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Predicting Silent Heart Attack Risk: A Wearable Biometric-Based Prediction Model

Abstract

Silent myocardial infarctions (SMIs), or silent heart attacks, occur when blood flow to the heart is blocked without the typical symptoms such as chest pain or shortness of breath. These events often go undetected, increasing the risk of severe cardiac damage and future life-threatening episodes. This project aims to develop a machine learning model to predict the presence of heart disease, a key risk factor for SMIs, using biometric data from wearable devices. Heart disease, particularly coronary artery disease, is the leading underlying cause of myocardial infarctions, including silent ones. The model employs techniques such as dimensionality reduction, SCANN (Synthesis of Compact and Accurate Neural Networks), and TUTOR (Training Neural Networks Using Decision Rules as Model Priors) to enhance prediction accuracy and computational efficiency. This model contributes to early detection by assessing unseen risk based on wearable biometrics, and ultimately aims to aid preventive healthcare through efficient, interpretable, and wearable-compatible heart disease risk assessment models.

1 Introduction

Cardiovascular disease is the leading cause of death worldwide, with myocardial infarctions (heart attacks) being a primary contributor [1][4]. While traditional heart attacks are often characterized by severe chest pain and other noticeable symptoms, silent myocardial infarctions lack these clinical symptoms [11][12]. Individuals may continue their daily activities unaware that they have suffered cardiac damage, significantly increasing their risk of further serious damage and death [11].

This project aims to develop a machine learning model that predicts the presence of heart disease, which is an established precursor to both symptomatic and silent myocardial infarctions, using biometric data collected from wearable medical devices. Rather than detecting an imminent cardiac event, the model focuses on assessing latent cardiovascular risk based on physiological indicators such as ECG readings, blood biomarkers, and other biometric signals. Accurate risk prediction enables earlier intervention and long-term monitoring for high-risk individuals.

To improve model efficiency and generalization, dimensionality reduction (DR) techniques are applied to alleviate the curse of dimensionality and enhance feature selection [1]. The model architecture integrates DR with SCANN, a methodology that employs architecture-altering operations to synthesize efficient, nonstandard feedforward structures suited to reduced-dimensionality datasets [8]. Additionally, concepts from TUTOR, a deep neural network synthesis framework, are incorporated to support learning with limited labeled data. TUTOR enhances model training by generating synthetic data from the same underlying distribution as the real data and applying decision rules as priors for training neural networks on tabular datasets [7].

Model performance will be evaluated using cross-validation to ensure robustness and predictive accuracy. Although the current dataset does not support real-time prediction of heart attacks, the ultimate goal of this research is to develop a reliable and computationally efficient wearable-compatible model for proactive cardiac risk assessment. Future extensions may include time-series analysis and integration with real-time alert systems that notify healthcare providers if critical thresholds are crossed and the patient is unresponsive. By combining advanced machine learning techniques with wearable biometric data, this project contributes to the early detection and prevention of adverse cardiac events.

2 Background

In this section, we will explore the medical and technical foundations of this research. We will discuss heart disease, myocardial infarctions (MIs), the role of machine learning in medical diagnostics, and previous research on heart disease prediction. Additionally, we will introduce

key techniques such as dimensionality reduction, SCANN, and TUTOR.

2.1 Cardiovascular and Heart Disease

Cardiovascular disease (CVD), encompassing a wide range of disorders affecting the heart and blood vessels, remains the leading cause of death globally, responsible for over 17.3 million deaths annually, with this burden expected to rise [21][22]. Heart disease includes various clinical conditions, most notably heart failure (HF), a major contributor to cardiovascular morbidity and mortality with poor long-term outcomes and high prevalence [3]. Inflammatory and structural conditions such as myocarditis, endocarditis, and valvular heart disease also fall under this umbrella [13].

The development of heart disease is strongly linked to modifiable risk factors, such as hypertension, hyperlipidemia, diabetes, smoking, and obesity [6][17], as well as lifestyle influences like inactivity and excessive alcohol use, alongside genetic predispositions [16]. Diagnosis typically combines clinical evaluation with tools such as electrocardiograms (ECGs), which can detect subtle myocardial injury and conduction abnormalities, and imaging techniques like echocardiography, cardiac MRI, and CT angiography for structural assessment [2][13]. One of the most severe and urgent manifestations of heart disease is myocardial infarction, commonly known as a heart attack.

2.2 Myocardial Infarction and Silent Heart Attacks

Myocardial infarction, a severe manifestation of coronary artery disease, occurs when coronary artery blockages restrict blood flow to the myocardium, leading to ischemic injury and potential tissue necrosis [9][18]. The primary cause is atherosclerosis, defined as a buildup of unstable plaques, lipids, white blood cells, and cholesterol in arterial walls [10]. Clinically recognized MIs often present with symptoms such as chest pain, nausea, shortness of breath, diaphoresis, fatigue, dizziness, or syncope, though not all cases exhibit these typical signs [10].

