Deep learning-based Heart disease Risk prediction using Soft Max deep Scaling Gated Adverbial Neural Network

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Abstract

Heart disease is one of the diseases that is responsible for the death of millions of people each year worldwide. It is considered one of the main diseases in middle-aged and elderly people. The increasing rate of heart disease cases, high mortality rate, and medical treatment expenses necessitate early diagnosis of symptoms. Prediction of cardio vascular disease is a critical challenge in the area of clinical data analysis Data science related Diagnosis and prediction of heart related diseases requires more precision, perfection and correctness. Deep Learning (DL) models are becoming increasingly popular for use in a wide range of clinical diagnostic tasks. Making accurate predictions is essential for such tasks because the results can have a big impact on patients and reduce mortality. DL algorithms for efficient identification of heart disease plays an important role in healthcare, especially in cardiology. Previously Machine learning algorithms used for feature extraction has some problems, there are less efficient for complex risk stages and increased computation time, and Feature extraction is inaccurate for classification, and unreliable. When extensive data exist, deep learning techniques can overcome some of those limitations.To overcome the issues, the performance of the deep learning-based Software Cost Estimation Technique using SoftMax deep Scaling Gated Adverbial Neural Network (SmDSAN2) for accurate software cost estimation. Initially we collected the dataset form standard repository and initially we started

the first step is data preprocessing for reducing null and unbalance values based on Min-Max-Z score normalization (Mm- Z-score). To utilizing the feature margin range is using the threshold values and it's based on Fuzzified Support Margin Impact Rate (FSMIR). And third step is Feature selection based on threshold values for selecting the maximum weighted range and also selecting the nearest values based on Particle Swarm Intelligence (PSI). It iteratively assigned to ranks feature importance, removes the least important, and rebuilds the model until desired feature subset is obtained. Final stage is classification is based on SoftMax deep Scaling Gated Adversial Neural Network (SmDSAN2) is evaluating the heart disease risk prediction and reducing the false rate for analyzing the It has the ability to predict the risks based on SmDSAN2algorithm has shown high accuracy for Predict the dataset. Predicting techniques used by categorizing the approximation of risk level developed using Fuzzified margin rate to identify in multiclass dataset. SmDSAN2algorithm will help the Healthcare environment to follow rules standard and also reduce the risk.

Keywords: Healthcare, Heart disease, Data science, Deep Learning, Margin rate, Fuzzified, Neural Network, Z-score, Accuracy, Rules.

1) Introduction

Cardio Vascular Diseases (CVDs) continue to be among the leading causes of death globally, while early and accurate prediction models remain paramount to reducing associated risks. With the help of state-of-the-art computation tools, large-scale clinical and physiological data have been used to risk models for heart disease [1,2]. Deep Learning (DL) has become widespread due to its ability to work with high-dimensional data, the possibility of obtaining relevant patterns, and its higher predictive performance compared to conventional machine learning methods [3,4]. DL is applied to cardiovascular diseases, including congenital heart disease (CHD), symptom regression analysis, and real-time hybrid systems [5].

However, some challenges are still key in the operation of CVD. First of all, it is still important to note that clinical datasets for cardiovascular diseases are often significantly unbalanced, affecting the model's quality and its ability to detect rare but quite significant cases [6,7].

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[1]T. Amarbayasgalan, et al., in IEEE Access, vol. 9, pp. 135210-135223, 2021, Doi: 10.1109/ACCESS.2021.3116974.
[2]S. Ghorashi et al., in IEEE Access, vol. 11, pp. 60254-60266, 2023, doi: 10.1109/ACCESS.2023.3286311.
[3]A. Kumar, K. U. Singh et al., "A Clinical Data Analysis Based Diagnostic Systems for Heart Disease Prediction Using Ensemble Method.
[4]B. Ramesh et al., in IEEE Access, vol. 12.
[5]V. Vision Paul et al., doi: 10.1109/ACCESS.2024.3430898.
[6]J. J. Gabriel et al.,"Accurate Cardiovascular Disease Prediction: Leveraging Opt_hpLGBM With Dual-Tier Feature Selection.
[7]S. Bebortta, et al., "DeepMist: Toward Deep Learning Assisted Mist Computing Framework for Managing Healthcare Big Data.

Secondly, original deep learning architecture may produce low interpretability results, which can be disconcerting to clinicians who may not be able to validate the results [8]. Third, there is a problem of overfitting or low generalization when working with other populations because of the insufficient development of methods for feature selection and model optimization [9]. In the same way, large-scale deep neural network learning models present a high computational complexity when deployed in real-time in low-end devices [10].

To overcome these challenges, this research investigates a new Soft Max Deep Scaling Gated Adversarial Neural Network (SMD-SGAN) to assess heart disease risk. The SMD-SGAN utilizes gated mechanisms to filter irrelevant noise while utilizing adversarial networks to address data imbalance and improve generalization. SoftMax deep scaling and other layers improve classification boundaries for prediction among groups and patients. This new architecture is intended to offer high interpretability, computational efficiency, and powerful performance, which can develop the foundation for hospital-effective, accurate, and practical heart disease risk prediction models.

2)Literature Survey

Heart disease (HD) is acknowledged as the primary cause of death globally, according to the author [11]. Improving patient outcomes and delivering prompt medical interventions depend heavily on early identification and precise HD prognosis. The Hybrid Deep Neural Networks (HDNN) approach was used to achieve the goal. The computational burden of this approach resulted from the integration of several networks. A Support Vector Machine (SVM) approach was used to fix the problem. Inference times may increase if ensemble models are heavily relied upon. Hyperparameter adjustment of the ensemble components impacts the SVM's performance [12].

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[8]Y. M. Ayano, et al., Interpretable Hybrid Multichannel Deep Learning Model for Heart Disease Classification Using 12-Lead ECG Signal," in IEEE Access.
[9]D. Cenitta, et al., Ischemic Heart Disease Prediction Using Optimized Squirrel Search Feature Selection Algorithm," in IEEE Access.
[10]M. Obayya, Jet al., Automated Cardiovascular Disease Diagnosis Using Honey Badger Optimization with Modified Deep Learning Model.
[11]M. S. A. Reshan, et al., "A Robust Heart Disease Prediction System Using Hybrid Deep Neural Networks.

[12]Rath, A., Mishra, D., et al., Imbalanced ECG signal-based heart disease classification using ensemble machine learning technique.

Although HD has a low global frequency, it is nonetheless a frequent condition that causes death, according to the author [13]. Thus, early MI signal detection can lower mortality. A Deep Convolutional Neural Network (DCNN) approach was used to achieve the goal. To help cardiologists identify HD early, DCNN with focal loss is a useful technique for making a quick and accurate HD diagnosis. Without investigating more straightforward interpretable models, it might not generalize for unknown datasets and rely too heavily on DL.Hybrid

Convolutional Recurrent Neural Network (HCRNet) technology was used to address the problem. Cardiologists can use it to promptly diagnose arrhythmias and accurately distinguish different types of heartbeats. For multi-class situations, HCRNet might be overly specialized, which would restrict generalization. High accuracy necessitates substantial hyperparameter optimization [14].

As one of the major causes of death, the author[15] commented upon how hard it is to predict cardiac conditions like heart attacks. This is because it is difficult and takes a lot of knowledge and expertise to foresee these conditions. This problem was fixed by using the Synthetic Minority Oversampling Technique (SMOTE). Artificial data artefacts could be introduced when employing methods such as SMOTE. Furthermore, it ignores class disparity across diverse real-world populations. To fix the problem, an Auxiliary Classifier Generative Adversarial Network (ACGAN) technique was used. It was applied to resolve the issues brought on by the dataset's imbalance. In the absence of extra layers or components, it could have trouble identifying temporal correlations in ECG data. Due to inadequate testing on external datasets, the results can exaggerate generalizability [16]. Extensive data preprocessing, the requirement for features engineering, and guaranteeing the accuracy of classification findings were the goals of the author [17].

