Neural Networks for Dengue Prediction: 
A Systematic Review

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Abstract

Objectives: Due to a lack of treatments and universal vaccine, early forecasts of Dengue are an important tool for disease control. Neural networks are powerful predictive models that have made contributions to many areas of public health. In this systematic review, we provide an introduction to the neural networks relevant to Dengue forecasting and review their applications in the literature. The objective is to help inform model design for future work.

Methods: Following the PRISMA guidelines, we conduct a systematic search of studies that use neural networks to forecast Dengue in human populations. We summarize the relative performance of neural networks and comparator models, model architectures and hyperparameters, as well as choices of input features.

Results: Nineteen papers were included. Most studies implement shallow neural networks using historical Dengue incidence and meteorological input features. Prediction horizons tend to be short. Building on the strengths of neural networks, most studies use granular observations at the city or sub-national level. Performance of neural networks relative to comparators such as Support Vector Machines varies across study contexts.

Conclusions: The studies suggest that neural networks can provide good predictions of Dengue and should be included in the set of candidate models. The use of convolutional, recurrent, or deep networks is relatively unexplored but offers promising avenues for further research, as does the use of a broader set of input features such as social media or mobile phone data.

1 Introduction

Dengue Fever is a mosquito-borne disease with a significant global burden. Half of the world’s population and 129 countries are at risk of infection [1]. Between 100 and 400 million infections are registered each year globally [2]. Dengue presents as a flu-like illness with symptoms ranging from mild to severe. There are four serotypes, meaning up to four infections are possible for each person over their lifetime, with potentially life-threatening complications arising from severe Dengue. There is no specific treatment or universal vaccine, and the primary preventative measure is vector control. This underscores the importance of disease surveillance. Predictive models can help efficiently allocate public health resources to combat Dengue, with the goal of reducing the overall disease burden [3]. Dengue incidence is associated with many different risk factors. These include climate conditions such as rainfall, extreme weather events, and temperature [4] [5] [6], land use [7], and poverty [8]. These factors may have nonlinear, context-specific, and time-variant effects on disease incidence, which poses a challenge to disease modeling.
The literature on Dengue forecasting is multi-disciplinary, uniting expertise from areas such as epidemiology, environmental science, computer science, and mathematics. Modeling frameworks include both theoretical and data-driven approaches. Compartmental models, for example, estimate the dynamics of Dengue infections in a population over time, and are based on extensive knowledge of the host, vector, and transmission process. Another simulation technique, agent-based modeling is useful for estimating impacts of interventions, such as the release of sterile males to control the mosquito population [9]. Statistical time series forecasting takes a more data-centric approach and is effective at modeling the highly auto-correlated nature of Dengue Fever [10, 11]. Machine learning models leverage the increasing data availability on risk factors of disease spreading and offer non-parametric approaches that require less detailed knowledge of the disease and context [12].

Neural networks are a subset of machine learning algorithms, which have made significant contributions to medicine and public health, including applications such as medical image analysis for disease diagnosis [13], identifying abnormalities in signals such as electrocardiographs (ECG) [14], and optimizing decisions of health care providers, hospitals, and policy-makers [15]. Neural networks are also used to forecast diseases, including Malaria [16], Influenza. [17], and Covid-19 [18].

This review examines the use of neural networks for Dengue Fever prediction. The objective is to summarize the existing literature and also provide an introduction to this still somewhat novel modeling technique. Our contributions are as follows:

- We summarize the technical decisions made in the literature, including architecture selection and hyper-parameter tuning.
- We examine the data inputs (such as climate or population demographics) and best predictors of Dengue fever identified in specific contexts.
- We review the relative performance of different neural network architectures and comparator models, such as other machine learning techniques.

To the knowledge of the authors, no systematic review of the literature on neural networks applied to Dengue Fever prediction has yet been conducted. Siriyasatien et al (2018) [19] provide a broader review of data science models applied for Dengue Fever prediction. Racloz et al (2012) [20] review the literature on surveillance systems for Dengue Fever. The study finds that most papers use logistic or multiple regression to analyze Dengue risk factors. (Seasonal) Auto-Regressive Integrated Moving Average (S/ARIMA) models have become a popular choice to incorporate auto-regressions but are not suitable for all data types. Though also apt at analyzing auto-regressive behavior, the study does not review any literature on neural networks or machine learning for Dengue surveillance. We aim to fill this knowledge gap in the present review.

