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A Comparative Study of Machine Learning Techniques for Multi-Class Classification of Arboviral Diseases

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Among the neglected tropical diseases (NTDs), arboviral diseases present a significant number of cases worldwide. Their correct classification is a complex process due to the similarity of symptoms and the lack of tests in Brazil countryside is a big challenge to be overcome. Given this context, this paper proposes a comparative study of machine learning techniques for multi-class classification of arboviral diseases, which considers three classes: DENGUE, CHIKUNGUNYA and OTHERS, and uses clinical and socio-demographic data from patients. Feature selection techniques were also used for selecting the best subset of attributes for each model. Gradient boosting machines presented the best result in the metrics and a good subset of attributes for daily usage by the physicians that resulted in a 76.58% recall on the CHIKUNGUNYA class.

Keywords: arboviral diseases, neglected tropical disease (NTD), machine learning, multi-class classification, dengue (DENV), Chikungunya (CHIKV)

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1 INTRODUCTION

In 2015, the 2030 Agenda[1] was conceived by representatives of the member states of the United Nations (UN), and its main purpose is focused on eradicating poverty in all forms and dimensions *via* the implementation of sustainable development around the world. To achieve this major objective, 17 sustainable development goals (SDGs) were developed. Among them, Goal 3 (health and well-being) seeks to promote well-being for all, at all ages. Target 3.3 aims to end epidemics of AIDS, tuberculosis, malaria, and neglected tropical diseases (NTD), as well as combating hepatitis, waterborne diseases and other communicable diseases by the year 2030.

Arboviral diseases are NTDs caused by viruses and are transmitted by mosquitoes as their vector. Currently, there are about 545 known species of arboviruses, of which about 150 of them cause diseases in humans (1). In addition to Dengue virus (DENV), in the last 10 years, the emergence of other arboviruses, such as Chikungunya virus (CHIKV), Zika virus (ZIKV) and West Nile virus (WNV), has been observed. According to Lima-Camara (2016), disorganised urban growth and the

[1] http://www.agenda2030.com.br

modification of the environment by human actions are some of the reasons that influenced the increase in this type of disease (2).

According to reports released by the Pan American Health Organization (PAHO)[2,3] in 2020, together Dengue and Chikungunya accounted for a total of 2,402,128 cases in the Americas. However, most of these cases were classified as suspected cases due to the difficulty involved in their confirmation. For example, only 43.81% of reported Dengue cases (1,007,939 cases) were actually confirmed, and for Chikungunya, as few as 39% (39,619 cases) were confirmed. The low proportion of confirmed cases is due to the high complexity in the classification of these diseases in terms of their signs and symptoms. According to the Health Library of Primary Health Care (from Portuguese *Biblioteca Virtual em* Saúde da Atenção Primária à Saúde) (BVS APS)[4], most of cases are limited to the patients' signs and symptoms and the local epidemiological status. In addition, rapid tests available at primary healthcare centers have low accuracy. Despite (3) state that "*cross-reactions with DENV or ZIKV infections are unlikely, because CHIKV is an alphavirus, while DENV and ZIKV are antigenically unrelated flaviviruses*", it can be a concern. Actually, the cross-reactivity is one of the issues that pose barriers to the correct diagnosis for all arboviruses diseases at low-level health units. However, the lack of tests is also a major issue in the Amazon countryside. Therefore, accurate testing require specific equipment and time, though this also presents operational costs.

As a tropical country, Brazil has a huge diversity of both flora and fauna, and this includes mosquitos, which play an important role as vectors of illnesses such as arboviral diseases (4). According to PAHO, Brazil had the highest number of Dengue cases in the Americas in 2020, with 1,040,481 cases (65% of the total). Clinical classification of an arboviral disease is particularly a complex task in Brazil because of concomitant circulation of other arboviruses, such as Mayaro virus (MAYV), Venezuelan equine encephalitis virus (VEEV), Eastern equine encephalitis virus (EEEV), and Rocio virus (ROCV), which present a similar clinical profile (2). Besides the difficulty in clinical classification, cross-reaction is an issue for the current rapid tests that are available and this reduces their accuracy (2). Although high lethality has not been evidenced so far, the occurrence of coinfection with several arboviruses or concomitant circulation is cause for concern.

The Brazilian Unified Health System (from Portuguese, *Sistema Único de Saúde*) SUS has suffered over the years from a reduction in funding and this imposes an additional barrier to expanding quality diagnostic testing and presents a major public health challenge, highlighting the need for a low-cost diagnostic approach. The use of Machine Learning (ML) techniques becomes an interesting alternative, as they are able to recognise and develop a classification without the need for immediate laboratory tests. This would avoid the costs of collecting them and running these tests. As stated by Bulbul and Unsal, "*compared to classical methods, the process of obtaining information is much more accurate and faster with data mining and ML*" (5). ML models estimate results by learning from previously entered information. In addition, these models do not require computational power and can be executed in tablets or cell phones.

