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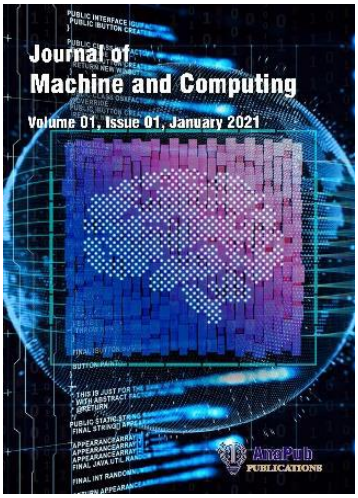

Chandra Babu J and Reddy Madhavi K

DOI: 10.53759/7669/jmc202505111

Reference: JMC202505111

Journal: Journal of Machine and Computing.

Received 10 October 2024

Revised form 30 January 2025

Accepted 30 March 2025

Please cite this article as: Chandra Babu J and Reddy Madhavi K, "Local Interpretable Model-Agnostic Explanation with Dual Path Network for Abnormality Detection and Classification in Biological Systems", Journal of Machine and Computing. (2025). Doi: https:// doi.org/10.53759/7669/jmc202505111.

Local Interpretable Model-Agnostic Explanation with Dual Path Network for Abnormality Detection and Classification in Biological Systems

[1]J. Chandra Babu, [2]K. Reddy Madhavi

[1]Research scholar, Department of CSE, School of Computing, Mohan Babu University, Tirupati, India.
[2]Professor, AI&ML, School of Computing, Mohan Babu University, Tirupati, India
[1]chandrababu1210@gmail.com, [2] kreddymadhavi@gmail.com
Corresponding Author: kreddymadhavi@gmail.com

Abstract –

Detection and classification of abnormalities in biological systems are critical tasks where early identification can significantly enhance intervention strategies and outcomes. Emerging technologies such as Deep Learning (DL) have opened new avenues for more accurate prediction and classification of disease-related conditions. While several machine learning algorithms can detect abnormalities at early stages to support preventive actions, many existing models suffer from limitations such as inaccuracy, bias, and overfitting. This work presents a novel approach for improving prediction accuracy by identifying essential features using advanced deep learning architectures. A new framework is proposed, combining the Dual Path Network (DPN-131), known for its robust feature extraction capabilities, with Local Interpretable Model-Agnostic Explanations (LIME) to enhance both model predictability and interpretability. The DPN-131 model effectively captures complex patterns in high-resolution biological data, enabling precise detection and classification of various abnormal conditions for cardiovascular disease. To address the interpretability challenges often encountered in deep learning models, LIME provides localized explanations that identify influential data regions and features associated with specific predictions. Experimental results on a large-scale biological dataset demonstrate that the DPN-131 model, supported by LIME, achieves state-of-the-art classification accuracy and produces interpretable, trustworthy explanations. This method provides a powerful and explainable tool to assist intelligent decision-making processes for early detection and management of abnormalities in biological systems.

Keywords - DPN-131, LIME, medical image classification, explainable AI, Deep Learning.

I. INTRODUCTION

Cardiovascular disease (CVD) is the most urgent medicinal concern at the moment. It's the most common cause of mortality in general and one of the deadliest chronic diseases. Over 20.5 million people die from cardiovascular disease every year, making for about 31.5% of all deaths globally, according to unconstrained data from the World Health Organization (WHO). Furthermore, it is anticipated that by 2030, there will be 24.2 million deaths each year. Heart attacks as well as strokes cause approximately 85% of cardiovascular disease-related deaths [1]. A heart attack happens when plaque builds up in the artery walls, limiting the supply of blood to the heart. The brain's blood supply is cut off when a blood clot plugs a brain artery, causing a stroke. Heart disease is mostly caused by the heart's inability to pump blood to specific parts of the body efficiently. Cold sweats, swollen feet, nausea, shortness of breath, chest pain, sudden disorientation, and an erratic heartbeat are some of the early symptoms. Increasing patient survival rates requires accurate heart disease prognosis and early detection. Obesity, sedentary lifestyles, high blood pressure, high cholesterol, alcohol and tobacco use, and genetic abnormalities all raise the risk of cardiovascular disease. Mortality can be reduced by early symptom identification and lifestyle changes such as regular exercise, quitting smoking, and making professional appointments for routine checkups [2].

Most current techniques for identifying and predicting heart disease rely on a patient's medicinal history, symptoms, and physical inspection results. Diagnosing heart disease can be challenging for physicians, with accuracy often reaching only up to 67%, as the diagnosis is typically based on symptoms observed in patients who have already been diagnosed [3]. Therefore, to improve heart disease prediction, the medicinal industry involves an automatic intelligent classification. The application of machine learning procedures, along with the extensive patient data available in healthcare, can help achieve this goal. Data science research teams have recently shown a great deal of importance in disease prediction. The availability of large health statistics and the quick improvement of computer methods in healthcare production are the main causes of this interest. Integrating cutting-edge deep learning and intelligent decision-making technologies could greatly improve the healthcare assistance that society receives [4]. The most important resource for learning new things and getting useful

information is data. Numerous sectors such as research, technology, commerce, educational institutions, and health deal with enormous volumes of data, or 'big data.' This data, whether unstructured or structured, is typically unprocessed. To store, process, analyze, manage, and visualize it, valuable information must first be extracted through data analysis [5].

Patient data and medical information are becoming increasingly accessible and growing in the healthcare sector. This raw data contains a great deal of imbalance and redundancy. Pre-processing is required to extract relevant attributes, speed up training computations, and increase classification accuracy. These processes are enhanced by recent advancements in computing power and machine learning capabilities, which also open new avenues for healthcare research [6], particularly in the primary detection of diseases like cancer and cardiovascular disease, thus increasing survival rates. Applications of machine learning extend to areas such as improved vehicle safety system design and the identification of risk factors for illnesses. Machine learning provides powerful predictive modeling techniques to address existing limitations. It can be used to develop predictive algorithms and interpret large datasets. By minimizing the discrepancy between estimated and observed effects, it leverages computing to understand composite, non-linear relationships among variables. The system predicts outcomes by applying patterns learned from the features in the current dataset to unseen data. When trained with suitable data, classification and an approach in supervised machine learning can effectively detect diseases [7].

