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Detecting Information on the Spread of Dengue on Twitter Using Artificial Neural Networks

Samina Amin[1,*], M. Irfan Uddin[1], M. Ali Zeb[1], Ala Abdulsalam Alarood[2], Marwan Mahmoud[3] and Monagi H. Alkinani[4]

[1]Institute of Computing, Kohat University of Science and Technology, Kohat, 26000, Pakistan
[2]College of Computer Science and Engineering, University of Jeddah, Jeddah, 21959, Saudi Arabia
[3]Faculty of Applied Studies, King Abdulaziz University, Jeddah, Saudi Arabia
[4]Department of Computer Science and Artificial Intelligence, College of Computer Sciences and Engineering, University of Jeddah, Jeddah, Saudi Arabia
[*]Corresponding Author: Samina Amin. Email: kustsameena@gmail.com
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Abstract: Social media platforms have lately emerged as a promising tool for predicting the outbreak of epidemics by analyzing information on them with the help of machine learning techniques. Many analytical and statistical models are available to infer a variety of user sentiments in posts on social media. The amount of data generated by social media platforms, such as Twitter, that can be used to track diseases is increasing rapidly. This paper proposes a method for the classification of tweets related to the outbreak of dengue using machine learning algorithms. An artificial neural network (ANN)-based method is developed using Global Vector (GloVe) embedding to use the data in tweets for the automatic and efficient identification and classification of dengue. The proposed method classifies tweets related to the outbreak of dengue into positives and negatives. Experiments were conducted to assess the proposed ANN model based on performance evaluation matrices (confusion matrices). The results show that the GloVe vectors can efficiently capture a sufficient amount of information for the classifier to accurately identify and classify tweets as relevant or irrelevant to dengue outbreaks. The proposed method can help healthcare professionals and researchers track and analyze epidemic outbreaks through social media in real time.

Keywords: Artificial neural network; classification; social media; GloVe; social networking sites

1 Introduction

Social networking sites (SNS) are extremely popular worldwide, and are redefining how people communicate and engage with one another. Such services as Twitter, Facebook, Instagram, LinkedIn, and blogs are used to not only share media and text content, but also to provide opportunities to users to share their perceptions or opinions on any topic, activity, or trending issue. SNS are also helpful for gathering situational information during disasters, like an earthquake or an epidemic outbreak. The rapid spread of epidemic outbreaks in recent years has highlighted the need for effective analytical techniques to understand the flow of information and plan according actions. The SNS can be used to efficiently deliver information for the detection of diseases for the public to reduce their spread [1].

Viral infections pose a major threat to public health. The timely and precise tracking of infectious diseases and their growth can help reduce their damaging effects. However, research on disease-related information on SNS has primarily targeted healthcare professionals and physicians tracking their patients' visits, and is used to identify the occurrence of diseases. Dengue fever is among the most rapidly rising mosquito-borne viral infections. An average of 389 million people are annually infected by it worldwide, of which 95–97 million exhibit medical symptoms [2]. The risk of dengue is expected to rise in the future owing to increased urbanization, an insufficient supply of clean water, and, possibly, climate change. The epidemiological nature of dengue is complicated, it is challenging to monitor, and mechanisms to track it are expensive and ineffective [3]. The number of regions affected by dengue has grown in recent years as cases continue to increase [2].

SNS have been utilized in various applications of disease surveillance [1,4]. Researchers have developed methods for the prediction of diseases using health-related data derived from Web 2.0 [1]. Moreover, Google search queries have incorporated a Web-based system to monitor early warnings in real time [5]. In recent years, SNS, in particular Twitter, have had a positive impact on disease identification, such as predicting the given state of spread as reported by the public [6,7], reporting traditional medical data, and detecting epidemic outbreaks [8,9].

This paper proposes an ANN-based model that uses optimization techniques along with the GloVe embedding dictionary-based approach [10]. It leverages SNS to detect and classify dengue outbreaks. The above-mentioned research on the identification and classification of diseases on SNS has used machine learning approaches, such as the support vector machine (SVM), naïve Bayes, k-nearest neighbor, the decision tree, and ANN techniques. The proposed model examines Twitter data to provide a useful way to detect epidemic outbreaks instead of formal data collection techniques. Formal methods of surveilling epidemic outbreaks use manually collected clinical data that take weeks, or even months, to become accessible and interpretable. We train an optimized ANN model on a corpus of tweets, using the GloVe embedding technique for feature extraction, to classify dengue-related tweets and determine whether they represent instances of infection.

The proposed work applies the ANN to make the following contributions to the literature:

1. It classifies tweets as "dengue positive" or "dengue negative" using the ANN with parameter tuning.
2. It uses a word embedding technique (GloVe) to efficiently learn the context of the word structure for better classification.
3. The proposed optimized model significantly outperforms prevalent methods in terms of precision, accuracy, recall, and the F1-score.

The proposed model was evaluated and tested on various domains to assess its performance, accuracy, and reliability (see Section 4). The results show that it offers many opportunities to detect and classify diseases, such as the novel coronavirus (COVID-19).

The remainder of this paper is organized as follows: Section 2 discusses related work in the area and Section 3 details the proposed method. Section 4 describes the results of experiments to assess its performance, and Section 5 offers the conclusions of this study as well as a set of research suggestions for future work in the area.

