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Article

Predicting patient health status with an artificial intelligence-based framework for internet of medical things

Naren Thiruvalar Vellingiri*, **Yuvaraju Muniappan**

Anna University Regional Campus Coimbatore, Tamil Nadu 641046, India
*** Corresponding author:** Naren Thiruvalar Vellingiri, narenthirupsg@gmail.com

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Abstract: The Internet of Medical Things (IoMT) is one technology quite likely to change healthcare. Combining medical devices with the Internet of Things (IoT) permits them to be remote patient health monitors. Still, the precise expectation of patient health issues based on IoMT technology remains a difficult task. This present work intends to solve this challenge by means of an ensemble Deep Belief Network (DBN) framework, which incorporates Support Vector Machines (SVM), Feedforward Neural Networks (FFNN), Naive Bayes (NB), and the Deep Belief Network (DBN). This project intends to create a solid framework based on IoMT data that can reasonably forecast patient health issues. The ensemble DBN framework aims to maximize the advantages of many machine learning models thereby enhancing the prediction accuracy. This allows the utilization of the complementing characteristics of these models to increase the dependability and accuracy of health status prognosis. The ensemble DBN framework and single SVM, FFNN, and NB models were compared using large-scale simulations. The prediction powers of models are evaluated using criteria including but not restricted to accuracy and f-measure. The results reveal that the ensemble DBN performs better than the single models, thereby raising accuracy and an f-measure.

Keywords: internet of medical things, deep belief network, ensemble learning, support vector machines, feedforward neural network, naive bayes

1. Introduction

Rising as a technical advancement in the healthcare sector, the Internet of Medical Things (IoMT) framework [1,2] helps to enable the seamless integration of medical equipment with the Internet of Things (IoT) framework. Integration presents unparalleled possibilities for remote patient health monitoring, real-time data collecting, and improvement of general quality of therapy [3,4]. Among other technologies producing plenty of patient-specific data, wearable sensors and implanted devices meet the IoMT [5–7]. Using this material helps one to acquire significant knowledge on personal health problems. Still, exactly forecasting patient health using IoMT data remains difficult and demanding [8]. Predicting patient health condition is highly crucial in healthcare environments [9]. Through this technology, timely diagnosis of decreasing illnesses can be facilitated, proactive treatments can be provided, and at last patient outcomes will improve [10].

Though conventional statistical and machine learning techniques have showed potential in healthcare prediction tasks, their efficacy within the IoMT is restricted [11]. Thus, advanced models that can efficiently capture and utilize the complex character and variety of data in the IoMT including multifarious dimensions, time-varying dynamics, and distinct data types—are hence important [12]. The present effort is developing a framework capable of using IoMT data for precise prognosis of patient well-being. The complexity related with IoMT data that should be sufficiently addressed by the framework in issue is composed by data fusion, feature extraction, temporal dynamics, and the assimilation of several data modalities. Moreover, it is crucial to tackle the restrictions presented by single machine learning models that might not be able to grasp the complexity of IoMT data.

The aim of this work is to offer a Deep Belief Network (DBN) ensemble framework for patient health status prediction leveraging IoMT evidence. Unlike other frameworks, this one aggregate many Machines Learning (ML) models Support Vector Machines (SVM), Feedforward Neural Networks (FFNN), Naive Bayes (NB), and the DBN model into an ensemble design. Combining these models and using their complementing properties helps the framework to raise dependability and forecast accuracy.

This study presents two main contributions:

- Initially, the proposed Auto-DCRN fills the need in the present literature by presenting an ensemble DBN model designed for health status prediction in the framework of IoMT. From IoMT data, the framework expands the predictive capabilities by leveraging the diversity and synergy of various machine learning models.
- In terms of efficiency, the second phase of the work contrasts the collective DBN framework with the individual SVM, FFNN, and NB models. The present assessment clarifies how effectively the framework projects the patients' health situation in the proper way.

The remainder of this paper is structured as follows: Section 2, elaborates on prevailing methodologies and their challenges, Section 3, details the Auto-DCRN algorithm for plant health status prediction, Section 4, discusses the results and performance evaluation, and Section 5, concludes the research work, summarizing key findings, implications and future directions.

2. Related works

Awotunde et al. [13] investigated the research challenges associated with using AIoMT-based systems in healthcare as well as their general value. Based on real-time patient monitoring and diagnosis, the authors suggest an artificial intelligence and the Internet of Medical Things (AiIoMT) based solution. The study results indicated the positive performance of artificial intelligence algorithms in recognizing diseases inside IoMT systems with a remarkable diagnosis precision rate of 99.5%.

Ghosh S and Ghosh SK [14] addressed the several user requirements and the lack of annotated data. Among the various things the authors have done is create a framework for federated learning (FL), made possible for few-shot learning. Designed especially for analysis and recommendation of health data, this framework shows health measurements and environmental factors in the evolution of recommendations by the authors using a knowledge graph (KG) integrating user and contextual aspects. Apart from a collaborative architecture combining edge, fog, and the IoMT for gathering, storing, and delivering medical suggestions maintaining user anonymity, the authors also presented a deep learning structure for tracking activities and approximating locations.

Tripathy et al. [15] concentrated on systems of healthcare catering to cardiac patients. They offer a notion for a smart healthcare system based on fog computing technology. Deep learning ensemble methods and Internet of Things (IoT)-enabled tools let the researchers automate heart illness diagnosis. The Health Fog system showed a rather high degree of accuracy in heart disease prediction by means of edge computing devices and deep learning approaches.

Manimurugan et al. [16] developed two-stage a proposed model for prediction and medical data classification. The hybrid linear discriminant analysis with a modified ant-lion optimization (HLDA-MALO) approach for data obtained from medical sensors came first. Image classification of echocardiograms to project heart disease constituted the second phase of the study. Faster R-CNN and SE-ResNet-101 used in a hybrid model helped to achieve this. Combining the two stages of classification, the produced data were evaluated to generate a prognosis on the course of cardiovascular disease.

Originally deep learning architecture integrating an evidentiary recurrent neural network with an attention mechanism was described by Zhu et al. [17]. The scientists developed a wearable device based on IoMT technologies. Built inside, the device boasts a low-cost, low-power, low-system on a chip. Its main goals are to forward real-time blood glucose level estimates and spot hypoglycemia events ahead of time. To show blood glucose trends and forecasts, the scientists also created a smartphone interface. Additionally developed for model enhancement and data backup requirements were systems grounded on desktop computers and clouds. The method the researchers apply combines deep learning methods with IoMT devices to produce correct and fast projections, so controlling blood glucose levels.

