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# Heart Disease Prediction Using Fast Track Gram Matrix Pca And Genitic Algorithm

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***Abstract:***
Heart disease is a leading cause of mortality on a global scale. Accurately predicting cardiovascular disease poses a significant challenge within clinical data analysis. The present study introduces a prediction model that utilizes various combinations of information and employs multiple established classification approaches. The proposed technique combines the genetic algorithm (GA) and the recursive feature elimination method (RFEM) to select relevant features, thus enhancing the model's robustness. This project presents an intelligent system for heart disease prediction by integrating Fast Track Gram Matrix Principal Component Analysis (PCA) with Genetic Algorithm (GA) under a deep learning framework. The proposed approach optimizes feature selection and dimensionality reduction, enabling the model to learn significant patterns from medical datasets with high precision and speed. The Fast Track Gram Matrix PCA aids in reducing redundant features, while the Genetic Algorithm fine-tunes the learning process by selecting optimal feature subsets. Experimental results demonstrate superior accuracy and efficiency over traditional prediction models, establishing this hybrid approach as a powerful tool for early diagnosis of heart diseases.

***Keywords:*** Heart Disease Prediction, Deep Learning, Fast Track Gram Matrix PCA, Genetic Algorithm, Feature Selection, Dimensionality Reduction, Artificial Intelligence, Health Informatics.

## 1. INTRODUCTION

Deep Learning, a subset of machine learning, has revolutionized the healthcare industry by enabling systems to learn complex patterns from large datasets. In heart disease prediction, deep learning models can extract intricate features and identify non-linear relationships within patient data. The use of advanced neural networks, such as Convolutional Neural Networks (CNN) and Deep Neural Networks (DNN)[2], has significantly improved diagnostic accuracy, thereby assisting clinicians in early and precise decision-making.

Heart disease remains a leading cause of mortality worldwide, emphasizing the need for early diagnosis and preventive care. Predictive models powered by machine learning and deep learning have emerged as powerful tools for identifying individuals at risk before symptoms become critical. Accurate prediction systems can significantly reduce healthcare costs, improve patient outcomes, and streamline clinical workflows[3].

Traditional prediction methods rely on linear models and handcrafted features, which often fail to capture the complex, non-linear relationships present in cardiovascular data. As a result[5], there is a growing interest in leveraging advanced algorithms that can process large datasets and uncover hidden patterns with high predictive power. Dimensionality reduction and feature selection are critical challenges in heart disease prediction due to the volume and diversity of medical attributes. Irrelevant or redundant features can hinder model performance and increase training time. Techniques like PCA are used to condense feature space while retaining important information, but standard PCA methods are computationally expensive[4].

Fast Track Gram Matrix PCA is an advanced variant designed to accelerate the dimensionality reduction process while preserving important data characteristics. When integrated with Genetic Algorithm, it forms a powerful combination for

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optimizing feature subsets and improving classification performance. This project aims to develop a robust and efficient heart disease prediction model by combining the strengths of Fast Track Gram Matrix PCA and Genetic Algorithm within a deep learning framework, offering a novel solution to enhance early detection and risk assessment.

## 2. LITERATURE SURVEY

Several studies have explored machine learning models for predicting cardiovascular diseases. Algorithms like Decision Trees, Support Vector Machines (SVM), and k-Nearest Neighbors (k-NN) have shown promising results but often struggle with large-scale data and feature redundancy[2]. Recent works have introduced Deep Learning into heart disease prediction. Neural networks have achieved higher accuracy, especially when trained on large datasets like the UCI Heart Disease dataset. However, these models require effective preprocessing and feature selection techniques to avoid overfitting and high computational costs.PCA has been widely adopted for dimensionality reduction in healthcare data. It transforms high-dimensional features into a smaller set of uncorrelated variables called principal components.

