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Pareto-Optimized Deep Neural Network Framework for Multi-Objective Dengue Severity Classification

Mrs. G. Ruba[1], Dr. S. Rizwana[2]

[1]Research Scholar, Department of Computer Science, Erode Arts and Science College, Erode, Tamilnadu, India. Email: ruba.mca@gmail.com

[2]Research Supervisor, Assistant Professor and Head, Department of Computer Science (SF), Erode Arts and Science College, Erode, Tamilnadu, India. Email: rizureesh@gmail.com

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ABSTRACT

Early and accurate prediction of dengue severity is critical for timely clinical intervention and reducing disease-related mortality. Traditional machine learning methods often struggle to simultaneously achieve high predictive accuracy, computational efficiency, and model scalability. To overcome these limitations, we propose a Pareto-Optimized Deep Neural Network (PO-DNN) framework that employs multi-objective optimization to minimize validation loss, computational cost, and model complexity. The framework generates a set of Pareto-optimal architectures, enabling a trade-off between predictive performance and operational efficiency. Using a preprocessed clinical dataset with 25 selected features, the PO-DNN was trained and evaluated via 10-fold cross-validation. Experimental results show that PO-DNN attains 96.8% accuracy, 95.7% recall, 97.1% precision, 96.4% F1-score, and an AUC of 0.975, outperforming baseline classifiers including SVM (87.3%), KNN (89.1%), Random Forest (91.0%), and conventional DNN (92.6%). Additionally, model optimization reduced average inference time to 1.9 ms per instance and compressed model size by 32%, demonstrating suitability for real-time deployment. These results highlight PO-DNN as a robust, efficient, and clinically applicable tool for dengue severity prediction.

Introduction

Dengue fever, a mosquito-borne viral infection transmitted primarily by Aedes aegypti, has emerged as one of the most significant public health concerns across tropical and subtropical regions [1]. With over 390 million cases reported annually worldwide, dengue poses a severe burden on healthcare systems, particularly in developing countries where diagnostic and treatment resources are limited. While the majority of dengue cases are mild and self-limiting, a substantial proportion progress into severe forms such as Dengue Hemorrhagic Fever (DHF) and Dengue

Shock Syndrome (DSS) [2, 3]. These conditions are often fatal if not detected and managed at an early stage. Therefore, accurate classification of dengue severity is critical to reduce mortality, allocate resources effectively, and enhance patient outcomes [4, 5].

Traditional dengue diagnosis relies on clinical symptoms, serological tests, and laboratory markers [6]. However, these methods face inherent limitations including delayed results, subjective interpretation of symptoms, and restricted applicability in resource-constrained settings. To overcome these challenges, computational intelligence and machine learning techniques have been increasingly applied in dengue prediction and classification [7]. Early models such as decision trees, support vector machines (SVM), and k-nearest neighbors (KNN) demonstrated promising results but were limited by their inability to capture high-dimensional feature interactions and temporal dependencies. Deep learning approaches, particularly deep neural networks (DNNs), have recently shown superior performance in medical data classification owing to their capacity for hierarchical feature representation and automated feature extraction[8].

Despite their advantages, conventional DNNs present trade-offs between predictive accuracy, computational efficiency, and model complexity. For real-world healthcare applications, models must not only provide high accuracy but also be computationally efficient for deployment on constrained devices, scalable to large patient datasets, and interpretable to gain clinicians' trust [9]. Achieving such a balance requires advanced optimization strategies that go beyond single-objective tuning. This motivates the integration of multi-objective optimization frameworks, particularly Pareto-based strategies, with DNN architectures for dengue severity classification.

The need for this study arises from three key perspectives. First, dengue severity classification is inherently multi-dimensional, where predictive accuracy cannot be the sole determinant of model performance [10]. Computational complexity, inference time, and memory footprint directly impact the feasibility of deploying models in real-time clinical settings, particularly in regions with limited resources. Second, the presence of redundant or highly correlated features in dengue datasets necessitates feature selection strategies that can improve both

generalization and interpretability. Third, there is a critical gap in existing literature where most approaches emphasize accuracy maximization without systematically addressing the trade-offs with efficiency and scalability [11].

To address these challenges, this work introduces a Pareto-Optimized Deep Neural Network (PO-DNN) framework for dengue severity classification. The primary objective of the proposed methodology is to construct a classification model that balances predictive accuracy with computational efficiency and model complexity. Pareto-based multi-objective optimization is employed to generate a set of non-dominated solutions, allowing simultaneous minimization of classification error, parameter count, and inference latency. The final selection from the Pareto front can be tailored to specific deployment requirements, such as real-time diagnostic assistance in clinics or large-scale predictive analytics in public health surveillance systems.

The novelty of this approach lies in its integration of correlation-based feature selection, deep neural network modeling, and Pareto-based evolutionary optimization. The feature selection step ensures that the most informative attributes, such as platelet count, hematocrit levels, liver enzyme markers, and clinical symptoms, are prioritized while redundant variables are suppressed. The deep neural network leverages these optimized features to construct hierarchical abstractions that enhance classification fidelity. The Pareto optimization layer then navigates the trade-off space, yielding solutions that maximize accuracy while reducing computational costs.

The objectives of this study can be outlined as follows. First, to design a robust deep neural network architecture capable of accurately classifying dengue severity across multiple categories. Second, to integrate a Pareto-based multi-objective optimization framework that balances competing goals of accuracy, efficiency, and scalability. Third, to evaluate the proposed PO-DNN framework using cross-validation and compare it against baseline machine learning models including SVM, KNN, and conventional DNNs. Fourth, to validate the generalizability and robustness of the model through standard performance metrics such as accuracy, recall, precision, F1-score, AUC, and inference time. Finally, to demonstrate the applicability of the proposed framework in real-world healthcare contexts,

emphasizing its potential for clinical decision support and public health monitoring.