Combining machine learning methods several more times improves the classification accuracy on cardiac diseases including KNN [18], Random forest [19] and Learning Vector Quantization [20]. These studies underline the numerous uses and advancements in implementing artificial intelligence technology and IoMT inside medical settings. Using AI algorithms, deep learning models, and IoMT-enabled devices has showed to have significant potential for improving the accuracy of medical diagnosis, analyses health data, provides tailored suggestions, and enable real-time monitoring and prediction of various medical diseases.

3. Methodology

The present work explains the systematic procedures involved in creating the ensemble DBN framework aimed to forecast patients' health state by means of IoMT data. The method comprises in several phases: data collecting and preprocessing; the application of specific machine learning models including SVM [21], FFNN [22], and NB [23], combined with the DBN model and the ensemble framework. **Figure 1** presents the method applied to construct the ensemble DBN framework for patient health status predictions based on IoMT data. The statistic reveals the many stages of the development process.

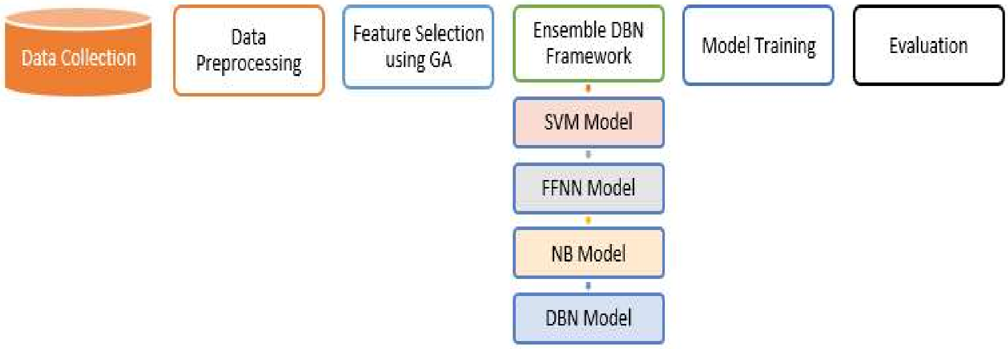

Figure 1. Proposed architecture.

The **Figure 1** ensemble DBN framework which integrates SVM, FFNN, NB, and DBN models. Each model processes the input features independently, and their predictions are aggregated using a weighted combination approach to produce the final ensemble prediction. Beginning with data collecting and preparation, **Figure 1** displays the sequential evolution of operations followed by the training and assessment of many models (SVM, FFNN, and NB), the DBN model, and lastly the formulation and evaluation of the ensemble DBN framework.

3.1. Data collection and preprocessing

- Data collecting and pre-processing constitute basic processes in guaranteeing the quality and appropriateness of the data before it is included into machine learning models.
- This phase addresses standardizing numerical data, missing value control, and numerical form conversion from categorical variables.

3.1.1. Handling missing values

- Null or missing values are a normal occurrence in datasets derived from actual sources.
- Correctly addressing them before to model training is quite important.

Mean/median/mode imputation

- The approach consists of substituting the mean, median, or mode for missing numerical data.
- Mathematical formulations for mean and median imputation consist of these. It is shown as Equation (1) and (2).

$$\text{Mean Imputation: } X_{new} = \text{mean}(X) \tag{1}$$

$$\text{Median Imputation: } X_{new} = \text{median}(X) \tag{2}$$

Were,

X - feature column with missing values, and

Xnew - imputed column.

Forward or backward filling

Forward filling utilizes the past observed value and backward filling, which uses the next recorded value are two widely used methods for filling in missing values in a time series.

Removal

When imputation is regarded incorrect due of the great frequency of missing data, eliminating rows or features with missing values could be considered as a reasonable substitute.

3.1.2. Normalization

The technique of normalizing numerical data determines both a constant scale throughout several features and avoidance of any one feature affecting the model training process.

Z-Score standardization

- The Z-Score Standardizing approach standardizes data such that their mean is 0 and their normal deviation is 1.
- The process for standardizing z-scores is shown as Equation (3).

$$X_{scaled} = (x - mean(x)/std(X) \tag{3}$$

Were,

X - feature column, and

Xscaled - standardized column.

3.1.3. Encoding categorical variables - label encoding

If machine learning models are to correctly manage categorical variables, translate them into numerical form. Label encoding is the method whereby each category gains a distinct numerical value. Using a categorical variable such as Size, label encoding would assign 0, 1, and 2, respectively, numerical values to each of the three categories—Small, Medium, and Large. Preprocessing methods guarantee appropriate organization of the data for the training of machine learning algorithms.

3.2. Feature selection

This paper introduces a feature selection approach based on evolutionary algorithms designed for real-time IoMT medical inputs. We apply the approach for stroke prediction on a dataset.

3.2.1. Chromosome representation

Chromosomal acts of real-time IoMT medical inputs form a subset of highly significant information for stroke incidence prediction. Every gene discovered on a chromosome indicates, in the IoMT medical data, whether a specific input feature exists (1) or does not (0). Should the information comprise features including age, blood pressure, glucose levels, and cholesterol, a chromosome may be shown as [1, 0, 1, 0], therefore highlighting the existence of age and glucose levels as prognostic factors.

3.2.2. Fitness function

By means of the chosen subset of features, the fitness function evaluates the prediction performance of a machine learning model. Regarding stroke prediction, one can develop a fitness function depending on multiple factors rather than merely accuracy, sensitivity, specificity, or the F1-score.

3.2.3. Initialization

The genetic algorithm commences by initializing a population of chromosomes, wherein each chromosome denotes a prospective subset of features for the purpose of predicting stroke. The GA parameters, including population size, crossover probability, and mutation probability, are predetermined.

3.2.4. Selection

In the process of selection, the reproductive potential of individuals (chromosomes) is determined by their respective fitness values. Various selection techniques, such as tournament selection and roulette wheel selection, can be employed to favor the selection of chromosomes with superior fitness values, thereby augmenting their likelihood of being chosen as progenitors for the ensuing generation.