Silent myocardial infarction involves infarctions with minimal, atypical, or absent symptoms [11][20]. It is typically identified through objective findings, such as new Q-wave abnormalities on electrocardiograms (ECGs) in individuals without a known MI history, and is often discovered retrospectively via routine screening [20]. SMIs may account for nearly 50% of all MIs, highlighting their clinical importance despite the absence of overt symptoms [14].

SMI is linked to increased risks of ischemic stroke, subsequent clinical MI, heart failure (HF), and sudden cardiac death (SCD) [14][20]. HF, in particular, affects about one in four acute MI patients and significantly contributes to long-term mortality and morbidity [9]. The prognosis of SMI is comparable to symptomatic MI, reinforcing the need to treat it as a serious clinical event [20]. Early detection and proactive management are therefore critical, especially in high-risk populations such as those with hypertension, diabetes, or a history of cardiovascular disease.

2.3 Machine Learning in Medical Diagnosis

Machine learning (ML) is increasingly employed in medical diagnostics to process large datasets and detect patterns indicative of early disease onset. It has demonstrated broad applicability in medical imaging, particularly in radiology and pathology, by aiding clinicians in interpreting diagnostic images and identifying subtle pathological features. ML has been effectively applied to conditions such as breast cancer and temporomandibular disorders, where it can detect patterns beyond human perception [5][15][23]. Additionally, ML methods offer consistent, objective image evaluations, reducing diagnostic variability and minimizing missed or delayed diagnoses [19].

Advanced ML techniques like SCANN enable automatic synthesis of compact and accurate deep neural networks (DNNs) through connection growth, neuron growth, and pruning [8]. SCANN employs a grow-and-prune paradigm to jointly optimize network weights and architecture, minimizing model size without sacrificing accuracy; when combined with dimensionality reduction, this approach is termed DR+SCANN [8]. Similarly, TUTOR is a DNN synthesis framework that uses decision rules as model priors and generates synthetic data, allowing effective

training with limited data and lower computational demands [7]. TUTOR improves classification accuracy and reduces data dependency [7].

2.4 Related Work

Machine learning (ML) has emerged as a transformative tool in heart disease prediction, offering the ability to analyze complex datasets and return accurate predictions. ML is particularly well-suited for high-dimensional data environments, such as those involving electrocardiographic (ECG) signals, where traditional statistical techniques may falter. ML algorithms have demonstrated superior performance compared to both practicing clinicians and commercial diagnostic systems in detecting subtle ischemic changes associated with occlusion myocardial infarction, as well as in predicting heart failure following myocardial infarction [2][9].

Previous research in heart attack prediction has leveraged various machine learning models, including logistic regression (LR), decision trees (DT), and deep learning (DL) approaches [1][4][18]. Dimensionality reduction methods such as Principal Component Analysis (PCA) are explored to improve the performance of machine learning models by decreasing the number of features, addressing the curse of dimensionality [1]. Feature selection techniques also help refine datasets for improved model accuracy [1][4]. By integrating these advanced methods, this project seeks to develop a robust and efficient heart attack prediction system.

3 Motivation

In this section, we will explain the motivation behind this project. We will highlight the broader public health implications of early heart disease detection, touch on the importance of early detection, discuss gaps in current predictive technologies, and explain how this project aims to address these shortcomings.

3.1 Public Health Implications

Cardiovascular diseases represent a critical global health challenge, claiming millions of lives annually [18]. More specifically, heart disease stands as a leading cause of disability and the second-leading cause of death worldwide [11]. Identifying cardiac events and predicting future risks is crucial for effective prevention strategies. Machine learning presents itself as a convenient, fast, and low-cost method for disease detection, offering a significant advantage in timely diagnosis. Such prediction systems would be especially advantageous to those in remote or underserved areas, who may not have the resources to easily access the appropriate healthcare professionals for regular check-ups. Ultimately, by alerting individuals and medical professionals in advance, such technology can lead to earlier intervention, personalized treatment plans, and a significant reduction in the overall burden of heart disease on public health.

3.2 Importance of Early Detection

Detecting an impending heart attack before it occurs can significantly reduce mortality rates by enabling early medical intervention. Traditional diagnostic methods include electrocardiograms (ECG), blood tests for cardiac biomarkers, and imaging techniques such as echocardiography [4]. However, these approaches typically detect heart attacks after they have occurred rather than predicting them in advance. Machine learning techniques have shown promise in analyzing complex biometric data patterns to identify early warning signs of cardiac distress [1][4][18].

