



International Journal of Artificial Intelligence and Machine Learning

Publisher's Home Page: <https://www.svedbergopen.com/>



Research Paper

Open Access

LIME-HyGRU: An Explainable Hybrid Machine Learning and GRU Algorithm for Predicting Vector-Borne Diseases

¹*K. Kavitha, ²T. Prabhu, ³A. ARUN

¹*Research Scholar, Department of Computer Applications, Dr. MGR Educational and Research Institute, Chennai, Tamilnadu, India-600 095. kavithak_csc@bwc.edu.in.

²Associate Professor and Dean, Department of Computer Applications, Dr. MGR Educational and Research Institute, Chennai, Tamilnadu, India-600 095. prabhu.cse@drmgrdu.ac.in.

³Head of Operations, Giggso India Pvt. Ltd. Chennai - 600 097. arunambashanker@gmail.com

Abstract

Vector-borne diseases remain a major global health concern, causing more than 700,000 deaths annually. These diseases are transmitted by vectors such as mosquitoes, ticks, flies, and fleas and are caused by a wide range of infectious agents, including bacteria, viruses, and parasites. Delayed diagnosis, particularly in regions with limited access to specialist healthcare results in increasing the complications and mortality. This leads the importance of developing a decision-support systems that can assist healthcare professionals in identifying these diseases at an early stage. This study proposes LIME-HyGRU, an explainable deep learning framework for the prediction of multiple vector-borne diseases by combining a Hybrid Gated Recurrent Unit (HyGRU) network with Local Interpretable Model-agnostic Explanations (LIME). This model enables both accurate disease prediction and transparent interpretation, allowing users to understand which clinical features contribute most to the final outcome. The combination of deep learning and explainable artificial intelligence (XAI) makes the model more suitable for clinical decision support. The framework is trained using labeled patient data and validated on previously unseen test samples to assess its predictive capability. Model performance is evaluated using widely accepted classification metrics, including accuracy, precision, recall, F1-score, confusion matrix, and receiver operating characteristic (ROC) analysis. The experimental findings indicate that LIME-HyGRU not only achieves reliable prediction performance but also offers meaningful explanations that improve the transparency and trustworthiness of the prediction process. These results demonstrate the potential of the proposed framework as an AI-assisted expert system for the early prediction and clinical management of vector-borne diseases.

Keywords: Vector Borne Disease Prediction, Random Forest, XGBoost, Gradient boosting, LIME, GRU.

1. Introduction

A mosquito, sandfly, or other bloodsucking vector may transmit an infectious illness known as a vector-borne disease (VBD). Some examples of these illnesses include Zika, chikungunya, dengue fever, leishmaniasis, and malaria. The global illness burden is rising due to these infections. The annual death toll from VBDs is 700,000, putting more than 80% of the world's population at danger [1]. A research found that there were 104 million dengue virus cases globally in 2017, compared to 23 million in 1990 [2]. The World Health Organisation (WHO) ranks dengue fever (DF) as one of the top ten global health concerns; the disease is believed to affect 40% of the world's population and has 390 million annual cases. More than 3,00 fatalities have been recorded, and there have been more than 16,000 severe cases and 7.6 million dengue cases registered for the year as of April 30, 2024, according to the World Health Organisation (WHO)[3]. Dengue fever is on the rise in regions that were previously untouched by globalisation and continuing climate change, despite the fact that the disease is most often seen in poor and developing nations. From moderate fever accompanied by symptoms including raised body temperature, eye discomfort, aching muscles and joints, synovitis, and headaches to more hemorrhagic severe fever and shock syndrome, dengue infections may manifest in a wide range of degrees.

Communicable and vector borne diseases make up a disproportionately high amount of India's mortality toll. Communicable and vector-borne diseases are disproportionately affecting rural areas, where healthcare providers are challenged to offer adequate treatment. certain diseases therefore cause more deaths per year in certain places. Most of the diseases transmitted by mosquitoes have similar symptoms that appear later in life. Many people die because the illness progresses owing to the delay in treatment. Technology (4) has become an important tool in developing expert systems that can assist in the accurate diagnosis of vector-borne diseases and recommend appropriate treatment options. Over the past few decades, there have been major technological advances related to vector-borne diseases (VBDs). Advances in both hardware and software have

improved the collection, data gathering, management and analysis of the disease, while the emergence of molecular tools for identification of vector species and pathogens. These advances enable us to predict, prevent and control VBDs to a far larger degree than previously [5].

Machine learning (ML) enables computers to learn patterns from data and improve their performance without being explicitly programmed for every task. Instead of relying solely on predefined rules, ML algorithms identify relationships within historical data and use this knowledge to make predictions on new data. It involves two stages: training where model learns from trained data and testing where unseen samples are evaluated. Machine learning has many practical uses, such as in voice recognition and spam filtering. Disease prediction is one area where this technology has found use in healthcare [6]. Machine learning (ML) is an important part of artificial intelligence (AI) and has been used as a powerful tool to effectively analyse large datasets obtained from biosensors and then extract important information [7]. Local Interpretable Model-Agnostic Explanations, or LIME for short, is a popular XAI framework for deciphering ML predictions [8].

Deep Learning plays its vital function in all the fields of Engineering and its applications. Deep learning has its impact in medical area, automobile industry, business forecasting/prediction, computer vision, video classification, pattern recognition, natural language processing, clustering, regression and voice recognition. In machine learning it is possible to predict and classify but are not scalable. In deep learning, we are adding numerous layers to reach a solution (in terms of categorization and prediction). The concept of deep learning is based on the structure of the brain and its neural system. The processing units are divided into the input layer, the hidden layer and the output layer. Weights are associated with each layer and adjusted in each cycle [9]. Deep learning algorithms were used for predicting directly transmitted infectious illnesses. Some of the advanced deep learning models like LSTM and gated recurrent unit (GRU) recurrent neural networks with a large number of discrete time steps have been employed in forecasting infectious diseases such as influenza, dengue incidence and hand, foot and mouth disease. GRU model has beaten other machine learning algorithms in accuracy prediction [10].

2. Literature review

Early identification and personalised treatment techniques of vector-borne illnesses were developed by Arun B. Prasad et al. [11] using machine learning models. Malaria, dengue fever, Lyme illness, Zika virus, and chikungunya were able to be reliably predicted by the model, which was constructed using a mix of SVM, DT, RF, and Naive Bayes classifiers. Multiple datasets comprising illnesses, whether city conditions or temporal series included, and symptoms were used to teach the physician or the process of going through these diagnoses and weather conditions, which included the patient's symptoms.

A technique to enhance the prediction of dengue fever outbreaks was devised by Tanvir Ferdousi et al. [12] using pertinent incidence data from outlying regions as characteristics. The researchers used windowed cross-correlation analysis on dengue case data to determine feature rankings. Within the time series, they suggested two ways to distribute correlation windows (size and position) in order to calculate correlation weights. They use a mix of criteria including correlation, distance, and prevalence to rank the periphery sites (PIC) of a target location (IC). By using the ranked feature sets, the predictive models are able to achieve model- and location-specific optimum performances using a limited fraction of information.

Nermeen Gamal Rezk et al. [13] employed the Voting Ensemble (VEL) model for the prediction of explainable heart disease and prognosis. The main objectives are to build predictive models and to improve their interpretability by using SHAP (SHapley Additive Explanations) and LIME (Local Interpretable Model-agnostic Explanations) analyses. They carefully develop their systems and test numerous hybrid ensemble learning approaches in order to discover the best model for HDP. The results of the model evaluation indicate that it could be an effective and sophisticated tool for cardiovascular risk assessment. In real-world scenarios, the model showed better performance than the alternatives with an accuracy percentage of 96.5%.

In their study on geographically extensive diseases, Debra P. C. Peters et al. [14] pointed out that one of the primary challenges is to predict the causes of incursion and expansion of vector-borne diseases. This is especially the case for diseases that spread because of climatic and other environmental heterogeneity. The researchers adopted a human-guided machine learning strategy to combine multi-scale big data models. They employed their approach to quantitatively examine the importance of over 400 globally distributed environmental variables for the development of EWS for vesicular stomatitis (VS), a common vector-borne vesicular illness affecting cattle in the Americas. " They believed that they can apply their big data approach of human and machine learning to other emerging diseases to help us understand, predict and treat vector-borne illnesses better."

To study the impacts of climate change on vector-borne illnesses, Andrew Endo et al. [15] were among the first to try to construct a mechanistic theoretical framework that combines life cycle theory, thermal biology,

population dynamics, and epidemiology. Instead of deducing processes from data, it proposes to explain them from fundamental principles, which is where its originality resides. To provide disease prevalence and dissemination estimates that are totally unrelated to population-level data (such time series), they use dynamical models that integrate temperature response functions that are generated from mechanics and parameterised using temperature response data. They make it possible to compare the model's projected time series of prevalence with comparable data for any place, with more degrees of freedom and statistical power.