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[13]Hammad, M., et al. Myocardial infarction detection based on deep neural network on imbalanced data.

[14]Luo, X., et al.,multi-classification of arrhythmias using a HCRNet on imbalanced ECG datasets. Computer Methods and Programs in Biomedicine, 208, 106258. https://doi.org/10.1016/j.cmpb.2021.10625

[15]Pandey, A... et al. Mitigating class imbalance in heart disease detection with machine learning. Multimed Tools Appl (2024). https://doi.org/10.1007/s11042-024-19705-8

[16]Du, C., et al., Classification of Imbalanced Electrocardiosignal Data using Convolutional Neural Network. Computer Methods and Programs in Biomedicine.

[17]Waqar, M., et al., 2021(1), 6621622. https://doi.org/10.1155/2021/6621622

An improved SMOTE technique was used to achieve the goal. It guarantees that cardiac attacks may be accurately predicted. RR intervals combined with Higher-Order Statistics with LSTM (RRHOS-LSTM) and CNN-Long Short-Term Memory (CNN-LSTM) were used to address the problem. It was successfully utilized to draw attention to aberrant heartbeat classes. The suggested approach may result in decreased interpretability and increased computing complexity and delay [18].

According to the author [19], creating efficient analytical models is essential to using ECG data for accurate heart disease identification. A Generative Adversarial Network (GAN) approach was used to achieve the goal. However, the unpredictability of precise ECG signals might not be adequately captured by the generated data. To prevent mode collapse or low-quality samples, careful training is necessary. A DL and Fuzzy Clustering (Fuzz-Cluster) methodology was used to fix the problem. This method categorized The ECG signals according to their corresponding cardiac conditions. Nevertheless, it might not scale effectively for real-time applications or big datasets. High-dimensional ECG features may be complex for the method [20].

According to the author, early detection of cardiac arrhythmias is essential to reducing their potentially dangerous effects [21]. However, manually analyzing ECG signals takes a lot of time and is prone to errors. A Synthetic Minority Over-Sampling (SMO-S) methodology was used to fix the problem. It was applied to enhance overall performance and dataset balance. Without appreciable accuracy gains, it may be redundant. It may thus struggle to adjust to various datasets. A Self-Organizing Map with Autoencoder (SOM-AE) methodology was used to fix the problem. Robustness may be limited by SOM-AE's higher training complexity [22].

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[18]E. Essa et al., in IEEE Access, vol. 9, pp. 103452-103464, 2021, doi: 10.1109/ACCESS.2021.3098986.

[19]Wang, Z., et al., Hierarchical deep learning with Generative Adversarial Network for automatic cardiac diagnosis from ECG signals.

[20]Kumar, S., et al.,Computers in Biology and Medicine, 153, 106511. https://doi.org/10.1016/j.compbiomed.2022.106511

[21]Zabihi, F., et al., An electrocardiogram signal classification using a hybrid machine learning and deep learning approach.

[22]Rath, A., et al., Informatics and Systems, 35, 100732. https://doi.org/10.1016/j.suscom.2022.100732

Using a feature selection approach, the author [23] sought to create a precise Machine Learning (ML) method for early detection of cardiac disease. ABoost approach was used to achieve the goal. It was used to determine which classifier produces the highest percentage of accurate predictions for heart disease. It might not perform as well as the most advanced DL techniques. The problem was solved by using a two-dimensional CNN approach. It successfully distinguishes between multi-cycle normal and pathological heartbeats. It lacks validation on external, noisy ECG datasets, is computationally costly, and is susceptible to noise [24].

The author covered the difficult task of predicting heart attacks from stroke patient data [25]. To fix the problem, an Under Sampling-Clustering-Oversampling (UCO) methodology was used. This methodology produces almost balanced data for training ML models for heart attack prediction. However, the complex temporal dynamics of ECG signals in stroke patients may be complicated for UCO to capture fully. A CNN-LSTM methodology was also used to fix the problem. In real-time settings, it might be slow and resource-intensive. Without sufficient regularization, the CNN-LSTM may overfit [26].

The author [27] used Principal Components Analysis with LSTM (PCA-LSTM) for classification and noise reduction. For lengthy ECG sequences, PCA-LSTM is vulnerable to exploding/vanishing gradient issues, and the preprocessed data's caliber significantly impacts how well it performs. A CNN-LSTM methodology was used to address this problem. It was employed to find irregularities in the heartbeat. CNN-LSTM frameworks are not comparable to other or simpler systems and frequently have enormous processing demands [28].

According to the author [29], addressing imbalanced datasets is a common challenge for classical ML algorithms forecasting cardiac disease. Wavelet Transformation and CNN (WT-CNN) were used to fix the problem. Healthcare practitioners can effectively employ the provided model to predict cardiac disease because the WT-CNN improves classification accuracy compared to previous classification methodologies. It might, however, miss crucial information or add noise, and it might not provide enough speed improvements to offset their increased complexity.

[23]H. F. El-Sofany, "Predicting Heart Diseases Using Machine Learning and Different Data Classification Techniques.

[24]Li, Y., Luo, J., et al., A deep learning approach to cardiovascular disease classification using empirical mode decomposition for ECG feature extraction.

[25]M. Wang, X. Yao and Y. Chen, "An Imbalanced-Data Processing Algorithm for the Prediction of Heart Attack in Stroke Patients," in IEEE Access.

[26]Rai, H.M., Chatterjee, K. Hybrid CNN-LSTM deep learning model and ensemble technique for automatic detection of myocardial infarction using big ECG data.

A ResNet with BiLSTM approach was used to fix the problem. Through the local feature extraction portion of the produced ECG feature map, the model successfully combines the position data of the closest neighbors. It might miss uncommon but clinically essential abnormalities, though. Furthermore, it could not be resilient to hidden ECG patterns [30].

3)Proposed Methodologies

In this section we briefly described about the proposed method which is used to predict the heart disease with accurate. To perform the proposed method with more accurate we use heart disease dataset which is available at Kaggle website. In this propose method we perform four phases like preprocessing, impact rate detection, feature selection, and classification. In the first phase we use Mm- Z-score, in second phase we employ FSMIR, then we perform PSI method and finally use SmDSAN[2] method for classification. In below figure 1 we illustrate the architecture diagram of the proposed method.

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[27]M. A. Khan and Y. Kim, “Cardiac Arrhythmia Disease Classification Using LSTM Deep Learning Approach.

[28]Sowmya, S., & Jose, D. (2022). Contemplate on ECG signals and classification of arrhythmia signals using CNN-LSTM deep learning model. Measurement: Sensors, 24, 100558.

[29]Mohammad, F. (2022). WT-CNN: A Hybrid Machine Learning Model for Heart Disease Prediction. Mathematics, 11(22), 4681. https://doi.org/10.3390/math11224681

[30]Ma, S., Cui, J., Xiao, W., & Liu, L. (2021). Deep Learning-Based Data Augmentation and Model Fusion for Automatic Arrhythmia Identification and Classification Algorithms.

