Detection of Dengue Disease Empowered with Fused Machine Learning

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***Abstract*— Dengue fever is a life-threatening illness that affects both industrialized and poor nations, including Pakistan. It is necessary to forecast the illness at an early stage to avoid it. Machine Learning (ML) methods outperform other computer approaches in terms of illness prediction. The model utilized in this study to predict dengue fever is fused with machine learning. Artificial Neural Networks (ANN) and Support Vector Machine (SVM) provide the foundation of the conceptual framework. The datasets employed in these models have been collected from a government hospital in Lahore, Pakistan for diagnosing dengue fever (positive or negative). 70% of the statistics in the dataset are training data, whereas 30% are testing data. This fused model's membership functions explain whether a dengue diagnostic is positive or negative, which controls the model's output. A cloud storage system saves the fused model based on patients' real-time information for future use. The proposed model has a 96.19 % accuracy rate, which is much greater than earlier research.**

Keywords*— *Dengue Fever (DF), Dengue Hemorrhagic Fever (DHF), Dengue Prediction, Prediction Fused Dengue Model (PFDM)

I. INTRODUCTION (*HEADING 1*)

Pakistan is an emerging country with limited assets and a high population. The high population density makes it difficult to take high risks, predominance, action, and other problems associated with dengue fever. In the pre-vaccination epoch, an epidemic can have several periods, each of which arises in a particular season. Dengue virus is spread to animals, as well as human beings, by mosquitoes. Dengue virus is transmitted by mosquitoes of the family Aedes aegypti and transmitted by the bite of female parasites [1]. Despite the short lifespan of dengue mosquitoes, the average time for the dengue virus to spread is 4 to 10 days after the larvae emerge from the eggs [2-4]. Dengue fever is increasing due to the combined effect of high temperature and precipitation [5]. Symptoms of dengue fever include nausea, discomfort in the extremities and joints, severe headache, and vomiting [1, 6]. Dengue fever and headache are common primary symptoms of this disease, but they can worsen over time. There are many types of dengue viruses, and four have been discovered so far: DENV1, DENV2, DENV3, and DENV4 [2]. According to the World Health Organization (WHO), 2.5 billion people worldwide are at risk of contracting dengue, except for Antarctica [1].

In recent years, Pakistan has seen many natural hazards and challenges, like water shortages, flooding, earthquakes, and terrorists, all of which have harmed the country's resources and put the entire public's health at risk. DF has also become a major concern as a result of a lack of immunization, poor hygiene, water contamination, overcrowding, and many migrants. As per the World health organization (WHO), around 50,000,000 dengue viral diseases occur each year around the world, putting two-fifths of the globe's population at risk [12]. In different regions of the world, viral crisis sickness, DHF, and DF have caused significant and growing mortality rates [13]. In at least eight tropical Asian nations, viral disease is single of the foremost reasons for humanity and hospitalizations among many children [14].

Dengue fever has increased 30-fold in more than 100 countries around the world in the past 50 years. Dengue has a feast to large populations in South-East Asia and the southwestern United States [7, 8]. Pakistan has a varied climate, comprising tropical and subtropical areas, deserts, and relatively cold northern regions. Dengue has developed resistance to various agents in Pakistan, and studies in recent years have shown that the cruelty of this disease has changed from slight to severe [9]. An intelligent ML-based diagnostic system is needed to detect this viral disease. An expert judgment system based on machine learning can correctly diagnose dengue patients at an early stage. To predict dengue, researchers analyzed different data sets. The ML-based framework requires a data set with the necessary features for training and validation. We proposed an ML-based model that can make accurate predictions by selecting appropriate and relevant features from the data set. This study uses a data set that we collected from a government hospital in Lahore.

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Our research focuses on Lahore, Punjab. We are currently investigating the spread of dengue fever across Lahore. Punjab is the most populous province of Pakistan, and its capital is Lahore. Lahore is the largest city in Pakistan with a population of 12 million. Big cities struggle to manage many sectors, as we saw in Lahore, where pollution (air and land) is rampant. For the duration of the monsoon period, Pakistan experiences heavy rainfall and an increase in dengue outbreaks [10]. Dengue fever was first reported in Pakistan in 1994, but it did not gain widespread attention until an outbreak in the port city of Karachi in the mid-2000s [11]. Early detection and suggestive cure are important to the long-term health and well-being of dengue patients. In terms of disease detection and avoidance, intelligent curative analytic systems based on signs, symbols, laboratory tests, and observations will be of great use. Artificial intelligence (AI) has also been used in various ways to detect diseases in curative analytic systems. Using a machine learning fusion approach, this study develops a framework for detecting dengue fever patients early. It's critical to comprehend how the solutions infer responses, that is, which predictors are linked to the replies. To make the model more robust, additional training data is required, and further research should be conducted. The lack of confirmation of the findings to other research populations, such as various dengue-endemic locations and age categories, is a drawback. A further drawback is the removal of children who appeared later inside the illness and cannot be representative of our research population; nonetheless, the patients in this study had a wide range of dengue symptoms, involving significant decompensation.

II. RELATED WORK

Researchers [15] note that the Dengue Virus (DENV) is the furthermost public and most prevalent virus globally. Although all 4-DENV serotypes circulate together in the countryside, the clinical agenda for these 4-types has not been established in Pakistan. The authors conducted cross-sectional relational learning to manuscript the prevalence of different arboviruses in Sindh. At this time, the authors define a group of patients detected with dengue fever within two years. In this study, the orthogonal NS1 antigen ELISA system was used, and RT-PCR was used to detect the DENV subtype. A complete of 168 NS1-positive patients were estimated, of whom 91 remained classified by RT-PCR. There existed no momentous variance in the risk of infection by sex and age, and the peak of transmission occurred in the fall. DENV2 is the greatest public serotype tracked by dengue virus1, 3, and 4. The information suggests that dengue virus1 patients are more probable to have unusual liver function examinations. Dengue virus2 patients are further expected to have joint pain and nervous warning sign. Dengue virus3 patients are more probable to complain of sweltering pain in the urinary tract, increased lymphocyte count, and decreased hematocrit, while dengue virus4 patients are more possible to statement headache and rash. It should be noted that none of the patients through primary or subordinate infection had DHF or other symptoms of unembellished DF. In this study, the authors said they remained capable to recognize more patients' positive for NS1 antigen than with RT-PCR. This study shows that all 4 types of dengue fever were prevalent and infected in Pakistan.

