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DESIGN AND ANALYSIS ON MEDICAL IMAGE CLASSIFICATION FOR DENGUE DETECTION USING ARTIFICIAL NEURAL NETWORK CLASSIFIER

P.K. Swaraj[1] **and G. Kiruthiga**[2]
[1]Department of Computer Science and Engineering, Government College of Engineering, Thirussur, India
[2]Department of Computer Science and Engineering, IES College of Engineering, India

Abstract

Dengue is regarded as a serious threats to humanity, globally and this is a vital disease with huge spreading of virus that affects the health of humans. The virus is spreading at a rapid rate through mosquitoes that even may kill the one who is affected with dengue. In this paper, we develop a quick response system that certainly finds the disease through a faster validation process. The study uses artificial neural network (ANN) as a deep learning model that classifies and predicts the condition or the infection status of a patient. The study uses a pre-processing model and a feature extraction model to prepare the image datasets for classification. The simulation is conducted to validate the effectiveness of the model over dengue image datasets i.e. the blood samples of humans. The validation shows that the proposed method effectively classifies the patients in a faster manner than the other deep learning models.

Keywords:

Machine Learning, Dengue, Classification, Diagnosis

1. INTRODUCTION

Dengue is a mosquito-borne disease, which occurs through Aedes mosquitoes in tropical regions. Long rains give molecules that bear these diseases more stagnant water to breed. According to the Indian Ministry of Health, 70 people are dead and over 36,000 have suffered from dengue since January. The majority of infections in Bengal and Orissa in the east and Kerala and Karnataka in the south [1] have been recorded.

More tests and fever reports, at least in towns and towns, are the main cause of the spike. Overall the number of infections is still growing: for example, the number of confirmed dengue cases alone soared from 28,292 in 2010, to almost 100,000 in 2015. During this time, there were between 110 and 242 official deaths annually from this disease. Dengue fever influences the body inducing high flu-like symptoms and fever. The infection of your blood triggers headache, rash, discomfort, queasiness, fatigue and fever. It can cause minor blood loss in the gums. The findings show that the dengue in the United States has a large economic burden. Dengue symptoms outweigh other viral conditions like human papillomavirus (HPV) or rotavirus [3].

In the public health world, early diagnosis of dengue fever is a must, and machine learning technologies can allow physicians to early diagnose and forecast diseased diseases, which not only help to improve classification accuracy, but also to save on time, expense and discomfort associated with pathological tests [5] [6]. Medical diagnostics using machine learning techniques have enabled the disease to be analyzed on the basis of clinical and laboratory symptoms and to provide reliable results.

Machine Learning (ML) methods have been applied in many disciplines in the last two decades to provide useful results from very heterogeneous data, such as geography, climate and epidemiology. Unlike statistical modeling based on many assumptions (for example, independence of predictor variables, homoscedasticity, and regular error distribution), machine learning facilitates the use of a large number of correlated variables, enables modeling of complex interactions between variables and can match complex models without presupposing a presupposition. In dengue prediction experiments, various ML methods are also used [7] [20]-[23]. In the light of their ability to resolve the prevalent issue of overfitting [24]-[28], where Random Forest (RF), which is another common ML algorithm, has shown to be predictable in comparison with the ML methods.

In various countries [29]-[33] random forests have been used for predicting dengue danger. Seasonal variables or social-demographic predictors were not always used in models, and they were found to enhance HIV [34] and Ebola [35] prediction accuracy. In addition, dengue models were designed to prevent dengue cases for particular administrative regions, irrespective of the application of time-series or ML approaches in a city or province [9]-[12] [20]-[23]. Models of universal dengue prediction, useful across various administrative regions, are scarce.

