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A novel approach to predict COVID-19 using support vector machine

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1. Introduction

The ongoing outbreak of Coronavirus disease (COVID-19) is an infectious disease caused by severe acute respiratory syndrome Coronavirus 2 (SARS-CoV-2) [1] was first reported in December 2019 in Wuhan City, Hubei province, China. Since then, the disease has spread globally at an exponential rate infecting more than 22,00,000 and killing more than 1,53,000 and still counting. Studies have shown that transmission takes place mainly via respiratory droplets and close contacts. The virus can survive for 72 h on the surface; as a result, the contaminated surface can become a source of transmission. Those infected with the virus have shown a wide range of signs and symptoms which includes fever (87.9%), dry cough (67.7%), fatigue (38%), shortness of breath (19%), sputum production (33.4%), persistent chest pain, headache (14%), sore throat (13.9%), chills (11%), nasal congestion (4.8%), nausea (5%), diarrhea (4%), hemoptysis (0.9%), and pink eyes and lips (0.8%) [1–3]. A person infected with COVID-19 generally starts to show signs and symptoms within 5–6 days after the infection. The occurrence of the first symptom of COVID-19 to death is estimated to be in a range of 6–41 days [4]. The range decreases for patients above 70 years old compared with those under the age of 70.

Certain similarities have been found in the symptoms between COVID-19 and SARS-CoV [5] patients. People infected with COVID-19 may show few mild diseases such as common cold, fever, and dry cough which are common in SARS-CoV. Such patients generally recover within two weeks. However, the upper respiratory tract symptoms like rhinorrhea, sneezing, and sore throat classified that COVID-19 targets the lower airway. Moreover, COVID-19 infected patients developed certain gastrointestinal symptoms like

diarrhea which was not so significant among the patients infected with MERS-CoV or SARS-CoV. The graveness of COVID-19 varies. Those infected with severe diseases like dyspnea, the high-respiratory frequency may take three to six weeks to recover. Many of those who died of COVID-19 progressed to the critical condition, which includes respiratory failure, septic shock, multiple organ failure [3,6]. Studies have shown that people with underlying conditions such as cardiovascular disease and hypertension [7] are more inclined to get infected with COVID-19. According to the reports by National Health Commission of China (NHC) [8] among the confirmed cases of COVID-19, many patients initially showcased heart palpitations and chest tightness. As per the report of NHC, 11.8% of the patients who died had substantial heart damage with elevated levels of cardiac arrest during hospitalization. The incidence of cardiovascular symptoms is pretty high in COVID-19 patients which leads to the immune system disorder during disease progression. In another report [9,10], where data of 1099 patients with laboratory confirmed COVID-19 cases extracted from 552 hospitals and 30 provinces, autonomous provinces and municipalities in mainland China, 173 had severe diseases with comorbidities of hypertension. Fever (43.8% on admission and 88.7% during hospitalization) and cough (67.8%) were found to be the most common symptoms. China CDC Weekly in Ref. [11] reported that the severity of the symptoms was classified as mild, severe, or critical. Respiratory frequency above 30 per minute, blood oxygen saturation less than 93%, respiratory failure and septic shock were considered as severe and critical cases exhibited by the patients. Based on the symptoms and exposure, clinical diagnosis of the suspected cases was carried out. Throat-swab samples were used to determine confirmed cases. Real-time reverse transcription polymerase chain reaction [6] performed on throat-swab specimens obtained from the upper respiratory tract of the patient has been the standard method of diagnosis [7]. However, there is no standard method for predicting the seriousness of the condition based on the early and mid-period symptoms. Owing to the unpredictability of the infection and the continuously evolving nature of the virus, proper judgment of the infection with just a handful of symptoms is not possible.

Our proposed method attempts to predict COVID-19 using a coined set of symptoms based on their severity and frequency. The key attributes in the feature set incline the prediction toward a particular class. The prediction has been classified into three classes, which are not infected, mildly infected, and severely infected. Among all the symptoms of COVID-19 cases, only a handful of them have been chosen. These include the most common symptoms (fever, breathing rate, cough) across 90% of the confirmed cases. Moreover, the reports mentioned in the previous paragraph solidify our selection of hypertension, heart diseases, chest pain, and acute respiratory syndromes as an attribute for the dataset. We apply the support vector machine (SVM) classifier to classify the features/symptoms into the mentioned classes. In our paper, we have also performed a comparative study on popular supervised learning models using visual programming.

