

Support for Medical Diagnosis of COVID-19 Using Machine Learning Algorithms on Chest CT Images: A Comparative Study of Supervised Classifiers

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RESUMO

A COVID-19, causada pelo vírus SARS-CoV-2, é uma doença respiratória altamente contagiosa com consequências graves. O diagnóstico preciso e rápido é fundamental para o controle da doença, mas os sintomas inespecíficos e a demora nos testes dificultam o processo. Os algoritmos de aprendizado de máquina têm se mostrado promissores ao proporcionar apoio a diagnósticos mais eficientes e rápidos. Nesse estudo, foram comparados quatro classificadores supervisionados usando imagens de tomografia computadorizada (CT) de 35 pacientes com COVID-19. A extração de características foi realizada usando a técnica de matriz de coocorrência de níveis de cinza e a seleção de características foi feita com classificadores Random Forest e Extra-Trees. Os modelos foram treinados, avaliados e ajustados para obter um melhor desempenho. O estudo tem como objetivo o suporte à decisão médica com o uso dos algoritmos de aprendizado de máquina no diagnóstico da COVID-19 com base em imagens de CT.

PALAVRAS CHAVE. COVID-19. Aprendizado de Máquina. Tomografia Computadorizada

Tópicos (PO na Área da Saúde, Estatística e Modelos Probabilísticos, Inteligência Computacional)

ABSTRACT

COVID-19, caused by the SARS-CoV-2 virus, is a highly contagious respiratory disease with serious consequences. Accurate and rapid diagnosis is crucial for disease control, but nonspecific symptoms and delays in testing hinder the process. Machine learning algorithms have shown promise in providing more efficient and faster diagnoses. In this study, four supervised classifiers were compared using computed tomography (CT) images from 35 patients with COVID-19. Feature extraction was performed using the gray-level co-occurrence matrix technique, and feature selection was carried out using Random Forest and Extra-Trees classifiers. The models were trained, evaluated, and adjusted to achieve best performance. The

study aims to support medical decision-making by utilizing machine learning algorithms in the diagnosis of COVID-19 based on CT images.

KEYWORDS. COVID-19. Machine Learning. Computed Tomography.

Paper topics (OR in Healthcare, Statistics and Probabilistic Models, Computational Intelligence)

1. INTRODUCTION

COVID-19, caused by the SARS-CoV-2 virus, is a highly contagious respiratory disease and may lead to acute respiratory distress, severe pneumonia, multiple organ failure and death. Its symptoms include fever, dry cough, and shortness of breath [Maior et al. 2021]. This disease has already caused millions of deaths worldwide, overwhelming healthcare systems and having a significant impact on the global economy [Fernandes 2020].

One of the challenges with COVID-19 is that the signs and symptoms of the disease are common to many viral infections, especially respiratory infections, and the absence of specific symptoms [Maior et al. 2022], making diagnosis without proper testing difficult. Additionally, the standard diagnostic method, a polymerase chain reaction (PCR) test, can take several days to produce results, delaying treatment and increasing the risk of transmission [Centers for Disease Control and Prevention [CDC] 2021]. In this context, early detection and treatment of COVID-19 are crucial to controlling the spread of the disease. Chest imaging, such as chest radiographs and computed tomography (CT) scans, is a valuable tool in detecting and monitoring the extent of lung lesions caused by COVID-19, which is especially important in patients with moderate to severe symptoms [Inui et al. 2021].

The use of machine learning algorithms for COVID-19 diagnosis and screening based on chest imaging has shown promising results [Nasiri & Alavi 2021]. These techniques can help provide a more efficient and accurate diagnosis, reducing the time needed to obtain results and allowing for earlier intervention. Additionally, machine learning algorithms have been applied to various tasks in medical image analysis, such as segmentation, classification, and detection. These algorithms can learn from a large number of annotated images and extract relevant features for diagnosis, providing a more objective and accurate assessment of medical images [Wang et al. 2020].

In this study, the objective is to investigate the use of machine learning algorithms for early detection and diagnosis of COVID-19 based on CT images. Specifically, four commonly used supervised classifiers were employed: Multilayer Perceptron (MLP), K-Nearest Neighbor (KNN), Random Forest (RF), and Support Vector Machine (SVM). The goal is to diagnose COVID-19 cases early by making predictions through supervised classification models.