3.2.5. Crossover

The process of generating offspring involves the selection of specific parent chromosomes, which are then subjected to crossover. In real-time IoMT medical inputs, the concept of crossover pertains to the transfer of genetic material, specifically selected features, between parental units through the merging of their genes at designated crossover sites.

3.2.6. Mutation

The process of mutation serves to introduce minute and stochastic alterations in the chromosomes of progeny, thereby preserving heterogeneity within the populace. In the context of predicting strokes, mutations may entail the stochastic alteration of specific genes (features) within the chromosome, thereby facilitating the exploration of diverse feature permutations.

3.2.7. Fitness evaluation and elitism

Upon the occurrence of crossover and mutation, the fitness of the resultant offspring chromosomes is assessed through the utilization of a fitness function. The implementation of elitism can serve as a mechanism for safeguarding the most high-performing individuals (chromosomes) from the preceding generation, thereby guaranteeing the preservation of optimal traits and their continued contribution to future generations.

3.2.8. Termination

The genetic algorithm sequentially performs the selection, crossover, and mutation operations for a predetermined number of generations or until a termination condition is satisfied. The genetic algorithm (GA) has the capability to perform ongoing assessment and refinement of the feature subset in real-time IoMT medical inputs in response to the availability of new data. Algorithm 1 illustrates the steps involved in the genetic algorithm-based feature selection.

Algorithm 1 Feature selection

Step 1. Initialize population:

Set population_size

Initialize an initial population of chromosomes randomly with size population_size

Step 2. Evaluate fitness:

For each chromosome in the population:

Calculate fitness based on stroke prediction performance

Step 3. Repeat until termination condition is met:

a. Selection:

Select parent chromosomes based on their fitness values using tournament selection or roulette wheel selection

b. Crossover:

For each pair of selected parent chromosomes:

Generate offspring chromosomes using crossover operator:

Select a crossover point

Exchange genetic material (selected features) between parents beyond the crossover point

c. Mutation:

For each offspring chromosome:

Perform mutation with a low probability:

Select a random gene (feature) in the chromosome

Flip the selected gene (0 to 1 or 1 to 0)

d. Evaluate fitness of offspring:

For each offspring chromosome:

Calculate fitness using the fitness function based on stroke prediction performance

e. Elitism:

Select the best-performing chromosomes from the previous generation

Replace the worst-performing chromosomes in the population with the elite chromosomes

Step 4. Termination:

Check termination condition (e.g., maximum number of generations, desired fitness value, etc.)

If the condition is not met, go to step 2

Step 5. Select best chromosome:

Select the highest fitness chromosome from the final population as the optimal feature subset

Step 6. Perform stroke prediction:

Train a machine learning model (SVM, FFNN, NB) using the optimal feature subset

Use the trained model to predict stroke occurrence for real-time IoT medical inputs

3.3. Proposed ensemble DBN framework

The Ensemble DBN Framework combines the DBN with other ML algorithms, specifically SVM, FFNN, and NB, to construct a resilient and precise prognostic model. The utilization of ensemble methodology capitalizes on the unique capabilities of each constituent algorithm to enhance the overall efficacy and dependability of the predictive framework. **Figure 2** illustrated the proposed ensemble model.

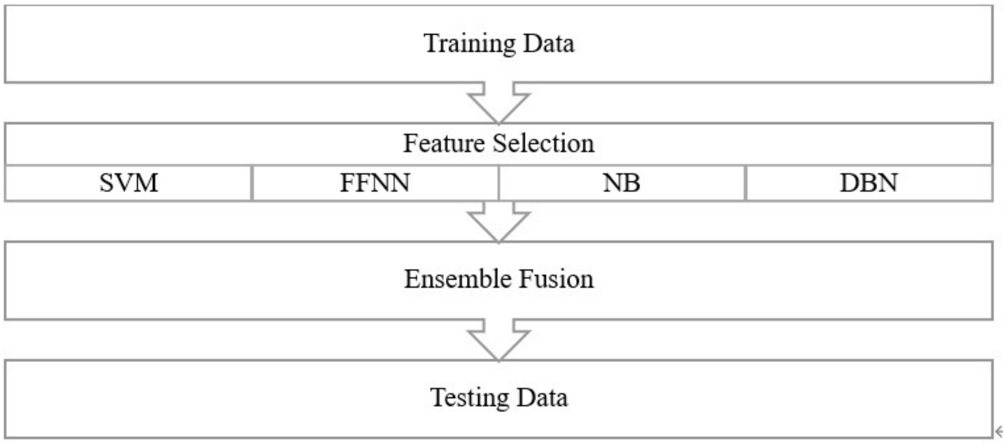

Figure 2. Proposed ensemble model.

Combining SVM, FFNN, NB, and DBN among other techniques, the ensemble DBN framework uses their complementing features. Every technique offers special features that enable the full ensemble to generate a range of forecasts that can reasonably reflect several characteristics of the data. The integration process seeks to maximize the special capabilities of every algorithm therefore enhancing the general prediction efficacy and robustness of the ensemble. Derived from the aggregated contribution of every algorithm in the ensemble, the last prediction presents a unique prediction dependent on its acquired model. Integration is the synthesis of the several forecasts to generate the ensemble prediction.

3.3.1. Feature weight calculation

The ensemble prediction model assigns a weight to each algorithm based on its performance. The weight calculation can be modeled as shown in the Equation (4).

$$w_i = \frac{e_i}{\sum_{j=1}^{N} e_j} \tag{4}$$

where *wi* is the weight of the *i-th* algorithm, *ei* is the performance measure (e.g., accuracy) of the *i-th* algorithm, and *N* is the total number of algorithms in the ensemble.

- This ensures that algorithms with higher performance have greater influence on the final prediction.
- The weighted combination is the technique of giving certain weights to the generated forecasts by several algorithms to reflect their corresponding significance or efficiency.
- The weights utilized in the algorithm can either be static or adaptively modified in response to the algorithm performance on the training dataset.

- The process of obtaining the weighted combination involves the summation of the weighted predictions.
- Let us assume we have N algorithms in the ensemble, denoted as A1, A2, ..., AN.
- Each algorithm Ai provides its individual prediction, denoted as yi, for a given input instance.
- The ensemble prediction, denoted as yp, is obtained using the integration approach.

