0.90, demonstrating superior and well-balanced classification performance.

Fig. 3. shows the confusion matrices of the four quantum-based classification models: the Quantum Support Vector Classifier (QSVC), Quantum Neural

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Network (QNN), Quantum k-Nearest Neighbors (QKNN), and Variational Quantum Classifier (VQC), tested on the test dataset. These confusion matrices give a detailed understanding of each model's behavior in terms of classification in which the true positives, true negatives, false positives, and false negatives are indicated. QKNN has the best overall classification performance of all the considered quantum models. It has a great number of true positive and true negative predictions, which means that it is effective in separating between diseased and non-diseased classes.

recall values in the range of 0.86–0.88, indicating consistent predictive capability across both classes. The Gradient Boosting model showed slightly lower performance, with an accuracy of 0.852, and F1-score and recall values around 0.84–0.85, suggesting a marginal reduction in classification effectiveness compared to the other models.

Overall, the recall values across these classical models remain relatively close, generally falling within the 0.85 to 0.89 range, which reflects their ability to correctly identify most of the true instances. The similarity between recall and F1-score values further

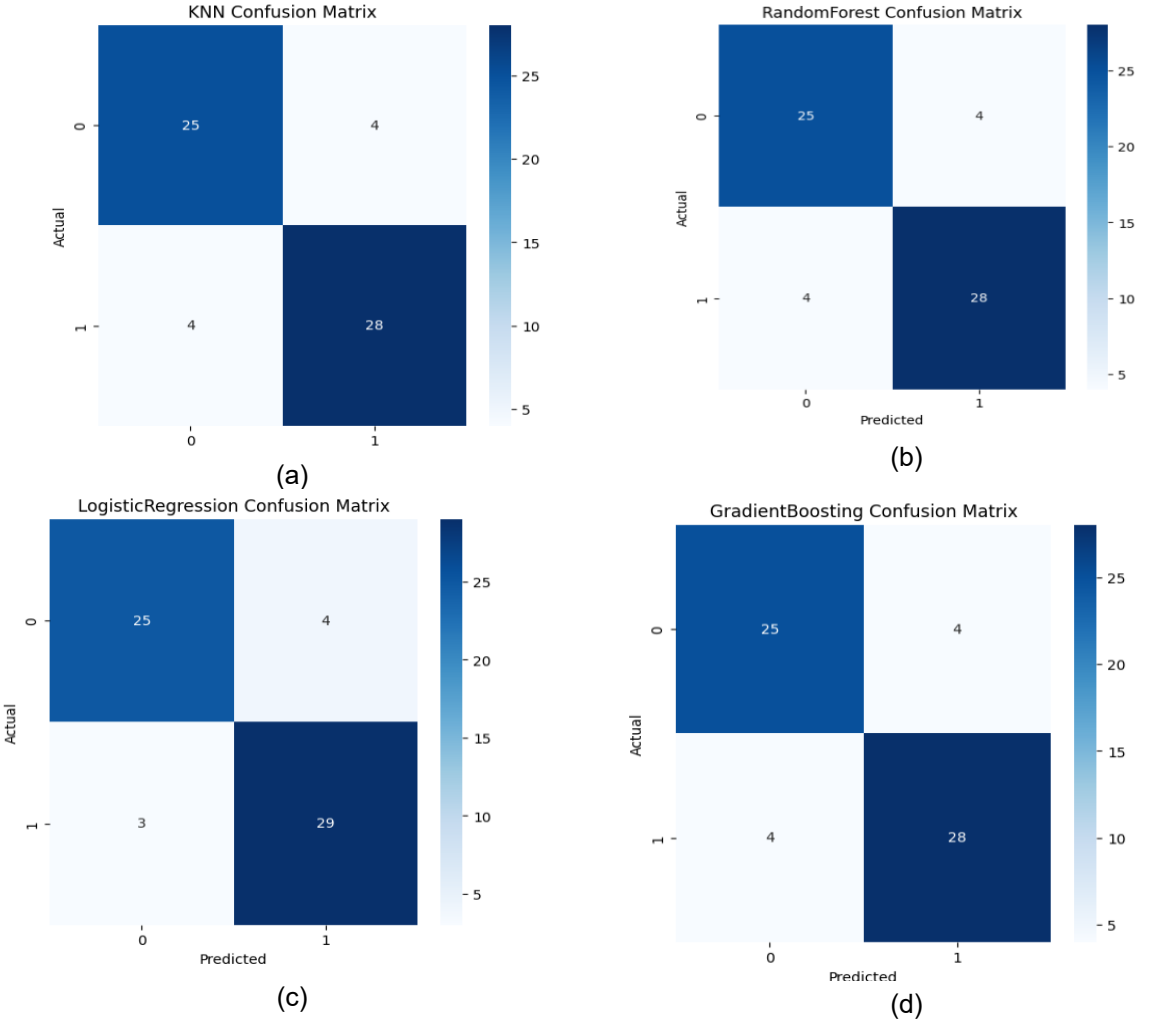


**Fig. 4. Confusion Matrices of Machine Learning Models (a) kNN, (b) Random Forest, (c)Logistic Regression, (d)Gradient Boosting respectively.**

The evaluation of classical machine learning models indicates that Logistic Regression achieved an accuracy of 0.885, with corresponding F1-score and recall values close to 0.88–0.89, demonstrating a strong and well-balanced classification performance. Similarly, both KNN and Random Forest models achieved accuracies of 0.868, with F1-scores and indicates a balanced trade-off between precision and sensitivity, without significant bias toward any particular class. These findings confirm that classical models provide strong baseline performance; however, their results are slightly lower than those of the best-performing quantum -inspired approaches, highlighting the potential advantage of hybrid models in achieving

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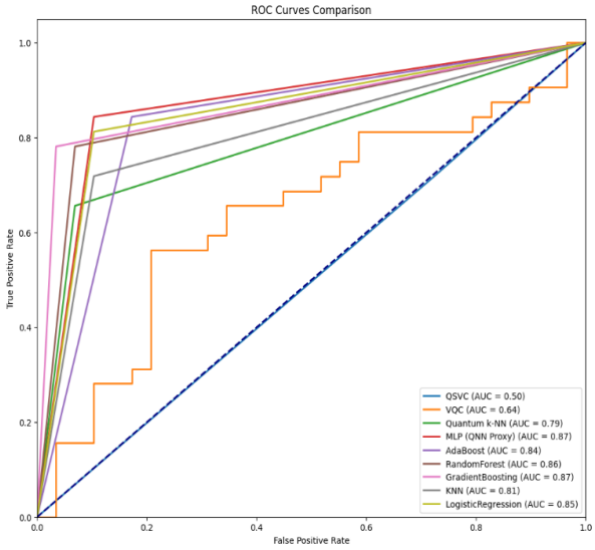