The letter is organized as: [Section 2](#) describes a review of related studies. [Section 3](#) presents a discussion of the proposed COVID-19 detection methodology. [Section 4](#) provides the experimental results and discussions. [Section 5](#) depicts the performance analysis of other supervised learning models using visual programming. Lastly, we present some concluding comments.

2. Related studies

In the recent past, a lot of work in the field of bioinformatics, face detection, text categorization, etc., has been done by using the support vector machine algorithm [12–16]. A brief review is presented here.

Liaqat Ali et al. in Ref. [17] have explained how the SVM is used in the early detection of heart failure, which can help cardiologists to improve the diagnosis process. This system uses two separate models first to eliminate irrelevant features, and the second model is used as a predictive model. From the results, it has been observed that the proposed model shows better performance compared to other machine learning (ML) models with an accuracy in the range of 57.85%–91.83%.

Zihe Yang et al. [18] proposed an improved SVM-based learning model for the diagnosis of diabetes. The system transformed the original problem into an unconstrained optimization problem by applying constraints reduction strategy. By using the gradient descent algorithm, the SVM results improved significantly, which outperforms other benchmark methods.

Y. Lebrini et al. [19] applied the SVM classification method based on phenological metrics to identify the changes and the main agricultural classes in the concerned area. This system classified the main classes into the irrigated annual crop, irrigated perennial crop, rainfed area, and fallow to control the illegal pumping zones based on the main agricultural system classes. The proposed model reached an overall accuracy of 88% and the values of F1-score greater than 0.76.

Joyati Chattopadhyay et al. [20] proposed the idea of facial expression recognition for humans using SVM classification. Based on the extracted facial features, they employed the SVM classifier to separate the facial expressions into six classes, which include happy, sad, disgust, angry, surprise, and fear. This system achieved an accuracy of 80% in detecting facial expressions.

Sajja Tulasi Krishna, Hemantha Kumar Kalluri in Ref. [21] proposed a system to predict the cancer tumors in the lungs by using an SVM classifier. They extracted the features from the CT image scan by using the local binary pattern. SVM kernels such as linear, polynomial, and radial basis functions were used for the classification, among which radial basis function yielded the highest accuracy of 88.76%.

J. S. Raikwal, Kanak Saxena in Ref. [22] analyzed the performance of SVM and k-nearest neighbor (kNN) algorithms to classify data and discover the data pattern to predict future disease. After evaluation, it was evident from the accuracy and resultant

graph that accuracy of kNN is higher compared to SVM for small dataset size. However, the accuracy drops down when the dataset size increases. The evaluation time is also better in SVM compared to kNN for large dataset.

Binh Thai Pham et al. [23] evaluated the predictive capability of SVM and Naïve Bayes Tress (NBT) methods for spatial prediction of landslides in a part of Uttarakhand state in India. It was observed that the SVM model outperforms the NBT model for classification of landslide and nonlandslide pixels.

Huseyin Polat, Homay Danaei Mehr, Aydin Cetin in Ref. [24] implemented SVM classification algorithm to diagnose Chronic Kidney Disease. Feature selection method was applied to reduce the dimension of the dataset. On applying SVM classifier by using the best first search engine, feature selection method produced an accuracy of 98.5% in the diagnosis of Chronic Kidney Disease which is higher than the other ML algorithms.

Ashfaq Ahmed K, Sultan Aljahdali, Syed Naimatullah Hussain in Ref. [25] used SVM and random forest (RF) to learn, classify, and compare cancer, liver, and heart diseases data on different dataset. It is noted that the accuracy varied with different kernel function for SVM. However, the results are observed to be much better with radial basis function with SVM and are comparable with random forest technique.

Vivek Patel in Ref. [26] introduced the concept of power quality disturbances classification by using software simulation of SVM using MATLAB. Means, Variance, and Standard Deviation of the signal were extracted for feature classification and simulated using SVM radial basis kernel function. The results generated from the simulation showcased that Field Programmable Gate Array (FPGA)-based SVM classification is fast and yields high-classification accuracy (CA).

