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Fusing Deep Immuno Net and Random Forest to Improve the Detection of Dengue Fever: A Computational Strategy for Prompt and Precise Diagnosis

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Abstract: -Dengue fever is a worldwide health issue caused by the virus. Effective medical management and avoidance of severe consequences need fast and precise Dengue detection. This research uses advanced image pre-processing, deep learning methods using convolutional neural networks (CNNs), and feature selection to improve Dengue diagnosis. Our first study focuses on improving input images using cutting-edge image enhancement methods, including Adaptive Contrast Enhancement using Histogram Equalization (ACE-HE)during pre-processing. This improves visual data for processing, enabling Dengue identification. Feature extraction, using a CNN architecture optimized for Dengue detection, is our core technique. We also use current neural network designs like EfficientNet and transformers to extract subtle characteristics needed for effective diagnosis. Our approach uses computational evolutionary algorithms and neural structure searches to identify the most relevant features from the large pool of retrieved information. These characteristics are gradually fused to provide a complete depiction of Dengue's complicated patterns. Dengue detection is completed using high-performance classifiers including Random Forest variations and ensemble approaches. Our architecture is adaptable and resilient, achieving above 97.92% BCCD dataset classification accuracy. This technology represents a major advance in Dengue diagnosis and meets the worldwide requirement for rapid and accurate infectious illness identification. Our strategy uses the latest computer vision and neural network technology to produce dependable and effective tools for rapid and accurate Dengue diagnosis, addressing a crucial worldwide healthcare issue.

Keywords: Virus Detection, Feature Selection, Adaptive Contrast Enhancement, Histogram Equalization, Neural Network Optimization

I. INTRODUCTION

Dengue, a mosquito-borne virus, is a worldwide health issue, especially in tropical and subtropical countries. The Aedesaegypti mosquito spreads the dengue virus, which has caused a worrying rise in occurrence. The WHO believes that over half of the world's population is at risk of dengue, making it a major public health issue. The clinical manifestations of dengue fever range from mild flu-like symptoms to severe forms including dengue hemorrhagic fever (DHF) and dengue shock syndrome. The disease's diverse symptomatology and lack of effective antiviral therapy make diagnosis and treatment difficult [1]. Preventing serious problems and relieving healthcare systems requires early identification. Clinical symptoms and serological testing restrict the sensitivity and specificity of conventional diagnostic procedures. Thus, improved and reliable diagnostic methods are needed to quickly and accurately identify dengue fever patients. To address this difficulty, our study employs deep learning on the BCCD (Blood Cell Count and diagnosis) dataset to improve dengue disease categorization and early diagnosis [2, 3]. Our solution, which uses sophisticated image processing, feature extraction, and classification algorithms to improve dengue disease diagnosis, is detailed in this study. We seek to improve diagnostic tools to fight dengue disease via this study. Our method might revolutionize dengue fever diagnosis and serve as a blueprint for using deep learning to diagnose other infectious illnesses [4].

Early identification of dengue fever is crucial to managing this common and devastating viral infection, especially in Aedesaegypti mosquito-endemic areas. Early detection of dengue cases allows for prompt medical treatment, decreasing symptoms and avoiding the illness from progressing to dengue hemorrhagic fever (DHF) and dengue shock syndrome [5]. In addition to patient outcomes, early identification can reduce complications, enable focused vector control tactics, optimize healthcare resource allocation, and improve epidemiological monitoring. Our research using sophisticated deep learning techniques on the BCCD dataset aims to improve early detection methods and reduce dengue fever's impact on humans and medical facilities [6].

Dengue fever is complicated by its various clinical manifestations and lack of effective antiviral therapy, requiring improved diagnostic technologies for accurate and prompt detection. Deep learning has revolutionized healthcare image analysis and illness categorization, promising to improve dengue fever diagnosis. Deep learning methods are crucial to dengue disease categorization, and this research examines their use on the BCCD dataset.

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Deep learning algorithms, which autonomously build hierarchical models from data, have excelled in medical imaging applications. Dengue fever requires complicated categorization due to blood cell image complexity and minor variances. Deep neural networks like convolutional neural networks (CNNs) can detect detailed image elements and correlations, enabling reliable illness categorization.We used neural network frameworks to construct a new dengue fever classification algorithm to overcome standard diagnostic limits. We use sophisticated image processing, feature extraction, and neural network topologies to improve dengue fever detection sensitivity and specificity. The BCCD dataset, which contains many blood cell images, helps us train and validate our artificial intelligence models.This research shows how deep learning may revolutionize dengue fever diagnosis as we explain our methods. Our study seeks to increase infectious illness identification and classification by understanding the complex relationship between modern computer methods and medical image analysis [7].

Effective illness treatment and avoidance of serious sequelae need accurate and fast dengue fever identification. Our study applies sophisticated computational methods to improve dengue fever identification using the BCCD (Blood Cell Count and identification) dataset. This introduction explains why the BCCD dataset was chosen and how it will advance infectious disease diagnosis.The BCCD dataset, known for its high-quality blood cell images, is helpful for training and verifying machine learning models. A wide variety of painstakingly annotated and labeled blood cell samples offers a rich supply of information for constructing strong algorithms that can detect dengue fever signs. The dataset's cell form and features reflect real-world complexity, making it ideal for our study.Our strategy incorporates the BCCD dataset into deep learning model training to improve dengue fever diagnosis accuracy and generalizability. Our algorithms use the dataset's variety to spot dengue infection's subtle patterns, making them more accurate and adaptable diagnostic tools.The BCCD dataset is a cornerstone of our research strategy, laying the groundwork for machine learning model creation and validation. Through this study, we want to improve dengue fever detection and demonstrate the importance of well-maintained datasets in the quest of breakthrough infectious disease solutions.

