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Research Article

Multi-Agent-Based Ensemble Learning Model with Feature Selection for Enhanced COVID-19 Detection

Rupinder Kaur Walia[1], Harjot Kaur[2]

[1]Research Scholar, [2]Assistant Professor, Department of Computer Science Engineering. Guru Nanak Dev University, Amritsar, Punjab, India.
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I N F O

Corresponding Author:
Rupinder Kaur Walia, Department of Computer Science Engineering. Guru Nanak Dev University, Amritsar, Punjab, India.
E-mail Id:
rupinder.walia84@gmail.com
Orcid Id:
https://orcid.org/0000-0001-9304-4050
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A B S T R A C T

Introduction: The ongoing COVID-19 pandemic has driven the attention of researchers for advanced and adaptable methods in disease detection. This research paper proposes a novel multi-agent-based model for detecting COVID-19 among patients with high accuracy.

Methods: Initially, all the necessary information is attained from a COVID-19 dataset that is available on GitHub. This data is then subjected to pre-processing because it contains a lot of null, missing and redundant values. The processed dataset is then passed to the proposed Deep Learning (DL) architecture for selecting only important and effective features. In order to make the process of feature selection in DL more effective, we have implemented the Layer-wise Relevance Propagation (LRP) and the Extra Tree technique on each layer of the DL model. The LRP and Extra tree evaluate the importance of each feature at each DL layer and finally, the output of two is combined to get the final feature set. After this, data is divided into training and testing sets in the proportion of 80:20. To introduce the concept of novelty, we have divided the training dataset into three agents (data subsets) which are then passed to three base models i.e., Support Vector Machine (SVM), Logistic Regression (LR) and K-Nearest Neighbor (KNN) separately. This was not the case in traditional models wherein the entire training dataset was passed to classifiers for training purposes.

Results: The outputs generated by three base models are then combined by using an ensemble learning voting mechanism to make the final prediction which determines whether a patient is COVID-19 positive or not. The efficacy of the proposed approach is validated using Python software, wherein, it outperforms traditional LR, SVM and Bernoulli NB models by attaining an accuracy of 97.5%.

Conclusion: The proposed multi-agent-based model for COVID-19 detection shows promising results in terms of accuracy and efficiency. By employing advanced techniques such as deep learning, feature selection, and ensemble learning, this approach addresses key challenges in disease detection and offers a significant improvement over traditional methods.

Keywords: COVID-19, Feature Selection, Biomedical Applications, Ensemble Learning

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Introduction

In the year 2020, World Health Organization also known as WHO declared COVID-19 as a global pandemic. COVID-19 is an extremely contagious disease that is usually caused by a Coronavirus strain named SARS-CoV-2.[1] It is highly infectious and has infected around 768,983,095 people around the world as of August 2, 2023. The epidemic started in Wuhan, China, in the last month of 2019, but as of the right moment, it has propagated across more than 200 nations. In order to control the virus's spread, many countries have primarily used non-clinical restraints (such as lockdowns).[2] The majority of the economies around the globe have been severely impacted by the virus, resulting in shutdowns or the global coronavirus recession.[3] Close contacts play a critical role in the transmission of the SARS-CoV-2 virus, with infection occurring when a susceptible person breathes in droplets containing the virus, released by an infected person during coughing or sneezing.[4] Moreover, the disease can also spread when a person comes into contact with infected materials physically and then touches their sensitive body parts like eyes, nose, or mouth.[5] Due to the method of dissemination, there are many non-pharmaceutical interventions (NPI) for prevention, including using masks, personal protective equipment (PPE), routinely hand-washing, remaining at home, and avoiding getting in crowded places.[6,7] Initial COVID-19 symptoms include fever, coughing, and exhaustion. However, massive alveolar damage and developing respiratory failure might result in mortality as the condition worsens.[8] Despite the fact that disease only has a 2% mortality rate, the quick spread of disease within individuals worsens the situation. The COVID-19 virus has a high incidence rate that falls between 1.5 and 3.5, making it very contagious.[9,10] As a result, it's critical to get a diagnosis promptly in order to curb the virus's propagation. This has proven to be exceedingly difficult, though, as the virus can remain dormant among people for over 5 days until symptoms appear.[11]