According to Omar Enzo Santangelo et al. [16], there are numerous study methodologies in the emerging field of using machine learning models for early or real-time verification of epidemics. This makes it challenging to compare studies methodologically, even though they all reach the same conclusion—that major infectious disease outbreaks can be monitored. There have been many global epidemics of infectious illnesses in the last few decades, and machine-learning models provide a way to track their emergence and progression. On top of that, their use in healthcare and scientific research is only going to increase.

G. Jeyakodi et al. [17] created OaRCM, a combination of a relation classification model driven by ontologies and a DL model. The OaRCM was tested on the SemEval-2010 Task 8 benchmark dataset and the MVAont-encoded, manually annotated MosqVecBA dataset. The model improves its classification performance by combining many sophisticated neural network designs, such as LSTM, BiLSTM, and BiGRU, with self-attention layers, dropout layers, dense layers, and an ensemble approach. In terms of learning capacity and classification performance, the results show that the ontology-encoded OaRCM outperforms conventional ML and DL models. Using contrastive data, Sandali Raizada et al. [18] presented a novel CNN-MDOP algorithm for multimodal epidemic prediction. No prior study has, as far as they are aware, concentrated on contrasting data in the field of medical data analysis. Their proposed CNN algorithm achieves a prediction accuracy of 88%.

Using Imagenet-trained Convolutional Neural Network (CNN) models, Nabeel Abdur Rehman et al. [19] annotated London landscape elements in satellite imagery. After that, they used a famous Susceptible-Infectious-Recovered epidemic model using dengue case data from 2012–2016 in Pakistan and landscape characteristics identified using CNN from satellite images of the country. They looked at ways to enhance the prediction model for each landscape component separately and evaluated the practicality of using labels from a different location for the images. Important for proactive and strategic control and monitoring programs, they discovered that using landscape data retrieved from satellites may enhance epidemic prediction.

Mokammel Hossain Tito et al. [20] reported that the application of ML models enhanced the predictive skills by discovering patterns and correlations among various data inputs such as climate, environmental parameters, host population dynamics, vector abundance, and historical disease incidence. The Support Vector Machine (SVM) was the best function classifier model that was used to predict vectorborne infections and several parameters were employed to determine this. The SVM model with only 0.3 seconds processing time and 90.87% accuracy is surely the model to use for public health interventions that need to be taken in real-time. It is a powerful instrument for early detection and preventive control of vector-borne disease outbreaks and represents a trade-off between high accuracy and fast processing.

3. Methodology

The LIME-Hybrid GRU Algorithm (LIME-HyGRU) as shown in Figure1, is a unique framework for vector-borne illness prediction that integrates deep learning, explainable AI techniques and machine learning to enhance the accuracy of predictions and the interpretability of models. First we need to get a huge dataset with 64 different health-related medical history factors. The first step is data preparation, which consists of cleaning the data by removing any extra or missing items, encoding the labels of any categorical variables, and normalising the data using the StandardScaler so that all features are scaled evenly. Feature selection is done in two parts. In the first step, predictions are made and features are ranked using a hybrid machine learning model. In the second step, LIME is used to identify the most significant characteristics used by the model to make judgments. This two-stage selection technique selects the twenty most essential medical criteria. Then, from the selected features, a new more complete dataset can be constructed by merging with certain relevant environmental metrics such as average humidity, rainfall, soil moisture and vegetation index. The last dataset is split into 2 parts, one for training and the other for testing with 80:20 ratio. We develop an Enhanced Gated Recurrent Units (GRUs) based deep learning model to explore the data's temporal and sequential patterns. We train the model with the training data and evaluate the model with the testing data. The system performance is comprehensively analyzed using the confusion matrix, accuracy, precision, recall, F1-score, and ROC curve, showing the applicability of the LIME-HyGRU framework for accurate and interpretable vector-borne illness prediction.

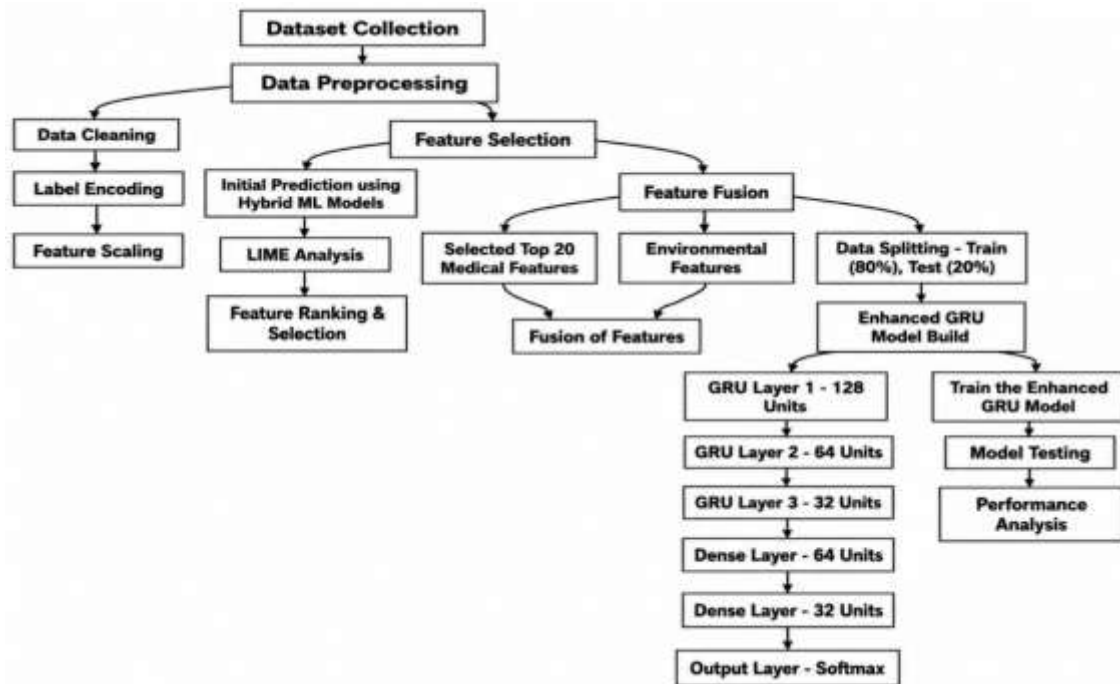


Figure1.Proposed Architecture

i. Dataset collection

The proposed methodology begins with the collection of a comprehensive and reliable dataset. For this study, a publicly available dataset obtained from Kaggle was used. The dataset contains detailed clinical records of patients exhibiting symptoms commonly associated with vector-borne diseases. Included in the dataset are:

- **64 medical features** such as fever, muscle pain, vomiting, rash, coma, jaundice, etc.
- **Prognosis/label** that indicates the diagnosis or disease outcome.

This dataset is essential for strong classification since it ensures a diverse range of symptoms, which is needed for model training. Table 1 shows the sample representation of the vector-borne disease dataset containing medical and prognostic features and Table 2 shows the data loading and exploratory analysis of the collected dataset.

Table 1 Data set used in this investigation

Index	Sudden fever	headache	Mouth bleed	Nose bleed	Muscle pain	Jointpain	vomiting	rash	diarrhea	hypotension	Pleural effusion	ascites	Gastro bleeding	swelling	nausea	chills
1	0	1	1	1	1	0	1	0	0	0	0	1	0	0	0	0
2	1	1	1	1	1	0	1	0	0	0	0	1	0	0	1	0
3	0	1	0	1	0	0	1	1	0	0	0	0	0	0	1	1
4	0	0	0	0	0	1	1	1	0	0	0	0	0	0	1	1
5	1	0	0	1	1	1	1	1	0	0	0	0	0	0	0	1
6	1	1	1	1	1	1	0	1	0	0	0	0	0	0	0	1
7	1	1	0	1	1	1	1	0	0	0	0	0	0	0	0	0
8	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	1
9	0	0	1	1	1	1	1	0	0	0	0	0	0	0	0	1
10	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	1

Table 2 Data Loading and Exploring

Symptom	Count	Mean	Std	Min	25%	50%	75%	Max
---------	-------	------	-----	-----	-----	-----	-----	-----