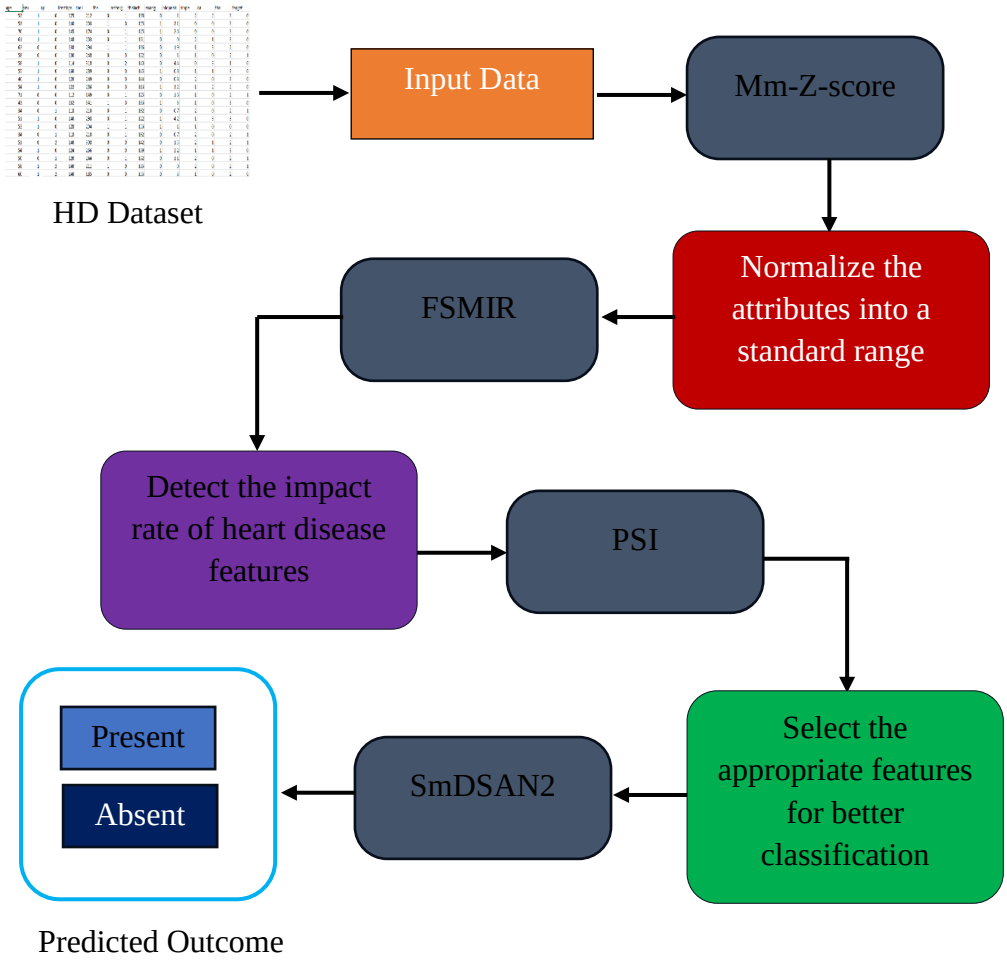

Figure 1. Architecture diagram of the proposed method

Mm-Z-score is an extension of the Min-Max scaling and Z-Score normalization in that it scales the features into a standardized range. That way, none of them is overloaded due to the size of the feature itself, which makes the dataset good for the DL algorithms. While all features of FSMIR affect the quantitative increase/decrease of the probability or certainty of the existence of heart diseases in a patient, FSMIR directly measures how significantly each distinctive feature influences the target variable. PSI also provides an ability to choose features with the highest statistical and predictive importance, by which only the most informative data will be given to the classifier. In the classification, PSI ensures that acme physiological parameters like maximum heart rate, resting blood pressure, and cholesterol levels are provided with a higher ranking. SmDSAN2 establishes itself as the state of the art in terms of performance using gating mechanisms, adversarial robustness, and deep scaling. SmDSAN2 has a high capacity for dealing with many data samples. It can be modified to accommodate different numbers and types of features depending on their use in specializations of clinical practice.

3.1) Dataset Assortment

In this paper, the proposed method is applied to the heart disease data set with the highest accuracy for finding the presence of heart disease. This dataset is collected from the Kaggle website: https:/ /www.kaggle.com/datasets/johnsmith88/heart-disease-dataset. This data set dates from 1988 and consists of four databases: Cleveland, Hungary, and Switzerland. Long Beach V. It has 76 features except for the decision feature we are predicting, but only 14 features are used for all reported experiments. The "target" field can be described as the identification of heart disease in the patient. Universal is an integer-valued variable, where 0 = no disease and 1 = disease.

age	sex	cp	trestbps	chol	fbs	restecg	thalach	exang	oldpeak	slope	ca	thal	target
52	1	0	125	212	0	1	168	0	1	2	2	3	0
53	1	0	140	203	1	0	155	1	3.1	0	0	3	0
70	1	0	145	174	0	1	125	1	2.6	0	0	3	0
61	1	0	148	203	0	1	161	0	0	2	1	3	0
62	0	0	138	294	1	1	106	0	1.9	1	3	2	0
58	0	0	100	248	0	0	122	0	1	1	0	2	1
58	1	0	114	318	0	2	140	0	4.4	0	3	1	0
55	1	0	160	289	0	0	145	1	0.8	1	1	3	0
46	1	0	120	249	0	0	144	0	0.8	2	0	3	0
54	1	0	122	286	0	0	116	1	3.2	1	2	2	0
71	0	0	112	149	0	1	125	0	1.6	1	0	2	1
43	0	0	132	341	1	0	136	1	3	1	0	3	0
34	0	1	118	210	0	1	192	0	0.7	2	0	2	1
51	1	0	140	298	0	1	122	1	4.2	1	3	3	0
52	1	0	128	204	1	1	156	1	1	1	0	0	0
34	0	1	118	210	0	1	192	0	0.7	2	0	2	1
51	0	2	140	308	0	0	142	0	1.5	2	1	2	1
54	1	0	124	266	0	0	109	1	2.2	1	1	3	0
50	0	1	120	244	0	1	162	0	1.1	2	0	2	1
58	1	2	140	211	1	0	165	0	0	2	0	2	1
60	1	2	140	185	0	0	155	0	3	1	0	2	0

Figure 2. Diagram for theattributes of heart disease dataset

3.2) Min-Max- Z score normalization (Mm- Z-score)

The Min-Max-Z Score Normalization (Mm-Z Score) pre-processing is a general data-preprocessing technique developed to enhance the information quality of datasets in heart disease. Missing values in such essential attributes as cholesterol and blood pressure are treated by imputation (mean, median, or mode). Min-max normalization follows to normalize numerical features like heart rate and blood pressure into comparable normalized forms between 0 and 1. Standardization is performed next by applying Z-score normalization on the scaled features to cancel out the effect of outliers, with means equal to 0 and standard deviations equal to 1. Lastly, another form of imbalance within the target variable, such as in the case of the presence and absence of heart disease, is balanced using SMOTE, which creates nearer synthetic samples. This combined pipeline ensures that the obtained dataset includes several modifications: cleaning, correcting the imbalance, and rescaling data that

helps machine learning models more accurately predict heart disease.In the equation 1 we perform the min-max normalization to scale the heart disease features,

$$F_s = \frac{F_v - F_{min}}{F_{max} - F_{min}} \quad (1)$$

Let assume, F_s as scaled features of the heart disease dataset, F_v as actual value of the feature (for instance, cholesterol, blood pressure, age, etc.,), F_{min} as minim um value in the feature column (minimum blood pressure value in the dataset), and F_{max} as maximum value in the feature column. Numerical features with different scales, such as blood pressure, heart rate, cholesterol levels, etc., are frequently included in datasets related to heart disease. To make these properties similar, min-max normalization scales them to a common range, like [0, 1]. This adjustment ensures all numerical features, such as blood pressure or cholesterol, fall between 0 and 1 for improved feature comparison.After Min-Max normalization we perform Z-score standardization through equation 2 to further normalize the scaled features,

$$Z_F = \frac{F_s - \mu_s}{\sigma_s} \quad (2)$$

Let assume, F_s as feature value of the min-max scaled, μ_s as mean of feature value of min-max scaled, and σ_s as standard deviation of feature value of min-max scaled. The Z-score assists in adjusting for different feature standard deviations and centering feature values around 0. This equation ensures that features like heart rate and cholesterol, which have varying spreads (variability), contribute evenly to the model. Because heart illness datasets frequently contain missing or null values in crucial characteristics like cholesterol, age, or heart rate, we handle the null values in the heart disease features using equation 3,

$$F_p = \begin{cases} F_v, & if\ F_v \neq 0 \\ F, & if\ F_v = 0 \end{cases} \quad (3)$$