2. LITERATURE REVIEW

Certain studies have investigated the use of chest CT scans for the diagnosis of COVID-19. For example, Li et al. (2020) found that chest CT had a high sensitivity in detecting COVID-19 cases, particularly in the early stages of the disease. Similarly, Fang et al. (2020) reported that chest CT scans could detect COVID-19 cases with a sensitivity of up to 98%. However, these studies also highlighted the need for further research to establish standardized protocols for the use of chest CT scans in the diagnosis of COVID-19.

In recent years, machine learning has shown great potential in medical imaging analysis, particularly for the detection and classification of various diseases. For example, Wang et al. (2020) designed a tailored deep convolutional neural network, called COVID-Net, for the detection of COVID-19 cases from chest X-ray images. Similarly, Hemdan et al. (2020) developed a deep learning framework, COVIDX-Net, to diagnose COVID-19 cases using chest X-ray images. However, there is still a need for more studies to evaluate the effectiveness and generalizability of these ML algorithms in different settings and populations.

Moradi et al. [Moradi Khaniabadi et al. 2022] also used Chest CT images to develop a two-step ML-based model to diagnose and predict involvement of lungs in COVID-19 and non COVID-19 pneumonia patients. They used three hundred CT scans and extracted 107 texture features, to train ML-based supervised algorithms (e.g., SVM, RF, KNN). A feature selection technique was implemented to reduce dimensionality and increase accuracy. This study showed great potential in assessing COVID-19 CT images towards improved management of patients and the possibility of predicting severity lungs involvement.

3. METHODOLOGY

Through CT images of the lungs of patients who had symptoms of COVID-19, it was possible to extract image features and use predictive models to classify, with some accuracy, whether or not a patient is infected with SARS-CoV 2.

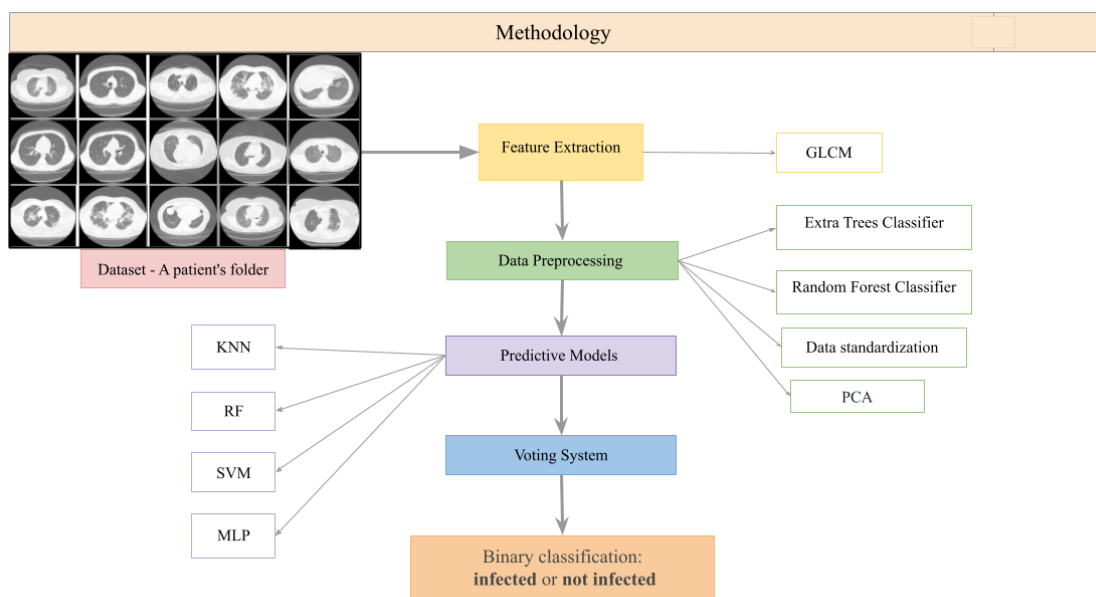


Figure 1: Simplified description of the methodology and technique used.

3.1. Dataset

For our research, we are using CT images of the lungs from patients showing evidence of COVID-19. The dataset was provided by Hospital das Clínicas, located in a city in Northeast Brazil. It consists of 35 patients, totaling 1276 images, with 553 images used for testing (10 patients) and 723 images used for training (25 patients). The data used in this work is related to a research project approved by the Research Ethics Committee of the Federal University of Pernambuco (CAAE 47459521.6.0000.5208).