ML models can be used to classify and forecast dengue outbreaks. The researchers assessed the enactment of the CART, Artificial Neural Network, Support Vector Machine, and Naive Bayes models to create new univariate epidemics of dengue established on weekly dengue outbreak records in Selangor and projected dengue outbreaks based on temperature variables. Using ML models to forecast dengue epidemics can give important information for healthcare organizations to better prepare for dengue outbreaks. Examining states as the most significant indicators of dengue occurrences can help modeling and anticipation at the native level. ML models have countless application potential in epidemiological studies and virus outbreaks [16]. In this study, the authors used GIS maps of the temporal and spatial severity of dengue. Dengue case map is plotted based on the different spatial units of the study area. The years most often affected by dengue were 2011 and 2013 (study period 2006-2017) 2011 was the most overwhelming time [23]. One possible reason is that torrential rains caused severe flooding in the country, but before that, cases of dengue fever started to rise in 2010 [16].

Studies have shown that the foremost reason for higher-than-normal DF in Lahore may remain automobile tyros imported from Thailand (one of the dengue hotspots in Asia) in 2011 and tyros' attacks by contaminated caterpillars. Dengue virus. Therefore, the prevalence is significant [17]. Surprisingly, there are hospitals with special equipment to combat dengue fever. Societies from distant regions of Pakistan (Sindh, Punjab, and Khyber Pakhtunkhwa) provinces commonly have to go to major towns to receive treatment for their illnesses. The DENV places more pressure on the current health care system during certain times of the year, such as unusual conditions such as above-average rainfall and below-average extremes. Therefore, there is a need to give mobile medical facilities in isolated areas [18]. The researchers used clinical laboratory data only to investigate retrospectively the classification of dengue and did not rely on X-rays, ultrasounds, or percentages of cannabis concentrations. The authors analyzed study data for children with severe feverish illness treated at 2 hospitals in Thailand.

Dengue Hemorrhagic Fever (DHF), Dengue Fever (DF), DF + other fever (OFI), dengue, OFI, severe dengue, and non-acute dengue + OFI using a multivariate logistic regression model. Information from the latter hospital was used for instance a confirmation group. There remained 1,227 patients in the exploration. The thoughtfulness of the model extended from 89.2% to 79.6%. This model shows a high sensitivity to the validation data set. This model can be used to compute probabilities and categorize patients centered on current clinical test center records and should be authenticated in other dengue epidemic areas [19]. The researchers investigated the combined effects of countryside and climate influences on mosquito incidence and dengue occurrence. Starting 2012 to 2014, data on insects, epidemics, and rainy season landscapes remained acquired from several government organizations in Manila, Philippines. Average temperature, rainfall, and foliage records remained achieved from side-to-side isolated detecting.

A random forest procedure was used to find land and environment variables. We then applied a model-based iterative division to test the mutual effects of landscape and weather features on the ovaries index and dengue occurrence using selected key variables. The frequent division egg index of MOB indicates that infestations of vector mosquitoes are

very sensitive to environmental conditions resulting from an amalgamation of high-density regions and little rainfall. In addition, MOB recursive zoning indicates that the occurrence of dengue is highly sensitive to the effects of rainfall in areas with high amounts of uptown and profitable zones [20]. A study in Indonesia used a GIS-based early threatening system to predict dengue outbreaks [21]. One more research from the Taipei University of Technology used a C-support vector classifier to predict the onset of dengue in Taiwan, and the acuteness of the radiated function model was 90.5% [22].

The author proposes a new contrast-learning method that embeds labels in the same embedded space as features and makes remote comparisons between features and labels in this common embedded space. Using the proposed model of two well-known intrusion detection data sets, NSL-KDD and UNSW-NB15, the proposed model is particularly useful for various unbalanced classification and noise problems [23,24]. The researchers used machine-learning methods to predict the switching activity conditions of several mobile IoT devices using both time-series and non-time-series approaches. All consequences are built on data from real mobile IoT devices. The ARIMAX time-series technique attained a precision of 93% among the tested methods but at a significant cost of training time. Non-time-series approaches generally need less training time than time-series approaches. In this work, the authors study different models of Deep Learning, optimize hyperparameters, and propose a new post-processing fusion framework (PFF). PFF attained a taxonomy precision of 99.33% on the Botanical Village data set. This method helps to overwhelm the confines of an individual DL model by choosing the correct organization from the outputs of respectively contributing model. It improves the accuracy and durability of the entire system [25, 26].

There are a number of approaches that may provide assistance in designing emerging solutions for the rising challenges in designing smart as well as autonomous management systems. Wireless sensor network [27], Fuzzy logic design [23, 36, 37], Machine learning [28, 29,35, 38-43, 42,47,48], computational intelligence [30, 31], artificial intelligence [32, 34], Particle Swarm Optimization (PSO) [41], round robin [43], equalization technique [44], explainable artificial intelligence [45], blockchain [46], IoT [49], and computational intelligence [50] are some of the approaches that are being used while employing and constructing a number of smart, and autonomous frameworks.