2 Related Work

Numerous epidemiological studies have been conducted on social media analysis to understand the role of public sentiment expressed on such platforms in disease detection [11]. The available information on epidemic outbreaks is highly dynamic given the temporal and spatial aspects of social media. The authors of [12] used spatio-temporal information to develop an unsupervised machine learning model to identify infectious diseases in a given location through sentimental analysis, rather than by using such background knowledge as the names of diseases and associated symptoms. Many researchers have applied content analysis and machine learning models, such as the SVM [13], linear or logistic regression [14,15], and k-nearest neighbors (KNN) [16], and have reported an accuracy of around 88% [11]. The goal of the research [11] was to monitor public concerns about diseases by classifying tweets into those conveying the symptoms of a given disease and those that did not.

Hussain-Alkhateeb et al. [17] proposed an early warning and response system (EWARS) that uses warnings and outbreak-related information to generate a prediction for the detection of dengue outbreaks at the district level. Guo et al. [18] developed a model for detecting dengue in China based on tweets by using a machine learning technique. They trained the support vector regression (SVR) model. According to the World Health Organization (WHO), dengue has been reported in almost every continent. Iqbal et al. [19] trained machine learning models to predict dengue outbreaks by using clinical data conducted from dengue patients discharged from hospital. Their proposed model was trained on such traditional machine learning models as the naïve Bayes, logistic boost, random forest, and SVM. Another interesting study was carried out by Gomide et al. [20], in which a framework was designed for monitoring dengue outbreaks through tweets by focusing on four aspects: Place, time, and opinion of the public. Two datasets were used, one from the Brazilian health department and the other based on Twitter data obtained using the keyword “#dengue,” to predict the outbreak using a linear regression model [20].

A large amount of Twitter data have been used to estimate the incidence of health issues in society. Cacheda et al. [21] focused on two languages, Portuguese and Spanish, in the Iberian Peninsula, and develop and tested an automated machine learning-based model. The goal was to detect four health conditions through tweets: Flu, anxiety, depression, and pregnancy [21]. This approach is limited in its implementation to other languages. Several approaches have been proposed to detect flu and ILI from tweets in real time. Aramaki et al. [8] used an SVM-based model to predict rates of influenza in Japan from Twitter data. The authors focused on detecting flu-related tweets based on frequency: The greater the number of tweets related to the disease was, the higher the chances were that it was spreading in the given region. However, frequency might not be a good indicator for determining whether someone is infected.

In this study, we extract dengue-related tweets (Section 3.1), i.e., tweets containing the word “dengue,” from Twitter to determine whether each of them conveys that someone has been infected. For example, “Today was the international day of dengue. I also gave a lecture on dengue” does not reflect that a person has been infected, even though the word “dengue” appears twice. However, “My daughter is suffering from dengue” reflects that a person has been infected. The classification of people infected by dengue based on tweets has not been examined in previous studies in the area. Current approaches to text classification based on the ANN have obtained important results [22]. Motivated by the accuracy of classification of ANN-based techniques, we use the network to classify tweets indicating infection by dengue. In the proposed model, the classification of infected people, which is the core task of disease detection, is not the ultimate target, but a means of distinguishing between tweets that do and do not convey infection. The aim is to provide a baseline for identifying other viral diseases, such as COVID-19, using social media content.

3 Proposed Method

Fig. 1 shows features and modules of the proposed model, including (i) data acquisition and data visualization, (ii) feature selection (ii) data splitting, and (iv) an overview of the model design and (v) model architecture by using example tweets. The details of each module are as follows.

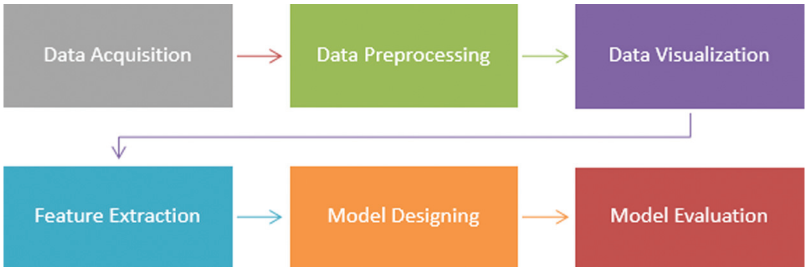


Figure 1: Flow of the proposed approach

3.1 Data Acquisition

The first step in developing a dengue classification model is the acquisition of the relevant data. For this purpose, we chose Twitter because it provides a larger amount of useful information regarding epidemic outbreaks rather than formal data collection techniques. To acquire tweets on dengue outbreaks, we used Twitter's Application Programming Interface (API) [23] designed for researchers to access the tweets in real time using the JavaScript Object Notation (JSON). The keywords used for querying and shortlisting the repository of relevant tweets included appropriate contextual words like #dengue, #denguemosquito, #denguefever, #denguevirus, #malaria, and #denguemalaria. We hence collected 141,435 tweets from June 2018 to November 2019, and stored them in JSON format. To abide by Twitter's terms and conditions, we extracted only a stripped-down version of the raw data containing a limited number of parameters, such as username, date, and tweet content.

3.2 Data Preprocessing and Building Ground Truth Dataset

The natural language processing (NLP) of an unstructured text corpus collected from Twitter is a new task because of the informal nature of tweets. It was used to eliminate unnecessary content from the dengue corpus to enhance the quality of the data deployed as features for further processing. This included the removal of hashtags, retweets, special characters, emoticons, Uniform Source Locators (URLs), and "@" mentions. Tweets posted in English were saved and those in any other language were eliminated. The saved tweets were then transformed to lowercase letters and checked for misspellings [24]. Stop words were then eliminated from the corpus.

To construct the dataset with a ground truth tag (concerning whether a given tweet conveys infection by dengue). Of the 141,435 tweets, a sample of 5,000 was selected for tagging. These tweets were tagged by three people to eliminate prejudice in the tagging procedure. Every tweet was tagged as either 1 or 0, where 1 represents infection by dengue (i.e., conveys the someone has been infected) while 0 represents no infection (the tweet presents other information about dengue). The tagged dataset consisted of features to understand the dataset description—for instance, six observations with their target labels are shown in Tab. 1.