The Artificial Neural Network (ANN) is an attempt to imitate the structure of the human brain. Many millions of tiny treatment devices, or neurons, operate in tandem in the human brain. Neurons are linked by neuronal links to each other. Each neuron receives feedback from a group of neurons. The input is then processed and the output is sent to a series of neurons. For further analysis, the output is collected by other neurons. The human brain is a complex neuronal network with connections that continue to break and form. Many human brain-like models were suggested [6]. The benefits of Neural Network are their ability to learn on the basis of training data, to organize themselves or represent the information they receive, and to operate in the real-time way in the meaning that Artificial Neural Network can perform simultaneous calculations and have high tolerance [6] [7]. Besides having the advantages of neural networks, they also need very large training data and slow convergence, so that the back propagation algorithm depends very much on the initial parameters, such as number of inputs, hidden nodes. There are several parameters to be determined when implementing the Neural Network. No standard guidelines are currently available in determining the parameters of the Neural Network so the approach used is an experimental method. Therefore we need a method to address these problems in order to improve the efficiency of the implementation of the neural network.

The aim of this paper is to forecast dengue fever using different algorithms for machine learning. This study identifies dengue signs in the patients first, and this recognition starts predicting them. In this paper, we develop a quick response system that certainly finds the disease through a faster validation process. The study uses Artificial Neural Network (ANN) as a machine learning model that classifies and predicts the condition or the infection status of a patient. The study uses a pre-processing model and a feature extraction model to prepare the image datasets for classification. The simulation is conducted to validate the effectiveness of the model over dengue image datasets i.e. the blood samples of humans. The validation shows that the proposed method effectively classifies the patients in a faster manner than the other deep learning models.

2. RELATED WORKS

In [4], the authors regarded the decision tree as a method for data mining and suggested a collection of valid attributes from time data. The experiment has four components. The decision tree technique uses two patient datasets to identify the dengue with a rating of 97.6% and 96.6% precision.

In [5], the author aims to extract dengue disease information, timelines and other relevant clinical data features from the named entity recognition. They develop a model to forecast whether or not the dengue disease exists and conduct frequency analysis that correlate the onset of the dengue and its symptoms over the months. As an input to the proposed system a number of annotated discharge summaries are used. In this work, measurements of performance are accuracy, Kappa statistics, mean absolute error, root mean square error and relative absolute error. The conclusion is that SMO algorithms perform better than other algorithms.

The authors in [6] suggested statistical techniques such as the regression of Multivariate Poisson. Statistics are well-established scientific methodology and helpful when the relationships are linear, when data mining technology is useful for the discovery of knowledge hidden in the data. The focus is on analyzing the linear correlation between dengue cases and infected mosquito data and shows the role women played in the dengue outbreak prediction, their infection and rate. This proposed model estimated the incidence of dengue efficiently and helped to monitor and control the outbreak of dengue in the early stages of the outbreak.

Real-time dengue risk forecasts were proposed in [7] for a small area. In place of a conventional early alert, aim monitoring and action mathematical model, these simulations used risk prediction models. In different cities, the accuracy of time and space can be conveniently adapted to various environments.

In [8], the authors employed the algorithm of decision tree and also explored the rule for future prediction in this field. The aim is to build a simulation model with a decision tree to forecast the probability of dengue diseases occurring in a tribal region. In order to produce an unattended model, the database is analyzed to determine the most important parameters of the region concerned and to estimate the chances of the disease using the supervised classification model. The precision of the model proposed is 97%.

3. PROPOSED METHOD

The prediction model for dengue occurrences operates in four steps. The four-phase workflow is seen in the Fig.1.