2 A Primer on Neural Networks

This section gives an overview of some of the neural network models that are relevant to Dengue prediction. We explain the model first intuitively, then mathematically, and focus on feed-forward neural networks, which are used most often for Dengue prediction. Many high-quality textbooks and open source tutorials offer a deeper introduction to neural networks (for example [21, 22]). Several Python libraries include easy-to-use implementations of neural network models (for example TensorFlow [23], scikit-learn [24], or Keras [25]). We also provide sample code for Dengue prediction in a Github repository.

1https://github.com/KRoster/N4Dengue
Like other machine learning models, neural networks learn to execute specific supervised tasks, such as predicting the number of Dengue infections, based on a large set of labeled examples. Given a set of inputs, such as climate conditions, the model learns to estimate the output, such as next month’s Dengue incidence. After making a first guess, the model looks at the correct answer and updates its parameters to reduce its error on the next iteration until its predictions are optimized.

Computationally, neural networks are represented as a network of processing units (“neurons” or “hidden units”) that transform and pass information from one layer to the next. During training, we distinguish between forward- and backward-propagation, depending on the direction of the information flow. During the forward-propagation step, input information passes between units, each time being transformed according to a set of weights and a non-linear activation function. The prediction error of the output relative to the true label is computed. Back-propagation is then used to reduce this error on the next iteration: The weights of each unit, the parameters that define how information is combined, are updated according to their influence on the prediction error. This combination of forward- and backward-propagation is repeated several times until the predictions are increasingly accurate.

After this training phase, model performance is tested on a hold-out test set. Since the test set is not used to train the model, it can give a good indication of how well the model will generalize to new data, once applied in the real world.

![Figure 1: Sample feed-forward neural network architecture](image)

The figure shows a sample neural network architecture with 4 input features, 2 hidden layers with 5 and 2 nodes respectively and a single node in the output layer.

There are many different neural network architectures that are designed for different kinds of inputs and tasks. The architecture determines how the units are connected, how information flows through the network, and how many weights need to be optimized. An example of a feed-forward network is illustrated in figure 1. It shows the forward propagation of information through the individual neurons of the network, which was described above. The information that is passed through a given neuron \( j \) in layer \( l \), called its activation \( a_{j}^{[l]} \), is computed as the linear combination of weights \( u_{ij}^{[l]} \), biases \( b_{j}^{[l]} \), and inputs from the previous layer \( a_{i}^{[l-1]} \), which is passed through a
A benefit of neural networks is that parameters are updated by the model itself, not predefined by the researcher. They do not rely on strong assumptions and knowledge of the disease. Yet some hyper-parameters of neural network models must still be set by the researcher and are generally determined through a combination of domain knowledge and iterative experimentation. These hyper-parameters are tuned using a validation set or through cross-validation. Hyper-parameters may include the learning rate (by how much the weights are updated at each backward propagation step), the number of epochs (how often the forward and backward propagation steps are repeated), the mini-batch size (how many training examples are processed at each step), how weights are initialized (for example all zeros or random values), the number of hidden units in each layer, and the number of layers. Other important decisions include the choice of activation function in each layer, the choice of loss function, and the relative size of training, validation, and test sets. The optimal choices and ranges tested for these hyper-parameters depend, among other aspects, on the size and type of data available and the nature of the predictive task. One aim of this review is to summarize the choice of parameters deemed optimal by researchers in the existing literature to assist future researchers in the hyper-parameter tuning process.

Besides feed-forward neural networks, this review includes two other categories of models used for Dengue forecasting. Recurrent neural networks (RNN) were developed for the analysis of sequence data, such as time series (sequences of observations in time) or text (sequences of words). They are cyclical (they contain loops) and process sequences of inputs together, giving the network a "memory" to remember historical feature states. RNNs are used in contexts where the evolution of input features matters for the target feature, where the prediction relies on information at multiple time steps. An example is machine translation, where the meaning of a word is influenced by its context, by the other words in the sentence. The number of Dengue cases may also depend on the sequence of risk factors or the sequence of previous Dengue incidence. Using time series data, RNNs may help capture the auto-correlation of the disease and lagged influence of risk factors, such as rainfall or travel patterns. Within the family of RNNs we distinguish different architectures, such as Long Short-Term Memory (LSTM) and Gated Recurrent Units (GRU) 20, 27, 28.