Table 1: Tweets with target labels

S#	Text/Tweet	Target
1.	She is suffering from dengue.	1
2.	Dengue has made my life miserable.	1
3.	Dengue, which is a viral disease and is spreading in our city, is a very dangerous disease and can possibly take your life; please stay safe.	0
4.	My friend lost her father due to dengue in Lahore.	1
5.	Every dengue season, messages calling papaya leaf extract and drugs made out of it a miracle cure for dengue are widely circulated.	0
6.	So we went back to the hospital only to find out that I had been infected with dengue again.	1

To render the tagged data more useful for further processing and classification, we performed tokenization and stemming. The former splits a given sentence (tweet) into word tokens whereas the latter shrinks the derived forms of a given word by retrieving its base word [25].

3.3 Feature Extraction

Feature selection is an essential part of processing text data. Raw data need to be interpreted and converted into numeric values for processing. In this paper, we used word embedding with the GloVe dictionary strategy for data processing. In text processing, a tweet needs to be interpreted as a weighted feature vector. For this purpose, it must be replicated as a weighted feature. The n-gram is a useful technique because it offers a sequence of words that allows for the allocation of probabilities to them. N-grams can thus be described as a sequence of words within a specified window size [26]. The proposed method derives n-gram features from input data acquired from the GloVe embedding layer.

GloVe is used to convert the tweet text into numeric vectors [10]. A GloVe is a count-based approach that generates a matrix of word coincidence to acquire word vectors by performing dimensionality reduction to a greater extent than the traditional term frequency-inverse document frequency (TF-IDF). For instance, the word "apple" can be given the numeric value 6234, whereas the word "windows" can be assigned an integer value, like 45. Similar words like "dengue," "headache," "flu," "body aches," and "dengue fever" are assigned integers that can easily be viewed graphically, as in Fig. 2. Relevant words thus appear together, rather than irrelevant words. GloVe captures global as well as local statistics by generating the word vectors of a corpus. As shown in Fig. 4, similar metrics deployed for closest neighbor analysis generate a single matrix multiplication that computes the connectedness among the words. As shown in Eq. (1), word embedding E: $\mathrm{Word}\,(\mathrm{w} \times \mathrm{u})$ is a parametrized function that plots words in a corpus to a high-dimensional space (100–500 dimensions). For instance, "fever" can be considered as similar to "dengue" in that both words represent symptoms of diseases.

$$\boldsymbol{E}\,(\mathrm{w} \times \mathrm{u}) = (\mathbf{0.2}, \mathbf{-0.4}, \mathbf{0.7}, \mathbf{0.9}, \ldots, \mathbf{0.8}) \tag{1}$$

where $E(w,u)$ is the weight matrix that converts the input values $x_1, x_2, x_3, \ldots, x_n$ into a hidden layer ($w.udimensionalmatrix$), and the transpose of $E'(u,w)$ is the matrix of weights that converts the output of the hidden layer into the actual output layer ($u.wdimensionalmatrix$).

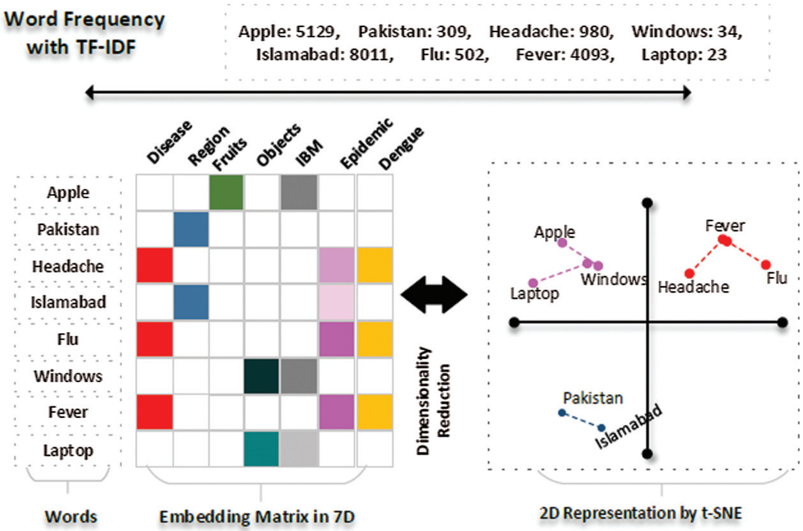


Figure 2: A sample demonstration of word embedding-based representation and TF-IDF

3.4 Data Splitting

This section presents the data splitting approach based on k-fold cross-validation [27]. Before training the model, we divided the tagged data into three sections—training, validation, and test sets—through 10-fold cross-validation. The k-fold validation scheme breaks the dataset in an 80:20 ratio, where 80% of the data are used to fit the model and the remaining 20% are used for model testing. We also further split the training data in a 60:20 ratio, where 60% of the data were used for model fitting and 20% for validation to tune the model parameters. This is done to determine whether the model efficiently works on the training data by removing overfitting and under-fitting.