**Fig. 5. ROC Curves comparison of all models**

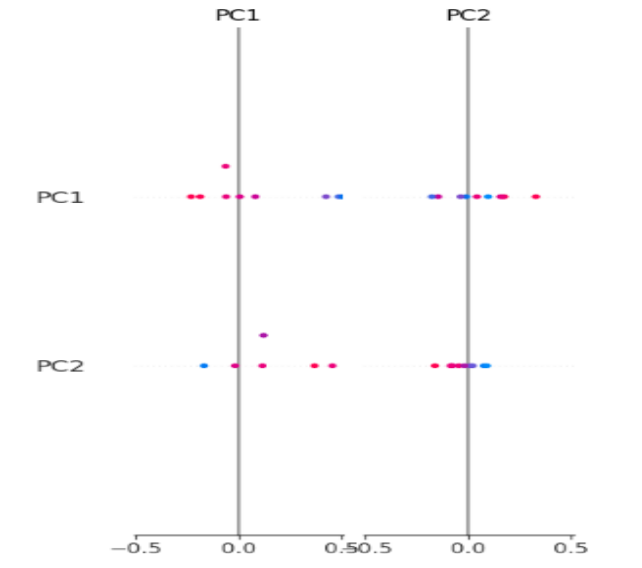


**Fig. 6. Feature Impact on Model Output using SHAP Analysis**

improved predictive accuracy and robustness. Fig. 4 presents the confusion matrices for several classical machine learning models, including k-Nearest Neighbors (kNN), Random Forest (RF), Logistic Regression (LR), and Gradient Boosting (GB). These models were evaluated using the test dataset. The confusion matrices offer a detailed view of each model's classification performance, illustrating the distribution of true positives, true negatives, false positives, and false negatives.

Explainable AI methods such as SHAP (Shapley Additive Explanations), LIME (Local Interpretable Model-agnostic Explanations), and DiCE (Diverse Counterfactual Explanations) were experimentally scaled across classical and quantum-inspired models to improve the transparency and clinical interpretability of models. SHAP analysis offered information on the importance of features across the globe by measuring the marginal contribution of each feature to the well-known predictions of the model, thus showing uniform clinical risk factors in models. In this study, the quantum models, such as Quantum Support Vector Classifier (QSVC) and Quantum Neural Networks (QNN), were implemented using a simulation-based environment. Due to the current limitations of quantum processors, including limited qubit availability, hardware noise, and restricted accessibility, the research was carried out using quantum circuit simulators executed on classical computing systems.

The simulation framework enables the implementation of quantum feature maps, parameterized quantum circuits, and variational quantum models while maintaining computational stability and reproducibility. In this approach, the behavior of quantum algorithms is emulated using classical resources, allowing the evaluation of quantum machine learning techniques without requiring physical quantum devices.

Fig. 5. demonstrates the Receiver Operating Characteristic (ROC) curves of all the classical and quantum machine learning models applied in this paper. The ROC curve is used to measure the strength of each model to diagnose by plotting the True Positive Rate (TPR) versus the False Positive Rate (FPR) at various classification thresholds. A curve that is nearer to the upper-left part denotes a model that has good discriminative power. Based on the comparison between the classical models, especially KNN, random forest, Logistic Regression, and gradient boosting, the smooth and steep ROC curves indicate the consistency of the discriminatory power and a high level of superiority. This is seen by the fact that they have a higher AUC (Area Under the Curve), which shows that these models have a higher balance between sensitivity and specificity with regard to thresholds. QKNN has the most desirable ROC behavior, and is in line with its high accuracy behavior. The ROC curves of QNN and QSVC have a medium level, and VQC has a relatively lower level, leading to a flatter curve and a smaller AUC. This implies that VQC has a hard time separating the two classes.

Fig. 6. shows a two-dimensional representation of the dataset with Principal Component Analysis (PCA) applied to it, i.e., the high-dimensional feature space is cast onto the two most important principal components in the dataset, i.e., PC1 and PC2. Each point in the plot represents a single sample, and the colors indicate the corresponding class labels (the presence or absence of heart disease). The separation tendency of the points along PC1 is clear, as a substantial amount of the variance of the classes that could be used to

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classify them is found in PC1. PC2, on the other hand, shows the partial overlap of classes, indicating that it is more effective at the representation of the variance,