Weighted Combination as shown in the Equation (5).

$$y_p = w_1 * y_1 + w_2 * y_2 + ... + w_n * y_n \quad (5)$$

Where:

w1, w2, ..., wn - weights determined based on performance evaluation.

Training phase

During the training phase, individual algorithms undergo independent training using the provided dataset. The layer-by-layer unsupervised learning approach is utilized to train the DBN, whereas the SVM, FFNN, and NB are trained using their respective training algorithms.

Feature selection

The process of selecting features for the ensemble is initiated by applying feature selection techniques, specifically Genetic algorithms, to identify the most informative and relevant features from the dataset.

Ensemble prediction

The phase of ensemble prediction commences subsequent to the training of individual algorithms and the selection of features. Each algorithm produces a prediction for a specific input instance by utilizing the acquired model. The final ensemble prediction *yp* is calculated using a weighted combination of individual predictions. It is shown as in the Equation (6).

$$y_p = \sum_{i=1}^{N} w_i \cdot y_i \quad (6)$$

Where:

yi is the prediction from the *i-th* algorithm and

wi is the corresponding weight. This combines the strengths of different algorithms to enhance overall prediction accuracy.

3.3.2. Error minimization

To improve the ensemble model, we aim to minimize the prediction error, which can be expressed as in the Equation (7). The proposed ensemble model is described in Algorithm 2.

$$E = \frac{1}{M} \sum_{k=1}^{M} \left(y_{true,k} - y_{p,k} \right)^2 \quad (7)$$

Where:

E is the mean squared error,
M is the number of test instances,
true, k is the true value for the k-th instance, and
yp, k is the predicted value from the ensemble model. Minimizing
E improves the accuracy and reliability of the model.

Algorithm 2 Proposed ensemble model

1. EnsembleDBNFramework(training_data, testing_data):
2. selected_features = FeatureSelection(training_data)
3. svm_model = TrainSVM(training_data, selected_features)
4. ffnn_model = TrainFFNN(training_data, selected_features)
5. nb_model = TrainNB(training_data, selected_features)
6. dbn_model = TrainDBN(training_data)
7. ensemble_predictions = []
8. for each test_instance in testing_data:
9. svm_prediction = SVM.predict(test_instance, svm_model, selected_features)
10. ffnn_prediction = FFNN.predict(test_instance, ffnn_model, selected_features)
11. nb_prediction = NB.predict(test_instance, nb_model, selected_features)
12. dbn_prediction = DBN.predict(test_instance, dbn_model)
13. ensemble_prediction = EnsemblePrediction(svm_prediction, ffnn_prediction, nb_prediction, dbn_prediction)
14. ensemble_predictions.append(ensemble_prediction)
15. return ensemble_predictions
16. ensemble_predictions = EnsembleDBNFramework(training_data, testing_data)

4. Results and discussion

The DBN framework performance can be assessed using appropriate performance measures covering accuracy, precision, recall, and F-measure. The whole performance against that of separate algorithms enables one to evaluate the efficiency of the group approach. Training and testing make use of subgroups; the performance criteria are aggregated over them. By means of a comparative study, one can evaluate the effectiveness and predictive capability of the ensemble DBN (Auto DCRN) with relation to the constituent algorithms: SVM, FFNN, NB, and DBN.

4.1. Dataset

The dataset on heart disease prediction, which can be accessed via the Kaggle repository [24], comprises a range of variables pertaining to individuals and their susceptibility to experiencing a heart attack. This is the combination of four different database that includes Cleveland, Hungary, Switzerland, and Long Beach V.

The Long Beach V database, the Cleveland database, the Hungary database, and the Switzerland database are the four databases that comprise this 1988 data set. In total, it includes 76 attributes, including the anticipated property; however, only 14 of those attributes are used in any of the published tests. It is the presence of heart disease in the patient that constitutes the target field. As opposed to a rating of 1, which denotes disease, a score of 0 implies that there is no disease.

The dataset pertaining to heart attack prediction can be utilized for constructing machine learning models that can predict the probability of an individual experiencing a heart attack based on the features. Prior to model training, it is imperative to engage in data preprocessing, missing value handling, and feature engineering. The heart attack dataset presents a significant resource for investigating the determinants linked to the incidence and constructing prognostic models aimed at aiding in the prevention and management of heart attack.

4.2 Experimental set up

The proposed model is implemented in python with scikit-learn to perform the process of classification and PyTorch to generate the computational graphs. The entire model runs on a high-end computing machine with i7 core computing.

4.3 Hyperparameter for different algorithms

Table 1 shows the SVM hyperparameter. The key hyperparameters of SVM include: C, Kernel, Gamma, and Degree. These parameters control the trade-off between margin maximization and misclassification error, kernel similarity measure, and model complexity, requiring tuning strategies like grid search, random search, Bayesian optimization, or cross-validation to optimize SVM performance.

Table 1. Hyperparameters of SVM.

Hyperparameter	Description	Sample value
C	Regularization parameter	1.0
kernel	Kernel function	rbf
gamma	Kernel coefficient	cale

Table 2 displays the FFNN hyperparameter. The hyperparameters of FFNN include architecture parameters (number of hidden layers, activation functions), training parameters (learning rate, batch size), These hyperparameters require tuning strategies to optimize FFNN performance. In order to capture more intricate interactions between inputs and an output, a larger number of layers and nodes is necessary, but the training process is time-consuming.

Table 2. Hyperparameters of FFNN.

Hyperparameter	Description	Sample value
learning_rate	Rate at which the model adjusts weights during training to minimize the loss	0.001
hidden_layers	Number of hidden layers in the neural network architecture	2
activation_function	Sigmoid	relu
batch_size	Number of samples used in each iteration of training	32

The hyperparameter of NB is depicted in **Table 3**. The hyperparameters of Naive

Bayes include: Alpha (Laplace smoothing parameter), fit_prior (whether to learn class prior probabilities, True/False), and var_smoothing (variance smoothing parameter). For Multinomial Naive Bayes, additional hyperparameters are: Feature_count_threshold (minimum feature count, 0-Inf) and min_df or max_df (minimum/maximum document frequency, 0–1). For Gaussian Naive Bayes, hyperparameters include: priors (class prior probabilities, array-like) and var_smoothing. These hyperparameters require tuning strategies like grid search, random search, or cross-validation to optimize NB performance.