All images were previously selected using a selection algorithm inspired by the method of Rahimzadeh et al. that utilizes parameters such as Dark Ratio (DR) and Threshold Ratio (TR) to adapt the image selection on an individual basis. The algorithm calculates the maximum dark pixel value (MPVp) for each patient based on the minimum and maximum pixel values in the images. Then, it uses the selection threshold (THLDp) to determine which images are retained. This selection process was applied to both the training and testing images, ensuring a consistent and personalized selection of the most relevant images for COVID-19 diagnosis.

3.2. Feature Extraction

A statistical method of examining textures is the gray-level co-occurrence matrix (GLCM). We can define texture analysis as a computer-assisted technique that allows the detection of mathematical patterns in the distribution of gray levels of pixels in digital images, it provides an objective characterization of the behavior of anatomical structures [Xian 2010].

The frequency of different combinations of neighboring pixel values that occur in an

image can be measured with GLCM and we can consider four directions (0°, 45°, 90° and 135°) in our analysis [Eichkitz et al. 2015]. For this reason, the algorithm output will be four different values for each texture feature. Then, the GLCM is created by calculating the frequency of occurrence of pixel pairs with specific values and in a spatial relationship. Thus, statistical measures are extracted from this matrix [Zulpe & Pawar 2012]. First, a probability matrix is calculated using the values of the GLCM matrix. The co-occurrence values for each of the four directions are determined. Then, the GLCM is normalized by the sum of the entries to get a kind of probability matrix. Finally, the probabilities are used for the calculation of the GLCM-based attributes [Eichkitz et al. 2015]. The ones we used are described in Table 1.

Table 1: Description of the features extracted from the GLCM

Features	Definition	Equations
Contrast	Evaluates the local variation of the gray level in pixel intensity values	$\sum_i \sum_j (i - j)^2 P(i, j) \quad (1)$
Dissimilarity	GLCM dissimilarity is a measure of the total variation present in each image object.	$\sum_i \sum_j P(i, j) \quad (2)$
Energy	The count of repeated pairs is calculated. If repeated pixel pairs are high, the energy should be high, since only the probability is used.	$\sum_i \sum_j P^2(i, j) \quad (3)$
Homogeneity	Tests the local homogeneity of the pixel pair. If the pixel values of each pair of pixels are identical, the homogeneity is supposed to be high	$\sum_i \sum_j \frac{P(i, j)}{1 + i - j } \quad (4)$
Correlation	Establishes a connection in the pixel pair between both pixels. If the pixel pair gray levels are strongly correlated, the correlation is supposed to be vital.	$\frac{\sum_i \sum_j (i - \mu_i)(j - \mu_j) P(i, j)}{\sigma_i \sigma_j} \quad (5)$

$P(i, j)$ is the probability that pixel intensity values are found in an image, and i and j are the numbers of rows and columns in the matrix. While σ_i, σ_j are the standard deviations and μ_i, μ_j are the means of the row and column. All the features were extracted using python language and its library *skimage.feature* [Haralick et al. 1973].

3.3. Preprocessing

3.3.1. Standardization

Standardization is a scaling technique that makes data scale-free by converting the statistical distribution of the data [Mulani 2022]. The standard score of a sample x is calculated as:

$$Z = \frac{(x - u)}{s} \quad (6)$$

Where u is the mean of the training samples or zero and s is the standard deviation of the training samples or one [Pedregosa et al. 2011]. All data were standardized using the StandardScaler function from the Sklearn library in the Python language.

3.3.2. Feature selection

3.3.2.1. Random Forest Classifier

Also as a preprocessing of the data, a selection of the most important features was performed using the random forest algorithm. The importance of a feature in a random forest algorithm is basically how much this feature is used in each tree of the forest [Kalousis et al. 2006]. Formally, Feature importance is calculated as the decrease in node impurity weighted by the probability of reaching that node. The node probability can be calculated by the number of samples that reach the node, divided by the total number of samples. The higher the value the more important the feature.

Different decision trees are constructed by selecting several subsequent feature sets. According to Kalousis et al., the feature selection result is proportional to the generated decision tree. Without a specific method, the first eight features were chosen, as you can see in Figure 3.