In this research, we proposed a novel method for cardiovascular disease detection and classification that combines LIME with DPN-131. The proposed structure leverages the model-agnostic interpretability features of LIME to improve transparency in critical decision-making procedures in medical requests. By comprising the DPN-131 architecture, known for its dual-path capability to detention both local and global feature demonstrations, our method advances organization accuracy and interpretability, making it a powerful tool for recognizing and categorizing cardiovascular circumstances with high precision.

1.1 Motivation of this research

The motivation for this paper originates from the rising occurrence of CVDs and the central need for precise, interpretable diagnostic tools to aid in early analysis and treatment. Traditional diagnostic methods frequently lack transparency, posing challenges to clinical trust and widespread use. This study goals to increase model interpretability while maintaining height accuracy in CVD diagnosis and organization by joining LIME with DPN-131. This hybrid method not only enhances predictive capacity but also offers clinicians insights into the decision-making process, fostering belief and enabling additional conversant, data-driven healthcare decisions.

1.2 Contribution of the research

- Suggested an advanced framework that combines the DPN-131, a deep learning architecture known for its robust feature extraction competencies, with LIME to increase the transparency and consideration of model predictions in CVD detection and organization.
- The DPN-131 model efficiently captures complex designs in high-resolution medical images, agreeing on precise identification and organization of diverse cardiovascular diseases.
- To address the interpretability challenge in DL, LIME is utilized to propose localized explanations, allowing doctors to envisage which regions and features of an image contributed to a specific diagnosis.
- Experimental results on a large CVD dataset determine that the DPN-131 model, augmented by LIME, completes state-of-the-art organization accuracy and provides credible, interpretable explanations that align with clinical CVD markers.

1.3 Outlines of the paper

Table 1: Outline of the paper

S.NO	Sessions
1.	Introduction
2.	Literature Review
3.	Proposed model
4.	Results
5.	Conclusion

II. LITERATURE REVIEW

CVDs are a major global cause of death and indisposition, emphasizing the dangerous need for enhanced categorization and recognition approaches. This literature survey examines recent advancements in CVD detection, focusing on approaches that leverage machine learning, signal handling, and image analysis to improve diagnostic accuracy. It explores state-of-the-art approaches for detecting various types of cardiovascular diseases, highlighting the strengths, limitations,

and trends in the current study. This review aims to provide insights into current approaches, analyze challenges, and propose future directions for successful early detection and personalized treatment of cardiovascular disease.

A Swarm-ANN-based model for forecasting heart disease was proposed by Nandy et al. [8]. In this model, the Swarm-ANN method is used to train a set of randomly constructed Neural Networks (NNs). The weights of the NN populations are altered throughout two weight-modification training sessions using a newly developing heuristic approach to improve the prediction accuracy for cardiovascular conditions. To aid physicians in the early identification of cardiac disease, Mahalakshmi et al. [9] developed effective feature optimization and organization algorithms. Initial steps include rescaling the collected data using the min-max normalization procedure. The optimal features and feature subsections are particularly using Recursive Feature Removal and Improved Particle Swarm Optimization (IPSO) methods. Ahmad et al. [10] suggested a convolutional neural network (CNN) technique utilizing a DL-based approach called BiLSTM to accurately predict cardiovascular disease. Feature selection is performed by ranking and selecting the most pertinent features. The hybrid CNN-BiLSTM model then varieties a prediction about cardiovascular health based on deep learning.

A major cause of death, heart disease, was the subject of a suggestion by Bharti et al. [11], who highlighted the significance of precise prediction in preventing potentially fatal situations. The study investigated various DL methods and ML procedures using the 14 principal features of the UCI ML Heart Disease dataset. The findings were promising, maintained by accuracy metrics and a confusion matrix. Additionally, the study explored the integration of these predictive techniques with multimedia technology, such as mobile devices, to increase accessibility and functionality. The results showed that the deep learning approach significantly enhanced accuracy, reaching 94.2%, outclassing earlier results obtained using ML methods such as SVM and conclusion trees. Sudha and Kumar [12] propose that CNNs are effective for identifying cardiac issues. The value of CNNs enhances as the network depth grows, enhancing their competence to interpret and convey information clearly and conceptually. A hybrid model that combines CNN and Long Short-Term Memory (LSTM) units, a type of recurrent neural network (RNN), was also proposed by them. By achieving greater classification accuracy, this combination made it possible for the model to effectively learn intricate aspects of the input. The hybrid model created encouraging results from investigations with 93% specificity, 89% accuracy, and 85% sensitivity.

A neonatal quiet sleep detection system was developed by Abbas S. F., et al. [13], utilizing a CNN architecture, EEG inputs, and decision support. The authors employed a CNN model consisting of binary convolutional layers, one ReLU layer, and pooling layers. To increase the long-term reliability of sleep stage organization, a smoothing filter was also applied. The accuracy of the proposed method is 97%. Sivaramani et al. [14] suggested an ML-based technique for predicting cardiovascular disease. To develop models that account for the training procedures and data observation strategies of various algorithms, the Heart Dataset was integrated with other organization models. The accuracy of the suggested technique is approximately 96%.

2.1 Research Gap

Existing models face a research gap in achieving reliable early detection, particularly in the asymptomatic stage, which can delay timely action. Most models are refined on homogeneous datasets, limiting their generalizability to diverse populations and underrepresented groups. Few methods effectively leverage real-time data from wearable devices for continuous CVD monitoring and prediction. Additionally, many deep learning models function as 'black boxes,' highlighting the need for interpretable models that clinicians can trust.

2.2 Limitation in the current study

- Many current systems rely on classical algorithms and rule-based models, which may lack accuracy, especially in early disease identification. This can result in greater rates of false positives and false negatives, impacting patient outcomes.
- Cardiovascular disease prediction methods often depend on specialized, high-quality datasets. However, variation in patient data across groups and geographies can limit the generalizability of these models.
  Most systems do not incorporate diverse data types (e.g., genetic, lifestyle, and environmental factors) that could enhance predictive accuracy, relying instead solely on clinical data.
- Advanced DL and ML models for detection sometimes require substantial computational resources, restricting their applicability in resource-constrained environments.