Sudden_Fever	504	0.5159	0.5002	0	0	1	1	1
Headache	504	0.4087	0.4982	0	0	0	1	1
Mouth_Bleed	504	0.5186	0.5001	0	0	1	1	1
Nose_Bleed	504	0.5476	0.4982	0	0	1	1	1
Muscle_Pain	504	0.5198	0.501	0	0	1	1	1
Joint_Pain	504	0.5039	0.5003	0	0	1	1	1
Vomiting	504	0.4032	0.4908	0	0	0	1	1
Rash	504	0.4096	0.4917	0	0	0	1	1
Diarrhea	504	0.4523	0.498	0	0	0	1	1
Hypotension	504	0.4285	0.4952	0	0	0	1	1
Pleural_Effusion	504	0.4407	0.4969	0	0	0	1	1
Ascites	504	0.4047	0.4903	0	0	0	1	1
Gastro_Bleeding	504	0.4442	0.4972	0	0	0	1	1
Swelling	504	0.4048	0.4908	0	0	0	1	1
Nausea	504	0.4254	0.494	0	0	0	1	1
Chills	504	0.4032	0.4908	0	0	0	1	1
Myalgia	504	0.4048	0.4908	0	0	0	1	1
Digestion_Trouble	504	0.4169	0.4935	0	0	0	1	1
Fatigue	504	0.3286	0.4705	0	0	0	1	1
Skin_Lesions	504	0.4166	0.4934	0	0	0	1	1
Stomach_Pain	504	0.4007	0.4905	0	0	0	1	1
Orbital_Pain	504	0.4206	0.4945	0	0	0	1	1
Neck_Pain	504	0.4463	0.4972	0	0	0	1	1
Weakness	504	0.4523	0.4982	0	0	0	1	1
Back_Pain	504	0.4325	0.4958	0	0	0	1	1

ii. Data preprocessing

Cleanup and standardization of raw environmental and clinical data in preparation for modelling is the focus of this lesson. Handling missing values is the first step in data cleansing, which is the first module in this. Table3 show the null value analysis during data preprocessing. The data is transformed after cleaning. Table 4 shows the conversion of categorical string features into numerical values using label encoding. An important step towards making categorical features compatible with ML and DL models is to encode them using Label Encoding, which transforms non-numerical labels into numerical values. After that, we scale the features using StandardScaler, which normalises them by lowering their variance and eliminating their mean. Feature normalization using StandardScaler is shown in Fig. 2. This normalisation process improves convergence stability and speed of machine learning algorithms, particularly those that are sensitive to variations in feature scales. Preprocessing step enhances the effectiveness of subsequent feature selection and facilitates the integration of environmental variables. The output of this stage is a clean, standardized, and well-structured dataset that is ready for model training and further analysis.

Table 3 Clean data for processing and - Null Value Checking Result	
Symptom	Value
Sudden_Fever	0
Headache	0
Mouth_Bleed	0
Nose_Bleed	0
Muscle_Pain	0
Ulcers	0
Toenail_Loss	0
Speech_Problem	0
Bullseye_Rash	0
Prognosis	0

Length	65, dtype: int64
--------	------------------

sudden_fever	headache	mouth_bleed	nose_bleed	muscle_pain	joint_pain	vomiting	rash	diarrhea
0	1	1	1	1	0	1	0	0
1	1	1	1	1	0	1	1	1
0	1	0	1	0	0	1	1	0
0	0	0	0	0	1	1	1	0
1	1	1	1	1	1	0	1	0
1	0	0	0	1	1	1	1	0
1	1	1	1	1	1	0	1	0
1	1	1	1	1	1	0	1	0

```
array([[ -1.03226633,  1.08278058,  0.96107446, ..., -0.45358751,
        -0.36760731, -0.37452836],
       [ 0.96874225,  1.08278058,  0.96107446, ..., -0.45358751,
        -0.36760731, -0.37452836],
       [ -1.03226633,  1.08278058, -1.0405021 , ..., -0.45358751,
        -0.36760731, -0.37452836],
       ...,
       [ -1.03226633,  1.08278058,  0.96107446, ...,  2.20464626,
         2.7202941 ,  2.67002477],
       [ -1.03226633, -0.92354815, -1.0405021 , ...,  2.20464626,
         2.7202941 ,  2.67002477],
       [ -1.03226633, -0.92354815,  0.96107446, ...,  2.20464626,
         2.7202941 ,  2.67002477]])
```

Figure2.Data Scaling using Standard Scaler

iii. Feature selection

This module is essential for improving model performance by keeping just the most important information and lowering dimensionality. An initial prediction is made utilising an internal decision-making process of a Hybrid Machine Learning model (e.g., a Random Forest and Gradient Boosting combo) that ranks the relevance of features.

A **Soft Voting Classifier** is used, combining three powerful models:

- **Random Forest:** Using several subsamples of the dataset, the Random Forest (RF) classifier employs a network of decision trees. Instead of utilising a decision tree to find the best segmentation point, it only uses randomisation to accomplish suboptimal segmentation. Because it controls overfitting and employs several decision trees on distinct subsets of information, it uses average predicted accuracy. With a big number of characteristics, it can build a classifier that is quite accurate [1].

- **XGBoost :** The XGBoost is an intuitive and adaptable ensemble method for machine learning. It offers a practical application of a gradient boosting machine learning model that is believed to be effective in healthcare [10].

- **Gradient Boosting:** One important technique to boosting is gradient boosting, which is an effective tool for developing predictive models. Building poor learners in a sequential fashion and then gradually merging them to improve overall performance is the basic idea of boosting [3]. Using Randomised Search Cross-Validation, we hyperparameter-tune each model to find the best possible configurations while keeping the computing cost to a minimum. Figure 3 shows the performance evaluation of the hybrid ensemble machine learning model

-

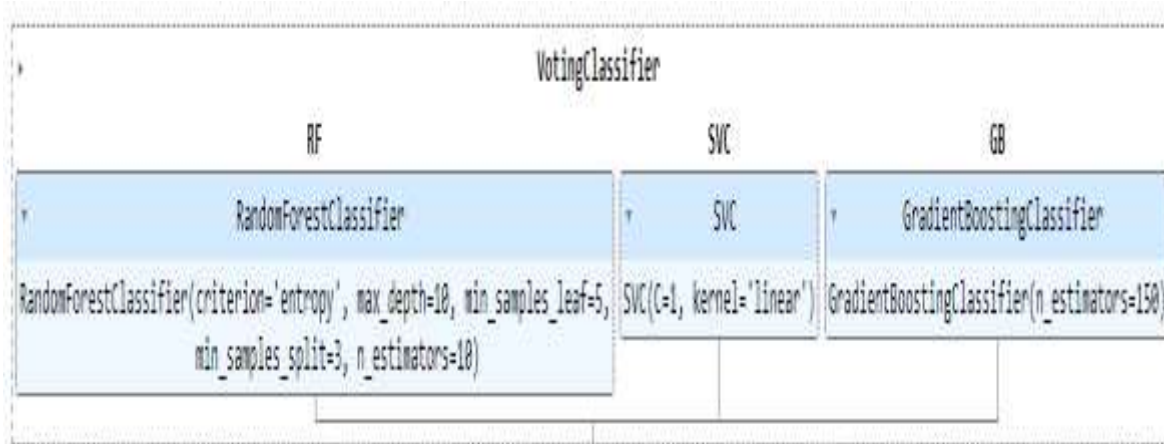


Figure3. Initial Prediction: Hybrid ML Model Performance

iv. Hybrid ML ensemble

- Models: Random Forest, SVC (probability=True), Gradient Boosting
- Hyperparameter Tuning: RandomizedSearchCV over parameter grids (e.g., RF n_estimators = [50,100,200], max_depth = [10,20,None]; SVC C = [0.1,1,10], γ = [0.001,0.01], kernel=rbf; GB learning_rate = [0.01,0.1], n_estimators = [50,100,200])
- Voting: Soft voting ensemble of the three tuned models

By using an interpretable model to locally approximate any classifier or regressor, LIME may provide a correct explanation for the predictions made by any of these algorithms. Among LIME's most important features are interpretable representation and proximity accuracy. The ability to interpret results helps to clarify the relationship between the variables used as inputs and the outcomes. Simultaneously, the veracity or accuracy of the model's output close to the anticipated instance is indicated by local fidelity. If an explainer algorithm is "model agnostic," it means it may use the original model as a "black box" and provide an explanation for any model. Explanations for tabular datasets, text-based models, and image classifications are all within LIME's purview. One or more of the following formats may be used to convey these explanations: text, numbers, or images [21]. It is possible to find the best possible configurations for each model with the least amount of computing effort by hyperparameter tuning them using Randomised Search Cross-Validation.

Every single prediction generated by any Machine Learning model may be better understood using this visualisation method. Since LIME assumes that all models are locally linear, it attempts to fit the model to a single observation in an effort to localise the global model's behaviour. LIME employs this elementary model to provide a local level explanation for the predictions made by the more complex models [8].

The LIME (Local Interpretable Model-Agnostic Explanations) approach is used to modify the selection process after initial prediction in order to add model interpretability. By making local approximations using interpretable models (like linear regression), LIME elucidates the predictions of complicated models and shows which aspects are most influential on individual predictions. The chosen traits are statistically significant and have semantic relevance since model-driven and interpretability-based insights are fused.

Based on their influence on prediction accuracy, the top 20 medical characteristics are chosen from the initial 64 features. Then, these chosen characteristics are combined with those of the surrounding environment. These variables enhance the contextual awareness of patient risk and are known to impact the transmission of vector-borne illnesses. A more robust prediction model is the outcome of merging individual medical records with geographical environmental variables in a fused dataset.

v. Feature fusion

Medical and environmental aspects are combined in the final dataset for modelling. Together, the five environmental variables and twenty medical features chosen by LIME create a 25-dimensional feature vector for each record. The GRU is able to learn how symptoms interact with environmental elements that promote vector proliferation because of this integration of ecological drivers and host clinical characteristics.