3.3.2.2. Extra-Trees Classifier

Another feature selection method was used in our analysis, aiming to compare the accuracy values. The Extra-Trees Classifier is an embedded method to extract relevant features. It is performed as a midway between feature extraction and classification [Baby et al. 2021]. Extra-trees work by generating individual decision trees from the entire training dataset. The algorithm selects a random split to divide the parent node into two random child nodes and this is repeated with the child nodes until reaching a node that had no children, called a leaf node [Alfian et al., 2022]. The Gini importance is a parameter of the model and it is computed for each feature, during construction of the forest. Thus, it was possible to choose the features with high importance value. We used the first three features, according to Figure 3.

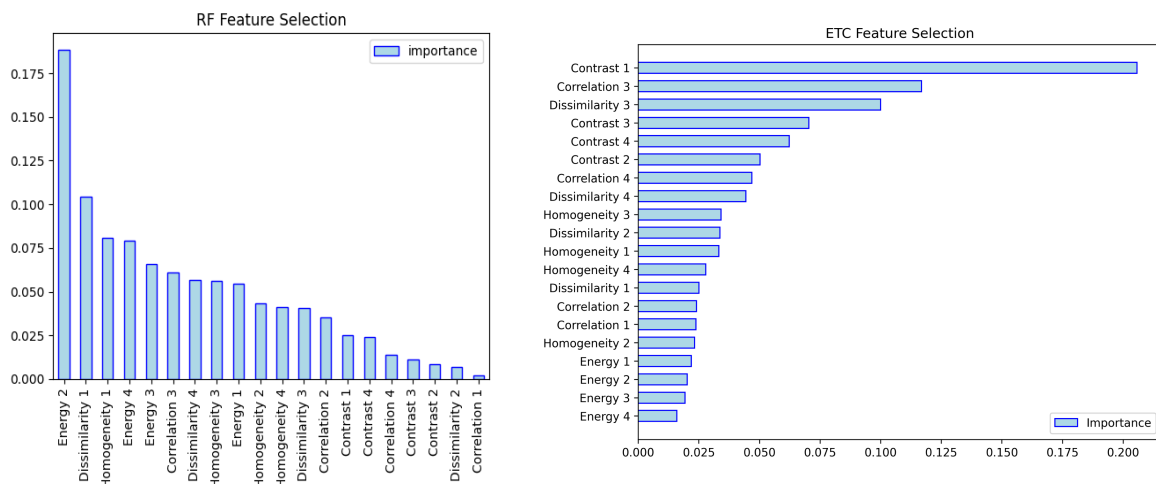


Figure 2: Example of the most important features of GLCM according to the feature selection Random Forest Classifier and Extra Tree Classifier using Sklearn Python.

3.3.3. Hyperparameter Tuning with GridSearchCV

Grid search is an approach to parameter tuning that will methodically build and evaluate a model for each combination of algorithm parameters specified in a grid [Ranjan et al. 2019]. Choosing the best hyper parameters have a big impact on the performance model [Ahmad et al. 2022]. In this context, we used the parameters given by the gridsearch algorithm aiming to achieve the best accuracy.

Table 2: Optimization results of hyperparameters using gridsearch

	Hyperparameters	Values
MLP	hidden_layer_sizes	x:[80,100], y:[0,5]
	activation	['identity', 'logistic', 'tanh', 'relu']
	solver	['lbfgs', 'sgd', 'adam']
	learning_rate	['constant', 'invscaling', 'adaptive']
KNN	algorithm	['auto', 'ball_tree', 'kd_tree', 'brute']
	n_neighbors	[5,2,23]
	weights	['uniform', 'distance']
RF	criterion	['gini', 'entropy']
	max_depth	[1,10]
	max_features	['auto', 'sqrt', 'log2']
	min_samples_leaf	[1,5,10]
	n_estimators	[10,100]
SVM	min_samples_split	[2,10]
	C	[2,4,8]
	kernel	['linear', 'poly', 'rbf', 'sigmoid', 'precomputed']
PCA	gamma	['scale', 'auto']
	n_components	[0.8,0.85,1,2,5,10,20]

3.3.4. Principal Components Analysis (PCA)

The PCA is one of the most fundamental tools of dimensionality reduction for extracting effective features from high dimensional vectors of input data [George 2012], identifying patterns in data, and expressing the data in such a way as to highlight their similarities and differences [Smith 2002]. For a better choice we used Grid Search CV to return a number of componentes to fill the parameter in PCA. For this, the algorithm was set with both methods of feature selection, once we are using them to evaluate the models.

