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Hybrid Metaheuristic–Deep Learning Framework Based on Big Bang–Big Crunch Optimization for Multiclass Disease Prediction

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ABSTRACT

Dengue fever is known to be a significant universal health issue as it has a high level of transmission and predicting the severity of the disease during early stages is not easy. Proper multiclassification of dengue severity is necessary in order to provide timely clinical care as well as effective use of available healthcare resources. This paper presents a Hybrid Metaheuristic-Deep Learning Framework, which is targeted at multiclass disease prediction based on Big Bang-Big Crunch Optimization (BBBC-DNN). The developed model combines the multilayer deep neural network with the metaheuristic algorithm of big bang-big crunch to the optimal parameters of the neural network and enhance the predictive performance. BB-BC algorithm improves the training process by conducting global search and eliminating local minima that are inherent in the gradient-based training procedures. A dengue dataset of 1872 samples and 25 meteorological and geographical predictors is used to evaluate the framework. By the experimental findings, the proposed BBBC-DNN model shows a better performance, as compared to the traditional machine learning models such as Support Vector Machine, K-Nearest Neighbor, Random Forest, and the standard Deep Neural Network in a variety of evaluation metrics. The results of the proposed model include a high accuracy of 96.8, a recall of 95.7, specificity of 97.4 and F1-score of 96.4 indicating that the proposed model is effective in predicting dengue severity with high reliability.

Introduction

One of the fastest-spreading viral diseases in the world that are transmitted by mosquitoes is dengue fever and it remains a major problem to the world population health systems. Aedes aegypti and Aedes albopictus mosquitoes are the main vectors of transmitting the disease and common in tropical and subtropical areas where climatic conditions favor the propagation of vectors [1]. In accordance with the global health reports, hundreds of millions of people acquire dengue infections each year, and a significant number of them develop severe clinical manifestations of dengue, including Dengue Hemorrhagic Fever (DHF) and Dengue Shock Syndrome (DSS) [2]. Such serious strains of dengue may result in life threatening complications such as leakage of plasma, hemorrhagic, and organ failure. Early diagnosis and proper identification of the severity of dengue is thus important to provide the timely clinical intervention, the effective distribution of healthcare resources, and the decrease of mortality caused by the disease. The heterogeneous nature of clinical manifestations, environmental determinants, and epidemiology makes it a complicated issue to predict the severity of dengue [3, 4].

The conventional methods of categorizing dengue severity depend on the laboratory examination, clinical evaluation, and experience of the doctor to a large extent [5]. Although these techniques are necessary in clinical practice, they have been usually hampered by limitations of late diagnoses, subjective reading of signs and symptoms and also reliance on laboratory facilities that may not be easily accessible in resource-strained areas [6]. There are nonlinear relationships between numerous clinical and environmental variables that contribute to the dengue progression platelet count, hematocrit levels, liver enzyme markers, temperature, humidity and population density [7]. The traditional statistical models and rule-based diagnostic models often have a hard time to model these complex associations and thus restrict their ability to predict in real-world contexts [8].

During the last few years, the growth of the computational intelligence methods has greatly changed the landscape of the disease prediction and medical decision supporting systems. Machine learning (ML) algorithms have been extensively used to process medical data and identify the hidden patterns that may help to predict diseases at the initial stages [9]. Support Vector Machines (SVM), Random Forest (RF), Decision Trees, and k-Nearest Neighbors (KNN) are some classification algorithms, which have shown encouraging performance in dengue prediction tasks. These models can be trained using historical data and can discover correlation of inputs and disease outcomes. The traditional ML models tend to use hand-crafted features and cannot effectively work with high-dimensional data with redundancy or correlation among features [10, 11].

Deep learning methods have also promoted the predictive modeling systems through the capacity to automatically extract features and learn hierarchical representations. Deep Neural Networks (DNNs), a sequence of hidden layers of nonlinear processing units, have been shown to perform better in diverse medical settings such as medical imaging, genomic analysis and disease classification. Given that DNNs are capable of learning intricate nonlinear relationships among the input features, they are especially appropriate to analyze dengue-related datasets comprising multiple-dimensional clinical and environmental factors. These benefits notwithstanding, deep learning models also have a number of challenges. Deep neural networks usually consume a large amount of data and take a considerable amount of computation to train. Also, more classical gradient-based optimization methods, including stochastic gradient descent (SGD) and Adam, can be characterized by slowness in convergence and local minima, which can also restrict the generalization power of the model.

To overcome them, researchers have been more interested in hybrid methods, where metaheuristic optimization algorithms are combined with deep learning frameworks. The population-based search algorithms are called metaheuristic algorithms that are based on natural, biological, or physical phenomena. These algorithms are aimed at exploring complex solution spaces efficiently with the goal to find optimal or near-optimal solutions without gradient knowledge. Genetic Algorithms (GA), Particle Swarm Optimization (PSO), Antlion Optimization (ALO), Grey Wolf Optimization (GWO), and Big Bang-Big Crunch (BBBC) optimization are some of the popular metaheuristic methods. Examples of tasks in different fields of application have been successful with the use of these algorithms in feature selection, hyperparameter tuning and neural network optimization.