3. Proposed COVID-19 detection methodology

The main problem for the detection of COVID-19 from the symptoms is because of the uncertainty of the data. As a result, no proper dataset is available to use as a reference. According to the results of the COVID-19–infected patients, the majority got hospitalized with high fever, cough with sputum, and shortness of breath. Patients with hypertension, cardiovascular disease, and high pulse rate [27] are quick to progress to the next stage once they get infected with COVID-19. Once the virus progresses to acute respiratory disease syndrome (ARDS), there could be respiratory failure, septic shock, and multiple organ failure [2,6]. The multicriteria [28–35,42–47] dataset thus has been created with the following symptoms as attributes (see Table 18.1):

Based on the symptoms, infected status is possible to find out by utilizing our proposed approach. The outcome, i.e., infected status, has been classified into three classes, which are not infected, mildly infected, and severely infected. The classes have been mapped to the numerical values as:

Severely Infected = 1; Mildly Infected = 2; Not Infected = 3.

Table 18.1 Summary of COVID-19 dataset.

Serial number	Attributes	Description
1	Temp	Temperature above 100°C is mild fever and above 103°C is high fever
2	Breathing rate	Above 30 breath/min is a critical condition
3	Hypertension	Stage 1: 140–159 blood pressure; stage 2: 160 and above
4	HBR	Heart beat rate; normal: 60–100 beats/min; high: above 100
5	ARDS	Acute respiratory disease syndrome causes respiratory failure
6	Chest pain	Persistent chest pain with breathing problem is critical
7	Heart disease	Patient with cardiovascular diseases is prone to COVID-19
8	CWS	Cough with sputum

3.1 Case 1: not infected

Cases assigned to not infected are showing symptoms only in a certain disease, which is quite natural for any human being. However, in certain instances, like the common cold, people can suffer from mild fever, dry cough, but only those conditions are not sufficient to ascertain COVID-19 infection.

3.2 Case 2: mildly infected

This class signifies that the symptoms do not confirm COVID-19 with certainty but can lead to severe consequences if proper measures are not taken. In cases like mild fever coupled with the mild breathing problem, we can say that the patient might be infected with COVID-19, but again this prediction has no certainty.

3.3 Case 3: severely infected

Patients with more than two to three symptoms, each of which has crossed their normal limits, have shown positive results for COVID-19 in the majority of cases. In cases where the patient is suffering from high fever, high-breathing rate, and has also developed acute respiratory syndrome is in a critical condition. The dataset is then passed on to the SVM classifier. The block diagram of Fig. 18.1 depicts the suggested methodology.

For this problem, SVM is chosen because it uses kernel trick to convert low-dimensional input space to high-dimensional space and thus converts the non-separable problem to separable problem. We have split the dataset into a train set and test set in the ratio of 7:3. Using the linear kernel, the SVM classifier linearly separates the data utilizing a hyper-plane. Each class of data is separated by parallel hyper-planes ensuring that the distance between them is as large as possible. We have taken the cost parameter $C = 10$. We are looking for a smaller margin hyper-plane to classify the infected classes more accurately with fewer miss-predictions; since we are dealing with a very high-priority situation of detecting COVID-19. The working principle of SVM for our paper is depicted in Fig. 18.2.