III. METHODOLOGY

3.1 Overall Architecture

This research presents a novel and unique technique to enhance the accuracy of CVD forecasts by recognizing essential traits using DL algorithms. The study introduces an innovative framework that combines DPN-131, a DL architecture renowned for its robust feature extraction competencies, with LIME to increase the transparency and interpretability of

model predictions in CVD detection and classification. The DPN-131 model effectively captures complex patterns in high-resolution medical images, enabling accurate detection and organization of various cardiovascular diseases. To address the interpretability challenges in deep learning, LIME provides localized explanations, helping clinicians identify which regions and attributes of an image contribute to a specific diagnosis. **Fig. 1** illustrates the architecture of DPN-131-LIME.

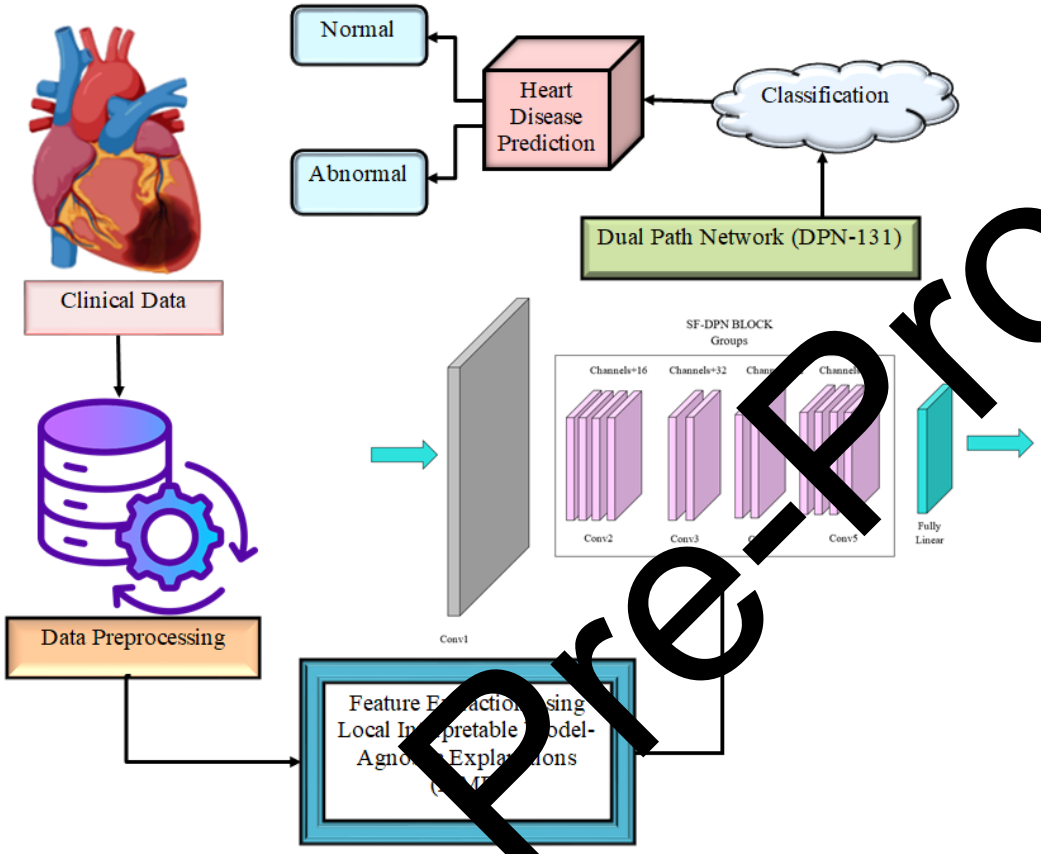

Fig 1. The architecture for DPN-131-LIME

3.2 Dataset

Three benchmark datasets, as shown in Table 1, were collected to evaluate the proposed study. The first dataset, which is referred to as the 2009 Cardiac MR Left Ventricle Segmentation Experiment data or Sunnybrook Cardiac Data (SCD), is shortened to HNET-DSI for this study. The second dataset, abbreviated as HNET-DSII, contains 1200 cardiovascular ECG recordings, with 300 for each of the four conditions under consideration. The original signals are from the MIT-BIH PhysioNet Database. ECG records from these four databases were divided into 4120 samples, resulting in 300 signals per condition. These signals are normalized based on the specified gain for each database and preprocessed using bandpass filters. The MODWPT (Multiple Discrete Wavelet Packet Transform) approach was employed to extract 54 features, represented as columns in the Comma-Separated Value (CSV) file included below. This file contains records with dimensions of 1200 × 54. The final dataset, HNET-DSIII, is a hybrid collection assembled from previously published studies. It includes data from 1300 participants in the UK Biobank imaging program, consisting of paired cardiac cine MRI images and electrocardiograms. Among the 1300 participants, 1150 were considered healthy, while 150 had at least one cardiovascular pathology.

3.3 Data Pre-processing

Large datasets are challenging to manage in healthcare systems; therefore, data preparation techniques are essential. To enhance model performance, data preprocessing may include data creation, manipulation, cleaning, and reading. Examples of data preprocessing techniques, such as picture standardization, noise reduction, data splitting, and image size standardization, are used to ensure consistency. In machine learning, optimal data representation requires thorough data preprocessing. The dataset can be prepared for successful training models using methods such as handling absent values, standard scaling (Standscale or SS), MaxAbs scaling, quantile transformation, zero-mean normalization, resilient scaling, and min-max scaling (MinMax). Further data preprocessing methods include predictive modeling, data cleansing, removing rows or columns with a high percentage of missing values, and substituting estimates for missing data. Analysis can be made simpler by eliminating independent variables (like symptoms) that take little to no consequence on the object

variable (like disease). Usually, the dataset's numerical properties are normalized to avoid some traits taking over the modeling process. Taking the appropriate rows out of the dataset is one way to deal with missing values [15].

Table 2: Dataset description

Dataset name	Dataset type and description	Web-link
HNET-DSI	• SCD and Cardiac MR Left Ventricle Integration Experiment data. • A collection of 450 cine-MRI images of various patients and disease conditions.	https://www.cardiacatlas.org/ Sunnybrook-cardiac-data/ (accessed on 2 March 2024)
HNET-DSII	• 1200 records of cardiovascular ECGs, with 300 records for each ailment. • Four databases of ECG records, segmented into 4120 samples each, forming 300 signals. • Each database contains records of size 1200 × 54.	https://www.kaggle.com/datasets/ah[illegible]2703/ec[illegible]-of-cardiac-ailments dataset (accessed [illegible] March [illegible]24)
HNET-DSIII	• Multimodal dataset consisting of paired MR images. • Voxel resolve of 1.8 × 1.8 × 8.0 mm³.	[illegible]ub

3.4 Dual Path Network (DPN-131)

The DPN-131 is a convolutional neural network archite[illegible]onsidered to increase feature sharing and aggregation across network layers. It associations the strengths of both resi[illegible]l and dense connections, creating a structure that efficiently reuses and aggregates feature representations. This network [illegible]nstruction is particularly powerful for deep learning tasks such as image organization [16]. **Fig. 2** shows [illegible] DPN architecture.