Medical systems around the world are still struggling to deal with a growing pandemic. They are facing a variety of challenges, such as the excessive need for hospital beds, lack of essential medical equipment, and the additional burden of infected healthcare workers.[12] Consequently, it is essential to have the ability to make quick clinical choices and use healthcare assets efficiently. In light of this, researchers have developed an RT-PCR (Reverse Polymerase chain reaction),[13] that finds the presence of COVID-19 ribonucleic acid (RNA) in respiratory tract instances, hence making it one of the most widely used detection methods. However, a lot of countries struggle to provide enough testing resources, which causes delays in getting precise results and restricts screening to people who have visible signs. Therefore, a demand for fast and more dependable screening techniques arises which may supplement or take the place of PCR testing in order to solve these constraints. Such screening methods can be utilised in conjunction with PCR testing to increase the accuracy of the diagnosis or as a substitute in locations wherein PCR screening is not readily available. Investigators now are working on developing COVID-19 diagnostic models based on artificial intelligence (AI) to help physicians react to the epidemic.

AI has been used by various researchers in the fight against COVID-19 as an aid in the prevention and tracking of infected patients.[14] In reality, governments were able to restrict the movement of individuals and find the persons they were interacting with by using specific geographical coordinates. Moreover, AI has proven to be advantageous in determining and categorising datasets and predicting forecasts.[15] Machine Learning (ML) algorithms are also specifically employed for this reason. Despite this, a majority of these methods exhibit lower computing effectiveness and precision. Because of these problems, determining the best approach with more accurate findings is very difficult. To put it another way, it's challenging to put forward a prediction system that can accurately identify and classify the virus. Specifically, discussing ML approaches, it is going to be extremely challenging to identify risks associated with public health in advance to improve the prediction rate of epidemiologic risks in the near future. In order to address these problems, agent-based techniques have been used in this research to increase the precision of ML models. Agent-based model (AGM) can be defined as a computational technique wherein simulated heterogeneous agents present in the system communicate with each other and their surroundings. While agent-based modelling is being used increasingly frequently in medical studies, the COVID-19 disease has yet to be detected using this technology.

Motivation

The ongoing COVID-19 pandemic has underscored the urgent need for accurate and adaptive detection methods to effectively curb the spread of the virus.[16–25] Traditional detection approaches were good but often struggled to capture the complex and evolving nature of the disease. Moreover, the current COVID-19 detection models have often treated the disease as a homogenous entity, overlooking its inherently heterogeneous nature. This may lead to inaccuracies in capturing the diverse transmission patterns, mutation rates, and behavioural changes exhibited by the virus. Keeping this in mind, an effective detection model must be presented that can handle heterogeneous data of COVID-19 with a high detection accuracy rate. After studying the literature, we observed that agent-based methods can significantly improve the detection rate by including data heterogeneity. By simulating

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individual agents representing different characteristics and behaviours of the virus within diverse populations, these models can paint a dynamic and nuanced picture of the disease's complexities. Their adaptability enables them to respond promptly to emerging variants and ever-changing epidemiological scenarios, ensuring real-time updates to enhance accuracy.

Research Contributions

In this paper, a highly accurate and effective COVID-19 detection model is presented that is based on multi-agent classification methods. The main contribution of our work is that we have introduced the concept of multi-agents in order to separate datasets into three subsets which are later on passed to three separate classifiers to predict the disease. The key contributions of our work are mentioned below:

1. To propose an effective feature selection technique in order to make an effective and informative dataset
2. After this, the concept of multi-agent is introduced through which we divide the feature set into three subsets or agents
3. To propose an effective classification model in which three classifiers i.e., KNN, SVM and Logistic Regression are used. The three feature subsets are separately given to three different classifiers and then a voting approach is implemented for predicting the final output
4. The performance of our approach is then validated by comparing it with a few traditional models in terms of various performance dependency factors

The remaining sections of the paper are categorised as follows: Section 2 represents a brief discussion about the latest COVID-19 detection methods. Section 3 discusses the proposed work and techniques employed in it. Section 4 represents the results obtained for the proposed model and finally, a conclusion of the paper is given in section 6.