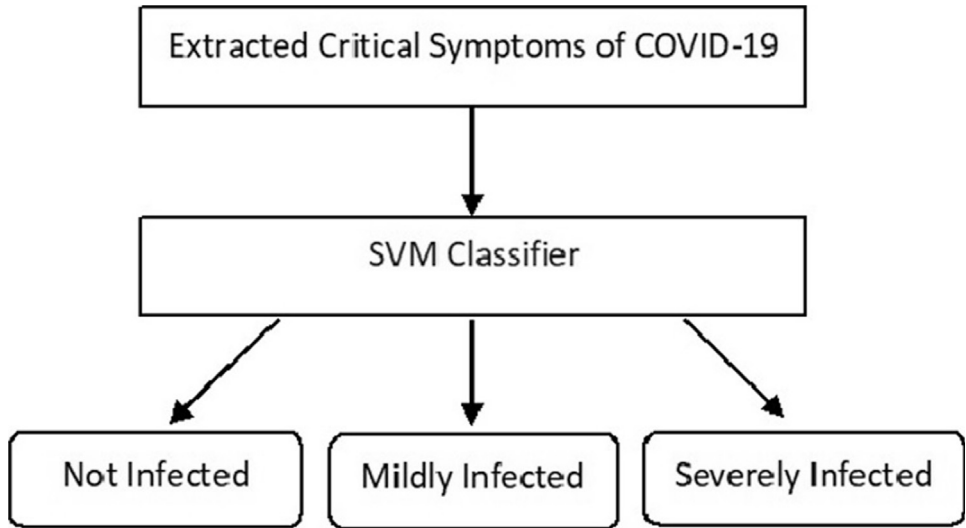


FIGURE 18.1 Block diagram of suggested COVID-19 detection methodology.

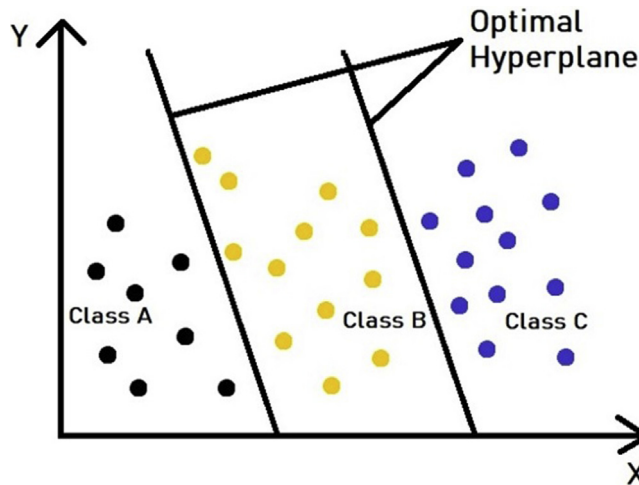


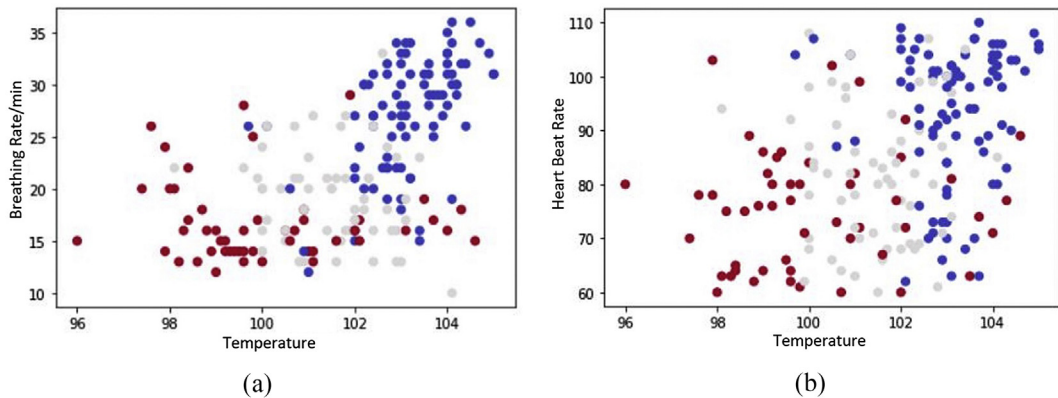
FIGURE 18.2 Working principle of support vector machine.

4. Experimental results and discussions

The dataset that has been created for this study contains 200 records, with eight attributes that are described in [Table 18.1](#). Authors are bound to employ the machine-learning algorithm on a minimal number of data set, as original data are not currently available because of the pandemic situation world wide. The authors also believe that the proposed technique will perform better provided with the real-time data set.

Table 18.2 Dataset snapshot.

Temp	Breathing rate	Hypertension	Heart beat rate	Acute respiratory disease syndrome	Chest pain	Heart disease	Cough with sputum	Infected
98.6	13	No	75	No	No	No	Yes	3
99.2	15	Stage 1	80	No	No	No	No	3
101.0	12	Stage 1	78	No	Yes	Yes	Yes	2
102.9	22	Stage 1	93	Yes	Yes	No	Yes	1
100.8	13	Stage 2	96	No	No	Yes	No	2

**FIGURE 18.3** Visualizing our prediction before applying support vector machine based on (A) temperature and breathing rate (B) temperature and Heart Beat.