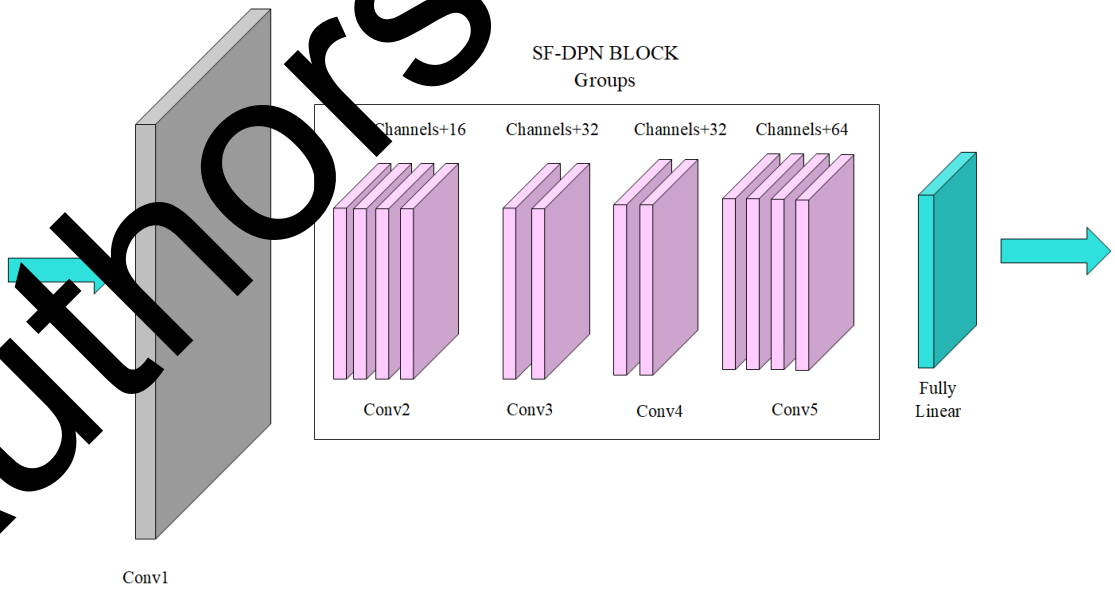

Fig 2. DPN diagram

DPN-131 comprises two pathways: one for learning new features to complete dense connections and another for reusing features via residual connections. This arrangement enables the network to maintain information flow across different layers, improving the network's expressive power without extreme growth in parameters.

1. **Residual Path**: The residual associates help maintain feature reuse, enabling stable gradients across layers.

   For a residual path, the connection container be represented as follows:

   Where $F\left(x,W\right)$ signifies the transformation function with weights W functional to the input x.

$$y = F\left(x,W\right) + x \tag{1}$$

2. **Dense Path**: The dense associates encourage new feature generation, where each layer has direct admission to all preceding feature maps.

   In a dense path, the output container be represented as follows:

$$x_l = H\left(\left[x_0, x_1, ..., x_{l-1}\right]\right) \tag{2}$$

   Where $H\left(.\right)$ denotes the composite function (convolution, batch normalization, etc.) and $\left[x_0, x_1, ..., x_{l-1}\right]$ represents the concatenation of all previous feature maps.

Dual Path Mechanism in DPN-132

In DPN-131, each block combines both residual and dense paths as follows:

$$y_l = F_{res}\left(x_l, W_{res}\right) + H_{dense}\left(\left[x_0, ..., x_{l-1}\right], W_{dense}\right) \tag{3}$$

Where $F_{res}\left(.\right)$ represents the residual transformation function and $H_{dense}\left(.\right)$ represents the dense transformation function. This dual structure allows each layer to reuse and expand features simultaneously.

1. **Feature Reuse**: Residual connections:

$$y_{res} = x + F\left(x, W_{res}\right) \tag{4}$$

2. **Feature Augmentation**: Dense connections:

$$y_{dense} = H\left(\left[x_0, x_1, ..., x_{l-1}\right], W_{dense}\right) \tag{5}$$

3. **Combined Output**:

$$y_l = y_{res} + y_{dense} \tag{6}$$

The DPN-131 achieves a balance between network depth and feature utilization, making it highly effective for complex vision tasks.

3.5 Feature Extraction using Local Interpretable Model-Agnostic Explanations (LIME)

To explain the predictions of complex black-box ML models, a technique called Local Interpretable Model-Agnostic Explanations (LIME) uses simpler, interpretable models to approximate each prediction locally [17].

Given a black-box model f that produces predictions, LIME explains the prediction for a specific instance x by perturbing x to create a set of new samples around it. These perturbations yield a new dataset $Z = \left\{\left(x_i', f\left(x_i'\right)\right)\right\}$, where x_i' are perturbed instances and $f\left(x_i'\right)$ are the black-box model's predictions for each perturbed instance.

Step-by-step LIME explanation

1. **Sampling Perturbations**: Perturbed instances x_i' are generated by slightly altering the values of x. For example, in text models, this might involve removing or replacing words, while in tabular data, it might involve adjusting feature values.

$$x_i' = x + \in \tag{7}$$

   Where $\in_i$: $N\left(0, \sigma^2\right)$ is random noise applied to each feature.

2. **Model Prediction**: For each perturbed instance x_i', the black-box model f generates predictions:

$$y_i' = f\left(x_i'\right) \tag{8}$$

   This step results in the dataset Z of perturbed instances and their corresponding predictions.