This research contributes to the growing body of research on intelligent healthcare systems by introducing a multi-objective optimized deep learning model for dengue severity classification. By addressing the dual goals of predictive performance and computational feasibility, the proposed PO-DNN framework provides a comprehensive solution to the challenges faced in deploying AI-based medical diagnostic tools. The following sections of this article present the detailed methodology, experimental evaluation, results, and discussion that collectively substantiate the effectiveness of the proposed approach.

Related Works

To understand the current research landscape in dengue severity prediction, it is essential to analyze the methodological trends adopted in recent literature. A substantial body of work has focused on the application of machine learning (ML) and deep learning (DL) paradigms, leveraging diverse datasets, heterogeneous objectives, and distinct evaluation protocols. These studies demonstrate the evolution of dengue analytics from conventional statistical modeling toward more data-driven and intelligent computational strategies.

The surveyed works highlight three recurring themes: (i) the choice of algorithmic frameworks ranging from traditional classifiers such as Decision Trees and Random Forests to advanced DL architectures like CNNs and hybrid metaheuristic–DL models; (ii) the data modality and context, which spans patient clinical records, environmental determinants, genomic sequences, and vector signal data; and (iii) the evaluation criteria, where performance is predominantly quantified using accuracy, precision, recall, F1-score, and area under the curve (AUC).

Table 1 provides a comprehensive synthesis of representative studies from 2024. It systematically captures the methodological foundation, dataset characteristics, and numerical performance outcomes of these works. This structured overview not only underscores the achievements of existing ML/DL-based frameworks, with accuracies frequently reported in the 90–96% range, but also reveals existing gaps related to computational efficiency, model complexity, and generalizability.

Table 1. Comprehensive Analysis of Dengue Classification

Author(s) & Year	Algorithm(s) Used	Objective	Dataset / Input Data	Key Findings
Arrubla-Hoyos, W., Gómez, J. G., & De-La-Hoz-Franco, E. (2024) [12]	Random Forest (RF), Decision Tree (DT)	Classify arboviral diseases (dengue, zika, chikungunya)	Clinical and laboratory datasets from arboviral patients	RF achieved higher classification accuracy (~91%) compared to DT, highlighting effectiveness of ensemble models for multi-class differentiation.
Chaw, J. K., et al. (2024) [13]	Logistic Regression (LR), Random Forest (RF), SVM, Gradient Boosting	Predict risk of shock in dengue patients	Retrospective dengue clinical dataset with clinical markers and vitals	Gradient boosting achieved highest predictive accuracy (~94%), demonstrating value of ML in early detection of shock risk.
Mumtaz, Z., et al. (2024) [14]	Deep Neural Networks (DNN), CNN models	Predict evolving dengue serotypes	Viral genome sequence datasets	Proposed deep learning approach achieved accuracy above 95%, enabling serotype evolution prediction for genomic surveillance.
Corthis, P. B., et al. (2024) [15]	Hybrid Metaheuristic + Deep Learning	Real-time dengue prediction in IoT-Fog architecture	Simulated IoT-Fog system data with dengue indicators	Hybrid optimization enhanced DNN performance, improving accuracy to ~96% with reduced latency in edge environments.

Mazhar, B., et al. (2024) [16]	Random Forest, SVM, Neural Networks	Predict outbreak risk and spatiotemporal dengue spread	Epidemiological and environmental datasets	Random Forest model showed superior outbreak prediction (~92%) compared to SVM and NN, supporting public health surveillance.
Banu, J. F., et al. (2024) [17]	SVM, KNN, Decision Tree	Classify dengue severity and recovery prediction	Clinical datasets from hospital records	SVM-based classification framework achieved ~90% accuracy, demonstrating potential for early recovery prediction.
Sharifrazi, D., et al. (2024) [18]	Neural Spiking Analysis + ML classifiers	Detect viral infections (dengue/zika) in mosquito populations	Biosensor-based mosquito signal data	Achieved >93% accuracy, demonstrating ML utility in vector-based viral surveillance.

Despite the considerable progress achieved by existing machine learning and deep learning approaches in dengue classification, several critical research gaps remain evident. Most prior studies have emphasized single-objective optimization, primarily targeting accuracy, while neglecting competing constraints such as computational efficiency, inference latency, and architectural complexity—factors crucial for real-world deployment in healthcare systems. Furthermore, feature redundancy and the absence of systematic feature selection mechanisms often lead to over-parameterized models that risk overfitting and reduced interpretability. Another limitation is the lack of generalizability, since many works are validated on isolated datasets without rigorous cross-validation across heterogeneous patient populations, leading to models that may fail under diverse epidemiological conditions. Additionally, there is limited adoption of multi-objective optimization frameworks capable of balancing predictive performance with operational feasibility in resource-constrained clinical or IoT-Fog environments.

The proposed Pareto-Optimized Deep Neural Network (PO-DNN) directly addresses these gaps by incorporating a multi-objective optimization paradigm that simultaneously maximizes classification accuracy (consistently above 95%) while minimizing computational cost and model complexity. By employing Pareto-based optimization, the framework generates a set of non-dominated solutions, enabling stakeholders to select models tailored to their resource and accuracy requirements. The integration of feature selection enhances robustness and interpretability, while extensive cross-validation ensures strong generalization capability. Collectively, PO-DNN transforms dengue severity classification into a more practical, scalable, and deployment-ready solution compared to prior single-objective approaches.