III. PROPOSED SYSTEM MODEL

There are several ML approaches to use, however in this study, we use classification algorithms to determine if the dengue is DHF or not. The Prediction fused dengue model (PFDM) is proposed in this paper as shown in Fig. 1. There are two main components in the PFDM model's initial stage. As a consequence, the training layer is the first segment, while the testing layer is the second. The training level is further segmented into five steps in the first segment of training: collecting, preprocessing, classification, efficiency, and machine-level combination. The core dataset for this research was obtained from a government hospital. During the data collection phase, we collected records with adequate characteristics to forecast dengue. This dataset includes dengue-related characteristics and tests. Data may be preprocessed at the preprocessing stage by using data gathering, oversampling, and data splitting. Following preprocessing, the data is recycled to train the ANN and SVM for learning criteria acquisition.

A. Data Gathering

After doing several searches at multiple hospitals, a portion of the dataset with reliable and independent variables have been compiled. We collect clinical feature and serological test data for this research. Only data from Dengue positive and negative patients is included in this dataset.

B. Dataset Description

Dataset has different parameters, as we now there are many attributes that we considered as including and excluding. The included attributes are shown in Tab. 1.

TABLE I. ATTRIBUTES OF DATASET

Parameters	Ranges	Units	Description
Gender	Male & Female	-	Select data of dengue patients both Male and Females
Age	12-55	Continues	Age 12 to 55 we select for this dataset.
HB	12.0-16.0	g/dl	HB level Increases
WBC	4-11.0	10^9/L	WBC level decreases
HCT	36.00-48.00	%	HCT level increases
PLT	150-450	10^9/L	PLT level decreases
NS1	1day	Serum test	From both primary and secondary infections, it is expected to be diagnosed as early as one day after the beginning of fever and to last up to nine days. The detection of the NS1 antigen is hampered.
IgM	3-5 days	Serum test	It is a core dengue infection that may be identified 3-5 days after the commencement of the illness.
IgG	1-2 days	Serum test	It's a secondary dengue infection that shows up 1-2 days after the first illness.

To achieve the needed accuracy, many machine learning methods may be used for the classification step. We chose two ML-based procedures for the suggested PFDM technique at first (SVM and ANNs). These algorithms were chosen based on preliminary tests that showed these strategies to be more successful for this challenge. We employed a range of accuracy metrics throughout the Performance Evaluation stage, containing Accuracy, Specificity, Sensitivity, Precision, and F1-score. If the suggested model fails to achieve the learning criteria, it will be reoriented. When the erudition desires are fulfilled, the outputs of ANN and SVM are utilized as input in an ML-fusion. The fused trained model is then kept in the cloud system. The testing layer is the structure's second section. Data is obtained from a database, and pre-processed train models are loaded from the cloud by the testing layer. A fused model is utilized to forecast whether a dengue identification is progressive or destructive. The predicted outcome is compared to the actual result to measure accuracy.

ANN models are trained using preprocessed training datasets. The preprocessed data has been split into train and test data at a ratio of 70:30 based on the class base split. To train the

records, we have used the Bayesian Ṛegularization function, in which 5 % of the data is used for testing, 5% for validating, and the remaining 90% is used for training. It consists of 6 hidden-layers neurons that separate input neurons from output-neuron. The input layer neurons represented by “w” are w1, w2, w3... w6, whereas v1, v2, v3... v6 represent hidden layer neurons. The word "outΨ" denotes output. "b1" and "b2" represent bias. An "outϱ" and "outϭ" are formed from Eq. 1 and Eq. 2.

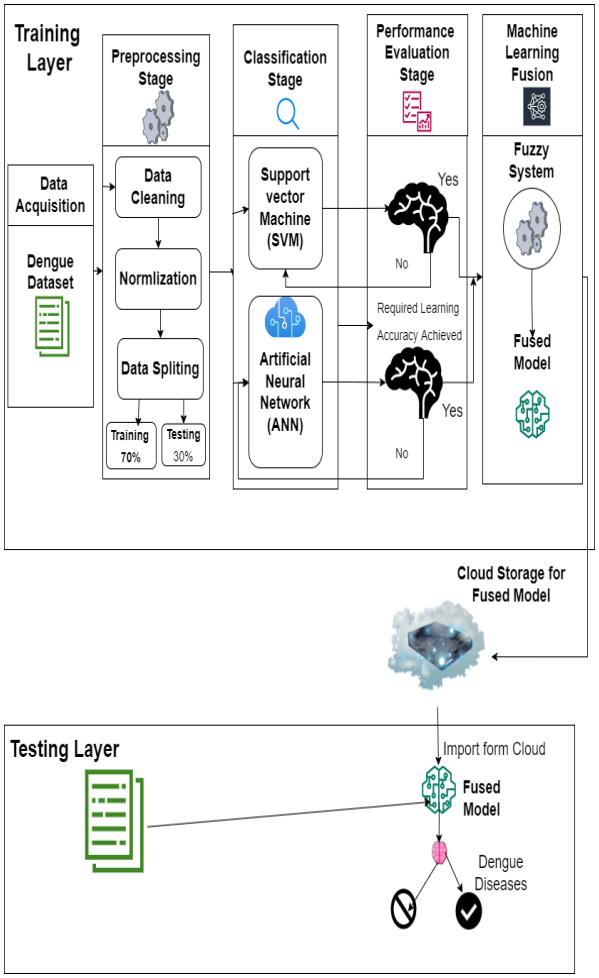


Fig. 1. Figure 1. Proposed Prediction Fused Dengue Model (PFDM).