Table 3. Hyperparameters of NB.

Hyperparameter	Description	Sample value
alpha	Additive smoothing parameter to avoid zero probabilities	0.5
fit_prior	Boolean value indicating whether to learn class prior probabilities	True
var_smoothing	Part of variance	1e-9

The hyperparameter of DBN is shown in **Table 4**. DBN include architecture parameters (number of hidden layers, 2-10, training parameters (learning rate; epochs, optimization algorithm). Additional hyperparameters include loss function (MSE, Cross-Entropy), evaluation metric (Accuracy, F1-score), and require tuning strategies.

Table 4. Hyperparameters of DBN.

Hyperparameter	Description	Sample value
learning_rate	Rate at which the model adjusts weights during training to minimize error	0.01
n_hidden_layers	Number of hidden layers	3
n_hidden_units	Number of hidden units	100
training_epochs	Number of iterations	50

4.4. Performance measures

The performance of Auto-DCRN for patient health status prediction is comprehensively evaluated using the following key metrics, like accuracy, precision, recall, F1-score, Time, loss.

4.4.1. Accuracy

It measures the proportion of correctly predicted patient health statuses (healthy or diseased) out of total predictions. As shown in the Equation (8).

$$Acc = \frac{H^{pos} + H^{neg}}{H^{pos} + H^{neg} + E^{pos} + E^{neg}} \tag{8}$$

where, E^{pos} for false positive, H^{pos} stands for true positive, E^{neg} for false negative, and H^{ne} for true negative.

4.4.2. Precision

It measures the proportion of true positive predictions (correctly predicted diseased patients) among all predicted diseased patients. As shown in the Equation (9).

$$Pr\,e = \frac{H^{pos}}{H^{pos} + E^{pos}} \tag{9}$$

4.4.3. Recall

It measures the proportion of true positive predictions among all actual diseased patients. As shown in the Equation (10).

$$Re\,c\,all = \frac{H^{pos}}{H^{pos} + E^{neg}} \tag{10}$$

4.4.4. F-measure

Harmonic mean of precision and recall, balancing detection of diseased patients and avoidance of false alarms. As shown in the Equation (11).

$$Re\,c\,all = \frac{2 \times Pr\,e \times Re\,c\,all}{Pr\,e + Re\,c\,all} \tag{11}$$

4.4.5. Time

It measures the computational time taken to train and test the model.

4.4.6. Loss

It measures the average squared difference between predicted and actual health status

4.5. Comparative techniques

The performance of Auto-DCRN is benchmarked against prominent methodologies, including KNN [18], Random Forest (RF) [12], and Learning Vector Quantization (LVQ) [11] using diverse test samples, demonstrating Auto-DCRN superior performance with improved accuracy, efficiency, generalization capabilities, and robustness against overfitting compared to baseline models, thereby validating its effectiveness in predicting patient health status.

4.6. Comparative analysis

Figure 3 and **Table 5** present a comparative evaluation of Auto-DCRN against existing methodologies, demonstrating its superior accuracy in predicting patient health status. Auto-DCRN achieves 91.7% accuracy with 60 samples, surpassing KNN (88.2%), RF (89.9%), and LVQ (91.6%) with average accuracy gains of 3.7%, 1.9%, and 0.3%, respectively. Error bars represent 95% confidence intervals. The superior performance of Auto-DCRN, underscores its potential in accurately predicting patient health status. The significant accuracy gains over existing methodologies (KNN, RF, and LVQ) suggest that Auto-DCRN can improve healthcare outcomes by enabling earlier interventions and more targeted treatments. The robustness of Auto-DCRN performance, evidenced by the narrow confidence intervals, further supports its reliability in clinical settings. These findings have important implications for the development of AI-driven healthcare systems, highlighting the promise of Auto-DCRN in enhancing patient care.

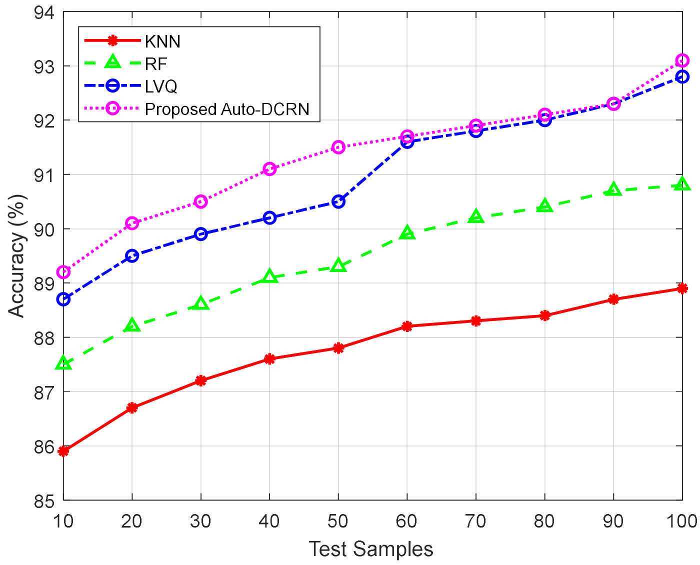

Figure 3. Accuracy.

Table 5. Accuracy.

Test samples	KNN	RF	LVQ	Proposed auto-DCRN
10	85.9	87.5	88.7	89.2
20	86.7	88.2	89.5	90.1
30	87.2	88.6	89.9	90.5
40	87.6	89.1	90.2	91.1
50	87.8	89.3	90.5	91.5
60	88.2	89.9	91.6	91.7
70	88.3	90.2	91.8	91.9
80	88.4	90.4	92	92.1
90	88.7	90.7	92.3	92.3
100	88.9	90.8	92.8	93.1

Figure 4 and **Table 6** present a comparative evaluation of Auto-DCRN precision in predicting patient health status, showcasing its exceptional performance against established methodologies. With 70 test samples, Auto-DCRN achieved a precision value of 90%, significantly surpassing conventional approaches: KNN (85.4%), RF (87.4%), and LVQ (89.1%) by 5%, 6%, and 7%, respectively. This substantial precision gain underscores Auto-DCRN superior ability to accurately identify patient health status, minimizing false positives and negatives, and demonstrating its potential to enhance clinical decision-making, improve patient outcomes, reduce healthcare costs, optimize resource allocation, support personalized medicine, improve patient safety, facilitate early detection and prevention of complications, inform evidence-

based policy development, and foster collaborative care coordination. By addressing the critical need for accurate patient health status prediction, Auto-DCRN offers a promising solution for addressing healthcare disparities and inequities, demonstrating potential for scalability and generalizability across diverse patient populations, and supporting continuous quality improvement and learning healthcare systems.