Most studies that deal with this problem have proposed models for diagnosing Dengue (6, 7); Chikungunya (8); or Zika (9) individually; and, to the best of our knowledge, only one study has provided a model for distinguishing of two arboviral diseases (Dengue and Chikungunya) (10), however the study also used laboratory data to perform the classification. Despite improving the results, we do not employ these types of data, as they, in addition to needing adequate equipment, would prevent the ML model from being used for a quick diagnosis at the time of the patient's arrival at the health unit. Furthermore, most of the existing works did not present a clear methodology that describes the pre-processing of data, hyperparameter optimization techniques, or feature selection. In our work, the entire data pre-processing and balancing are systematically presented, as well as a comparison of feature selection techniques with grid search. We present not only the best attributes for each model, but also the best configuration for each scenario. We also provide a discussion regarding the model that was trained with the best features selected by the sequential feature algorithm (SFA) techniques and a model designed with features selected by health specialists.

The present work proposes different ML models and compares them for multi-class classification of Dengue, Chikungunya and other diseases, using the clinical and socio-demographic data of the patients. The objective is to assist the physician in a rapid diagnosis at the time of arrival of the patient at the health unit by providing an auxiliary tool for decision making.

2 MATERIALS AND METHODS

2.1 Feature Selection

Feature selection is a technique that is used to reduce the dimensionality of the data set, which leads to better learning performance and/or lower computational cost. This technique selects the most relevant attributes in the data set by removing noisy, irrelevant and redundant features (11). Different feature selection techniques can be found in the literature, and can be categorised according to the search strategy. There are three main approaches: filter, wrapper, and embedded (11).

In this work, the wrapper approach is used, since it makes use of a learning algorithm to determine the best subset of attributes, called features, where an evaluation is usually made in terms of predictive accuracy. Due to the use and dependence of a learning model, this type of approach can become computationally expensive, though the possibility of selecting irrelevant features is less likely (12). Among the wrapper techniques, we used the SFA. This technique has four different types, and each type

[2] https://www3.paho.org/data/index.php/es/temas/indicadores-dengue.html, accessed Nov 11, 2020

[3] https://www3.paho.org/data/index.php/es/temas/chikv-es.html, accessed Nov 11, 2020

[4] https://aps.bvs.br/aps/qual-a-especificidade-e-sensibilidade-do-teste-rapido-da-dengue-e-que-tipos-existem/

differs in the way it selects or removes features from the data set: sequential forward selection (SFS), sequential backward selection (SBS), sequential forward floating selection (SFFS) and sequential backward floating selection (SBFS).

2.2 Grid Search

Grid search is an exhaustive search technique for setting hyperparameters of a given model. With it, it is possible to analyse the results of a ML model, and then decide which configuration best fits the target problem. According to Bergstra and Bengio (13), despite having limitations, this technique is widely used along with the manual search technique.

2.3 Machine Learning Techniques

ML is a branch of artificial intelligence that is composed of several techniques that have been widely used for pattern learning (8, 14–18). The ML models used in this work are Random Forest (RF), Adaptative Boosting (Adaboost), Gradient Boosting Machines (GBM), eXtreme Gradient Boosting (Xgboost), k-Nearest Neighbours (KNN), Naive Bayes (NB) and Multilayer Perceptron (MLP).

2.4 Evaluation Metrics

The following metrics are used: accuracy, precision, sensitivity and F1-Score. With the exception of accuracy, in the other metrics, the value of the metric in each class and the macro average of each one of them is also analysed.

2.5 Data Set

In this work, data regarding Dengue and Chikungunya notifications from the state of Amazonas and the city of Recife, Pernambuco from 2015 to 2020 are used. Regarding the state of Amazonas, data were retrieved from the Health Problem and Notification Information System, from Portuguese *Sistema de Informação de Agravo de Notificação* (SINAN)[5]. SINAN is the official system for disease reporting in Brazil. Diseases from the national list of compulsory notification must be reported, and this list includes Dengue and Chikungunya. This data set contains 57,445 entries and 146 variables and hereafter is referred to as "SINAN-db".

The data set for Recife was retrieved from an open data set named Portal de Dados Abertos do Recife (19), maintained by the Recife Health Department, whose primary source is also the SINAN, and therefore it follows the same dictionary pattern, and allows integration without further issues. This data set contains 83,073 registers and 124 variables and is referred to as "Recife-db" in this work.

Figure 1 illustrates the steps taken during the pre-processing of the data set. First, both data sets were integrated. Variables available in only one of the data sets were disregarded. The resulting data set from the integration of SINAN-db and Recife-db has 140,518 registers and 120 variables.

The output classes were grouped into three distinct classes:

- DENGUE: Patients with confirmed Dengue;
- CHIKUNGUNYA: Patients with confirmed Chikungunya; and
- OTHERS: Patients classified as "inconclusive" or "negative" for both Dengue and Chikungunya.

Only records confirmed or denied by clinical diagnoses were selected. Registers that did not relate signs or symptoms were discarded since they are the most important information for classification models. Moreover, variables with more than 50% of data missing were also removed. Besides the original variables, a new one (DIAS) was created so that the time (in days) from onset of these symptoms to the date of notification could be added to the models. For the selection of attributes, specialists were consulted. After coding variables as numbers, duplicates were removed, and missing values were replaced by "not informed" for each variable. Registers with missing values for all variables were also removed. Finally, the clean data set consisted of 17,948 registers in the DENGUE class, 5,724 in the CHIKUNGUNYA class and 16,704 in the OTHERS class, totalling 40,376 registers with 27 variables. In data science, a higher number of registers of a specific class compared to another in the same data set is known as imbalance and it can bias the ML model, which favours the classification of the class that has the largest number of registers (20).

