Evaluation of Machine Learning Models to Forecast COVID-19 Relying on Laboratory Outcomes Characteristics in Children

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Abstract. An outbreak of the 2019 novel Coronavirus epidemic (COVID-19) has rapidly spread worldwide. The coronavirus (COVID-19) has also spread among children, but it has been less severe than in adults. The characteristics of COVID-19 laboratory findings play a significant role in clinical manifestations, diagnosis, and treatment. Since the numbers of COVID-19 cases increased, it takes more time to interpret the lab outcomes and provide an accurate diagnosis. Little information about the clinical symptoms and epidemiological of COVID-19 is known. There is a need to investigate the characteristics of laboratory findings for the clinical decision-making system using predictive algorithms. This study aims to classify and validate machine learning approaches for detecting COVID-19 in children. The five well-known machine learning approaches: the artificial neural network (ANN); random forest (RF); support vector machines (SVM); decision trees (DT) which include classification and regression trees (CART); and gradient boosted trees (GBM) were used. All these approaches have been considered in the classification, and to determine the most suitable model. The performance of each model test was by conducted using a standard 10-fold cross-validation procedure. Given these results for classification performance and prediction of accuracy, CART is the best predictive model for classifications for children with COVID-19. The results of the study illustrate that the best classification performance was achieved with CART model to provide 92.5% accuracy for binary classes (positive vs. negative) based on laboratory findings. Leukocytes, Monocytes, Potassium, and Eosinophils, were among the most important predictors which indicate that those features may play a crucial role in COVID-19. Ultimately, our model may be helpful for medical experts to predict COVID-19 and can help invalidate their primary laboratory findings of children. ML methods can be a convenient tool for providing predictions for COVID-19 laboratory findings among Children.

Keywords. COVID-19, Coronavirus, Laboratory findings, Machine learning approaches.
1. Introduction

The new Coronavirus, which is called "SARS-CoV-2", is caused by the emergence of COVID-19 in Wuhan, China, in December 2019 [1-3]. Worldwide, more than 1,350,000 patients and 79,000 deaths from the COVID-19 virus were recorded as of April 8, 2020 [4]. Currently, COVID-19 is increasingly spreading around the world globally, causing many fatalities and global economic crises. Since the beginning of the coronavirus pandemic, more than 741,000 children in the US have been diagnosed positive for the COVID-19 (The American Academy of Pediatrics), and the rate of new cases among kids continues to rise. However, the number of adults who have been infected with COVID-19 is greater than that of children; therefore, children may be less likely to be susceptible to COVID-19. Most children with COVID-19 have slight symptoms. However, several children may get severely sick from COVID-19. They can be in need for hospitalization, and in the operating room they might die. Most studies focused on adults; there is no studied focus on children. The early action of identifying the presence of SARS-CoV-2 is vital in providing the best care possible to patients and contact persons, preventing further spreading of this infectious virus. An acquaintance of diagnostic tests for COVID-19 is still developing, and interpretation of their findings is critical. Laboratory medicine supplies a base contribution to clinical decision-making in numerous infectious illnesses, including SARS-CoV-2. Our challenge was to predict COVID-19 from clinical and laboratory, to shed light on the diagnosis of laboratory, and observing COVID-19 in children. For the first time, classification methods using machine learning (ML) are considered commonly used techniques in medicine, where the aim is to build classifiers capable of predicting COVID-19. These classifiers have been built employing training groups of data in which factors of COVID-19 are well known. Hence, methods of predictive and investigative nature such as ML algorithms are crucial to make intelligent decisions that may help to avoid COVID-19. ML approaches have been successfully practical to many healthcare complications [5] due to their high ability to estimate patient results compared with classical approaches in numerous disease conditions. The previous research suggests that machine learning methods may ameliorate the ability of decision-making in the laboratory. To the best of our knowledge, no study conducted a sufficient investigation into the use of machine learning approaches to estimate clinical findings. ML is considered a pivotal parameter supporting character in the competition in contradiction of COVID-19 and can highly contribute to solutions prompt than we wish otherwise fulfill in many scops and applications. Early detection of severe COVID-19 patients remains a significant challenge. To address this knowledge gap, data has been analyzed to improve machine learning-based triage samples that predict COVID-19 based on laboratory findings characteristics in children. Moreover, to specify the best model their prediction performance has been compared.