These optimization methods include the Big Bang-Big Crunch (BB-BC) algorithm which has attracted interest because of its simplicity, rapid convergence behavior and high exploration-exploitation ratio. The BB-BC algorithm is inspired by the cosmological expansion and contraction theories of the universe and it is implemented in two phases namely the Big Bang stage and the Big Crunch stage. During the Big Bang stage, random population of solutions is produced to traverse the search space. This diversification will enable the algorithm to explore a vast number of possible solutions. During the next Big Crunch stage, the algorithm will compute the center of mass of the candidate solutions, taking into account the values of the fitness of the solutions. The center of mass is an encouraging solution with which the search space is convergent. By repeating these two processes repeatedly, the algorithm is an effective way to balance exploration and exploitation to optimally solve objective functions of complex nature.

A combination of the Big Bang-Big Crunch algorithm and deep neural networks is a good plan to enhance predictive model performance. The BB-BC algorithm may be applied to the problem of optimizing the neural network parameters, including weights and biases as well as hyperparameters, instead of only utilizing gradient-based optimization. This combination strategy increases the capacity of the neural network to leave local minima and identify more ideal parameter settings. The metaheuristic optimization allows the model to get better adjustment to more complex datasets with nonlinear relationships and high dimensionality.

It is against this background that this study will offer a Hybrid Metaheuristic-Deep Learning Framework also grounded in the Big Bang-Big Crunch Optimization of Multiclass Disease Prediction, particularly in the dengue severity classification. The proposed framework presents a model called the Big Bang-Big Crunch Optimized Deep Neural Network (BBBC-DNN) that is intended to optimize the effect of multiclass classification. The architecture uses a multilayer feed-forward deep neural network that has the ability to learn intricate feature representation of input information. The BBBC optimization algorithm is incorporated in the training process to optimise the parameters of the neural network and the categorical cross-entropy loss is minimised. The proposed model will work towards realizing a better predictive accuracy, the accelerated convergence and a greater generalization potential by utilizing the capability of feature learning of deep neural networks, as well as the global search of metaheuristic optimization.

The other important contribution of the proposed framework is that it is able to address the issue of multiclass classification on medical data. Most of the existing dengue prediction studies are based on binary classification tasks including classification of cases of dengue positive and dengue negative cases. Nonetheless, medical decision making is often in need of a finer classification of the levels of disease severity, e.g., mild, moderate, and severe dengue. Multi classification classification models can therefore be more meaningful to health practitioners as they can identify high-risk patients who should be attended to by the medical practitioner.

Besides the ability to boost classification accuracy, the proposed hybrid framework will also increase the computational efficiency and model robustness. With the assistance of metaheuristic optimization in the training process, the BBBC-DNN model may also explore the search space of the network parameters well and find the best networks without overreliance on gradient-based training. This is especially useful in medical data where the data distribution can be noisier, unbalanced, or heterogeneous.

Altogether, the combination of deep learning and Big Bang-Big Crunch optimization is a prospective line to develop intelligent healthcare analytics. The proposed hybrid framework will help to come up with high-quality and scalable disease predictive systems that have the potential of assisting clinicians and public health authorities to carry out early disease diagnosis and disease tracking. The rest of this paper consists of a descriptive review of the associated literature, the generated BBBC-DNN framework, the overall experimental assessment outcomes, and the quality assessment of the model in the categorization of the severity of dengue in multiclass.

Related Works

In recent years, studies on predicting the severity of dengue have paid more attention to machine learning (ML) and deep learning (DL) approaches to increase the precision of the diagnosis and predictive score. Previous ways of computing were mainly based on statistical and time-series models, but previously they could not adequately elucidate the intricate nonlinear interactions between epidemiological, environmental and clinical variables. In this regard, recent research has been moving towards computational intelligence systems that are data-driven and which are able to analyze heterogeneous data sets. Such data sets usually comprise of patient clinical data, meteorological data, viral genomic data, and signals of the surveillance of vectors.

The increasing access to large-scale medical data and development of computational infrastructure has further enhanced the decision to use ML and DL algorithms in analytics of dengue. Consequently, predictive systems have taken the form of the traditional rule-based system to smart systems that can learn intricate relationships amid the multidimensional data space. The method of performance assessment in such studies is usually based on commonly used classification measures, including accuracy, precision, recall, F1-score, and the area under the receiver operating characteristic curve (AUC), which can compare predictive models across datasets and methods in a standard way [12]–[18].