- **Medical subset:** 20 LIME-selected features
- **Environmental set:** Avg. Temperature, Humidity, Rainfall, Soil Moisture, Vegetation Index
- **Combined input:** 25 features per instance

By combining patient symptoms with environmental factors into a single dataset, this fusion phase guarantees that the model can learn both internal health signals and external ecological determinants of vector-borne illness risk. Fusion of clinical and environmental features into the final dataset can be seen in Table5.

Table 5 Module 4 – Features Fusion New Dataset

prostration	convulsion	hypotension	weakness	tremor	Avg_Temperature	Humidity	Rainfall	Soil_Moisture	Vegetation_Index
0	0	0	0	0	27.5126	62.041	298.6984	22.6079	0.5606
0	0	0	0	0	32.8795	75.7593	228.8627	10.6642	0.8106
0	0	0	0	0	25.5699	76.7351	197.7079	11.9507	0.7419
0	0	0	0	0	34.4781	78.467	5.7705	20.1983	0.5864
0	0	0	0	0	29.8076	48.4672	288.4201	38.2101	0.1078
0	0	0	0	0	36.0833	89.1607	27.1153	21.8257	0.7461
0	0	0	0	0	32.0937	45.7215	181.1519	30.458	0.4768
0	0	0	0	0	27.679	84.3416	291.4975	39.8943	0.1846
0	0	0	0	0	20.9036	58.739	155.9859	30.1907	0.4887
0	0	0	0	0	26.8224	48.5917	286.3528	38.4976	0.7661
0	0	0	0	0	32.0956	61.5015	182.0359	26.3041	0.4312

vi. Building enhanced GRU model

An Enhanced Gated Recurrent Units (GRU) version of recurrent neural networks (RNNs) is recognised for effectively learning temporal and sequential patterns in time-series or organised tabular data, and this fundamental module is responsible for building and training a deep learning model based on this variety. When computing economy is paramount, GRU's equivalent performance and simpler design make it the preferred choice over more conventional RNNs and LSTMs.

An enhanced recurrent neural network, GRU is essentially a stripped-down version of LSTM that merges the input and forgetting gates into a single update gate. Since GRU lacks an extra memory cell, it is limited to controlling information inside the unit; its components are an update gate and a resets gate [10]. Figure 4 describes the internal architecture of the enhanced GRU network.

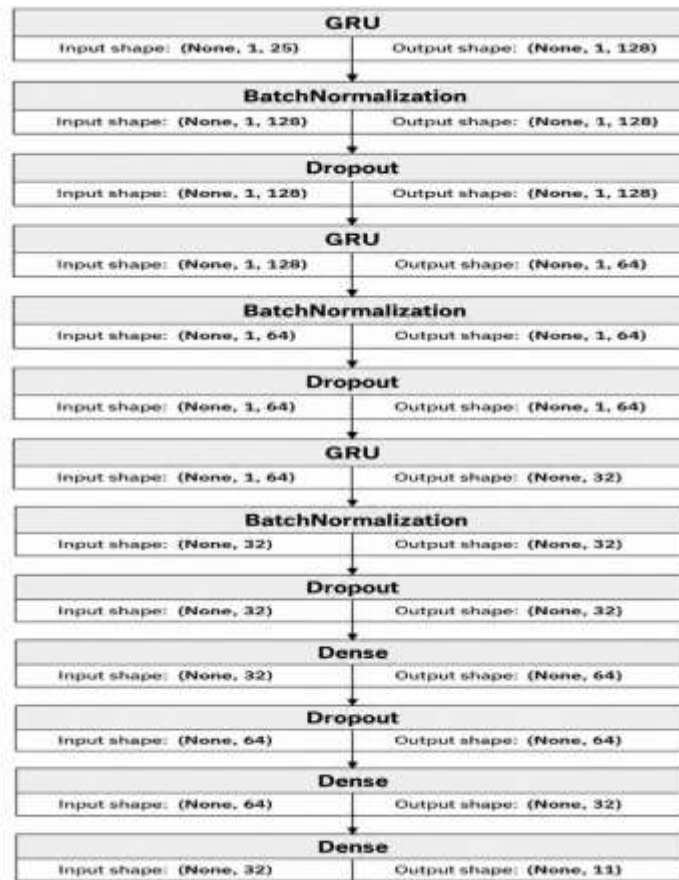


Figure4. Enhanced GRU Architecture

The Long Short-Term Memory (LSTM) unit and the Gated Recurrent Unit (GRU) are conceptually identical and, in some situations, provide identical results. By using two gates, namely the update and reset gates, GRU is able to address the issue of vanishing gradient. The amount of historical data that needs to be sent on in the future is determined by the update gate, whereas the amount of historical data that needs to be erased is determined by the reset gate. GRU is a small, quick model that outperforms LSTM in terms of both memory consumption and execution speed because to its reduced parameter requirements. Without the need for cell memory units, GRU units regulate the flow of data [6].

The GRU model takes the enhanced feature set output by the prior module as its input. An 80:20 split is used to divide the dataset into training and testing subsets. A stacked GRU (Gated Recurrent Unit) architecture is a part of the improved GRU model architecture that models complicated patterns in the data. The stacking process begins with three GRU layers:

- GRU(128, return_sequences=True) followed by BatchNormalization and Dropout(0.3),
- GRU(64, return_sequences=True) followed by BatchNormalization and Dropout(0.3),
- GRU(32, return_sequences=False) followed by BatchNormalization and Dropout(0.3).

GRUs solve the vanishing gradient issue and allow the network to recall long-term relationships using gating mechanisms, which are recurrent layers with update and reset gates. Two fully-connected layers are added after the recurrent stack: one with Dense(64) activation and ReLU activation, followed by Dropout(0.2), and another with Dense(32) activation and ReLU. Last but not least, the eleven illness classes' probability are generated by the Dense(11, softmax) output layer. Training may be stabilised by batch normalisation after each GRU, and overfitting can be prevented via dropout layers. In the end, the model produces a disease probability distribution after learning sequential patterns in the fused characteristics. The training architecture of the proposed stacked GRU model is presented in Fig. 5.

- Layer 1: GRU with 128 units (return_sequences=True), BatchNormalization, Dropout rate=0.30.
- Layer 2: GRU with 64 units (return_sequences=True), BatchNormalization, Dropout rate=0.30.
- Layer 3: GRU with 32 units (return_sequences=False), BatchNormalization, Dropout rate=0.30.
- Dense Layers: Dense(64, activation='relu') + Dropout(0.20), then Dense(32, activation='relu').

- Output Layer:Dense(11) with softmax activation for 11-class probabilities.
- Gating Mechanism: Each GRU unit uses update/reset gates to control memory (mitigating vanishing gradients)
- Activation: ReLU in hidden Dense layers; Softmax in output.

Layer (type)	Output Shape	Param #
gru (GRU)	(None, 1, 128)	59,520
batch_normalization (BatchNormalization)	(None, 1, 128)	512
dropout (Dropout)	(None, 1, 128)	0
gru_1 (GRU)	(None, 1, 64)	37,248
batch_normalization_1 (BatchNormalization)	(None, 1, 64)	256
dropout_1 (Dropout)	(None, 1, 64)	0
gru_2 (GRU)	(None, 32)	9,408
batch_normalization_2 (BatchNormalization)	(None, 32)	128
dropout_2 (Dropout)	(None, 32)	0
dense (Dense)	(None, 64)	2,112
dropout_3 (Dropout)	(None, 64)	0
dense_1 (Dense)	(None, 32)	2,080
dense_2 (Dense)	(None, 11)	363

Total params: 111,627 (436.04 KB)

Trainable params: 111,179 (434.29 KB)

Non-trainable params: 448 (1.75 KB)

Figure5. Build Enhanced GRU Model & Training

vii. Model Training

The training set is used to construct and train the model. For our multi-class classification tasks, we use the Adam optimiser in conjunction with categorical crossentropy loss. The main statistic being tracked is accuracy. With a batch size of 32, the model sees the complete training set 50 times in mini-batches of 32 samples during training, which is run for 50 epochs. We keep the train/test split at 80:20. Adam iteratively updates the model's weights during training, adjusting learning rates using estimations of lower-order moments. For the sake of future analysis, the training history is documented, including the loss and accuracy each epoch.

viii. Model Testing

This section assesses the trained GRU model using the 20% hold-out dataset. The model is applied to unseen fused feature vectors and the class with the greatest softmax probability is selected to provide predictions. To evaluate the effectiveness of generalization, the anticipated labels are contrasted with the actual labels.

ix. Performance Analysis

Testing the trained GRU model for accuracy and consistency is the last unit's main emphasis. To provide a thorough review, we employ a variety of quantitative evaluation metrics. A categorisation model's effectiveness may be measured by many factors. The confusion matrix shows true positives, true negatives, false positives, and false negatives to illustrate the model's performance and identify errors. Accuracy measures the model's

overall prediction accuracy. When classes are unbalanced, accuracy and recall (sensitivity) reveal more information. Precision demonstrates how accurate the model's positive predictions are, while recall shows how effectively it finds all relevant positive cases. One statistic, the F1-score, measures accuracy and recall. Balanced assessments are beneficial when class distributions are uneven. Finally, the ROC curve and AUC (Area Under the Curve) graphically and scalarly indicate the TPR-FPR trade-off. These assist evaluate model performance at different thresholds.