In this dataset (see [Table 18.2](#)), the output column, i.e., the infected column, is an integer-valued from one to three, which are mapped to not infected, mildly infected, and severely infected. Visualizing our prediction before applying SVM is shown in [Fig. 18.3](#).

Each row provides the data regarding the symptoms for individual patients. We replaced the string values (yes, no) of the attributes (ARDS, chest pain, heart disease, cough with sputum) with integers 1 and 0, respectively. For hypertension, the data have been mapped as no = 1, stage 1 = 2, stage 2 = 4. The dataset is then fed to SVM classifier to classify the symptoms into the three classes discussed earlier. We have kept the kernel as “linear.” The model has been trained using 70% of the data from the dataset. [Fig. 18.4](#) shows the prediction plot based on temperature and breathing rate. The confusion matrix describes the performance of classification on a set of test data where the true values or correct results are known, which is shown in [Fig. 18.5](#).

We have shown the scatter plots based on temperature, breathing rate, and heart beat rate because these three are the most common symptoms of COVID-19. Moreover, these three attributes have numeric values, while the rest of the set has character values (yes/no).

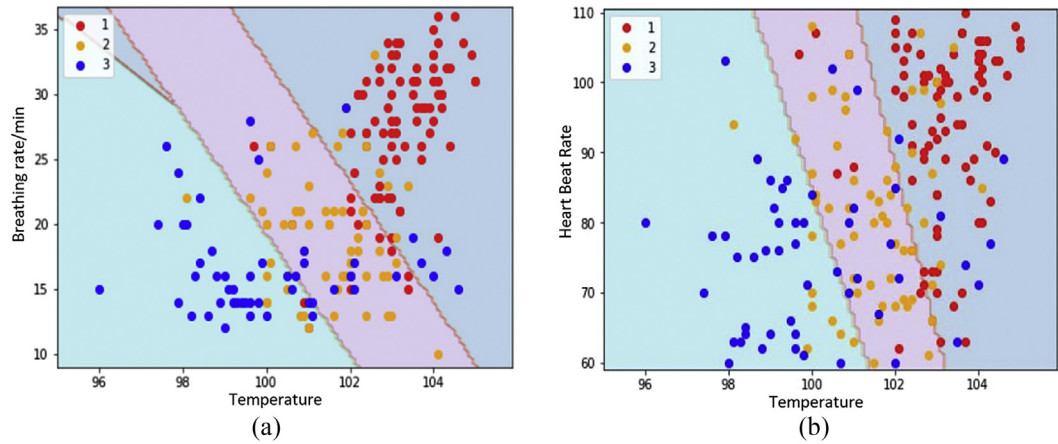


FIGURE 18.4 Prediction plot based on (A) Temperature and Breathing Rate (B) Temperature and Heart Beat Rate.

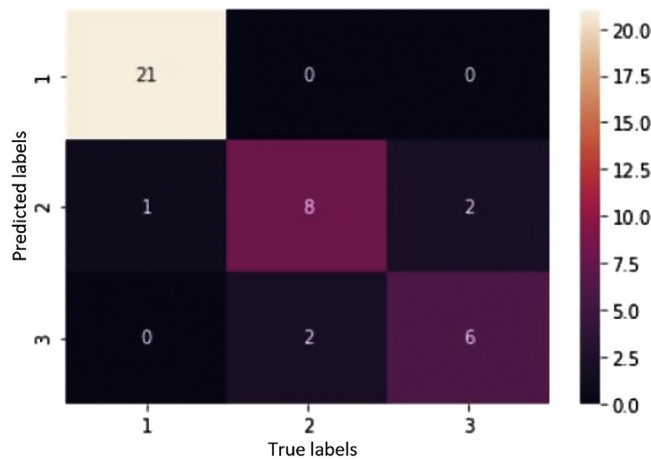


FIGURE 18.5 Confusion matrix.