$$out_{\varrho} = \frac{1}{1+e^{-(b_1 \sum_{\check{r}=1}^{m}((\mu \check{r}_{,\varrho} * w))}}$$

$$out_{\varrho} = \frac{1}{1+e^{-(b_1 \sum_{\check{r}=1}^{m}((\mu \check{r}_{,\varrho} * w))}} \quad (1)$$

$$where, \Psi = 1, 2, 3, \ldots . nwhere, \Psi = 1, 2, 3, \ldots . n$$

$$out_{\square} = \frac{1}{1+e^{-(b_1 \sum_{\varrho=1}^{n}((s_{\varrho,\square} * out_{\varrho}))}}$$

$$out_{\square} = \frac{1}{1+e^{-(b_1 \sum_{\varrho=1}^{n}((s_{\varrho,\square} * out_{\varrho}))}} \quad (2)$$

$$where, \square = 1, 2, 3, \ldots . \check{r}$$

With the squared error function, the errors in all output-neuron can be computed, and then sum to determine the total error.

$$\varepsilon = \frac{1}{2} \sum_{\square} (\tilde{\imath}_{\square} - out_{\square})^2 \; \varepsilon = \frac{1}{2} \sum_{\square} (\tilde{\imath}_{\square} - out_{\square})^2$$

(3)

The formula in eq.4 can be used to adjust these weights.

$$\Delta w \propto -\frac{\partial \varepsilon}{\partial w}$$

$$\Delta w \propto -\frac{\partial \varepsilon}{\partial w} \quad (4)$$

The weights among the hidden and output layers are updated by eq.5.

$$\Delta \hbar_{\varrho,\square} = -\varepsilon \frac{\partial \varepsilon}{\partial \hbar_{\varrho,\square}}$$

$$\Delta \hbar_{\varrho,\square} = -\varepsilon \frac{\partial \varepsilon}{\partial \hbar_{\varrho,\square}} \quad (5)$$

$$\Delta \hbar_{\varrho,\square} = -\varepsilon \frac{\partial \varepsilon}{\partial out_{\square}} \times \frac{\partial out_{\square}}{\partial out_{\square}} \times \frac{\partial out_{\square}}{\partial \hbar_{\varrho,\square}}$$

$$\Delta \hbar_{\varrho,\square} = -\varepsilon \frac{\partial \varepsilon}{\partial out_{\square}} \times \frac{\partial out_{\square}}{\partial out_{\square}} \times \frac{\partial out_{\square}}{\partial \hbar_{\varrho,\square}} \quad (6)$$

$$\Delta \hbar_{\varrho,\square} = \varepsilon(\tilde{\imath}_{\square} - out_{\square}) \times out_{\square}(1 - out_{\square})(out_{\varrho})$$

$$\Delta \hbar_{\varrho,\square} = \varepsilon(\tilde{\imath}_{\square} - out_{\square}) \times out_{\square}(1 - out_{\square})(out_{\varrho}) \quad (7)$$

Eq.8 and Eq.9 explain the updating of weights b/w input-layer neurons and hidden-layer neurons

$$\Delta v_{i,\varrho,} \propto -\left[\sum_{\square} \frac{\partial \varepsilon}{\partial out_{\square}} \times \frac{\partial out_{\square}}{\partial net_{\square}} \times \frac{\partial net_{\square}}{\partial out_{\square}}\right] \times \left[\frac{\partial out_{\varrho}}{\partial net_{\varrho}} \times \frac{\partial net_{\varrho}}{\partial v_{i,\varrho}}\right]$$

$$\Delta v_{i,\varrho,} \propto -\left[\sum_{\square} \frac{\partial \varepsilon}{\partial out_{\square}} \times \frac{\partial out_{\square}}{\partial net_{\square}} \times \frac{\partial net_{\square}}{\partial out_{\square}}\right] \times \left[\frac{\partial out_{\varrho}}{\partial net_{\varrho}} \times \frac{\partial net_{\varrho}}{\partial v_{i,\varrho}}\right]$$

(8)

$$\Delta v_{i,\varrho,} = \mathrm{Ɪ}\mathrm{Ɪ}\left[\sum_{\square} (\tilde{\imath}_{\square} - out_{\square}) \times out_{\square}(1 - out_{\square}) \times \hbar_{i,\vartheta} \times out_{\square}(1 - out_{\square}) \times w_i\right]$$

$$\Delta v_{i,\varrho,} = \mathrm{Ɪ}\mathrm{Ɪ}\left[\sum_{\square} (\tilde{\imath}_{\square} - out_{\square}) \times out_{\square}(1 - out_{\square}) \times \hbar_{i,\vartheta} \times out_{\square}(1 - out_{\square}) \times w_i\right]$$

(9)

Eq. 10 is the equation for adjusting the weights between hidden-layer and output-layer neurons.

$$\Delta v_{i,\varrho}(t+1) = \Delta v_{i,\varrho}(t) + \lambda \Delta v_{i,\varrho}$$

$$\Delta v_{i,\varrho}(t+1) = \Delta v_{i,\varrho}(t) + \lambda \Delta v_{i,\varrho} \quad (10)$$

SVMs create a class-based hyper-plane to categorize data. SVM is used to classify dengue symptoms into Positive and Negative categories. Drawing a line is the first step in the process of separating classes in a hyperplane. The equation of the line is eq.11.

$$y = ax + by = ax + b$$

(11)

Here, “a” represents the slope, besides “b” is a PowerPoint of the intersection. The following is the formula:

$$ax - y + b = 0ax - y + b = 0$$

(12)

If $\bar{x}\bar{x}$ = (x, y) £ & $w'''w'''$ = (a, −1), then, utilizing the aforementioned phrase, we can frame an eq.13 using the above expression.

$$w.\bar{x} + b = 0$$

$$w.\bar{x} + b = 0 \quad (13)$$

The support vectors formula is important for three-dimensional vector analysis. According to Eq. 14, the vector of $\bar{x}\bar{x}$ = (x, y) is denoted by ww.

