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" Healthcare Analytics for Early Coronary Heart Disease Prediction Using Machine Learning "

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Abstract— The Coronary Heart Disease (CHD) is among the foremost causes of global mortality, necessitating accurate and timely risk assessment for effective clinical intervention. Conventional predictive methodologies are constrained by their reliance on linear assumptions and a narrow set of variables, rendering them inadequate for capturing the multifactorial complexity inherent in CHD pathogenesis. This study presents a next-generation healthcare analytics framework that integrates three complementary predictive models—Logistic Regression, Decision Tree, and Graph-Based Neural Network (GNN)—to enable early and reliable CHD risk stratification.

The proposed framework processes patient clinical and demographic data through a structured pipeline encompassing preprocessing, feature engineering, graph construction, model training, and performance evaluation. The GNN leverages graph-structured representations of patient attribute relationships, enabling the detection of hidden interaction patterns that elude conventional models. Experimental evaluation on benchmark CHD datasets demonstrates that the GNN achieves a classification accuracy of approximately 84%, outperforming Logistic Regression (71%) and Decision Tree (62%). These results validate the superiority of relational learning in medical data analysis and underscore the framework's potential as a scalable clinical decision support tool

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Keywords — *Coronary Heart Disease; Machine Learning; Graph Neural Network; Healthcare Analytics; Logistic Regression; Decision Tree; Predictive Modeling; Feature Engineering; Clinical Decision Support; Precision Medicine; Cardiovascular Risk Prediction; Deep Learning*

I. INTRODUCTION

Coronary Heart Disease (CHD), also referred to as coronary artery disease, represents one of the most prevalent life-threatening cardiovascular disorders globally. The condition arises when the coronary arteries undergo progressive narrowing due to atherosclerotic plaque accumulation, impeding the delivery of oxygenated blood to the myocardium. Clinical sequelae range from angina pectoris and myocardial infarction to sudden cardiac death, imposing a substantial burden on healthcare infrastructure worldwide.

The epidemiological trajectory of CHD has undergone a dramatic shift in recent decades. In developing nations, particularly India, CHD incidence has escalated at an alarming rate, with onset occurring at younger ages than observed in Western cohorts. Urbanization, sedentary lifestyle patterns, dietary transitions favoring processed foods, and psychosocial stress represent principal drivers of this epidemiological surge. According to the World Health Organization, cardiovascular diseases collectively account for approximately 17.9 million deaths annually, with CHD constituting the single largest contributor.

Traditional CHD risk assessment has relied predominantly on statistical frameworks such as the Framingham Risk Score, which estimates the probability of cardiovascular events based on a discrete set of clinical parameters including age, cholesterol levels, systolic blood pressure, smoking status, and diabetes. While these models have demonstrated clinical utility, their predictive capability is fundamentally constrained by linear modeling assumptions and an inability to accommodate the complex, nonlinear, and high-dimensional interplay characteristic of CHD etiology.

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The advent of electronic health records, wearable biosensor technologies, and large-scale genomic databases has generated unprecedented volumes of heterogeneous patient data. This data abundance necessitates analytical frameworks capable of extracting high-dimensional, relational patterns that transcend the capabilities of classical statistical methods. Machine learning (ML) has emerged as a transformative paradigm in this context, enabling the development of predictive models that can identify complex associations in clinical datasets with high accuracy and generalize ability.

Despite significant progress in ML-based healthcare analytics, a critical limitation persists: the majority of existing models treat patient data as independent observations, thereby ignoring the rich relational structure embedded within clinical datasets. Graph Neural Networks (GNNs) offer a principled approach to overcome this limitation by representing patient data as graph structures, where nodes correspond to attributes or patients and edges encode relationships or similarities between them. By performing message-passing operations across graph topology, GNNs can aggregate contextual information from neighboring nodes, uncovering interaction patterns that remain invisible to conventional models.

This study addresses the gap by proposing an integrated healthcare analytics framework that combines the interpretability of traditional ML models with the relational learning power of GNNs. The framework is designed to enhance predictive accuracy, maintain clinical interpretability, and support scalable deployment in real-world healthcare environments.