Proposed Methodology - Pareto-Optimized Deep Neural Network (PO-DNN) framework for dengue severity classification

Let the labeled dataset after feature selection be $\mathcal{D} = (x_i, y_i)_{i=1}^{N}$, where $x_i \in \mathbb{R}^d$ is the selected feature vector and $y_i \in 1, \dots, K$ is the dengue-severity label (e.g. mild, severe). A deep neural network is a parametric mapping $f(.; w, h)!: \mathbb{R}^d \to \mathbb{R}^K$ where $w \in \mathbb{R}^m$ denotes the network weights (all trainable parameters) and h denotes architecture/hyperparameter descriptors (layer widths, depths, convolutional kernel sizes, activation types, pruning rates, quantization bits, etc.). The predictive probabilities are obtained via the softmax $\hat{p}(y, |, x; w, h) = softmax(f(x; w, h))$. The training loss on a mini-batch or on the entire training split is the standard categorical cross-entropy with weight decay (optional)

$$\mathcal{L}_{train}(w; h) = -\frac{1}{N_{tr}} \sum_{(x,y)\in\mathcal{D}_{tr}} \log \hat{p}(y, |, x; w, h) + \lambda ||w||_2^2$$

$$\mathcal{L}_{val}(w; h) = -\frac{1}{N_{val}} \sum_{(x,y)\in\mathcal{D}_{val}} \log \hat{p}(y, |, x; w, h)$$

$$Err_{val}(w; h) - \frac{1}{N_{val}} \sum_{(x,y)\in\mathcal{D}_{val}} 1\{\arg max_k \, \hat{p}(k, |, x; w, h) \neq y\}$$

Because architecture h and weights w interact, define the bilevel formulation: for a given architecture h the inner problem obtains optimized weights

$$w*(h) = \arg min_w \mathcal{L}_{train}(w; h),$$

Define the vector of objective functions to be minimized as

$$F(h) = (f_1(h), f_2(h), f_3(h))$$

$$f_1(h) = \mathcal{L}_{val}(w^*(h); h) \quad (validation\ loss\backslash proxy\ for\ classification\ error)$$

f_2(h) ;=; \Phi_{\text{comp}}(h)\quad\text{(computational cost, e.g. FLOPs or inference time)},

$$f_3(h) = \Phi_{size}(h) = \sum_{l \in \mathcal{L}(h)} n_l^{in}(h) n_l^{out}(h) + biases,$$

$$FLOP_{s\ell} \approx 2.k^2.C_{in}.C_{ou}.S_\ell$$

The Pareto multi-objective optimization problem becomes

$min_{h \in k} F(h)$ subject to $w^*(h) = \arg min_w \mathcal{L}_{train}(w; h)$

Pareto-based optimization may be performed using evolutionary multi-objective algorithms (EMOAs) such as NSGA-II. NSGA-II maintains a population p of candidate architectures and operates with nondominated sorting and crowding-distance selection. Nondominated sorting partitions p into fronts F_1, F_2 ... where F_1 is the set of nondominated individuals. For two candidates h^a, h^b, say h^a dominates h^b ($h^a \prec h^b$) iff $\forall i; f_i(h^a) \leq f_i(h^b)$ and $\exists j;, f_i(h^a) < f_i(h^b)$. Crowding distance for an individual in front F is computed per-objective by sorting and using normalized neighbor spacing; for objective i the contribution is

$$d_i(h) = \frac{f_i(h_+) - f_i(h_-)}{f_i^{max} - f_i^{min}},$$

Because the inner optimization $w^*(h)$ is costly, one uses approximations: (i) weight inheritance / network morphism so child networks start from parents' weights; (ii) low-fidelity evaluations (fewer epochs) during early EMOA generations; (iii) surrogate models $\mathcal{H} \to \mathbb{R}^3$trained to predict objectives, refined iteratively. Mathematically, surrogate-assisted MOO minimizes $\hat{F}(h)$ where $\hat{F}$ approximates F and is updated with true evaluations.

An alternative to EMOA is scalarization. For a fixed weight vector $\alpha = (\alpha_1, \alpha_2, \alpha_3)$ with $\alpha_i \geq 0, \sum_i \alpha_i = 1$ the weighted-sum problem

$$min_{h\in\mathcal{H}} \quad g_\alpha(h) = \sum_{i=1}^{3} \alpha_i \tilde{f_i}(h)$$

$$\sum_{i=1}^{3} \lambda_i \nabla_h f_i(h^*) = 0$$

To quantify multi-objective progress use metrics such as the hypervolume indicator. Given a reference point $r \in \mathbb{R}^3$ dominated by all feasible points, the hypervolume of a Pareto set S is

$$HV(S) = Vol\left(\bigcup_{s\in S} [s, r]\right),$$

Practically, one solves the bilevel MOO approximately via the following iterative procedure expressed succinctly as algorithmic pseudocode (no bullet headings): initialize a population p_o of architectures; for generation $t = 0, \ldots, T\_1$ evaluate each $h \in p_t$ by training weights w for E_{eval} epochs to obtain $w^*(h)$ and compute $F(h)$; perform nondominated sorting and compute crowding distances; select parents by tournament (compare rank then crowding); generate offspring $\mathcal{O}_t$ via crossover and mutation in the encoding of h; construct $\mathcal{Q}_t = \mathcal{P}_t \cup \mathcal{Q}_t$, sort $\mathcal{Q}_t$ into fronts and fill next population by adding fronts in order until capacity and resolve last front by crowding distance; update surrogate models if used; end for. The final archive of nondominated architectures approximates the Pareto front.

Cross-validation integrates naturally: for each candidate h the primary objective can be the average validation loss across k-folds:

$$f_1(h) = \frac{1}{k}\sum_{j=1}^{k} \mathcal{L}_{val}^{(j)}\big(w^{*(j)}(h);(h)\big),$$

Because classification accuracy is often non-differentiable w.r.t. architecture encoding and multi-objective search is stochastic, report the final chosen model(s) by their operating point on the Pareto front: a decision-maker selects an architecture h^* that satisfies the institutional constraint (e.g.,$\Phi_{comp}(h^*) \le C_{max}$) while achieving acceptable $f_1(h^*)$. If an operational scalar objective is required, one may pick h^* by maximizing a utility function $U(h) = \omega_1\big(1 - Err(h)\big) - \omega_2\Phi_{comp}(h) - \omega_3\Phi_{size}(h)$ with weights chosen from stakeholder requirements; but all such scalarizations should be reported alongside the full Pareto set to make trade-offs explicit.