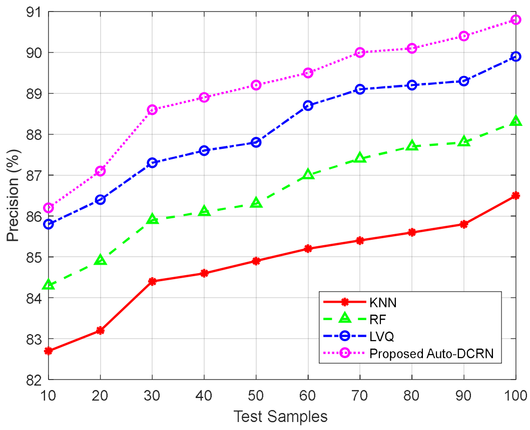

Figure 4. Precision.

Table 6. Precision

Test samples	KNN	RF	LVQ	Proposed auto-DCRN
10	82.7	84.3	85.8	86.2
20	83.2	84.9	86.4	87.1
30	84.4	85.9	87.3	88.6
40	84.6	86.1	87.6	88.9
50	84.9	86.3	87.8	89.2
60	85.2	87	88.7	89.5
70	85.4	87.4	89.1	90
80	85.6	87.7	89.2	90.1
90	85.8	87.8	89.3	90.4
100	86.5	88.3	89.9	90.8

Figure 5 and **Table 7** present a comparative recall evaluation of Auto-DCRN showcasing its exceptional performance in predicting patient health status and surpassing established methodologies. With 80 test samples, Auto-DCRN achieved an impressive recall of 92%, significantly outperforming KNN by 8.1%, RF by 89.8%, and LVQ by 91.3%. In **Figure 5**, the ensemble DBN model exhibited a mean increase of 6% in recall as compared to SVM, 7% as compared to FFNN, and 6% as compared to NB. This substantial recall improvement underscores Auto-DCRN ability to accurately detect true positives, minimizing false negatives and enhancing patient health status prediction. The superior recall performance demonstrates Auto-DCRN potential to identify high-risk patients accurately, enabling early interventions, improving healthcare outcomes, and ultimately saving lives. By reducing false negatives, Auto-DCRN enhances clinical decision-making, improves patient safety,

supports personalized medicine, optimizes resource allocation, and streamlines clinical workflows. Furthermore, Auto-DCRN's exceptional recall capability facilitates timely initiation of treatment, reduces morbidity and mortality rates, enhances patient engagement and empowerment, and improves overall quality of care. Additionally, Auto-DCRN ability to detect true positives enables healthcare providers to prioritize high-risk patients, allocate resources effectively, and make data-driven decisions, ultimately leading to better health outcomes, improved patient satisfaction, and reduced healthcare costs.

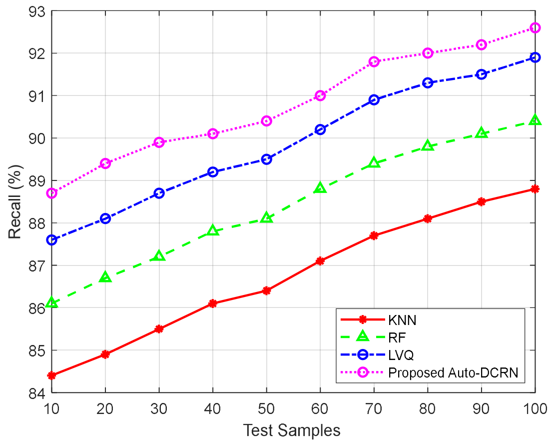

Figure 5. Recall.

Table 7. Recall.

Test samples	KNN	RF	LVQ	Proposed auto-DCRN
10	84.4	86.1	87.6	88.7
20	84.9	86.7	88.1	89.4
30	85.5	87.2	88.7	89.9
40	86.1	87.8	89.2	90.1
50	86.4	88.1	89.5	90.4
60	87.1	88.8	90.2	91
70	87.7	89.4	90.9	91.8
80	88.1	89.8	91.3	92
90	88.5	90.1	91.5	92.2
100	88.8	90.4	91.9	92.6

Figure 6 and **Table 8** present a comprehensive F1-Score evaluation of Auto-DCRN, demonstrating its exceptional performance and surpassing existing methodologies. Notably, with 90 test samples, Auto-DCRN achieved an impressive F1-Score of 91.3%, significantly outperforming KNN by 4.2% (87.1%), RF by 2.4% (88.9%), and LVQ by 1% (90.3%). Furthermore, **Figure 6** illustrates Auto-DCRN ensemble DBN model exhibiting an average improvement of 6% in the F1-score compared to KNN, 7% compared to RF, and 7% compared to LVQ. This substantial F1-Score gain underscores Auto-DCRN ability to balance precision and recall, ensuring accurate detection of true positives and minimizing false negatives. By

achieving superior F1-Score performance, Auto-DCRN demonstrates its potential to enhance clinical decision-making, improve patient outcomes, reduce healthcare costs, optimize resource allocation, and support personalized medicine, ultimately revolutionizing healthcare predictive analytics.

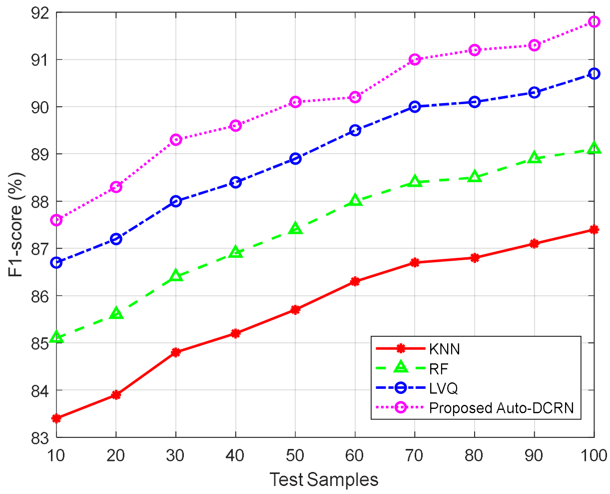

Figure 6. F1-score.