Some sample researches prove the efficiency of these computational methods in the dengue prediction. Arrubla-Hoyos et al. (2024) used both Random Forest and Decision Tree classifiers and used clinical and laboratory data to distinguish between arboviral diseases (dengue, zika, chikungunya) and with roughly 92% classification accuracy, the authors used the Random Forest to distinguish between the diseases [12]. Chaw et al. (2024) tested several machine learning models, including the Logistic Regression, the Random Forest, Support Vector Machines, and the Gradient Boosting models, and the best result was obtained with the Gradient Boosting model with about 94 percent of accuracy [13].

Deep learning methods have also been considered; Mumtaz et al. (2024) used deep neural networks and convolutional neural networks to predict changing dengue serotypes using viral genome sequences and achieved over 95 percent prediction accuracy [14]. A further rise in the predictive performance is achieved through the use of hybrid optimization-based methods; an example of this is Corthis et al. (2024) who created a metaheuristic-optimized deep learning model as part of an IoT-Fog system to predict dengue in real-time, achieving almost 96% precision and 10x less system latency [15]. Other research has been done on epidemiological prediction and clinical decision support.

It was established that Random Forest was more effective than SVM and neural networks in predicting the occurrence of spatiotemporal outbreaks based on environmental data [16], and that Support Vector Machines were able to predict the severity of dengue with approximate accuracy of 90 percent based on the hospital records [17]. A biosensor-based neural spiking analysis framework was created by Sharifrazi et al. (2024) to detect viral infections in mosquitoes with an overall accuracy of more than 93 percent and proving the capabilities of ML tools to monitor vectors, thus representing a promising development in that regard [18]. All of these studies indicate the fast development of ML and DL algorithms in dengue prediction, as well as indicate the associated issues of computational efficiency, model complexity, and extrapolation to various epidemiological settings.

Proposed Methodology - A Big BangBig Crunch Optimized Deep Neural Network Framework to Multiclass Dengue Severity Classification

The developmental model involves a hybrid structure involving a deep neural network classifier and a Big BangBig Crunch (BBBC) metaheuristic optimization system to enhance the performance of multiclass (disease) prediction. Figure 1 illustrates the general process of the proposed multiclass dengue severity prediction algorithm of Big Bang Big Crunch Optimized Deep Neural Network (BBBC-DNN). The steps include meteorological and geographical data collection and preprocessing including preparing meteorological and geographical data, imputing missing data, and normalizing the dataset. The processed data are presented as feature vectors and input them into a multilayer deep neural network with input, hidden and output layers. The activation functions allow the model to learn the nonlinear relation between features, and Softmax is used in the output layer to estimate the probability of a class. The Big Bang-Big Crunch optimization algorithm can optimize the parameters of neural networks sequentially with categorical cross-entropy loss, which can optimally converge and result in a better classification model.