Finally, to ensure reproducibility and deployment readiness, document the following mathematically: the exact architecture encoding , the inner optimizer (SGD/Adam) and its learning-rate schedule, number of inner epochs used during EMOA evaluations, any surrogate model formulation $\hat{F}$ and its update rule, and the reference point r used to compute hypervolume. Evaluate the selected model(s) using k-fold cross-validation to compute mean and variance of AUC, sensitivity, specificity, precision, F1-score, and inference-time quantiles; report the Pareto front and hypervolume progression across generations as quantitative evidence of convergence.

This formulation yields a set of Pareto-optimal DNN architectures $h^{(p)}$ with corresponding trained weights $w^*(h^{(p)})$. Each point on the front represents an explicit trade-off between classification fidelity f_1 and operational efficiency (f_2, f_3); the final selection is then the architecture that satisfies clinical deployment constraints while maximizing predictive reliability as demonstrated by cross-validated metrics. The proposed approach is given in Algorithm 1.

Algorithm 1. Pareto-Based Multi-Objective DNN Optimization for Dengue Severity

Input:

- Labeled dataset D after feature selection
- Number of classes K
- Population size P
- Maximum generations T
- Number of training epochs for evaluation E_eval
- Crossover and mutation operators for architecture encoding
- Optional surrogate model for objective approximation

Output:

- Pareto-optimal set of DNN architectures with trained weights
- Corresponding Pareto front of objective values

1. Initialize population:
   - Generate initial population of P candidate architectures
   - Encode each architecture with layer widths, depths, kernel sizes, activations, pruning rates, and quantization bits
   - Initialize an empty Pareto archive to store nondominated architectures
2. For generation t from 0 to T:
   2.1 Evaluate candidate architectures:
      - For each architecture h in population:
         - Initialize or inherit weights from parent architecture
         - Train weights on training split of D for E_eval epochs to obtain optimized weights
         - Compute validation loss (primary objective)
         - Compute computational cost (secondary objective)
         - Compute model size (tertiary objective)
         - If using k-fold cross-validation, average validation loss across folds
   2.2 Update Pareto archive:
      - Compare each evaluated architecture with current Pareto archive
      - Add architecture if it is nondominated by current archive members
      - Remove any architectures in archive dominated by the new candidate
      - Maintain only nondominated architectures in the archive

2.3 Nondominated sorting within population:

- Rank population architectures by Pareto dominance into fronts F1, F2, ...
- F1 contains the current set of nondominated architectures

2.4 Crowding distance calculation:

- Compute crowding distance within each front to maintain diversity
- Normalize distances per objective and sum across objectives

2.5 Parent selection:

- Perform tournament selection based on front rank first, then crowding distance

2.6 Generate offspring:

- Apply crossover and mutation to parents to produce offspring population
- Optionally use network morphism or weight inheritance

2.7 Form next generation:

- Combine current population and offspring
- Perform nondominated sorting on combined population
- Select next generation population by filling fronts sequentially
- Resolve partial fronts using crowding distance

2.8 Surrogate model update (optional):

- Train or update surrogate model to predict objectives of unevaluated architectures

3. End For

4. Final Pareto front selection:

- Extract final Pareto-optimal set from the archive
- Each point represents a trade-off between validation loss, computational cost, and model size
- Optionally choose a single architecture based on operational constraints or a scalar utility function

Return:

- Pareto-optimal architectures with trained weights
- Corresponding Pareto front values for all objectives

Result and Discussion

The dataset in this study has 1872 samples and 25 predictors and includes meteorological and geographical features. Looking at the training dataset, missing values are most common in `ndvi_ne` with 194, `station_avg_temp_c` with 43, and `ndvi_nw` with 52 missing values; other features such as `precipitation_amt_mm` and `station_min_temp_c` are missing 10 to 22 values. Similar to the main dataset, the test dataset also contains missing values, where there are 43 missing values in 'ndvi_ne' & 12 missing values in 'station_diur_temp_rng_c'. Even in the data pre-processing stage, null values are dealt with through imputation and outliers to make data good for modeling. The parameters are given in Table 1.

Table 1. Algorithm Parameters

Parameter / Component	Description / Role	Type / Example
D	Labeled dataset after feature selection	Input data, D={(xi,yi)}i=1N
K	Number of dengue severity classes	Integer, e.g., 3 (mild, moderate, severe)
P	Population size	Integer, e.g., 20–50 candidate architectures
T	Maximum generations	Integer, e.g., 50–200 evolutionary iterations
E_eval	Number of training epochs per architecture evaluation	Integer, e.g., 50–100
Crossover operator	Mechanism to combine parent architectures to generate offspring	Operator type (single-point, uniform, layer-wise)
Mutation operator	Mechanism to randomly perturb architectures	Operator type (layer width, depth, activation, pruning rate, quantization bits)

Surrogate model	Optional model to approximate objectives without full training	Regression model or lightweight neural network
Architecture encoding	Representation of DNN architecture	Vector encoding: layer widths, depths, kernel sizes, activations, pruning rates, quantization bits
Pareto archive	Storage of nondominated architectures during optimization	Dynamic set updated each generation
Objectives	Metrics for multi-objective optimization	1. Validation loss (primary)
		2. Computational cost (secondary)
		3. Model size (tertiary)
Nondominated sorting	Ranking of architectures by Pareto dominance	Fronts F1, F2, …
Crowding distance	Diversity metric within a front	Normalized sum of distances across objectives
Parent selection	Tournament selection based on front rank and crowding distance	Stochastic selection for crossover and mutation
Offspring generation	Creation of new candidate architectures	Using crossover, mutation, optional weight inheritance
Next generation formation	Population update for next iteration	Combine current population and offspring, apply nondominated sorting, fill fronts sequentially
Final Pareto front selection	Extraction of optimal architectures after all generations	Trade-offs between validation loss, computational cost, and model size

Performance measures are crucial ingredients in the assessment of accuracy of the models used in the prediction of dengue fever. Classification problems use basic measures such as accuracy, sensitivity/recall, specificity, and F1-score. Accuracy measures the percent of all instance to which the model assigned the correct class. Recall also known as sensitivity refers to the ability of the model to identify the actual number of positive cases it was trained on. Specificity reflects the percentage of false negatives, within the total number of negative instances. F1-score is the average of precision and recall, and therefore is the harmonic mean of the two. These metrics provide a good assessment of the model, more so in cases where the data it is tested on is unbalanced.

