A Regression Based Approach for Leishmaniasis Outbreak Detection

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Abstract: Leishmaniasis is part of a group of diseases called Neglected Tropical Diseases (NTDs) that affects poor and forgotten communities and reports more than 5,000 cases in regions like Brazil, Peru, and Colombia being categorized as endemic in these. In this study, we present a machine-learning model (Random Forest) to predict cases in the future and predict possible outbreaks using meteorological and epidemiological data of the province of la Convencion (Cusco - Peru). Understanding how climate variables affect leishmaniasis outbreaks is an important problem to help people to perform prevention systems. We used several techniques to obtain better metrics and improve our model performance such as synthetic data and hyperparameter optimization. Results showed two important climate factors to analyze and no outbreaks.

1 INTRODUCTION

Neglected Tropical Diseases (NTDs) are a group of diseases caused by a diverse group of pathogens such as parasites, bacteria, and viruses. Affecting more than 1 billion people worldwide, this group of diseases mainly affects poor and forgotten communities leading to economic and social consequences[1]. Leishmaniasis part of the NTDs, is a parasitic disease caused by a protozoa parasite and transmitted to humans by the bite of infected sandflies. Cutaneous leishmaniasis (CL) is the most common form of the disease with more than 700,000 new cases each year[2]. Americas is one of the regions where leishmaniasis had more impact, reporting cases of CL in 20 countries and categorizing 18 of them as endemic, regions with the most cases of Cl are Brazil, Colombia, and Peru with more than 5,000 cases reported only in 2021[3]. According to the Peruvian Center for disease control (CDC), 4,768 cases of CL were reported with a cumulative incidence of 14.35 cases per 100,000, 847 and 529 of the total cases correspond to the regions of Madre de Dios and Cusco[4]. In La Convencion province located in the region of Cusco, 364 cases of CL were registered in 2022[5]. Covid-19 pandemic cause an impact on different programs especially those related to the detection of NTDs delaying case detection and stopping some programs due to the prioritization of the combat of the pandemic. Identifying the elements that cause increases or outbreaks of leishmaniasis cases is the main challenge to creating models that predict those scenarios and trying with them to help in creating early prevention systems. Several studies are related to the study of different diseases and their epidemics. In (Nejad and Varathan, 2021) the authors use different ML models like Bayes net, Support Vector Machine, Naive Bayes, and Decision Tables. Their main objective was to identify climatic risk factors that cause dengue outbreaks using techniques like the Pearson Correlation Coefficient (PCC). Then, they found an important factor that combines the average temperature of the last 5 weeks and the accumulative rainfall of the last 2 weeks.

In (Xu et al., 2020), authors use LSTM, a deep learning model to compare it with regression models like SVR, GBM, or GAM. This approach uses as well meteorological data but this time in a monthly

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[1] United States Agency for International Development (USAiD) - https://www.usaid.gov/global-health/health-areas/neglected-tropical-diseases

[2] Centers for Disease Control and Prevention (CDC) - https://www.cdc.gov/parasites/leishmaniasis/epi.html

[3] World Health Organization (WHO) - https://www.who.int/data/gho/data/themes/topics/topic-details/GHO/leishmaniasis

[4] Peruvian Center for disease control - https://www.dge.gob.pe/epipublic/uploads/boletin/boletin_202252_31_153743.pdf

[5] Cusco Regional Health Management - http://www.diresacusco.gob.pe/inteligencia/epidemiologia/boletines.htm

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way. However, this process would not allow for better disease tracking due to a monthly forecast and not following the progress of the disease through days or weeks. The key components of our approach are mainly composed in the model of machine learning, Random Forest, which is an ensemble method that consists of the use of decision trees with the method of bagging. Then, we train and test the model with weekly data of confirmed cases of leishmaniasis from 2017 to 2022, obtained through a request form to the Cusco Regional Health Management (GERESA - CUSCO)[6] and meteorological data obtained from the official web app of the National Meteorological and Hydrological Service of Peru (SENAMHI)[7].

Our main contributions are as follows:

- We build an ML model for weekly prediction of CL cases based on meteorological data and confirmed cases.
- We have identified meteorological risk factors and possible cases in La Convencion through weekly predictions from 1 to 4 weeks ahead in 2023 as well as reporting possible outbreaks.
- We have conducted an experimental analysis to show the feasibility of our approach.