In order to balance the data set, the random undersampling technique was performed. In this technique, the class with the least number of registers defines the amount of the other classes, so that all classes have the same number of registers. After balancing, the data set still had 27 attributes and 17,172 records, with 5,724 for each of the three classes. The 27 variables resulting from the pre-processing are described in **Table 1**. The data set can be accessed in Mendeley Data (21).

2.6 Experiments

The experiment is divided into three main steps: *(a)* optimisation of hyperparameters and attribute selection, using Grid Search and SFA; *(b)* evaluation of models performance; and *(c)* specialist evaluation.

2.6.1 Optimisation of Hyperparameters and Attribute Selection

The grid search technique was performed for each model individually and, on each model, not only were the combinations of the hyperparameters tested, but we also defined which SFA technique offers the best subset of attributes.

Figure 2 illustrates how the grid search process was executed considering the model's hyperparameters together with the SFA techniques. We used the Python library sklearn GridSearchCV[6], using the training set (70% of the data set). The cross-validation technique (22) with k=10 was used. At the end of the grid search of each model, the result was the best combination of model hyperparameters and the best subset of data set attributes for the same configuration.

Table 2 shows the hyperparameters of each model that were tested in the grid search and their respective value ranges.

[5] http://portalsinan.saude.gov.br/

[6] https://scikit-learn.org/stable/modules/generated/sklearn.model_selection.GridSearchCV.html

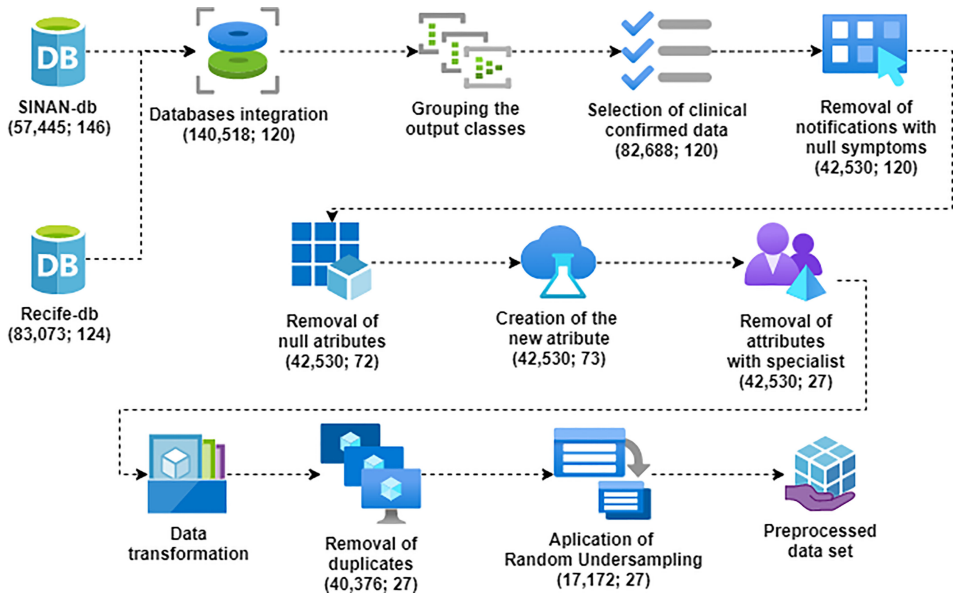

FIGURE 1 | Data set pre-processing steps.

All models, except Xgboost, were executed using the Python library sklearn.

The Adaboost was executed with the AdaBoostClassifier[7] and two hyperparameters were tested: *learning_rate* and *n_estimators*. *n_estimators* is the maximum number of stumps that the model will produce in the training, and *learning_rate* is a weight applied to each stump at each iteration. A higher *learning_rate* increases the contribution of each classifier. The higher the *learning_rate*, the greater the contribution of stumps during training. Low values decrease correct classification, while high values are associated with model instability (23).

The RF was executed with the RandomForestClassifier[8] and two hyperparameters were tested: *criterion* and *n_estimators*. *n_estimators*, as in Adaboost, is the maximum number of Decision Tree (DT) that the model produces and *criterion* is the function that determines which are the best splits in each node.

The GBM was executed with the GradientBoostingClassifier[9], and two hyperparameters were tested, *max_depth* and *n_estimators*. *max_depth* is the level of depth that each DT within the model has. The higher the level, consequently, the more nodes the DT has. *n_estimators*, as in Adaboost and RF, is the maximum number of DT that the model produces.

The Xgboost was executed with the Python library XGBoost[10] and two hyperparameters were tested, *max_depth* and *eta*. *max_depth*, as in GBM, is the level of depth that each DT within the model has; and *eta*, also known as learning rate, is the shrinkage in update to prevent overfitting.

The KNN was executed with the KNeighborsClassifier[11] and three hyperparameters were tested, namely, *metric*, *n_neighbors* and *weights*. *n_neighbors* is the number of neighbours that is used in the training. *weights* contains the function that determines the weights each neighbour has in the training, and *metric* is the function used to calculate the distance to each neighbour.

The MLP was executed with the MLPClassifier[12] and two hyperparameters were tested, in this case, *hidden_layer_sizes* and *learning_rate*_init. *hidden_layer_sizes* defines the number of hidden layers and the number of neurons that each layer has. *learning_rate*_init is the value that determines how often the weights of each layer will be updated during training.

Lastly, the NB[13] was executed with the GaussianNB. As NB does not have hyperparameters, the Grid Search of this model was executed only with SFA techniques.

