Forecast of Dengue Cases based on the Deep Learning Approach: A Case Study for a Brazilian City

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Abstract: According to the World Health Organization (WHO), dengue is an endemic disease in more than 100 countries, with about 50 million people infected each year and 2.5 billion living in risk areas. Dengue requires a major research effort in countries affected by the disease, as its incidence is strongly determined by nonlinear local processes, such as climatic conditions, social characteristics and habits of populations (Falcón-Lezama, 2016). In this scenario, forecasting models can be important tools for outbreak control, allowing health institutions to anticipate the mobilization of resources. In this article, we use deep learning, including long and short-term memory (LSTM) and dense layers of perceptrons to implement a forecast model of dengue cases for 5 epidemiological weeks ahead with a mean accuracy of 93%.

1 **INTRODUCTION**

Predicting the future and based on that, intervening in current processes is a fundamental task since the adoption of mechanisms for analyzing and

forecasting health incidents contributes to reducing expenditure and decreasing the mortality rate and the number of people affected by the diseases. Nevertheless, forecasting should not be considered the final answer, but rather a tool to increase

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understanding and highlight important processes and guide action (De la Sante, 1999).

Machine Learning (ML) is data-driven and does not involve intense prior assumptions, enabling the mapping of non-linear functions, even if the relationships between the data are not known (Wang et al., 2015). According to Cortes et al (2018), in the last decades, non-linear models of automatic learning have attracted the attention of researchers because they present good performance for forecasting nonstationary time series when compared with models of Autoregressive Integrated Moving Averages (ARIMA).

ML-based models have been used successfully in dengue outbreak forecasting problems. Adhikari et al (2019) presented a neural network called EpiDeep, which learns patterns of historical epidemic incidence curves and predicts future incidences. The EpiDeep model seeks similarities between the most recent evolutionary stage and past epidemic crises to make predictions and anticipate actions to control and mitigate the impacts of the disease.

In that sense, Anggraeni et al. (2019) used Artificial Neural Network to predict the number of cases of hemorrhagic dengue fever in the region of Malang Indonesia. The results of the model are presented on a web page that uses the Google Maps API to display the dissemination of cases grouped by health centers.

In our study, we used a LSTM prediction model suggested by Xu et al (2020), adding dense layers of perceptrons, to predict weekly dengue cases. Furthermore, we propose a method for non-trivial determination of the sampling window of points in the current series.

2 METHOD

Predicting the behavior of complex nonlinear processes is in the domain of machine learning (ML) applications. Typically, behavior is estimated and extrapolated into the future from a known subset of past data (Haykin, 2009).

Long-term dependency is a property observed in the time series of dengue cases (Cortes, F. et al., 2018). In this case, the model of eq. 1 describes the variation of the indicator over time:

$$\rho(n) = f(\rho(n-1), \rho(n-2) \dots \rho(n-m)) + g(\alpha_1(n), \alpha_2(n) \dots \alpha_l(n))$$
(1)

in which n represents the epidemiological week when a measure ρ of dengue cases is obtained, m is a positive integer value that determines a specific moment from which the correlation with the value of the nth measurement is negligible. In eq. 1, f is a nonlinear function that connects the current dengue cases to the values that have occurred over time and g is a possibly non-linear function that links the factors, α , that influence the spread of the disease, such as environmental, socioeconomic conditions and actions to control and prevent the mosquito.

Haykin (2009) suggests the application of Recurrent Neural Networks (RNN) as non-linear H-steps-forward filters, to project future time series values with long-term dependence. In this case, the neural network is fed with previous m values (sampling window) of the series, , and its output, v, estimates the next H values (forecast horizon) of the series itself. Then:

$$\boldsymbol{u} = [\rho(m), \rho(m-1) \dots \rho(1)]$$
(2)
$$\boldsymbol{u} \in \mathbb{R}^{m},$$

$$\mathbf{v} = [\rho(m+1), \rho(m+2) \dots \rho(m+H)]$$
(3)

$$\boldsymbol{v} \in \mathbb{R}^{H}$$

The relationship between \boldsymbol{u} and the next values of the time series, \boldsymbol{v} , is given by the vector equation shown in eq. 4.