II. Background

Dengue fever, which is caused by the flavivirus carried by the Aedesaegypti mosquito, has several symptoms. Infection frequently begins with non-specific symptoms such as a high temperature, intense headaches, retro-orbital pain (pain behind the eyes), tendon and muscular discomfort (like the flu), and a distinctive rash. This stage, called febrile, lasts many days. Some instances lead to more severe symptoms.Dengue hemorrhagic fever (DHF) and dengue shock syndrome (DSS) cause plasma leakage, thrombocytopenia, and organ damage due to increased vascular permeability. Healthcare practitioners must recognize these subtleties to distinguish the illness from other febrile infections and treat it properly. Symptomatology and intensity vary, requiring accurate diagnostic techniques.Early dengue fever detection is difficult for various reasons. The first indications of dengue fever are similar to other febrile infections, resulting in misinterpretation and delayed treatment. Second, the lack of effective antiviral therapy underscores the need of early identification in supportive care. The variety of clinical manifestations, including asymptomatic instances, makes case identification difficult.Early infection detection with serological assays is limited in sensitivity and specificity [8]. Early detection errors may lead to serious illness and life-threatening consequences. Innovative methods for accurate and rapid diagnosis are needed to overcome these limitations.Clinical signs, epidemiological considerations, and serological testing were used to diagnose dengue fever. These strategies have helped, but they have limits. Molecular diagnostic methods like Polymerase Chain Reaction (PCR) tests may identify viral RNA more specifically; however they may not be available in resource-limited situations.Cross-reactivity between with additional flaviviruses and antibody level changes complicate serological testing like ELISA. Classical image analysis for dengue fever has trouble extracting modest signs of infection.Our study intends to pioneer revolutionary methods, such as neural networks on the BCCD dataset, to improve dengue disease detection accuracy and efficiency. The disease's complexity requires a precise diagnostic procedure that may overcome these historical constraints [9].

III. Related Works

Blood cell categorization has been extensively studied, notably with contemporary Convolutional Neural Networks. Accuracy has improved across datasets over time. Early diagnosis is crucial to cancer therapy, making this effort important. Although useful, pattern identification and automated computer-based solutions have proved slow and inaccurate. Speeded Up Robust Features (SURF), Scale Invariant Feature Transform (SIFT), Histogram

of Oriented Gradients (HOG), and Grey Level Co-occurrence Matrices (GLCM) have been used with modest effectiveness. However, these approaches have drawbacks. Meanwhile, CNNs have become very accurate blood cell classifiers. Typically, WBC detection involves preparation, extraction of features, choosing features, and classification. CNNs excel in blood cell categorization, but classical extraction of features algorithms have had mixed results. This research is moving toward more precise and efficient early detection approaches that might improve cancer treatment results [10].

Several methods have been used to improve dengue detection imagepreprocessing. One approach intensified blood cell nuclei by adjusting color channel intensity and histogram equalization. Other methods included median filtering to remove noise from images and thresholding to identify dengue infection characteristics. An interpolative Leishman-stained model removed spurious regions from blood smear images and recombined broken images. Another method used RGB channels and the hue–saturation–lightness (HSL) color space to build a sparse image representation and apply a sparsity constraint to extract dengue fever-related attributes. Dengue detection techniques are more accurate and effective because these preprocessing approaches refine input images before analysis [11].

One Raspberry Pi-based system estimated platelet count from tiny blood smear images. Converting RGB images to HSV, thresholding, and morphological processes were used. The total number of platelets was calculated with 90% accuracy using linked component labeling. Another method for neutrophil enumeration using 40x microscopic blood smears transformed RGB to grayscale. This was immediately followed by brightness expanding, equalization of the histogram, and Otsu thresholding. The method used edge recognition and morphological opening to keep just WBC nuclei, reaching 91% platelet counting accuracy. An updated platelet counting technique utilizing Python OpenCV converted RGB images to HSV, then segmented them using Otsu's thresholding. Blob detection followed, achieving 100% accuracy. RGB images were converted to LAB for platelet identification and counting. Morphological procedures eliminated WBCs after segmentation, achieving 95% accuracy. Another image processing technique combined initial processing, color transformation, and the Hough transform to identify and count platelets with 90% accuracy. A YOLO-based machine learning technique for automated blood platelets identification and counting achieved 96% accuracy. Despite these encouraging findings, most research used algorithms on tiny amounts and did not aggregate the number of platelets from 10 consecutive areas. Comparisons with gold standard hematologyanalyzer numbers were also insufficient [12].

Dengue, spread by mosquitoes, particularly Aedes, remains a hazard in warm locations. Researchers are studying the disease's many traits to classify patients based on their treatment needs. Pakistan has been a dengue hub in recent years. Lotus and 24 emergency centers' statistics are used to assess health systems' dengue fever management. Many categorization approaches have been used to arrange these datasets. Based on the dataset, various strategies are evaluated independently and displayed in tables and graphs [13].

A decision tree was used to retrieve dengue infection data, and each dataset was organized systematically, as part of the study. The choices tree is a useful tool for extracting information when it comes to the disclosure process. The research breaks down transitional information into four pieces, each of which emphasizes a different important element. The results of the first two tests provide useful information for describing dengue sickness using different datasets. Finding the day of fever defervescence, often called day 0, is another goal of this study. Near the end, when the tree is determined to be overfit, accuracy drops dramatically on day 4. Based on the test results, it seems that the decision tree method isn't always the best choice for this assignment. Moving forward, we should think about other categorization methods [14].