When the Random Forest feature selection method was used to select the best features and these ones were used with Grid Search, it returned a number of componentes equal to 5. Similarly, it returned 2 for number os componentes with Extra Trees Classifier in feature selection method. In our project, dimension reduction was tested with PCA in all the classification models we used, however, only Random Forest showed an improvement in its performance.

4. PREDICTIVE MODELS

In order to analyze the model with better accuracy from our data, we tested MLP, KNN, RF, and SVM for comparing the results. These algorithms were chosen for their effectiveness in handling classification problems and their wide application in various domains.

4.1. Random Forest (RF)

Random Forest is a machine learning method used for problems involving classification or regression. It is based on a collection of decision trees $\{h(x, \theta_k), k = 1, \dots\}$ where the $\{\theta_k\}$ are independent and identically distributed random vectors. We can think of a decision tree as a graphical representation for a given decision process. Trees are formed by nodes, which store information (questions). The root node is the node that has the highest hierarchical level and, from it, branches the child nodes. A node that has no children is known as a leaf or terminal node. [Breiman 2001]

4.2. Multi-Layer Perceptron (MLP)

MLP works with supervised learning technique called backpropagation for training the neural network. A multi-layer perceptron is an artificial feedforward neural network model that maps input data into a set of appropriate output data. MLP consists of a directed graph with several layers of nodes, where each layer is connected to the next. Each node is a processing element (or neuron) with a nonlinear activation function, except for the input nodes. [Sabancı & Köklü 2015].

4.3. K-Nearest Neighbor Algorithm (KNN)

Concerned with classification problems, KNN is a supervised learning algorithm that classifies by analyzing image features in order to assign the class that was named in advance. The important thing is determining the features of each category in advance. The algorithm uses extracted features to determine the nearest neighbors for classifying new instances. It assigns the class based on the majority vote from the k nearest neighbors. The k value represents the number of neighbors considered. In our model, we used the square root of the training sample size as 'K'. [Sabancı & Köklü 2015] [Subramanian 2022].

4.4. Support Vector Machine (SVM)

SVM is an algorithm that was originally created for binary classification problems. However, it is currently widely used for multi-class and regression problems. Nowadays, the algorithm is frequently used in medical image processing applications. The main purpose of the SVM is to find a hyper-plane that separates data [Saygılı 2022]. It is known that the SVM algorithm uses kernel functions (e.g., polynomial, gaussian, sigmoid), aiming to map data to a different feature space [Saygılı 2022]. The choice of kernel function among other factors could greatly affect the performance of an SVM model [Shujun Huang et al. 2018]. In this sense, we used gridsearch as a tool to choose the best kernel.

5. VOTING SYSTEM

We can analyze the accuracy of the models per patient by gathering all the images of a single patient, along with the label of each image indicating whether it is positive or negative for COVID-19. Then, we would count the images labeled as positive and negative, considering the chosen threshold in the voting system. For example, considering a threshold of 0.2 means that if at least 20% of the total images of the patient are labeled as COVID-19 positive, the patient would be labeled as infected. The same process would apply to thresholds of 0.3 and 0.5. These steps are illustrated in Figure 4 .

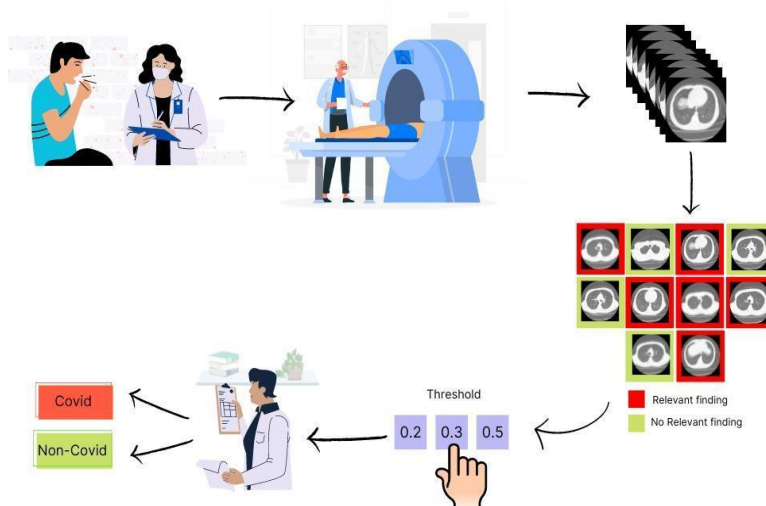


Figure 3: Representation of voting system

These steps would help determine whether a patient would be labeled as having COVID-19 based on the number of images classified as positive and the defined threshold. However, it is important to emphasize that a medical diagnosis is still necessary to confirm the disease, as the research aims to provide support for medical decision-making to expedite the patient's diagnostic process.