Related Work

In recent years, the field of COVID-19 detection has witnessed rapid advancements, particularly with the emergence of machine learning (ML) and artificial intelligence (AI) based models. As the COVID-19 pandemic continues to pose significant global challenges, researchers and practitioners have turned to popular academic platforms such as Google Scholar, Springer, Hindwai, Elsevier, and IEEE to explore innovative approaches for accurate and efficient COVID-19 detection. The literature was obtained by using some specific keywords like; COVID-19 detection methods, ML-based COVID-19 detection methods, AI-based diagnostic methods and so on. This literature review aims to critically analyse the state-of-the-art ML and AI-based COVID-19 detection approaches published on these renowned platforms, shedding light on their effectiveness, and potential for improving public health outcomes. To begin with, a few authors[26] tried to develop a unique detection model wherein they utilised ML and IoT techniques for detecting individuals with COVID-19, particularly in smart hospitals. They utilised NB, RF and SVM models in their work which were trained and validated on laboratory databases. Results showcased that out of three models, SVM showed the highest accuracy rate of 95%. Similarly, Painuli et al. examined the performance of various ML algorithms and the best models were included in their study.[27] Their analysis showed that RF and Extra tree were better at detecting COVID-19 with an accuracy of 90% and hence utilised in their work. Upon utilising these classifiers in their work, the extra tree outperformed the RF model by attaining a detection accuracy rate of 93.62%. Furthermore, Ardabili et al. tried to improve the performance of ML models by using an optimisation algorithm in their study.[28] They used the ANN classifier along with the GWO algorithm for identifying COVID-19 in the given dataset. The training and testing were performed by using different time series datasets. They analysed the model's efficacy in terms of MAPE which came out to be 6.23 on training data, 13/15 on testing data and 11.4 on validating datasets.

In contrast to the aforementioned methods, Chowdhury et al. aimed to detect COVID-19 by analysing cough sounds while simultaneously determining models which show improved results on various cough databases.[29] To accomplish this task, the authors proposed an ensemble learning-based MCDM (Multi Criteria Decision Making) model for identifying the best-performing ML model for disease detection. Results showcased that the extra tree classifier shows incredible results with an AUC, precision and recall of 95%, 100% and 97% respectively. A factorial experiment was utilised by authors for assessing the performance of various ML models using x-ray images for healthy, pneumonic and COVID patients.[30] The model underwent data-balancing, feature engineering and hyperparameter optimisation methods to achieve good results. Among all the models, SVM and RF were proven to be more effective in detecting and categorising patients in the three classes. Likewise, an effective ML model was presented for detecting COVID-19 in X-ray images.[31] The model was designed in such a way that it can predict four classes of normal, pneumonic, viral pneumonia and COVID-19 using CXR images. Results revealed that their model yielded an accuracy rate of 92.4% on training data, 88.24% on testing data and 87.13 on validating data respectively. Furthermore, Shaheed et al. proposed an automated COVID-19 detection model using CXR images that was based on DL and ML models.[32] They employed Gaussian filter and logarithmic operator techniques in the pre-processing phase and then features were extracted

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using CNN and GLCM. The feature set was then given to the RF classifier for detection and categorisation into three categories. Their proposed model achieved an accuracy of 97% on the given dataset. Furthermore, Awotunde et al. utilised 3 ML classifiers which include RF, XGBoost and LGBM for detecting and categorizing COVID-19 in patients.[33] Out of all ML classifiers, the LGBM model was able to generate accuracy, precision and ROC of 97% and recall and F1-score of 96% respectively.

To further increase the accuracy of COVID-19 detection, Gupta et al. utilised a hybrid CNN model using CXR images. They used 4 pre-trained CNN models (VGG-19, InceptionV3, MobileNetV2, and DenseNet) and developed 4 hybrid models which are VID, VMI, VMD and IMD.[34] The efficacy of the suggested approach was examined using five-fold cross-validation. Results revealed that the suggested hybrid VMD model was giving more accurate results with a testing accuracy of 97.3%. In addition to this, Asif et al. again proposed a CNN-based detection model wherein 6 pre-trained models i.e., VGG16, DenseNet201, MobileNetV2, ResNet50, Xception, and EfficientNetB0 were used.[35] The efficacy of the proposed model was examined on datasets containing a total of 3886 CXR images. Results revealed that the CNN-based VGG16 model was detecting COVID-19 with an accuracy of 97.84% and a precision of 97.89% respectively.