This paper is distributed in the next sections: First, we review in Section 2 studies related to the study and prediction of epidemics of viral infections and neglected tropical diseases, and their risks. In section 3, we will discuss the main contribution of our research, introduce background and overview related to the prediction and forecast of epidemics, to finally explain the method of our approach. Then, in Section 4, we present all the experiments performed with the model of ML their metrics, and how we improve those metrics. Finally, in Section 5 conclusions of our work will be presented.

2 RELATED WORKS

Epidemiological study has been showing a big growth in different diseases in recent years. The covid-19 pandemic set a huge increase in different studies and approaches in areas like machine learning and deep learning. Therefore, this area has diverse methods to detect, predict or forecast using models of ML and DL applying techniques like classification and regression. The next articles show a brief outlook on several studies related to NTDs and the methods they used to predict cases.

In (Zhao et al., 2020), the authors propose a Random Forest (RF) model that will compete against an Artificial Neural Network (ANN), searching for the best results at predicting dengue cases in Colombia, with pooled national data and department data, this data uses various predictors, like previous dengue cases, air temperature, population counts and education. Both models are evaluated with Mean Absolute Error (MAE) and then compared using the Relative MAE. Instead, we are predicting cases of leishmaniasis using RF, using data from a specific region in Cusco called La Convencion, besides we don't include data like population or socio-economic factors, since we only look for a correlation between climate data and its impact in the number of new cases.

In (Harvey et al., 2021), the authors use a combination of Gaussian Processes and Random Forest Regressors to predict malaria cases over a period of 13 weeks in Burkina Faso, so it can validate a warning system for a potential epidemic. They use data from the Integrated e-Diagnostics Management of Childhood Illness (IeDA) for the confirmed diagnosis of malaria, and after a selective process, they decide to use rainfall, because it improves the precision of the algorithm. Instead, we use data of confirmed cases obtained from health organizations in Peru using it as a target. The predictors that we use are: precipitation, humidity, and temperature. And we only use Random Forest for the prediction because, to the best of our knowledge in the literature, we found that RF is the most robust model for our scenario.

In (Elsheikh et al., 2021), the authors propose an LSTM model to predict confirmed cases, recovered cases, and deaths of COVID-19 in Saudi Arabia three weeks ahead. Also, they compare the proposed model with a statistical model called AutoRegressive Integrated Moving Average (ARIMA), and an AI model called Nonlinear AutoRegresive Artificial Neural Networks (NARANN). The data they utilize to train the models are from the official report from the Ministry of Health using the confirmed cases, recovered cases, and deaths in three different periods of time. The evaluation criteria, they use, for the models are seven RMSE, R^2, MAE, EC, OI, COV, and CRM. On the other hand, our approach uses only confirmed cases, because mortality rates of CL in Peru are low having 1 confirmed death in 2022[5], and data of recovered cases are hard to obtain.

In (da Silva et al., 2021), the authors propose a method that combines Ensemble Empirical Mode Decomposition (EEMD) with Autoregressive Integrated Average Exogenous inputs (ARIMAX), named EEMD-ARIMAX to analyze the correlation between human mobility and meteorological data with the

[6]https://sites.google.com/view/geresacusco/inicio
[7]https://www.senamhi.gob.pe/?&p=estaciones

number of COVID-19 cases in the capitals of Brazil. For their data of COVID-19 cases, they use Brasil.io, which is a website that compiles newsletters from the State Health Secretariats of Brazil, for the meteorological data they use data from the Centro de Previsa o de Tempo e Estudos Climáticos and used Minimum and Maximum Temperature, Humidity, and Rainfall, and the human mobility data they use the COVID-19 Community Mobility Reports given by Google, it shows the trends of mobility in certain places, like Retail and recreation, Parks, Workplaces, etc. Using RMSE, ME, and MAE they evaluate the predictions for their method, and they compare it with ARIMAX. They normalized their data, showing an improvement in their method in metrics like RMSEW. In contrast, we use meteorological data and confirmed cases to find correlations and predict the number of cases weeks ahead, instead of finding patterns with the trends of population or climate data using a time series model like ARIMA.