3.5 Classification Approach

The ANN is a special form of machine learning technique inspired by biological neural networks [28]. The ANN contains an input and an output layer as well as one or more than one hidden layers of neurons that process the input values to generate the output. An ANN incorporating more than one hidden layer is also known as a deep neural network. It can obtain knowledge from the data and deliver solutions to problems of classification, forecasting (prediction), and detection. The ANN is a nonlinear mathematical technique that incorporates multifaceted input–output relationships to find a new pattern. ANNs make use of machine translation, text classification, speech recognition, image recognition, and facial racemization. They are structured into two forms, as feed-forward neural networks (FFNNs) and feedback neural networks (FBNN). In the FFNN data processing occurs only in one way/direction from input to output. In the FBNN, the output is transferred internally to the model by calculating the error and propagating it back to earlier layers to achieve optimized results [28].

3.6 *Parameter Tuning*

This section analyzes the hyperparameters used in the development of the proposed model. Of eight deployed ANNs, the best four formulations for the proposed method in terms of performance are reported in Tab. 2.

Table 2: Overview of formulations of the ANN

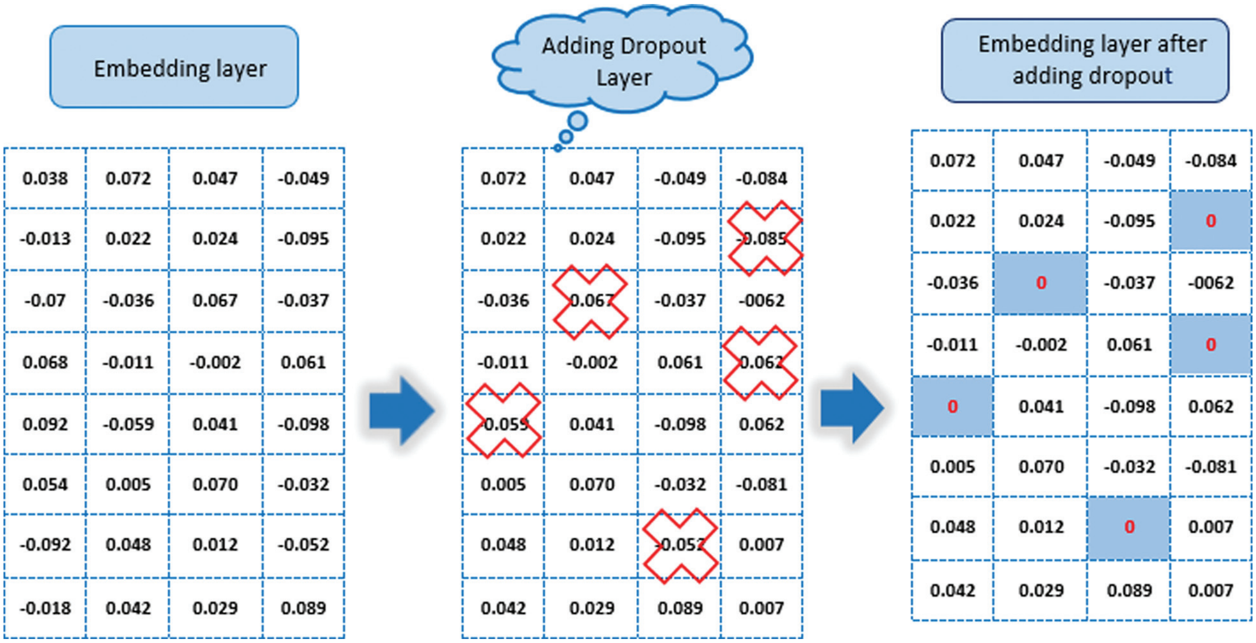
Formation	Max_features	No. of hidden layers	No. of nodes in layer 1	No. of nodes in layer 2	No. of nodes in layer 3	Emb_dim	Dropout
ANN-1	8,000	1	32	–	–	100	–
ANN-2	8,000	2	16	4	–	100	0.3
ANN-3	8,000	3	64	32	16	100	0.5
ANN-4	8,000	3	128	64	32	100	0.5

Tab. 2 represents the settings of the formulations of the ANN, where "hidden layers" represent a set of neurons positioned between the input and the output layers to impose various modifications on the input features. With each input is associated a corresponding *weight* that represents the magnitude of the links between neurons [29]. A weight close to zero indicates that the input is not altered by the output, whereas a negative value indicates that the output will be reduced by enhancing the input. This determines the degree to which the input affects the output. In addition, the sharpness (gradient) of the activation function is enhanced by the weight, which indicates that the weight determines how rapidly the activation function is actuated. A *bias* is added to the weighted sum to control the triggering of the activation function. The calculated value is then passed to the activation function to produce the output (i.e., positive or negative) in a way best suited for the provided data. An *epoch* is one instance (iteration) of compilation of the dataset (such as one forward as well as one backward pass). An epoch becomes too large to pump into the machine simultaneously [30], because of which it is split into smaller batches to optimize the training data. Furthermore, the *batch size* is the number of training examples of the dataset in a single batch. Compiling an epoch for the required number of batches is known as an *iteration*. The other parameters are maintained at fixed sizes in the model, including the maximum numbers of features (Max_features) and embedding dimensions (Emb_dim) (Tab. 2).

DNNs are efficient machine learning models with a large number of parameters. Overfitting is a significant issue in them. The models are also challenging to develop. Overfitting is handled by integrating the outputs of several deep learning models during the evaluation phase. Dropout is a regularization technique in ANN models used to solve this problem (overfitting) [31]. The main role of the dropout layer is to randomly turn off or drop the activation of the units along with their links in a model during training. Removing neurons from a model means deleting them from the model temporally, including all their links (e.g., both incoming and outgoing links). The work of the dropout layer is graphically represented in Fig. 3, which shows the embedding layer containing the vector dimension (actual value representation) for the tweet: "Oh I am diagnosed with dengue again." Consequently, some vector values of the embedding layer are temporally disabled to "0" at random after applying the dropout layer.