6. RESULTS

The classification results using different machine learning algorithms are presented in Tables 3, 4 and figure 5. The RF, KNN, SVM, and MLP models were evaluated in terms of average accuracy per image after being run 30 times for each analysis.

Considering that RF and MLP models are based on probabilities, we conducted an analysis utilizing the mean of the precision rates. We incorporated a loop mechanism that facilitated the iterative running of the machine learning model for a total of 30 iterations. The primary aim was to get the mean of the resulting precision rates, thus acquiring a more resilient evaluation of the model's efficacy.

Table 3: Best results per image.

Per image				
	RF	KNN	SVM	MLP
Accuracy (mean)	0.718	0.772	0.817	0.777
Feature Selection	RF	RF	RF	ETC
Preprocessing	PCA + standardization	PCA + standardization	Standardization	PCA

Table 4: Best results per patient.

Per patient				
	RF	KNN	SVM	MLP
Accuracy (mean)	0.854	0.8	0.9	0.884
Feature Selection	RF	ETC	ETC	RF
Preprocessing	PCA	Standardization	PCA	-
Threshold	0.2	0.2	0.2	0.2

In Table 3, the SVM model achieved the highest average accuracy, reaching 81.7%. In terms of feature selection, the RF classifier performed the best in three out of the four models in the image analysis context. For data preprocessing, standardization was applied to all classifiers except SVM, which used only standardization. Additionally, PCA was used in conjunction with standardization in some cases.

In the analysis of results per patient, as shown in Table 4, once again, the SVM model obtained the highest average accuracy, reaching 90%. The selection of features varied between RF and Extra-Trees Classifier (ETC), depending on the classifier used. Preprocessing also involved the use of PCA in some cases, while in others, only data standardization was applied. A threshold of 0.2 achieved the best performance in all cases, as expected, indicating that at least 20% of a patient's images should indicate COVID-19 to be considered as COVID-19. It is important to note that a threshold of 0.2 can lead to "false positives," but, on the other hand, it can be more sensitive in diagnosis.