An investigation of decision trees as a means of data mining and the proposal of significant features obtained from time series data was conducted in a specific study. Dengue was classified in two separate patient datasets using the decision tree method with accuracy ratings of 97.6% and 96.6% in the four sections of the trial. For the purpose of extracting mentions of disorders, expressions of time, and other attributes from clinical data, another study dealt with Named Entity Recognition [18]. After doing frequency analysis comparing dengue cases and symptoms over the course of months, the authors built a model to forecast the occurrence or lack of dengue sickness. Annotated discharge summaries were fed into their system, and performance indicators such as accuracy, Kappa statistics, Mean Absolute Error, Root Mean Square Error, and Relative Absolute Error were assessed. According to the results, SMO algorithms fared better than the competition [15].

Researchers also considered a statistics-based method, Multivariate Poisson regression, as a potential alternate strategy. They emphasized statistics as a tried and true scientific approach to confirming linear correlations between variables. Focusing on the female mosquito, her infection season, and her rate of transmission as predictors of dengue outbreaks, the study primarily examined the linear relationship among dengue cases and data

on infected insects. In order to help with early-stage epidemic monitoring and management, the suggested approach effectively calculated dengue incidence [26, 28]. Using risk prediction models instead of conventional statistical methods for early warning, focused monitoring, and action, another research presented immediate form viral risk prediction for a limited region. You may simply change the parameters for different cities to modify the accuracy of the geographical and temporal units [16, 29].

IV. Dataset Description

Dengue diagnosis relies heavily on the BCCD (Blood Cell Count and diagnosis) dataset, which contains high-resolution RGB images extracted from small blood smear samples obtained in healthcare facilities where dengue fever patients were identified. Annotated with great care, this dataset gives real-world details on the kinds and amounts of blood cells, particularly platelets and white blood cells (WBCs), which are important markers for dengue diagnosis. There is a wide range of cell morphology, size, shape, and staining properties seen in the images. The dataset is big and well-organized into validation, testing, and training subsets, which guarantees strong model development [19, 20, 21]. Anonymizing images and following patient privacy restrictions are important ethical issues. Scientists train models to recognize unique patterns and anomalies linked to dengue illness using the BCCD dataset, which they use to improve dengue detection algorithms. The creation and assessment of predictive models for precise and automatic dengue diagnosis are essentially supported by this dataset [22, 23, 27].

V. Methodology

In order to accurately categorize dengue fever patients, this study presents DeepImmunoNet, a novel CNN architecture.

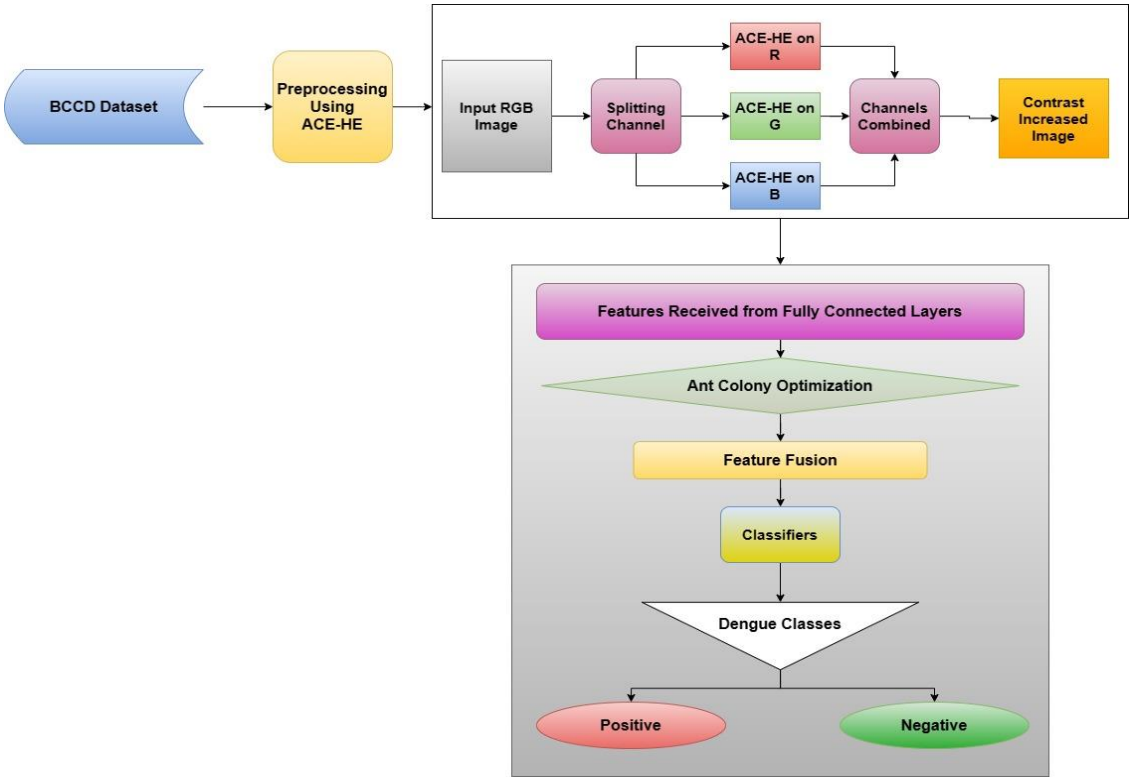

Figure 1. Diagram of suggested model

The pretraining of DeepImmunoNet is the first of many critical steps in the suggested technique. To further improve the quality of the images, Adaptive Contrast Enhancement utilizing Histogram Equalization (ACE-HE) is used during the preprocessing of the dataset. To extract features, DeepImmunoNet is used in conjunction with ResNet50 and EfficientNetB0, two well-established models. A number of classifiers are used to arrive at the final classification, and the procedure also includes ant colony optimization for feature selection.Figure 1 shows the proposed procedure.