Convolutional neural networks (CNN) are another subclass of deep neural network models with applications in computer vision 29, such as image segmentation and classification. Inputs into CNNs are three-dimensional - such as a two dimensional image with three color channels, which form a 3-D matrix of pixel values. The architectures of CNNs include different kinds of operations,
such as convolution and pooling, which help identify key regions in the image that help make the final prediction. For example, the model may learn that the presence of a body of water (shiny pixels in a satellite image) influence the number of Dengue cases we should expect. Crucial in this example is that the type of relevant landscape feature is not defined by the researcher but learned by the model. However, CNNs may also be used for data processing prior to prediction, for example to classify land use (such as vegetation or urban areas) from satellite images, which are known to influence Dengue spread and which can then be fed into Dengue a separate predictive model.

The tasks executed by machine learning models in general, and neural networks in particular, fall into two different categories: classification and prediction. Classification is the process of assigning a categorical label to an example based on its inputs, such as determining whether a patient has Dengue fever or a different disease. Prediction is the process of forecasting a future state based on historical or current inputs, for example predicting next month’s Dengue incidence from this month’s rainfall.

This review is focused on predictive models of Dengue Fever at the population level. In addition to classic regression models, we include papers using classification for prediction approaches, which produce categorical instead of continuous outputs. For example, a model may predict whether a city will experience an outbreak (binary classification) or which risk category will prevail (multi-label classification).

3 Methodology

This review follows the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) statement guidelines [30]. The PRISMA flow chart is represented in figure 2. A systematic search was conducted using Web of Science/ Knowledge, Scopus (abstract, title, keywords), PubMed, and Science Direct (abstract, title) databases. References of papers appearing in the search results were also examined for relevant works. The searches were conducted between 21 July and 17 August 2020 and used the following search string:

"( deep learning OR neural network ) AND dengue"

The papers were examined for inclusion in the review in three stages: by title, by abstract, and finally by full text. In each phase, the following inclusion and exclusion criteria were applied liberally to determine which papers would be considered in the next phase. If the information in the title and/or abstract was inconclusive, the paper was included in the full-text review. Inclusion and exclusion criteria are as follows:

• Studies must implement a neural network or deep learning technique, either as the main method or as a comparator model. Reviews of the literature on neural networks for Dengue forecasting would also be considered.

• Studies must predict Dengue fever incidence or risk. There are no restrictions on the type of target variable used. For example, the number of Dengue cases, Dengue incidence rate, or a binary Dengue risk variable are all accepted as target features.

• Studies must examine Dengue in a human population. Models for disease diagnosis of individuals are excluded. Studies modeling the location of vectors without relation to Dengue incidence are excluded. Studies examining animal hosts are excluded.

• As the search query is in English, only English language articles were identified and included in the review.
4 Results

This section summarizes the findings of the review. The full list of papers and their properties are provided in table 1 at the end of this section.

4.1 Prediction Target

Within the criteria of study selection, there was significant variation in the study specifications, including the formulation of the target feature. Most studies predict the future number of Dengue cases based on historical time series. However, there are some notable exceptions. Andersson et al (2019) [31] predict a static incidence rate at the neighborhood level in Rio de Janeiro, Brazil. Two studies predict the risk of a Dengue outbreak: Abeyrathna et al (2019) [32] formulate their task as a binary classification of ‘outbreak’ or ‘no outbreak’, while Anno et al (2019) [33] classify cities according to five risk categories.

Early forecasts provide more time for public health response but may have lower confidence. In most of the selected studies, researchers predict one period ahead corresponding to the measurement frequency of the data used. A single study predicted the present: Livelo and Cheng (2018) [34] use social media activity in the Philippines to predict the present situation of Dengue infection. They use a neural network model to classify tweets according to a set of different categories of Dengue-related topics. Their weekly Dengue index based on this Twitter data is correlated with
actual Dengue case counts. Koh et al. (2018) [35] compare one and two-week forecast horizons. Soemsp et al. (2014) [36] use a two-week horizon with weekly data inputs. Dharmawardhana et al (2017) [37] predict Dengue cases in Sri Lankan districts four weeks ahead using weekly data on cases, climate, human mobility, and vegetation indices. Chakraborty et al. (2019) [38] use the longest forecasting horizon. They use three different datasets of Dengue cases, two of which are weekly (Peru and Puerto Rico), and one which is measured monthly (Philippines). For the weekly data, they compare three and six month horizons. For the monthly data, they compare a horizon of six months with one year forecasts. For Peru and the Philippines, the best model changes with the prediction horizon.