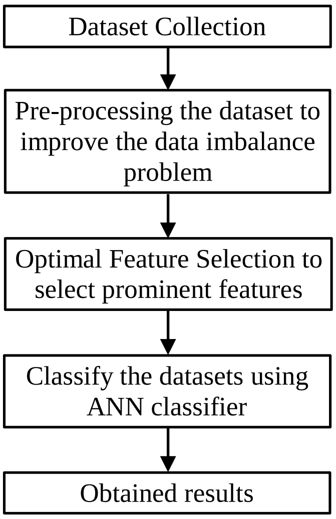

Fig.1. Proposed prediction model

- **Phase 1**: Real time data collection for dengue disease
- **Phase 2**: Data Pre-processing.
- **Phase 3**: Feature selection by weighted score
- **Phase 4**: Classification using ANN

Medical (clinical) data refers to the personal information that is involved or part of a clinical trial scheme with routine patient treatment. This covers digital copies of personal care data [19], electronic health reports. The collection, storage, processing, analysis or dissemination of medical data is a broad volume [20]-[22]. Data samples from Dengue Disease are obtained from different health centers across India as part of the real-time data collection process.

3.1 PREPROCESSING

Due to the enormous volume of diagnostic information from the different sources, it is possible to cope with certain problems, including lost values, noise, mislabeling, high dimensionality and imbalances. This proposed research applies the preprocessing task to manage imbalanced data, which is the Symmetric Minority Over Sampling Technique (SMOTE). This improves the accuracy of the classification of different traditional classifiers. These findings give improved results over the balanced dataset. The results are better. For the balanced dataset, the following formula is used:

$$\left(A'_{new_1}, A'_{new_2}\right) = \left(A_{11}, A_{12}\right) + rand\left(0-1\right) * \left(A_{new_1}, A_{new_2}\right) \quad (1)$$

where

$A_{new_1} = A_{21} - A_{11}$ and $A_{new_2} = A_{22} - A_{12}$

A_{11} - first attribute of first instance,

A_{21} - first attribute of second instance,

A_{12} - second attribute of first instance and

A_{22} - second attribute of second instance.

$rand(0\text{-}1)$ - random number.

Following the pre- mission, conventional feature selection methods like Genetic Algorithm (GA), Correlation based Feature Selection (CFS) and Particle Swarm Optimization (PSO) are evaluated by using the SMOTE over imbalanced data sets for the pre-processor. Afterwards, the findings are analyzed using the balanced dataset.

3.2 FEATURE EXTRACTION

In order to calculate the degree of complexity of the knowledge quality, 'Entropy' proposed by Shannon is used. The uses entropy-weighted methods in our proposed approach to derive objective weights of associated attributes. The proposed solution is given in following steps:

Step 1: Create decision matrix with the weighted score.

Step 2: Normalize the decision matrix to pre-process the data.

Step 3: Generate the weighted score matrix.

Step 4: Optimize weights using entropy weighted method.

Step 5: Compare weighted score.

Step 6: Rank weighted score values to predict attributes.

Step 7: Evaluate the accuracy.

The first step is to transform the dataset into a new dataset, using the suggested approach, using the chosen optimal attributes for the decision making procedure, by retaining the details of the attribute the same. Next, the weight of the experts is obtained by entropy. The same ranking subset obtained is regarded as the better alternative for the separate values. The results are then calculated based on the current system of comparison.

The first is to combine the weighted value of the weighted score with the average weighted score operator. Secondly, for any alternate collective total data subset the score functions are estimated. Third, according to the score values, the best alternative is chosen. Finally it is possible to compute the score values and produce the ranking data. Various order positions are achieved with the various approaches, but the distinctions are subtle.

The findings of this work are also more rational, and the approach suggested is more flexible than the method proposed in the current study. The findings of the comparative study confirms that it is an accurate and realistic method to forecast medical diseases in the context of the decision-making phase in the healthcare system.

3.3 CLASSIFICATION

ANN A total of 480 people were classified by the clinical and demographic features in this sample into two groups, for example, dengue impaired and dengue not affected. Participants were inscribed in several health centres from the outpatients and hospitals. The collection and examination of blood samples was carried out on the basis of the prescribed norm. In addition, dengue was diagnosed or dengue was not provided to patients with any standard values, or below or above standard values.