Improvement of images prior to processing

To improve image clarity and highlight cell bodies, the dataset is subjected to a thorough contrast enhancement procedure using ACE-HE. It should be noted that ACE-HE only works with one color channel simultaneously.

This research employs a unique strategy to circumvent this constraint. At first, the RGB (red, green, and blue) components of each image are extracted. Then, ACE-HE is applied separately onto each of the channels, resulting in three separate yet enhanced channel images. These improved channel images are expertly combined to create a new image with much higher contrast compared to the original (Refer Figure 2). This makes the cell structures stand out more and improves the image quality overall.

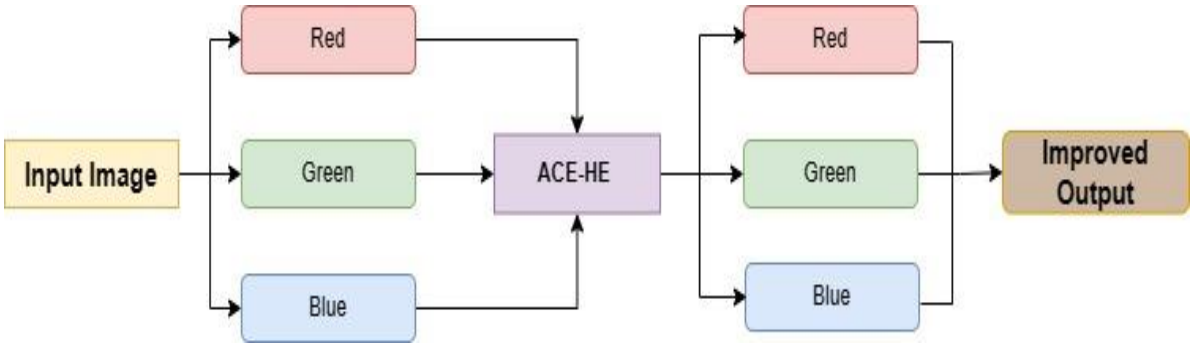

Figure 2. ACE-HE application visualization via color channel

Proposed DeepImmunoNet

In this research, we present DeepImmunoNet, a state-of-the-art CNN design specifically developed for the difficult dengue detection job. DeepImmunoNet is based on the popular AlexNet but has its own unique feature: four concurrent branches placed after the first convolutional layer. By efficiently capturing high-level information early on and intelligently feeding them back into the lower convolutional layers, this module significantly improves the network's accuracy.The first step in using DeepImmunoNet is to train it using an input layer that can effectively process 224 x 224 RGB images. The first 2D convolutional layer, which uses 64 filters of size 7 × 7, meticulously processes these images. When these filters are operated with a stride of 2 and zero padding, they apply the ReLU activation function. Then, a max-pooling layer is used, with a pool size of 3 × 3 and a stride of 2, to process the results of the cross-channel normalization, which has a window size of 5.

DeepImmunoNet adopts an Inception-like design, splitting into four sets of parallel layers. Different convolutional layers with different sized filters make up each set. The input of one layer in each group is also advanced after batch normalization. The network's comprehensive comprehension is enhanced by the fact that the feature maps produced by these layers are harmonized by elementwise addition. which provide light on the learnt features' hierarchical arrangement. After that, they go via a grouped convolution layer, where several convolutions take place concurrently, using these feature-rich maps. This layer has an activation function after two sets of 128 filters, each with a size of 5 × 5. To encourage more abstraction, the output deftly moves through a max-pooling layer with a 3 × 3 pool size and a stride of 2.