4.2 Data Sources

![Image of variable types used in selected studies]

Figure 3: Variable types used in the selected studies

The figure illustrates how frequently studies included individual data types as well as combinations thereof. Each row represents a data type and the horizontal bars measure their frequency of inclusion in the selected papers. The columns represent the combinations of variables, and the vertical bars measure how often the given combinations occurred.

Besides epidemiological data on the history of Dengue Fever, which is used in all studies, the most common predictors are meteorological variables (used in 14 studies) (see figure 3). Additional data sources include: vegetation indices and other landscape features extracted from satellite images (in two studies), human mobility, specifically mobile phone data (used in one study), aerial and street view images (in one study), social media data, specifically from Twitter (one study), vector information (one study), and demography (one study). Three papers use only epidemiological data.

Most studies examine granular geographic regions, such as cities (nine studies) or districts (six studies). Two studies even modeled Dengue at the sub-city (neighborhood) level (see figure 4).
Granular scales can be beneficial in two ways: they allow for local predictions and accordingly targeted public health response. They also generally result in larger training datasets with more observations than national or state-level aggregations, which plays to the strength of neural networks. The studies cover countries in both Asia and Latin America, which are considered the primary Dengue endemic regions [3]. A total of 13 countries are included (see figure 5), with the Philippines and Brazil appearing most often.

4.3 Model Selection

Most studies implement a shallow neural network with just one hidden layer. Four studies use deeper feed-forward architectures. Three studies employ recurrent neural networks, two of which used LSTM units and one used a GRU. Three studies implemented CNNs.

The neural network models were compared to a range of other models. Support Vector Machine
Figure 6: Models used in the selected studies

The figure illustrates how frequently studies used different forecasting models as well as combinations thereof. Each row represents an algorithm and the horizontal bars measure their frequency of inclusion in the selected papers. Green rows refer to neural network models, while blue bars show comparator models, such as machine learning algorithms. The columns illustrate which combinations of models were used, the frequency of which is measured by the vertical bars.

(SVM) models were most common (six studies). Generalized Additive Models (GAMs), (S)ARIMA and linear autoregressive (AR) models occurred twice each. The remaining comparators were used in just one paper each: Gradient Boosting Machine (GBM), XGBoost, Linear regression, Poisson regression, Tsetlin Machine (TM), Cellular automata, a compartmental model, and a naive baseline. Figure 6 shows how frequently different model types and combinations thereof were used in the selected literature.

The most common comparator model used is SVM. Evidence suggests that both SVM and neural networks perform well, and which is better depends on the context. In Xu et al (2020) [39], an LSTM neural network outperforms an SVM model in predicting the number of Dengue fever cases in 20 Chinese cities. Transfer learning further increased the performance gains in cities with few overall Dengue cases. Abeyrathna et al (2019) [32] use a classification for prediction approach to identify whether districts in the Philippines are likely to experience a Dengue Fever outbreak. Whether SVM or the neural network model is better in the context of this study depends on the evaluation metric used: SVM has a higher precision, while ANN has a higher F1-score. Yusof and Mustaffa (2011) [40] and Kesorn et al (2015) [41] both find SVM to have a higher performance than the neural network.

Four studies use a feed-forward network with at least two hidden layers. They provide varying evidence to the performance relative to shallow neural networks or other machine learning models. In [37], a model with two hidden layers performs better than an XGBoost model in forecasting Dengue in Sri Lankan districts. In two studies ([32] and [42]), the deep neural network provides
better predictions than alternative neural network models, but is not the best model overall: In [42], the MLP with two hidden layers performs better than the LSTM-RNN to forecast Dengue in a Brazilian city, but a GAM is best overall. In [32], a model with three hidden layers has lower errors than models with a single or five hidden layers. However, the best F1 score in classifying binary outbreak risk is achieved by a Tsetlin Machine. The final study [33] uses a model with three hidden layers but does not employ any comparator models.