4. Results and discussion

a. Performance metrics

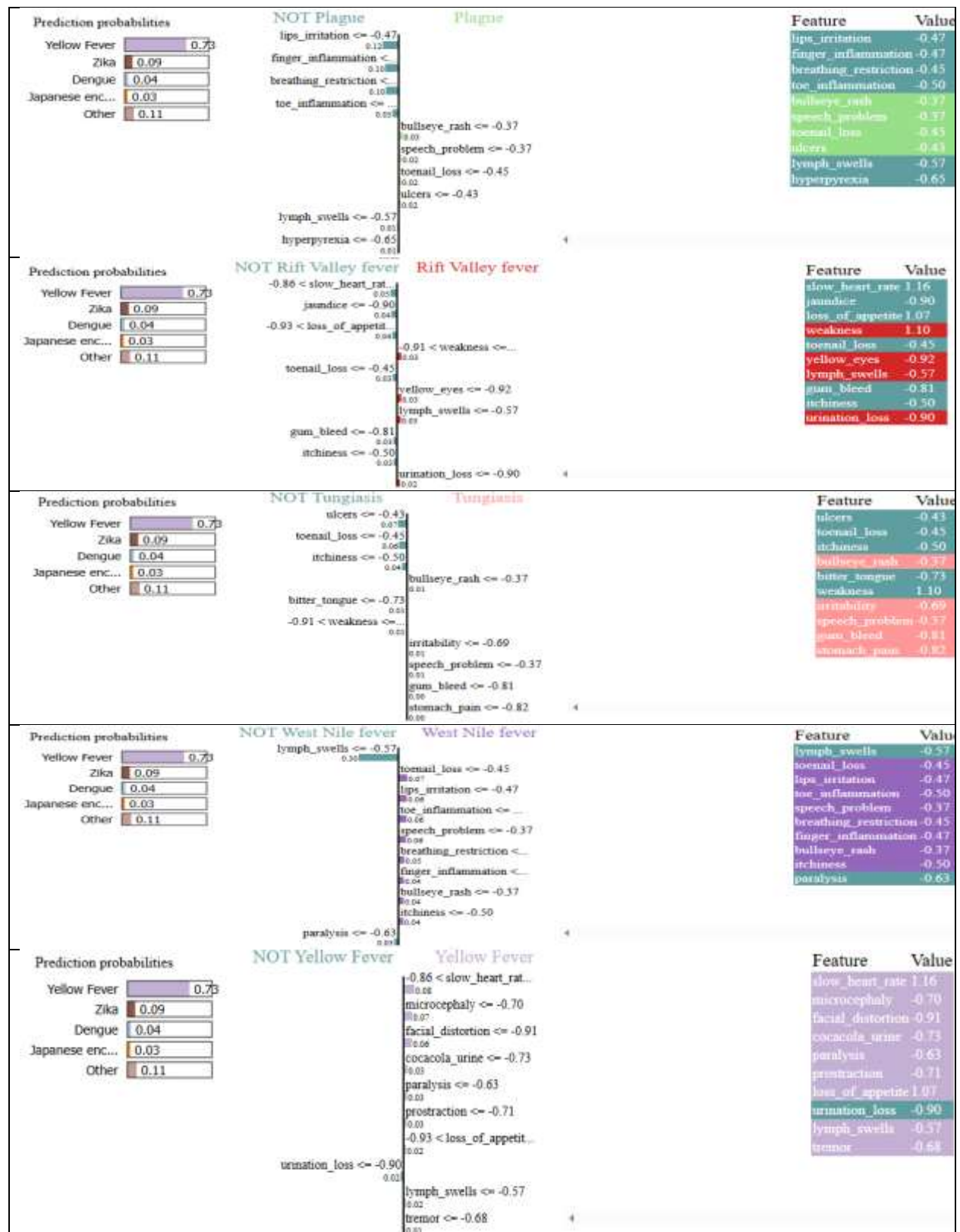
With an accuracy of 96.04%, the hybrid ML model proved to be quite accurate in predicting which vector-borne illnesses would be most effective in eradicating. A high level of accuracy in detecting positive occurrences with few false positives is shown by the precision of 96.76%. The model's reliability to catch relevant instances is validated by high detection rate of true positives as evidenced by recall value of 96.04%. Also, we can see that we have achieved a decent balance between recall and precision, with an F1 Score of 96.07%, thus giving equal weight to sensitivity and accuracy. The model's ability to use specific attributes to reliably forecast illness classes is shown by these high-performance measures.

b. LIME based influence Features analysis for all Classes

This study uses LIME to explain the predictions made by the hybrid machine learning model for each disease class, highlighting the top influential features for accurate classification, and provides a comprehensive understanding of the influence of various features in predicting the probabilities of multiple disease classes. Table 6 explains the step-by-step LIME analysis for different disease classes.

Table 6 Step-by-step analysis on different disease

Prediction probabilities Yellow Fever 0.73 Zika 0.09 Dengue 0.04 Japanese enc... 0.03 Other 0.11	NOT Chikungunya -0.95 < yellow_skin <= ... -0.94 < hypotension <= ... -0.90 < coma <= 1.11 -0.86 < slow_heart_rat... <= ... Chikungunya pleural_effusion <= ... urination_loss <= -0.90 itchiness <= -0.50 digestion_trouble <= ... breathing_restriction <= ... toe_inflammation <= ...	Feature Value yellow_skin 1.05 pleural_effusion -0.89 hypotension 1.07 urination_loss -0.90 itchiness -0.50 coma 1.11 digestion_trouble -0.83 slow_heart_rate 1.16 breathing_restriction -0.45 toe_inflammation -0.50
Prediction probabilities Yellow Fever 0.73 Zika 0.09 Dengue 0.04 Japanese enc... 0.03 Other 0.11	NOT Dengue toe_inflammation <= ... -0.86 < slow_heart_rat... <= ... -0.98 < light_sensitivit... <= ... -0.87 < nausea <= 1.15 -0.87 < weight_loss <= ... -0.91 < weakness <= ... -0.84 < dizziness <= 1.19 Dengue -0.94 < hypotension <= ... lymph_swells <= -0.57 urination_loss <= -0.90	Feature Value toe_inflammation -0.50 hypotension 1.07 lymph_swells -0.57 slow_heart_rate 1.16 urination_loss -0.90 light_sensitivity 1.02 nausea 1.15 weight_loss 1.15 weakness 1.10 dizziness 1.19
Prediction probabilities Yellow Fever 0.73 Zika 0.09 Dengue 0.04 Japanese enc... 0.03 Other 0.11	NOT Japanese encephalitis paralysis <= -0.63 irritability <= -0.69 tremor <= -0.68 Japanese encephalitis lymph_swells <= -0.57 toe_inflammation <= ... headache <= -0.92 -0.98 < light_sensitivit... <= ... bullseye_rash <= -0.37 speech_problem <= -0.37 stomach_pain <= -0.82	Feature Value lymph_swells -0.57 paralysis -0.63 irritability -0.69 tremor -0.68 toe_inflammation -0.50 headache -0.92 light_sensitivity 1.02 bullseye_rash -0.37 speech_problem -0.37 stomach_pain -0.82
Prediction probabilities Yellow Fever 0.73 Zika 0.09 Dengue 0.04 Japanese enc... 0.03 Other 0.11	NOT Lyme disease bullseye_rash <= -0.37 speech_problem <= -0.37 toenail_loss <= -0.45 toe_inflammation <= ... lips_irritation <= -0.47 itchiness <= -0.50 ulcers <= -0.43 confusion <= -0.61 breathing_restriction <= ... irritability <= -0.69 Lyme disease	Feature Value bullseye_rash -0.37 speech_problem -0.37 toenail_loss -0.45 toe_inflammation -0.50 lips_irritation -0.47 itchiness -0.50 ulcers -0.43 confusion -0.61 breathing_restriction -0.45 irritability -0.69
Prediction probabilities Yellow Fever 0.73 Zika 0.09 Dengue 0.04 Japanese enc... 0.03 Other 0.11	NOT Malaria cocacola_urine <= -0.73 rigor <= -0.69 convulsion <= -0.70 hypoglycemia <= -0.68 prostration <= -0.71 Malaria tremor <= -0.68 lymph_swells <= -0.57 paralysis <= -0.63 confusion <= -0.61 -0.85 < skin_lesions <= ...	Feature Value cocacola_urine -0.73 rigor -0.69 tremor -0.68 convulsion -0.70 lymph_swells -0.57 paralysis -0.63 hypoglycemia -0.68 confusion -0.61 skin_lesions 1.18 prostration -0.71





The impact of characteristics was carefully examined by conducting independent LIME studies for each target class, including Chikungunya, Dengue, Zika, Japanese encephalitis, yellow fever, and others. For each class, the analyses prioritised the important attributes according to how much they improved the model's prediction. Features with consistent effect across numerous classes and those with distinct significance for certain illnesses were identified via this step-by-step research.