3. **Weighting Perturbations**: Perturbed instances are weighted founded on their comparison to the original example x using a kernel function $\pi\left(x, x_i'\right)$, typically an exponential kernel with Euclidean distance:

$$\pi\left(x, x_i'\right) = \exp\left(\frac{\| x - x_i' \|^2}{\sigma^2}\right) \tag{9}$$

4. **Fitting Interpretable Model**: An interpretable model g (e.g., linear regression) is trained on the dataset Z with instance weights $\pi\left(x, x_i'\right)$. The objective is to minimize a weighted loss function:

$$Loss\left(f, g, \pi\right) = \sum_{i=1}^{|Z|} \pi\left(x, x_i'\right).\left(f\left(x_i'\right) - g\left(x_i'\right)\right)^2 \tag{10}$$

5. **Generating Explanation**: The interpretable method g is used to approximate f the local vicinity x. For a linear g, the coefficients β_j of each feature j indicate the feature's contribution to the prediction:

$$g\left(x\right) = \beta_0 + \sum_{j-1}^{p} \beta_j x_j \tag{11}$$

   This process yields feature weights that provide an interpretable explanation of how f made its prediction x, with higher β_j values indicating stronger influence. LIME's model-agnostic nature allows it to explain any model f, regardless of complexity or structure.

3.6 Implementation

- The implementation of the DPN-131 model, a hybrid neural network that combines the strengths of residual and densely connected networks, is trained using a dataset of cardiovascular images and patient data. DPN-131 efficiently captures compound patterns and dependencies in the data, with successful organization accuracy across various CVD cases.
- To interpret the model's predictions, we utilized LIME, a post-hoc explanation tool. LIME provides interpretable clarifications by perturbing the input data and detecting variations in the model's output, highlighting elements that are most significant to specific predictions.
- After DPN-131 predicts the class (e.g., the type of cardiovascular disease), LIME is employed to generate local explanations, revealing the model's decision-making process. This step helps clinicians understand the model's predictions, fostering confidence in the outcomes.
- Finally, the DPN-131-LIME arrangement is estimated on a test dataset using relevant metrics, validating both the model's strong presentation and interpretability.

3.7 Advantages of the proposed model

- The model offers local, interpretable explanations, enabling doctors to understand and trust its predictions for specific cases, which is important in healthcare.
- This model-agnostic technique can be functional to any prediction model, making it flexible and adaptable across various algorithms and scenarios in cardiovascular diagnostics.
- The DPN-131 architecture employments a dual-path structure that combines global and local features, enhancing its accuracy in detecting subtle patterns in cardiovascular data.

IV. RESULTS AND DISCUSSION

4.1 Experimental setup

The paper was conducted using pooled cardiac disease data from the HEART-DSI dataset. Different outcomes are predicted by each dataset based on whether cardiac disease is present or not. The proposed approach was evaluated through simulations implemented in Python, running on an Intel i3 CPU with a 1 TB hard drive and 4 GB of RAM.

4.1.1 Optimized hyperparameter

We utilized 20% of the data for testing and 80% for training. In this research, we proposed a hybrid DL-based method to accurately determine if a patient has cardiovascular disease. During training, the ADAM optimizer is used to continuously update the parameters of the proposed network model. Adjusting the hyperparameters of the proposed network yields the most important improvements in presentation. Table 3 shows the updated parameters.

Table 3: Optimized hyperparameter settings

Hyperparameters	Range
Mini batch size	64
L2 regularization	$1.0000e^{-0.4}$
Gradient decay factor	0.9000
Maximum number of epochs	100
Initial learning rate	0.001

4.2 Comparative Methods

Swarm-Artificial Neural Network (Swarm-ANN) [8]: To train and evaluate the structure based on the constancy of its solutions, a predefined number of Neural Networks (NNs) is randomly created using the proposed Swarm-ANN method.

CNN with bidirectional long/short-term memory (CNN + BiLSTM) [10]: According to this study, a CNN with bidirectional long short-term memory is a DL-based system that can be utilized to predict cardiovascular disease since patient data.

Chi-square and principal component analysis (CHI-PCA) [18]: CHI-PCA, a combination of major component investigation and chi-square analysis, is used for feature decrease.

XGBoost [19]: Accurate cardiovascular disease prediction results are provided by the XGBoost classifier in conjunction with wrapping techniques.

4.3 Performance Metrics

Accuracy: The percentage of properly classified examples out of all examples is known as accuracy. While it provides an overall measure of the classifier's performance, it can be misleading in imbalanced datasets.

$$Accuracy = \frac{True\ Positives\,(TP) + True\ Negatives\,(TN)}{Total\ Ins\tan ces\,(TP + TN + FP + FN)} \tag{12}$$

Where:

- FN = False Negatives
- TN = True Negatives
- FP = False Positives
- TP = True Positives

Precision: Precision, sometimes referred to as positive predictive value, is the proportion of genuine positive predictions to all of the model's positive predictions. When false positives have a high cost, it is helpful.

$$\Pr ecision = \frac{True\ Positives\,(TP)}{True\ Positives\,(TP) + False\ Positives\,(FP)} \tag{13}$$

Recall: Recall, or sensitivity, is the ratio of true positive predictions to actual positive suitcases. It is essential in situations where identifying every positive instance is critical, even if some false positives are allowed.

$$\mathrm{Re}\,call = \frac{True\ Positives\,(TP)}{True\ Positives\,(TP) + False\ Negatives\,(FN)} \tag{14}$$

F1-Score: The F1 score calculates the harmonic mean of recall and precision to ensure stability between the two. It is most beneficial when you require a single statistic that accounts for both precision and recall.

$$F1 - Score = 2 \times \frac{\mathrm{Pr}ecision \times \mathrm{Re}\,call}{\mathrm{Pr}ecision + \mathrm{Re}\,call} \tag{15}$$

Fallout Rate: The fallout rate, also known as the false positive rate, is the percentage of negative examples wrongly categorized as positive. Understanding the likelihood of false alarms is critical.

$$Fall\ Rate = \frac{False\ Positives\,(FP)}{False\ Positives\,(FP) + True\ Negatives\,(TN)} \tag{16}$$

Processing Time: Processing time is the time essential for the model to complete its predictions. It is crucial for applications that need real-time or near-real-time responses. Measured in seconds, milliseconds, etc., processing time can vary widely depending on hardware, model complexity, and dataset size.