Let assume, F_p as feature value after handling null values, F_v as original feature value, and F as mean value of feature, by following equation we compute the F,

$$F = \frac{\sum_{x=1}^{n} F_x}{n} \quad (4)$$

Before normalization, these missing values must be fixed to prevent computational problems. To preserve data integrity, null values are substituted with the mean, median, or mode. Mode imputation is favored for categorical characteristics (e.g., gender, type of chest pain). Since the target variable (e.g., 0 for no disease, 1 for disease) is frequently unbalanced in heart disease datasets, we then utilize equation 5 to correct the class imbalance. So, we use resamples technique like SMOTE (Synthetic Minority Oversampling Technique) to balance the dataset,

$$F_N = F_M + \delta.(F_C - F_M) \quad (5)$$

Let assume, F_N as synthetic feature value which is developed to minority class, F_M as previous feature value from minority class, F_C as nearest neighbor feature value, and δ as

random value in the range [0,1]. This equation generates synthetic samples for the minority class (e.g., patients with heart disease) to balance the class distribution, ensuring unbiased model performance. Imputation methods help ensure all values required in an analytic model are gathered and processed, not missing the all-important null values; on the other side, SMOTE deals suitably with providing balance in the target variable where it is skewed. The proposed hybrid pipeline also improves the data set's general quality and repeatability, allowing the models to learn meaningful patterns easily. Altogether, the Mm-Z Score enhances the accuracy, stability, and fairness of heart disease prediction systems and can successfully be used in the preprocessing stage of healthcare analytics and machine learning tasks.

3.3) Fuzzified Support Margin Impact Rate (FSMIR)

The Fuzzified Support Margin Impact Rate (FSMIR) is aimed explicitly at feature selection, where the margin range of the features obtained from the threshold value can be applied to datasets concerning heart disease. In FSMIR, fuzzy logic is used to measure the contribution of each feature to separating between classes after spotting their membership in specific support and importance ranges. Then, the support margin of each feature is computed, meaning how much the feature can contribute towards the generation of classification boundaries. A quantitative degree of membership scale is used to partition the feature in the defined fuzzy sets, for example, low, medium, high, and so on, depending on the proximity of this value to a certain constructed threshold. Through aggregating the membership degrees, FSMIR determines features that enjoy fair margins toward improving the classification and reducing overlap. It is further beneficial with heart disease datasets since FSMIR aids in somehow identifying the suitable feature selection for enhancing performance yet negating feature noise for the disease.In equation 6 we compute the support margin $S$of heart disease dataset,

$$S(f_y) = \frac{1}{n}\sum_{x=1}^{n}\left|i_{x,y}^{+} - i_{x,y}^{-}\right| \quad (6)$$

Let assume, f_y as value for patient s with heart disease (positive class), $i_{x,y}^{+}$ as value of feature, and $i_{x,y}^{-}$ as value for patients without heart disease. Age, heart rate, cholesterol, and blood pressure are essential in the heart disease dataset. This formula determines how well a characteristic like cholesterol distinguishes people with and without heart disease. A more significant margin indicates a more discriminative trait.Then we filter the margin-based Threshold T through equation 7,

$$T(f_y) = \begin{cases} 1, & if\ S(f_y) \geq \theta \\ 0, & otherwise \end{cases} \quad (7)$$

We use statistical analysis or domain expertise to determine the threshold, θ. For instance, only features (such as systolic blood pressure variations between classes) with a support margin of at least five will be allowed to get through the filter if $\theta = 5$. While less significant factors might be eliminated, characteristics like "age" might survive the filter since older

people may exhibit different patterns between groups.By following we perform fuzzy membership function through equation 8,

$$\mu_k(f_y) = \begin{cases} 0, & if\ f_y \le o_k \forall f_y \ge q_k \\ \frac{f_y - o_k}{p_k - o_k}, & if\ o_k \le f_y \le p_k \\ \frac{q_k - f_y}{q_k - p_k}, & if\ p_k \le f_y \le q_k \end{cases} \quad (8)$$

Let assume, $\mu_k(f_y)$ as membership degree of feature in subset (low, medium, and or high), k as fuzzy, and o_k, p_k, q_k as parameters defining the triangular membership function for k. Linguistically, features are classified into "low," "medium," and "high." Cholesterol levels below 200 may be classified as "low" in the fuzzy set. A cholesterol level in the "medium" fuzzy set may be between 200 and 240. Above 240, cholesterol may fall into the "high" fuzzy set. The fuzzy membership function captures minute differences in feature values by assigning each feature to these sets in a graded manner.Then we compute the FSMIRZ through equation 9,

$$Z(f_y) = \sum_{k=1}^{K} u_k \,.\, \mu_k(f_y) \quad (10)$$

Let assume, $Z(f_y)$ as fuzzified support margin impact rate for feature, K as total number of fuzzy sets, u_k weight assigned to fuzzy set, and $\mu_k(f_y)$ as membership degree of feature in k. The FSMIR value of each feature is calculated by summing up its memberships in fuzzy sets that have been given weights. Since "high cholesterol" is closely linked to heart disease, it might be heavy. "Low cholesterol" might weigh less. This formula offers a single metric to assess how significant characteristics such as "maximum heart rate" or "resting blood pressure" differentiate between patients with and without cardiac disease.Then we rank$R$ the feature through equation 11,

$$R(f_y) = s\left(Z(f_y)\right), \quad \forall f_y \in A \quad (11)$$

Let assume, $R(f_y)$ as rank of feature on the basis of Z value, s as sorting of features, and A as set of all features in the dataset.Features including "age," "exercise-induced angina," "cholesterol levels," and "resting ECG results" are ranked according to their Z values. While variables with lower Z values might not be as important, those with higher Z values, such as "maximum heart rate during exercise," are probably more useful for predicting heart disease.After ranking we deploy threshold to select the top features through equation 12,

$$A_S = \{f_y \in A | Z(f_y) \ge \tau\} \quad (12)$$

Let assume, A_S as set of selected features, and τ as selection threshold for Z values. This ensures that only the most relevant features, such as "exercise-induced angina" or "ST depression," are used for model training, improving interpretability and reducing overfitting.By selecting the most suitable features from the context, the FSMIR method is specifically ideal for datasets, such as those about heart disease, for which classification of

the core features is required. Using the support margin and fuzzy logic allows FSMIR to address the complexity and subtleties in an attribute such as cholesterol level or blood pressure. The equations guarantee that the adopted features offer the highest ability to distinguish between classes, enhance prediction efficiency, and can be explained by clinicians.