The main purpose of this research is to realize accuracy and recognize the factors behind laboratory findings characteristics in children. The study also aimed to develop a machine learning method to determine the most significant features that can estimate true COVID-19 positive status. In this study, using binary logistic regressions have been analyzed by assuming the COVID-19 positive cases as independent. The main contribution of this research is to find a better prediction that will help doctors and other healthcare workers to discover if children are positive or negative for COVID-19 according to laboratory findings. The outlines of this paper are: section 2 presents the related work; section 3 discusses the data and methodology; section 4 characterizes the results and discussion. While the conclusions and possible future works are introduced in section 5. Is it necessary?

2. Related work

There is adequate related work in this area of research directly related to this manuscript. Machine Learning (ML) approaches have been implemented to produce the highest precision prediction in the medical field including the prediction of heart disease [6-9], breast cancer diagnosis [10-12], predicting pneumonia mortality [13-15], and mortality risk adjustment in critical care [16-19]. These studies assist the medical experts to grasp and assess clinical outcomes better. In this work, classifying and validating various machine learning approaches for the detection of COVID-19 in children were conducted. In the literature, there is limited similar studies concerning the clinical prediction of
COVID-19. Authors in [20] have used ML models to predict the number of upcoming patients affected by COVID-19 and the threatening factors of COVID-19. Data were obtained from the GitHub repository offered by Johns Hopkins University/Systems Science and Engineering Center. They used four standard forecasting models, including linear regression (LR), exponential smoothing (ES), the least absolute shrinkage and selection operator (LASSO), and support vector machine (SVM). Each model has three prediction types, including the number of recently infected cases, the number of recoveries within the next 10 days, and the number of deaths.

The performance of each classifier was evaluated using different measures including (R2: R-Squared score), (R2 adjusted: Adjusted R-Squared Score), (MSE: mean square error), (MAE: mean absolute error), and (RMSE: root mean square error). The results showed that the ES produced the best performance, followed by LR and LASSO. In contrast, SVM performed inadequately in all the prediction scenarios given the available dataset. In another study [21], the clinical severity of the coronavirus was predicted using ML techniques. The dataset was obtained from two hospitals in Wenzhou, Zhejiang, China. They considered eleven predictive features and applied six different classifiers, such as Logistic regression, (KNN: K the nearest neighborhood), decision tree depending upon Gain Index, decision tree depending upon Gain Ratio, random forests, and (SVM: support vector machines). The execution of the classifiers was tested considering only values of accuracy. SVM classifier showed the best accuracy value of 80% gathered from Hospital Israelite Albert Einstein-São Paulo-Brazil. They trained five different ML classifiers including logistic regression, neural networks, SVM, random forests, and gradient boosted trees (XGB). The performance of the classifiers was evaluated based on areas under the receiver operator curve (AUC), the precision-recall curve (AUPR), specificity, sensitivity, and specificity at higher than 95% sensitivity. They indicate that the best-set models by AUC. XGB was used for predicting COVID-19 test results of 66% for the test set, RF for predicting hospital admissions for COVID-19 positive patients of 92% for the test set, and SVM and LR for predicting ICU admission for COVID-19 positive patients of 98% for the test set. Authors in [22] have applied five machine learning algorithms involving (NN: neural networks), (FR: random forests), (XGB: gradient boosting trees), (LR: logistic regression), and (SVM: support vector machines) to investigate the danger of positive COVID-19 diagnosis and considered fifteen predictive features. Data were collected from 235 adult patients, in the Hospital Israelite Albert Einstein/São Paulo/Brazil. The predictive performance was measured by computing the area under the ROC curve (AUC), specificity, sensitivity, Brier score, F1-score, (PPV: positive predictive value), and (NPV: negative predictive value). The best predictive rendering was achieved by SVM and RF algorithms with an AUC of 85% for the test set.

3. Methodology of predictive modeling for binary classification
In this present work, five ML methods were applied and developed for the prediction of the COVID-19, as shown in Figure 1. In the first stage, the COVID-19 dataset and patient cohort was identified. Then, machine learning methods were developed to be suitable for model design. Also, the evaluation and validation of all models of machine learning techniques are applied. In the final stage, models using various performance metrics are tested to make sure of achieving fit results.
Figure 1. The methodology of Predictive modeling for binary classification.