$$\boldsymbol{p} = \boldsymbol{f}(\boldsymbol{u}) + \boldsymbol{g}(\boldsymbol{\alpha}) \tag{4}$$

 $\alpha = [\alpha_1, \alpha_2, \dots \alpha_l]$ Thus, the prediction problem consists in providing an estimate for the next values of the time series:

$$\boldsymbol{v}'(k) = \boldsymbol{f}'(\boldsymbol{u}) + \boldsymbol{g}'(\boldsymbol{\alpha}) \tag{5}$$

where v'(k) is an estimate of $v(n) \in f' \in g'$ are the corresponding approximations of f and g.

The input layer of the forecast model corresponds to the offset sampling window of the dengue cases records in the previous epidemiological weeks and the output layer provides the forecast in the desired period (forecast horizon).

RNNs (Fig. 1) are structures that can scale to very long-time sequences. The internal states h_t of the processing units of an RNN change as the inputs are presented over time (t), forming conditions similar to a memory. RNNs use equation 6 to adjust the values in their internal processing units. When it is trained to perform a task that requires predicting the future from the past, the recurrent network uses h_t as a kind of memory of the relevant aspects of the previous sequence ($x_{(t-1)}, x_{(t-2)}, x_{(t-3)}$...) from entries to t. (Hochreiter and Schmidhuber, 1987).

$$h_t = f(h_{t-1}, x_t) \tag{6}$$

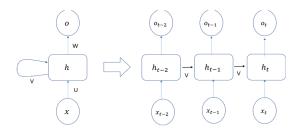


Figure 1: Graph of a Recurring Neural Network.

A. Perceptrons Layers - PL

PL (Fig.2) are structures with feedforward architecture of processing elements (artificial neurons). Most of the information needed for processing is extracted in the layer, which encodes them through synaptic weights and thresholds of its neurons. The network training process is usually performed with the backpropagation algorithm, which uses input and output pairs to adjust the weights and thresholds of the network employing an error correction mechanism (Haykin, 2009).

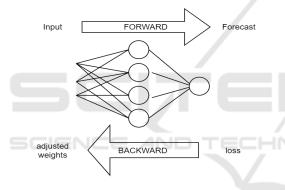


Figure 2: Graph of a PL.

B. Evaluation Metrics

Building prediction models based on ML demand the adjustment of parameters such as learning rate, number of neurons, and sampling window to minimize the loss function (evaluation metrics) related to the training process (Faceli et al., 2011). The most popular loss metrics are:

Root Mean Squared Error – RMSE:

$$RMSE = \sqrt{\frac{\sum_{i=1}^{n} (y_i - \dot{y}_i)^2}{n}}$$
(7)

Mean Absolute Error - MAE:

$$MAE = \frac{1}{n} \sum_{i=1}^{n} |y_i - \dot{y}_i|$$
(8)

Mean Absolute Percentage Error - MAPE:

$$MAPE = \frac{\sum_{i=1}^{n} |(y_i - \dot{y}_i)/y_i|}{n} \cdot 100$$
 (9)

Where $y_i e \dot{y}_i$ denote the observed value and the estimated value of the model, respectively, and n is the number of samples used.

C. Software to Forecast Study

The forecast study was performed using the Keras-TensorFlow package (Chollet, 2017). The other packages employed were (i) Pandas libraries for structuring the data, (ii) Matplotlib for constructing graphs, (iii) scikit-learn for linear regression and normalization of the data, and (iv) NumPy for the vector structure and mathematical functions (Géron, 2017). The version of the software used was the latest version available on March 15, 2021, in the Python Package Index (PyPI), for the programming language Python 3.6. All the software used is free and open source.