In (Nguyen et al., 2022), the authors searched a model that can accurately predict dengue cases in Vietnam with meteorological factors, for this, they compared Convolutional Neural Network (CNN), Transformers, Long Short-Term Memory (LSTM), and Attention-enhanced LSTM (LSTM-ATT) with more traditional machine learning models like XGBoost, Super Vector Regressor (SVR), etc. Their data was constituted with monthly incident confirmed cases and deaths for dengue and meteorological data like average monthly temperature, maximum average monthly temperature, monthly rainfall, monthly average relative humidity, monthly evaporation, total monthly sunshine hours, etc.

For the evaluation of models in a time period of one to three months, they use RMSE and MAE, they also assessed the months between outbreaks or not for the model LSTM-ATT, for this epidemic detection they used four metrics, which are: accuracy, precision, sensitivity, and specificity. In contrast, we use weekly data, due to that type of format data gives us an opportunity to follow and visualize if there are meteorological patterns that could increase the spread of CL, since the granularity of weekly data may cause a loss of patterns.

3 CONTRIBUTION

3.1 Preliminary Concepts

Definition 1 (Regression (Chandramouli et al., 2018)). *Regression is the process of finding an association or relation of a dependent variable, which is the variable that we want to predict, with independent variables that are known as predictors.*

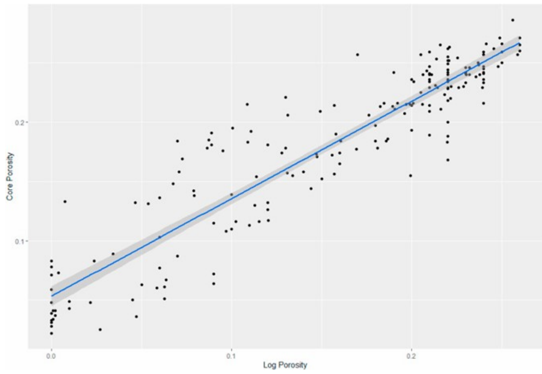


Figure 1: Example of linear regression (Al-Mudhafar, 2020).

Example 1 (Regression). *Figure 1 represents the structure of a linear regression model, showing the relationship between two variables.*

Definition 2 (Ensembled Models (Zhou, 2021; Sarkar and Natarajan, 2019)). *It's a technique that combines the outputs of different models of machine learning to get a better result in comparison to each model on their own, for this reason, they are usually built with simpler models but it also applied to stronger models so it can use less of them.*

The ensemble has various techniques that include: Averaging (taking the average of the outputs between all the models to get its final result), Boosting (using weak learners and, through multiple iterations, converts them into strong learners, focusing on the mistakes of the hypothesis), Bootstrapping (the model obtains a sampling that will be used as an input for the models and the output will be the most voted or an average if the case is a regression), Bagging (based on bootstrap sampling, it takes a dataset with a number of samples, takes a random sample, and copies it in the sampling set, it keeps the sample so it can be chosen again and repeats the process several times).

Definition 3 (Decision Trees (Zhou, 2021)). *It's a representation of the choices and decisions a person can make in each situation in the structure of a tree, being the branches as the multiple decisions that a person can take, and the leaves being nodes of the outcomes or states of every decision, and the root is the initial state of the situation.*

Definition 4 (Random Forest (Zhou, 2021)). *It works as an extension of the bagging method, using the randomness of bootstrapping to create decision trees so they are different from each other, so it can reduce overfitting and make the outcome more precise. It*

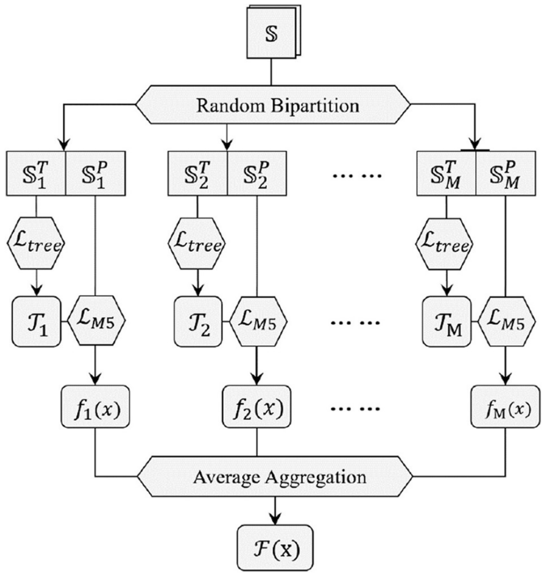


Figure 2: Structure of Random Forest (Ao et al., 2019).

usually starts with a lower performance with fewer trees but with more learners it can get better performance, also it has a low computational cost.