$$w = \frac{\bar{x}}{|\bar{x}|} + \frac{\bar{y}}{|\bar{x}|}w = \frac{\bar{x}}{|\bar{x}|} + \frac{\bar{y}}{|\bar{x}|} \quad (14)$$

$$where\ i = 1,2,3 \ldots . n$$

$$where\ i = 1,2,3 \ldots . n$$

Eq.15 describes how to write n-dimensional matrices.

$$w \cdot \bar{x} = \sum_{i=1}^{n} w_i \bar{x}_i w \cdot \bar{x} = \sum_{i=1}^{n} w_i \bar{x}_i$$

It is possible to determine if data has been categorized accurately using eq.15.

$$\dot{D}_i = y_i(w.\bar{x} + b)\dot{D}_i = y_i(w.\bar{x} + b) \quad (15)$$

The functional margins of a dataset are denoted by ℕℕ and are represented as

$$\mathbb{N} = \min_{i=1,2,\ldots m} \dot{D}_i \mathbb{N} = \min_{i=1,2,\ldots m} \dot{D}_i$$

The Ǥeometric-Bargin ℕℕ of the dataset will provide the hyperplane, which is the optimal hyperplane when used with the Łagrangian-function

$$ꝺ(w, b, \mathfrak{P}) = \frac{1}{2} w.w - \sum_{i=1}^{m} \mathfrak{P}_i [y(w.x + b) - 1] \quad (16)$$

$$\Delta w ꝺ(w, b, \mathfrak{P}) = w - \sum_{i=1}^{m} \mathfrak{P}_i y_i x_i = 0 \quad (17)$$

$$\Delta b ꝺ(w, b, \mathfrak{P}) = -\sum_{i=1}^{m} \mathfrak{P}_i y_i = 0 \quad (18)$$

It can be represented as follows when simplified:

$$w = \sum_{i=1}^{m} \mathfrak{P}_i y_i x_i = 0 w = \sum_{i=1}^{m} \mathfrak{P}_i y_i x_i = 0$$

And

$$\sum_{i=1}^{m} \mathfrak{P}_i y_i = 0 \sum_{i=1}^{m} \mathfrak{P}_i y_i = 0 \quad (19)$$

Substituting the Łagrangian-function ꝺ.

$$w(\mathfrak{P}, b) = \sum_{i=1}^{m} \mathfrak{P}_i - \frac{1}{2} \sum_{i=0}^{n} \sum_{i=1}^{m} \mathfrak{P}_i \mathfrak{P}_j y_i y_j x_i x_i \quad (20)$$

Therefore, the above Equation can also be defined by Eq.10.

$$max\ \mathfrak{P} \sum \mathfrak{P}_i - \frac{1}{2} \sum_{i=1}^{m} \mathfrak{P}_i \mathfrak{P}_j y_i y_j x_i x_i$$

$$max\ \mathfrak{P} \sum \mathfrak{P}_i - \frac{1}{2} \sum_{i=1}^{m} \mathfrak{P}_i \mathfrak{P}_j y_i y_j x_i x_i$$

For avoiding containment inequalities, put the ĸĸṬ (Ƙarush-Kuhn-Ṭucker) condition on the Łagrangian multiplier procedure.

$$\mathfrak{P}i\ [\ \gamma i\ (\ wi \cdot x^* + b\ ) - 1\ ] = 0$$

$$\mathfrak{P}i\ [\ \gamma i\ (\ wi \cdot x^* + b\ ) - 1\ ] = 0 \quad (21)$$

Here x^*x^* represents an optimal opinion, and Ϙ has a positive value; while the value for other opinions is nearly zero. The equality is expressed through Eq. 22 here

$$[\ \gamma i\ (wi \cdot x^* + b\ ) - 1\ ] = \theta$$

$$[\ \gamma i\ (wi \cdot x^* + b\ ) - 1\ ] = \theta \quad (22)$$

The nearest arguments to the hyper-plane are identified through support vectors. Such issues are discussed in eq.23.

$$w - \sum_{i=1}^{m} \mathfrak{P}i \Upsilon i x_i = 0 w - \sum_{i=1}^{m} \mathfrak{P}i \Upsilon i x_i = 0 \quad (23)$$

To put it another way, it can be inscribed as:

$$w = \sum_{i=1}^{m} \mathfrak{P}i \Upsilon i x_i$$

Eq.24 calculates b when it is computed.

$$\Upsilon i\ [(w_i \cdot x^* + b\ ) - 1\ ] = 0$$

$$\Upsilon i\ [(w_i \cdot x^* + b\ ) - 1\ ] = 0 \quad (23)$$

In other words, the in cooperation sides of the eq. are reproduced by Υi:

$$\Upsilon i^2\ [(y_i \cdot x^* + b\ ) - 1\ ] = 0$$

$$\Upsilon i^2\ [(y_i \cdot x^* + b\ ) - 1\ ] = 0 \quad (24)$$

γi 2 is equivalent to 1.

$$b = \Upsilon i - [w_i \cdot x^*] b = \Upsilon i - [w_i \cdot x^*] \quad (25)$$

$$b = \frac{1}{\acute{U}} \sum_{i=1}^{u} (y_i - [w_i \cdot x^*]\ )$$

$$b = \frac{1}{\acute{U}} \sum_{i=1}^{u} (y_i - [w_i \cdot x^*]\ ) \quad (26)$$

Eq. 27 determines the number of SV Ú and the number of predictions on the hyperplane. The hypothesis function is labeled in Eq. 27.

$$H(w_i) = \begin{cases} +1 \text{ if } (w_i \cdot x^* + b\ ) \geq 0 \\ -1 \text{ if } (w_i \cdot x^* + b\ ) < 0 \end{cases}$$

$$H(w_i) = \begin{cases} +1 \text{ if } (w_i \cdot x^* + b\ ) \geq 0 \\ -1 \text{ if } (w_i \cdot x^* + b\ ) < 0 \end{cases} \quad (27)$$

Dengue positivity is shown by points immediately above the hyper-plane, i.e. 1, and Dengue negativity is indicated by specific points below the hyper-plane, i.e. - 0. Support vectors are just the coordinates of each observation. The Classification method is a standard that effectively differentiates two classes (positive and negative).