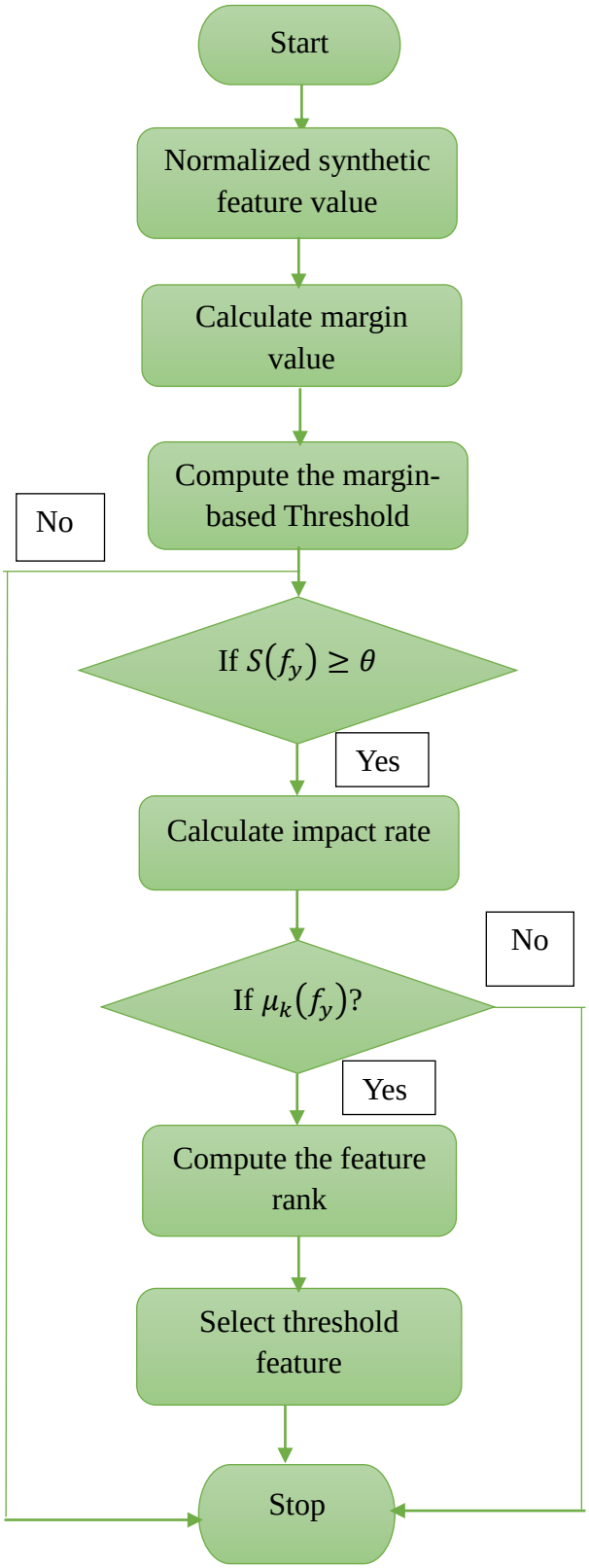

Figure 3. FSMIR Flowchart Diagram

The FSMIR flowchart illustrated in Figure 3 helps determine the marginal range of features from the initial values. This chart employs fuzzy logic to assess the contribution of each feature regarding the dataset associated with heart disease.

3.4) Particle Swarm Intelligence (PSI)

Particle Swarm Intelligence (PSI) is a bio-inspired optimization algorithm derived from the swarm behavior of a particular group of particles, birds, or fish. When applied to the heart disease dataset for feature selection, the PSI can be employed to recognize those features making the most impact via a thresholding strategy. Individual and collective knowledge pertains to particles and how they pass from one location to another in the search space; each particle corresponds to a subset of features among the dimensions. The fitness of a particle is assessed with a fitness function that estimates how appropriate the selected features are to the goal result. This method establishes value limit factors to serve as a range of the best maximum feature weights and then identifies those approaching the ideal weight value. In discrete movements, particles shift the position and velocity parameters of their particles. It continues to improve feature subsets using the maximum relevance corresponding to the weighted threshold range pairs, with the features of weights nearest to the threshold. When synthesizing the present thresholding-based selection with the dynamic PSI, the future subset selection works efficiently in modeling heart-diseased datasets to boost the general model performance and interpretability. The PSI algorithm implies that each particle can be a subset of the features of the heart disease dataset. For instance, if a dataset has n features (a list of features may include age, cholesterol level, blood pressure, etc.), each particle is represented by a vector of binary variables. Through the equation 13 we compute the feature subset,

$$i_x = [i_{x1}, i_{x2}, \dots, i_{xn}] \tag{13}$$

In this equation illustrate $i_{xy} \in \{0,1\}$ for select the feature in the heart disease dataset, by selected 1, or not 0. Then we perform fitness function for feature selection through equation 14 to evaluate the quality of a feature subset based on two main criteria like prediction accuracy of classification method, and simplicity of subset which is used toselecting fewer features for reduce complexity,

$$F(i_x) = \alpha . A(i_x) - \beta . \frac{S(i_x)}{T} \tag{14}$$

Let assume, F as fitness, i_x as feature subset, S as number of selected features, T as total number of features in the i_x, and α, β as weight coefficients which is used to balance the importance of accuracy and feature reduction. Higher fitness values correspond to subsets that maximize prediction accuracy while minimizing the number of selected features. After evaluate the quality of feature we update the velocity$v$ of each particle through equation 15 to determines how its position (feature subset) changes over iterations,

$$v_{xy}(p+1) = u . v_{xy}(p) + a_1 . s_1 . \left(q_{xy} - i_{xy}(p)\right) + a_2 . s_2 . \left(d_y - i_{xy}(p)\right) \tag{15}$$

Let assume, $v_{xy}(p+1)$ as updated velocity for feature y of the particle x at time p, u as inertia weight controlling exploration and exploitation, a_1, a_2, as acceleration coefficients for personal and global best influences, s_1, s_2 as random values in the range [0.1] to add stochasticity, q as personal best solution and d as global best solution. In this equation the best subset discovered by the particle so far and the best subset discovered by the entire swarm. By following we update the feature position on the basis of its velocity through equation 16,

$$i_{xy}(p+1) = \begin{cases} 1, if\ Sigmoid\left(v_{xy}(p+1)\right) > Z \\ 0, \quad otherwise \end{cases} \tag{16}$$

Let assume, Z as threshold, by following we perform sigmoid function through equation 17,

$$Sigmoid\left(v_{xy}\right) = \frac{1}{1+e^{-v_{xy}}} \tag{17}$$

In this equation if the sigmoid function output is greater than the predefined threshold (e.g., 0.5), the feature is selected $\left(i_{xy} = 1\right)$, otherwise 0 the feature is not selected. To further refine the selection process, the algorithm incorporates feature weights derived from their importance. In equation 18 we perform weight function,

$$u_y = \frac{FI(y)}{\sum_{k=1}^{n} FI(k)} \tag{18}$$

Let assume, u_y as normalized weight of feature which ensure all weights sum to 1, FI as feature importance. Thresholds are used to prioritize features that contribute significantly to heart disease prediction, such as cholesterol level, age, and blood pressure. Then we perform the convergence on output function of the PSI method through equation 19,

$$d = \arg\max\left(F(i_1), F(i_2), \ldots, F(i_m)\right) \tag{19}$$

The basic steps of the present PSI algorithm are as follows: 'the algorithm cycle is repeated until there is no better fitness value amplified in the entire process and that the maximum number of iterations is achieved.' The last step is the feature subset that ranks in the global best position g, which leads to the maximum accuracy and minimum restiveness feature subset. In the case of a heart disease dataset, the PSI algorithm may select Age, Resting blood pressure, Cholesterol level, Fasting blood sugar, Maximum heart rate reached, and Exercise-induced ST depression. These features are significant for diagnosing strokes, and selecting them increases model performance and decreases complexity. On the other hand, the PSI-based technique ensures that only the essential features are kept, making the predictions believable and straightforward.

3.5) SoftMax deep Scaling Gated Adversial Neural Network (SmDSAN^2)