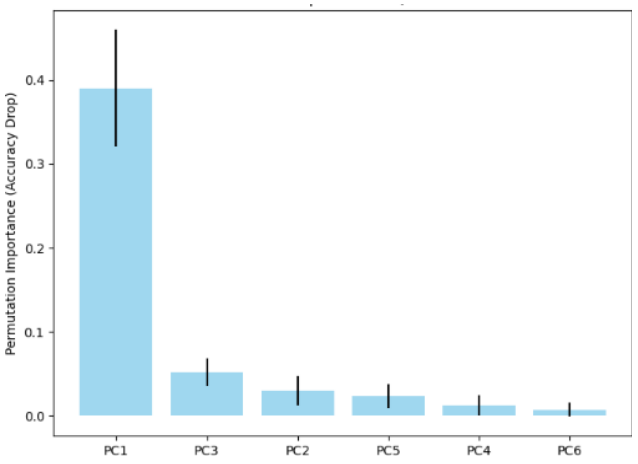


**Fig. 7. Permutation Feature Importance of QkNN on PCA features using LIME**

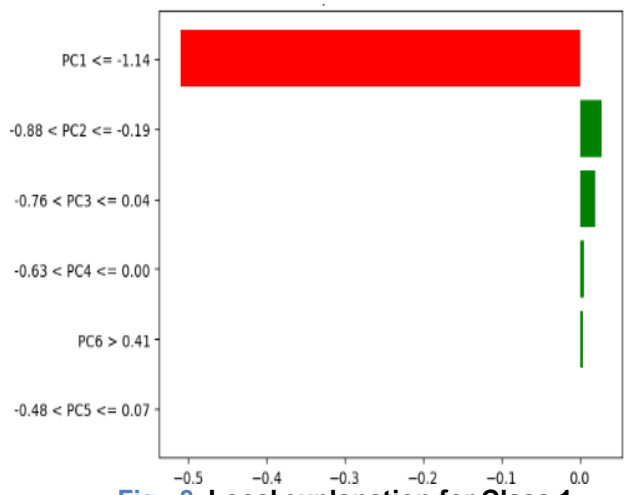


**Fig. 8. Local explanation for Class 1**

though it is less effective at separating the classes.

The analysis of the permutation feature importance of the Quantum kNN (QkNN) model trained on the features transformed by PCA is shown in Fig. 7. The x axis indicates the principal components (PC1-PC6) and the y-axis indicates the reduction in model accuracy when each of the features is randomly permuted. A more significant drop creates a higher significance of that feature to the model performance. The outcome shows clearly that PC1 has the most significant impact, since the permutation of this component will bring the most significant decrease in the model accuracy (about 0.39). This implies that most of the discriminative information that the QkNN acquires is likely to be contained in the first principal component. PC3 and PC2 are of moderate significance, and they add smaller though significant accuracy drops.

The other components (PC5, PC4, and PC6) have low influence, meaning they contribute little to the model's predictive performance. The error bars are the standard deviation of the results of multiple runs of permutation, and this shows that the importance estimates are stable and reliable. On the whole, this discussion confirms that QkNN mainly depends on the most significant PCA variations, which proves the effectiveness of dimensionality reduction and emphasizes the most important features of transformation, which play a crucial role in the precise prediction of heart disease.

Fig. 8. demonstrates a local explanation using LIME of a single prediction that is of Class 1 (heart disease present). In contrast to global feature importance methods, LIME attempts to explain the action of the model on a single instance by locally approximating the intricate model with an interpretable linear model. The red bars in this visualization indicate those features that reduce the likelihood of being in Class 1, and the green bars indicate those that augment the likelihood of being in Class 1. The size of each bar shows the contribution that it will make towards the final prediction.

## IV. Discussion

### A. Accuracy

Altogether, the findings reveal that classical models are still very competitive in predicting heart diseases, whereas quantum-inspired algorithms, in particular, QkNN with an accuracy of 90%, show potential and should be explored further with the development of quantum devices and algorithms. Besides, a gap in performance is observed, which demonstrates the significance of effective feature mapping and circuit design in quantum models. The findings also indicate that hybrid quantum-classical solutions can be used to address this gap by relying on the power of both paradigms. With the development of quantum technologies, predictive performance is likely to improve due to the improved circuits with high scalability and noise resistance. These results support the usefulness of further investigation into quantum-enhanced clinical decision support system machine learning. Overall, the results indicate that classical machine learning approaches remain highly competitive for heart disease prediction, while quantum-inspired techniques, particularly QkNN, exhibit promising potential for future exploration.