3 FORECAST MODELING

Fig. 3 shows the reported dengue cases by epidemiological week, counted from 2011 to 2020 for a Brazilian city with a demographic density of 1.8 hab/km² and was carried out based on information available in the SINAN (Sistema de Informação de Agravos de Notificação) (SINAN, 2022). The time series histogram is shown in Fig. 4. In previous experiments, a considerable loss for forecast model accuracy was found for highest incidence values because of sampling bias for smaller values. Fig. 5 and 6 shows the time series and histogram with the logarithmic function.

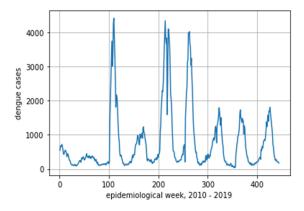


Figure 3: Dengue cases by epidemiological week, counted from 2010 to 2020 for a Brazilian city with a demographic density of 1.8 hab/km².

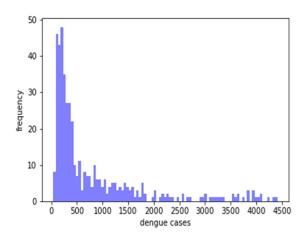


Figure 4: Histogram of the dengue time series.

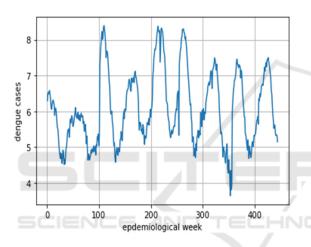


Figure 5: Dengue cases by epidemiological week, counted from 2010 to 2020 for a Brazilian city with a demographic density of 1.8 hab/km² - logarithmic function.

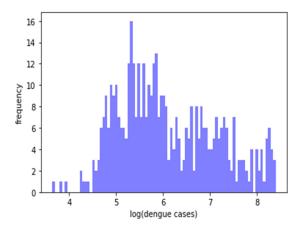


Figure 6: Histogram of the dengue time series - logarithmic function.

D. Sampling Window

Determining the sampling window to be used as input for the forecast model is not trivial, especially when working with data visualization platforms, in which the user can choose a new time series for the projection at any time. The algorithm must, therefore, adapt different models for the forecast horizon in question, according to the real data of the chosen series as input to the neural network. For this, we propose to use lags to the forecast horizon, H, for which the values of the Autocorrelation Function (ACF) are greater in module than the statistical confidence limits (Samohyl, 2009).

The ACF measures the correlation degree of a variable with itself in previous time units (lag), allowing to infer the long term of the time series (Samohyl, 2009). The autocorrelation coefficient for the lag, θ , is given by:

$$r_{\theta} = \frac{Cov(X_t, X_{t-\theta})}{V(X_t)} \tag{10}$$

where $Cov(X_t, X_{t-\theta})$ is the covariance of the series values lagged by θ and $V(X_t)$ the variance at t.

Fig. 7 shows the ACF for the dengue cases series of the Brazilian city studied. The score for lags greater than 10 epidemiological weeks tends to values between 0.4 and -0.4, which, according to Samohyl (2009), are considered of lesser statistical significance. Thus, for this series, the lags for the sampling window are x_{t-0} , $x_{t-1} \dots x_{t-(10-H)}$.

The metrics defined in eq. 7, 8, and 9 are generally used in TSF applications but with different behaviors. For example, MAE and MAPE are very smooth when the average error is small. Conversely, the RMSE is highly sensitive to outliers. A cost function that combines the best properties of these metrics is the logcosh function (Chollet, 2017) that works as the RMSE, but is attenuated for outliers. Thus, the logcosh cost function was used in all the models implemented in the research.

As proof of concept, in Fig. 8, the input data consist of the log-values of the dengue cases. The output data are the forecasting dengue cases in the subsequent weeks (forecast horizon - H). This implementation uses an RNN and was named LSTM - PL Model. It has an input layer corresponding to the records of dengue cases in the lag window, a hidden layer containing 70 LSTM cells, and a second hidden PL with 64 neurons and a dropout rate of 0.5, used to minimize the overfitting. Finally, the output layer provides the dengue cases forecast. Table 1 shows the LSTM-PL Model average loss for different forecast horizons (H) in the training step. In this research, we considered the five-week epidemiological forecast horizon as a useful value for decision making, still maintaining an acceptable loss rate.