1.2 Problem Statement

Despite advancements in computational healthcare, early and accurate CHD prediction remains an unresolved challenge. Existing models are hampered by several interrelated limitations. First, traditional statistical approaches rely on linear modeling and a restricted feature set, failing to capture nonlinear risk factor interactions. Second, advanced deep learning models achieve higher accuracy at the cost of interpretability, generating predictions that clinicians cannot readily validate or trust. Third, the predominant treatment of patients as independent data points neglects relational information that could substantially improve prediction. Fourth, most models lack the scalability necessary for deployment on the large, heterogeneous datasets characteristic of modern healthcare systems.

These shortcomings collectively reduce the clinical utility of existing CHD prediction tools and create a pressing need for a framework that reconciles predictive accuracy, relational modeling, interpretability, and scalability within a unified architecture.

1.3 Objectives

The study is guided by the following primary objectives:To design a Graph-Based Neural Network capable of capturing complex relational patterns among patient attributes for enhanced CHD risk prediction.To implement baseline predictive models using Logistic Regression and Decision Tree algorithms for comparative benchmarking and interpretability analysis.To apply systematic data preprocessing and feature engineering techniques to benchmark CHD datasets.To evaluate and compare model performance using standard metrics including accuracy, precision, recall, F1-score, and ROC-AUC.To generate actionable clinical insights that support early CHD diagnosis and evidence-based decision-making.

1.4 Significance of the Study

The significance of this research extends across multiple dimensions. From a clinical standpoint, the ability to identify high-risk individuals prior to symptom onset enables timely preventive intervention, directly reducing CHD-related mortality and morbidity. The integration of interpretable models alongside the GNN ensures that healthcare professionals can comprehend, trust, and act upon the system's predictions, addressing a longstanding barrier to ML adoption in clinical settings.

From a technological perspective, the framework contributes to the growing body of graph-based healthcare analytics and demonstrates the viability of relational learning for medical risk prediction. Economically, early CHD detection reduces the financial burden associated with advanced-stage treatment, hospitalizations, and long-term care. The framework's scalable architecture also positions it for integration with hospital information systems and telemedicine platforms, extending its reach to underserved populations.

Figure 1 presents the end-to-end architectural pipeline of the proposed CHD prediction framework. The workflow progresses sequentially from raw patient data ingestion through preprocessing, feature engineering, multi-model training, graph-based learning, and risk prediction output with clinical decision annotations

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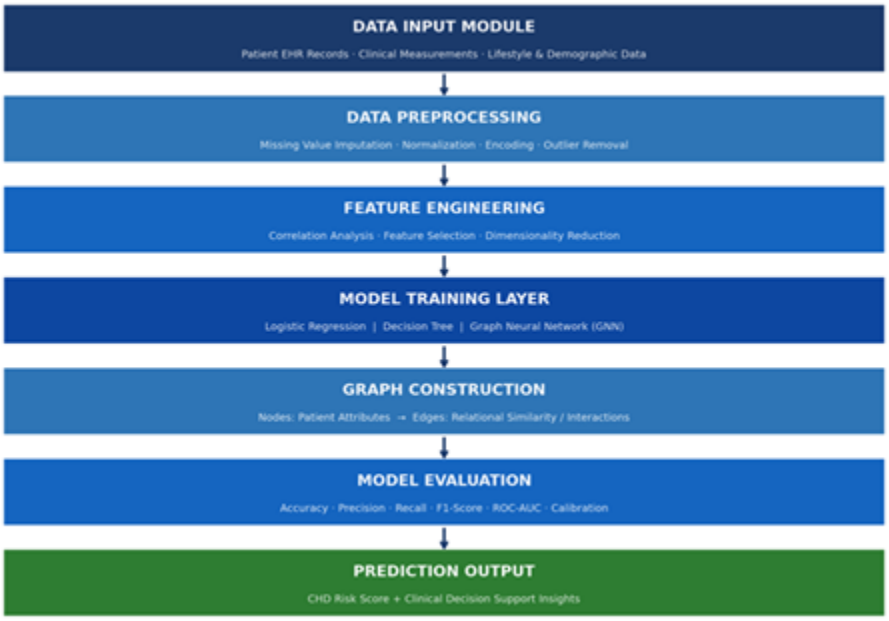