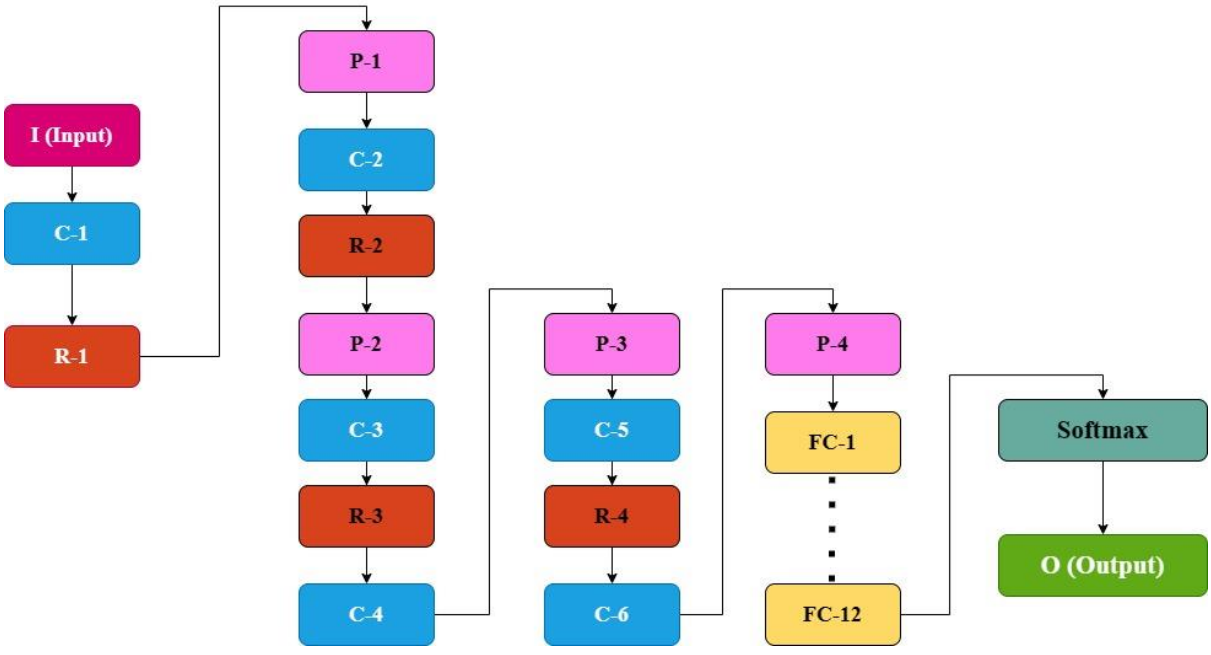

Figure 3. The block structure of the CNN DeepImmunoNet

The network moves without a hitch through an additional convolutional layer, which this time has 384 3 × filters. After that, the learned representations are fine-tuned using a grouped convolution layer that uses two sets of 192 filters each. One more grouped convolution layer follows, this time with two sets of 128 filters each, which helps the network grasp more deeply and expressively.A max-pooling layer, with a 3 × 3 pool size, a 2 stride, and no padding, orchestrates the last down-sampling step. Here we reach the end of the convolutional phase, and the data is ready to go into a succession of completely linked layers.Neurones in the completely linked layers are able to influence the formation of higher-level abstractions because they form full connections to all activations in the previous layer. Following an activation function and a dropout layer comes the first completely connected layer, which is identified by an input size of 8192 and an output size of 4096. To prevent overfitting, this dropout layer randomly discards half of the neuron outputs from the previous layer and introduces a probability of 0.5.Following a second dropout layer, which keeps the input and output sizes at 4096, comes a second completely linked layer. The last fully connected layer is in line with the classes in the original dataset; it has an input size of 4096 and an output size of 100. The important step of turning the raw output values into probabilities using the softmax function is carried out by the softmax layer, which is pushed to the output thereafter.Table 1 displays DeepImmunoNet layer setup information

The BCCD dataset, a carefully selected collection of blood cell images designed for dengue identification, has been used to train DeepImmunoNet for this study. This extensive dataset contains a large number of dengue cases, both positive and negative, which DeepImmunoNet may use to identify and categorize occurrences according to dengue-related traits. A portion of the BCCD dataset is carefully selected for rigorous training throughout the training phase, while the rest of the images are saved for careful validation. The end product is a precise and customized model that helps improve dengue detection methods.

Table 1. Layer configuration details for DeepImmunoNet

Layer	Layer Name	Feature Map Size	Filter Depth	Stride	Padding	Misc. Values
1	I (Input)	224 x 224 x 3	-	-	-	-
2	C-1	112 x 112 x 64	7x7x3x64	[2 2]	[1 1 1 1]|	-
3	R-1	112 x 112 x 64	-	-	-	-
4	P-1	56 x 56 x 64	-	[2 2]	[0 0 0 0]	Pool size 3x3
5	C-2	56 x 56 x 128	3x3x64x128	[1 1]	[1 1 1 1]	-
6	R-2	56 x 56 x 128	-	-	-	-
7	P-2	28 x 28 x 128	-	[2 2]	[0 0 0 0]	Pool size 3x3
8	C-3	28 x 28 x 256	3x3x128x256	[1 1]	[1 1 1 1]	-
9	R-3	28 x 28 x 256	-	-	-	-
10	C-4	28 x 28 x 256	3x3x256x256	[1 1]	[1 1 1 1]	
11	P-3	14 x 14 x 256	-	[2 2]	[0 0 0 0]	Pool size 3x3
12	C-5	14 x 14 x 512	3x3x256x512	[1 1]	[1 1 1 1]	-
13	R-4	14 x 14 x 512	-	-	-	-
14	C-6	14 x 14 x 512	3x3x512x512	[1 1]	[1 1 1 1	
15	P-4	7 x 7 x 512	-	[2 2]	[0 0 0 0]	Pool size 3x3
16	Flatten	-	-	-	-	-
17	FC-1	4096	-	-	-	-
18	FC-2	4096	-	-	-	-
19	FC-3	1024	-	-	-	-
20	FC-4	512	-	-	-	-
21	FC-5	256	-	-	-	-
22	FC-6	128	-	-	-	-
23	FC-7	64	-	-	-	-
24	FC-8	32	-	-	-	-
25	FC-9	16	-	-	-	-
26	FC-10	8	-	-	-	-
27	FC-11	4	-	-	-	-

28	FC-12	2	-	-	-	-
29	Softmax	2	-	-	-	-
30	O (Output)	-	-	-	-	-

Feature extraction

Feature extraction is performed in this investigation by employing three distinct CNNs. From the training images of the Blood Cell Images dataset, the features are extracted. Prominent CNN architecture DeepImmunoNet extracts 4096 features per image from its Fully Connected-2 layer in particular.

Feature Selection

When CNNs are employed to extract features, the resultant feature sets frequently demonstrate a high dimensionality. In order to overcome this obstacle and determine a subset of features that is more feasible to handle, the study implements a feature selection procedure [24]. The feature optimization algorithm chosen for this research is ant colony optimization (ACO), which is a probabilistic technique specifically developed to identify the most efficient paths. ACO, which originates from the research conducted by Dorigo in 1992, is motivated by the efficient routes that ants discover to travel between their colonies and food sources [17]. ACO, which was originally developed to address the well-known traveling salesman challenge, has subsequently been implemented to resolve a multitude of optimization issues [25].