It is evident from the above literature that numerous scholars from around the world have contributed to the automated diagnosis of COVID-19 by studying different databases.[36] With the advent of technology, ML- and DL-based approaches have gained a lot of attention for detecting COVID-19.[37,38] However, it has been noted that current DL methods are not highly effective and have lower detection rates. Similarly, many authors have utilised ML classifiers in their work but they fail to handle huge datasets and undergo overfitting issues, which lower their accuracy rate. Furthermore, we observed that feature selection is an important step in classification models that helps to improve the accuracy rate by removing unnecessary features. By doing so, one can reduce the training time of the model and increase its accuracy, therefore, an effective Feature selection technique must be utilised in detection models. Keeping these facts in mind, an effective automated COVID-19 detection model is presented in this study that is based on multi-agent systems and ensemble learning methods.

Material And Methods

Present Work

This section gives a brief introduction to the proposed COVID-19 detection model. The main aim of the proposed approach is to overcome the shortcomings of current COVID-19 diagnosis methods and increase the detection accuracy rate. To accomplish this objective, we have utilised a COVID-19 dataset that is accessible online on GitHub. A detailed description of the healthcare dataset is needed.[26] However, we cannot utilise this raw dataset directly in our work, as it contains a lot of null, missing and unnecessary values that can degrade the detection accuracy rate, therefore, a pre-processing technique is implemented. During pre-processing null values are eliminated, missing values are filled and strings are converted into numeric values to make the dataset more informative. The processed dataset contains only informative features related to COVID-19 detection, but all these features cannot be utilised for model training and must be refined further to reduce the complexity of the model and also solve dataset dimensionality issues. Nonetheless, the features generated are highly dimensional and hence more effective techniques need to be implemented. In the proposed work, we have utilised the Deep Learning-based architecture for analysing the features at different layers. To further optimise this process, we will be implementing LRP (Layer Wise Relevance Propagation) which generates the weights of features in each layer to describe their importance. Moreover, we have also implemented the Extra Tree-based feature selection technique that determines the importance of various features in the dataset created by the DL model. The outputs obtained by two techniques i.e., LRP and Extra trees are then combined to form the final feature vector database that contains only the 10 most important and relevant features. Now, this dataset is split into training and testing data in the ratio of 80:20. The majority portion of data i.e., 80% is further divided into three subsets or agents to perform the classification process. The novelty contribution of our study is that we have created three subsets from training data which serve as agents, and each subset is passed to different classifiers i.e., KNN, SVM and LR to make separate predictions, which is not the case in the traditional model wherein entire training dataset is passed to classifiers to predict the final output. The final prediction in our approach is made by utilising the ensemble learning voting mechanism. The primary principle behind this voting method is that by combining the specific decisions using a majority voting system, errors in each method can be eradicated. Therefore, we aimed to improve the performance of the proposed multi-agent approach COVID-19 detection system. The proposed architecture of the proposed model is shown in Figure 1.

Dataset Information and Preparation

In the proposed work, we have utilised a COVID-19 database that is easily available on GitHub. This database contains laboratory samples of individuals who were admitted to Israelita Albert Einstein Hospital, located in Sao Paulo, Brazil. The researchers collected data samples during the earlier days of 2020 for detecting COVID-19 in patients.

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A total of 111 laboratory samples were collected from a total of 5644 patients. Moreover, the data collected showed that the positive rate of patients was only 10%, out of which 2.5% of patients needed critical care and 6.5% of patients needed hospitalisation. It must be noted here that the dataset contains no information about the gender of patients. Furthermore, in order to make the dataset balanced the researchers observed that only 18 laboratory samples play a critical role in detecting COVID-19, therefore, they eliminated the rest of the samples. The refined dataset now contains only 18 laboratory samples taken from 600 patients. However, even these 18 samples are unknown to a few patients, and because of this, they decreased the number of patients from 5644 to 600. Now, out of these 600-patient data, we don't have any findings for 520 patients and the remaining 80 were COVID-19 patients. Figure 2 represents the graph for count which indicates the total COVID-19 positive and negative patients. The utilised dataset can be accessed via https://github.com/burakalakuss/COVID-19-Clinical.

The graph (Figure 2), represents the non-COVID samples by '0' and positive COVID samples by '1' respectively. The graph clearly shows data imbalance because a majority of the samples were negative and only a few samples were positive. As mentioned earlier, to reduce this misbalancing only 18 laboratory samples were preserved and the rest were eradicated but still, the data needs to be refined.