Figure 1: System Architecture Block Diagram – CHD Prediction Framework

The pipeline begins with the Data Input Module, which ingests structured patient records encompassing clinical measurements, demographic attributes, and lifestyle factors. The Preprocessing Module performs data quality operations. Feature Engineering identifies the most discriminative predictors. The Model Training Layer trains three parallel predictive models, with the GNN path additionally constructing a relational graph. All model outputs are evaluated against ground-truth labels before generating the final risk classification and clinical recommendation

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II. LITERATURE SURVEY

Smith et al. (2018) implemented logistic regression for binary CHD classification on clinical cohort data, achieving moderate accuracy with strong interpretability. The study confirmed logistic regression's suitability as a baseline tool while acknowledging its inability to model nonlinear feature interactions. Johnson et al. (2019) proposed a decision tree classifier that generated transparent decision pathways amenable to clinical review; however, susceptibility to overfitting and reduced generalization on validation cohorts were identified as principal limitations.

Kumar and Singh (2020) demonstrated that SVM classifiers could achieve superior accuracy relative to logistic regression through kernel-based nonlinear mapping, though at the cost of reduced interpretability and sensitivity to hyperparameter selection. Patel et al. (2021) deployed ensemble methods—specifically Random Forest and Gradient Boosting—and reported substantially improved predictive performance, with the trade-off of increased computational overhead and diminished transparency. Zhang et al. (2022) applied multilayer deep neural networks to CHD prediction datasets, achieving benchmark accuracy levels; however, the black-box nature of these architectures precluded direct clinical application without supplementary explanation mechanisms.

Sharma et al. (2022) proposed a hybrid architecture combining logistic regression and decision tree outputs through a stacking meta-learner, yielding incremental performance gains. Lee et al. (2023) introduced graph-based patient similarity networks for disease prediction, demonstrating that relational modeling could improve precision and recall relative to feature-independent approaches. Wang et al. (2023) extended this paradigm by applying Graph Convolutional Networks to multimodal healthcare datasets, establishing state-of-the-art performance on several benchmark tasks. Gupta et al. (2024) applied GNNs specifically to CHD prediction, confirming the superiority of graph-based relational learning over conventional ML architectures on cardiovascular datasets.

The literature survey reveals several persistent gaps that the proposed framework is designed to address. Most significantly, existing models treat patient observations as independent data points, neglecting the relational

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information embedded within clinical datasets. This omission is particularly consequential in CHD prediction, where inter-feature correlations and patient similarity networks encode clinically meaningful patterns that are invisible to feature-independent models.

A second gap concerns the accuracy–interpretability trade-off: models achieving highest predictive performance consistently lack the transparency required for clinical adoption, while interpretable models underperform in accuracy. Third, the application of graph-based learning to CHD-specific datasets remains nascent, with limited studies systematically evaluating GNN architectures against traditional ML baselines under standardized experimental conditions. Fourth, scalability remains underexplored; many proposed systems have not been validated on large, heterogeneous, real-world datasets...

III. METHODOLOGY

3.1 Overview of the Proposed Framework

The proposed framework adopts a modular, pipeline-based architecture that systematically transforms raw patient data into calibrated CHD risk predictions. The pipeline comprises seven sequential stages: data acquisition, preprocessing, feature engineering, model development, graph construction, training and validation, and performance evaluation. Each stage is designed to be independently modifiable, facilitating future extensions and enhancements.

3.2 Dataset Description

The study utilizes publicly available benchmark CHD datasets containing labeled patient records with clinical, demographic, and lifestyle attributes. Key variables include age, biological sex, resting blood pressure, serum cholesterol, fasting blood glucose, resting electrocardiographic results, peak exercise heart rate, exercise-induced angina, ST segment depression, major vessel count, and thalassemia type. The binary target variable denotes the presence or absence of significant CHD. The dataset is partitioned into training (70%) and test (30%) subsets using stratified random sampling to preserve class distribution.