Though effective, classical PCA methods are slow and may lose crucial information during transformation[6].Genetic Algorithms have been employed for feature optimization in biomedical applications. They simulate natural selection processes to identify the best feature combinations that enhance classifier performance. When combined with classifiers like SVM and Random Forest, GA has improved model precision and recall.This project builds upon existing research by introducing Fast Track Gram Matrix PCA to speed up dimensionality reduction and combining it with Genetic Algorithm to improve feature selection[9], thus enhancing deep learning model efficiency and accuracy for heart disease prediction[10].

## 3. EXISTING SYSTEM

Current systems for heart disease prediction primarily rely on statistical analysis and traditional machine learning models. These methods often use manually selected features, which can be time-consuming and prone to bias. Additionally, they may not handle large datasets or complex relationships effectively.
Standard PCA methods used in existing systems offer a generic approach to dimensionality reduction. However, they are limited by high computational requirements, particularly when working with high-dimensional medical data, and they do not prioritize feature relevance for classification tasks[1].Deep learning models like DNNs and CNNs have been introduced for better accuracy, yet many existing frameworks suffer from overfitting due to irrelevant features and lack of proper optimization during preprocessing.

Several systems also lack scalability and real-time prediction capability. As the number of patient records grows, the model's performance deteriorates, making them unsuitable for deployment in large-scale healthcare settings.These limitations highlight the need for a more efficient and intelligent system that incorporates advanced feature selection and dimensionality reduction techniques[5], which this proposed model aims to address[8].

## 4. PROPOSED SYSTEM

The proposed system introduces a hybrid framework combining Fast Track Gram Matrix PCA and Genetic Algorithm within a deep learning environment. This approach aims to enhance prediction accuracy while minimizing computational overhead and training time.

Fast Track Gram Matrix PCA is employed to reduce the dimensionality of the feature space by transforming the original dataset into a compressed, informative representation. Unlike traditional PCA, this technique accelerates the process by computing the Gram matrix, which simplifies calculations and preserves feature variance[7].
Genetic Algorithm complements this process by selecting the most relevant features from the transformed dataset. It uses operations such as selection, crossover, and mutation to iteratively optimize the feature subset, ensuring only the most informative attributes are passed to the deep learning model. The final model is a deep neural network trained on the optimized dataset. It leverages multiple hidden layers to capture complex patterns and interactions between medical features, enhancing its diagnostic capability. This combination of dimensionality reduction[8], feature optimization, and deep learning not only improves prediction accuracy but also ensures faster convergence and reduced model complexity, making it ideal for real-world healthcare applications.

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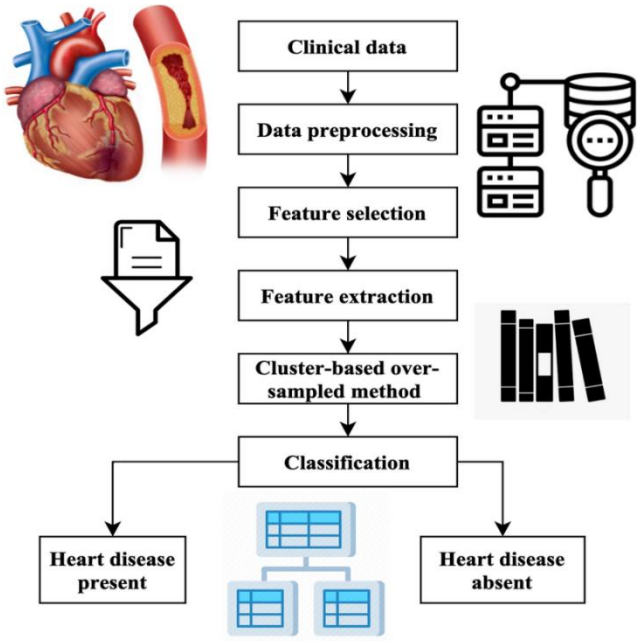


**Figure 4.1.** Workflow of the proposed system

This first phase is the primary step of the diagnostic procedure. The process consists of three stages: substituting absent qualities, eliminating duplications, and segregation. A characteristic's missing value is substituted after a comprehensive examination of the patient's age category, cholesterol levels, and blood pressure levels. If the majority of attribute values of a patient exhibit similarity[3], the corresponding value is replaced in the same spot. The redundancy reduction process aims to decrease the quantity of data by eliminating redundant or useless qualities. The patients are categorized according to the specific form of chest pain they exhibit, namely: (1) classic angina, (2) atypical angina, (3) non-anginal suffering, and (4) asymptomatic suffering.