3.7 *Classification Results*

This section presents the graphical visualization of tweet processing using the ANN. The aim of the proposed method is to analyze tweets and classify them according to whether they convey



Embedding layer

0.038	0.072	0.047	-0.049
-0.013	0.022	0.024	-0.095
-0.07	-0.036	0.067	-0.037
0.068	-0.011	-0.002	0.061
0.092	-0.059	0.041	-0.098
0.054	0.005	0.070	-0.032
-0.092	0.048	0.012	-0.052
-0.018	0.042	0.029	0.089

Adding Dropout Layer

0.072	0.047	-0.049	-0.084
0.022	0.024	-0.095	~~0.085~~
-0.036	~~0.067~~	-0.037	-0062
-0.011	-0.002	0.061	~~0.062~~
~~0.059~~	0.041	-0.098	0.062
0.005	0.070	-0.032	-0.081
0.048	0.012	~~0.052~~	0.007
0.042	0.029	0.089	0.007

Embedding layer after adding dropout

0.072	0.047	-0.049	-0.084
0.022	0.024	-0.095	0
-0.036	0	-0.037	-0062
-0.011	-0.002	0.061	0
0	0.041	-0.098	0.062
0.005	0.070	-0.032	-0.081
0.048	0.012	0	0.007
0.042	0.029	0.089	0.007

Figure 3: Structure of the dropout layer

the fact that someone has been infected with dengue, or contain only information about the disease. Since the ANN cannot process text data directly, they were converted into numeric vectors for computation. In NLP, the textual data were converted into numerical values, and vector values were computed for all words in the corpus using the GloVe embedding technique.

The embedded vectors were fed into the ANN to train the model for classification. The ANN with a single hidden layer was selected only to demonstrate the method through which tweet text was processed and the numbers computed in each step. At the output layer, two units were created to classify the data into a negative or a positive class. In the first step, the data were converted into vectors as discussed above. Around 8,000 vectors values (referred to as features) were obtained for the entire training dataset. In the training phase, the data (i.e., vector values of text) were processed by the ANN as shown in Fig. 4. After training, the values of the weight (w) and bias (b) were optimized using the gradient descent algorithm. We then used the values of w^t and b for classification.

Example: The processing and numerical computation of each layer of the ANN with some example tweets (i.e., positive and negative) are graphically provided in accordance with the guidelines discussed in the Section 3.

Suppose the two tweets—*"she is suffering from dengue" and "stay safe dengue is viral"*—are considered as disease positive and disease negative, respectively. Disease positive means that someone is infected from dengue while disease negative tweet represents that tweet contains some information about the dengue disease. Then, the tweets are analyzed through the ANN. Figs. 5 and 6 show the way in which they were classified by the ANN. The relevant vector is represented by vector X in these figures, and the other values were all zero in these examples. Then, the corresponding weights of the hidden layer were calculated as shown by vector W^1. The following operations were performed (Eqs. (2) and (3)).

$$Z^1 = np.dot\left(W^{1T}.X\right), \quad \text{and} \quad A^1 = ReLU\left(Z^1\right) \tag{2}$$

$$\boldsymbol{Z^2 = np.dot\left(W2^T.A^1\right), \quad and \quad A^2 = Sigmoid\left(Z^2\right)} \tag{3}$$

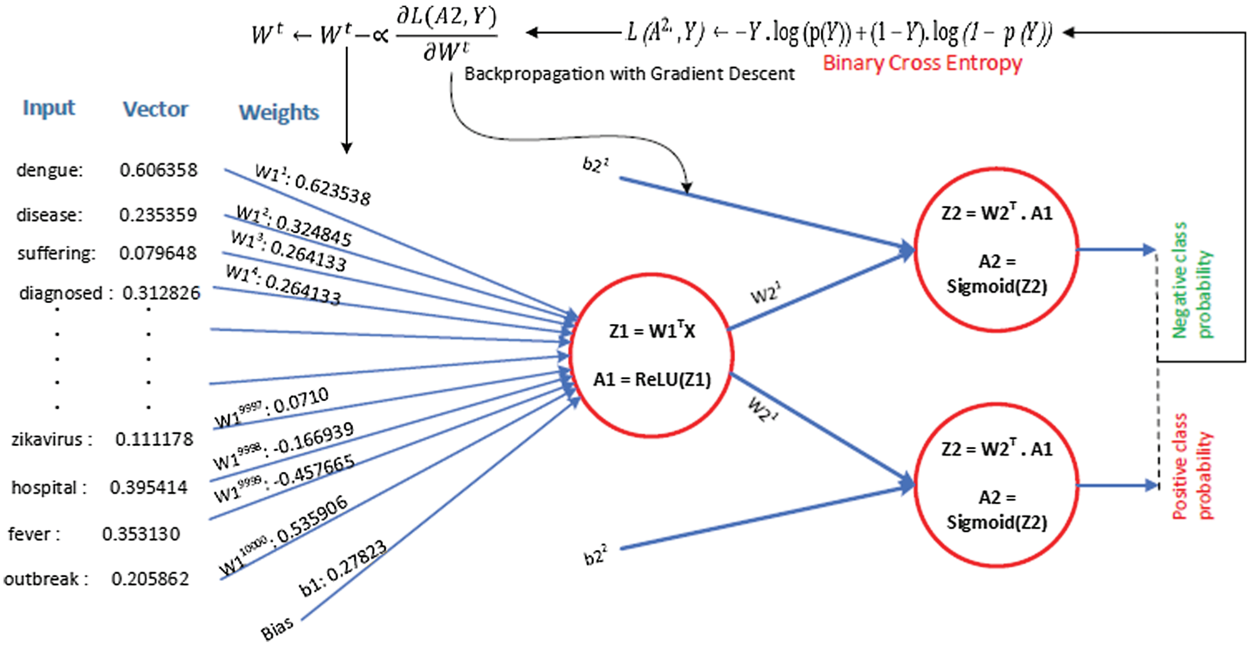


Figure 4: Example—ANN structure for processing embedded training data

A^2 contains two probabilities. The first number shows the probability of the given tweet belonging to the negative class and the second shows the probability of it belonging to the positive class. The negative class probability in Fig. 5 was 0.24 and the positive class probability was 0.8. This means that the ANN classified the first tweet as belonging to the positive class tweet at an accuracy of 80%.