3.1. Data description and data correlation
During the study period, 5664 children with COVID-19 were admitted to obtaining treatment in the medical centers. The data were obtained from the Kaggle [23] which allows data analysts to compete in solving real and complex data knowledge problems. This study included children who had taken test COVID 19 and laboratory features and were aged ≤ 18 years at admission. There were 29 features out of which 24 features have been applied to this model including the SARS-Cov-2 exam result variable, as presented in Table 1. The response variable is the SARS-COV-2 exam result. Three features were not included because they don’t have any impact on the model.

| Number | Parameters                                | Type of variable                                      |
|--------|-------------------------------------------|-------------------------------------------------------|
| 1      | ID                                        | Discrete(0-18 years old)                              |
| 2      | Patient age quantile                      | Discrete(0-18 years old)                              |
| 3      | SARS-Cov-2 exam result                    | Categorical (1 = negative; 2 = positive)              |
| 4      | Patient admitted to regular ward          | Categorical (1 = yes, 0 = no)                         |
| 5      | Patient admitted to semi-intensive unit   | Categorical (1 = yes, 0 = no)                         |
| 6      | Patient admitted to intensive care unit   | Categorical (1 = yes, 0 = no)                         |
| 7      | Hematocrit                                | Continuous                                            |
| 8      | Hemoglobin                                | Continuous                                            |
| 9      | Platelets                                 | Continuous                                            |
| 10     | Mean platelet volume                      | Continuous                                            |
| 11     | Red blood Cells                           | Continuous                                            |
| 12     | Lymphocytes                               | Continuous                                            |
| 13     | Mean corpuscular hemoglobin concentration (MCHC) | Continuous                                      |
| 14     | Leukocytes                                | Continuous                                            |
| 15     | Basophils                                 | Continuous                                            |
| 16     | Mean corpuscular hemoglobin (MCH)         | Continuous                                            |
| 17     | Eosinophils                               | Continuous                                            |
| 18     | Mean corpuscular volume (MCV)             | Continuous                                            |
| 19     | Monocytes                                 | Continuous                                            |
| 20     | Red blood cell distribution width (RDW)   | Continuous                                            |
| 21     | Serum Glucose                             | Continuous                                            |
| 22     | Neutrophils                               | Continuous                                            |
| 23     | Urea                                      | Continuous                                            |
| 24     | Proteina Creativa mg/dL                   | Continuous                                            |
3.2. Data preprocessing

Data preprocessing is a critical stage before developing machine learning models. Many modeling techniques require the predictors to specify a standard scale of measure. Most transformations are centering and scaling which perhaps help to improve the constancy of numerical calculations. Also, it can be useful for taking off the skewness of the predictors by implementing methods like the Cox and Box transformations. Then, before fitting any model, a suitable analysis of missing values and outliers is required. Special techniques such as Box plot by the interquartile range (IQR) method was used for eliminating outliers. IQR was used, which is a measure of statistical dispersion between upper Q3 and lower quartiles Q1. Moreover, missing values have been conserved suitably, which helps to remove the highly correlated predictors without loss of predictive performance. Therefore, “filter methods” have been used to avoid this problem and measure the relationship between each predictor and objective. Further, Principal Component Analysis (PCA) was used to minimize the variables number. Finally, because machine learning models are based on mathematical calculations which is a necessary step before fitting any model encoding nominal or categorical variables into numerous dummy variables. It would cause some problems if we keep the text as the categorical variables in the equations. Normalization is important to ensure that all the feature values are on the same scale and treated with equal weight. A Min-Max normalization was performed to transform each numerical attribute into the range [0, 1].

3.3. Machine learning approaches

This study included five well-known machine learning approaches including decision trees, support vector machines (SVM), artificial neural network (ANN), random forest (RF), and classification and regression trees (CART). While, the gradient boosted trees was considered a classification. The method used in this study is as follows:

3.3.1. Gradient boosting machine. A Gradient Boosting Machine (GBM) is an ensemble (combination) of regression or classification trees. GBMs are one of the most powerful ensemble algorithms that are often first-in-class with predictive accuracy. GBM is a fixed size decision tree-based learning algorithm that associates many simple predictors. It constructs the model in a stage perceptive method as boosting approaches, and it amounts them up by allowing the improvement of self-confidence lack of function differently, as illustrated in Figure 2. Gradient boosting is measured using a gradient descent model. Gradient descent is a very general optimization model accomplished by discovering the best results for a varied variety of problems.

![Gradient boosting machine](image)

Fig. 2. Gradient boosting machine.