Example 2 (Random Forest)**.** *In Figure 2, we see the structure of a Random Forest with the partitions of samples for every decision tree, the outputs of these, and the final solution made with average aggregation.*

3.2 Method

The method designed to predict leishmaniasis outbreaks consists of a group of stages. The whole process begins with collecting the data, then we continue with Data preprocessing, which is involved the process of cleaning the data detecting missing values and removing noisy data; Data resampling, where we change the format of the dataset to weekly variables and we also apply feature engineering in this process to get new variables like the average temperature of the week. After the preprocessing stage, we have the model stage, where we start setting the partition of our dataset for training and testing. This second stage is made with the Random Forest Regressor, we train and test the model and we analyze the first results of the model in the evaluation stage with regression metrics. The third stage corresponds to the optimization process, different techniques will be used to get the best parameters for our model and improve error predictions and improve our metrics (Figure 3).

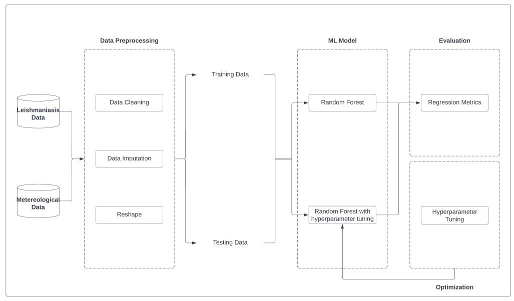


Figure 3: Method Diagram.

3.2.1 Data Preprocessing

Two datasets were collected for this study, one of them corresponds to meteorological data that was obtained from the official website of the Meteorological Service of Peru[8] from 2017 to 2022. The data was provided hourly, with attributes like temperature, humidity, precipitation, wind direction, and wind speed. Leishmaniasis data was obtained through a request form to the Cusco Regional Health Management (GERESA - CUSCO)[9], this dataset contains only confirmed cases of leishmaniasis from the province of La Convencion in a weekly format.

Data cleaning is the first technique used in this stage, the meteorological dataset had a lot of missing values that were handled imputing those hours and dates that were missing, then the meteorological values were imputed with a linear interpolation method. The percentage of missing values is presented in Table 1. The Leishmaniasis dataset had 28 weeks of missing data, to solve this problem we removed those values in order to avoid noise. Classic imputation techniques can't be applied directly to this type of data due to the different behavior of the disease through the weeks and its spread. Then, we have the resampling process, due to the formats of the datasets (hourly format and weekly format). This process has two stages:

1. We resample the meteorological dataset in a daily format here we also apply feature engineering to get new variables: minimum, maximum, and average temperature and humidity of the day.
2. In the second stage, we resample the dataset to a weekly format and we combine the whole dataset with leishmaniasis cases.

After applying feature selection and considering epidemiological variables we found that wind direction and wind speed won't impact to the prediction of the cases, due to their correlation coefficients (0.045,

[8]https://www.senamhi.gob.pe/?&p=estaciones
[9]https://sites.google.com/view/geresacusco/inicio

Table 1: Missing Values %.

	Attribute	Missing Values (%)
1	Temperature	8.47%
2	Humidity	8.53%
3	Precipitation	21.36%
4	Wind Speed	8.68%
5	Wind Direction	8.68%

0.12). The final dataset resulted in 233 rows, and 7 variables: mintemp, maxtemp, avgtemp, minhum, maxhum, avghum and prec.

3.2.2 Synthetic Data

This technique consists in creating new artificial data for the training set based on our existing dataset. We propose this method due to a lack of data and its future impact on the performance of the model. We use Synthetic Data Vault (SDV) (Patki et al., 2016) to build the new training dataset for our model. This process consists in prepare the data for the training of the SDV model, here we load the data and define the format of each variable. Then we have the modeling stage, SDV provides different models called synthesizers, for this project FAST ML[10] was used. The model learns from the existing data and then we sample new data based on the number of new rows that we want.