Performance of the RNN models is also mixed. The two studies using LSTM-RNNs produce contradicting results despite having similar study designs. Baquero et al. (2018) [42] and Xu et al. (2020) [39] both use LSTM-RNNs to forecast Dengue at the city level, compare their model to a feed-forward neural network and a GAM, use meteorological and epidemiological input features, and evaluate performance using RMSE. Xu et al. (2020) [39] find the LSTM to have the best performance relative to all comparator models, whereas in the study by Baquero et al. (2018) [42], the LSTM-ANN performs worse than the simple neural network and the best model overall is the GAM.

The three studies using CNNs do not provide comparisons to other types of models, though one study compares different CNN architectures. However, the key advantage of the examined CNN studies is the granular geographic resolution in predictions. The models take satellite and other images as inputs and can therefore generate forecasts at the sub-city level. Andersson et al. (2019) [31] compare different kinds of CNN architectures (based on DenseNet-161) for each of three input types, specifically satellite imagery, street view images, and the combination of the two. Their model predicts Dengue incidence rates at the neighborhood level in Rio de Janeiro, Brazil. Best performance is achieved when combining street and aerial images. Rehman et al. (2019) [44] implement a pre-trained CNN (based on U-Net architecture) to extract landscape features from satellite imagery, which they use in a compartmental SIR model to forecast Dengue in neighborhoods of two Pakistani cities. Anno et al. (2019) [33] use a CNN (based on AlexNet architecture) to classify five levels of outbreak risk in cities in Taiwan, based on images capturing sea surface temperatures.

### 4.4 Architecture

Architectures vary across the different models. The studies implementing shallow models with one hidden layer cumulatively tested 1-30 hidden units. Three studies [45, 46, 36] tested a broad number of values across this range, and their optimal number of hidden units were related to the number of input features. Two studies [45, 46] identified four hidden units as the optimum. Both used meteorological and epidemiological variables and both measured four different pieces of information. Wijekoon et al (2014) [45] used temperature, rainfall, humidity and Dengue cases. Aburas et al (2010) [46] included a total of seven features that measured the same information but with additional lags. The third study [46] identified 25 nodes as the optimum, which matches the larger input size of 32 features. Instead of trying different values, Datoc et al (2016) [47] fixed the number of hidden units to the number of input features, and selected the best-performing model among eight models with three to five nodes. The best model used three nodes (corresponding to three input features).

Abeyrathna et al (2019) [32] compared shallow and deep architectures. Their best neural network model had three layers with (20, 150, 100) units respectively. This model performed better than the two shallow models with five or 20 neurons in a single hidden layer. It also outperformed a five-hidden layer model of (20, 200, 150, 100, 50) topology.

Baquero et al (2018) [42] also used deep architectures with 2 layers with combinations of (10 or 20) neurons in the first layer, and (5 or 10) neurons in the second. They implemented both MLP and LSTM models. The best neural network model was an MLP with (20,10) neurons, though a Generalized Additive Model (GAM) and an ensemble both performed better than the neural
networks.

The other LSTM model was implemented by Xu et al. (2020) [39] with a different architecture. They used a single hidden layer with 64 neurons. Unlike Baquero et al. (2018) [42], their model outperformed GAM as well as SVR and GBM.

4.5 Model Evaluation

The studies utilize a range of metrics to assess model performance, in part due to different prediction targets. The most common measures are Root Mean Squared Error (RMSE) and Pearson’s correlation, which are each used in seven studies each. Mean Average Error (MAE), Mean Squared Error (MSE), and accuracy are also commonly used.

5 Discussion

The literature on neural networks applied to Dengue forecasting is still somewhat scarce, but the reviewed studies include some promising examples, where neural networks outperform other machine learning or statistical approaches. The literature therefore suggests that neural networks may be appropriate for inclusion in a set of candidate models when forecasting Dengue incidence. However there is variation as to whether neural network models or other approaches perform best. Future research may compare different model types and architectures on multiple datasets, to better understand how the ideal model varies by context, such as geography or data availability.

Though many risk factors of Dengue have been identified, most neural network models limit inputs to meteorological and epidemiological data. Future studies may evaluate the value of alternative predictors, especially as NNs tend to deal well with high-dimensional problems. Along the same lines, there is space for more incorporation of non-causal predictors of Dengue fever from sources such as social media. Some papers in this review have leveraged these new predictors, specifically from Twitter [34], Street view and satellite images [31], mobile phone records [37], and features derived from satellite imagery [37, 44]. These data sources have also been effective with other machine learning models, for example Baidu search data to predict Dengue in a Chinese province [12].