3.3 Gaps in Existing Research

Despite advancements in medical diagnostics, critical gaps remain in the prediction and management of heart disease. Machine learning has shown promise in analyzing complex health data, but challenges persist, including data quality issues [1], inconsistent healthcare datasets [18], and the need for improved model accuracy and interpretability [4]. Additionally, the etiology of heart disease is still not fully understood, making the selection of optimal predictive features and algorithms an ongoing challenge [18]. Many ML-based prediction systems also struggle with transparency, integration into clinical workflows, and scalability for diverse patient populations [4]. This project addresses these gaps by leveraging DR+SCANN to synthesize a compact and accurate neural network architecture, reducing

model complexity while maintaining high predictive performance [8]. Additionally, TUTOR enhances training efficiency by incorporating synthetic data and decision-rule-based learning, improving accuracy even with limited real-world datasets [7]. By combining advanced ML techniques with real-time biometric data processing, this system aims to bridge the gap between retrospective diagnostics and proactive, life-saving interventions.

4 Methodology

In this section, we will describe the proposed approach for developing a machine learning-based system for the early detection of heart disease using biometric data from wearable medical devices. The methodology involves dimensionality reduction through Principal Component Analysis (PCA), model development using DR+SCANN and TUTOR, and performance evaluation through 3-fold cross-validation.

4.1 Experimental Setup

The experimental setup utilized the Heart Disease dataset from the UCI Machine Learning Repository [24], containing 13 features and 303 instances. All experiments were conducted using Python 3 in a Jupyter Notebook environment on Google Colab, leveraging a T4 GPU for acceleration. The entire pipeline, from baseline to model evaluation, took approximately 1 hour and 15 minutes to execute. Specifically, the baseline model ran in 5 minutes, SCANN Schemes A and B each took 5 minutes, TUTOR Scheme A required 35 minutes, and TUTOR Scheme B completed in 25 minutes.

4.2 Data Preprocessing and Dimensionality Reduction

As shown in the "START" → "Data Preprocessing" → "Dimensionality Reduction" pathway (Fig. 1), biometric features from the dataset were initially loaded and preprocessed to handle missing values. The target variable, indicating the presence of heart disease, was binarized such that values greater than zero were encoded as 1 (presence of disease) and zero as 0 (absence of disease). To normalize feature scales magnitudes. This cycle of connection growth, and improve model convergence, standardization was applied using z-score normalization. Dimensionality reduction was performed using Principal Component Analysis (PCA), retaining 95% of the variance in the training set. The PCA transformation was fitted on the standardized training data and subsequently applied to both training and testing sets. This step reduced input dimensionality and improved the computational efficiency of subsequent model training.

4.3 Baseline DNN Model Development

Following dimensionality reduction, the PCA-transformed data was passed to the "Baseline Model Development" step (Fig. 1). A baseline deep neural network was constructed to classify the presence of heart disease. The model architecture consisted of an input layer, two fully connected hidden layers with 200 and 100 units respectively, each followed by LeakyReLU activation ($\alpha = 0.01$), and a sigmoid-activated output layer for binary classification. The model was compiled with the Adam optimizer and binary cross-entropy loss. Training was performed over 1500 epochs with early stopping and learning rate reduction callbacks, using a batch size of 32 and class weighting to address class imbalance.

4.4 DR+SCANN Implementation

The baseline model was further refined through architecture optimization in the "Apply DR+SCANN" stage (Fig. 1). Two schemes, A and B, were explored.

4.4.1 Scheme A

Scheme A was implemented using a grow-and-prune synthesis paradigm to iteratively optimize the deep neural network's architecture for heart disease classification. Initially, binary masks were applied to the dense layers to control trainable connections. The model was trained on PCA-transformed inputs, and gradients from a mini-batch were used to guide the selective growth of dormant connections with high magnitude gradients. After each growth phase, the architecture was expanded by adding new hidden units with noise-initialized weights. The model was then retrained, and pruning followed, targeting connections with the lowest gradient

model expansion, and pruning was repeated over 10 iterations.

4.4.2 Scheme B

Scheme B employed an alternating prune-and-grow strategy to iteratively refine a deep neural network initialized with 300 hidden units. Each model was trained on PCA-reduced features and initialized with binary masks that selectively activated network connections. The training began with aggressive pruning, removing 95% of connections based on gradient magnitude to reduce redundancy. The network was then fine-tuned before dormant connections with the highest gradient magnitudes were reintroduced at a 90% growth rate. This cycle of pruning, fine-tuning, and growth was repeated over 10 iterations. Mini-batches were used to guide the pruning and growth steps. This scheme emphasized compactness and adaptability through dynamic architectural optimization at each iteration.