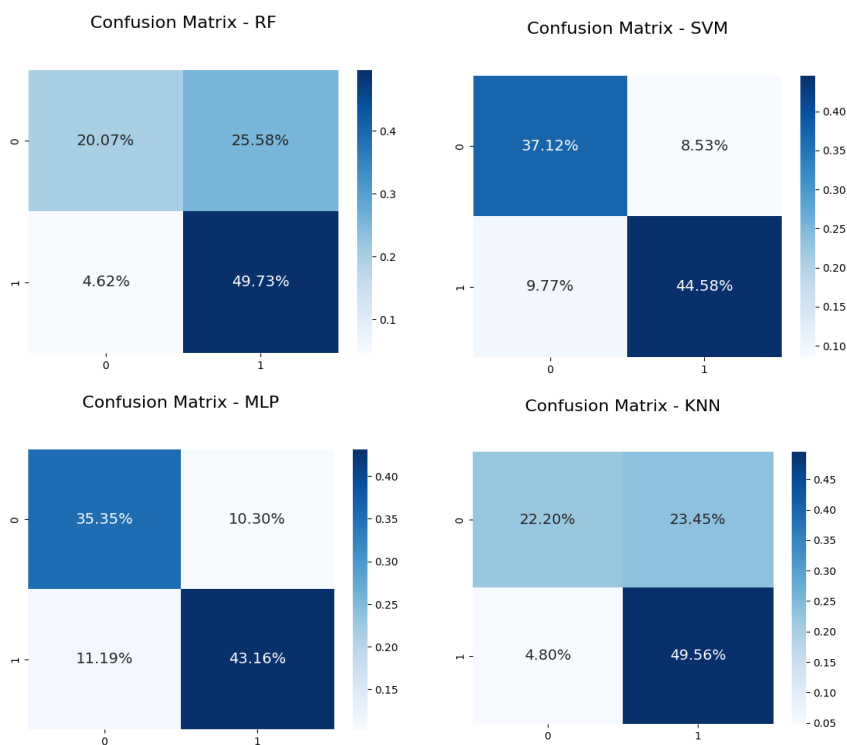


Figure 4: Confusion Matrix of the models

Analyzing the true positive and true negative rates in the confusion matrices, we can observe the performance of the models in classification. The SVM model achieved a true positive rate of 37.12%, meaning that it correctly classified 37.12% of the images that were actually related to COVID-19. Additionally, the SVM had a true negative rate of 44.58%, indicating that it correctly classified 44.58% of the images that were not related to COVID-19. These results show a moderate performance of the SVM in identifying both COVID-19-related and non-related images. In comparison, the MLP had a true positive rate of 43.16% and a true negative rate of 35.35%. This indicates that the MLP had a slightly lower performance than the SVM in correctly classifying COVID-19-related and non-related images. On the other hand, the RF achieved a true positive rate of 49.73% and a true negative rate of 20.07%. These results indicate that the RF had a relatively good performance in identifying COVID-19-related images, but its true negative rate was lower, meaning that it misclassified a significant portion of the

non-related images. Finally, the KNN had a true positive rate of 49.56% and a true negative rate of 22.20%. The KNN had a similar performance to the RF in correctly classifying COVID-19-related images, but its true negative rate was also lower. This analysis shows that the SVM had the best performance in terms of true positive and true negative rates, followed by the MLP, RF, and KNN respectively.

During the additional tests, different configurations were explored, including the use of thresholds of 0.2, 0.3, and 0.5, as well as the application of preprocessing techniques such as PCA and data standardization. The detailed results of these tests can be found in the Attachment providing a more comprehensive view of the performance and optimization of the models under different tested configurations.

7. CONCLUSION

The present work involves the use of CT images as a tool to support diagnosis of COVID-19 by exploring machine learning models. Some techniques of accuracy increase were tested, willing to develop satisfactory models (i.e., feature selection, hyperparameters tuning). Furthermore, we could evaluate the precision of the models per image and also per patient. The best models were SVM and MLP that showed high accuracy in both ways of analysis.

It is important to emphasize that we ran 30 times all the models to analyze performance and the behavior of RF and MLP, which are probabilistic models. Based on this, RF presented low variance in tests per patient, what suggests a better precision than MLP, since the model is assertive even after testing it n times.

In addition, it is relevant to highlight that some limitations must be overcome such as the number of available data, performance of models, and the difficulties to find accuracy enhancement techniques, in order to have better precision in the diagnosis of the disease.

ACKNOWLEDGMENTS

The authors thank the following Brazilian research funding agencies for the financial support: Fundação de Amparo à Ciência e Tecnologia de do Estado de Pernambuco (FACEPE), APQ-0607-3.08/22; Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq), 308924/2021-5 and 310892/2022-8; Coordenação de Aperfeiçoamento de Pessoal de Nível Superior (CAPES), Finance Code 001. We also thank the Human Resources Program 38.1 (PRH 38.1) entitled "Risk Analysis and Environmental Modeling in the Exploration, Development and Production of Oil and Gas", financed by Agência Nacional de Petróleo, Gás Natural e Biocombustíveis (ANP) and managed by Financiadora de Estudos e Projetos (FINEP), 044819.

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ATTACHMENT

Per image:

	Standardized data				Without standardization			
	Random Forest							
Without PCA	KNN	SVM	RF	MLP	KNN	SVM	RF	MLP
mean	0.772646	0.81705	0.578507	0.557786	0.6571936	0.669626	0.572765	0.766075
std	2.26E-16	1.13E-16	0.017466	0.078566	0	1.13E-16	0.013444	0.068521
time (s)	0.01	0.02	0.26	0.37	0.02	0.04	0.30	0.82
With PCA 5	KNN	SVM	RF	MLP	KNN	SVM	RF	MLP
mean	0.772647	0.813499	0.71794	0.566371	0.657194	0.666075	0.707638	0.745471
std	2.26E-16	2.26E-16	0.029303	0.071525	0	2.26E-16	0.011074	0.068898
time (s)	0.02	0.01	0.25	0.33	0.01	0.04	0.30	0.62
Extra Tree								
Without PCA	KNN	SVM	RF	MLP	KNN	SVM	RF	MLP
mean	0.726465	0.776199	0.440616	0.586264	0.463588	0.541741	0.444227	0.449793
std	2.26E-16	0	0.06208	0.139582	1.69E-16	1.13E-16	0.061211	0.123983
time (s)	0.01	0.01	0.29	0.29	0.01	0.06	0.24	0.82
With PCA 2	KNN	SVM	RF	MLP	KNN	SVM	RF	MLP
mean	0.74778	0.761989	0.583481	0.540261	0.460036	0.527531	0.474423	0.777205
std	1.13E-16	1.13E-16	0.013208	0.120528	0	1.13E-16	0.032706	0.072616
time (s)	0.01	0.01	0.21	0.16	0.01	0.01	0.24	0.44