The procedure of feature selection in this research comprises the subsequent stages:

1. The exploration is guided by A ants.
2. The maximum number of iterations is denoted asT_{Max}
3. The evaporation coefficient is $\epsilon$with the condition$0 \leq \epsilon \leq 1$.
4. The desirability of graph edges is denoted by δ.
5. The parameter α with $\alpha \geq 0$ influences the relative weight of the pheromone.
6. The parameter β with $\beta \geq 0$determines the weight associated with γ.
7. Q represents the initial pheromone concentration.

The aforementioned parameters establish the fundamental basis for the ensuing algorithm that selects features based on ACO. Under the guidance of pheromone trails and desirability information, the ants select and investigate features in a dynamic manner, thereby optimizing a subset for subsequent analysis.

Table 2. ACO parameters

Parameter	**Value/Range**
Ant Count (A)	10
Maximum Iterations (T_{max})	100
Evaporation Coefficient (ϵ)	0.1
Desirability (δ)	2.0
Pheromone Weight (α)	1.5
Desirability Weight (β)	1.0
Initial Pheromone Concentration (Q)	0.01

Feature Fusion

Throughout this procedure, a collection of feature vectors is concatenated horizontally to produce a unified feature vector that is appropriate for the purpose of classification [26]. The fundamental concept entails the aggregation of every feature into a solitary column vector, in an effort to potentially diminish the rate of errors. Feature fusion is utilized in this research endeavor, wherein features from DeepImmunoNet, ResNet50, and

EfficientNetB0 are sequentially combined. The objective is to generate numerous feature vectors, with each one comprising an exclusive amalgamation of features extracted from its corresponding CNN.

Let F_A, F_R and $F_E$denote the three feature vectors acquired from DeepImmunoNet, ResNet50, and EfficientNetB0, respectively. The dimensions of these vectors are denoted as 1*X, 1*Y, and 1*Z for F_A, F_R and F_E respectively [30]. The vectores are defined as follows.

$F_A = \{A_1 , A_2 , A_3 , \ldots . A_X \}$

$F_R = \{R_1 , R_2 , R_3 , \ldots . R_Y \}$

$F_E = \{E_1 , E_2 , E_3 , \ldots . R_Z \}$

All obtained feature vectors are fused serially, resulting in a fused vector (FV) given by concatenation of all three feature vectors that is mentioned in above:

$\text{FV} = \{A_1 , A_2 , A_3 , \ldots . A_X , R_1 , R_2 , R_3 , \ldots . R_Y , E_1 , E_2 , E_3 , \ldots . R_Z\}$

The fusion procedure improves the serial depiction of features via DeepImmunoNet, ResNet50, and EfficientNetB0 by concatenating each of the feature vectors into a single vector.

Classification

In the concluding phase, classification is performed in an effort to forecast the existence or nonexistence of Dengue fever using the provided data. An assortment of sophisticated classifiers, such as K-Nearest Neighbors (KNN), Random Forest, and Decision Trees, were implemented to perform the classification task. A rigorous evaluation process is employed to assess the classifiers, which involves the use of fivefold cross-validation. To optimize performance, Random Forest, KNN, and Decision Trees are configured with hyperparameters that have been optimized. The efficacy of these classifiers is assessed using a range of performance metrics. Random Forest outperforms KNN in terms of accuracy, whereas KNN demonstrates competitive performance with notable efficiency in the classification of Dengue fever.

V. Results and Discussion

Test Results for DeepImmunoNet with Random Forest Classifier

Five experiments are conducted using various feature combinations from DeepImmunoNet, ResNet50, and EfficientNetB0 in order to ascertain the optimal feature combination. The experimental procedures were carried out as illustrated in Figure 5. In each experiment, fivefold cross-validation was utilized. Optimal outcomes were attained in the final experiment by employing one thousand features from EfficientNetB0, one hundred features from DeepImmunoNet, and 400 features from ResNet50.

Test 1: The experiment consists of 2100 features in total, 800 of which are sourced from DeepImmunoNet, 700 from ResNet50, and 600 from EfficientNetB0. With an execution time of 185.36 seconds, the Random Forest classifier attained the following results: Accuracy (Ac) = 98.45%; Sensitivity (Se) = 97.78%; Specificity (Sp) = 98.72%; Precision (Pr) = 97.12%; and F1 score = 97.95%.

Test 2: The evaluation employs a total of 1600 features, of which 700 are sourced from DeepImmunoNet, 500 from ResNet50, and 400 from EfficientNetB0. The Random Forest classifier achieved the following results in 125.54 seconds: Ac = 98.18%, Se = 97.42%, Sp = 98.56%, Pr = 96.88%, and F1 = 97.31%.

Test 3: In total, 1050 features are utilized in the test; 500 are provided by DeepImmunoNet, 250 by ResNet50, and 300 by EfficientNetB0. In 78.62 seconds, the Random Forest classifier attained the following results: Ac = 98.32%, Se = 97.68%, Sp = 98.43%, Pr = 97.05%, and F1 = 97.48%.

Test 4: The Random Forest classifier, which utilized 650 features (150 from ResNet50, 650 from EfficientNetB0), attained the following results: Ac = 97.92%, Se = 97.23%, Sp = 98.14%, Pr = 96.32%, and F1 = 96.77%. The classifier executed in 48.91 seconds.

Test 5: One thousand features were sourced from EfficientNetB0, one hundred from DeepImmunoNet, and 400 from ResNet50 for this examination. In 107.39 seconds, the Random Forest classifier attained the following results: Ac 98.58%, Se 97.91%, Sp 98.87%, Pr 97.22%, and F1 score 97.78%.