3.2.3 Random Forest

RF is an ensemble model that uses decision trees with a bagging method, so it can prevent overfitting. RF has many decision trees that use different samples of data and train separately from each other, each tree produces different results that are ranked and selecting the best result. In this stage, we use the sklearn library of the Random Forest Regressor[11]. For our RF model, we define training and testing in a different way, with our approach of using synthetic data we cannot use all the original dataset to generate new data, because while testing, the model will overfit, to avoid this problem we split the original dataset having only the 2022 data to testing and only generating new data based on years 2017 - 2021.

3.2.4 Evaluation

The evaluation methods that will be used to evaluate the regression model predictions are Mean Absolute Error (MAE) and Root Mean Squared Error (RMSE). MAE calculates the sum of all the absolute differences between the actual and the predicted value and then divided by the total number of data points. RMSE is the square root of MSE, and Mean Squared Error (MSE) is basically the squared difference between actual and predicted value.

Both metrics represent similarities because they determine how close is the prediction to the actual values on average, even detecting large errors in the case of RMSE. Low values of MAE and RMSE indicate that de model is correctly predicting and larger values represent poor prediction.

3.2.5 Optimization

In order to optimize our model and get better results in our metrics we will use hyperparameter tuning. This technique uses different methods to obtain the best set of hyperparameter values that produce better results in the model's performance. Random forest has several hyperparameters that can be modified to get better performance. Getting the best set of hyperparameters can be challenging if we do it manually, so in this study, we will use different methods such as random search, grid search, and Three-based Pipeline Optimization (TPOT).

- Grid Search (GS). GS is one of the most common techniques to optimize hyperparameters. Its functionality is relatively simple, we create a grid of different hyperparameters values then GS fits in every combination, saves every performance for each set created, and selects the best performance as output.
- Random Search (RS). This technique uses a method that chooses random values of a predefined set of hyperparameters, then in each iteration fits the model with a set chosen and returns the best set after several iterations. Random Search performs better when we have a large search space and also takes less time than GS to show results.
- Three-Based Pipeline Optimization (TPOT) (Le et al., 2020). It's a machine learning tool that uses genetic programming to help to find the best pipeline for a machine learning model. For this study, we use TPOT to get the best set of hyperparameters for Random Forest.

[10]https://docs.sdv.dev/sdv/single-table-data/modeling/synthesizers/fast-ml-preset

[11]https://scikit-learn.org/stable/modules/generated/sklearn.ensemble.RandomForestRegressor.html

4 EXPERIMENTS

4.1 Experimental Protocol

All our was conducted with Google Colab, a free version of a Python environment. Colab provides 12.7 GB of ram and 107.7 GB of disk to write and execute Python code and store files for up to 12 hours. Dataset files were stored in google drive and imported with a Python library gdown. For the optimization stage, a dictionary of parameters was determined and the possible values for each parameter are shown in Table 2. Our code is publicly available in: https://github.com/RyzewitchChicken/LMR-Code.git

4.2 Results

The proposed work carried out several experiments in order to get better metric values and reduce error prediction. Those experiments are presented in different scenarios where we defined hypotheses and present the results of them.

Scenario 1. The first scenario performed is related to training and testing the model with the original dataset. The experiment resulted in MAE and RMSE values, 3.97 and 4.91 respectively.

Scenario 2. After several tests with synthetic data, we concluded by adding 10,500 new rows of data to the original dataset based on the results of MAE values, see Table 3. In this experiment, we got better value metrics in comparison with the original dataset, 3.77 in MAE and 4.56 in RMSE. The distribution of new data in comparison with real data is shown in Figure 4. Until this scenario, random forest hyperparameters were not modified, so settings were used by default based on the sklearn library.

Scenario 3. Table 4 shows the optimizers' best results according to the values established in Table 2. Random search performs slightly better in comparison to TPOT and grid search, having a better value in RMSE with 4.42 (Table 5) and being faster than others because of the random selection of hyperparameters. On the other hand, grid search also has good results but performs badly in RMSE getting 4.51, due to its search space and all combinations evaluation, grid search tends to be computationally slow.