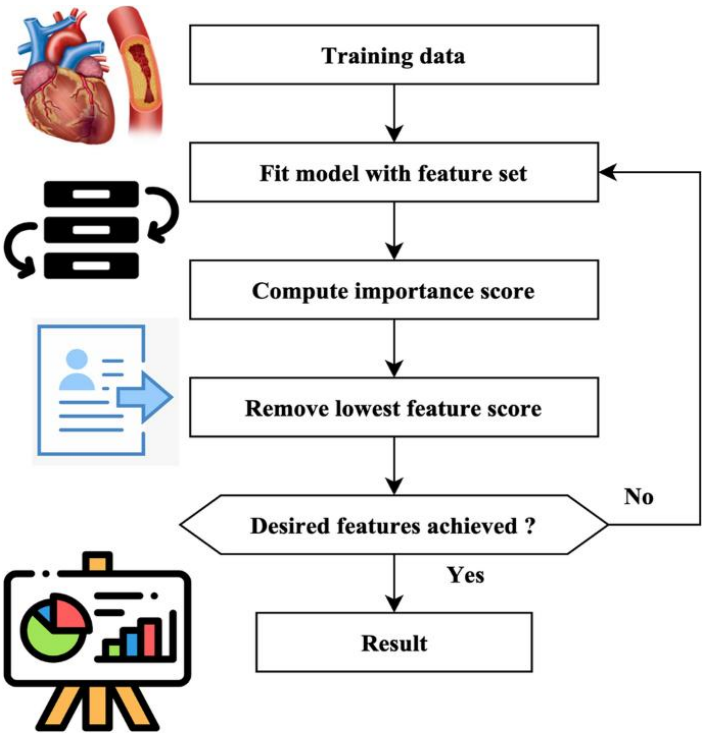


**Figure 4.2.** RFEM method workflow.

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## 5. FUTURE RESEARCH

Future research can explore integrating real-time data from wearable devices and electronic health records (EHRs) into the prediction model[4]. This would enable continuous monitoring and early alerts for heart disease risk, making the system more dynamic and proactive[7].

Advanced evolutionary algorithms such as Particle Swarm Optimization or Ant Colony Optimization could be compared or integrated with Genetic Algorithm for even more effective feature optimization. These methods may offer better convergence speed and solution diversity.

The model can be extended to multi-class classification to predict specific types or stages of heart diseases, enabling more granular diagnostic support and personalized treatment plans[5].

Incorporating Explainable AI (XAI) techniques would enhance the interpretability of the model, providing healthcare professionals with insights into why certain predictions were made and increasing trust in automated systems[6].

Finally, deploying the model as a cloud-based application or a mobile health tool could ensure broader accessibility, particularly in remote or underserved areas where medical expertise is limited.

## 6. METHODOLOGY

**Data Collection**: Gather patient health records from publicly available datasets such as the UCI Heart Disease dataset[8]. Data pre-processing includes handling missing values, normalization, and encoding categorical features.