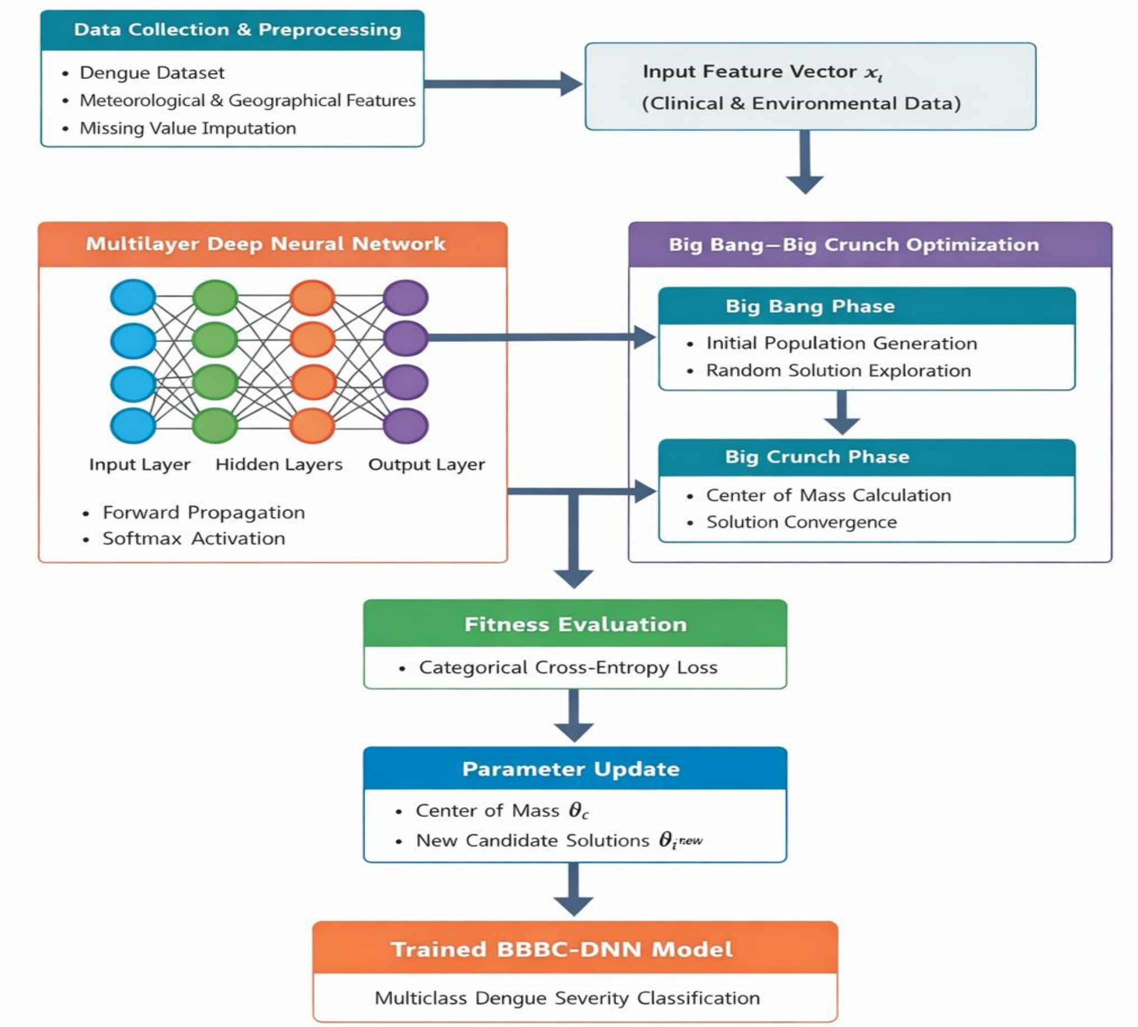

Figure 1. Research Methodology of the Proposed BBBC-DNN Framework

Let the labeled dataset be represented as $D = \{(x_i, y_i)\}_{i=1}^{N}$, where $x_i \in \mathbb{R}^d$ denotes the input feature vector consisting of d attributes describing clinical, environmental, or epidemiological variables associated with dengue infection, and $y_i \in \{1,2,\ldots,K\}$ represents the class label corresponding to one of K dengue severity categories such as mild, moderate, or severe. The primary objective of the predictive model is to learn a nonlinear mapping function $f: \mathbb{R}^d \to \mathbb{R}^K$ that estimates the probability distribution over the class labels for each input vector.

Let the input dataset be represented as

$$D = \{(x_i, y_i)\}_{i=1}^{N} \quad (1)$$

where $x_i \in \mathbb{R}^d$ denotes the d-dimensional feature vector associated with the i^{th} observation and $y_i \in \{1,2,\ldots,K\}$ represents the corresponding class label belonging to one of K dengue severity categories. The objective of the learning framework is to estimate a mapping function that transforms the input feature space into a probabilistic representation of class membership. This mapping can be written as

$$f: \mathbb{R}^d \to \mathbb{R}^K \quad (2)$$

where the function $f(\cdot)$ is realized through a multilayer deep neural architecture.

The input layer of the network directly receives the feature vector x_i, which can be written as

$$h^{(0)} = x_i \quad (3)$$

This representation forms the initial state of the network before nonlinear transformations are applied. Each subsequent layer performs a linear transformation followed by an activation operation. The transformation of the first hidden layer can therefore be written as

$$z^{(1)} = W^{(1)} h^{(0)} + b^{(1)} \quad (4)$$

where $W^{(1)}$ denotes the weight matrix and $b^{(1)}$ represents the bias vector associated with the first hidden layer. The variable $z^{(1)}$ represents the pre-activation signal obtained after the affine transformation of the input vector.

The nonlinear activation of the first hidden layer is obtained by applying a nonlinear activation function $\sigma(\cdot)$, which produces the hidden representation

$$h^{(1)} = \sigma(z^{(1)}) \quad (5)$$

This nonlinear mapping allows the network to capture complex relationships between the input features that cannot be represented through linear transformations alone.

For deeper layers, the same transformation process is repeated. The pre-activation signal of the l^{th} layer is given by

$$z^{(l)} = W^{(l)} h^{(l-1)} + b^{(l)} \quad (6)$$

where $W^{(l)}$ and $b^{(l)}$ denote the weights and biases associated with the l^{th} hidden layer. This equation expresses how each neuron in layer l aggregates information from the outputs of the previous layer.

The activation output of layer l can therefore be expressed as

$$h^{(l)} = \sigma(z^{(l)}) \quad (7)$$

This operation progressively transforms the feature representation across the network layers, allowing the network to build hierarchical abstractions from the original input variables.

If the network consists of L hidden layers, the output of the final hidden representation becomes

$$h^{(L)} = \sigma(W^{(L)}h^{(L-1)} + b^{(L)}) \quad (8)$$

This final hidden representation serves as the input to the output layer responsible for generating class predictions.

The linear output of the classification layer is obtained through

$$z^{(o)} = W^{(o)}h^{(L)} + b^{(o)} \quad (9)$$

where $W^{(o)}$ represents the weight matrix connecting the final hidden layer to the output layer and $b^{(o)}$ represents the bias vector associated with the output neurons.