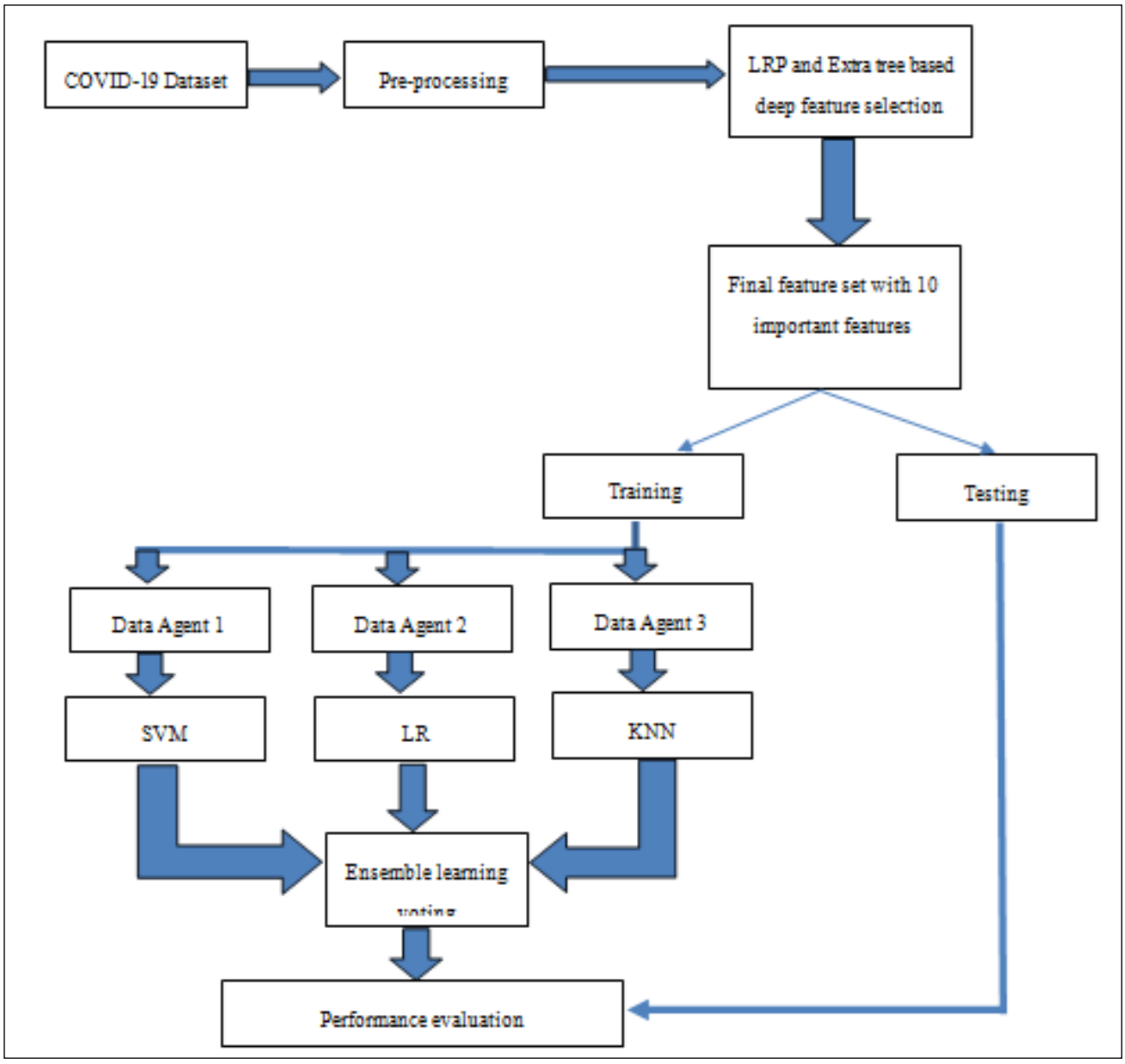

Figure 1.Proposed COVID-19 Detection Model

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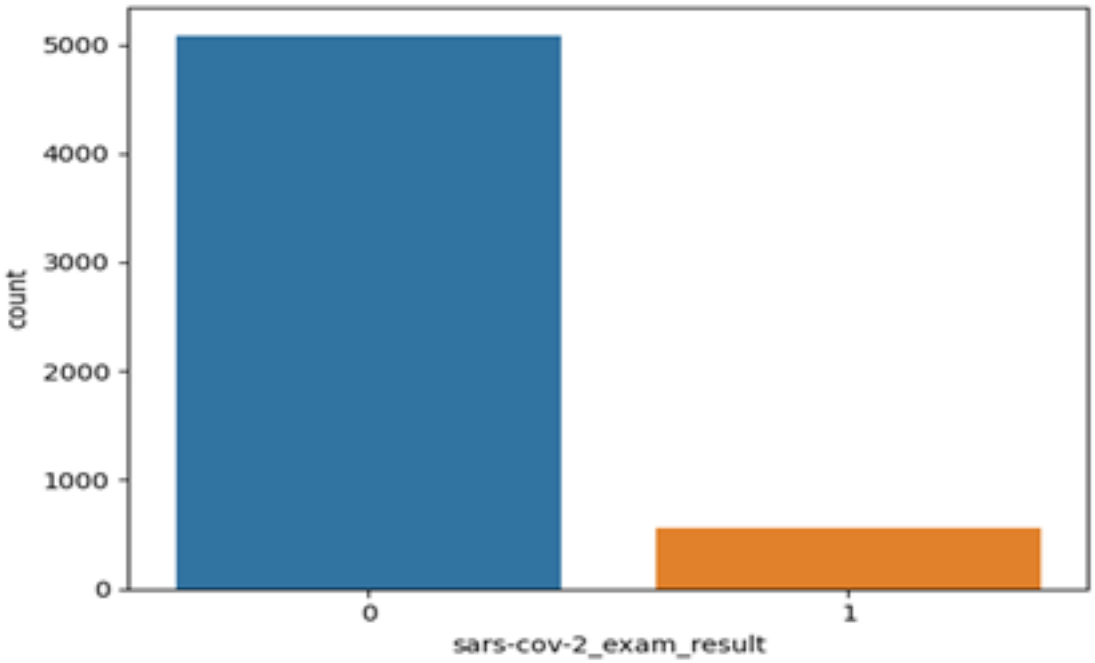

Figure 2.Count of COVID-19 Samples in Dataset

After collecting the necessary data from available sources, we utilise it in the proposed model for further implementations. Despite the fact that they removed some unnecessary samples from the dataset, it still contains a lot of null or missing values which can deteriorate the detection accuracy rate of the proposed model. Thus, before implementing advanced techniques like feature engineering and multi-agent methods, we pre-process this raw dataset. During the pre-processing phase, the null or missing values were identified in the dataset and removed by using the mean imputation method. It is one of the simplest and most effective methods for filling the null values by replacing them with the mean of available values in the same column. Moreover, we have implemented a level encoder technique for converting the strings in the dataset into numeric values for quantitative analysis. Moreover, by converting strings into numeric values, the features of the dataset can be represented in a consistent and standardised manner within the given feature space, which in return makes it easier for the algorithms to understand relationships and patterns. In our proposed approach, a total of 43 rows of data are attained after applying pre-processing techniques. The details of these attributes are given in Table 1, along with their data type.

Table 1 represents the total 43 features present in the dataset after implementing the pre-processing technique to the raw dataset. The table shows the numeric value for each attribute along with its data type. However, these features are still high in number and we need to refine them for solving dimensionality and complexity issues.

Feature Engineering Using DL

Feature engineering is considered one of the critical steps in the classification process. During this process, only important and crucial features are selected from the processed dataset, which not only makes the dataset more informative but also reduces its complexity and solves dimensionality issues. Since, the features obtained after pre-processing are highly dimensional and cannot be used directly in the proposed work, therefore, Deep Learning (DL) architecture is used in the proposed work for selecting the features obtained from the dataset after pre-processing. The network is initialised by defining various important parameters of the DL model. Table 2 demonstrates the configuration parameters of the proposed DL model.