4.5 TUTOR Implementation

In parallel, a complementary strategy using synthetic data and decision-rule priors was implemented, as shown in the "Apply TUTOR" step (Fig. 1).

4.5.1 Scheme A

Scheme A integrated a hybrid data-centric and model-centric approach, beginning with a real-data-driven synthetic generation pipeline. A kernel density estimator (KDE) with bandwidth selected via log-likelihood maximization was fit to the training data and used to sample 20,000 synthetic feature vectors. To ensure semantic validity, a random forest classifier was trained to predict categorical attributes from continuous features, and only synthetics with consistent predictions were retained. These verified samples were labeled using a separately trained random forest model optimized for depth via accuracy-based grid search. The resulting synthetic dataset was used to pretrain a neural network with 200 hidden units. This model was subsequently fine-tuned on real training data.

capable of continuously monitoring biometric

4.5.2 Scheme B

TUTOR Scheme B introduced a dual-network fusion framework that separately leveraged synthetic and real data representations. Synthetic samples were generated via kernel density estimation, followed by semantic integrity filtering using a categorical-classifier-based screening process. A random forest model trained on real data was again used to label these synthetics, with the model optimized for depth via accuracy-based grid search. Two neural networks were then independently trained: one on the filtered synthetic data and the other on the real training set. Each model learned distinct representations, extracted from their respective layers. These representations were passed into a composite neural architecture that concatenated the embeddings and produced a final classification output through a shared dense prediction layer. The combined model was trained end-to-end using both sets of embeddings as input.

4.6 Model Validation and Performance Evaluation

To assess model generalization, a 3-fold stratified cross-validation framework was employed across all schemes, including the Baseline DNN, SCANN A/B, and TUTOR A/B, as seen in the "Baseline Model Development" "Apply TUTOR" "Apply DR+SCANN" → "Performance Evaluation" pipeline (Fig. 1). Each fold involved splitting the data into training and testing subsets while preserving class distributions. Performance was evaluated using accuracy, precision, recall, and F1-score, averaged across folds to ensure robustness and comparability of results. These metrics were calculated on the held-out test fold in each split and then averaged across the three folds to ensure reliable comparisons. After evaluation, all models were compared in the "Compare Models" block (Fig. 1), and the best-performing model was selected.

4.7 Real-Time Prediction and Response Systems

The selected model will be integrated into a real-time prediction framework, as shown in the "Real-Time Prediction System" step (Fig. 1), and will be deployed on wearable medical devices

signals. The system will process incoming data in real-time, applying the predictive model to detect abnormal patterns associated with heart disease. This system enables early identification of cardiac irregularities, allowing for proactive intervention before symptoms escalate. By integrating with wearable sensors, the model continuously analyzes data such as heart rate, blood pressure, and other physiological indicators. Upon detecting high-risk signals, the pipeline proceeds to the "Alert System" (Fig. 1), which issues immediate notifications to patients. Users receive rapid alerts through connected devices, prompting them to seek medical attention. This response mechanism ensures that at-risk individuals can act quickly, potentially preventing severe outcomes. This integration of real-time analytics with alert protocols forms a system designed to reduce cardiac event-related morbidity and mortality.

5 Experimental Results

This section presents the performance outcomes of the baseline deep neural network (DNN) model and its optimized variants using SCANN and TUTOR schemes. The baseline model serves as a reference point, demonstrating balanced accuracy, precision, recall, and F1-score.

5.1 Baseline DNN Performance

The baseline deep neural network achieved an accuracy of 82.2%, precision of 82.4%, recall of 78.2%, and an F1-score of 80.1% (Fig. 8). The confusion matrix, aggregated over all folds, yielded 137 true negatives, 107 true positives, 30 false negatives, and 23 false positives (Fig. 2). These results demonstrate that the baseline model provides a solid starting point, with reasonable performance across metrics.