The membership functions are used in the fuzzy-logic approach. To compute its inputs, this approach employs SVM and ANN outputs. The rubrics that are put on to inputs/outputs are defined by the features that can make up the membership model. Artificial Neural Network and

Support Vector Machine used fuzzy logic to govern if a patient's concerns were connected to dengue fever. A fuzzy decision is defined mathematically as follows:

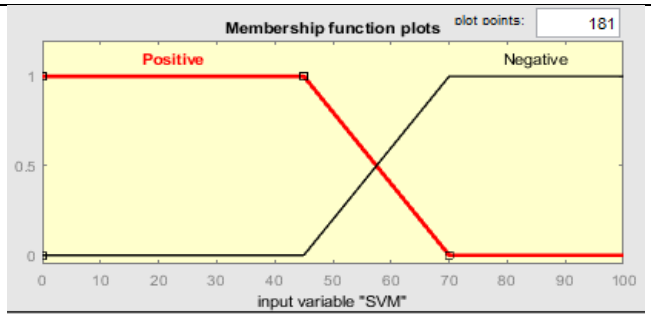
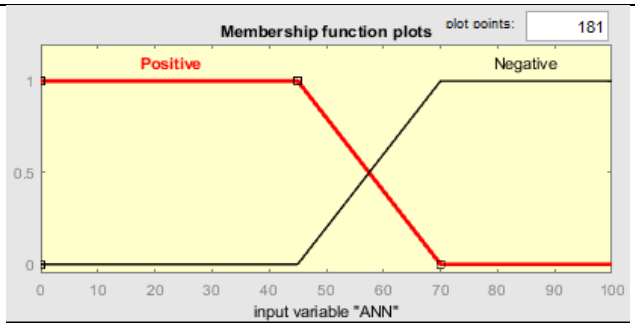
$$\mu_{ANN} \cap \mu_{SVM}(a,s) = \min[\mu_{ANN}(a), \mu_{SVM}(s)]$$

$$\mu_{ANN} \cap \mu_{SVM}(a,s) = \min[\mu_{ANN}(a), \mu_{SVM}(s)]$$

(28)

The membership function of an ANN has been defined as ŲANNŲANN, while the membership function of an SVM has been defined asŲSVMŲSVM. The result parameters are either 0 or 1 based on the findings as shown in Tab. 2.

TABLE II. MEMBERSHIP FUNCTION FOR PFDM SYSTEM

SVM = **SVM =**	$\mu_{SVM,Pos}(s) = \{max(min(1, \frac{70-s}{25}),$ $\mu_{SVM,Pos}(s) = \{max(min(1, \frac{70-s}{25}),$ $0)\}0)\}$ $\mu_{SVM,Neg}(s) = \{max(min(1, \frac{s-45}{25}),$ $\mu_{SVM,Neg}(s) = \{max(min(1, \frac{s-45}{25}),$ $0)\}0)\}$	
ANN = **ANN =**	$\mu_{ANN,Pos}(a) = \{max(min(1, \frac{70-a}{25}),$ $\mu_{ANN,Pos}(a) = \{max(min(1, \frac{70-a}{25}),$ $0)\}0)\}$ $\mu_{ANN,Neg}(a) = \{max(min(1, \frac{a-45}{25})$ $\mu_{ANN,Neg}(a) = \{max(min(1, \frac{a-45}{25})$ $,0)\},0)\}$	

To forecast whether the patient is dengue or not a decision level fusion is used. The following is a representation of fuzzy inference.

$$Ru^{e} = s^{e} \times a^{e} Ru^{e} = s^{e} \times a^{e}$$

(29)

$$\mu ANN \cap SVM \mu ANN \cap SVM =$$

$$\mu_{svm\ (s)} \cap \mu_{ANN\ (a)} \mu_{svm\ (s)} \cap \mu_{ANN\ (a)}$$

(30)

Where a fuzzy relation Ю⁴Ю⁴is well-defined with the rules

$$Ю^{4} = \cup_{e=1}^{4} Ru^{e} Ю^{4} = \cup_{e=1}^{4} Ru^{e}$$

(31)

$$З_{R}(Decision) = max_{1<x<4}[\prod_{z=1}^{4}(\mu_{ANN_x} \mu_{SVM_n})$$

$$З_{R}(Decision) = max_{1<x<4}[\prod_{z=1}^{4}(\mu_{ANN_x} \mu_{SVM_n})]$$

(32)

The proposed model uses the centroid method de-fuzzier, which may be implemented using a variety of ways such as the center-of-area method (COA), the weighted average method, and the mean of maxima method (MOM), and the maximum membership standard. The interface engine generates fuzzy output that is turned into frangible output using comparable functionality as the fuzzier. Equation 33 deals with crisp points.

$$\dot{F} = \frac{З Ю_{\mu R}(R) ð R}{З Ю_{\mu R}(R) ð R} \dot{F} = \frac{З Ю_{\mu R}(R) ð R}{З Ю_{\mu R}(R) ð R}$$

(33)