Similarly, Fig. 6 shows the negative class probability (0.765) and positive class probability (0.231) of the tweet “dengue is viral stay safe.” It shows that the model classified this tweet as a negative tweet with an accuracy of 76.5%.

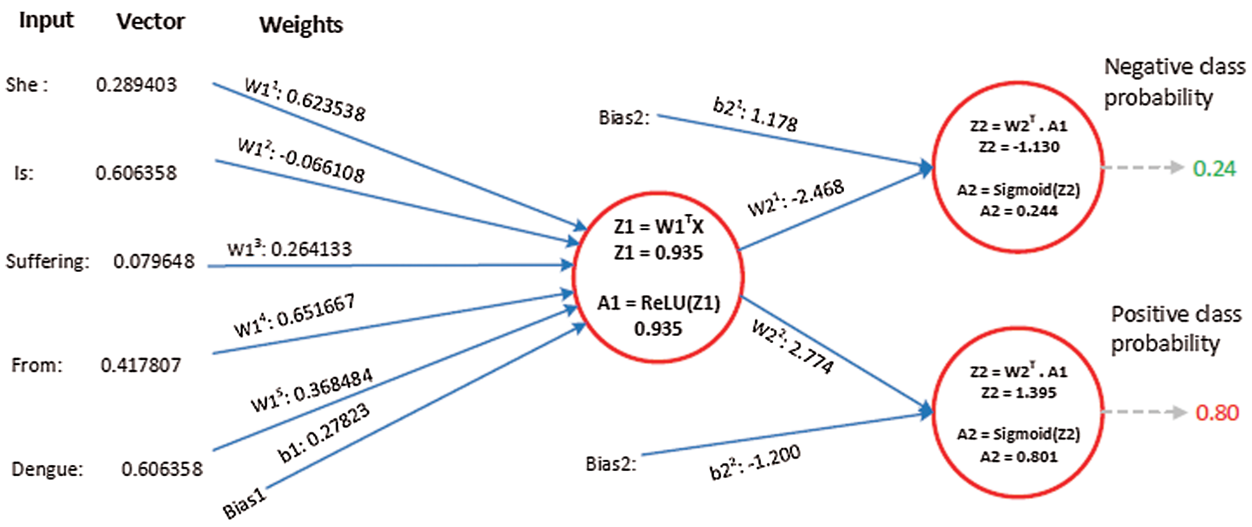


Figure 5: The processing of the tweet "she is suffering from dengue" as an example of a tweet belonging to the positive class

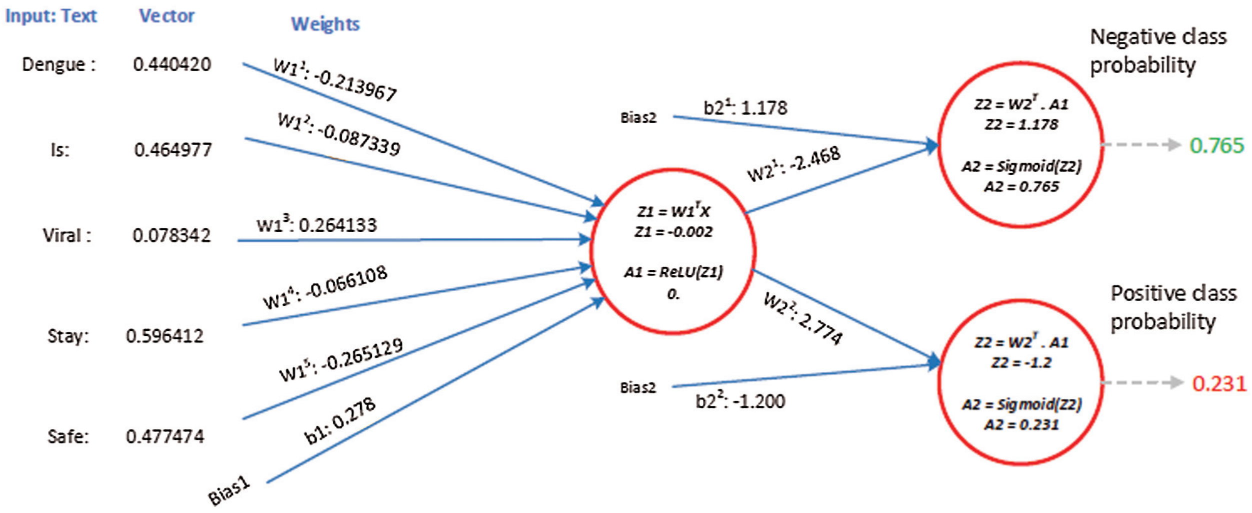


Figure 6: The processing of the tweet "dengue is viral stay safe" as an example of a negative class tweet

4 Experimental Results and Discussion

This section presents the results of experiments to validate the proposed method. The experiments were performed on Anaconda Python 3.6 with the TensorFlow, Keras, and scikit learning modules [32–35]. The preprocessed data were formulated for analysis using the two classes of dengue positive and dengue negative.