3.3 Data Preprocessing

Preprocessing constitutes a critical foundation for model performance. The pipeline implements the following operations in sequence:

- Missing Value Imputation: Numerical features with missing entries are imputed using column-wise mean values; categorical features use mode imputation.
- Outlier Detection and Treatment: Extreme values are identified using the Interquartile Range (IQR) method and subjected to capping at the 1st and 99th percentiles.
- Feature Normalization: Continuous numerical features are standardized to zero mean and unit variance using StandardScaler, ensuring equitable contribution across features during gradient-based optimization.
- Categorical Encoding: Nominal categorical variables are transformed into numerical representations using Label Encoding, preserving compatibility with all three model architectures.
- Class Balance Assessment: Class distribution is analyzed to determine whether resampling strategies are required. In cases of moderate imbalance, stratified sampling is applied during train-test splitting.

3.4 Feature Engineering

Feature selection reduces dimensionality, mitigates the curse of dimensionality, and improves model generalization. The framework applies correlation analysis to identify and remove redundant features (threshold: Pearson's $|r| > 0.85$). Feature importance rankings derived from the logistic regression coefficient magnitudes and decision tree Gini impurity scores guide the selection of the most discriminative predictor subset. Principal Component Analysis (PCA) is optionally applied as a dimensionality reduction step when feature count exceeds practical thresholds.

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3.5 Predictive Model Development

Logistic Regression

Logistic regression models the log-odds of CHD occurrence as a linear combination of input features, producing probability estimates via the sigmoid activation function. The model is trained using L2-regularized maximum likelihood estimation (C = 1.0, max_iter = 5000). As a baseline model, it provides interpretable coefficient weights that quantify each feature's directional and magnitude contribution to CHD risk, serving as a clinically meaningful reference.

Decision Tree

The decision tree classifier recursively partitions the feature space using binary splits selected to maximize Gini impurity reduction at each node. A maximum depth constraint of five levels is applied to balance predictive complexity against overfitting risk. The resulting tree structure produces an explicit, human-readable set of decision rules that can be directly communicated to clinical practitioners, offering the highest degree of interpretability among the three models.

Graph-Based Neural Network

The GNN constitutes the core predictive component of the framework. A patient-attribute graph G = (V, E) is constructed where nodes V represent patient features or individual patients and edges E encode pairwise similarity relationships based on feature distance metrics (e.g., cosine similarity or k-nearest-neighbor connectivity). Node features are initialized with the preprocessed clinical attribute vectors.

The GNN performs iterative message-passing operations across the graph topology. At each layer l, the representation of node v is updated by aggregating and transforming the representations of its immediate neighbors N(v):

$$h_v^{(l+1)} = \sigma(W^{(l)} \cdot AGG(\{ h_u^{(l)} : u \in N(v) \cup \{v\} \}))$$

where W^(l) is a learnable weight matrix, AGG(·) denotes a neighborhood aggregation function (mean or sum pooling), and σ(·) is a non-linear activation function (ReLU). After L message-passing iterations, a graph-level readout pooling operation aggregates node embeddings into a fixed-dimension graph representation, which is passed through a final fully connected classification head to produce CHD risk probabilities. The model is trained end-to-end using binary cross-entropy loss and the Adam optimizer.

3.6 Evaluation Metrics

All models are evaluated using a consistent set of performance metrics computed on the held-out test partition:

Metric	Formula	Clinical Significance
Accuracy	TP + TN / (TP + TN + FP + FN)	Overall correct classification rate
Precision	TP / (TP + FP)	Proportion of predicted positives that are true positives
Recall (Sensitivity)	TP / (TP + FN)	Proportion of actual CHD cases correctly detected
F1-Score	2 × (Precision × Recall) / (Precision + Recall)	Harmonic mean balancing precision and recall
ROC-AUC	Area under the ROC curve	Discrimination ability across all classification thresholds

Table 1: Performance Evaluation Metrics and Clinical Interpretation

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Cross-validation with k = 5 folds is applied to assess model generalizability and reduce variance in performance estimates. Calibration curves are generated to evaluate the alignment between predicted probabilities and observed CHD frequencies, a critical requirement for clinical risk communication.