4.3.1 Performance measure for the proposed technique

Table 4 and Fig.3 present the presentation metrics of the suggested model for three changed configurations: HNET-DSI, HNET-DSII, and HNET-DSIII. HNET-DSII shows the most comprehensive presentation, with an accuracy of 97.80%, precision of 95.73%, recall of 94.14%, and F-score of 92.55%, indicating strong classification reliability and precision. HNET-DSIII follows with high accuracy (89.39%) and an exceptional F-score (90.56%), suggesting a balanced precision and recall. In contrast, HNET-DSI has the lowest metrics, with an accuracy of 65.20% and an F-score of 75.35%, indicating comparatively lower performance. Overall, the HNET-DSII configuration appears to be the most effective.

The graphical representation in Fig. 4 demonstrates that the proposed technique achieves high precision, recall, and accuracy across the different datasets. When applied to HNET-DSI, the technique achieved outstanding results, by an F-score of 97.80%, accuracy of 95.73%, precision of 94.14%, and recall of 92.55%.

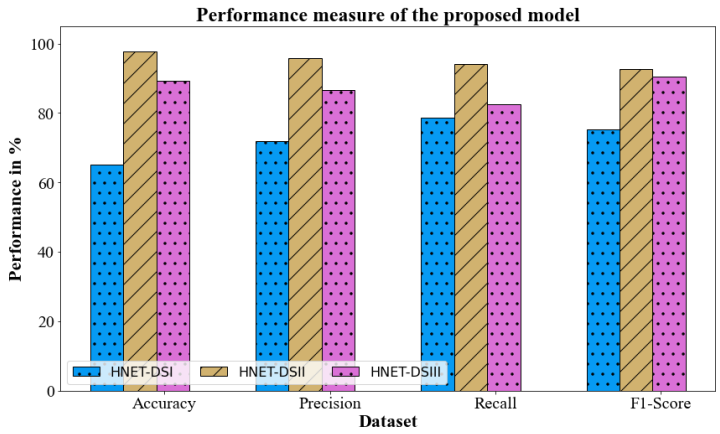

Fig 3. Performance measure for the proposed model

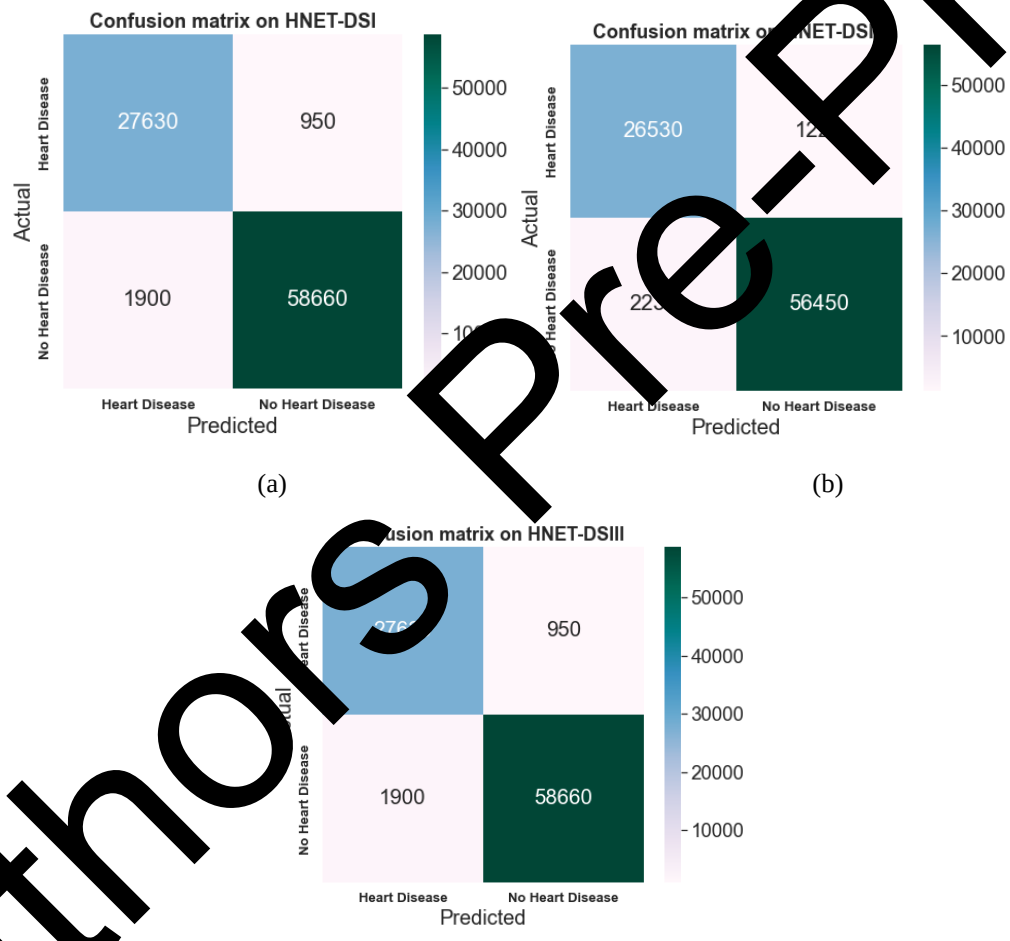

Fig 4. HNET-DSI, HNET-DSII, and HNET-DSIII confusion matrices are presented as follows: (a) The suggested model's actual versus predicted response rate on HNET-DSI; (b) the actual response rate on HNET-DSII compared to the model's predictive; (c) the model's actual versus predicted response rate on HNET-DSIII.

Table 4: Performance measure for the proposed technique

Metrics	HNET-DSI	HNET-DSII	HNET-DSIII
Accuracy	65.20	97.80	89.39
Precision	71.93	95.73	86.64
Recall	78.69	94.14	82.52
F-Score	75.35	92.55	90.56

4.3.2 Fallout Rate Analysis

Table 5: Fallout Rate Analysis for DPN-131-LIME method

Dataset	Swarm-ANN	CNN-BiLSTM	CHI-PCA	XGBoost	DPN-131-LIME
HNET-DSI	54.58	47.93	39.24	62.83	24.32
HNET-DSII	57.47	43.81	42.36	60.37	25.63
HNET-DSIII	58.39	40.39	37.73	58.39	26.23