### B. Confusion Matrices for Quantum Models

The confusion matrix analysis for the quantum machine learning models Fig. 3. reveals notable variations in classification performance for heart disease prediction. The QSVC model shows relatively poor performance, with 8 true negatives (TN) and 25 true positives (TP), but a high number of misclassifications, including 21 false positives (FP) and 7 false negatives (FN). This

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indicates that the model struggles to correctly identify healthy cases, leading to a high false alarm rate.

The QNN model demonstrates improved and more balanced performance, achieving 24 TN and 26 TP, with 5 FP and 6 FN. This reflects a more stable classification capability, with relatively fewer misclassifications across both classes. The quantum-inspired KNN model achieves the best performance among all quantum models, with 28 TN and 27 TP, and minimal errors consisting of 1 FP and 5 FN. This indicates strong capability in distinguishing between healthy and diseased patients, with very low false-positive rates and comparatively few missed cases. In contrast, the VQC model exhibits the weakest performance, with 15 TN and 12 TP, and a high number of misclassifications, including 14 FP and 20 FN. The large number of false negatives is particularly critical in a medical context, as it reflects a failure to identify patients with heart disease. Overall, the results indicate that while quantum models such as QNN and quantum-inspired KNN provide promising and reliable performance. The presence of false negatives across models suggests that certain patient cases exhibit overlapping or complex feature patterns, making accurate classification challenging. Among all models, the quantum-inspired KNN demonstrates superior reliability and is better suited for clinical decision support due to its lower misclassification rates.

The observed performance degradation suggests that the PCA-based quantum feature representation, combined with the selected variational circuit depth, may not sufficiently capture the complex nonlinear relationships required for accurate heart disease classification. The study explores various quantum machine learning models, emphasizing the significance of feature mapping, circuit design, and model selection in achieving dependable quantum-enhanced classification results.

### C. Confusion Matrices for Machine Learning Models

Among the classical models assessed, Logistic Regression demonstrated the highest overall classification accuracy. It accurately classified most instances of both positive (heart disease present) and negative (heart disease absent) classes, with minimal misclassifications. The confusion matrix analysis demonstrates that the evaluated classifiers exhibit comparable performance across both classes in heart disease prediction. For the KNN, Random Forest, and Gradient Boosting models Fig .4. the number of correctly classified instances is similar, with 25 true negatives (TN) and 28 true positives (TP), while misclassifications include 4 false positives (FP) and 4 false negatives (FN). This indicates that these models maintain a balanced classification performance across both healthy and diseased cases.

In contrast, the Logistic Regression model shows slightly improved performance, achieving 29 true positives and 25 true negatives, with 4 false positives and only 3 false negatives. The reduction in false negatives is particularly significant in the context of heart disease prediction, as it reflects improved sensitivity in identifying patients with the disease. The balanced distribution of true positives and true negatives suggests that Logistic Regression achieves high sensitivity and specificity, making it a particularly

**Table. 2: Comparison of proposed model with state of art models.**

| Reference | Methodology | Dataset | Accuracy |
|---|---|---|---|
| [15] | Multilayer perceptron (MLP) , Particle swarm optimization (PSO) | Cleveland Heart Disease | 84.61% |
| [19] | Naïve Bayes Classifier, Federated Logistic Regression, Shapley, , Local Interpretable Model-agnostic Explanations | Cleveland Heart Disease | Naive Bayes- 81.1% Federated Logistic Regresion – 78.2% |
| [20] | Adaptive curve grey wolf optimization (ACGWO) algorithm into neural network backpropagation | Cleveland Heart Disease | 86.8% |
| [26] | Chi Squared Test, Support Vector Machines | Cleveland Heart Disease | 85% |
| [28] | Chi-square statistical test, Light Gradient Boosting Machine (LightGBM) | Cleveland Heart Disease | 88.5% |
| Proposed Model | OCA+ Quantum based feature mapping+Genetic Algorithm+ PCA+QkNN classifier + Shapley+LIME+DiCE | Cleveland Heart Disease | 90% |