The learning rate determines the adjustment for the neural network weights when using the Descending Gradient Method (DGM) in the training stage. In this research, the Adam version of the DGM was used with an adaptive learning rate. According to Haikin (2009), the method is computationally efficient, requires less memory, is invariant for the diagonal scaling of gradients and is suitable for problems with large amounts of data.

To find the best learning rate, experiments were started with the value of 0.001 and then other values were verified. For a five-week epidemiological forecast horizon, the best learning rate was observed to be 0.01. Fig. 9 shows the forecast of the LSTM-PL Model versus observed values, for the training set.

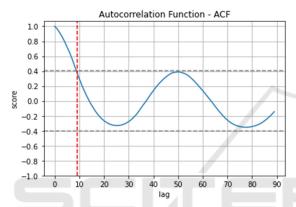


Figure 7: ACF for the dengue cases series of a Brazilian city studied.

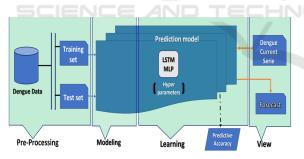


Figure 8: Proof of concept.

Table 1: LSTM-PL Model average loss versus forecast horizons (H).

Forecast horizon - H (weeks)	Average loss (%)
3	4.9
4	5.3
5	6.9
6	10.3
7	20.8
8	43.5
9	50.6

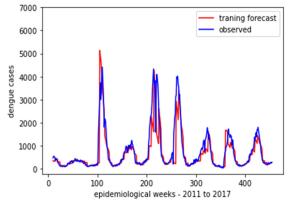


Figure 9: Forecast of the LSTM-PL Model for the training set.

4 RESULTS

Fig. 10 presents the predicted cases for visualizations carried out from the 20th to the 40th epidemiological week of 2020, with a forecast horizon of 5 weeks for each observation (observations indicated by the arrow).). The LSTM-PL Model average predictive accuracy using the MAPE (section II, B) metric is 93%. The control chart has a central curve (MCL) that, in this research, represents the average behavior of the incidence of dengue in the previous epidemiological period (52 weeks). This curve is close to two others that are determined according to the variability (standard deviation) of the data in the time series, called Upper Control Limit (UCL) and Lower Control Limit (LCL). In this research we use the Exponentially Weighted Moving Average (EWMA), discussed in Montgomery (2009), to calculate the MCL, LCL, and UCL control curves.

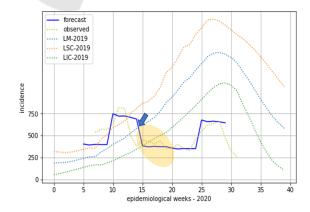


Figure 10: Control Diagram for dengue cases and the forecast given by the LSTM-PL Model for 5^{th} to 40^{th} epidemiological week, 2020.

In Fig. 10, the control chart shows early and consistently a likely occurrence of case underreporting, for observations carried out from the 14th week. Thus, the alert, duly validated by other indicators, would give the manager the opportunity to trigger corrective actions 5 weeks in advance.

5 CONCLUSIONS

In this research, we implemented a model based on ML to make predictions of dengue cases and present them in control charts that we intend to make available in dashboards of digital health platforms.

The use of ACF proved to be a practical approach for determining the sampling window (lag). This method is easy to automate for use on digital health platforms. Note that we use weekly measurements, which leads to great data variability over time. However, we believe that this granularity is the most suitable for timely decision-making.

It is not uncommon for epidemic outbreaks to occur suddenly and unexpectedly. However, even when out of control, epidemic outbreaks do not occur by chance, and the effort to analyze time series is justified precisely to anticipate and prevent them.

For predicting non-stationary time series, as is the case of dengue, it is crucial to capture the long-term dependence contained in the data. Periodic patterns can be difficult to recover, but the results from this research show that this can be achieved by ML-based models. In contrast to classic statistical methodologies, such as ARIMA and SARIMA modeling (Cortes et al, 2018), the proposed solution requires very little intervention by the analyst.

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