Per patient:

	Random Forest								Extra Tree							
	Standardized data				Without standardization				Standardized data				Without standardization			
	Threshold 0.2															
without PCA	KNN	SVM	RF	MLP	KNN	SVM	RF	MLP	KNN	SVM	RF	MLP	KNN	SVM	RF	MLP
mean	0.6	0.8	0.8	0.66	0.7	0.7	0.8	0.88	0.80	0.7	0.72	0.64	0.7	0.9	0.71	0.85
std	0	0	0	0.12	0	0	0	0.08	0	0	0.06	0.16	0	0	0.07	0.08
time (s)	0.02	0.11	2.03	3.41	0.04	0.19	2.04	8.32	0.03	0.09	2.2	1.56	0.05	0.24	2.4	5.57
with PCA	KNN	SVM	RF	MLP	KNN	SVM	RF	MLP	KNN	SVM	RF	MLP	KNN	SVM	RF	MLP
mean	0.6	0.7	0.8	0.68	0.7	0.7	0.72	0.74	0.8	0.8	0.6	0.67	0.7	0.9	0.85	0.75
std	0	0	0	0.14	0	0	0.06	0.11	0	0	0	0.14	0	0	0.05	0.09
time (s)	0.02	0.15	2.42	3.81	0.03	0.25	2.44	6.39	0.04	0.13	3.	1.93	0.05	0.34	2.9	4.19
Threshold 0.3																
without PCA	KNN	SVM	RF	MLP	KNN	SVM	RF	MLP	KNN	SVM	RF	MLP	KNN	SVM	RF	MLP
mean	0.6	0.8	0.8	0.61	0.6	0.6	0.8	0.74	0.7	0.7	0.69	0.57	0.6	0.7	0.65	0.78
std	0	0	0	0.13	0	0	0	0.09	0	0	0.04	0.13	0	0	0.07	0.12
time (s)	0.02	0.11	2.05	3.53	0.04	0.19	2.47	8.19	0.03	0.10	2.3	1.52	0.06	0.27	2.4	5.45
with PCA	KNN	SVM	RF	MLP	KNN	SVM	RF	MLP	KNN	SVM	RF	MLP	KNN	SVM	RF	MLP
mean	0.6	0.7	0.70	0.62	0.6	0.6	0.59	0.73	0.7	0.8	0.6	0.65	0.6	0.9	0.70	0.64
std	0	0	0.07	0.14	0	0	0.06	0.12	0	0	0	0.13	0	0	0.02	0.13
time (s)	0.03	0.15	2.43	3.89	0.03	0.27	2.49	6.50	0.04	0.14	3.0	2.03	0.05	0.35	2.9	4.24
Threshold 0.5																
without PCA	KNN	SVM	RF	MLP	KNN	SVM	RF	MLP	KNN	SVM	RF	MLP	KNN	SVM	RF	MLP
mean	0.5	0.8	0.69	0.57	0.5	0.4	0.68	0.73	0.6	0.7	0.47	0.54	0.5	0.5	0.45	0.71
std	0	0	0.03	0.11	0	0	0.04	0.09	0	0	0.11	0.15	0	0	0.08	0.12
time (s)	0.02	0.12	2.04	3.65	0.04	0.18	2.04	8.33	0.03	0.11	2.4	1.56	0.06	0.27	2.5	5.10
with PCA	KNN	SVM	RF	MLP	KNN	SVM	RF	MLP	KNN	SVM	RF	MLP	KNN	SVM	RF	MLP
mean	0.5	0.4	0.47	0.58	0.5	0.4	0.47	0.58	0.6	0.8	0.5	0.56	0.5	0.5	0.6	0.6
std	0	0	0.07	0.12	0	0	0.07	0.12	0	0	0	0.15	0	0	0.03	0.13
time (s)	0.03	0.27	2.45	6.59	0.03	0.27	2.45	6.59	0.03	0.14	3.0	2.01	0.04	0.38	3.0	4.22