The process of classifying a heart disease dataset using the SoftMax Deep Scaling Gated Adversarial Neural Network (SmDSAN2) is a technical manner of trying to predict the various aspects related to heart disease risks and disposition while simultaneously trying to

ensure that the prediction does not lead to high rates of false prediction. SmDSAN2 applies adversarial neural networks, gating mechanisms, and SoftMax scaling for processing patient biometrics like heart rate, cholesterol levels, etc. This model employs gated units to control and filter out essential features. It also combines adversarial training to mitigate noise or imbalance in the dataset. While using SoftMax scaling, SmDSAN2 can produce correct class probabilities, which enhances the interpretability of the generated model outputs. This framework optimizes risk assessment and diagnosis by providing a more robust risk stratification method and improves true positive and negative rates. It allows for prompt and effective clinical decision-making to benefit the patient.In equation 20 we illustrate the input data,

$$I = \{i_1, i_2, \dots, i_n\}, i_x \in \mathbb{R}^s \quad (20)$$

Let assume, I as input dataset, i_x as single patent features (like, heart rate, cholesterol), n as total number of samples in dataset, and s as dimensionality of the feature space. This equation represented as a multidimensional feature vector, where each sample includes patient-specific features. It may include ECG readings, maximum heart rate achieved during stress tests, etc. Then we perform gated mechanism$d$ for feature selection through equation 21,

$$d(i) = \sigma(U_d . i + b_d) \quad (21)$$

Let assume, $d(i)$ as output of gate activation, U_d as weight matrix for gating layer, b as bias term, and σ as sigmoid activation function which is used to ensures output between 0 and 1. The gating mechanism ensures that only the most relevant features for predicting heart disease (e.g., heart rate, blood pressure) are prioritized.For example, the gating mechanism may give higher importance to features like elevated cholesterol or abnormal heart rate for identifying patients at higher risk. By following we perform adversarial training for improve robustness and generalization where a generator network introduces perturbations, and a discriminator learns to distinguish between real and adversarial samples. In the equation 22 we perform Generator,

$$i_{adv} = i + \epsilon . sign\big(\nabla_x \mathcal{L}(i, j)\big) \quad (22)$$

Here, we perform the Discriminator H loss,

$$\mathcal{L}_H = -\mathbb{E}\big[\log\big(H(i)\big)\big] - \mathbb{E}\big[\log\big(1 - H(i_{adv})\big)\big] \quad (23)$$

Let assume, i_{adv} as adversarial output developed through adding perturbation to the i original input, ϵ perturbation input, $\nabla_x \mathcal{L}(i, j)$ as gradient of the loss function with respect to the input, $H(i)$ as discriminator probability that i is real sample. Adversarial training improves the model's robustness by generating slightly perturbed versions of the dataset (e.g., small variations in heart rate or cholesterol) and training the model to handle these variations.For heart disease data, adversarial examples might involve small changes in HR, BP, or CH to simulate real-world noise or sensor inaccuracies. By following we perform deep

scaling process for multilayer extraction across layers to capture hierarchical patterns in the dataset through equation 24,

$$o^{(l+1)} = \alpha^{(l)}.f\left(U^{(l)}.o^{(l)} + b^{(l)}\right) \quad (24)$$

Let assume, $o^{(l+1)}$ output of the layer l, U as weight matrix, b as bias, $f(.)$as non-linear activation function (ReLU, Tanh), and α as scaling factor. Deep scaling allows the model to focus on both high-level (e.g., patient age group) and low-level features (e.g., exact cholesterol levels).For heart disease, earlier layers might learn basic patterns like high cholesterol, while deeper layers might capture complex interactions between HR, BP, and AGE. Then we perform SoftMax function for the final classification step through equation 25,

$$Q(j = k|i) = \frac{\exp(P_k)}{\sum_{y=1}^{K}\exp(P_y)} \quad (25)$$

Let assume, $Q(j = k|i)$ as probability of input belongs to class, P as logit also unscaled output, K as total number of classes (like heart disease present or absent).The SoftMax layer predicts the probability of heart disease presence or absence based on the processed features.For example, the SoftMax output might predict $Q(j = 1|i)$, indicating an 85% chance of heart disease. Then we perform $\mathcal{L}$ for optimization through equation 26,

$$\mathcal{L} = \mathcal{L}_C + \lambda.\mathcal{L}_{adv} \quad (26)$$

Let assume, $\mathcal{L}_C$ as cross entropy loss, λ as weighting parameter to balance the two loss components, and $\mathcal{L}_{adv}$ as adversarial loss from the discriminator. In equation 27 we perform $\mathcal{L}_C$ for classification,

$$\mathcal{L}_C = -\frac{1}{n}\sum_{x=1}^{n}\sum_{k=1}^{K} j_{x,k}\log\left(Q(j = 1|i_x)\right) \quad (27)$$

The loss function combines classification accuracy and robustness. This equation makes it possible for the model to predict heart disease accurately, but simultaneously, it is secure from adversarial perturbation. The SmDSAN2 model seamlessly uses a systematic approach to group the heart disease datasets. It starts with a gated mechanism that screens out facets like HR, BP, and CH, where only facets most related to heart ailments are allowed. For example, performing some adversarial training guarantees the model's resistance against noise, which would more or less mimic realistic distortions in medical readings. There is an extraction of hierarchical patterns in deep scaling that can comprehend essential and complex attributes of the feature. The SoftMax layer estimates the possibility of the presence of heart diseases, and a combined loss function also maintains the effectiveness and robustness of the network. This model allows calculating precise risk values with low false-positive and false-negative values for practical clinical application.

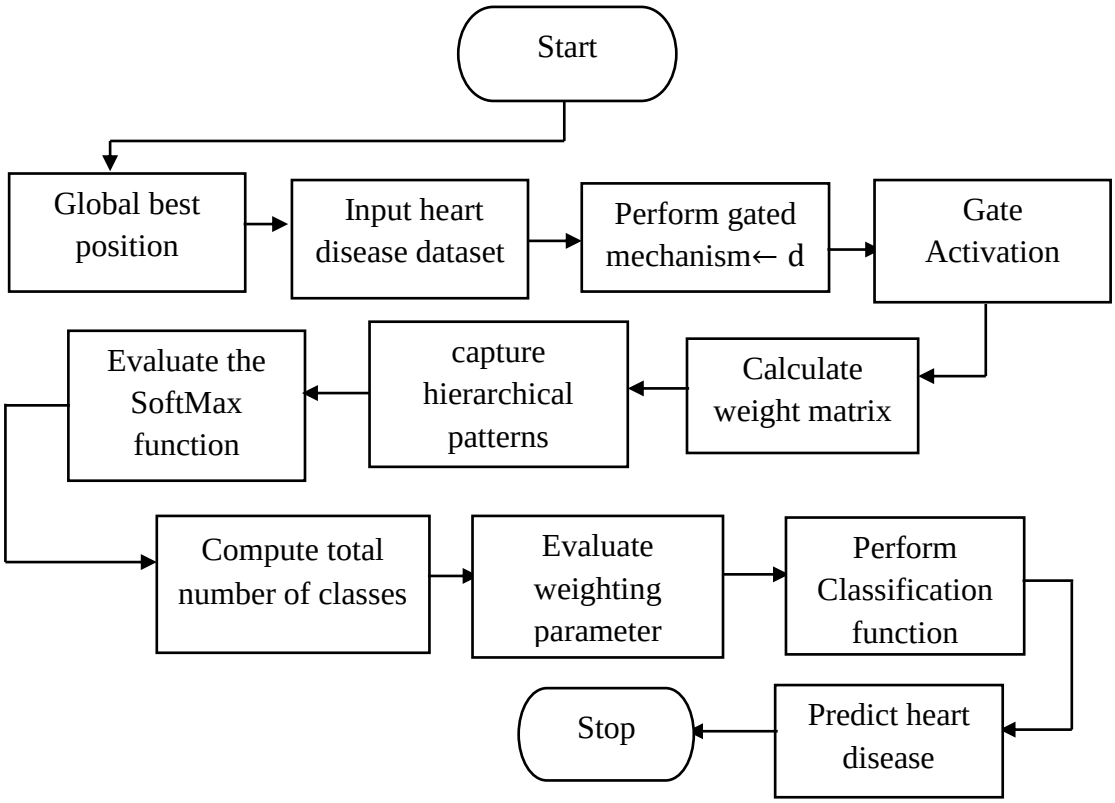

Figure 4. Proposed SmDSAN^2 Method Flowchart Diagram

The SmDSAN^2 method aims to assess heart disease risk probability through the flowchart in Figure 4, determine the existence of heart disease using the SoftMax layer, and predict different features associated with heart disease risk.

4) Result and Discussion

The SmDSAN2 method proposed in this study utilizes various performance measures to predict heart disease and can detect HD using a Python-based Jupyter Notebook. With them, specificity, sensitivity, precision, F1-Score, accuracy, and time complexity can be used to obtain a valid estimate for predicting heart disease.