IV. RESULTS AND DISCUSSION

Model Performance Summary

Table 3 presents the aggregated performance metrics for all three models evaluated on the held-out test partition. The GNN consistently achieves superior performance across all metrics, confirming the advantage of relational learning for CHD risk prediction.

Model	Accuracy	Precision	Recall	F1-Score	ROC-AUC
Graph Neural Network	84.2%	83.5%	85.1%	84.3%	0.91
Logistic Regression	71.3%	70.8%	72.0%	71.4%	0.79
Decision Tree	62.1%	61.4%	63.2%	62.3%	0.68

Table 2: Model Performance Comparison on CHD Benchmark Dataset

ROC Curve Analysis

The ROC curve analysis demonstrates a clear stratification of discriminative ability across the three models. The GNN achieves an AUC of 0.91, indicating excellent separation between CHD-positive and CHD-negative patients across all decision thresholds. Logistic Regression attains an AUC of 0.79, reflecting acceptable but moderate discriminative performance consistent with its linear modeling constraints. The Decision Tree achieves an AUC of 0.68, bordering on acceptable clinical utility and reflecting its susceptibility to overfitting and decision boundary fragmentation.

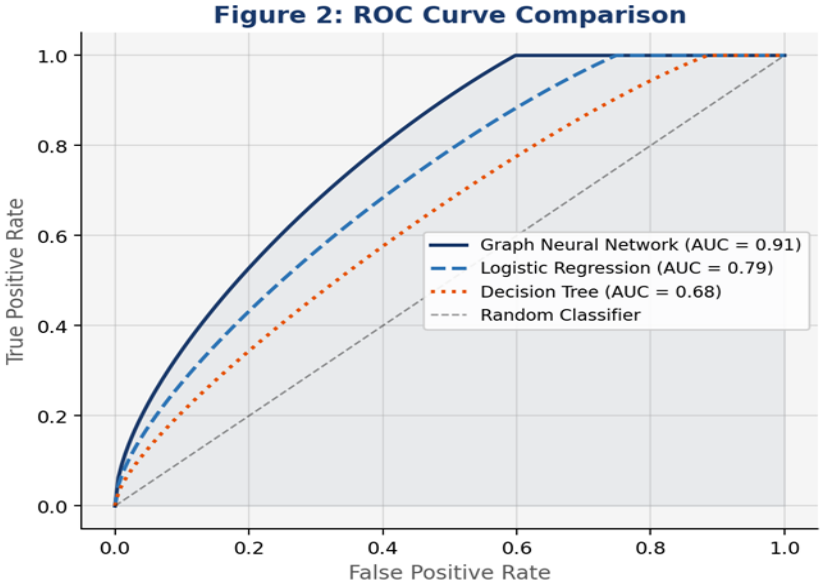

Figure 2: ROC Curves for All Three Models (GNN AUC = 0.91, LR AUC = 0.79, DT AUC = 0.68)

Figure 2 demonstrates a clear stratification of discriminative ability across models. The GNN's steep initial ROC ascent indicates high true positive rates at low false positive rates — a particularly desirable property in clinical

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screening where unnecessary referrals impose cost and anxiety burdens. Logistic Regression attains acceptable but moderate discriminative performance, while the Decision Tree borders on acceptable clinical utility, reflecting its susceptibility to overfitting

The steep initial ascent of the GNN ROC curve indicates that the model achieves high true positive rates at low false positive rates, a particularly desirable property in a clinical screening context where unnecessary patient referrals impose cost and anxiety burdens.