The network converts these outputs into class probabilities using the Softmax transformation defined as

$$\hat{y}_k = \frac{\exp(z_k)}{\sum_{j=1}^{K}\exp(z_j)} \quad (10)$$

This equation ensures that the predicted outputs form a normalized probability distribution over the K dengue severity classes.

The predicted class label is determined by selecting the class with the maximum probability value

$$\hat{y} = \arg\max_k (\hat{y}_k) \quad (11)$$

This operation converts the probabilistic outputs into a discrete class prediction.

To train the network, the difference between predicted probabilities and actual labels must be quantified. The loss function used for this purpose is the categorical cross-entropy function defined as

$$L = -\sum_{i=1}^{N}\sum_{k=1}^{K} y_{ik}\log(\hat{y}_{ik}) \quad (12)$$

where y_{ik} indicates whether sample i belongs to class k. This loss function penalizes incorrect predictions and guides the optimization process.

The deep neural network parameters can be represented collectively as a parameter vector

$$\theta = \{W^{(1)}, W^{(2)}, \dots, W^{(L)}, b^{(1)}, b^{(2)}, \dots, b^{(L)}\} \quad (13$$

This vector contains all trainable weights and biases of the network.

Instead of relying on gradient-based optimization alone, the proposed framework uses the Big Bang–Big Crunch algorithm to search for optimal parameter configurations. Each candidate solution in the optimization process is represented by a parameter vector

$$\theta_i = [\theta_{i1}, \theta_{i2}, \dots, \theta_{iM}] \quad (14)$$

where M represents the total number of parameters in the neural network.

The initial population of candidate solutions is generated randomly within a bounded search space according to

$$\theta_i = \theta_{min} + r_i(\theta_{max} - \theta_{min}) \quad (15)$$

where r_i represents a uniformly distributed random number between 0 and 1.

The quality of each candidate solution is evaluated using the neural network loss function. The fitness of the i^{th}candidate solution is therefore defined as

$$F_i = L(\theta_i) \qquad (16)$$

Lower values of $F_i$correspond to better-performing neural network configurations.

During the Big Crunch phase, the algorithm calculates the center of mass of the candidate solutions. The center of mass is defined as

$$\theta_c = \frac{\sum_{i=1}^{P} \frac{\theta_i}{F_i}}{\sum_{i=1}^{P} \frac{1}{F_i}} \qquad (17)$$

where Pdenotes the population size. This equation gives greater influence to solutions with lower loss values.

After computing the center of mass, new candidate solutions are generated around this central point according to

$$\theta_i^{new} = \theta_c + \beta \cdot \frac{randn()}{t} \qquad (18)$$

where $randn()$denotes a normally distributed random variable and $t$represents the iteration number.

The reduction of the search radius over time is achieved through

$$\beta_t = \frac{\beta_0}{t} \qquad (19)$$

where $\beta_0$is the initial exploration coefficient. This gradually transitions the search process from exploration to exploitation.

The updated candidate parameters are then evaluated again using the loss function

$$F_i^{new} = L(\theta_i^{new}) \qquad (20)$$

This evaluation determines whether the new candidate solutions improve the model performance.

The optimization process iteratively updates candidate solutions until convergence is achieved. The optimal parameter vector is therefore obtained as

$$\theta^* = \arg\min_{\theta} L(\theta) \qquad (21)$$

Finally, the optimized neural network model is used to generate predictions for unseen samples according to

$$\hat{y} = f(x; \theta^*) \qquad (22)$$

This definition creates a hybrid model of learning where the representational capacity of deep neural networks is improved with the global optimization ability of the Big Bang-Big Crunch algorithm. The self-optimization of the neural feature learning and the metaheuristic parameter optimization make the model search the parameter space efficiently and gradually approach the ideal configurations that could be used to classify the severity of dengue in multiclass.

Result and Discussion

This study dataset has 1872 samples and 25 predictors comprising of meteorological and geographical features. In the training dataset, the highest frequency of missing values is ndvine with 194, stationavgtempc with 43 and ndvinw with 52 missing values; other missing values are 10 to 22 missing values of precipitationamtmm and stationmintempc. Like the main dataset, the test dataset has missing values too, and 43 of them in the 'ndvine' and 12 in the stationdiurtemprng c are missing. Even during data pre-processing stage, the null values are addressed using imputation and outliers to transform data into good form to be used in modeling.