The results that the textual content of the tweets was converted into feature vectors by the GloVe embedding technique. The GloVe dictionary efficiently captured a sufficient amount of information for the selected ANN to use the hyperparameters to classify the tweets as dengue positive or negative. Its performance was evaluated in terms of precision, recall, and the F1-score [36].

Tab. 3 lists the performance of the proposed method in training, validation, and testing, and lists the training times in seconds for the given formulations of the ANN. Its test accuracy gradually increased with the training time, with some deviations in orientation. ANN-3 yielded the best result using three hidden layers, 64, 32, and 16 nodes in layers 1–3 respectively, and 0.5 as the value of the dropout layer.

Table 3: Accuracy of the proposed classifiers

Formation	Training accuracy (%)	Validation accuracy (%)	Test accuracy (%)	Training time (s)
ANN-1	81.30	79.00	79.30	983
ANN-2	83.80	80.01	81.08	1120
ANN-3	**90.04**	**88.40**	**89.80**	1211
ANN-4	89.10	86.50	87.40	1491

Tab. 4 reports the performance of the proposed method in terms of precision, recall, and the F1-score) for various formulations of the proposed ANN model. ANN-3 achieved the best results in terms of precision (88%), recall (88%), and the F1-score (88%).

Table 4: Evaluation metrics of the proposed method

Formation	Precision (%)	Recall (%)	F-score (%)
ANN-1	79	77	78
ANN-2	82	81	81
ANN-3	**88**	**88**	**88**
ANN-4	84	83	83

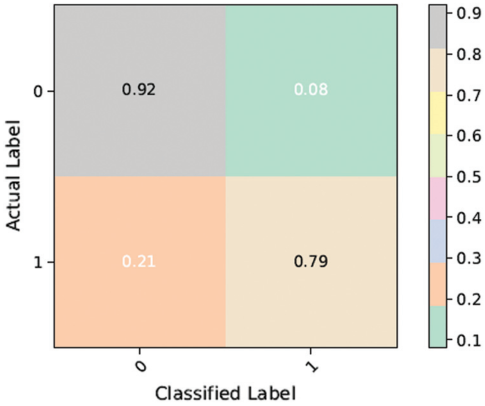


Figure 7: Confusion matrix for ANN-1

The model was also evaluated by deploying confusion matrices and the receiver operating character curve (ROC curve) [36]. The confusion matrix compared the classified data with actual labeled data, whereas the ROC curve is a graphical visualization that shows the investigative capability of a binary classification problem as its discrimination threshold is varied. In the graphs below, for the confusion matrix, the y-axis represents the actual label whereas the x-axis represents the classified data (i.e., the data detected by the model). Similarly for the ROC curve, the y-axis shows the true positive rate and the x-axis shows the false positive rate (tweets that did not represent infection but were judged by the model as dengue positive). Moreover, a micro-average ROC curve was used for the most populous class (negative class) and a macro-average ROC curve for the least populous class (positive class). If the macro-average value was smaller than the micro-average value of the ROC curve, it showed that the most populous class featured a significant number of instances of incorrect classification, whereas smaller class labels were correctly classified. If the macro-average was slightly smaller than the micro-average, this indicated that smaller labels were improperly classified by the model while the larger class was properly classified. Fig. 7 shows that ANN-1 was not efficient at classifying tweets indicating dengue without the optimization techniques. The ROC curve reflects this in Fig. 8. However, as shown in Figs. 9 and 10, ANN-2 performed better than ANN-1 owing to the slight optimization of the hyperparameters (see Tab. 2).