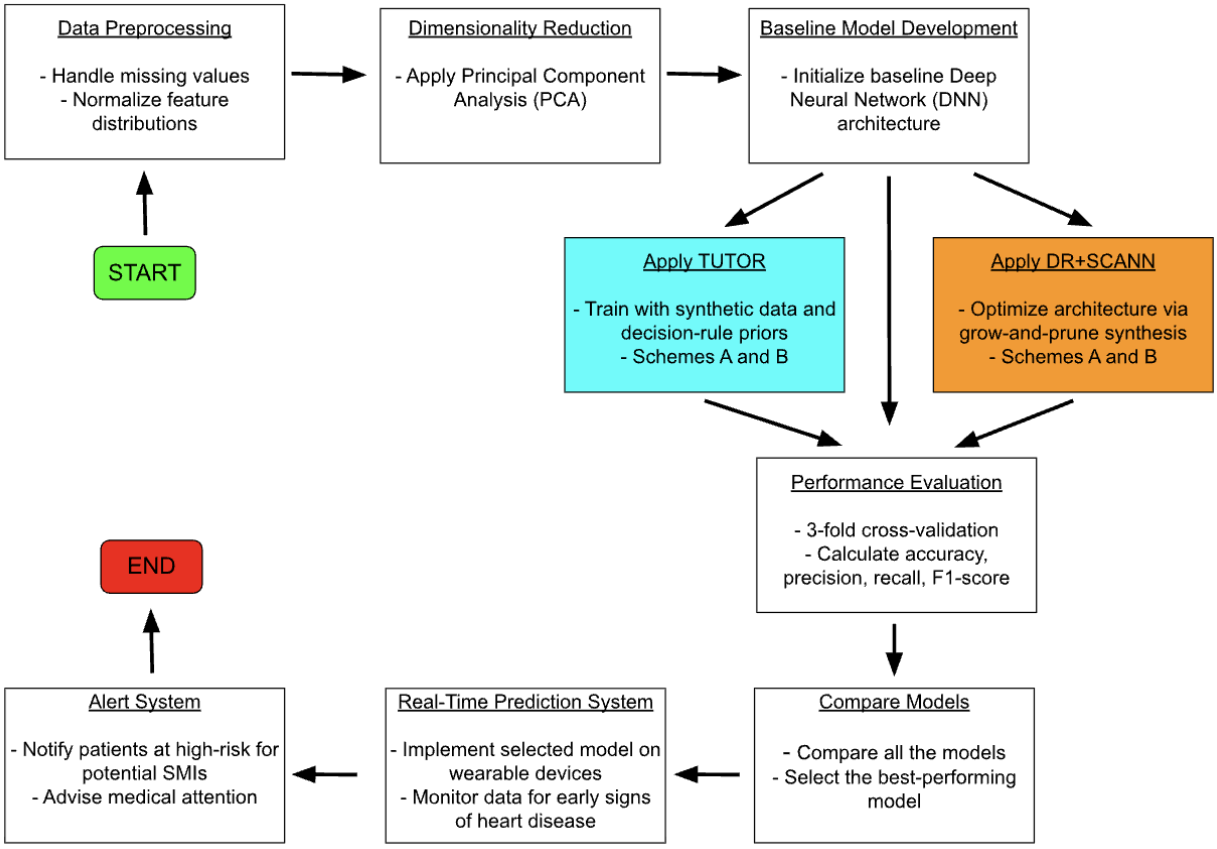

Figure 1: Top-Level Flowchart

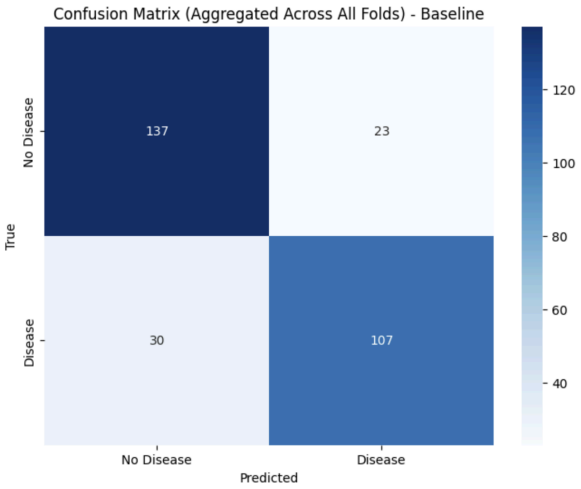

Figure 2: Baseline Confusion Matrix

5.2 DR+SCANN Results

Both SCANN variants maintained or exceeded baseline precision while introducing compactness and efficiency through architectural refinement. Scheme A, in particular, demonstrated strong generalization performance.

5.2.1 Scheme A

SCANN Scheme A achieved an accuracy of 84.8%, precision of 86.7%, recall of 79.6%, and an F1-score of 82.8%, outperforming the baseline across all metrics (Fig. 8). Its confusion matrix showed 147 true negatives, 109 true positives, 28 false negatives, and 17 false positives, indicating improved discrimination and reduced misclassification rates (Fig. 3).