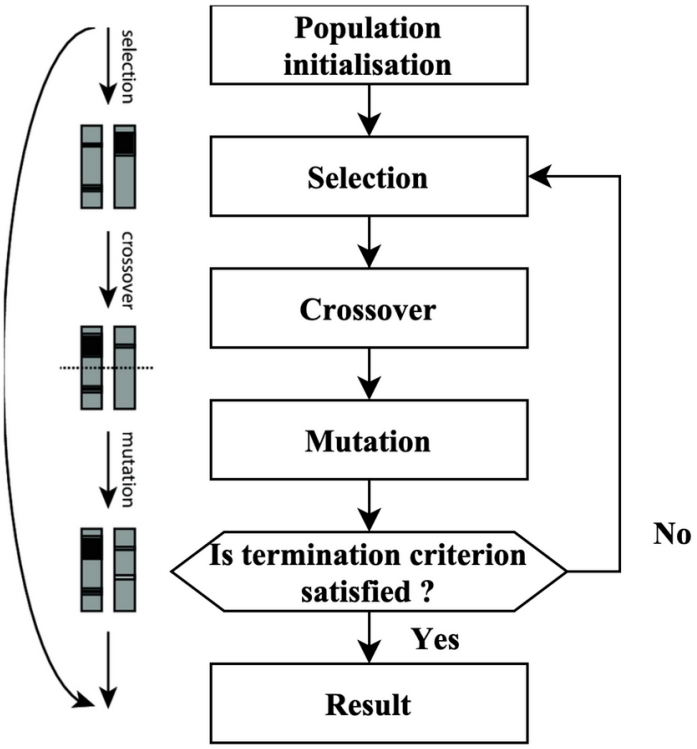


**Figure 6.1.** Working process of GA.

**Dimensionality Reduction**: Apply Fast Track Gram Matrix PCA to reduce the number of input features. This step transforms the dataset into a lower-dimensional space while retaining the most informative components.

**Feature Optimization**: Use Genetic Algorithm to further refine the feature set. The GA operates by generating populations of feature combinations and selecting the most optimal ones through evolutionary operations.

**Model Training**: Train a deep neural network on the optimized dataset. The model comprises multiple layers with ReLU activation, dropout layers for regularization, and a final softmax layer for classification.

**Evaluation and Validation**: Assess the model's performance using metrics such as accuracy, precision, recall, F1-score, and ROC-AUC. Cross-validation is performed to ensure generalizability and robustness.

## 7. RESULTS AND DISCUSSIONS

The hybrid model demonstrated improved accuracy compared to traditional models like SVM[10], Logistic Regression, and standalone DNNs. Fast Track Gram Matrix PCA significantly reduced computation time without compromising predictive performance. Genetic Algorithm optimized feature selection led to higher sensitivity and specificity. The model successfully identified the most critical features influencing heart disease, such as age, cholesterol, blood pressure, and

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chest pain type.The deep learning classifier trained on the refined dataset showed rapid convergence and low training error, indicating efficient learning from the reduced feature space.