2.6.2 Evaluation of Models

After the execution of the grid search, the models were evaluated using the remaining 30% of the data set that was not part of the training, which was called the test set. The models were evaluated using the metrics described in subsection 2.4. The tests were executed 30 times and the metrics were averaged in order to be

[7] https://scikit-learn.org/stable/modules/generated/sklearn.ensemble.AdaBoostClassifier.html
[8] https://scikit-learn.org/stable/modules/generated/sklearn.ensemble.RandomForestClassifier.html
[9] https://scikit-learn.org/stable/modules/generated/sklearn.ensemble.GradientBoostingClassifier.html
[10] https://scikit-learn.org/stable/modules/generated/sklearn.ensemble.GradientBoostingClassifier.html
[11] https://scikit-learn.org/stable/modules/generated/sklearn.neighbors.KNeighborsClassifier.html
[12] https://scikit-learn.org/stable/modules/generated/sklearn.neural_network.MLPClassifier.html
[13] https://scikit-learn.org/stable/modules/generated/sklearn.naive_bayes.GaussianNB.html

TABLE 1 | Database attributes after pre-processing.

Attribute	Description
NU_IDADE_N	Patient age
CS_SEXO	Patient sex
CS_GESTANT	Gestational Age of the Patient (Quarter), in case CS_SEXO=F
CS_RACA	Patient Race
CS_ZONA	Residence area
FEBRE	Symptom - Fever
MIALGIA	Symptom - Myalgia
CEFALEIA	Symptom - Headache
EXANTEMA	Symptom - Rash
VOMITO	Symptom - Vomiting
NAUSEA	Symptom - Nausea
DOR_COSTAS	Symptom - Back Pain
CONJUNTVIT	Symptom - Conjunctivitis
ARTRITE	Symptom - Arthritis
ARTRALGIA	Symptom - Arthralgia
PETEQUIA_N	Symptom - Petechiae
LACO	Symptom - Tourniquet test
DOR_RETRO	Symptom - Eye pain
DIABETES	Pre-existing disease - Diabetes
HEMATOLOG	Pre-existing disease - Haematological diseases
HEPATOPAT	Pre-existing disease - Liver diseases
RENAL	Pre-existing disease - Kidney disease
HIPERTENSA	Pre-existing disease - Hypertension
ACIDO_PEPT	Pre-existing disease - Peptic acid disease
AUTO_IMUNE	Pre-existing disease - autoimmune disease
DIAS	Days that the patient is feeling the symptoms
CLASSI_FIN	Final patient classification

compared. The model chosen was the one that best fitted the needs of the experiment. After that, the model was submitted to specialists so that the application in the health care routine could be assessed.

3 RESULTS

The scenario of low-income countries and limited-resource settings requires physicians to make a diagnosis often using only clinical parameters and without laboratory data support. ML techniques can aid in the classification of arboviral diseases using only these clinical parameters. Therefore this work evaluated seven ML techniques using only clinical and socio-demographic features.

Overall and per-disease baseline characteristics are presented in **Table 3**. Baseline characteristics show an overall mean (SD) age over 30 years and a predominance of men and in urban areas for each arboviral disease. Fever (85.3%), headache (60.6%), myalgia (58.4%), and arthralgia (51.1%) were the most frequent symptoms.

Our results are presented in three parts: *(a)* the results obtained from each model using grid search; *(b)* evaluation of the models using the configurations found by the grid search; and *(c)* comparison of the best model with a model designed with features selected by health specialists.

3.1 Grid Search

Table 4 presents the results from the Grid Search technique of the seven models: Adaboost, RF, GBM, Xgboost, KNN, MLP and NB.

Regarding SFA, the techniques that presented the best performance were SFFS and SBS. The size of the subset of attributes ranged between 10 and 20 attributes, and the most common attributes were CS_RACA, CS_ZONA, FEBRE, EXANTEMA, NAUSEA, ARTRALGIA, DOR_RETRO, which appeared in all subsets. **Table 5** shows the attributes selected by the SFA techniques for each model.

The model that best performed was the Xgboost model, using the SFFS technique with 20 attributes (the largest subset size in this experiment), *eta* = 0.3 and *max_depth* = 2, which obtained 62.3% accuracy. On the other hand, the KNN model with 19 attributes, selected by the SBS technique, *metric* = *euclidian*, *n_neighbors* = 2 and *weights* = *uniform*, was the worst model in the grid search, with 57.39% accuracy.

3.2 Evaluation of Models

Table 6 presents the results of accuracy and macro medians from recall, precision and F1-score. The GBM model outperformed all the models. It is interesting to note that the MLP model showed poor performance in comparison with the result it presented in the grid search. This difference may indicate that the MLP model failed to generalize the data during training and underfitting probably occurred and, as consequence, the MLP model did not performed well when using the test set.

The results of the CHIKUNGUNYA class are presented in **Table 7**. This class obtained the highest results, achieving more than 80% recall in KNN and MLP, although, those same models demonstrated the lowest values of precision. The other models had a better balance between these two metrics. For the F1-score metric, the situation is very similar, with the only difference being that the MLP outperformed the NB. In general, the GBM model obtained the best results.