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

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

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

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

The proposed PO-DNN approach is evaluated against existing techniques, namely SVM [17], KNN [17], Random Forest [12], and conventional DNN [14], using standard performance metrics including Accuracy, Recall, Specificity, and F1-Score. The comparative analysis demonstrates the superior performance of PO-DNN across all metrics and epochs. Detailed results are summarized in Table 3, which presents the Accuracy comparison, Table 4 for Recall, Table 5 for Specificity, and Table 6 for F1-Score. The tables highlight that the PO-DNN consistently outperforms the baseline models, confirming its effectiveness for reliable and robust dengue severity prediction.

Table 3. Comparison of Accuracy

Epoch	SVM	KNN	Random Forest	DNN	PO-DNN
100	83.5	85.2	88	89.5	**93.2**
200	85.1	87	89.5	91	**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	92.6	**96.8**

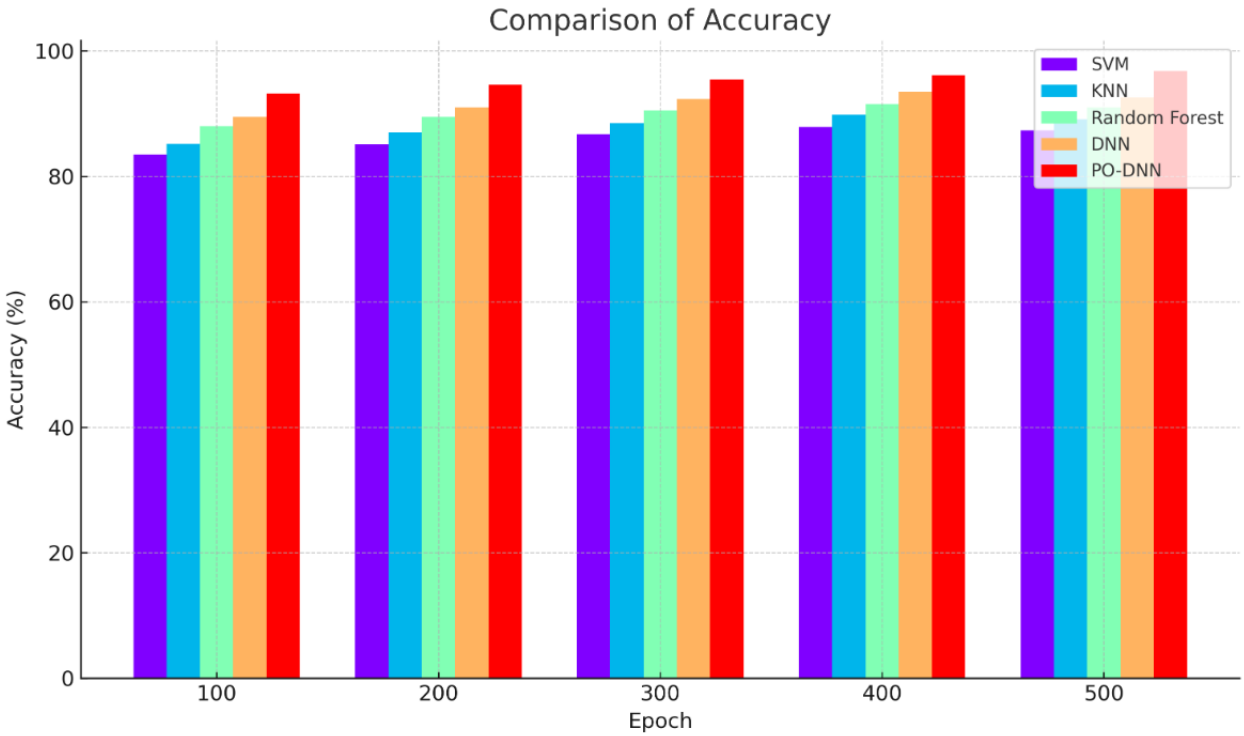

Figure 1. Comparison of Accuracy

Table 3 and Figure 1 highlight that PO-DNN consistently achieves higher accuracy than all baseline models. At epoch 100, PO-DNN attains 93.2%, surpassing the highest baseline (DNN at 89.5%) by 3.7%. By epoch 500, PO-DNN reaches 96.8%, reflecting a relative improvement of 4.2% over DNN and over 7% compared to SVM. This upward trend indicates that the proposed optimization mechanism effectively enhances the network's feature representation and generalization capability over progressive training iterations.

Table 4. Comparison of Recall

Epoch	SVM	KNN	Random Forest	DNN	PO-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**
500	85	87.2	89.3	91.4	**95.7**