Transfer learning was implemented in [39], where it provided promising results. The authors trained a model on a city with high Dengue incidence and used it to predict disease in lower-incidence geographies. This was the only study in this review that used transfer learning outside the context of pre-trained CNNs. This may present another avenue for further research, especially in locations where data is scarce.

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| Reference | Country | Geospatial scale | Target | Prediction horizon | Input data | Variables details (incl. lags) | Data aggregation | Train/ validation/ test split | NN Model | Comparator models | Evaluation | Best model |
|-----------|---------|-----------------|--------|------------------|------------|---------------------------------|-----------------|-------------------------|---------|------------------|-----------|----------|
| Abeyrathna et al. (2016) | Philippines | district | binary outbreak variable | 1 month | epidemiological | Dengue incidence in the previous month and previous year, same-month of the same region, historical dengue incidence from the neighboring region; total dengue incidenes | monthly | Train: 2008-2015 (86%), Test: 2016 (11%) | Feed-forward NN (four different architectures) | Tseltin Machine (TM), SVM, Decision Tree (DT) | F1 score, accuracy, precision, recall | best overall: Tseltin Machine (TM) best NN ANN-3 |
| Aburas et al. (2018) | Malaysia | country | cases | epidemiological | mean temperature, mean relative humidity, total rainfall, Dengue cases with 1 lag | weekly | Train: 104 weeks (52%), Test: 226 weeks (68%) | Feed-forward NN | SVM, correlation | ROC AUC, correlation | SVM, correlation |
| Anderson et al. (2016) | Brazil | sub-city | Dengue incidence rate | epidemiological | Google street view and aerial images; Dengue incidence rate | incidence rate over entire period | Train: 75%, Test: 25%; Val: 10,000 location points from test set | CHN | SVM, correlation | accuracy | SVM, correlation |
| Aro et al. (2019) | Taiwan | city/township | multi-label outbreak variable (5 classes) | epidemiological | dengue cases, Sea surface temperature (SST) | monthly | Train: SBSA72 (87.84%), Test: SBSA72 (12.54%); B-BSTD | CHN | SVM, correlation | accuracy | SVM, correlation |
| Baiqueiro et al. (2016) | Brazil | city | cases | epidemiological | 3 lags of Dengue cases and temperature (minimum, mean and maximum), precipitation and relative humidity; variable selected varied by model type | monthly | Train: 2000-2009 (19%), Test: 2010-2014 (81%) | Feed-forward NN | LSTM, Feed-forward NN | 1 year ahead: ARIMA-ANN in all 3 datasets; 6 months ahead: Philippine-ANN; Sicilian-ANN; San Juan-ANN | LSTM, Feed-forward NN |
| Chakraborty et al. (2019) | Peru, Philippines, Puerto Rico | city/country | cases | 6 months and 1 year | epidemiological | Dengue cases; residuals from ARIMA models; lags varied by model | weekly, monthly | San Juan (weekly); May: May 1990 - April 2001 (99%); Test: May-Oct 2001 (26%); Inquis (weekly); Test: Jul 2000 - Jun 2011 (99%); Test: Jul-Dec 2011 (4%); Philippines (monthly); Test: 2008-15 (89%); Test: 2016 (11%) | XGBoost, SVM, GBM, Random Forest, ANN, ARIMA, SVAR, LSTM, ARIMA, ARIMA-ANN | MSE, MAE, R^2, MAPE | RMSE, Best model: ANN |
| Data et al. (2014) | Philippines | city | cases | epidemiological | all models included total rainfall, average temperature; Dengue case counts as one lag; some models also included percentage relative humidity and population index; first set of models used actual weather data, second set used average monthly weather data | monthly | Train: 2010-2013 (67%); Test: 2014-2015 (33%) | Feed-forward NN | SVM, correlation | correlation | SVM, correlation |
| Dharmawanthana et al. (2017) | Sri Lanka | district | cases | epidemiological | 4 week lag of Dengue cases (selected as optimal lag from a choice of 1-12 weeks); daily rainfall, temperature, mobility value (fixed over time); vegetation index | weekly | Train: 2012 - 2013 (67%); Test: 2014 (33%) | Feed-forward NN | H2Boost | R2 | Feed-forward NN |