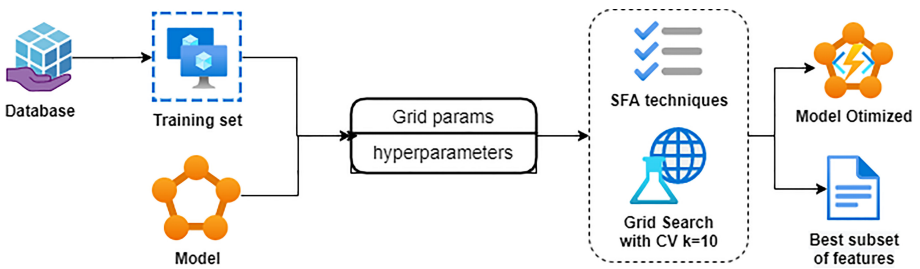

FIGURE 2 | Grid Search flowchart with SFA.

TABLE 2 | Parameters used in Grid Search.

Model	Parameters	Values
Adaboost	learning_rate	[0.36, 1, 1.5]
	n_estimators	[25, 50, 100]
RF	criterion	[gini, entropy]
	n_estimators	[50, 100, 200]
GBM	max_depth	[1, 3, 5]
	n_estimators	[50, 100, 200]
Xgboost	eta	[0.3, 0.5]
	max_depth	[2, 6]
KNN	metric	[euclidean, manhattan]
	n_neighbors	[2, 5, 10]
	weights	[uniform, distance]
MLP	hidden_layer_sizes	[(100), (100,100), (100,100,100)]
	learning_rate_init	[0.001, 0.01, 0.1]

The results for DENGUE class are presented in **Table 8**. Recall values were below 50% for all models, which were the lowest values. The results of the precision and F1-score were not much better either, i.e., below 60%. Overall, the GBM model obtained the best results again.

Table 9 presents the results of recall, precision and F1-score for the OTHERS class. Results were similar and were around 60%, with the exception of the KNN model, which had a considerable drop in recall (34.83%), and the MLP and NB models, which also showed poor performance regarding the precision metric (51.49% and 54.32%, respectively). In this class, none of the models stood out, and GBM, Xgboost and NB models obtained the best values for recall, precision, and F1-score, respectively. GBM and Xgboost model were considered the best for classifying this class.

3.2.1 Specialist Evaluation

The specialists analysed the attributes used in the GBM model, called GBM-SFA, and requested the removal of four attributes: CS_RACA, CS_ZONA, ACIDO_PEPT and AUTO_IMUNE. As a result, the remaining attributes (**Table 10**) were used as input for training a new GBM model, called GBM-Specialist. In order to achieve maximum performance, another grid search was executed,

TABLE 3 | Clinical and socio-demographic findings of patients at baseline.

Variables	Total N=17172	Dengue N=5724	Chikungunya N=5724	Others N=5724
Gender Women, %	7267/17172 (42.3)	2540/5724 (44.4)	2200/5724 (38.4)	2527/5724 (44.1)
Age, Mean (SD)	32.6 (20.1)	31.0 (19.8)	36.6 (20.0)	30.1 (19.9)
Race, %				
White	690/17172 (4.0)	223/5724 (3.9)	203/5724 (3.5)	264/5724 (4.6)
Black	156/17172 (0.9)	53/5724 (0.9)	56/5724 (1.0)	47/5724 (0.8)
Yellow	34/17172 (0.2)	10/5724 (0.2)	11/5724 (0.2)	13/5724 (0.2)
Admixed	5292/17172 (30.8)	1806/5724 (31.6)	954/5724 (16.7)	2532/5724 (44.2)
Indigenous	176/17172 (1.0)	104/5724 (1.8)	22/5724 (0.4)	50/5724 (0.9)
Missing	10824/17172 (63.0)	3528/5724 (61.6)	4478/5724 (78.2)	2818/5724 (49.2)
Pregnant, %				
1st Quarter	53/17172 (0.3)	9/5724 (0.2)	13/5724 (0.2)	31/5724 (0.5)
2nd Quarter	77/17172 (0.4)	25/5724 (0.4)	22/5724 (0.4)	30/5724 (0.5)
3rd Quarter	75/17172 (0.4)	17/5724 (0.3)	27/5724 (0.5)	31/5724 (0.5)
Ignored gestational age	19/17172 (0.1)	4/5724 (0.1)	7/5724 (0.1)	8/5724 (0.1)
Missing	16948/17172 (98.7)	5669/5724 (99.0)	5655/5724 (98.8)	5624/5724 (98.3)
Residence area, %				
Urban	14658/17172 (85.4)	4775/5724 (83.4)	5187/5724 (90.6)	4696/5724 (82.0)
Rural	175/17172 (1.0)	27/5724 (0.5)	9/5724 (0.2)	139/5724 (2.4)
Periurban	5/17172 (0.0)	2/5724 (0.0)	2/5724 (0.0)	1/5724 (0.0)
Missing	2334/17172 (13.6)	920/5724 (16.1)	526/5724 (9.2)	888/5724 (15.5)
Fever, %	14647/17172 (85.3)	5190/5724 (90.7)	5300/5724 (92.6)	4157/5724 (72.6)
Myalgia, %	10029/17172 (58.4)	3948/5724 (69.0)	3364/5724 (58.8)	2717/5724 (47.5)
Headache, %	10406/17172 (60.6)	4020/5724 (70.2)	3316/5724 (57.9)	3070/5724 (53.6)
Rash, %	4395/17172 (25.6)	1765/5724 (30.8)	1637/5724 (28.6)	993/5724 (17.3)
Vomit, %	3312/17172 (19.3)	1440/5724 (25.2)	992/5724 (17.3)	880/5724 (15.4)
Nausea, %	3517/17172 (20.5)	1610/5724 (28.1)	1076/5724 (18.8)	831/5724 (14.5)
Back pain, %	2612/17172 (15.2)	1088/5724 (19.0)	877/5724 (15.3)	647/5724 (11.3)
Conjunctivitis, %	678/17172 (3.9)	297/5724 (5.2)	222/5724 (3.9)	159/5724 (2.8)
Arthritis, %	1641/17172 (9.6)	638/5724 (11.1)	715/5724 (12.5)	288/5724 (5.0)
Arthralgia, %	8770/17172 (51.1)	2394/5724 (41.8)	4890/5724 (85.4)	1486/5724 (26.0)
Petechiae, %	802/17172 (4.7)	421/5724 (7.4)	211/5724 (3.7)	170/5724 (3.0)
Tourniquet test, %	290/17172 (1.7)	207/5724 (3.6)	38/5724 (0.7)	45/5724 (0.8)
Retroorbital pain, %	2555/17172 (14.9)	1407/5724 (24.6)	622/5724 (10.9)	526/5724 (9.2)
Diabetes, %	216/17172 (1.3)	57/5724 (1.0)	103/5724 (1.8)	56/5724 (1.0)
Haematological diseases, %	58/17172 (0.3)	22/5724 (0.4)	16/5724 (0.3)	20/5724 (0.3)
Liver diseases, %	72/17172 (0.4)	21/5724 (0.4)	25/5724 (0.4)	26/5724 (0.5)
Kidney disease, %	50/17172 (0.3)	10/5724 (0.2)	20/5724 (0.3)	20/5724 (0.3)
Hypertension, %	454/17172 (2.6)	128/5724 (2.2)	191/5724 (3.3)	135/5724 (2.4)
Peptic acid disease, %	97/17172 (0.6)	27/5724 (0.5)	28/5724 (0.5)	42/5724 (0.7)
Autoimmune disease, %	42/17172 (0.2)	10/5724 (0.2)	16/5724 (0.3)	16/5724 (0.3)
Symptom time in days, Mean (SD)	21.0 (217.3)	17.0 (32.8)	22.6 (58.2)	23.3 (370.5)