The Weka tool is used for model prediction to test the dengue dataset. Different medical applications use the weka platform for cancer and other disease diagnostics. The biggest benefit of using weka is helping to diagnose the thousands of characteristics of the dataset. In this procedure, classical classifications such as Naïve Bayes (NB), J48, MultiLayer Perceptron (MLP) and Support Vector Machine (SVM) using the Weka tool test the features chosen by the proposed solution. In addition, a dengue dataset is considered to assess the disease prevention in order to verify our strategy with 480 instances and 20 attributes. Cross-validation tests are carried out to assess the consistency of the model and other success metrics including accuracy, recall, True Positive Rate, False Positive Rate and the Receiver Operating Characteristic (ROC).

The J48 appears to be the best classifier for complete datasets among four traditional classifiers, Naïve Bayes (NB), Decision Tree (J48), Multi Layer Perceptron (MLP) and SVM. However, this is not satisfactory for the forecast of the survival of dengue fever on the basis of data set symptoms. For the comparative study of several classifiers on the dengue dataset, the following output metrics, such as the accuracy, TP rate, FP rate, precision, reminder, F-method and ROC, are examined. The J48 classifier appears to be the best among the other classifier with 95% maximum precision before implementing any function selection algorithm. Before using any algorithm, i.e. evaluation of the completed data set on classifier, Table.2 and Table.3 indicate different Output metrics.

As their name implies, artificial neural networks are the computer networks that aim to grossly replicate the mechanism of decision making in nervous cell (neurons) networks of the central nervous biological (human or animal) system [17] [18]. As seen in Fig.1, the ANN structure consists of three major strata. First, an input layer that binds a weight set with the input signal to the neuron. The secret layer then weighs the weight values of the neuron and sums up the input and bias values. Finally, the neuron output amplitude is limited by means of the activation transfer mechanism by means of an output layer. In order to maximize or decrease the net performance of the neuron, a bias is often applied to the neuron [19].

MLP is a network created by a backpropagation learning algorithm that uses and reverts to the mistake made by the network and is composed by at least one hidden layer and an output layer. RBF is a neural network which acts as an activation function on a radial basis. The various types of radial functions exist, but the Gaussian function is the most common type. The RBF is very similar in design to that of the multilayer perceptron and has three layers for RBF: the input layer, the secret layer and the escape layer, whereby MLS have more [24, 25]. This is a very similar architecture. For a more detailed overview of the various forms of ANN schemes, please see [26].

4. RESULTS AND DISCUSSIONS

In the medical fields, several methods for calculating precision indexes that includes are used: sensitivity, specificity [34]. In this paper, the accuracy, sensitivity, and specificity for test data sets are calculated to assess the efficiency of classification model [15, and the variability thereof in several test sets obtained from randomized dataset partitions.

$$Accuracy=\frac{TP+TN}{TP+TN+FP+FN} \tag{2}$$

$$Sensitivity=\frac{TP}{TP+FN} \tag{3}$$

$$Specificity=\frac{TN}{TN+FP} \tag{4}$$

where

TP is the number of cases correctly identified as patient,

FP is the number of cases incorrectly identified as patient,

TN is the number of cases correctly identified as healthy and

FN is the number of cases incorrectly identified as healthy.

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Table.1. Accuracy before applying feature selection Algorithm

Classifier	Accuracy	TP Rate	FP Rate	Precision	Recall
NB	91.17	0.93	0.08	0.72	0.93
J48	96.24	0.93	0.02	0.93	0.93
MLP	93.70	0.78	0.02	0.92	0.78
SVM	94.97	0.93	0.02	0.93	0.93

Table.2. ROC before applying feature selection Algorithm

Classifiers	F-measure	MCC	ROC Area
NB	0.810	0.775	0.948
J48	0.935	0.920	0.970
MLP	0.844	0.819	0.992
SVM	0.935	0.920	0.967