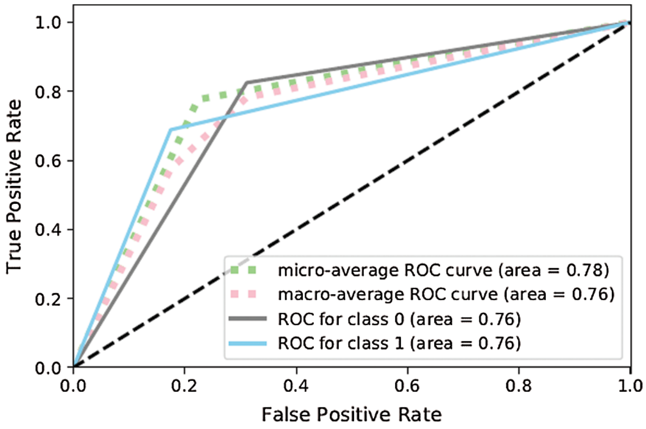


Figure 8: ROC curve for ANN-1

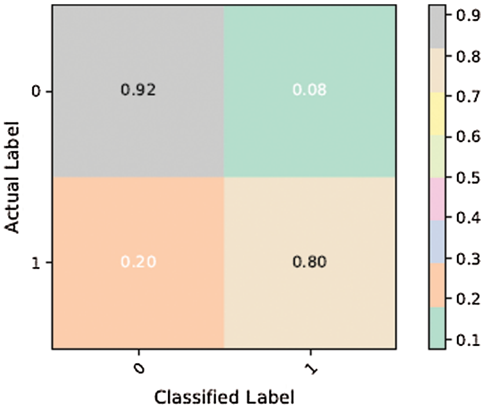


Figure 9: Confusion matrix for ANN-2

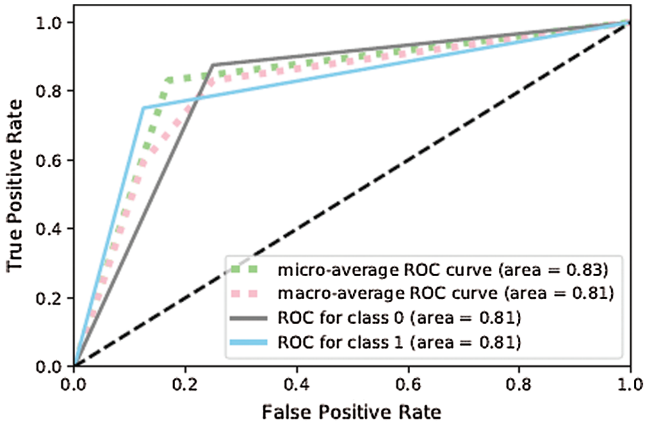


Figure 10: ROC curve for ANN-2

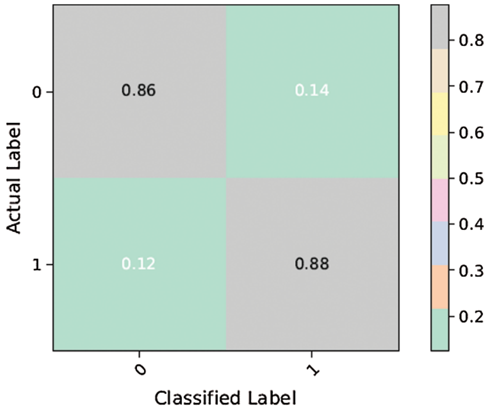


Figure 11: Confusion matrix for ANN-3

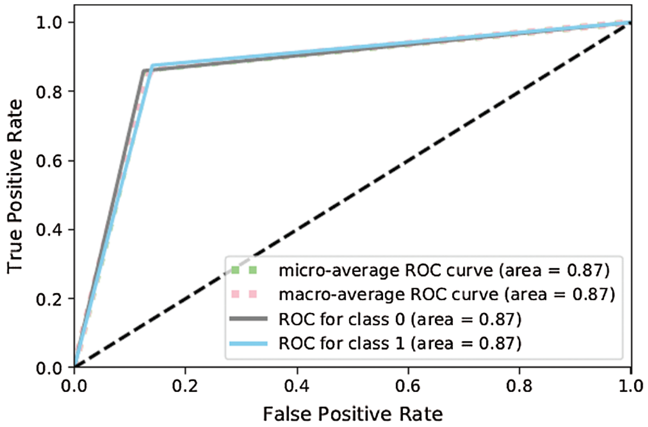


Figure 12: ROC curve for ANN-3

The results above show that the performance of ANN-3 (Figs. 11 and 12) for the class of disease-positive tweets (88%) was significantly better than the other formulations as it used different hyperparameters. Moreover, Figs. 13 and 14 show that ANN-4 delivered poorer performance (81%) because with its limited number of nodes, it works efficiently on medium-sized data but not on large corpora (5,000 tagged data items were used in this study).

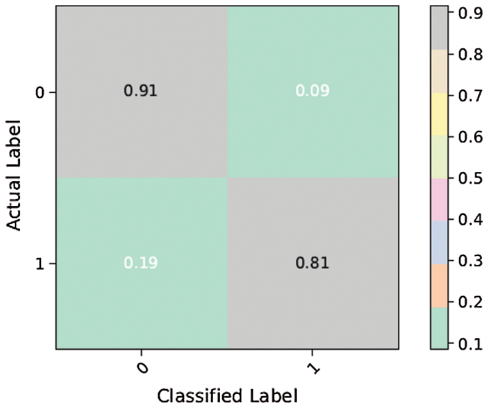


Figure 13: Confusion matrix for ANN-4

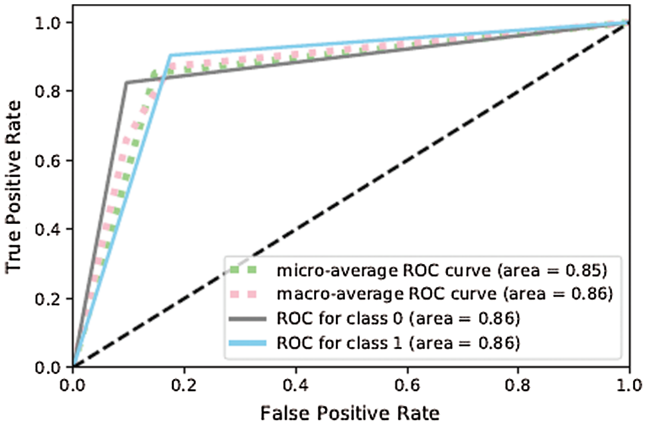


Figure 14: ROC curve for ANN-4

5 Conclusion

In recent years, Twitter has emerged as the most popular social media platform for sharing health-related information in real time. We explored ANN techniques in this study to classify dengue-related tweets into positive and negative classes. A ground truth dataset was used for experiments. It was passed through modules for (i) data acquisition, (ii) data preprocessing, (iii) feature extraction, and (iv) classification. The proposed model was then trained and evaluated in terms of its ability to correct classify tweets into positive and negative classes, according to whether they did or did not indicate that someone had been infected, respectively. We used several evaluation metrics to assess the model. The synthetic and semantic relationships among the words were also checked by uses features of the GloVe embedding technique with bi-grams. The results showed that the proposed method can efficiently learn the context of the word structure. In future, the proposed model may also be applicable as a surveillance system to quickly detect the transmission of COVID-19.

Despite substantial findings revealed by the proposed model, it has certain drawbacks. Supervised learning was used in this research, because of which the data used for model training needed to be labeled. The model should be trained in an unsupervised way to avoid requiring labeled data.

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