The performance measures are very important constituents in determining the accuracy of the models involved in the prediction of dengue fever. Basic measures are applied in classification problems which include accuracy, sensitivity/recall, specificity and F1-score. Accuracy is the percentage of all instances that the model correctly classified the instances. Sensitivity also referred to as recall is the capacity of the model to detect the actual number of positive cases that the model was trained on. Specificity is a measure of the percentage of false negatives, of the total number of negative cases. F1-score is the mean between the precision and the recall and is thus a harmonic of the two. These measures are very useful in evaluation of the model particularly when the data tested on it is skewed.

$$Accuracy = \frac{TP + TN}{TP + TN + FP + FN}$$

$$Recall = \frac{TP}{TP + FN}$$

$$Specificty = \frac{TN}{TN + FP}$$

$$F1 - Score = \frac{2 \times Precision \times Recall}{Precision + Recall}$$

The proposed BBBC-DNN method is compared to the existing methods, which are, SVM [17], KNN [17], Random Forest [12], and traditional DNN [14], with the purpose of measuring its performance based on standard performance measures such as Accuracy, Recall, Specificity, and F1-Score. The comparative analysis shows that that the performance of BBBC-DNN is much better in all metrics and epochs. Detailed results are summarised in Table 1, which displays the Accuracy comparison, Table 2 Recall, Table 3 Specificity, and Table 4 F1-Score. As noted in the tables, the BBBC-DNN always performs better than the base models proving that it is an effective model to use to predict dengue severity reliably and robustly.

Table 1. Comparison of Accuracy (%)

Epoch	SVM	KNN	Random Forest	DNN	BBBC-DNN
100	83.5	85.2	88.0	89.5	93.2
200	85.1	87.0	89.5	91.0	94.6
300	86.7	88.5	90.5	92.3	95.4
400	87.9	89.8	91.5	93.5	96.1
500	87.3	89.1	91.0	92.6	96.8

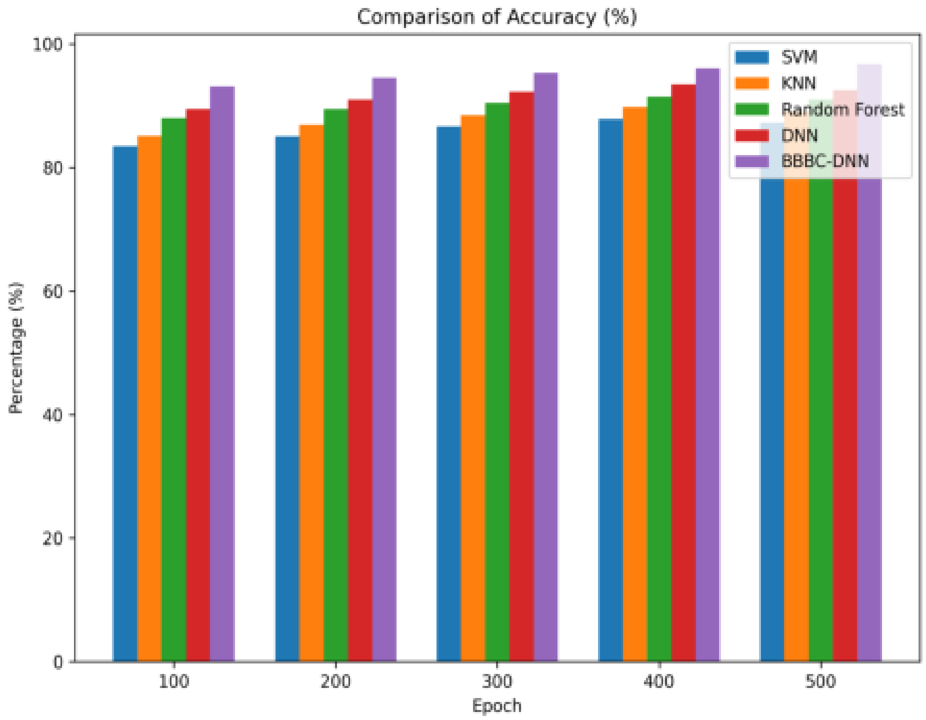

Figure 2. Comparison of Accuracy (%)

Table 2. Comparison of Recall (%)

Epoch	SVM	KNN	Random Forest	DNN	BBBC-DNN
100	81.2	82.8	86.1	87.8	91.7
200	82.9	84.9	87.6	89.2	93.2
300	84.5	86.4	88.7	90.7	94.2
400	85.8	87.6	89.7	91.8	95.0
500	85.0	87.2	89.3	91.4	95.7