3.3.2. Neural Network (NN). It is composed of neurons that are arranged in layers to convert an input vector into an output. The first layer is known as the input layer, and the last is the output layer. Between the input and output are the hidden layers, which can consist of a few or many neurons. A nonlinear function applied for each input unite that passes the output to the next layer. The architecture of a feedforward NN shows the output of layers the input
for the following layer, as shown in Figure 3. The hidden layer converts its inputs to the output layer that applies activations on the vectors of the inputs for the last predictions. In this study, the construction process is the first stage. This stage is for testing three layers with a hidden layer. The hidden layer has half the number of neurons associated with the input layer, as shown in figure 4. The functions used in this study are the linear functions, the threshold functions, and the sigmoid functions. The hidden and output layers activation functions were tested. The NN for 50 epochs were trained using stochastic gradient descent that was optimized by Adam. The error function of categorical cross-entropy for binary classification was applied as a function of loss.

![Figure 3](image-url)  
*Figure 3.* The architecture of a Feedforward.

![Figure 4](image-url)  
*Figure 4.* Neural Network (NN).

### 3.3.3. Random forest model (RF)

This is similar to a decision tree and it has a flowchart-like structure, as shown in Figure 5. It is used to control the overfitting process [24]. RF has many internal nodes. Each node tests whether one or numerous features match certain conditions. Depending on the result of the test, branches can be taken from the testing nodes to either different descendant nodes or prediction outcomes. However, instead of using all features for decision-making, a random tree randomly selects a subset of features for use. The principle of this method is to combine the set of binary decision trees referred to as CART. Therefore, the prediction made by a random forest classifier is obtained by averaging the predictions made by individual decision trees. This prevents the model from overfitting. Bootstrap is the method that performs a random sampling with a resample. As every tree constructed by bootstrap is randomly chosen with a different dataset, it eliminates the bias, and it can test the stability of a solution. In this study, the initial depth is one that improved gradually until (i) the model started to overfit or (ii) the accuracy, recall of the train, and exam sets start to diverge. Thus, the RF models trained with
different numbers of trees. This study started first with only one tree and the number of trees kept increasing until the error stopped decreasing to get the final model of RF. Each decision tree uses Gini to measure the excellence of split.

![Random Forest Model](image1.png)

**Figure 5.** Random forest model.

3.3.4. **Support vector machine (SVM).** It is a flexible, well-known, and supervised machine learning process which is used for both tasks; classification and regression. SVM concept is a hyperplane in multidimensional space to discrete dissimilar classes. SVM creates optimal hyperplane that is used to minimize an error. As shown in Figure 6, our study focused on non-Linearity. The kernel method was used in this study to increase the efficiency of the computation and also improve the accuracy of the prediction outcome. Therefore, a non-linear region is required by the classifier to separate such classes. Numerous kernel types such as linear, sigmoid, kernels, and polynomial, were tested. The best methods were tested with linear and radial kernels. Then, different models with varying C values were trained.

![Support Vector Machine](image2.png)

**Figure 6.** Support vector machine (SVM).

3.4. **Model development, and validation**

The assessment of the classifier is achieved by separating the whole data set into two groups. The first subset is utilized to train the model while the second subset is for testing. Dataset was sectioned into a training set and testing set by 70%, and 30% respectively. To validate the model, cross-validation was used and it was so useful during the comparison of different models. Also, cross-validation provided the estimated performance of model. In the process of validation, the method of K-fold has been implemented in this study. In the training dataset of 5-fold cross-validation, each fold was divided into five-folds, as shown in figure 6. One partition to fit the model and the remaining partitions to test the
model. The current fold was selected as a test-set and the remaining folds as a training-set. Figure 7 demonstrates the 5-fold cross-validation.

![Figure 7. Five-fold cross-validation.](image)

3.5. Performance evaluation for the classification methods
Later than the previous step, a training set model was tested and evaluated on the test set. This method divides the training data set into five partitions at random. The classification performance of the model was evaluated based on the performance of each model of the learning in terms of the confusion matrix, precision, negativity, accuracy, F-Measure, Area Under the Curve (AUC) and Receiver Operating Characteristic (ROC). These measures are suitable for binary classification responsibilities. The various evaluation criteria in our approach are as follows:

3.5.1. A confusion matrix. It demonstrates the number of predictions correct and/or incorrect, which is introduced by the classification model. Moreover, the actual findings were compared to the findings of the classification model. Two classes (Positive and Negative) of the confusion matrix $2 \times 2$ were displayed, Table 2. It is significant to evaluate the classifier's performance when obtaining the classification model using one or more ML methods. The decision process is based on a threshold value “cutoff point” which classifies the scores of a continuous variable called “classifier” into two classes: positive vs. negative. If the classifier more than or equal the cutoff point, the subject will be classified as positive while if the classifier, the subject will be classified as [24], Figure 8.

| Predicted Class | Actual Class | Positive | Negative |
|-----------------|--------------|----------|----------|
|                 | Positive     | True Positive (TP) | False Negative (FN) |
|                 | Negative     | False Positive (FP) | True Negative (TN) |
| Precision       | TP/(TP+FP)   |                      | TN/(TN+FN) |
| Sensitivity     | TP/(TP+FN)   |                      |                      |
| Negative Predictive Value | TN/(TN+FN)   |                      |                      |
| Specificity     | TN/(TN+FP)   |                      |                      |

Table 2. Confusion matrix.
3.5.2. **Accuracy.** This is the fractional value of the total number of correctly predicted samples to the entire number of present samples in a dataset [25]. Accuracy is the first measure of performance for the ML classifier.

\[
Accuracy = \frac{TP + TN}{TP + TN + FP + FN}
\]  

(1)

3.5.3. **Sensitivity.** Is the second performance measure, which is the division of the true positive predictions to all the positively predicted predictions. From all the positive predicted values, precision states which values are correctly predicted and precisely match the computed values. Sensitivity measures the ratio of positives anticipated which are real positives [26].

\[
Sensitivity = \frac{TP}{TP + FP}
\]  

(2)

**Figure 8.** Four possible outcomes when intersecting prediction with a classifier.

3.5.4. **Precision.** It is the third measure of performance. Precision provides the fractional value of the correctly predicted samples to the total samples in a dataset. Precision measures the proportion of actual positives correctly classified [27].

\[
Precision = \frac{TP}{TP + FN}
\]  

(3)

3.5.5. **Area Under the Curve (AUC).** The Receiving Operating Characteristic (ROC) curve is used as a metric to calculate the classification model's quality. AUC represents the area under the curve of ROC. AUC shows how satisfactory it is for the probabilities to isolate the positive groups from the negative ones. The area under the curve of 0.5 represents a random classifier, while AUC for a typical classifier is equal to 1. The curve of ROC is plotted with TPR versus the FPR. TPR represents the y-axis and FPR represents the x-axis. The correct positive rate or TPR is in the range of trues. The calculations were carried out, as shown in Figure 9.

**Figure 9.** The Receiving Operating Characteristic (ROC) curve.
4. Result and discussion

4.1. Description statistics

Python programming was used to analyse the data. A total of 5,664 patients' records were tested for COVID-19 in this study. Twenty-one predictor variables were used with the class variable to predict COVID-19 based on Laboratory Findings Characteristics in Children. Furthermore, the work aims to classify and identify the most important variables that contribute to the detection of COVID-19 in children. Visualizing the data with the correlation among variables was applied. The correlation mentions the common link among the variables. Correlation Matrix statistics for each variable were evaluated using correlations as appropriate using the Pearson Correlation Coefficient (PCC), as presented in Figure 10. This study has focused on studying correlation with the class label. Some features displayed strong relationships among the COVID-19, which was the class label. Typically, characteristic variables with higher linkage with response variables have a more significant influence throughout the training phase. Figure 11. demonstrates a correlation matrix that provides a diagnosis of the pairwise connection between each variable. The correlation matrix reveals that a large positive rate which is nearby to 1.0 shows a strong positive correlation, i.e. (RDW and hematocrit). RDW and hemoglobin also are a strong positive correlation. This means if the rate of one of the variables increases, the rate of the other variable increases as well. Therefore, there is a large negative value since the rate is close to -1.0. It also shows a strong negative correlation, i.e., (Neutrophils and Lymphocytes). This means if one value of feature increases, the value of the target variable decreases. Figure 10 illustrates that some characteristics were extremely correlated with the category label, and they may simplify the sensibly accurate detection model training for the COVID-19. The presence of high inter-character correlations suggest that some dismissed features may need to be excluded to further advance the detection of the model. Consequently, we could select relevant features from data utilizing feature importance and correlation matrix. Figure 10 displays the difference in the distribution of each attribute by class value. We can also see whether COVID-19 is positive or negative for each feature.