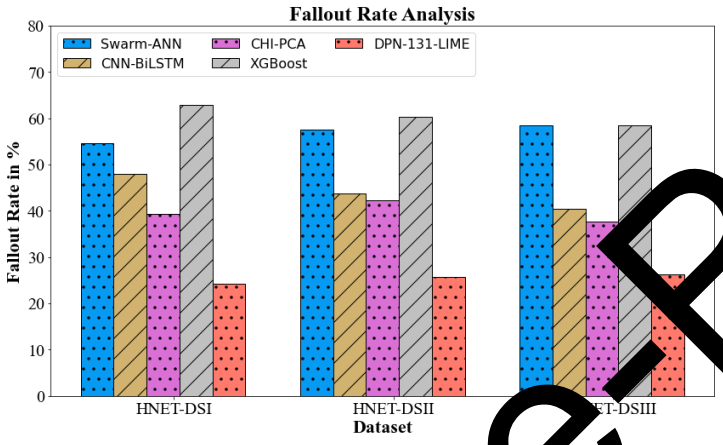

Fig 5. Fallout Rate Analysis for DPN-131-LIME method

4.3.3 Processing Time Analysis

Table 6: Processing Time Analysis for DPN-131-LIME method

Dataset	Swarm-ANN	CNN-BiLSTM	CHI-PCA	XGBoost	DPN-131-LIME
HNET-DSI	12.472	14.982	15.384	11.324	10.213
HNET-DSII	12.943	14.893	15.721	11.733	10.473
HNET-DSIII	12.434	14.6	15.349	11.921	10.324

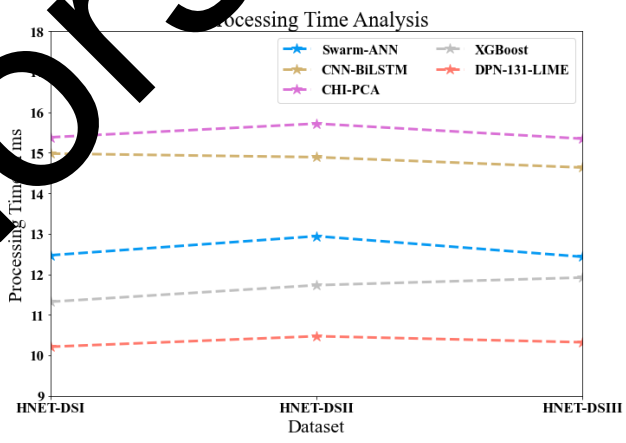

Fig 6. Processing Time Analysis for DPN-131-LIME method

Table 5 and **Fig. 5** associate the fallout rate of the DPN-131-LIME technique with various machine learning models (Swarm-ANN, CNN-BiLSTM, CHI-PCA, and XGBoost) on three datasets: HNET-DSI, HNET-DSII, and HNET-DSIII. The DPN-131-LIME approach consistently achieves the lowest fallout rates across all datasets, recorded at 24.32%, 25.63%, and 26.23% for HNET-DSI, HNET-DSII, and HNET-DSIII, respectively. This indicates superior performance in minimizing false positives, outperforming models such as Swarm-ANN and XGBoost, which exhibit significantly higher

fallout rates across datasets. The results demonstrate DPN-131-LIME's capability to effectively categorize with minimal false-positive errors, establishing it as a strong candidate for this application.

Table 6 and Fig. 6 compare the processing durations of various approaches, including Swarm-ANN, CNN-BiLSTM, CHI-PCA, XGBoost, and the DPN-131-LIME approach, across three datasets (HNET-DSI, HNET-DSII, and HNET-DSIII). The DPN-131-LIME technique consistently demonstrates the shortest processing time across all datasets, with durations of 10.213, 10.473, and 10.324 seconds for HNET-DSI, HNET-DSII, and HNET-DSIII, respectively. This efficiency highlights DPN-131-LIME's potential as a faster processing model compared to other approaches, with XGBoost performing closest in speed. CNN-BiLSTM and CHI-PCA have the longest processing times, making them less suitable for applications requiring quick responses.

4.4 Training and Testing Validation

Cardiovascular Disease-Based Training and Testing with Loss and Accuracy method involves utilizing ML methods to forecast the possibility of cardiovascular disease (CVD) in patients. The training procedure employs a loss model to minimize the change between expected and actual results, thereby optimizing the model's presentation. Following training, an accuracy model is used to estimate the model's efficacy by determining how accurately it predicts CVD outcomes on previously unobserved test data. This approach subsidizes the improvement of predictive models for early analysis, risk assessment, and personalized treatment improvement for CVD patients.

4.5 Discussion

The accuracy, precision, recall, and F-score metrics for three datasets (HNET-DSI, HNET-DSII, and HNET-DSIII) estimated using a variety of models, including Swarm-ANN, CNN-BiLSTM, CHI-PCA, XGBoost, and DPN-131-LIME, are revealed in the table below. HNET-DSII outperforms the other two datasets (HNET-DSI and HNET-DSIII) across the board, achieving the highest values for accuracy, precision, recall, and F-score. Furthermore, the datasets exhibit different model presentations, with Swarm-ANN and XGBoost generally outperforming CNN-BiLSTM and CHI-PCA. Additionally, DPN-131-LIME constantly has the shortest processing times across all datasets, indicating additional effectual computational presentation. The table also shows inference time (in seconds).

4.6 Ablation Study

All components in the proposed model are important. This section discusses the proposed DPN-131-LIME model alongside existing models, including CNN-BiLSTM, Swarm-ANN, CHI-PCA, and BDLSTM, along with their rationale, using a series of ablation experiments on the HNET-DSI, HNET-DSII, and HNET-DSIII datasets. To examine presentation enhancements and demonstrate the motivation behind our suggested DLFF-HELM model, we incrementally add different features extracted by the model in a stepwise manner.