TABLE 4 | Results from Grid Search.

Model	Hyper parameters	QTD. Att	SFA	Accuracy
Adaboost	Learning_rate: 0.36 n_estimators: 25	10	SBS	0.5972
RF	criterion: gini n_estimators: 200	16	SFFS	0.6061
GBM	max_depth: 3 n_estimators: 200	18	SFFS	0.6218
Xgboost	eta: 0.3 max_depth:2	20	SFFS	0.6230
KNN	metric: euclidean n_neighbors: 2 weights: uniform	19	SBS	0.5739
MLP	hidden_layer_sizes: (100), learning_rate_init: 0.1	15	SFFS	0.6153
NB	–	10	SBFS	0.585

with the same GBM hyperparameters that are presented in **Table 2**. The best configuration for hyperparameters was *max_pedth* = 5, higher than the GBM-SFA, and *n_estimators* = 100 half the GBM-SFA, with a validation accuracy of 60.15%.

Table 11 shows the results of all metrics for the GBM-SFA and GBM-Specialist models. The GBM-SFA presented the best performance for all metrics, except in the precision of the DENGUE class, though with only a very small difference.

3.3 Discussions

The grid search results did not present a large variation, ranging from 57% to 62% accuracy. In addition, none of the models presented accuracy above 70%, which shows the difficulty involved in classifying arboviral diseases using only clinical and socio-demographic data.

It was possible to observe that the DENGUE class was the class with the lowest performance, thus highlighting the difficulty in classifying this disease with the data used. However, there are some reasons that may explain this: *(a)* the classification is a multi-class task, which makes it difficult to generalize the three classes;*(b)* the applying of the undersampling technique to balance the data may also have affected the DENGUE class, as at the end of the pre-processing there were almost 18,000 Dengue registers that could have been used, but this number had to be reduced to almost 6,000 due to the low amount of Chikungunya registers; *(c)* lack of laboratory attributes often associated to Dengue such as leucocyte count, haematocrit or thrombocytes.

Any model intended to predict Dengue would need to be applied earlier in the illness to identify who must be closely monitored for plasma leakage (24). Although, in early phases, Dengue is often indistinguishable from other arboviral diseases (25). Using only clinical and socio-demographic data, as proposed in our work, may be a limitation in Dengue diagnosis. However, in remote areas that lack human and laboratory resources, the models can play an essential role in surveillance by identifying possible epidemics.

The OTHERS class performed a little better than the DENGUE class, but still showed weak performance. In this case, the great diversification may be the main cause, as this class includes all patients who were admitted with a suspected case of arbovirus, but were classified as inconclusive and discarded, so here the patients may include a wide variety of diseases.

The CHIKUNGUNYA class presented the best results in this work, principally in regards to the recall metric, with over 80%. These results show that, besides the difficulty, it is possible to make a good classification using only clinical and socio-demographic data.

TABLE 5 | Attributes select by the SFA techniques for each model.