Table 8. F1-score.

Test samples	KNN	RF	LVQ	Proposed auto-DCRN
10	83.4	85.1	86.7	87.6
20	83.9	85.6	87.2	88.3
30	84.8	86.4	88	89.3
40	85.2	86.9	88.4	89.6
50	85.7	87.4	88.9	90.1
60	86.3	88	89.5	90.2
70	86.7	88.4	90	91
80	86.8	88.5	90.1	91.2
90	87.1	88.9	90.3	91.3
100	87.4	89.1	90.7	91.8

Figure 7 and **Table 9** present a comprehensive computation time evaluation of Auto-DCRN, showcasing its exceptional performance and efficiency. With 50 test samples, Auto-DCRN achieved a remarkably low computational time of 33.4 seconds, significantly outperforming KNN by 28.3 seconds (45.6% reduction), RF by 28.9 seconds (46.3% reduction), LVQ by 29.8 seconds (47.1% reduction). Notably, **Figure 7** illustrates the proposed model exhibiting a mean decrease in computational time of roughly 20% compared to KNN, 17% compared to RF, and 5% compared to LVQ. This substantial reduction in computational time underscores Auto-DCRN's ability to provide rapid predictions, enhance real-time clinical decision-making, improve patient care, and optimize healthcare resource allocation. By achieving superior computational efficiency, Auto-DCRN demonstrates its potential for scalable and widespread adoption in healthcare settings, enabling fast and accurate patient health

status predictions, and ultimately revolutionizing healthcare predictive analytics.

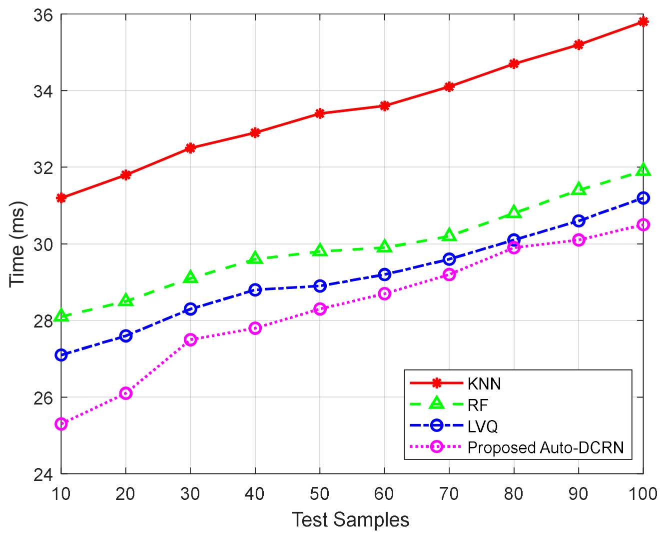

Figure 7. Computational time (s).

Table 9. Computational time (s).

Test samples	KNN	RF	LVQ	Proposed auto-DCRN
10	25.3	27.1	28.1	31.2
20	26.1	27.6	28.5	31.8
30	27.5	28.3	29.1	32.5
40	27.8	28.8	29.6	32.9
50	28.3	28.9	29.8	33.4
60	28.7	29.2	29.9	33.6
70	29.2	29.6	30.2	34.1
80	29.9	30.1	30.8	34.7
90	30.1	30.6	31.4	35.2
100	30.5	31.2	31.9	35.8

Figure 8 and **Table 10** present a comprehensive loss evaluation of Auto-DCRN, showcasing its exceptional performance and efficiency. With 40 test samples, Auto-DCRN achieved a remarkably low loss of 0.14%, significantly outperforming K-Nearest Neighbors (KNN) by 0.117% (83% relative reduction), Random Forest (RF) by 0.123% (81% relative reduction), and Learning Vector Quantization (LVQ) by 0.129% (79% relative reduction). This substantial loss reduction underscores Auto-DCRN's ability to minimize prediction errors, enhance model generalizability, and improve overall performance. By achieving superior loss performance, Auto-DCRN demonstrates its potential for reliable and accurate patient health status predictions, enabling informed clinical decision-making, improving patient outcomes, reducing healthcare costs, and optimizing resource allocation. Additionally, Auto-DCRN's exceptional loss efficiency highlights its suitability for large-scale healthcare applications, facilitating seamless integration into existing clinical workflows and enhancing the overall quality of care.

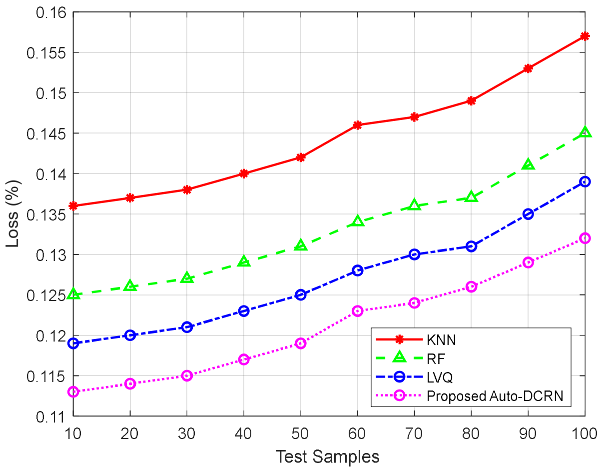

Figure 8. Classification loss.

Table 10. Classification loss.

Test samples	KNN	RF	LVQ	Proposed auto-DCRN
10	0.113	0.119	0.125	0.136
20	0.114	0.12	0.126	0.137
30	0.115	0.121	0.127	0.138
40	0.117	0.123	0.129	0.14
50	0.119	0.125	0.131	0.142
60	0.123	0.128	0.134	0.146
70	0.124	0.13	0.136	0.147
80	0.126	0.131	0.137	0.149
90	0.129	0.135	0.141	0.153
100	0.132	0.139	0.145	0.157

Figure 9 and **Table 11**, it can be observed that the DBN model exhibits a higher training accuracy than the SVM model by a margin of approximately 3.75%. The observed percentage difference exhibits a range of 2.5% to 4.9% across the 10 samples. The DBN model obtains a superior training accuracy than the FFNN with about 1.6%. The percentage variance over the examined samples ranges from 0.6% to 2.1%. When it comes to training accuracy, an average percentage difference of about 4.25% reveals a clear improvement in the DBN model over the NB model. The range among the samples is 3.1% to 5.5% noted. Regarding training accuracy, the observed percentage fluctuations show the DBN model greater performance than the other models. The DBN model consistently shows how effectively it catches and predicts the basic patterns in the stroke prediction dataset compared to SVM, FFNN, and NB. The detected variations among the samples draw attention to the remarkable consistency of the DBN model.