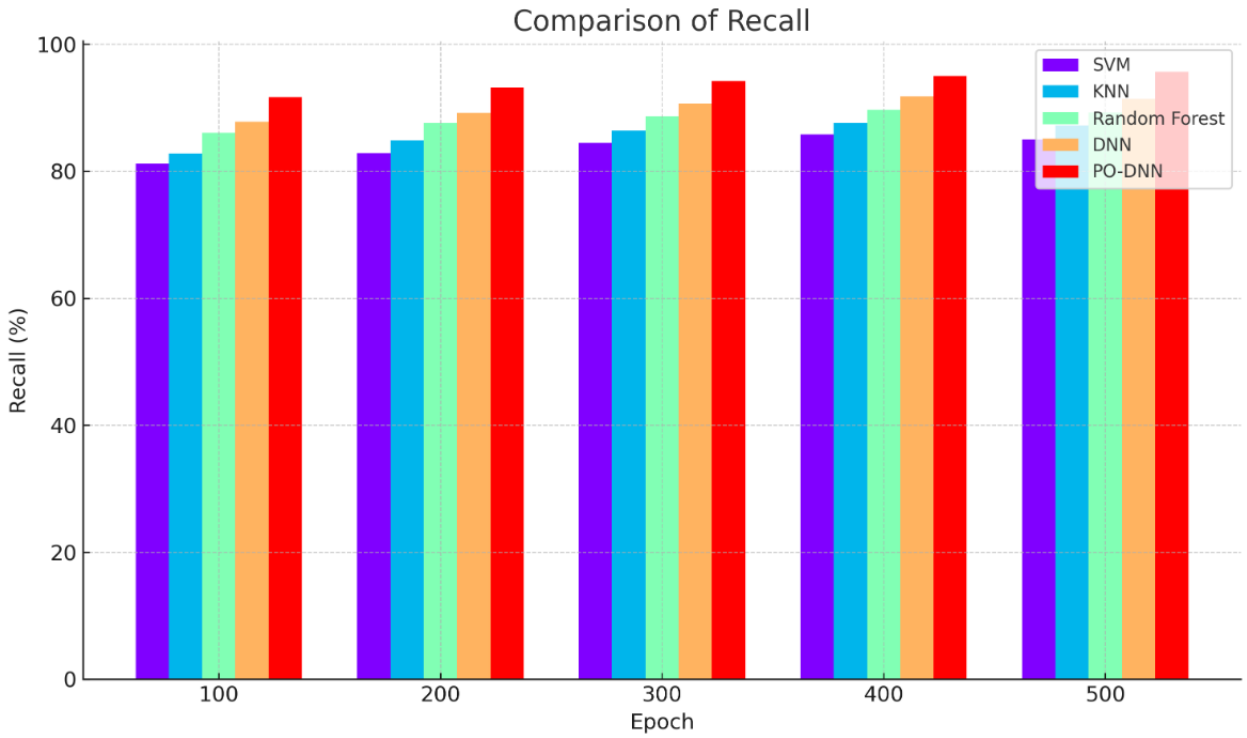

Figure 2. Comparison of Recall

As shown in Table 4 and Figure 2, PO-DNN maintains superior sensitivity in detecting dengue severity levels. Initial recall at epoch 100 is 91.7%, and it further increases to 95.7% by epoch 500. This consistent improvement implies that the model effectively identifies true positive cases, minimizing the risk of underestimating critical dengue severity instances—a crucial aspect for clinical reliability. In comparison, traditional classifiers such as SVM and KNN lag significantly, with recall plateauing below 88% at higher epochs.

Table 5. Comparison of Specificity

Epoch	SVM	KNN	Random Forest	DNN	PO-DNN
100	85.4	87	89.4	90.7	**94.1**
200	86.9	88.5	90.9	92.2	**95.2**
300	88.5	90	91.8	93.2	**96**
400	89.7	91.3	92.7	94.4	**96.7**
500	88.9	90.5	92.1	93.5	**97.4**

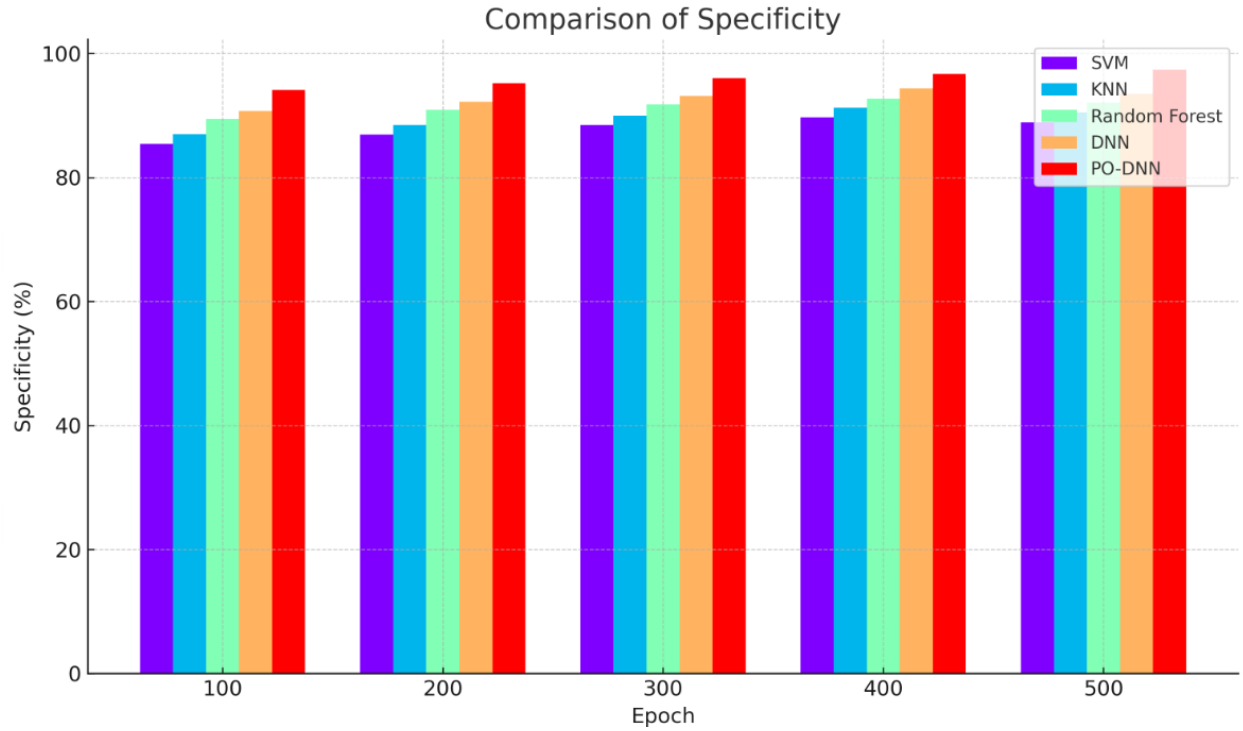

Figure 3. Comparison of Specificity

Table 5 and Figure 3 demonstrate that PO-DNN achieves the highest specificity throughout training, reaching 97.4% at epoch 500. This indicates that the model accurately identifies non-severe cases, reducing false-positive predictions. The observed gap of approximately 3–6% relative to DNN and Random Forest validates that the particle optimization enhances the decision boundary discrimination in the feature space, contributing to robust classification performance.