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reliable choice for medical diagnostic applications. The kNN classifier performed well in predicting outcomes, successfully identifying many negative cases. However, its confusion matrix showed slightly more false negatives than Logistic Regression, indicating a possible decrease in sensitivity when detecting heart disease. Gradient Boosting also performed competitively, achieving high overall accuracy and capturing complex relationships in the data. Overall, the comparison of the confusion matrices highlights Logistic Regression as the most consistent and reliable classical model for heart disease prediction in this study. While kNN, Random Forest, and Gradient Boosting showed strong classification performance, their slightly higher false negative rates suggest potential limitations in detecting all disease-positive cases. These findings emphasize the importance of model selection in healthcare applications, where minimizing false negatives is critical to avoid missed diagnoses.

**D. Model Explainability Analysis**

The plot clustering patterns indicate that the compressed feature space contains structural information from the original data that is meaningful. The interconnection of classes also emphasizes the instability of the prediction of heart diseases, in which they are not always possible to separate in a linear way. All in all, this visualization confirms that PCA is an effective preprocessing step of both classical and quantum-inspired models by confirming that it reduces the dimensionality without losing critical discriminatory information. It is clear that the condition PC1 ≤ -1.14 has the greatest effect, and this dominates the decision of the model, whereby it shifted the prediction away from Class 1. On the other hand, feature ranges that are less strong, like PC2 = -0.88 and less than PC3 = 0.04, have a positive impact on predicting Class 1, though lesser. Features PC4, PC5, and PC6 show comparably low effects, and this shows that these features are not important in the prediction of this particular case. This LIME description is, on the whole, an explanation of how the model uses a combination of multiple features transformed to a PCA to make a local decision to enhance the transparency of the models and aid clinical interpretability because it shows which features contributed to the prediction to the greatest degree.

The comparative analysis presented in Table 2 demonstrates that the proposed model outperforms several existing state-of-the-art approaches on the Cleveland Heart Disease dataset. Previous studies have employed a variety of machine learning and optimization techniques to improve prognosis accuracy. For instance, the study in [15] utilized a Multilayer Perceptron (MLP) combined with Particle Swarm Optimization (PSO) and achieved an accuracy of 84.61%. The work in [20] integrated the Adaptive Curve Grey Wolf Optimization (ACGWO) algorithm with neural network backpropagation and obtained an accuracy of 86.8%. Similarly, the method proposed in [26], which employed the Chi-Squared Test and Support Vector Machines (SVM), achieved an accuracy of 85%, demonstrating the effectiveness of statistical feature selection techniques in improving classification performance. Furthermore, the study in [28] used a Chi-square statistical test along with the Light Gradient Boosting Machine (LightGBM), resulting in a higher accuracy of 88.5%.

The proposed framework achieved an accuracy of 90%, which is higher than all the compared methods. This improvement can be attributed to the hybrid integration of optimization, dimensionality reduction, quantum-inspired feature mapping, and explainable AI techniques. In contrast to earlier approaches that mainly relied on conventional machine learning classifiers, the proposed model combines OCA, Genetic Algorithm, PCA, and Quantum k-Nearest Neighbor (QkNN) classifier to enhance feature extraction and classification efficiency. Additionally, the incorporation of explainability methods such as Shapley, LIME, and DiCE improves the interpretability of prediction outcomes, a need only partially addressed in prior studies such as [19].

The findings indicate both similarities and differences compared to previous studies. Similar to existing research, the proposed work confirms that feature optimization and selection play a significant role in improving heart disease prediction accuracy. However, unlike earlier methods, the proposed framework integrates quantum-based feature mapping and explainable AI techniques into a unified prediction model, leading to enhanced predictive accuracy and interpretability. Therefore, the results demonstrate that the proposed hybrid approach is more effective and reliable for heart disease prediction when compared with the state-of-the-art methods presented in Table 2.