Our model has an accuracy of 87%. From the classification report, we see that our methodology has a high success rate of predicting severely infected cases, which is very crucial for COVID-19 prediction. The score for the rest two classes is on the lower side because of the variable nature of COVID-19 because people with no symptoms are also getting infected with COVID-19. We cannot predict with certainty that a person showing mild symptoms or no signs at all will not get affected by COVID-19. Because of these uncertainties in the dataset, the accuracy is on the lower side (see Table 18.3).

In Table 18.3, the classifier has shown higher precision for severely infected class, which means that very few cases have been labeled as severely infected, while not infected and mildly infected class have shown lower precision compared to severely infected class. The classifier has shown perfect result for predicting the cases which

Table 18.3 Classification report.

Class	Precision	Recall	f1-score	Support
Not infected	0.75	0.75	0.75	12
Mildly infected	0.82	0.74	0.78	19
Severely infected	0.94	1.00	0.97	29

belong to severely infected class since it has recall = 1 but has shown a moderate result for the other two classes. As an f1-score, which is the average of precision and recall, is high for severely infected and a bit low for not infected and mildly infected. The final column support is the number of true values for each class.

5. Performance analysis of other supervised learning models using visual programming

Our analysis on COVID-19 dataset depicts that among all the other supervised models, SVM works best in predicting COVID-19 cases with maximum accuracy. To bolster our claim, we have performed a comparative study on popular supervised learning models. As we know that the severity of COVID-19 is so critical that turnaround time for COVID-19 cases becomes one of the utmost important factors. From current data, we also understand that the symptoms of COVID-19 have evolved over the months since its first inception and they are still evolving. Therefore, the new symptoms and data will further increase the number of predictors for COVID-19 data analysis and prediction. Keeping this in mind, we need a software tool to quickly analyze the data with new set of predictors and see their efficiency in predicting the disease.

Thus, we propose the usage of a visual programming methodology using Orange [36]. It is an open source ML and data visualization toolkit especially designed to reduce coding overheads and easy analysis of data using ML models [38–41] for researchers from any background. Thus, to introduce this novel toolkit, we have performed our comparative analysis between different machine-learning models using Orange. Fig. 18.6 depicts the block diagram of the methodology. First COVID-19 data are parsed and the features are ranked based on their predictive scores. This step is basically a dimensionality reduction which is generally employed to reduce the number of features and select only the features that have the best correlation with the target. Furthermore, the linearly varying redundant features can also be identified using this “Rank” block and thereby overall computation time while working with large dataset gets reduced, thereby making the methodology robust, fast, and scalable. For ranking purpose, popular scoring methods [37] like Info, Gain, Gini, ReliefF, and FCBF are employed. Next, the top features are selected, and they are fed into the ML models for training and prediction. “Test and Score” module helps in evaluating the results of the prediction and provides comparison metrics to evaluate the performance of various supervised machine-learning models viz.