Table 1. Simulation Parameter

Simulation	Values
Name of the Dataset	Heart Disease Dataset
No of Dataset	1026
Training	754
Testing	272
Tool	Jupyter
Language	Python

As mentioned in Table 1, they use Python-based Jupyter Notebook to get the correct accuracy and detect HD with the support of the dataset.

- $A_{ccuracy} = {\mathcal{T}^{\mathcal{P}} + \mathcal{T}^{n}}/{\mathcal{T}^{\mathcal{P}} + \mathcal{T}^{n} + \mathcal{F}^{\mathcal{P}} + \mathcal{F}^{n}}$
- $S_{ensitivity} = {\mathcal{T}^{\mathcal{P}}}/{\mathcal{T}^{\mathcal{P}} + \mathcal{F}^{n}}$
- $S_{pecificity} = {\mathcal{T}^{n}}/{\mathcal{T}^{n} + \mathcal{F}^{\mathcal{P}}}$
- $P_{recision} = {\mathcal{T}^{\mathcal{P}}}/{\mathcal{T}^{\mathcal{P}} + \mathcal{F}^{\mathcal{P}}}$
- $F1_{score} = {2 \times p_{recision} \times S_{ensitivity}}/{p_{recision} + S_{ensitivity}}$

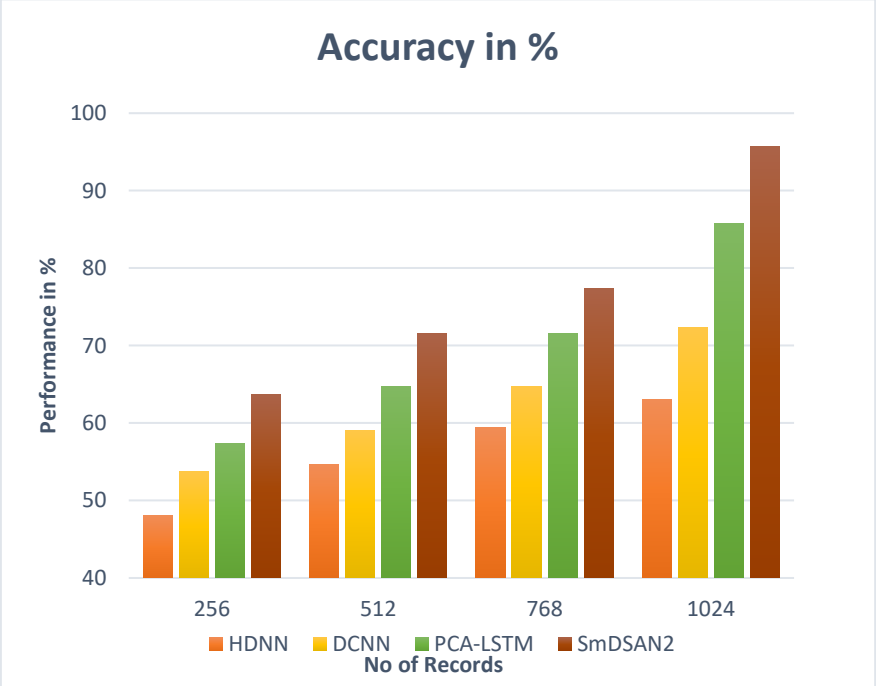

Figure 5. Accuracy performance in %

Therefore, in Figure 5 and Table 2, we depict the accuracy performance of the deployed method and the existing methods. HDNN archives stand at 63.1%, DCNN at 72.4%, PCA-LSTM at 85.7%, and the deployed method at 95.7%. According to the comparison, the SmDSAN2 stores data with higher accuracy than other techniques. Another advantage of its high accuracy is that the model often diagnoses patients with or without heart disease. This lowers the overall diagnosis error percentage and offers clinicians a solid method of planning additional medical tests.

Table 2. Performance of Accuracy in %

No of Records	HDNN	DCNN	PCA-LSTM	SmDSAN2

256	48.1	53.7	57.4	63.7
512	54.7	59.1	64.7	71.5
768	59.4	64.7	71.5	77.4
1024	63.1	72.4	85.7	95.7

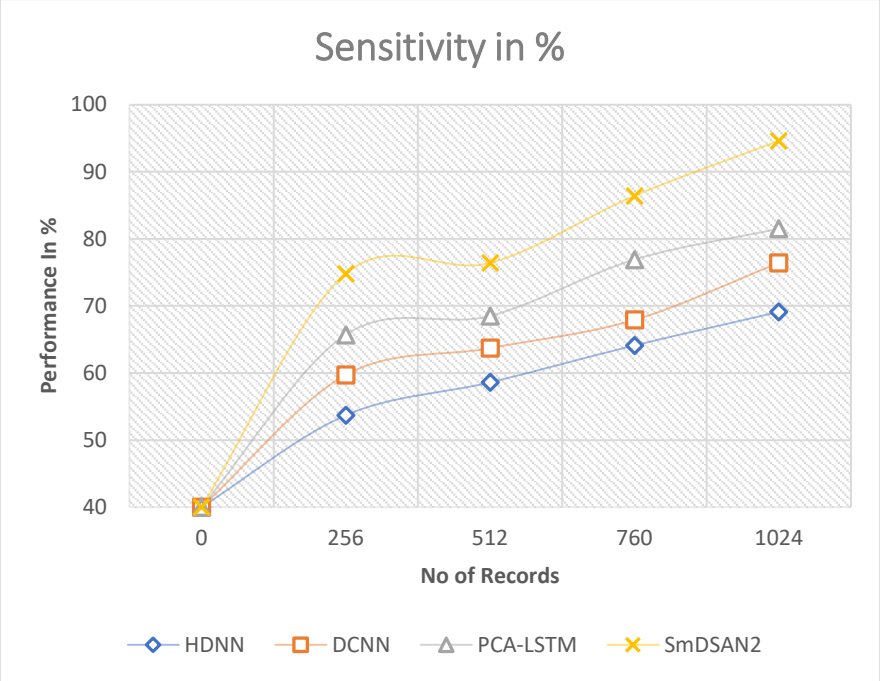

Figure 6Sensitivity performance in %

To compare the sensitivity performance of the deployed method and the existing methods, we present it as follows in figure 6 and table 3. The accuracy rates for HDNN archives are at 69.1%, DCNN is at 76.4%, PCA-LSTM at 81.5%, and the accuracy rates for the deployed method are at 94.6%. Although the SmDSAN2 employed method is compared to other methods, it achieves higher sensitivity when deployed. That is why sensitivity makes the model discover as many cases of heart disease as possible. High sensitivity reduces the risk of having a high percentage of patients with heart disease being overlooked. This is important as one may be suffering from heart problems but they have not been diagnosed, this can be life endangering.

Table 3. Performance of sensitivity in %

No of Records	HDNN	DCNN	PCA-LSTM	SmDSAN2

256	53.7	59.7	65.7	74.8
512	58.6	63.7	68.5	76.4
760	64.1	67.9	76.9	86.4
1024	69.1	76.4	81.5	94.6

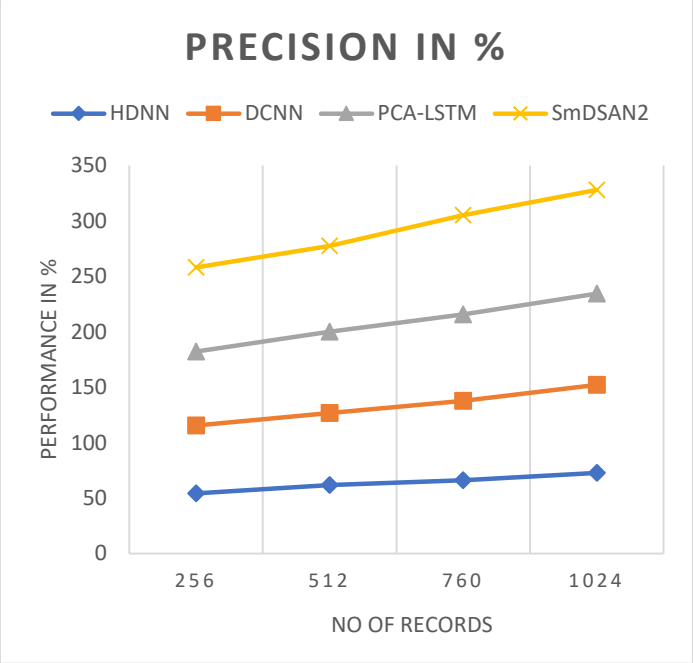

Figure 7. Precision performance in %

In Figure 7 and Table 4, we highlight the precision performance of the deployed method and the existing methods. The HDNN stores 72.6%, DCNN is 79.5%, PCA-LSTM attains 82.3%, while the proposed method achieves 93.7%. As is revealed by comparing the deployed method with other methods, the SmDSAN2 stores a higher precision value. Precision, therefore, befits the situation by ensuring that when the model says there is heart disease, it is very accurate. Less false positives (where the AI system injudiciously diagnoses a person with heart disease), lower stress, medical procedures, and additional expenses when the individual is healthy.