Scenario 4. In order to get better metric values, we propose a hypothesis that our model tends to perform badly due to the low case periods and according to our research approach (predict outbreaks) we consider that low case periods would be not necessary. In this scenario, we performed two experiments: i) We considered that cases lower than 5 cause low performance. Our model struggles to predict minor values causing large prediction errors and resulting in higher MAE and RMSE values. We conducted an experi-

Table 2: Values for optimization.

Parameter	Possible Value
Number of estimators	100, 200, 300, 400, 500 - 1500
Max features	sqrt, log2
Max depth	10, 20, 50, 65, 70, 90, 110, none
Min samples split	2, 5, 10
Min samples leaf	1, 2, 4

Table 3: Synthetic data values test.

Quantity of rows	MAE
1,500	3.91
4,500	3.90
7,500	3.91
10,500	**3.77**
13,500	3.89

Table 4: Result of Optimizers.

Optimizer	Quantity of estimators	Min samples split	Min samples leaf	Max features	Max depth
Random Search	700	10	2	sqrt	10
Grid Search	1200	5	4	log2	90
TPOT	400	2	2	sqrt	65

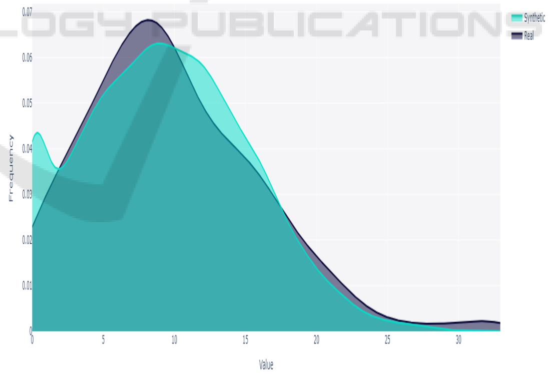
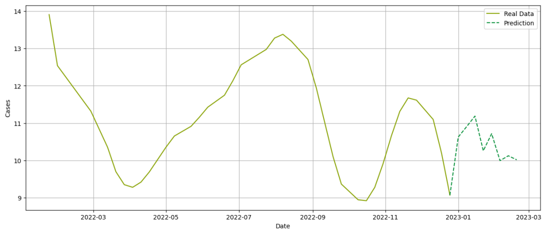


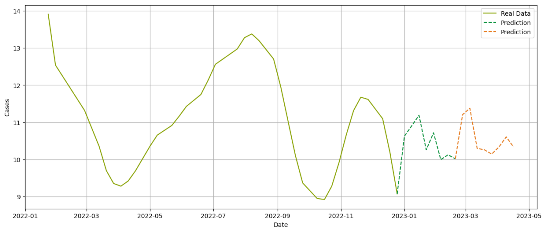
Figure 4: Distribution comparison between synthetic and real data.

Table 5: Metric Results.

Experiment	MAE	RMSE
Random Forest (Original Dataset)	3.97	4.91
Synthetic Data	3.77	4.56
Random Forest + Random Search	**3.65**	**4.42**
Random Forest + Grid Search	3.67	4.51
Random Forest + TPOT	3.64	4.47
Random Forest + Cases > 5	2.79	3.48
Random Forest + Cases > 7	**2.27**	**2.93**



(a) 8 weeks ahead.



(b) 16 weeks ahead.

Figure 5: Predicting Outbreaks.

ment where we deleted values lower than 5 and we got better results, having 2.79 in MAE and 3.48 in RMSE. And, ii) for the second experiment we tested values higher than 7. In this case, we even got better results in our metric error, MAE 2.27 and 2.93 in RMSE, an improvement of 18.64% in MAE in comparison to the previous MAE value. Important to mention that scenario 4 experiments were conducted with our best model and the optimizer (Random Forest + Random Search), a big improvement considering that MAE dropped from 3.65 to 2.27 and that our model has problems predicting low values. All metric values of the different experiments performed are shown in Table 5.