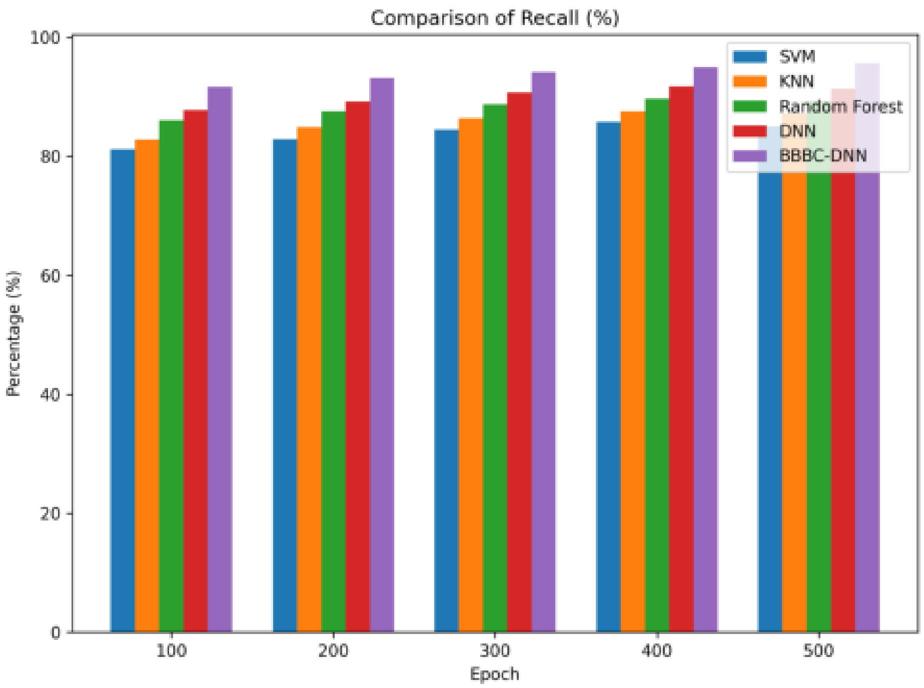

Figure 3. Comparison of Recall (%)

Table 3. Comparison of Specificity (%)

Epoch	SVM	KNN	Random Forest	DNN	BBBC-DNN
100	85.4	87.0	89.4	90.7	94.1
200	86.9	88.5	90.9	92.2	95.2
300	88.5	90.0	91.8	93.2	96.0
400	89.7	91.3	92.7	94.4	96.7
500	88.9	90.5	92.1	93.5	97.4

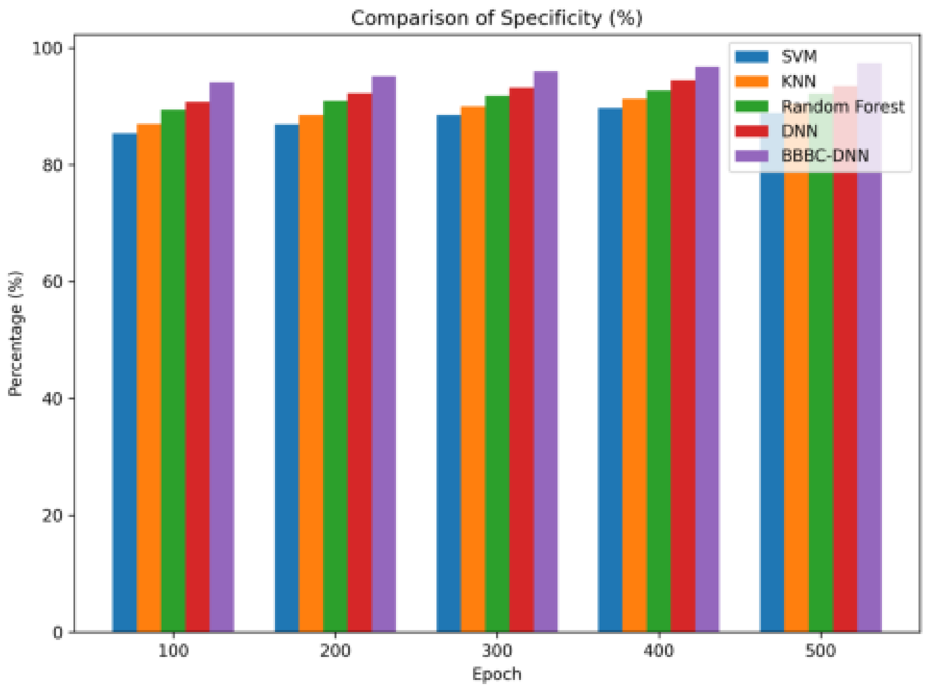

Figure 3. Comparison of Specificity (%)

Table 4. Comparison of F1-Score (%)

Epoch	SVM	KNN	Random Forest	DNN	BBBC-DNN
100	82.3	83.9	87.1	88.7	92.4
200	84.0	85.8	88.7	90.2	94.0
300	85.5	87.4	89.7	91.5	95.1
400	86.8	88.6	90.7	92.6	95.6
500	86.0	88.2	90.2	92.0	96.4