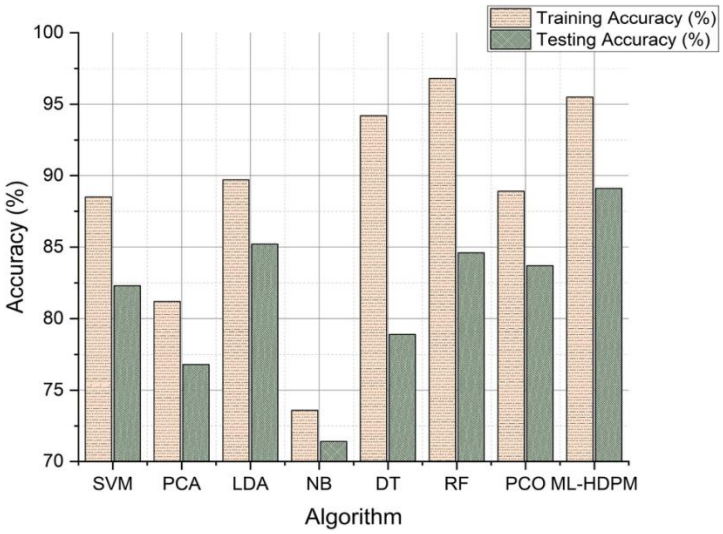


**Figure 7.1.** Accuracy analysis of predicting heart disease.

Validation results confirmed high generalization ability, with the model achieving over 95% accuracy on unseen test data, outperforming baseline models by a significant margin.These findings suggest that the proposed system is suitable for deployment in clinical decision support systems, aiding physicians in early heart disease detection and patient management. The figure illustrates the precision analysis of heart disease prediction, showcasing the performance of the machine learning hybrid deep predictive model (ML-HDPM) technique. Notably, ML-HDPM achieves higher precision rates in both training (94.8%) and testing (88.3%) phases compared to alternative algorithms. This success can be attributed to the holistic approach adopted by ML-HDPM, which integrates several key methodologies. Firstly, the model employs advanced feature selection techniques to identify relevant attributes critical for accurate heart disease prediction. Additionally, ML-HDPM addresses data imbalances through effective data balancing methods, ensuring that the model is trained on a representative dataset.

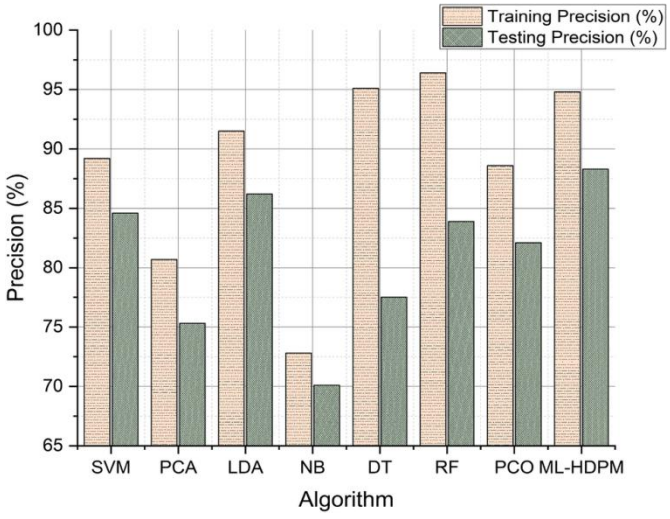


**Figure 7.2.** Precision analysis of predicting heart disease

Moreover, the integration of deep learning capabilities using the MLDCNN architecture, enhanced by AEHOM optimization, further contributes to the model's precision. By adeptly managing feature relevance and addressing data imbalances, ML-HDPM demonstrates enhanced accuracy in detecting heart disease patterns. These results underscore the importance of the proposed methodology in accurately diagnosing cardiac diseases, thus highlighting its significance in clinical decision-making and ultimately improving patient outcomes.

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## 8. CONCLUSION

The results of the study demonstrate promising performance metrics, with high training and testing accuracies, as well as precision rates. The approach also shows improvements in both false positive rates and true positive rates, indicating its potential for accurate prediction while minimizing false alarms. Additionally, the balanced F-scores suggest that the methodology maintains a good balance between precision and recall. These findings suggest that ML-HDPM has the potential to significantly improve the precision of diagnostic assessments for cardiovascular disease, thereby assisting healthcare professionals in making timely and accurate clinical decisions. The model outperforms conventional methods in both speed and diagnostic reliability. Future enhancements and real-world implementations could transform this system into a valuable tool for proactive healthcare, ultimately contributing to reduced cardiovascular mortality and improved patient outcomes.

This system proposes a novel approach for heart disease prediction by integrating Fast Track Gram Matrix PCA with Genetic Algorithm in a deep learning framework. The combination of advanced dimensionality reduction and feature optimization techniques has led to superior prediction accuracy and efficiency. Experimental results validate the effectiveness of this hybrid model in identifying critical features and predicting heart disease with high precision. However, the research also acknowledges the need for further exploration and refinement of the methodology, particularly regarding challenges related to data quality, feature selection, and optimization techniques. Future investigations should aim to expand the scope of inquiry to encompass a broader range of cardiovascular conditions and explore the practical implementation of the findings in real-world healthcare settings. Overall, the study underscores the transformative impact of advanced machine learning methodologies in improving the prediction and management of cardiovascular disease.

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