Prediction. With our previous results in the fourth scenario, we can finally generate predictions having our best model. In Figure 5a and Figure 5b, we generate an 8-week and 16-week prediction, all these predictions correspond to the first 4 months of 2023 (January, February, March, and April). Both Figures present the cases of 2022 and the predictions generated, in both, we can see that the province of La Convencion won't show outbreaks and the trend shows no outbreaks for the incoming months. The way that we detect an outbreak is by using the Z-score method if we detect an outlier in our set of predictions we define that as an outbreak.

4.3 Discussion

Metrics. In order to get better metric values and reduce MAE and RMSE we performed several experiments (Table 5). Considering that the lowest MAE and RMSE value we get is the better our model performs, we proposed a few techniques to achieve. The first experiment gave us a perspective on how the model is performing with the original dataset, we found that missing values and zero values cause noise and reduce our dataset size, therefore, our model performed badly with high metric values and a higher RMSE value of 4.91. Synthetic data helped us to get more rows with a similar distribution to the original dataset, showing that with this technique we can reduce error prediction going from 3.97 in MAE to 3.77 and 4.91 in RMSE to 4.56.

We compared three optimizer techniques where Random Search performed a bit better than TPOT, having similar results in MAE with 3.65 and 3.64 and a slight difference in RMSE with 4.42 and 4.47. Grid Search also performs similarly in MAE (3.67) but struggles to get a good RMSE value getting 4.51. On the other hand, we have Table 4 results. We put out attention to the number of estimators and "max_depth", Grid Search costs a high computationally performance due to the values in estimators 1200 and 90 in max_depth, more estimators and higher depth for a tree tend to have a higher training time. Random Search and TPOT have different results, with more estimators for RS with a lower depth tree but fewer estimators for TPOT with a higher depth tree. Even with more estimators RS performed a little faster than TPOT, this is caused because of the depth. In RF, max_depth defines the number of splits for each decision tree, so in the case of RS takes less time for the model to train due to fewer splits. This experiment shows that hyperparameter tuning was a good approach because reduces significantly error prediction, we went from 3.77 with synthetic data without modifying hyperparameters and using it based on the setting of sklearn to 3.65 testing different combinations of hyperparameters.

Our last experiment proposed a hypothesis based on how our model was performing until the last scenario. We have shown that zero values caused noise in the model and produced bad performance, but going deeper into the experiments, we noticed that the model was still struggling with low values. Two tests were conducted with a similar approach, dropping those values that may cause trouble for the model. These two experiments showed that having cases values higher than 5 and 7 caused better metric values, in MAE and RMSE improved error prediction from 3.65 to 2.79 and 2.27, in the case of RMSE from 4.42 to 3.48 and 2.93. These major changes helped us in predicting larger values to detect outbreaks in the future which makes our model better to predict larger cases but worst to predict lower cases.

Model. Feature importance is an important technique to analyze our model and how our attributes are contributing to predicting leishmaniasis cases. Based on our analysis maximum humidity is the most important feature in the prediction, representing 18%. Average temperature and minimum humidity represent another 15% and 14% of contribution while precipitation represents the lowest importance with 11%. We can see that humidity has a good correlation with leishmaniasis cases while there is a low correlation between precipitation and our target variable (cases), but we noticed that this might be related to the meteorological dataset.

5 CONCLUSION

In this work, we used a Random Forest model to predict leishmaniasis cases and possible outbreaks in the future. As an ensembling model, RF shows good results in predicting cases. We performed several tests to get a better model with less error prediction, showing that our original dataset was really small and caused problems for the model. Even with synthetic data, our error prediction was high, so an optimization process was necessary. Optimizers showed great results, Random Search and a genetic algorithm (TPOT) performed better than an approach like Grid Search reducing error prediction in metrics like MAE from 3.77 to 3.64-65.

Our first approach was deleting 0 values due to the noise that causes, but we noticed that low values cause trouble. We proposed two experiments where we considered that low values won't be necessary. After several tests, we conclude that cases greater than 5 and 7 contribute to getting better metrics values with an improvement of 24% and 38% (MAE) respectively. That experiment causes a model that is better at predicting high values but worst at low values. Finally, we noticed that humidity and temperature are the most important predictors.

As an extension of this work, a better and bigger dataset is necessary to get a better model with the correct recollection of meteorological data and epidemiological data. On the other hand, NTDs have several diseases that cause problems in different parts of the world.

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