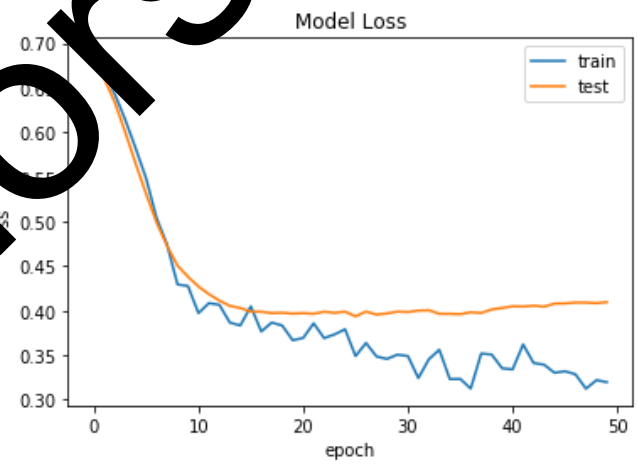

Fig 7. Training and Testing Validation Analysis

4.6.1 Influence of the LIME

The application of the LIME technique offers insights into complex models used for predicting cardiovascular disease by providing interpretable, locally faithful explanations for individual predictions. In cardiovascular disease prediction, machine learning models may achieve high accuracy but often lack transparency, making it difficult for healthcare

providers to understand how a model arrives at its decisions. LIME addresses this by creating simplified, interpretable models that estimate the behavior of the compound model for specific predictions. This helps clinicians understand the factors influencing each prediction, thereby aiding in decision-making and potentially improving patient outcomes.

4.6.2 K-Fold Cross Validation

K-Fold cross-validation is a resampling method utilized to estimate a model's presentation. The final performance estima is obtained by averaging the results across the K iterations of this method, where each fold serves as validation data once. When K is set to 5, the dataset is divided into five equivalent parts for the experiments. In each of the five training and validation cycles, four subsets are utilized for training, and the remaining subset is used for validation. This pr confirms that each subset is utilized once for validation, provided that a more reliable performance estimate by av aging the results from all five iterations.

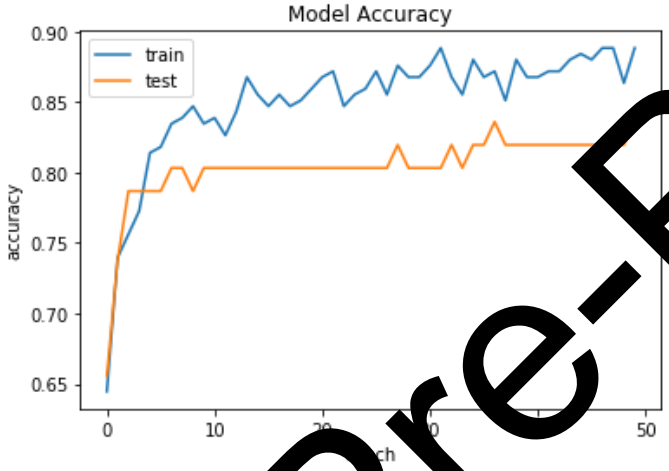

Fig 8. Training and testing validation analysis

4.6.3 Comparison of the proposed model.

Table Comparison of the proposed model

Reference	Model	Year	Accuracy (%)
Bhavekar et al [24]	RNN-LSTM	2022	95.06
Dileep et al [ ]	C-BiLSTM	2023	94.78
Li et al [ ]	Naïve Bayes (NB)	2022	88.7
Nandy et al 21]	Swarm-ANN	2023	95.78
Sabo al [ ]	XGBoost	2022	91.8
ur M l]	DPN-131 + LIME	2024	97.80

Table 7 and Fig 9 associate the presentation of the suggested model with recent models from previous studies. The models listed diff in architecture, with Dileep et al. (2023) using a C-BiLSTM to achieve 94.78% accuracy and Nandy et al. (2023) emp ing a Swarm-ANN model to slightly surpass it at 95.78%. Older techniques, such as Li et al.'s Naive Bayes (202 and Sa r et al.'s XGBoost (2022), achieve lower accuracies of 88.7% and 91.8%, respectively. Bhavekar et al. (2022) hieve a competitive 95.06% with an RNN-LSTM model. However, the proposed model, which combines DPN-31 and LIME, outperforms all others with an impressive accuracy of 97.80%, demonstrating its superior classification p ce.

4.7 Challenges and Limitations

One of the main challenges in combining Local Interpretable Model-Agnostic Explanations (LIME) with Dual Path Networks (DPN-131) for cardiovascular disease detection and classification is balancing interpretability and model complexity. Although LIME is useful for the contained interpretability of model forecasts, it may fail to capture global behavior, particularly in complex models like DPN-131. Moreover, the robustness of LIME explanations depends on feature importance and data quality, which can affect medical reliability. The dual-path architecture also significantly

enhances computational demands, requiring considerable resources and time, thus limiting scalability in real-world, resource-constrained healthcare environments.

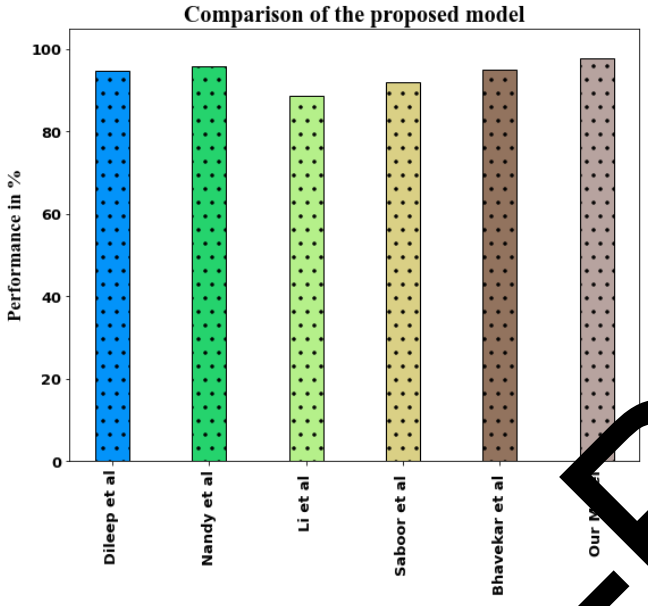

Fig 9. Comparison of the proposed model.

V. Conclusion

In conclusion, the arrangement of LIME and DPN-131 offers an effective, interpretable strategy for identifying and categorizing cardiovascular illnesses. This model improves diagnostic accuracy by leveraging DPN-131's powerful feature extraction and LIME's explainability, providing explicit insights into decision-making processes—critical for clinical requests. Our study determines that this technique can assist clinicians identify crucial aspects of cardiovascular health, improving diagnostic precision and therapy planning. Further research could refine and broaden this paradigm to cover other complex medicinal conditions. Future studies should explore transfer learning methods to adapt DPN-131 for other medical image association tasks, thereby extending its usability beyond cardiovascular diseases to other areas of healthcare and maximizing its analytic perspective.

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