The combination of bio-inspired optimization methods, including Genetic Algorithms, emphasizes their possible application in the process of selecting the most efficient sets of features in the complex medical data, which enhances performance as well as resiliency. In addition, the usage of explainable AI methods (SHAP, LIME, and DiCE) is designed to support important clinical needs of transparency, interpretability, and trust in AI-based healthcare systems.

From a broader perspective, this research provides a basis for further investigation into quantum-enhanced medical decision support systems. With the maturation of quantum hardware, the suggested framework may be translated and implemented on actual quantum devices, potentially enabling additional benefits to performance. Also, the approach can be applied to other clinical prediction tasks, which will contribute to

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the creation of effective, interpretable, and the next generation of intelligent healthcare solutions.

## V. Conclusion

This paper introduced a hybrid pipeline based on classical and quantum-inspired predictive models used in heart diseases, combining statistical features selection, evolutionary optimization, dimensionality reduction via PCA, and quantum-enhanced learning. The suggested framework integrated ANOVA, Mutual Information, and RFE in a systematic way to create a powerful hybrid feature set, which was optimized further via Genetic Algorithms to come up with an optimal set of six-dimensional PCA space to be used with quantum models. Classical machine learning models, as well as quantum models, such as QSVC, QNN, QKNN, and VQC, were trained and tested to learn the relative predictive power of the models. It was revealed in experiments that classical algorithms like kNN (87%), Random Forest (87%), Logistic Regression (89%), and Gradient Boosting (85%) were all capable of performing excellently on the heart disease data. The most effective quantum model, namely QKNN (90%), was able to compete successfully with the best classical models. QNN and QSVC performed moderately, and VQC exhibited generalization. Permutation Feature Importance, SHAP, LIME, and DiCE interpretability analyses showed that PC1 was the most important variable to the model decisions, which highlighted the importance of PC1 in the transformed quantum feature space. On the whole, the findings indicate that classical models are still very effective in structured clinical data, although quantum-inspired models, especially QKNN, prove to be potentially effective, especially when enhanced by feature engineering and dimensionality reduction methods. Future work can extend the proposed hybrid classical–quantum framework in several more specific directions that directly address the current study's limitations. First, the framework can be evaluated on larger multi-modal medical datasets that combine structured clinical records with other data types. Examples include integrating electronic health records (EHR) with medical imaging data such as echocardiograms or cardiac CT scans, wearable sensor data capturing heart rate and activity patterns, and genomic or biomarker information. Such multi-modal datasets would allow the proposed framework to capture more comprehensive cardiovascular risk factors and improve predictive performance beyond the single structured Cleveland dataset used in this study. Second, federated or privacy-preserving quantum learning could be explored to address data privacy challenges commonly encountered in healthcare environments. In a federated learning setting, multiple hospitals or medical institutions could collaboratively train the hybrid model while keeping patient data locally stored. Only encrypted model parameters or gradients would be shared with a central aggregation server. This approach would help maintain patient confidentiality, comply with healthcare data protection regulations, and enable the use of larger distributed datasets without direct data sharing. Integrating federated learning with quantum-inspired models could therefore improve model generalization while preserving data privacy. By addressing these directions, future studies can overcome the current limitations related to dataset size, privacy constraints, and interpretability challenges, thereby improving the practical applicability and reliability of hybrid quantum learning systems for medical decision support.

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### Data Availability

The dataset analysed during this study is publicly available. The UCI Machine Learning Repository Heart Disease Dataset is accessible at https://archive.ics.uci.edu/dataset/45/heart+disease
.

### Author Contribution

Rashmi Mothkur contributed to the conceptualization, methodological design, model development, technical implementation and manuscript drafting. Swetha C B contributed in data processing, experimental validation, result analysis and manuscript drafting. Both authors reviewed and approved the final manuscript and agreed to be accountable for all aspects of the work.

### Declarations

### Ethical Approval

All procedures adhered to ethical guidelines for research involving human subjects.

### Consent for Publication Participants.

Consent for publication was given by all participants

## Competing Interests

The authors declare no competing interests.

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