Table 4. Performance of precision in %

No of Records	HDNN	DCNN	PCA-LSTM	SmDSAN2
256	54.2	61.3	66.7	75.8

512	61.7	64.9	73.6	77.2
760	66.1	71.5	78.2	89.5
1024	72.6	79.5	82.3	93.7

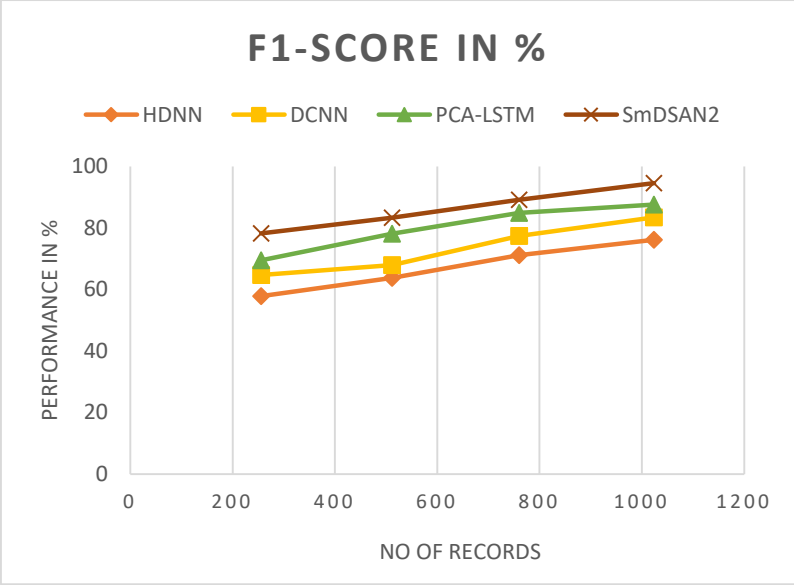

Figure 8. F1 Score performance in %

In Figure 8 and Table 5, we exhibit the F1-Score performance of the deployed method and the existing techniques. The corresponding architectures of the HDNN archives is 76.2%, DCNN is 83.5%, PCA-LSTM is 87.6%; the architectures of the deployed method are 94.6%. The SmDSAN2 saves the trained F1 Score performance by evaluating deployed methods with other techniques. The F1-Score measures the ratio between the True Positive rate and an average of the False Positive rate and False Negative rate, which is very important when false positives and false negatives are costly. Thus, the high F1-Score shows that the model has a reasonable rate of diagnosing heart disease without compromising precision or sensitivity. It helps provide precise and detailed predictions at the same time.

Table 5. Performance of F1 Score in %

No of Records	HDNN	DCNN	PCA-LSTM	SmDSAN2
256	57.8	64.7	69.5	78.3
512	63.8	67.9	78.2	83.4

760	71.2	77.4	84.9	89.2
1024	76.2	83.5	87.6	94.6

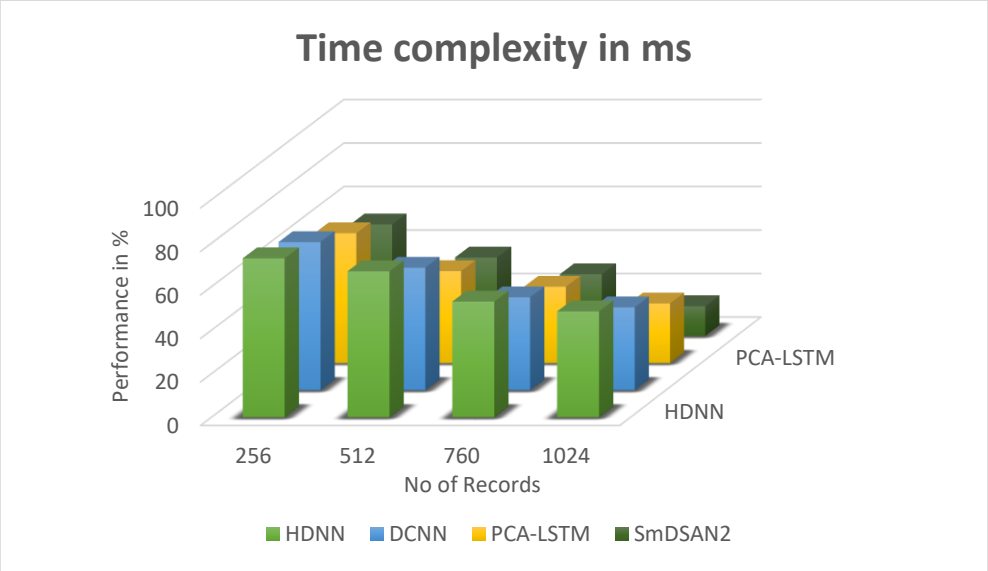

Figure 9. Time Complexity performance in ms

In Figure 9, and Table 6 we plot time complexity analysis of the presented and typical approaches used in the deployment phase. The HDNN, in our experiments, saves 48.7 ms, while the DCNN saves 38.1 ms, the PCA-LSTM saves 27.4 ms, and the deployed method saves 13.7 ms only. SmDSAN2 uses the deployed method to achieve low time complexity compared to other methods in the literature. Low time complexity enables prediction, and this will not be time-consuming even when processing big data or raw data in real-time, for instance, monitoring patients in intensive care units. Quick predictions enhance timely medical choices that are enormously vital in cases of emergency situations where early diagnosis of heart diseases may help to avoid heart attacks and other related complications.

Table 6. Performance of Time Complexity in ms

No of Records	HDNN	DCNN	PCA-LSTM	SmDSAN2
256	73.1	68.1	59.7	51.3
512	67.1	56.3	42.3	36.1
760	53.2	42.7	35.1	28.4

1024	48.7	38.1	27.4	13.7

5) Conclusion

This research evaluates a risk prediction model for heart disease using an improved DL algorithm, SoftMax Deep Scaling Gated Adversarial Neural Network (SmDSAN2). By utilizing the heart disease dataset available on Kaggle, the proposed method achieves high accuracy and reliability through a structured four-phase workflow: Feature pre-processing, identification of impact rate, selection of features, and finally, classification of the data. The first phase uses Mm-Z-Score to normalize the data, standardize features, and eliminate the effects of outliers. In the second stage, FSMIR defines core features with the most significant shared impact on the disease, discarding any unimportant factors. The third phase applies the PSI method to select the most essential features for inclusion in the feature subset since including all features increases the processing time and leads to over-emphasis of some features. Last, in the SmDSAN2 model, we apply novel solutions such as the gating mechanisms, adversarial robustness, and deep scaling to attain accurate, interpretable, and robust classification. This approach eliminates almost all the false-positive and false-negative results, which are always undesirable in biomedical applications. It clearly shows the framework has the potential to help clinicians in the timely identification of pathologies and treatment plans to provide better patient care and cost-effective infrastructure in the healthcare system.