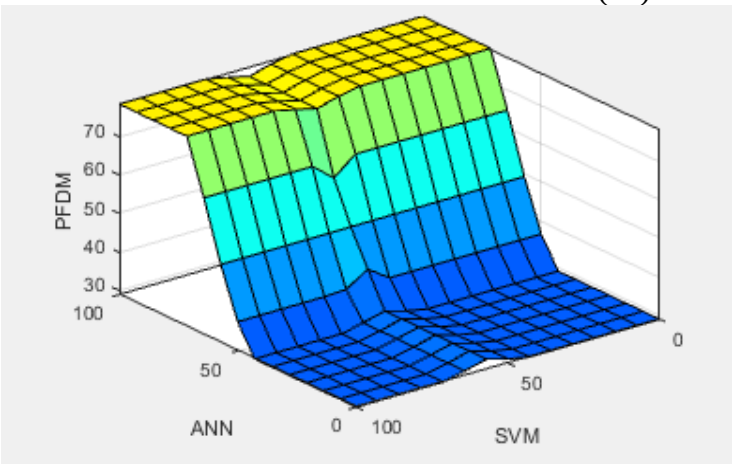


Fig. 2. Figure 2: Rule surface of PFDM

The x-axis corresponds to SVM, the y-axis to ANN, and the z-axis to the PFDM solution, as shown in Fig. 2. The PFDM Framework can be used to compare dengue ANN and SVM outputs. The result is if both approaches predict no dengue, PFDM Structure predicts no dengue; when both models

predict dengue as a yes, PFDM Structural also forecasts dengue as a 1.

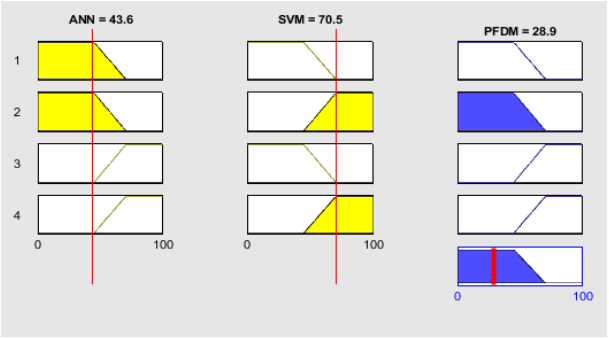


Fig. 3. Figure 3: PFDM system outcomes with dengue (Positive)

Fig. 3 demonstrates that if the ANN predicts yes (1) dengue and the SVM predicts not (0) dengue, the fused model predicts yes (1) dengue as well. Fig. 4 shows that If ANN predicts no (0) dengue and SVM predicts no (0) dengue, the fused model also predicts no (0) dengue. The proposed framework's testing layer entails real-time diagnosis and categorization of dengue patients. The proposed PFDM model uses real-time patient data to enhance the illness detection system.

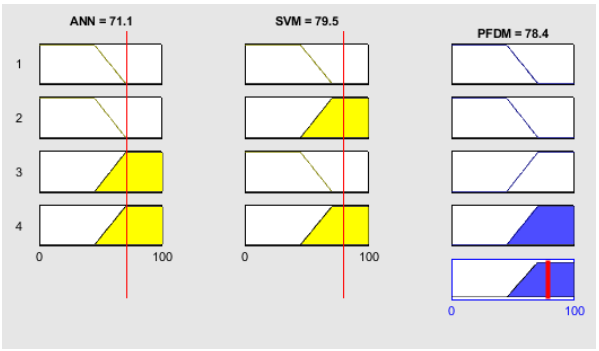


Fig. 4. PFDM system outcomes with dengue (Negative)

IV. Discussion and Result

MATLAB R2018a was used to simulate the proposed model. ANNs and SVMs are employed in the prediction phase. Datasets for dengue patients collect from the government hospital of Lahore, Pakistan. Dataset has a total number of rows are 347 and has 7 columns. The number of cases utilized to train the ANN is 242, as shown in Tab. 2.

TABLE III. TABLE 2. ANN-BASED RESULTS DURING TRAINING

	True Class	Output Values	
Input Values	Total=242	Positive $\hat{O}R_1$	Negative $\hat{O}R_2$
	Positive $\acute{E}R_1$	106	8
	Negative $\acute{E}R_2$	3	125

The instances of each class are described in Tab. There are 114 cases in Class 1 (Positive), with 106 cases correctly anticipated and 8 cases incorrectly predicted. Class 0 (Negative) has a total of 128 cases, with 125 cases correctly predicted and three cases incorrectly predicted. The number of examples utilized to test the ANN is 156, as shown in Tab. 3.

TABLE IV. ANN-BASED RESULTS DURING TESTING

	True Class	Output Values	
Input Values	Total=105	Positive $\hat{O}R_1$	Negative $\hat{O}R_2$
	Positive $\acute{E}R_1$	42	4
	Negative $\acute{E}R_2$	0	59

The instances of each class are described in Tab. 4. There are 46 cases in Class 1 (Positive), 42 of which are correctly anticipated and 4 of which are incorrectly predicted. There are 59 cases in Class 0 (Negative), with 59 cases correctly predicted and 0 cases incorrectly predicted. The confusion matrices of SVM training using five-fold cross-validation are described in Tab. 6. The number of cases utilized to train the SVM is 242, as shown in Tab. 4.

TABLE V. SVM BASED RESULTS DURING TRAINING

	True Class	Output Values	
Input Values	Total=242	Positive $\hat{O}R_1$	Negative $\hat{O}R_2$
	Positive $\acute{E}R_1$	106	10
	Negative $\acute{E}R_2$	3	123

There are 116 cases in Class 1 (Positive), with 106 cases correctly predicted and 10 cases incorrectly predicted. There are a total of 125 cases in Class 0 (Negative), with 123 cases correctly predicted and three cases incorrectly predicted. The number of examples utilized to test the SVM is 105, as shown in Tab. 5.

TABLE VI. SVM BASED RESULTS DURING TESTING

	True Class	Output Values	
Input Values	Total=105	Positive $\hat{O}R_1$	Negative $\hat{O}R_2$
	Positive $\acute{E}R_1$	40	3
	Negative $\acute{E}R_2$	4	58

The instances of each class are: Class 1 (Positive) has a total of 43 cases, 40 of which are correctly anticipated and three of which are incorrectly predicted. There are 62 examples in Class 0 (Negative), 58 of which are correctly predicted and 4 of which are incorrectly predicted. The number of instances utilized to test the PFDM is 105, as shown in Tab. 6.