![A correlation matrix showing the correlations in the data.](image-url)
4.2. Comparison of different prediction models

Six prediction models were assessed to predict COVID-19 based on Laboratory Findings Characteristics in children as shown in Figures 12 and 13. In this study, accuracy, specificity, sensitivity, and ROC (AUC) are used to assess the classifier performance. In the expression of the precision value over the data, the CART model delivers the most reliable performance among all models. Also, the only model that performed significantly better than Bagged, SVM, and RF is the CART model. Overall, in the test set, the CART model shows the highest accuracy with a 92.5% value among all models. Meanwhile, the Bagged, SVM, and NN models have an accuracy of approximately more than 80%. The RF model has lower accuracy values for all models in the test group 78.3%.

As shown in Figure 13, RF, the average sensitivity of the classifier is close to 0.78, which is not a good result. The precision score of the RF model is 0.761, which is the least sensitive of the six models.

The average score for both sensitivity and precision of the NN classifier is 0.81, which is close to the SVM classifier. SVM utilizes quadratic programming to solve the support vector. Solving quadratic programming includes matrix calculation. The average score of the SVM linear classifier is 0.832, which ranks third out of the six. The Precision score of the Bagged classifier is 0.854, which ranks in second place, and is only a little less Precision than the CART model approximately 0.90. The results presented in Figure 14 demonstrate that all machine-learning models, except the RF, achieved an accuracy of more than 80%. The highest precision, sensitivity, and precision were 0.90 and 0.87, found in the CART followed by 0.854, and 0.836 respectively in the Bagged Following the SVM. According to sensitivity and precision values over all the data, the CART and Bagged model delivers the most reliable performance among all models. For the predictors model, the area under the ROC curves is drawn as presented in Figure 14.

For all predictors model, the area under the ROC curves was significantly more than 0.5. The CART model shows the greatest area under the ROC curve compared with other prediction models. There was no considerable variation among any of the prediction models utilizing the criteria of 95% confidence interval. Even so, the p values of the CART model and all else models were less than the other comparisons. Moreover, only the CART model performed significantly best prediction power than others according to the area under the ROC curve. The CART model, SVM linear, SVM radial, and NN were 0.98, 0.92, 0.83, and 0.8 respectively. Consequently, this study confirms that the CART model was a great predictor of COVID-19 based on Laboratory Findings Characteristics in children. The area under ROC curves was more pairwise related to variables.
Figure 12. Comparison of accuracy between different predictive models.

Figure 13. Comparison of sensitivity and precision between different predictive models.

Figure 14. The area under ROC curves.
4.3. Feature importance

Feature importance is the technique of choosing features that are most helpful for our prediction [28]. After evaluating the performance of the model, the feature importance was compared. Features selection by RF, SVM, NN, and CART, are displayed in Figures 15 (a, b, c, and d).

Compared with the features of a significant difference between ML. Therefore, RF, CART, NN, and SVM were selected to analyze the important features. Figure 14 shows the top four predictor variables in the RF (Figure 15(a )) and CART models (Figure 15 (b)). In both models, Leukocytes, Monocytes, Potassium, and Eosinophils, were among the most important predictors, which indicate that those features could play a remarkable role in COVID-19. However, the top four predictor variables were not completely similar in both NN and SVM (Figures15(c) and 15 (d)), including Leukocytes, Monocytes, Potassium, and Eosinophils. Then the variable will be used to form the model. NN and SVM also had a significant difference in the common feature rankings than RF and CART. Although the top second feature “Leukocytes “is the same in both NN and SVM with linear and radial kernels, the other's most important features had differences between them. Leukocytes indicate that this feature may play an essential role in COVID-19. Eosinophils was also an important feature in all ML techniques. In general, since the best model was CART, four variables are important to be used.

(a) Feature importance RF.

(b) Feature importance CART.
5. Conclusions
This study applied the machine learning model to reveal COVID-19 in children. The outcomes realized that the CART model was the best model to predict the COVID-19 based on Laboratory Findings Characteristics. However, the RF model was the least sensitive in all models. Four features were chosen as important features that might yield to be desired results depending on this study. The model has an ability to predict the likelihood of contracting COVID-19 laboratory-based which will ameliorate the doctors' capability to recognize COVID-19 in children in the early stages through the use of clinical features of prediction. Further investigations can be carried out to define whether similar datasets with big datasets will help to improve power to avoid these restrictions and further expand the accuracy of prediction.

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