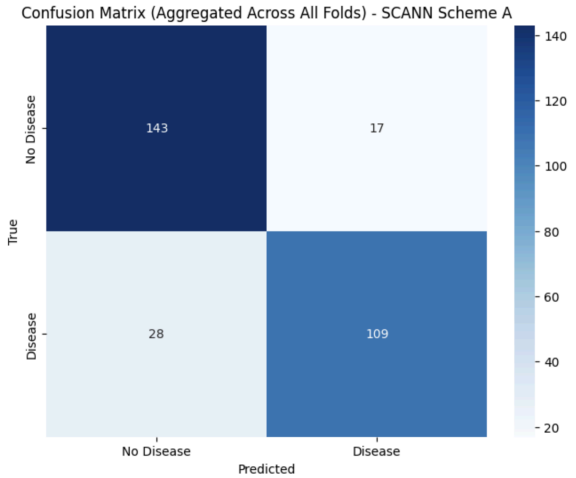

Figure 3: SCANN-A Confusion Matrix

5.2.2 Scheme B

In contrast, SCANN Scheme B yielded slightly lower performance, with an accuracy of 81.1%, precision of 82.3%, recall of 75.3%, and F1-score of 78.2% (Fig. 8). The corresponding confusion matrix recorded 138 true negatives, 103 true positives, 34 false negatives, and 22 false positives (Fig. 4). While still competitive, Scheme B's aggressive pruning early in training may have limited its capacity to recover critical features, resulting in slightly reduced recall and F1-score compared to Scheme A.

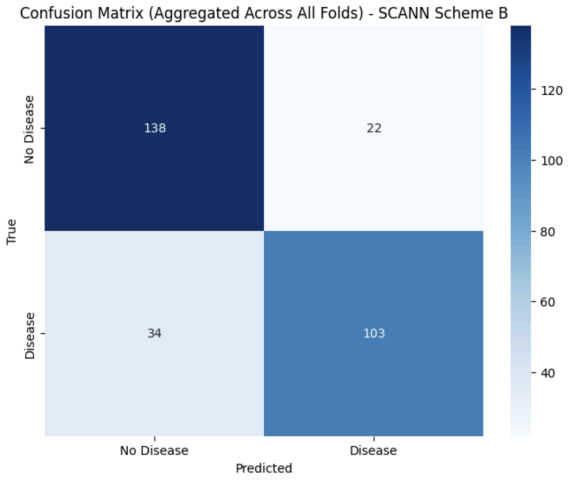

Figure 4: SCANN-B Confusion Matrix

5.3 TUTOR Results

Both TUTOR models underperformed relative to the baseline and SCANN models across all metrics. Nonetheless, the models maintained moderate sensitivity, which may be beneficial in applications prioritizing the detection of at-risk individuals, despite a higher false alarm rate.

5.3.1 Scheme A

TUTOR Scheme A achieved an accuracy of 70.7%, precision of 67.7%, recall of 69.4%, and an F1-score of 68.4% (Fig. 8). The confusion matrix indicated 115 true negatives, 95 true positives, 42 false negatives, and 45 false positives (Fig. 5). While the recall was moderate, the elevated number of false positives contributed to reduced precision and overall accuracy.

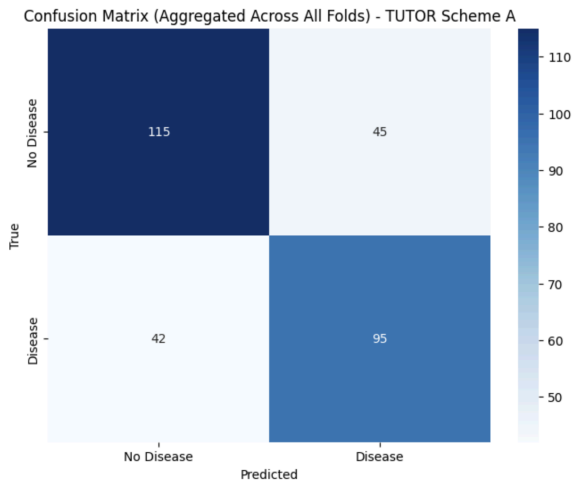

Figure 5: TUTOR-A Confusion Matrix

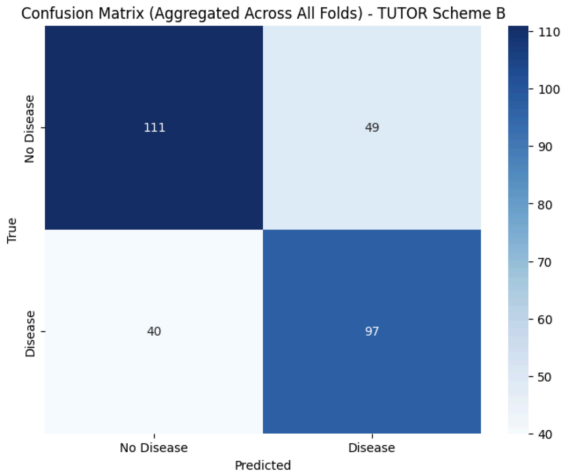

Figure 6: TUTOR-B Confusion Matrix

5.3.2 Scheme B

TUTOR Scheme B produced comparable performance, with an accuracy of 70.0%, precision of 66.4%, recall of 70.9%, and an F1-score of 68.4% (Fig. 9). Its confusion matrix recorded 111 true negatives, 97 true positives, 40 false negatives, and 49 false positives (Fig. 6). Despite a slightly higher recall, this scheme also struggled with false positive reduction, resulting in similar overall performance to Scheme A.