Table.3. Accuracy on NB classifier

Classifier	Accuracy	TP Rate	FP Rate
GA + J48	95.546	0.937	0.120
PSO + J48	97.501	0.976	0.165
CFS + J48	85.730	0.872	0.882
ANN + J48	100.003	0.962	0.167

Table.4. ROC on J48 classifier

Classifier	Precision	Recall	F-measure	MCC	ROC Area
GA + J48	0.922	0.942	0.932	0.77	0.983
PSO + J48	0.952	0.972	0.962	0.881	0.861
CFS + J48	0.871	0.871	0.881	0.881	0.871
ANN + J48	0.942	0.962	0.952	0.831	0.902

Table.5. Accuracy on MLP

Classifier	Accuracy	TP Rate	FP Rate
GA + MLP	93.703	0.942	0.122
PSO + MLP	96.276	0.942	0.942
CFS + MLP	94.412	0.972	0.162
ANN + MLP	99.250	0.962	0.172

Table.6. ROC on MLP classifier

Classifier	Precision	Recall	F-measure	MCC	ROC Area
GA + MLP	0.922	0.942	0.932	0.770	0.983
PSO + MLP	0.942	0.952	0.962	0.952	0.962
CFS + MLP	0.952	0.972	0.962	0.881	0.983
ANN + MLP	0.942	0.962	0.952	0.831	0.902

Table.7. Accuracy on SVM

Classifier	Accuracy	TP Rate	FP Rate
GA + SVM	93.703	0.942	0.122
PSO + SVM	95.455	0.972	0.162
CFS + SVM	96.235	0.962	0.162
ANN + SVM	96.235	0.962	0.172

Table.8. ROC on SVM classifier

Classifier	Precision	Recall	F-measure	MCC	ROC Area
GA + SVM	0.922	0.942	0.932	0.770	0.983
PSO + SVM	0.952	0.972	0.962	0.881	0.861
CFS + SVM	0.942	0.962	0.952	0.831	0.902
ANN + SVM	0.942	0.962	0.952	0.831	0.902

Table.9. Performance on original set and reduced set.

Classifiers	GA	PSO	CFS	ANN
NB	85.548	95.222	93.703	97.501
C4.5	95.546	97.501	85.730	100.003
MLP	93.703	96.276	94.412	100.003
SVM	93.703	95.455	96.235	96.235

Table.10. Accuracy

Classifier	Accuracy	TP Rate	FP Rate
ANN + NB	97.501	0.937	0.120
ANN + J48	99.550	0.962	0.167
ANN + MLP	96.255	0.962	0.167
ANN + SVM	96.235	0.962	0.167

Table.11. ANN with other classifiers

Classifier	Precision	Recall	F-measure	MCC	ROC Area
ANN + NB	0.861	0.861	0.861	0.770	0.922
ANN + J48	0.942	0.962	0.952	0.831	0.902
ANN + MLP	0.942	0.962	0.952	0.831	0.902
ANN + SVM	0.942	0.962	0.952	0.831	0.902

The Feature Selection allows us to improve the detection efficiency of the different classifiers with the appropriate model preparation, deleting all irrelevant and redundant features, and extracting the best possible features from the initial feature collection. In addition, we expected to reduce the number of original features and reduce the time required to train without compromise. The proposed weighted score significantly improved the dengue prediction accuracy of different classifiers. NB, DT and ANN classifiers were significantly improved.

5. CONCLUSIONS

In this paper, ANN offers fast reactions by a quicker confirmation process. The ANN categorizes and forecast patient infection. In the analysis, the image data sets for classification are prepared using a preprocessing model and a feature extraction model. The simulation is carried out to test how the model works for image data sets of dengue, i.e. human blood samples. The validation indicates that patients are efficiently classified more quickly than the other deep learning models by the proposed approach. In all performance measures, such as accuracy, accuracy, recall, and f-measure. ANN gives the best outcomes, the best classification classifier for a person with or without dengue disease.

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