Model	Attributes
Adaboost	NU_IDADE_N, CS_RACA, CS_ZONA, FEBRE, CEFALEIA EXANTEMA, NAUSEA, ARTRALGIA, LACO, DOR_RETRO
RF	CS_RACA, CS_ZONA, FEBRE, MIALGIA, CEFALEIA, EXANTEMA, NAUSEA, ARTRITE, ARTRALGIA, PETEQUIA_N, DOR_RETRO, DIABETES, HEMATOLOG, HEPATOPAT, RENAL, AUTO_IMUNE
GBM	CS_RACA, CS_ZONA, FEBRE, MIALGIA, CEFALEIA, EXANTEMA, NAUSEA, DOR_COSTAS, CONJUNTVIT, ARTRITE, ARTRALGIA, PETEQUIA_N, DOR_RETRO, DIABETES, HIPERTENSA, ACIDO_PEPT, AUTO_IMUNE, DIAS
Xgboost	NU_IDADE_N, CS_RACA, CS_ZONA, FEBRE, MIALGIA, CEFALEIA, EXANTEMA, VOMITO, NAUSEA, DOR_COSTAS, CONJUNTVIT, ARTRITE, ARTRALGIA, PETEQUIA_N, DOR_RETRO, DIABETES, HEMATOLOG, HIPERTENSA, ACIDO_PEPT, DIAS
KNN	CS_GESTANT, CS_RACA, CS_ZONA, FEBRE, MIALGIA, CEFALEIA, VOMITO, NAUSEA, DOR_COSTAS, CONJUNTVIT, ARTRITE, ARTRALGIA, PETEQUIA_N, LACO, DOR_RETRO, DIABETES, HEMATOLOG, HIPERTENSA, ACIDO_PEPT
MLP	CS_SEXO, CS_RACA, FEBRE, MIALGIA, CEFALEIA, EXANTEMA, VOMITO NAUSEA, ARTRALGIA, PETEQUIA_N, LACO, DOR_RETRO, DIABETES, HEMATOLOG, HEPATOPAT
NB	CS_RACA, CS_ZONA, FEBRE, MIALGIA, EXANTEMA, NAUSEA, ARTRALGIA, LACO, DOR_RETRO, ACIDO_PEPT

TABLE 6 | The result from accuracy and macro median of recall, precision, and F1-score.

Model	Accuracy	Recall	Precision	F1-score
Adaboost	0.5879	0.5903	0.5837	0.5782
RF	0.6011	0.6033	0.5965	0.5949
GBM	**0.6240**	**0.6257**	**0.6205**	**0.6196**
Xgboost	0.6153	0.6173	0.6116	0.6093
KNN	0.5411	0.5410	0.5519	0.5222
MLP	0.5380	0.5424	0.5569	0.4967
NB	0.5798	0.5833	0.5782	0.5704

In bold: These were the results that stood out, i.e., the highest value of each metric.

TABLE 7 | The result from recall, precision, and F1-score for CHIKUNGUNYA class.

Model	Recall	Precision	F1-score
Adaboost	0.7992	0.6045	0.6884
RF	0.7667	0.6360	0.6943
GBM	0.7787	**0.6561**	**0.7122**
Xgboost	0.7881	0.6382	0.7053
KNN	**0.8396**	0.5365	0.6546
MLP	0.8100	0.5902	0.6745
NB	0.7190	0.6272	0.6699

In bold: These were the results that stood out, i.e., the highest value of each metric.

TABLE 8 | The result from recall, precision, and F1-score for DENGUE class.

Model	Recall	Precision	F1-score
Adaboost	0.4020	0.5582	0.4674
RF	0.4355	0.5638	0.4919
GBM	**0.4870**	**0.5949**	**0.5356**
Xgboost	0.4589	0.5842	0.5140
KNN	0.4352	0.5033	0.4668
MLP	0.2202	0.4843	0.2902
NB	0.3637	0.5642	0.4423

In bold: These were the results that stood out, i.e., the highest value of each metric.

TABLE 9 | The result from recall, precision, and F1-score for OTHERS class.

Model	Recall	Precision	F1-score
Adaboost	0.5695	0.5882	0.5787
RF	0.6085	0.5881	0.5982
GBM	0.6115	0.6104	**0.6110**
Xgboost	0.6049	**0.6123**	0.6086
KNN	0.3483	0.6161	0.4450
MLP	0.6463	0.5149	0.5714
NB	**0.6673**	0.5432	0.5989

In bold: These were the results that stood out, i.e., the highest value of each metric.

TABLE 10 | Attributes selected by the specialist.

Attribute	Description
FEBRE	Symptom - Fever
MIALGIA	Symptom - Myalgia
CEFALEIA	Symptom - Headache
EXANTEMA	Symptom - Rash
NAUSEA	Symptom - Nausea
DOR_COSTAS	Symptom - Back Pain
CONJUNTVIT	Symptom - Conjunctivitis
ARTRITE	Symptom - Arthritis
ARTRALGIA	Symptom - Arthralgia
PETEQUIA_N	Symptom - Petechiae
DOR_RETRO	Symptom - Eye pain
DIABETES	Pre-existing disease - Diabetes
HIPERTENSA	Pre-existing disease - Hypertension
DIAS	Days that the patient is feeling the symptoms

In bold: These were the results that stood out, i.e., the highest value of each metric.

TABLE 11 | Comparison between the GBM model with SFA attributes and GBM model with specialist attributes.