5.4 Model Comparison

A comparative analysis across all five models reveals distinct trade-offs in classification performance. The SCANN Scheme A model achieved the best overall results, with the highest accuracy (84.8%), precision (86.7%), and F1-score (82.8%), indicating a strong balance between precision and recall. The baseline DNN also performed well, particularly in precision (82.4%), though with slightly lower recall.

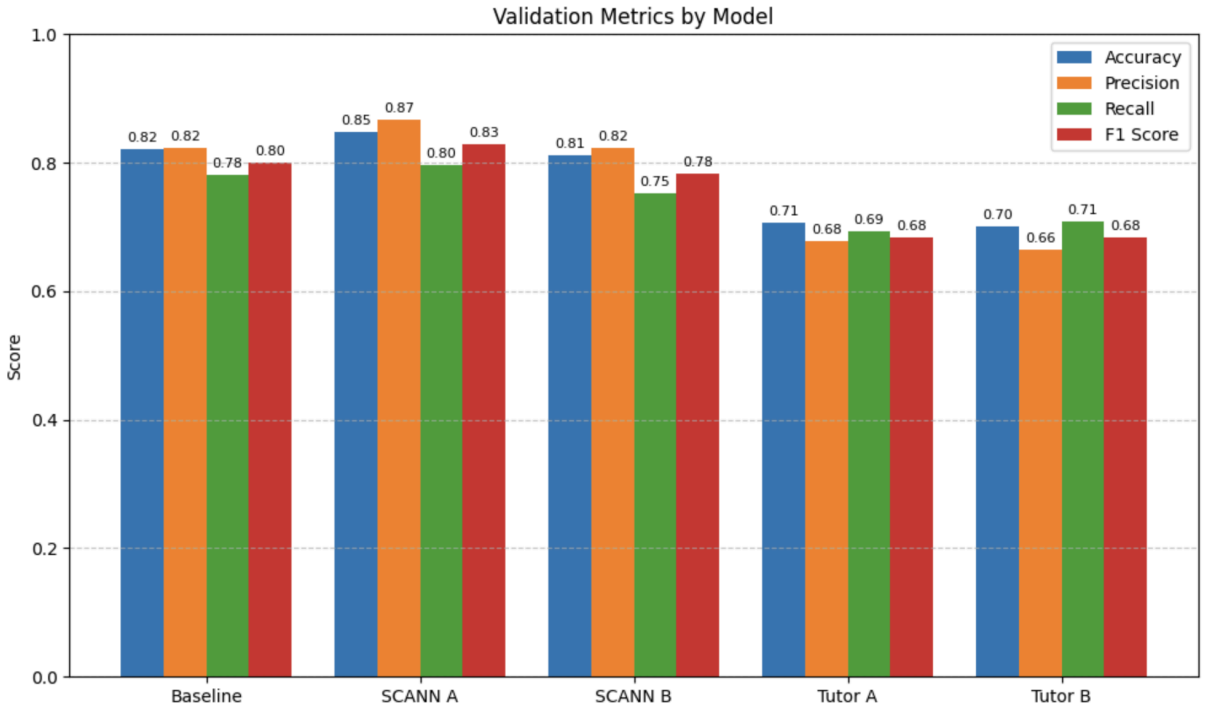

Figure 7: Bar Plot of Validation Metrics by Model

Model	Accuracy	Precision	Recall	F1-Score
Baseline DNN	82.2%	82.4%	78.2%	80.1%
SCANN A	84.8%	86.7%	79.6%	82.8%
SCANN B	81.1%	82.3%	75.3%	78.2%
TUTOR A	70.7%	67.7%	69.4%	68.4%
TUTOR B	70.0%	66.4%	70.9%	68.4%

Figure 8: Validation Metrics by Model

SCANN Scheme B showed competitive performance but lagged slightly behind Scheme A. In contrast, both TUTOR models underperformed across all metrics. Despite moderate recall (~70%), they exhibited lower precision and accuracy, likely due to a high false positive rate, limiting their effectiveness for precise diagnosis.

6 Discussion

This section explores the performance of SCANN's architectural optimization and TUTOR's synthetic data integration, highlighting their respective strengths and limitations. It concludes with an examination of the dataset and methodological constraints that influenced model performance.