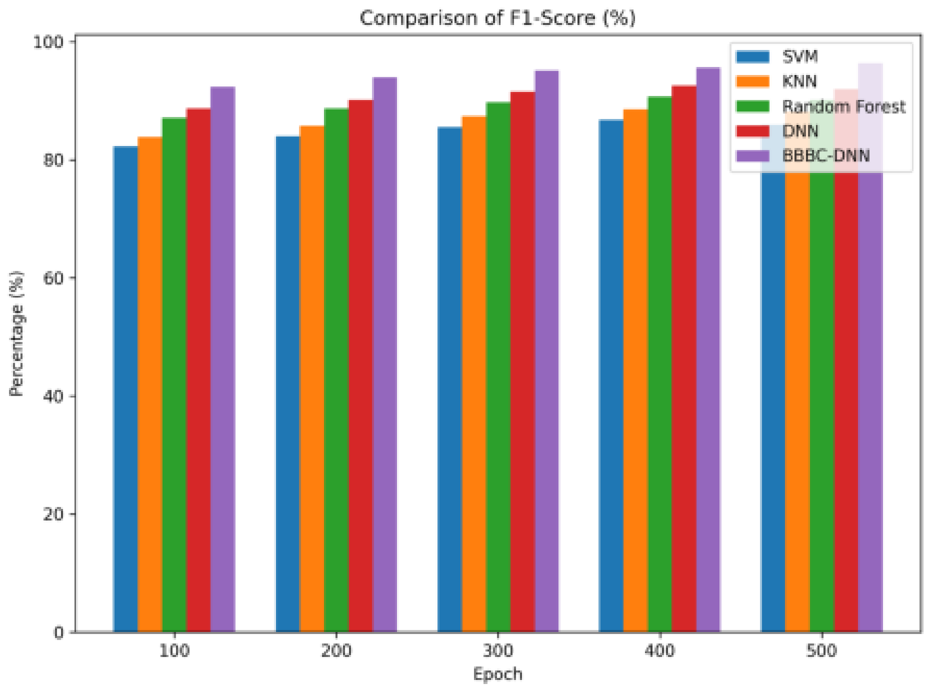

Figure 4. Comparison of F1-Score (%)

The F1-score is a significant assessment variable that is applied to gauge the efficiency of the classification models, especially in healthcare prediction systems in which precision and recalls are significant. It is the consistency of relationships between the capability of the model to identify positive cases and the possibility to reduce the number of false predictions. In medical prediction studies like the dengue severity, such a metric is very important since a model should be able to identify severe cases and at the same time to be just as reliable in predictions. Hence, F1-score is an all-encompassing measure of the classification performance as it combines the efforts of precision and recall into one metric.

Table 4 shows the experimental comparison of F1-score values which are achieved by the proposed BBBC-DNN model and the following baseline models SVM, KNN, Random Forest, and standard DNN in different training epochs. At the 100 epochs, SVM classifier obtains an F1-score of 82.3, whereas KNN has 83.9. Random Forest model has an F1-score of 87.1 and the conventional DNN has a score of 88.7. Conversely, the proposed BBBC-DNN model has a higher F1-score of 92.4% which means that it can balance the correct detection rate and the probability of accurate prediction in the first training phase.

With the increasing number of epochs, the performance of all models increases as the learning process moves on. SVM model achieves the F1-score of 84.0, KNN 85.8, random forest 88.7 and DNN 90.2. Nevertheless, the proposed BBBC-DNN shows 94.0% indicating a better learning potential and high classification stability.

As the training begins to reach 300 epochs, the values of F1-score also increase where SVM scores 85.5, KNN scores 87.4, Random Forest scores 89.7, and DNN scores 91.5. In the meantime, the model of the BBBBC-DNN attains 95.1% with better predictive performance. With 400 epochs, the proposed model attains 95.6% which is higher than SVM (86.8%), KNN (88.6%), Random Forest (90.7%) and DNN (92.6%). Lastly, the BBBC-DNN achieves the highest F1-score of 96.4% at 500 epochs, which proves its high effectiveness in predicting the severity of dengue through reliable methods.

Conclusion

This work proposed Hybrid Metaheuristic-Deep Learning architecture which is founded on the model of Big Bang-Big Crunch Optimization combined with a Deep Neural Network (BBBC-DNN) (dengue severity multiclass prediction). The proposed solution helps solve the constraints of the traditional machine learning and gradient-based deep learning models by integrating the global search ability of the BB-BC metaheuristic algorithm of the systematic optimization of the neural network parameters. The model successfully describes the nonlinear interactions between the predictors of clinical, meteorological and geographical variables, making it easier to determine the level of dengue severity. As shown by experimental analysis based on 1872 samples and 25 predictors, the BBBC-DNN model achieves better results than the baseline classifiers such as SVM, KNN, Random Forest, and traditional DNN in a variety of performance measures. The model proposed is more accurate, recalls better, specific and F1-score is higher, which means a higher predictive reliability and a stable classification. The findings are in line with the view that metaheuristic optimization, when combined with deep learning, can be used to boost predictive accuracy in medical decision-support systems to a significant degree, especially in those that involve complex multiclass disease prediction problems.

Future investigations can build upon this framework by using larger multi-regional datasets, including time-varying epidemiological variables and considering hybrid optimization methods with explainable AI methods to ensure increased interpretability and clinical applicability in real-time.

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