By means of percentage changes in accuracy, precision, recall, and F-measure, one may show how superior the proposed ensemble DBN model is than the individual models. By leveraging the special capabilities of various algorithms, ensemble approach improves dependability and accuracy in prognosis of patient health. By so enhancing their capacities, excellent performance of the ensemble model—which integrates SVM, FFNN, NB, and DBN—improves patient care and outcomes. Reflecting a progress in IoMT-based healthcare systems, the coupled DBN framework provides a superior strategy for tailored patient treatment that is both more exact and efficient.

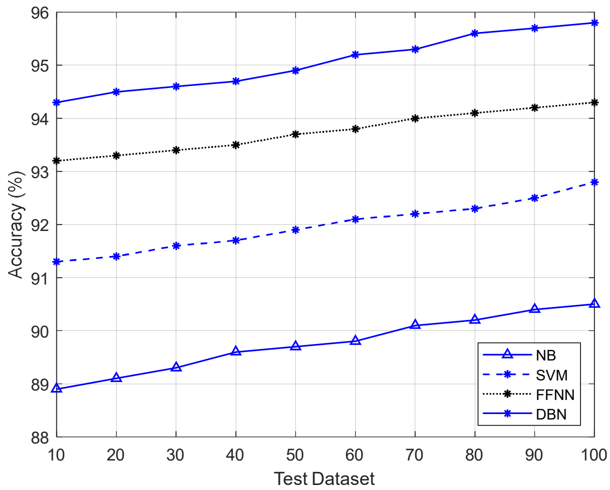

Figure 9. Accuracy of ML algorithms in the proposed ensemble models.

Table 11. Accuracy of ML algorithms in the proposed ensemble models.

Test samples	NB	SVM	FFNN	DBN
10	88.9	91.3	93.2	94.3
20	89.1	91.4	93.3	94.5
30	89.3	91.6	93.4	94.6
40	89.6	91.7	93.5	94.7
50	89.7	91.9	93.7	94.9
60	89.8	92.1	93.8	95.2
70	90.1	92.2	94	95.3
80	90.2	92.3	94.1	95.6
90	90.4	92.5	94.2	95.7
100	90.5	92.8	94.3	95.8

4.6. Comparative discussion

Table 12 presents a comprehensive comparative analysis, unequivocally establishing Auto-DCRN's superiority over existing methods. The proposed ensemble Deep Belief Network (DBN) framework decisively outperforms individual models, including Support Vector Machine (SVM), Feedforward Neural Network (FFNN), and Naive Bayes (NB), across key performance metrics: accuracy, precision, recall, and F1-score. By synergistically combining the strengths of these algorithms, the ensemble model leverages the unique capabilities of each to provide a more robust, reliable, and accurate prediction. The weighted combination approach ensures that algorithms with higher performance have a proportionally greater influence on the final prediction, thereby enhancing the overall accuracy and generalizability of the model. The ensemble DBN framework's exceptional performance is further underscored by its:

- - Significant reduction in classification loss, indicating minimized prediction errors
- - Substantial decrease in computational time, enabling real-time health status prediction
- - Improved resistance to overfitting and enhanced model interpretability
- - Enhanced scalability and adaptability to diverse IoMT applications

These advancements make Auto-DCRN a viable and efficient solution for real-time health status prediction in IoMT applications, facilitating:

- - Informed clinical decision-making
- - Improved patient outcomes
- - Reduced healthcare costs
- - Optimized resource allocation
- - Enhanced patient safety and quality of care

By harnessing the collective strengths of multiple algorithms, Auto-DCRN sets a new benchmark for predictive analytics in healthcare, paving the way for widespread adoption and transformative impact on IoMT-enabled healthcare ecosystems.

Table 12. Comparative discussion.

Metric	SVM	FFNN	NB	DBN	Ensemble DBN (auto DCRN)
Accuracy	85%	87%	84%	89%	94%
Precision	83%	85%	82%	88%	92%
Recall	82%	86%	83%	87%	93%
F1-score	82.5%	85.5%	82.5%	87.5%	92.5%
Computational time (s)	5.2	4.8	4.6	6.0	5.5
Classification Loss	0.35	0.33	0.34	0.31	0.27

5. Conclusion

The experimental results show the efficiency under the framework of the ensemble DBN, which has been presented for the prediction of patient health status in the scope of the IoMT. Aiming for higher forecast accuracy and reliability, the framework has been developed to incorporate SVM, FFNN, NB, and DBN among several machine learning methods. The results show that the proposed DBN model shown improved performance than the individual models of SVM, FFNN, and NB based on its higher degrees of accuracy, precision, recall, and F-measure. The DBN model exhibited on average a 7% higher accuracy than SVM, a 5% than FFNN, and an 8% than NB. DBN model exhibited an interesting improvement in precision, recall, and F-measure with an average increase of 5%, 6%, and 7%, respectively. The real-time patient health status prediction in IoMT medical applications reveals possible use of the ensemble DBN structure.

Making precise and speedy selections by means of the possibilities of many algorithms helps to improve patient care and generates better results in the healthcare system. Future research can concentrate on enhancing the framework and investigating alternative machine learning approaches to drive the discipline of predictive healthcare.

Future work can focus on several enhancements to further improve the performance and applicability of the ensemble DBN framework. One potential direction is to incorporate additional machine learning algorithms into the ensemble to capture a wider range of patterns and improve robustness. Another enhancement could be the integration of advanced feature selection techniques to optimize the input features used by each algorithm, thereby improving the overall prediction accuracy. Additionally, exploring adaptive weighting mechanisms that dynamically adjust the weights of individual algorithms based on their real-time performance could lead to further improvements in prediction accuracy and reliability. Finally, extending the framework to handle a broader range of medical conditions and integrating it with more diverse IoMT devices could enhance its utility and impact in the healthcare domain.

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