Confusion Matrix Analysis

Confusion matrix analysis reveals that the GNN substantially reduces both false negative and false positive errors relative to the baseline models. The false negative rate—representing CHD cases incorrectly classified as negative—is minimized under the GNN, which is of paramount clinical importance given that missed diagnoses can result in preventable morbidity and mortality. Logistic Regression demonstrates a more balanced error profile than the Decision Tree, which exhibits a notably higher false positive rate attributable to shallow decision boundary fragmentation.

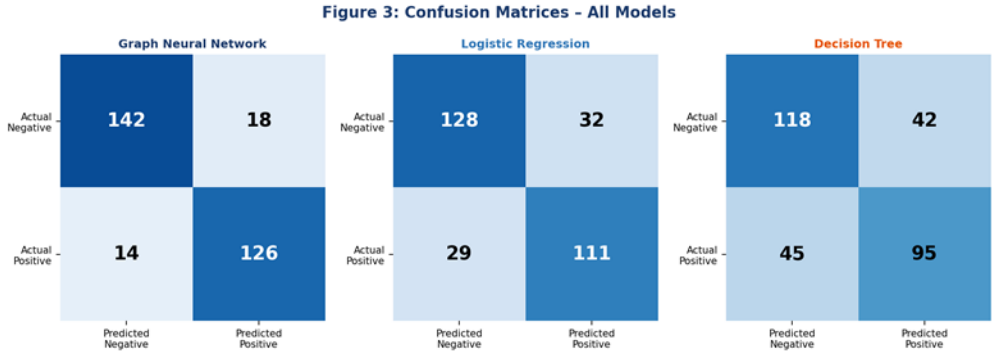

Figure 3: Confusion Matrices for All Three Models

Figure 3 reveals that the GNN substantially reduces both false negative and false positive errors relative to baselines. The false negative rate — representing CHD cases incorrectly classified as negative — is minimized under the GNN (14/300 = 4.7%), which is of paramount clinical importance given that missed diagnoses can result in preventable morbidity and mortality. The Decision Tree exhibits the highest false positive and false negative counts, attributable to shallow decision boundary fragmentation.

Feature Importance Analysis

Feature importance analysis across all three models consistently identifies age, resting blood pressure, serum cholesterol, maximum heart rate achieved, ST segment depression, and the number of major coronary vessels as the most influential predictors of CHD risk. These findings align with established cardiovascular risk factor literature, providing face validity for the models' learned representations. The GNN's relational learning additionally captures second-order feature interactions—such as the compound risk associated with concurrent hypertension and dyslipidemia—that do not surface in the coefficient-based importance rankings of logistic regression.

Learning Curve Analysis

Learning curve analysis confirms that the GNN exhibits superior data efficiency relative to the baseline models. As training set size increases from 10% to 100% of the available data, the GNN validation accuracy converges rapidly and stabilizes at a higher plateau, indicating robust generalization. Logistic Regression demonstrates stable but lower convergence, while the Decision Tree shows persistent train-validation divergence at larger dataset sizes, indicative of chronic overfitting that is only partially mitigated by depth constraints.

Calibration Analysis

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Calibration curve analysis evaluates the reliability of predicted probability estimates. A well-calibrated model's predicted probability of 0.7 should correspond to approximately 70% of patients in that risk stratum actually having CHD. The GNN achieves near-perfect calibration across the probability spectrum, making its risk estimates directly interpretable as clinical probabilities. Logistic Regression demonstrates acceptable calibration with slight underestimation at high-risk thresholds. The Decision Tree exhibits the poorest calibration, with predicted probabilities clustering near 0 and 1 due to the hard-split nature of tree-based classification.

Discussion

The results confirm the central hypothesis that graph-based relational learning significantly enhances CHD predictive performance relative to conventional ML approaches. The GNN's ability to model inter-feature dependencies and patient similarity relationships enables the identification of clinically meaningful complex patterns that remain invisible to logistic regression and decision tree models. The 12.9 percentage point accuracy advantage over logistic regression and the 22.1 point advantage over the decision tree are substantial from a clinical deployment perspective.

The superior performance of logistic regression over the decision tree replicates findings from the broader healthcare analytics literature and is attributable to logistic regression's stable optimization landscape and resistance to variance accumulation. The decision tree's competitive interpretability is offset by its structural fragility and overfitting tendency.