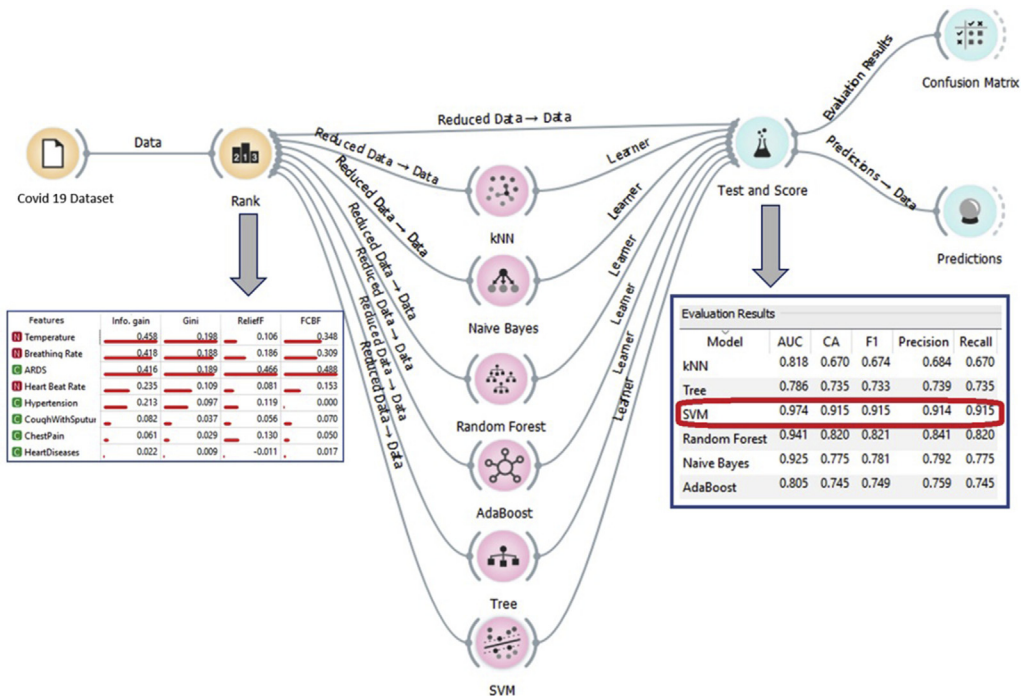


FIGURE 18.6 Comparative analysis of Supervised Learning algorithms using visual programming on COVID-19 Dataset.

kNN, Naïve Bayes, RF, AdaBoost, Binary Tree, and SVM. The evaluation results of the models are depicted in Fig. 18.6, and SVM outperforms all other models that are tested. We have done our prediction based on the parameters like area under ROC, CA, F1 Score, Precision, and Recall. The confusion matrix for all the models has been summarized in Fig. 18.7, illustrating the superiority of SVM in predicting COVID-19 [48–51] efficiently.

6. Concluding remarks

This paper aims to develop a model that can predict whether a person is affected by COVID-19 or not using SVM classification. All the possible conditions of infection based on the symptoms have been meticulously looked upon, and accordingly the dataset has been framed. It's hard to reflect accurate prediction since persons without any signs or symptoms of COVID-19 are also getting affected. The nature of the virus is very uncertain, and the symptoms are evolving and changing day by day. Keeping in mind the criticality of this infected, only those symptoms which are very common and critical have been kept in framing the dataset. The mildly infected class has been kept as a warning sign because the patient's symptoms have inclined toward COVID-19 infection. The not infected class doesn't signify that the patient is free from the shackles of COVID-19, but for the time being, signifies that they are free from immediate danger.

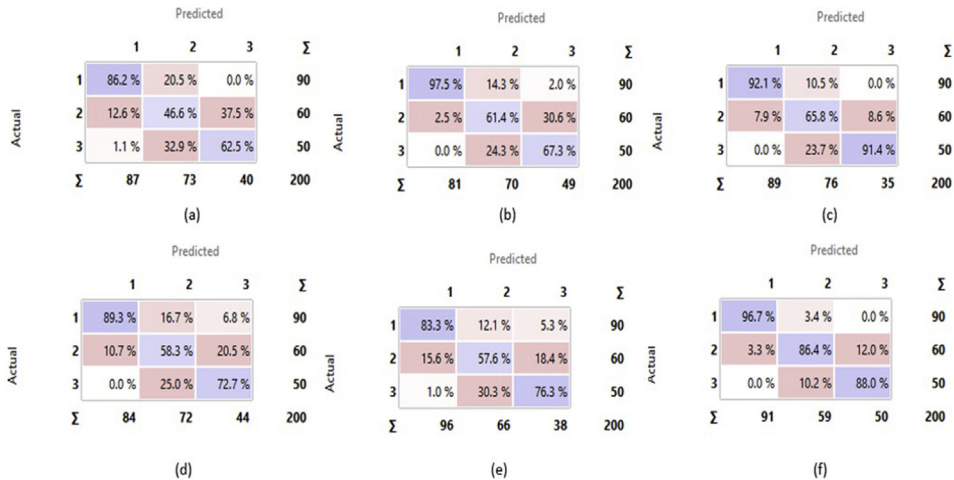


FIGURE 18.7 Confusion Matrix of respective Supervised Learning Algorithms (A) kNN (B) Naïve Bayes (C) Random Forest (D) AdaBoost (E) Binary Tree (F) support vector machine.

Patients who are in the critical class should immediately undergo proper medication to overcome the disease. Furthermore, proper utilization of visual programming toolkit for visualizing and analyzing the data may pave the way for easier and faster COVID-19 data analysis scheme for researchers from multidisciplinary background.

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