Table 7 Selected Top 20 Features	
Feature	Importance Score
lymph_swells	0.6141
toe_inflammation	0.2615
speech_problem	0.2366
bullseye_rash	0.2350
paralysis	0.2225
toenail_loss	0.2142
lips_irritation	0.2074
slow_heart_rate	0.1887
breathing_restriction	0.1640
urination_loss	0.1582
cocacola_urine	0.1517
microcephaly	0.1442
finger_inflammation	0.1425
itchiness	0.1366
tremor	0.1161
ulcers	0.1045
irritability	0.0953
hypotension	0.0858
prostration	0.0856
light_sensitivity	0.0787

The top 20 features in each class were determined using the LIME-based feature selection procedure, which took into account their combined significance rankings and presented in Table 7. In order to improve the model's prediction ability in differentiating between different vector-borne illnesses, the most important symptoms and traits were determined.

Lymph Swells (0.6141): This characteristic stood up as the most important, suggesting a robust correlation with several different types of diseases. Diseases such as Dengue, Zika, and Yellow Fever often manifest with swollen lymph nodes, which becomes an important diagnostic marker.

Toe Inflammation (0.2615): In cases where there is inflammation in the toes, it might be a sign of a local infection or an inflammatory reaction across the body, especially in cases when there is a virus or bacterium involved. Its high impact score implies it might be useful for identifying certain conditions.

Neurological symptom (0.2366): This symptom may be used to diagnose diseases of the central nervous system, such as severe dengue fever or Japanese encephalitis.

Bullseye Rash (0.2350): This cutaneous manifestation is characteristic of Lyme disease and other vector-borne diseases, but may also be a diagnostic aid for other disorders.

Paralysis (0.2225): Paralysis is a critical feature for the correct diagnosis because it is a severe symptom that may indicate severe cases of diseases such as Zika and Japanese encephalitis.

Loss of Toenails (0.2142): Loss of toe nails is less common but can occur in extreme cases as a result of long term infection or consequences of a systemic illness; This contributes to the predictive value of the model.

Lips Irritation (0.2074): This is a crucial symptom to note for diagnosis as it might be a symptom of diseases affecting the mucous membranes like Dengue or Zika.

Slow Heart Rate (0.1887): The diagnostic use of Bradycardia (slow heart rate) is illustrated by the fact that it is a systemic reaction found in severe infections such as yellow fever.

Breathing Restriction (0.1640): Respiratory distress is a major symptom in severe cases of several illnesses such as Japanese encephalitis and dengue fever.

Urination Loss (0.1582): This sign is indicative of involvement of the kidneys or urinary system and can be caused by a severe viral infection or hemorrhagic sickness.

Cocacola Urine (0.1517): Important diagnostic criteria include dark-colored urine, which may suggest significant infection, dehydration or hemorrhagic symptoms.

Microcephaly (0.1442): There is strong evidence that this neurological symptom may help in the diagnosis of Zika, a virus that causes congenital microcephaly.

Finger Inflammation (0.1425): This trait, like inflamed toes, helps distinguish between systemic and localised inflammation, which is useful for diagnosing diseases.

Itchiness (0.1366): As a first indicator of a viral infection, skin irritation and itching are typical symptoms.

Tremor (0.1161): Tremors and other neurological symptoms are essential for diagnosing disorders that impact the nervous system, such Japanese encephalitis.

Ulcers (0.1045): Ulcers on the skin or in the mucous membranes help doctors distinguish between serious infections and those affecting the whole body.

Irritability (0.0953): When diagnosing encephalitis or other infections affecting the central nervous system, this symptom is critical.

Hypotension (0.0858): In diseases like Dengue Shock Syndrome, a dangerously low blood pressure reading is a telltale sign of systemic infection or serious involvement.

Prostration (0.0856): Severe or advanced stages of infection may be identified by signs of extreme weariness and prostration.

Light Sensitivity (0.0787): As a neurological sign, photophobia (light sensitivity) is seen in encephalitic infections and other serious viral disorders.

The most diagnostically important symptoms across a variety of vector-borne illnesses are summarised in this top feature set. This decision also increases the interpretability of the model and guides clinician's attention to the crucial clinical signs, which are required for the accurate diagnosis and efficient treatment planning.

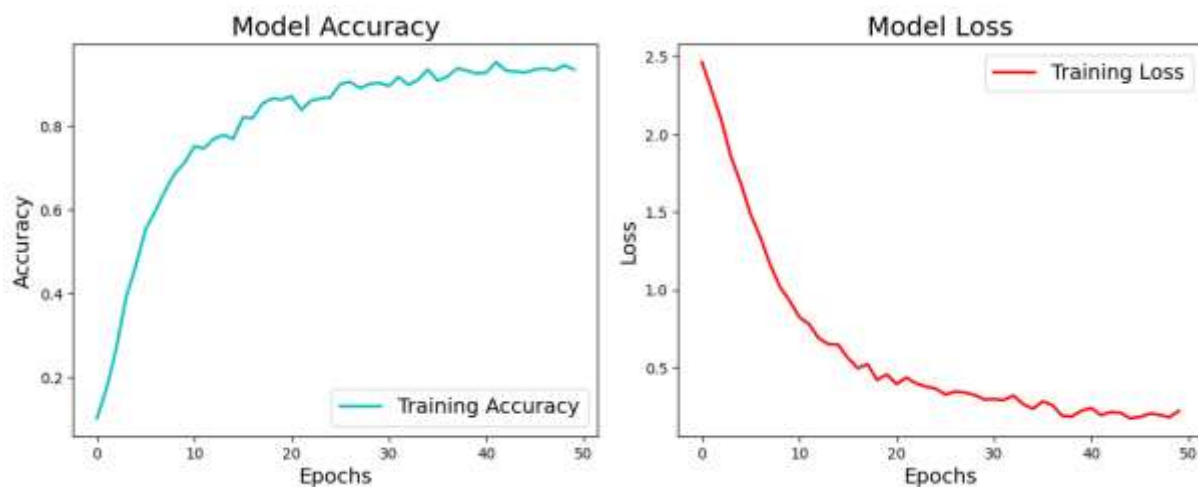


Figure6. Training Accuracy and training loss

The accuracy and loss numbers acquired during the training phase of the GRU model showed that it learnt quite well. With a training accuracy of 99.50%, the model was able to learn the patterns in the training dataset with very little misclassification. At the same time, a training loss of 0.0181 was noted, which indicates a small margin of error and successful model convergence during training. A very constant learning curve with very few oscillations is shown by the graphical depiction of loss and accuracy across the training epochs (50). The model

seems to have a balanced generalization capacity, as shown by this steady trend, and is neither overfitting nor underfitting. Training accuracy and loss convergence curves of the proposed GRU model can be seen in Fig. 6. A comparison between actual and predicted disease classes are shown in Table 8.

Table 8 Model Testing and Evaluation		
Index	Actual Result	Predicted Result
0	8	8
1	0	0
2	3	3
3	9	9
4	6	6
5	9	9
6	7	7
7	2	2
8	7	7
9	3	3
10	7	7
11	7	7
12	9	9
13	6	6
14	4	4
15	4	4
16	5	5
17	5	5
18	4	4

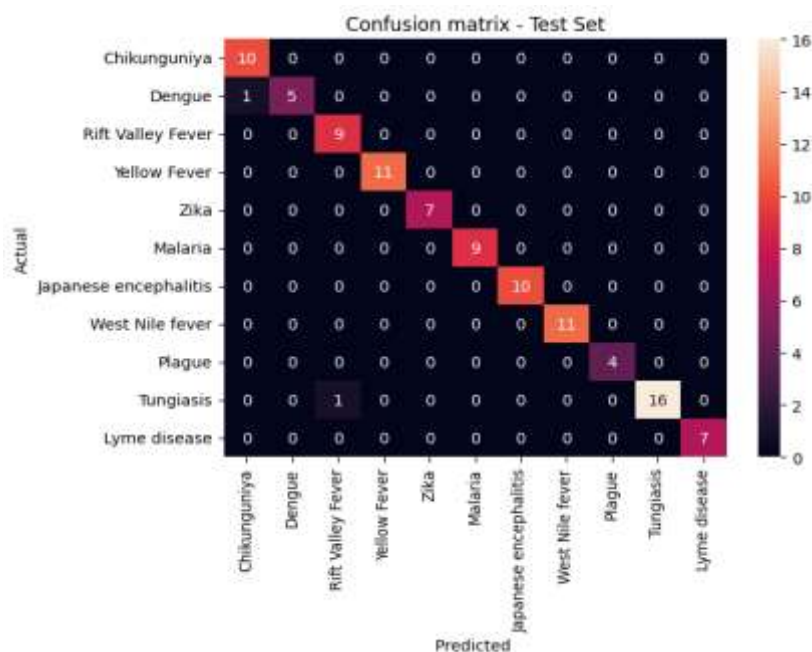


Figure7. Confusion Matrix

Confusion matrix of the proposed LIME-HyGRU model is shown in Fig. 7, which provides detail about the number of right and wrong classifications for each class, is an essential tool for prediction tasks since it provides insights into the performance of a model. Specifically, in this dissection:

The accuracy with which the model predicted each category of vector-borne diseases is detailed in each cell of the confusion matrix. The model's accuracy in classifying the test set's various illness classifications is shown by the confusion matrix. The algorithm was able to forecast with remarkable accuracy and classify perfectly for classifications such as Yellow Fever, Lyme Disease, Rift Valley Fever and Japanese Encephalitis. West Nile disease

and chikungunya demonstrated high accuracy, which shows efficient learning and strong separation of features. However, only a few cases of misdiagnosis like Dengue and Tungiasis were identified which might be related to similarities in characteristics. Due to its efficient learning of the illness patterns and feature qualities, the model demonstrated strong classification skills with few misclassifications.