6.1 SCANN's Architectural Optimization

SCANN Scheme A demonstrated superior performance compared to both the baseline and Scheme B, with a 2.6% improvement in accuracy and a notable reduction in false positives. This performance gain aligns with the grow-and-prune strategy described in the SCANN framework, which enables dynamic architectural refinement by regrowing pruned connections that prove valuable during training. The result is a more compact yet expressive model that maintains strong feature discrimination, which is critical in clinical prediction tasks where misclassification carries significant consequences.

In contrast, Scheme B exhibited lower recall, highlighting the tradeoff between model compactness and predictive performance. Its performance suggests that aggressive pruning early in training may have led to the irreversible loss of key diagnostic features. While this approach may yield gains in model efficiency, it risks undermining clinical reliability, especially in datasets where feature redundancy is limited. These findings highlight the importance of balanced pruning strategies that preserve essential information while promoting architectural sparsity.

6.2 TUTOR's Synthetic Data Challenges

TUTOR models showed a significant performance gap compared to the baseline, with a 12% drop in accuracy, highlighting challenges in leveraging synthetic data for medical prediction. The effectiveness of synthetic data generation hinges on accurate density estimation. However, the heart disease dataset likely contains complex, nonlinear relationships that exceed the representational capacity of methods like KDE, leading to distributional mismatches that impair model generalization.

Despite the overall decline in performance, TUTOR maintained moderate recall, suggesting that the synthetic data did capture some high-risk signal patterns. This outcome is expected, as

rule-based labeling strategies can preserve core decision boundaries but often fall short when modeling subtle feature interactions. While TUTOR's precision was adversely affected, evidenced by elevated false positive rates, its recall indicates potential for use in recall-critical applications, where detecting as many at-risk cases as possible is prioritized over minimizing false alarms.

6.3 Limitations

This study faced several dataset and methodological constraints that likely influenced model performance. First, the limited dataset size of only 297 instances post-split posed a challenge for TUTOR's synthetic data generation. Effective density estimation requires substantial data coverage, which is difficult to achieve with such a small sample. Additionally, the possible underrepresentation of key biomarkers may have further degraded the fidelity of generated samples, compounding errors in downstream predictions.

Methodologically, SCANN's grow-and-prune optimization introduces considerable computational overhead. These cycles demand careful hyperparameter tuning, which may hinder scalability and generalization to larger, more diverse datasets. Meanwhile, TUTOR's reliance on rule-based labeling through random forests introduces its own risks. If the baseline forest fails to capture rare but important risk patterns, those biases can be inherited by the synthetic data, limiting the model's ability to generalize beyond the initial training distribution. These constraints emphasize the importance of both data quality and methodological flexibility in developing robust predictive models for clinical applications.

7 Conclusion and Future Directions

This study demonstrates the importance of balancing model efficiency and diagnostic accuracy in heart attack prediction. SCANN's grow-and-prune methodology proved effective, enhancing accuracy and reducing false positives by preserving critical connections during training. Scheme A's performance showed that dynamic architectural refinement can optimize both compactness and feature discrimination. In contrast, Scheme B's aggressive pruning sacrificed recall, highlighting the risks of excessive efficiency at the cost of predictive power. TUTOR's performance revealed challenges in leveraging synthetic data for medical prediction, particularly due to distributional mismatches and the complexity of nonlinear relationships. However, TUTOR's moderate recall suggests potential value in applications prioritizing recall over precision.

Future improvements to heart attack prediction models could focus on several key areas to enhance their accuracy and applicability in real-world clinical settings. First, expanding the models to incorporate multimodal data, such as genomic sequences and medical imaging, could significantly improve predictive power. This would require developing novel growth-prune strategies capable of handling the complexities of combining diverse data types, potentially utilizing techniques like Bayesian optimization for efficient feature fusion.

Additionally, federated learning could be explored to enable privacy-preserving collaboration between institutions. By training models across distributed datasets without sharing patient data, federated learning would allow for the aggregation of diverse clinical information while maintaining privacy. Overcoming the challenges of data heterogeneity and computational costs will be essential to fully realize its potential.

Another promising direction is the integration of multiple clinical data sources, such as electronic health records and laboratory results, to provide more comprehensive risk profiles. Advanced data harmonization techniques would be needed to address inconsistencies between sources and ensure accurate predictions.

Finally, developing adaptive models that can account for demographic diversity is crucial. Fine-tuning models to different population groups, considering factors like age, gender, and ethnicity, will be important for improving fairness and generalizability, ensuring that predictive models work effectively across all patient demographics.

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Appendix

https://github.com/emilyz04/ece-heart-disease