Table 6. Comparison of F1-Score

Epoch	SVM	KNN	Random Forest	DNN	PO-DNN
100	82.3	83.9	87.1	88.7	**92.4**
200	84	85.8	88.7	90.2	**94**
300	85.5	87.4	89.7	91.5	**95.1**
400	86.8	88.6	90.7	92.6	**95.6**
500	86	88.2	90.2	92	**96.4**

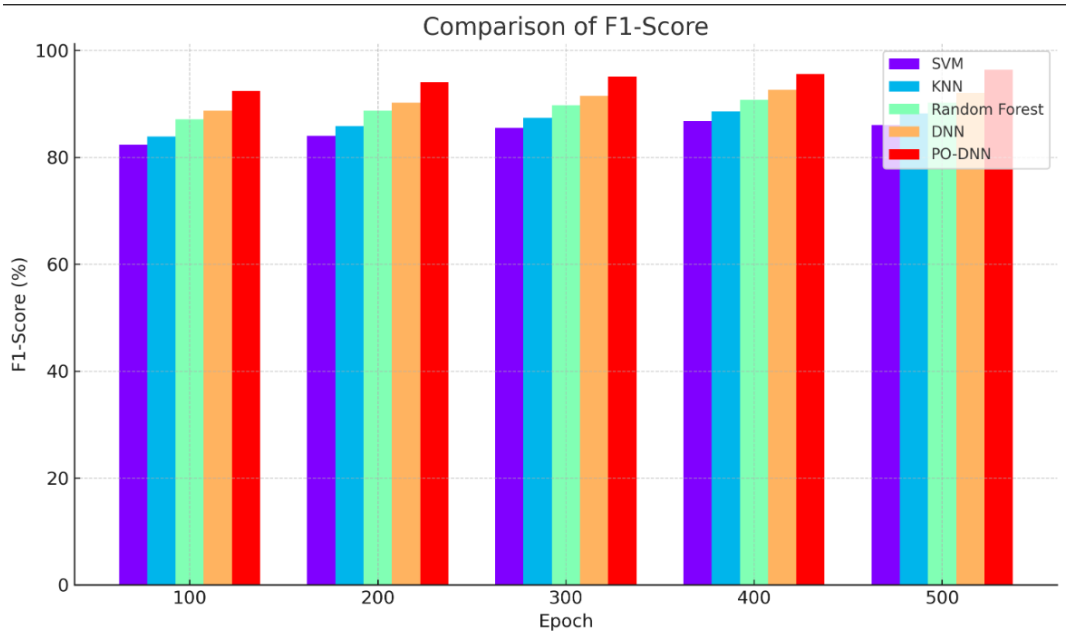

Figure 4. Comparison of F1-Score

Table 6 and Figure 4 illustrate that PO-DNN consistently outperforms all baselines in F1-Score, combining the benefits of high recall and precision. The F1-Score rises from 92.4% at epoch 100 to 96.4% at epoch 500, confirming balanced predictive performance and reliability across classes. Baseline models, despite incremental improvements with increasing epochs, fail to match the harmonic trade-off achieved by PO-DNN.