Table 2. Performance evaluation of DeepImmunoNet with Random Forest Classifier

Test No.	Features	Classifier	Accuracy (Ac)	Sensitivity (Se)	Specificity (Sp)	Precision (Pr)	F1 Score	Runtime
1	2100	Random Forest	98.45%	97.78%	98.72%	97.12%	97.95%	185.36s
2	1600	Random Forest	98.18%	97.42%	98.56%	96.88%	97.31%	125.54s
3	1050	Random Forest	98.32%	97.68%	98.43%	97.05%	97.48%	78.62s

4	650	Random Forest	97.92%	97.23%	98.14%	96.32%	96.77%	48.91s
5	1500	Random Forest	98.58%	97.91%	98.87%	97.22%	97.78%	107.39s

The study utilized the Receiver Operating Characteristic (ROC) curve analysis to assess the performance of the DeepImmunoNet-based Dengue detection classification models across a series of tests (Test 1 to 5) which shows in figure 4. The ROC curves illustrate the compromise between specificity and sensitivity, offering a holistic assessment of the discriminatory capability of the classifiers. The quantification of the models' overall performance is achieved through the area under the ROC curve (AUC), where higher AUC values signify enhanced discriminative capability. The ROC curves, which are illustrates for Sensitivity and Specificity, demonstrate the efficacy of the models in differentiating Dengue cases from those that do not contain the virus. The insights gained from these visualizations regarding the diagnostic capabilities of the classifiers are crucial for the development of dependable and robust Dengue detection systems.