Tab. 6 describes the instances of each class: Class 1 (Positive) has a total of 47 instances in which 43 cases are truly predicted while 4 cases are wrongly predicted. Class 0 (Negative) has a total of 58 instances in which 58 cases are truly predicted while 0 cases are wrongly predicted.

TABLE VII. PROPOSED PREDICTION FUSED DENGUE MODEL (PFDM) BASED RESULTS DURING TESTING

	True Class	Output Values	
Input Values	Total=105	Positive $\hat{O}R_1$	Negative $\hat{O}R_2$
	Positive $\acute{E}R_1$	43	4
	Negative $\acute{E}R_2$	0	58

$$\text{Accuracy} = \frac{\left(\acute{O}R_1/_{ER_1} + \acute{O}R_2/_{ER_2}\right)}{ER_1 + ER_2} \quad (35)$$

$$\text{Miss Rate} = \frac{\left(\acute{O}R_2/_{ER_1} + \acute{O}R_1/_{ER_2}\right)}{ER_1 + ER_2} \quad (36)$$

$$\text{PPV} = \frac{\left(\acute{O}R_2/_{ER_2}\right)}{\left(\acute{O}R_2/_{ER_2} + \acute{O}R_1/_{ER_2}\right)} \quad (37)$$

$$\text{NPV} = \frac{\left(\acute{O}R_1/_{ER_1}\right)}{\left(\acute{O}R_1/_{ER_1} + \acute{O}R_2/_{ER_1}\right)} \quad (38)$$

$$\text{Specificity} = \frac{\left(\acute{O}R_1/_{\acute{O}R_1}\right)}{\left(\acute{O}R_2/_{ER_2} + \acute{O}R_1/_{ER_2}\right)} \quad (39)$$

$$\text{Sensitivity} = \frac{\left(\acute{O}R_2/_{ER_2}\right)}{\left(\acute{O}R_2/_{ER_1} + \acute{O}R_2/_{ER_2}\right)} \quad (40)$$

$$\text{FDR} = \frac{\left(\acute{O}R_2/_{\acute{O}R_1}\right)}{\left(\acute{O}R_2/_{ER_1} + \acute{O}R_1/_{ER_1}\right)} \quad (41)$$

$$\text{FPR} = 1 - \text{Specificity} \quad (42)$$

$$\text{FNR} = 1 - \text{Sensitivity} \quad (43)$$

$$\text{F1 Score} = 2 \times \frac{\text{PPV} \times \text{Sensitivity}}{\text{PPV} \times \text{Sensitivity}} \quad (44)$$

Both the ANN and SVM models, as well as the suggested PFDM model, are compared in Tab. 7. On test data, the suggested PFDM model beat both ANN and SVM.

TABLE VIII. OUTCOMES OF SVM, AND ANN PROPOSED PFDM

	ANN Train %	ANN Test %	SVM Train %	SVM Test %	PFDM%
Accuracy	95.45	95.24	94.63	93.33	96.19
Miss-arte	4.55	4.76	5.37	6.67	3.81
Sensitivity **Sensitivi**	97.25	97.67	97.25	90.91	1
Specificity Specifici	93.98	93.55	92.48	95.08	93.55
PPV	92.98	91.30	91.38	93.02	91.49
NPV	97.66	98.31	97.62	93.55	1
FPR	6.02	6.35	7.52	4.92	6.45
FNR	2.75	2.33	2.75	9.09	0
F1-Score	95.07	94.38	94.22	91.95	95.56

Tab. 8 shows that the proposed model gives 96.19% accuracy which is higher than the state-of-the-art previous published articles.

TABLE IX. TABLE 8: COMPARISON OF PFDM WITH PREVIOUS WORK

Papers	Year	Dataset	Techniques	Accuracy
[15]	2021	Generation of a synthetic dataset	CART, SVM, Naïve Bayes, ANN	70%, 70%, 62%, 66%
[16]	2021	Ministry of Health Malaysia (MOH), and Malaysian Meteorological Department (MMD).	Bayes Net, SVM	92.35% 88%
[19]	2018	Continue and Discrete dataset of Dengue patients	CART, ANN	88%, 92%
[20]	2015	District Headquarter Hospital Jhelum	Bayesian, RT, Random forest	92%, 76%, 76%
[14]	2018	Kaurna Medical Hospital, Kerala	Naïve Bayes, J48, Random forest	63.3%, 76.6%, 83.3%
Proposed Model	2022	Health Department	PFDM	96.19%

V. CONCLUSION

Dengue fever has recently grown in Pakistan, to the extent that it has become a severe public health problem. Dengue fever must thus be recognized early to control and avoid the disease's negative effects on the body. One of the most challenging problems facing the healthcare profession is detecting dengue disease in its early stages. Our research-based method can accurately predict dengue fever. Machine learning approaches are being used to evaluate a range of medical data to better diagnose and advise optimum treatment of major health concerns. This study suggests a machine-learning-based automated dengue decision-assistance system. The suggested model includes two commonly known ML approaches, SVM and ANN, using fuzzy logic. The fuzzy decision system's accuracy was 96.19 percent, which was a high number when compared to comparable systems. We have also compared our technique to the most recent one. Hybrid classification approaches, data mining optimization, and fuzzy logic procedures are all used.

To enable physicians and patients to evaluate dengue fever much more rapidly and accurately, data mining methods must be employed implicitly, aligning both F and HF illnesses. According to the conclusions of this study, class imbalance is a crucial component in classification, and accuracy rates alone do not fully indicate classification efficiency. We will also create a website or mobile application for dengue patients in the future.

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Conflict of interest

The authors declare there is no conflict of interest.

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