Table 9. Accuracy, precision, recall and f1-score			
Class	Precision	Recall	F1-Score
0	0.9091	1.0000	0.9524
1	1.0000	0.8333	0.9091
2	0.9000	1.0000	0.9474
3	1.0000	1.0000	1.0000
4	1.0000	1.0000	1.0000
5	1.0000	1.0000	1.0000
6	1.0000	1.0000	1.0000
7	1.0000	1.0000	1.0000
8	1.0000	1.0000	1.0000
9	1.0000	0.9412	0.9697
10	1.0000	1.0000	1.0000

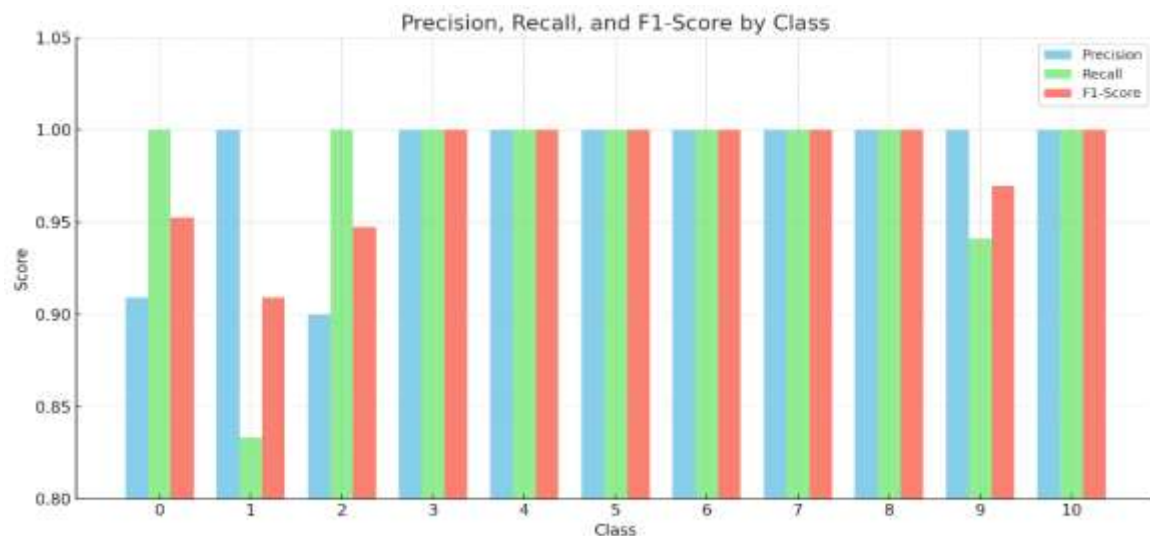
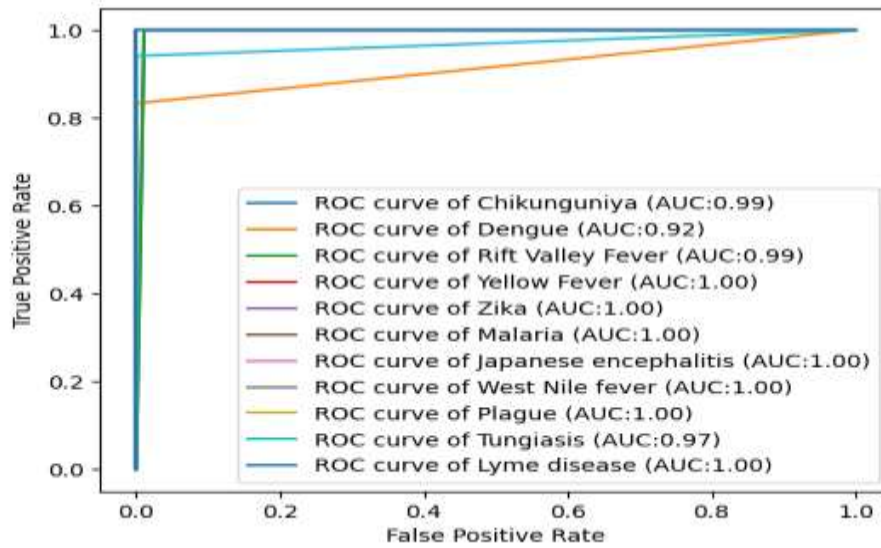


Figure 8. Accuracy, precision, recall and f1-score

The performance of the proposed LIME-HyGRUmodel across all classes is thoroughly evaluated in the classification report. With a total accuracy of 98.02% on the test set, the model clearly has excellent predictive power. In the majority of classes, precision, recall, and F1-score values are consistently high, with weighted and macro averages close to 0.98. Class 1 does have a somewhat lower recall of 0.8333, however, which might mean that some detections or misclassifications were missed. It is clear from the model's excellent recall and accuracy scores for other classes that it successfully differentiates between different types of diseases, keeping its sensitivity and specificity in check across the dataset. Table 9 provides class-wise precision, recall, and F1-score of the proposed model. Further, finding the twenty most important characteristics that discriminated across illness classes to the best of our ability was the primary goal of the feature selection procedure, which was guided by a hybrid ML model and LIME analysis. This pick comprised key symptoms that were very impactful across multiple illness categories such as swollen lymph nodes, inflamed toes, and slow heart rate. In addition, we included environmental variables together with medical history data to enhance the model's generalisability to external risk factors. This gave us an opportunity to consider putative environmental factors affecting symptoms and disease presentation, and enhanced our ability to anticipate. Figure 8 shows the comparative visualization of precision, recall and F1-score for all disease groups.



ROC AUC score: 0.988756873987053

Figure 9 ROC Curve

The Receiver Operating Characteristic (ROC) curve analysis for the prediction of 11 vector-borne diseases yielded a high Area Under the Curve (AUC) value of 0.9887. This number is a good measure of the model's ability to discriminate between positive and negative examples of each disease. AUC is a measure of the model's discriminative power, and greater values indicate better performance. AUC is between 0 and 1. The very high area under the curve (AUC) of 0.9887 demonstrates the ability of the model to very well distinguish between all classes using projected probabilities. The model's high prediction accuracy and dependability in identifying patients with the relevant vector-borne illnesses are confirmed by this result, which significantly above the baseline of random guessing (AUC = 0.5). The proposed model's ROC curve and AUC analysis results are shown in Fig. 9.

Table 10 Performance comparison of proposed and existing model.

Disease	Precision	Recall	F1-score	Accuracy
Random forest	98.95	93.07	95.92	92.16
SVC	97.87	91.09	94.36	89.32
GBT	97.83	89.11	93.26	87.38
RF-SVC-GB	100.00	96.04	97.98	96.04
LIME-HyGRU	98.26	97.95	97.99	98.02