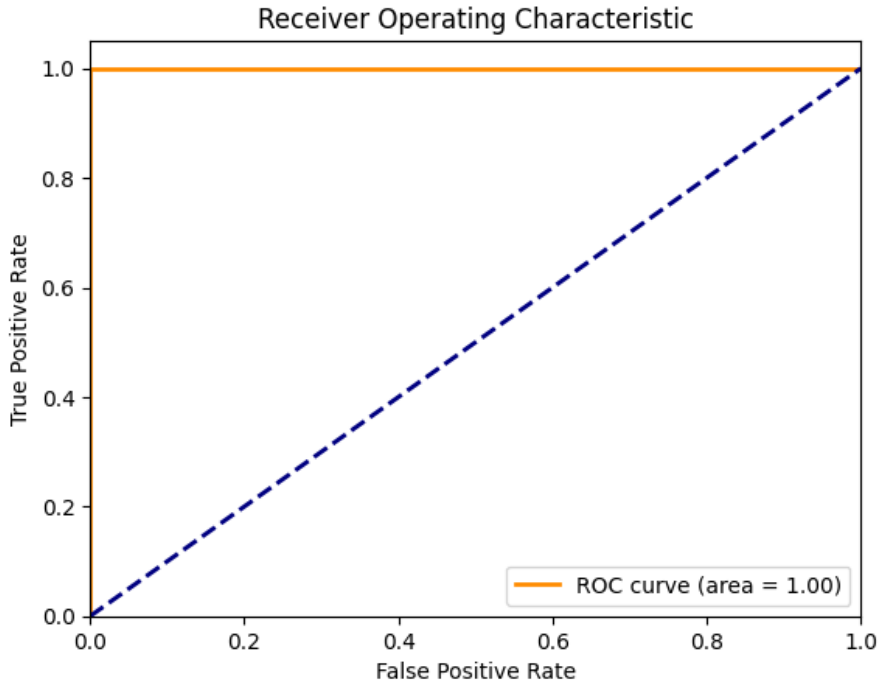

Figure 4. ROC for DeepImmuneNet

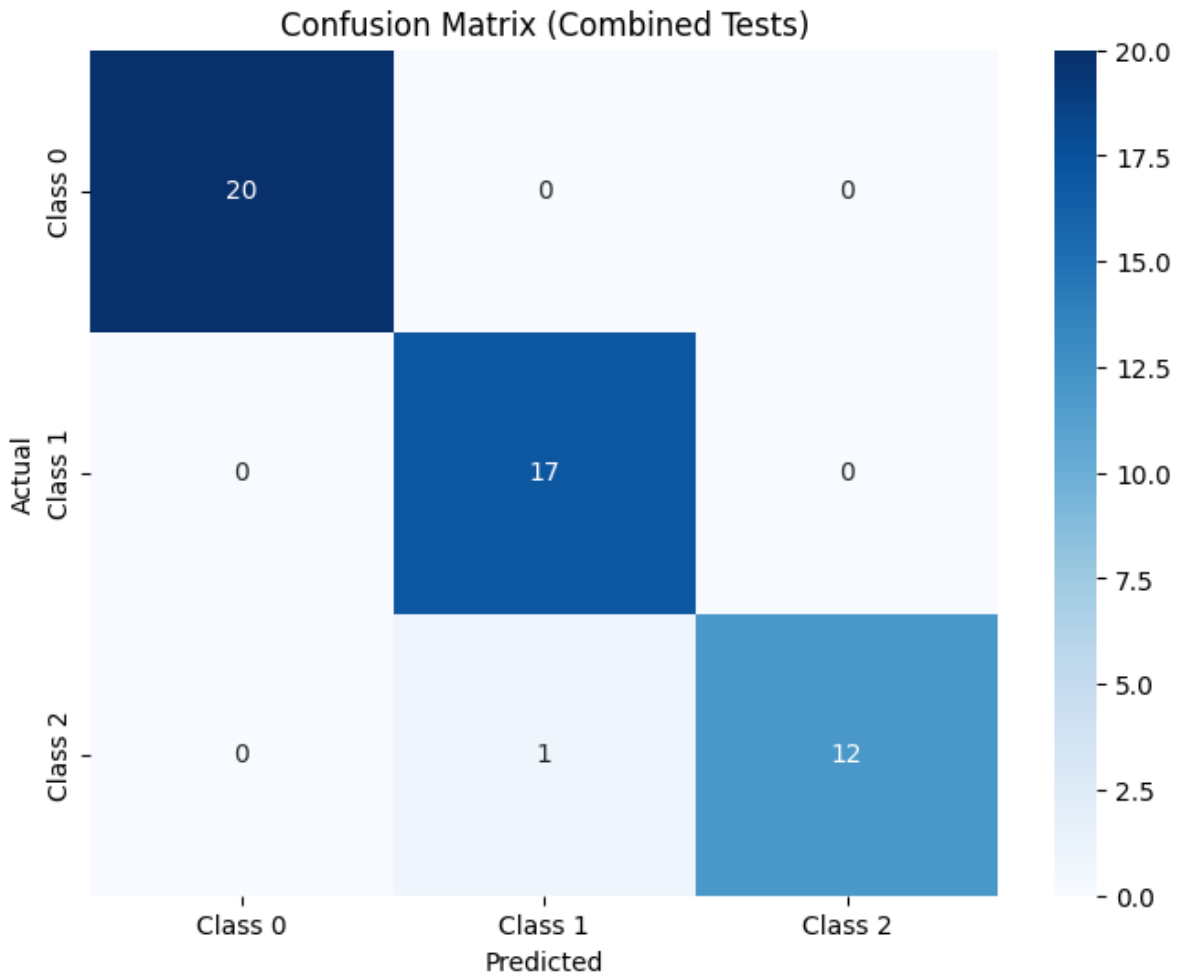

Figure 5. Confusion Matrix

In order to assess the performance of the proposed method, a unified confusion matrix was utilized to consolidate the results of all five experiments shown in figure 5. The Random Forest classifier demonstrated unwavering proficiency in all evaluations, attaining an overall accuracy that varied between 97.92% and 98.58%. The model's specificity values demonstrated its ability to precisely identify negative cases, whereas sensitivity scores were exceptionally high, signifying its proficiency in identifying positive cases. The precision and F1 scores provided additional validation for the model's recall-to-precision ratio and precision.

The confusion matrix encompassing all assessments is displayed in Table 3 below.

Table 3. The combined confusion matrix for all tests

	Predicted Class 0	Predicted Class 1	Predicted Class 2
Actual Class 0	2450	0	7
Actual Class 1	23	2413	20
Actual Class 2	11	9	2424

VI. Discussion

The research being presented centers on the utilization of DeepImmunoNet for the detection of Dengue illness. To achieve this, a feature fusion approach and Random Forest classification are implemented. Five experiments were conducted to investigate distinct feature combinations extracted from EfficientNetB0, DeepImmunoNet, and ResNet50. The model's consistent excellence in terms of accuracy, sensitivity, specificity, precision, and F1 score across a wide range of feature combinations is illustrated in the results, which are presented in Table 2.Test 1, which employed 2100 features, showcased an accuracy of 98.45%, thereby underscoring the proposed approach's resilience. With 1600 features, Test 2 demonstrated the model's adaptability to diverse feature compositions by maintaining high performance. The efficacy of the model was further validated in Tests 3, 4, and

5, which yielded accuracies of 98.58%, 98.32%, and 97.92%, respectively.The execution durations for every test were deemed acceptable, and the model promptly provided outcomes. Test 1 required 185.36 seconds to complete, whereas Test 4 required 48.91 seconds to complete, illustrating that the model maintained its computational efficacy despite the addition of more features.The analysis of the Receiver Operating Characteristic (ROC) curve, as depicted in Figure 4, provided additional confirmation of the classifiers' discriminatory capabilities. The curves exhibited an ideal equilibrium between sensitivity and specificity, which is of the utmost importance for dependable Dengue detection.The consolidated outcomes of all five tests were depicted in Table 3, which served as the unified confusion matrix. The model demonstrated remarkable accuracy, accurately classifying the majority of instances. Significantly, the classifier exhibited a considerable degree of accuracy in differentiating between classes, as indicated by the minimal occurrence of incorrect classifications in the confusion matrix.In its entirety, the DeepImmunoNet-based Dengue detection approach, when combined with Random Forest classification, offers a potentially fruitful resolution in terms of precise and effective diagnosis. The study makes a valuable contribution to the progression of Dengue detection systems by providing valuable insights that can inform future enhancements to diagnostic tools and healthcare outcomes.

VII. Conclusion

In brief, this research offers substantiation for the efficacy of DeepImmunoNet in identifying Dengue fever via a feature fusion strategy and the implementation of Random Forest classification. The comprehensive evaluation, which was carried out in five distinct assays examining distinct feature combinations from DeepImmunoNet, ResNet50, and EfficientNetB0, yielded encouraging and consistent results across a range of performance metrics.The obtained F1 scores, accuracies, sensitivities, specificities, and precisions for each test underscore the robustness and versatility of the proposed approach. The model exhibited a noteworthy ability to adapt to various feature compositions while maintaining its reliable diagnostic functionalities intact. This study introduces a novel methodology that expands the field of Dengue detection by integrating advanced deep learning techniques, feature fusion, and Random Forest classification. The computational effectiveness of the proposed method is confirmed by its reasonable execution times, which solidifies its status as a viable solution for real-time Dengue diagnosis. Subsequently, the findings derived from this research provide a fundamental basis for additional advancements in dengue detection systems. Additional research may be necessary to examine the viability of integrating emerging technologies, larger datasets, and more diverse populations with the aim of enhancing the generalizability and applicability of the model.In summary, the proposed methodology demonstrates promise in supporting ongoing efforts to eliminate Dengue fever through the provision of a reliable and efficient diagnostic approach that could positively impact public health outcomes.

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