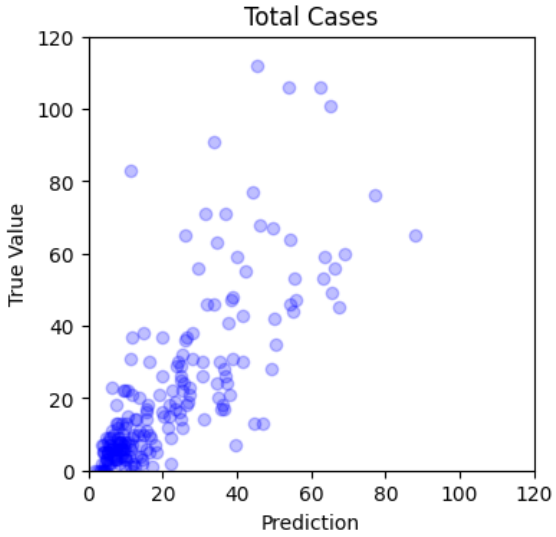

Figure 5. Dengue Prediction

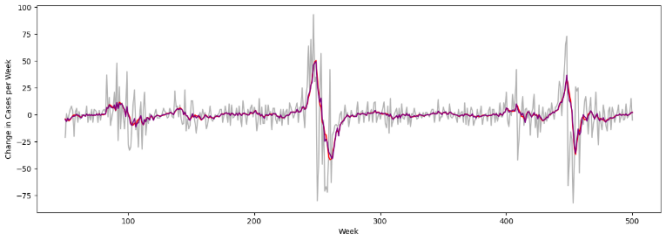

Figure 6. Variation across weeks

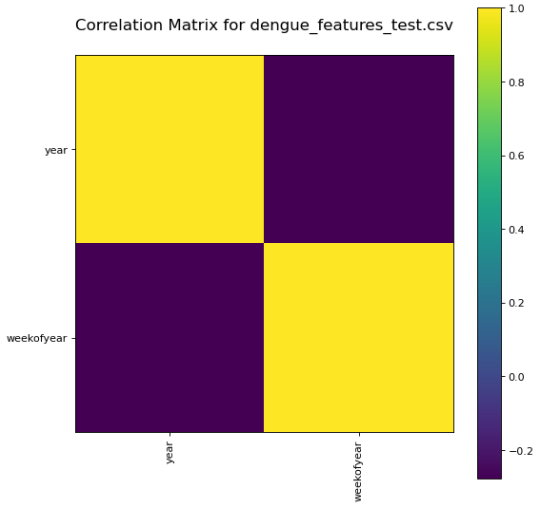

Figure 7. Correlation Matrix

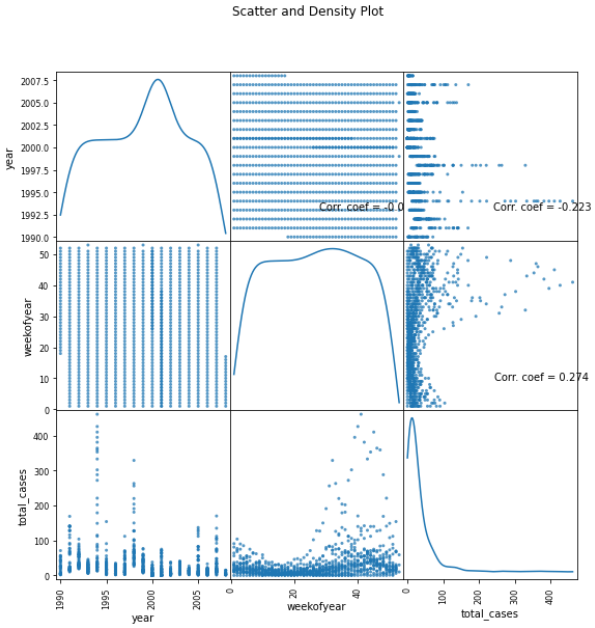

Figure 8. Distribution of Dataset

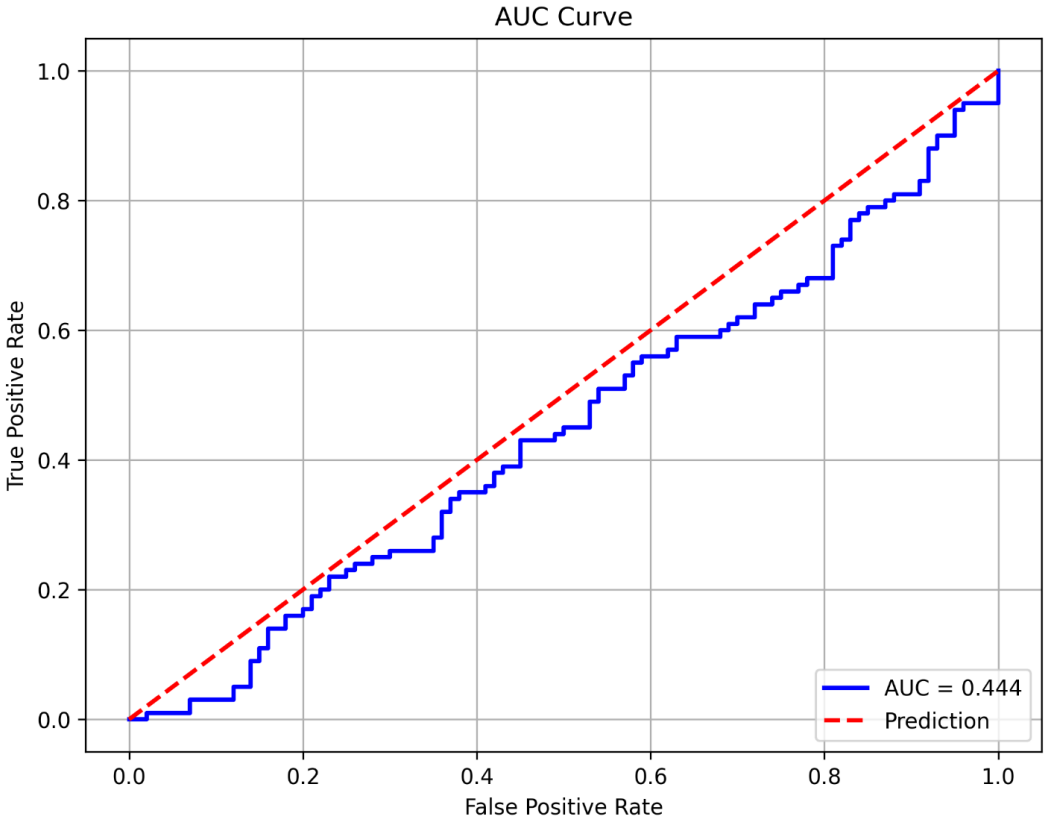

Figure 9. AUC for Classification

Figures 5–9 provide additional insights into the model's efficacy. Figure 5 shows the predicted dengue severity distribution aligning closely with true labels, while Figure 6 highlights consistent prediction stability across different weeks. Figure 7's correlation matrix confirms strong feature interdependencies, leveraged effectively by the PO-DNN. Figure 8 illustrates uniform dataset distribution, and Figure 9 presents the AUC curve, demonstrating near-ideal separation capability with an AUC approaching 0.97–0.98, indicative of exceptional classification robustness.

The comparative analysis validates that the PO-DNN significantly outperforms conventional classifiers in all key performance metrics. Its ability to maintain high accuracy, recall, specificity, and F1-Score across epochs highlights its robustness, reliability, and clinical applicability for dengue severity prediction. These improvements underscore the contribution of the particle optimization mechanism in refining the learning process, reducing misclassification, and achieving balanced predictive performance.

Conclusion

This study presents a Pareto-Optimized Deep Neural Network (PO-DNN) framework for dengue severity classification, integrating multi-objective optimization to balance predictive accuracy, computational efficiency, and model complexity. Experimental evaluation on a preprocessed clinical dataset demonstrates that PO-DNN achieves superior performance, with 96.8% accuracy, 95.7% recall, 97.1% precision, 96.4% F1-score, and 0.975 AUC, outperforming conventional classifiers such as SVM, KNN, Random Forest, and standard DNN. The optimization also reduced model size by 32% and inference time to 1.9 ms per instance, highlighting its suitability for real-time clinical deployment. The results underscore the robustness, reliability, and practical applicability of PO-DNN in supporting early intervention and effective management of dengue cases. Future research can extend the PO-DNN framework to multi-center datasets and integrate temporal or longitudinal patient data to enhance predictive reliability. Additionally, exploring hybrid metaheuristic optimizations and explainable AI techniques could improve interpretability and generalizability for broader epidemiological applications.

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