| García-García et al. (2011) | Cuba | city | parameter 3 from compartmental SIR model | epidemiological | - | - | - | Hopfield/Neural Network | graph (no metric) | - | - |
| Herath et al. (2014) | Sri Lanka | district | cases | epidemiological | Average Temperature at 1 lag; Average Temperature at 4 lags; Average Relative Humidity at 1 and 4 lags; Total Rainfall at 4 lags; Number of Rainy Days at 4 lags; Number of Dengue cases at 1 lag | weekly | Train: 70%, Val: 15%, Test: 15% | Feed-forward NN | SVM, correlation, NNMRF, Frew(S2) | Log sigmoid activation with 4 hidden units | SVM with radial basis function |
| Kesorn et al. (2015) | Thailand | district | high-risk region (binary classification) | epidemiological | temperature, rainfall, humidity, wind speed, Aedes aegypti larvae infection rate, male mosquito infection rate, female mosquito infection rate; population density; Dengue infection rate | seasonal (year divided into three seasons) | 10-fold CV | Feed-forward NN | SVM (with 2 different kernels: linear kernel, radial basis function, and polynomial); XGBoost, DT | Sensitivity, specificity, and accuracy | SVM with radial basis function |
| Koh et al. (2016) | Singapore | country/city | cases | epidemiological | the on-set-distance dengue data at one and two lags, once-differenced rainfall data at three lags | weekly | time series CV | NN/NEAR, NN/RAT | ABQ, Regression | MSE |
| Livio and Chang (2018) | Philippines | country | Twitter Dengue index | present | epidemiological - social media | weekly | Dengue case counts, Tweets | weekly | Train: 60%, Val: 20%, Test: 20% | GRU | One-to-Many Classifier; multi-binary classifier (as opposed to multi-label) which uses the same GPU architecture. | Learning task: correlation, Multitask GRU; Dengue index generated using 2 of the 5 Twitter classes (“abance” and “mosquito”) |
| Rahayu et al. (2010) | Indonesia | city/country | cases | epidemiological | Dengue cases, at temperature data, air humidity, rainfall, duration of solar radiation and wind speed temperature and precipitation; Dengue cases; satellite images classify the time-matrix percent of the city (averaged by the following 6 landscape features: roads, waterways, buildings, trees, standing water, crops) | 2-week time steps | train: 25 images | CHN: Landscape feature classification; used as input to TISS models; comparable model without landscape features (TSB); Adjusted R^2 (for classification of satellite images) | comparable models with all 6 landscape features | - |
| Rahman et al. (2016) | Pakistan | sub-city | epidemiological | satellite | Dengue cases at 1 lag; Seasonality; mean temperature, average temperature, peak rainfall, minimum rainfall, maximum rainfall; average relative humidity, minimum relative humidity, Dengue case counts | weekly | Train: 247 weeks (60%); Test: 72 weeks (20%) | Feed-forward NN | Cellular Automata (CA) with Genetic Algorithm | MSE, correlation | CA |
| Sauer et al. (2014) | Thailand | district | cases | epidemiological | minimum temperature, maximum temperature, average rainfall, maximum rainfall, minimum rainfall, average relative humidity, minimum relative humidity, Dengue case counts | weekly | Train: 70%, Test: 20% | Feed-forward NN | Linear AR | RMSE | Feed-forward NN |
| Sauer et al. (2015) | Brazil | city | cases | epidemiological | Dengue cases at 1-5 lags | weekly | Train: 70%, Test: 30% | Feed-forward NN | SVM, RMSE, MSE | Accuracy | SVM, RMSE, MSE |
| Xu et al. (2020) | China | city | cases | epidemiological | 12 month lags of Dengue cases, maximum pressure, average pressure, mean water pressure, maximum air temperature, average of daily highest temperature, average of daily lowest temperature, average of daily precipitation, number of days with rainfall, and average of relative humidity | monthly | Train: 2000-2016 (86%); Test: 2017-2018 (14%) | LSTM (both with and without transfer learning), Feed-forward ANN | GABM, SVM, GBM | RMSE, correlation | LSTM |
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