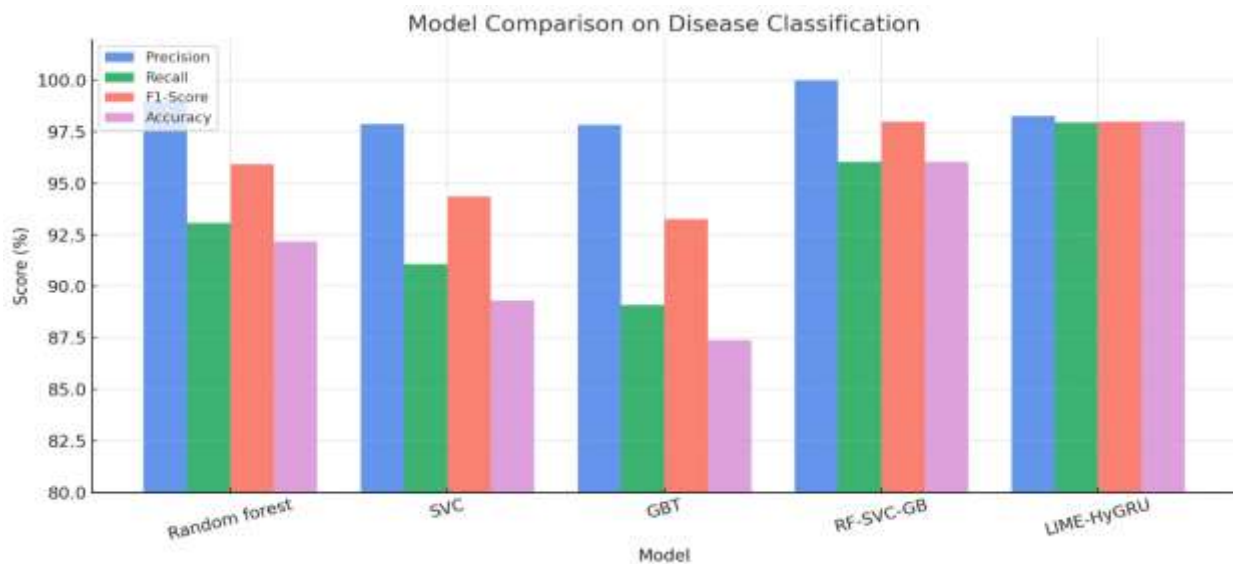


Figure 10 Comparison chart of proposed and existing model

The comparison Table 10 shows the effects of five models such as Random Forest, SVC, GBT, RF-SVC-GB, and LIME-HyGRU on the Precision, Recall, F1-Score, and Accuracy measures. Among them, LIME-HyGRU displays the best overall performance, notably excelling in Accuracy (98.02%) and maintaining balanced, high values across all other measures. A comparative performance chart of proposed and existing prediction models are presented in Figure 10. The hybrid RF-SVC-GB model likewise does very well, with a perfect Precision score (100%) and a good F1-Score (97.98%). Random Forest does better than SVC and GBT on their own, notably in F1-Score and Accuracy, hence it may be used as a standalone model. SVC does well, but it doesn't do as well as Random Forest on any of the criteria. GBT has the worst job in Recall and Accuracy, which means it would have trouble finding all the relevant illness cases compared to the other models.

5. Conclusions

Many people, particularly in underdeveloped regions, get sick or die as a result of vector-borne diseases (VBDs), which are becoming more common. The World Health Organisation (WHO) has focused control efforts on vector-borne diseases (VBDs) since they make up seven out of ten neglected infectious diseases that disproportionately impact low-income and marginalised communities. This study presents a novel LIME-HyGRU model for the prediction of vector-borne diseases. The LIME-HyGRU model combines the two existing algorithms, HyGRU (Hybrid GRU Algorithm) and LIME. With a total accuracy of 98.02% on the test set, the model clearly has excellent predictive power. In the majority of classes, precision, recall, and F1-score values are consistently high, with weighted and macro averages close to 0.98. The findings demonstrate that our suggested model outperforms other current models and offers a potential strategy.

To improve the outcomes of future endeavours, we might explore other hybrid models. Further, information on certain vector-borne diseases may be used for forecasting purposes.

References

1. Javaid, M., Sarfraz, M. S., Aftab, M. U., Zaman, Q. uz, Rauf, H. T., & Alnowibet, K. A. (2023). WebGIS-Based Real-Time Surveillance and Response System for Vector-Borne Infectious Diseases. *International Journal of Environmental Research and Public Health*, 20(4). <https://doi.org/10.3390/ijerph20043740>
2. Nanda, A. K., Thilagavathy, R., Gayatri Devi, G. S. K., Chaturvedi, A., Jalda, C. S., & Inthiyaz, S. (2024). Forecasting deep learning-based risk assessment of vector-borne diseases using hybrid methodology. *Technology and Health Care*, 32, 1–21. <https://doi.org/10.3233/thc-240046>
3. Chowdhury, A. H. (2025). *Comparison of Deep Learning and Gradient Boosting : ANN Versus XGBoost for Climate - Based Dengue Prediction in Bangladesh*. 1–10. <https://doi.org/10.1002/hsr2.70714>
4. Karn, S., Sangole, S., Gawde, A., & Joshi, J. (2019). Prediction and classification of vector-borne and communicable diseases through artificial neural networks. *2019 International Conference on Intelligent Computing and Control Systems, ICCS 2019, Iccics*, 1011–1015. <https://doi.org/10.1109/ICCS45141.2019.9065500>
5. Eisen, L., & Eisen, R. J. (2011). Using geographic information systems and decision support systems for the prediction, prevention, and control of vector-borne diseases. *Annual Review of Entomology*, 56, 41–61. <https://doi.org/10.1146/annurev-ento-120709-144847>
6. Bhatia, G. (2017). *A Novel Approach towards Prediction of Mosquito- Borne Diseases*. VII(I), 209–212.
7. Vaiyapuri, T. (2024). Utilizing Explainable AI and Biosensors for Clinical Diagnosis of Infectious Vector-Borne Diseases. *Engineering, Technology and Applied Science Research*, 14(6), 18640–18648. <https://doi.org/10.48084/etasr.9026>
8. Rao, S., Mehta, S., Kulkarni, S., Dalvi, H., Katre, N., & Narvekar, M. (2022). A Study of LIME and SHAP Model Explainers for Autonomous Disease Predictions. *IBSSC 2022 - IEEE Bombay Section Signature Conference, December*, 1–6. <https://doi.org/10.1109/IBSSC56953.2022.10037324>
9. Doni, A. R., & Sasipraba, T. (2020). Lstm-Rnn Based Approach for Prediction of Dengue Cases in India. *Ingenierie Des Systemes d'Information*, 25(3), 327–335. <https://doi.org/10.18280/isi.250306>
10. Kamana, E., Zhao, J., & Bai, D. (2022). Predicting the impact of climate change on the re-emergence of malaria cases in China using LSTMSeq2Seq deep learning model: a modelling and prediction analysis study. *BMJ Open*, 12(3). <https://doi.org/10.1136/bmjopen-2021-053922>
11. Prasad, A. B. (2025). *Detection of early spread of vector borne disease with personalized treatment strategies using machine learning*. 316–321. <https://doi.org/10.1201/9781003559085-56>

12. Ferdousi, T., Cohnstaedt, L. W., & Scoglio, C. M. (2021). A Windowed Correlation-Based Feature Selection Method to Improve Time Series Prediction of Dengue Fever Cases. *IEEE Access*, 9, 141210–141222. <https://doi.org/10.1109/ACCESS.2021.3120309>
13. Rezk, N. G., Alshathri, S., Sayed, A., El-Din Hemdan, E., & El-Behery, H. (2024). XAI-Augmented Voting Ensemble Models for Heart Disease Prediction: A SHAP and LIME-Based Approach. *Bioengineering*, 11(10). <https://doi.org/10.3390/bioengineering11101016>
14. Peters, D. P. C., McVey, D. S., Elias, E. H., Pelzel-McCluskey, A. M., Derner, J. D., Burruss, N. D., Schrader, T. S., Yao, J., Pauszek, S. J., Lombard, J., & Rodriguez, L. L. (2020). Big data–model integration and AI for vector-borne disease prediction. *Ecosphere*, 11(6). <https://doi.org/10.1002/ecs2.3157>
15. Endo, A., & Amarasekare, P. (2022). Predicting the Spread of Vector-Borne Diseases in a Warming World. *Frontiers in Ecology and Evolution*, 10(April). <https://doi.org/10.3389/fevo.2022.758277>
16. Santangelo, O. E., Gentile, V., Pizzo, S., Giordano, D., & Cedrone, F. (2023). Machine Learning and Prediction of Infectious Diseases: A Systematic Review. *Machine Learning and Knowledge Extraction*, 5(1), 175–198. <https://doi.org/10.3390/make5010013>
17. Gopal, J. (2025). *OaRCM: An Amalgamation of Ontology and Deep Learning Approach for Effective Relation Classification of Mosquito Vector Biocontrol Agents* *OaRCM: An Amalgamation of Ontology and Deep Learning Approach for Effective Relation Classification of Mosquito Vector Biocontrol Agents*. March. <https://doi.org/10.1177/15705838241312424>
18. Raizada, S., Mala, S., & Shankar, A. (2020). Vector borne disease outbreak prediction by machine learning. *Proceedings of the International Conference on Smart Technologies in Computing, Electrical and Electronics, ICSTCEE 2020*, 213–218. <https://doi.org/10.1109/ICSTCEE49637.2020.9277286>
19. Rehman, N. A., Saif, U., & Chunara, R. (2019). *Deep Landscape Features for Improving Vector-borne Disease Prediction*. <http://arxiv.org/abs/1904.01994>
20. Tito, M. H., Jannat, M. H. E., Aktar, M. T., Saha, B., Das, P., Hossain, A., Islam, N., Chohan, M. S., & Khan, S. (2024). *Letters in Animal Biology*. 04(1), 17–22.
21. Vimbi, V., Shaffi, N., & Mahmud, M. (2024). Interpreting artificial intelligence models: a systematic review on the application of LIME and SHAP in Alzheimer's disease detection. *Brain Informatics*, 11(1), 1–29. <https://doi.org/10.1186/s40708-024-00222-1>