Classes	Metrics	GBM-SFA	GBM-Specialist
Macro	Accuracy	**0.6240**	0.6075
	Recall	**0.6257**	0.6094
	Precision	**0.6205**	0.6053
	F1-score	**0.6196**	0.6021
DENGUE	Recall	**0.4870**	0.4600
	Precision	0.5949	**0.5993**
	F1-score	**0.5356**	0.5204
CHIKUNGUNYA	Recall	**0.7787**	0.7658
	Precision	**0.6561**	0.6313
	F1-score	**0.7122**	0.6921
OTHERS	Recall	**0.6115**	0.6025
	Precision	**0.6104**	0.5860
	F1-score	**0.6110**	0.5941

In bold: These were the results that stood out, i.e., the highest value of each metric.

As such, our models can be used as a low-cost and rapid alternative, which would be useful in a resource-limited scenario (10). Note that arthralgia is considered a very common presentation in Chikungunya fever. Together with high fever, it has a specificity of 99.6% and a positive predictive value of 84.6% for infection classification. Since other arboviruses infections such as ZIKV, DENV and other alphaviruses also present with arthralgia, the epidemiological scenario must be considered before classifying every case as CHIKV infection based only on this symptom (26).

The tree-based models (Adaboost, RF, GBM and Xgboost) presented the best overall results. Tree-based models are generally the best models for problems that use tabular data. The MLP model presented the worst results, and a drop in performance was observed compared to training with grid search, thus indicating a possible underfitting.

The GBM model obtained the best results, and its attributes were analysed by the specialists and a new GBM model was designed. Despite obtaining slightly inferior results, it did have better interpretability for physicians and these results show that the GBM-SFA model is the most accurate model. On the order hand, the GBM-Specialist model is more interpretable and consequently would be more accepted for use by physicians. According to Ozaydin et al. (2021), "*interpretability and accuracy may often have to be sacrificed for each other*" (27). It is useless for a model to be precise if physicians cannot use it daily because they do not trust the model or do not understand the attributes used, for example. In this sense, the GBM-Specialist has a big advantage over the GBM-SFA model and, despite achieving lower performance, the difference in results is around 2% for each metric.

Although multi-class classification better represents real-world problems, most classification techniques are focused on binary classification (28). This happens, among other factors, due to the high complexity of training a model to be able to generalize more than two classes. This greater complexity contributes to multi-class models having lower performance when compared to binary models.

As future work, we plan to make an ensemble of two binary models, one trained to classify Dengue and another trained to classify Chikungunya. In this way, we can use more data from Dengue notifications, and we believe that with more data for training it is possible to improve the results of the DENGUE class.

4 CONCLUSIONS

Arboviruses are diseases that have similar symptoms, which makes it difficult to make decisions regarding their treatment. For this reason, the correct classification of arboviral diseases when the patient arrives for treatment becomes a very useful tool in the daily life of hospitals. To help solve this problem, ML models were proposed for multi-class classification of Dengue, Chikungunya, and other common illnesses in Brazil, using only clinical and socio-demographic data.

In this work, seven ML models were evaluated: Adaboost, RF, GBM, Xgboost, KNN, MLP and NB. A grid search was executed for each model along with a SFA technique for optimization of the hyperparameters and attribute selection. The tree-based models (Adaboost, RF, GBM and Xgboost) presented the best overall results. The MLP model presented the worst results, and a drop in performance was observed compared to training with grid search, indicating a possible underfitting. The GBM model, named GBM-SFA, obtained the best results and its attributes were analysed by the specialists and a new GBM model was designed and named the GBM-specialist model.

When comparing the metrics of the GBM-SFA and GBM-specialist models for classification of both classes, the GBM-SFA outperformed the GBM-specialist model, showing that despite professionals being specialists in the field of infectious diseases, the difficulty and limitations of human clinical diagnosis of these arboviruses is real, as the signs and symptoms are very similar and arboviruses circulate concomitantly in Brazil (29–31).

The models evaluated in this work showed high sensitivity rates in relation to the CHIKUNGUNYA class. However, more sensitive ML models could aid in the identification and classification of arbovirus cases, and provide clinicians with a diagnostic tool based on real data that would complement clinical judgment, as well as being an effective surveillance tool in a pre-epidemic period. More specific models should be explored to identify laboratory-confirmed arbovirus cases during peak and post-peak periods, as the number of cases increases dramatically during these periods (17).

Our results showed that, in addition to the difficulty, it is possible to make a good classification using only clinical and socio-demographic data. Our models can be used as a low-cost and quick alternative, and would be useful in a scenario of limited resources in which only information from the patient that is obtained at the health unit is available.

DATA AVAILABILITY STATEMENT

Publicly available datasets were analyzed in this study. This data can be found here: https://data.mendeley.com/datasets/bv26kznkjs/1.

ETHICS STATEMENT

All methods were performed in accordance with the Brazilian regulations that do not require consent for studies using unidentified data from the Brazilian data health systems.

AUTHOR CONTRIBUTIONS

TT, SN, IT, and PE conceived the methodology and the design of the experiments of the work. TT, SN, and IT performed to the pre-processing of the data set and the experiments with the ML models. SO, MA, and VS performed the statistical analysis. PE analysed the experiments and the statistical analysis. SO, MA, and VS acted as health specialists. All authors contributed to the writing and review of the manuscript, read and approved the submitted version.

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SUPPLEMENTARY MATERIAL

The Supplementary Material for this article can be found online at: https://www.frontiersin.org/articles/10.3389/fitd.2021.769968/full#supplementary-material

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