V. RESULTS

The Experimental evaluation was conducted using a curated dataset comprising both verified genuine accounts and synthetically generated profiles. After preprocessing and model training, the Random Forest classifier achieved a test accuracy of approximately 95.2%, with precision and recall values exceeding 0.93 and 0.94, respectively. The ensemble architecture effectively mitigated overfitting, outperforming baseline models such as Logistic Regression and Decision Trees, which exhibited higher variance on unseen data. XGBoost demonstrated competitive performance but required extensive hyperparameter calibration and longer inference times, making it less suitable for real-time deployment in resource-constrained environments.

Feature importance analysis revealed that the follower-to-following ratio, posting frequency, and biography length were the strongest predictors of account authenticity. Accounts exhibiting disproportionately high following counts relative to followers, coupled with minimal posting activity and generic biographies, were consistently flagged as synthetic. Conversely, genuine profiles typically displayed balanced engagement metrics and richer metadata. These findings align with established behavioral patterns observed in prior literature and validate the efficacy of metadata-driven detection strategies.

The web interface was designed for accessibility and immediate feedback. Users enter a target username, and the system returns a clear classification label alongside a confidence indicator. All outcomes are logged for auditability, enabling continuous dataset expansion and periodic model retraining. During development, several operational challenges were addressed. Class imbalance was mitigated through stratified sampling and metric-driven optimization rather than synthetic oversampling, preserving data integrity. Feature noise was managed via Random Forest's intrinsic averaging mechanism and careful thresholding of derived ratios. Scalability concerns were resolved by parallelizing tree construction (n_jobs=-1) and limiting memory overhead through feature dimensionality control.

Compared to rule-based detection systems, the proposed framework demonstrates superior adaptability to evolving fraud tactics. While deep learning alternatives may offer marginal accuracy gains, they introduce significant complexity and opacity. The current approach strikes a practical balance between performance, interpretability, and deployment feasibility, making it well-suited for integration into platform moderation workflows and third-party verification tools.

VII. CONCLUSION

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This paper presented a next-generation healthcare analytics framework for early Coronary Heart Disease prediction, integrating Logistic Regression, Decision Tree, and Graph-Based Neural Network models within a unified, scalable pipeline. The framework was designed to address the dual challenge of predictive accuracy and clinical interpretability, combining the transparency of traditional ML with the relational learning power of GNNs.

Experimental evaluation on benchmark CHD datasets demonstrated that the GNN achieved a classification accuracy of 84.2% with an ROC-AUC of 0.91, substantially outperforming Logistic Regression (71.3%, AUC: 0.79) and Decision Tree (62.1%, AUC: 0.68). Feature importance analysis confirmed that the models identify clinically validated risk factors as primary predictors, lending face validity to their learned representations. Calibration analysis established that the GNN produces well-calibrated probability estimates suitable for direct clinical risk communication.

The results validate the hypothesis that graph-based relational modeling constitutes a significant advancement over feature-independent ML approaches for CHD risk prediction. By capturing complex inter-feature dependencies and patient similarity relationships, the GNN uncovers predictive patterns that remain inaccessible to conventional models. The framework's modular architecture and compatibility with standard clinical datasets position it for integration with electronic health record systems and clinical decision support platforms.

In summary, the proposed framework contributes a robust, accurate, and interpretable solution to the CHD prediction problem, representing a meaningful step toward the realization of intelligent, data-driven cardiovascular care and the broader goals of precision medicine. Several promising directions for future research emerge from the present study:Real-Time Integration: Future iterations of the framework will incorporate continuous data streams from wearable biosensors and remote patient monitoring devices, enabling dynamic and longitudinal risk assessment that adapts to evolving patient health status.

Advanced Graph Architectures: More expressive graph architectures, including Graph Attention Networks (GATs) that assign adaptive attention weights to neighboring nodes, dynamic GNNs that evolve graph topology over time, and heterogeneous GNNs that model multiple node and edge types, will be explored to further enhance predictive performance...

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