Table 1.Information of Attributes after Pre-processing

Numeric Value	Attributes	Non-Null	Count	Data Types
0	patient_age_quantile	5644	Non-null	int64
1	sars-cov-2_exam_result	5644	Non-null	int64
2	Hematocrit	5644	Non-null	float64
3	serum_glucose	5644	Non-null	float64

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4	respiratory_syncytial_virus	5644	Non-null	int64
5	0mycoplasma_pneumoniae	5644	Non-null	float64
6	neutrophils	5644	Non-null	float64
7	Urea	5644	Non-null	float64
8	proteina_c_reativa_mg/dl	5644	Non-null	float64
9	potassium	5644	Non-null	float64
10	influenza_b,rapid_test	5644	Non-null	int64
11	alanine_transaminase	5644	Non-null	float64
12	gamma-glutamyltransferase	5644	Non-null	float64
13	total_bilirubin	5644	Non-null	float64
14	Ionized_calcium	5644	Non-null	float64
15	strepto_a	5644	Non-null	int64
16	Magnesium	5644	Non-null	float64
17	pco2_(venous_blood_gas_analysis)	5644	Non-null	float64
18	fio2_(venous_blood_gas_analysis	5644	Non-null	float64
19	rods_#	5644	Non-null	float64
20	urine_-_esterase	5644	Non-null	int64
21	urine_-_aspect	5644	Non-null	int64
22	urine_-_ph	5644	Non-null	int64
23	urine_-_hemoglobin	5644	Non-null	int64
24	urine_-_ketone_bodies	5644	Non-null	int64
25	urine_-_nitrite	5644	Non-null	int64
26	urine_-_sugar	5644	Non-null	float64
27	urine_-_leukocytes	5644	Non-null	int64
28	urine_-_crystals	5644	Non-null	int64
29	partial_thromboplastin_time (ptt)	5644	Non-null	float64
30	relationship_(patient/normal)	5644	Non-null	float64
31	international_normalized_ratio_(inr)	5644	Non-null	float64
32	lactic_dehydrogenase	5644	Non-null	float64
33	prothrombin_time_(pt), _activity	5644	Non-null	float64
34	vitamin_b12	5644	Non-null	float64
35	creatine_phosphokinase (cpk)	5644	Non-null	float64
36	ferritin	5644	Non-null	float64
37	arterial_lactic_acid	5644	Non-null	float64
38	lipase_dosage	5644	Non-null	float64
39	d-dimer	5644	Non-null	float64
40	Albumin	5644	Non-null	float64
41	arteiral_fio2	5644	Non-null	float64
42	Phosphor	5644	Non-null	float64

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Table 2.DL Configuration Parameters

Deep Learning Parameters	Values
No. of layer	4
Optimiser	Adam
Loss	Binary cross-entropy
Metrics	Accuracy
Epochs	50
Batch size	32

The DL model is trained over the processed dataset during which it learns important features automatically. The proposed model comprises four layers, one input and output layer and two dense layers. The layers are arranged sequentially with the first input layer, then two dense layers and finally an output layer. By adding two dense layers in the architecture, the model can learn increasingly complex and abstract representations from the given data. Figure 3 shows the architecture of the proposed DL model utilised for analysing features.

The description of these four layers used in the proposed DL architecture is briefly explained below:

1. **Input Layer:** The first layer of the proposed DL architecture is the sequential input layer, which takes the featured dataset obtained after implementing the pre-processing technique.
2. **Dense_1 Layer:** The outcome of the first layer is then passed to the second layer which comprises 43 units and the RelU activation function. The 43 units in the layer signify the presence of 43 neurons which determines its dimensionality. Moreover, the RelU activation function is used for adding non-linearity to the network, which is essential for the network's ability to learn complex patterns and relations in data.
3. **Dense_2 Layer:** In the next phase, data is passed through the second dense layer which has the same configuration of 43 units and RelU activation function. This layer helps the model to learn more intricate patterns and representations effectively.
4. **Output Layer:** The final layer of the proposed architecture is an output dense layer with 1 unit and a sigmoid activation function for binary classification.

As the main motive is to reduce the complexity and dimensionality of the proposed COVID-19 detection model, therefore, we aim to optimise the working of the DL model for feature selection. Our main contribution in this phase is that we have implemented two effective techniques i.e., LRP and Extra Tree on each layer of the DL model for selecting only those features that can enhance the detection accuracy rate. The LRP is utilised at each layer of the DL model to evaluate the importance of each feature. It is basically a technique in which back-propagation is used for explaining the networks. By utilising the configuration on the trained model itself, LRP assigns Relevance values "Ri" to significant inputs in order to explain the classifier's judgement for a unique data point. It is utilised in many applications particularly where the predicted value is used for determining the relevance value for lower layers.

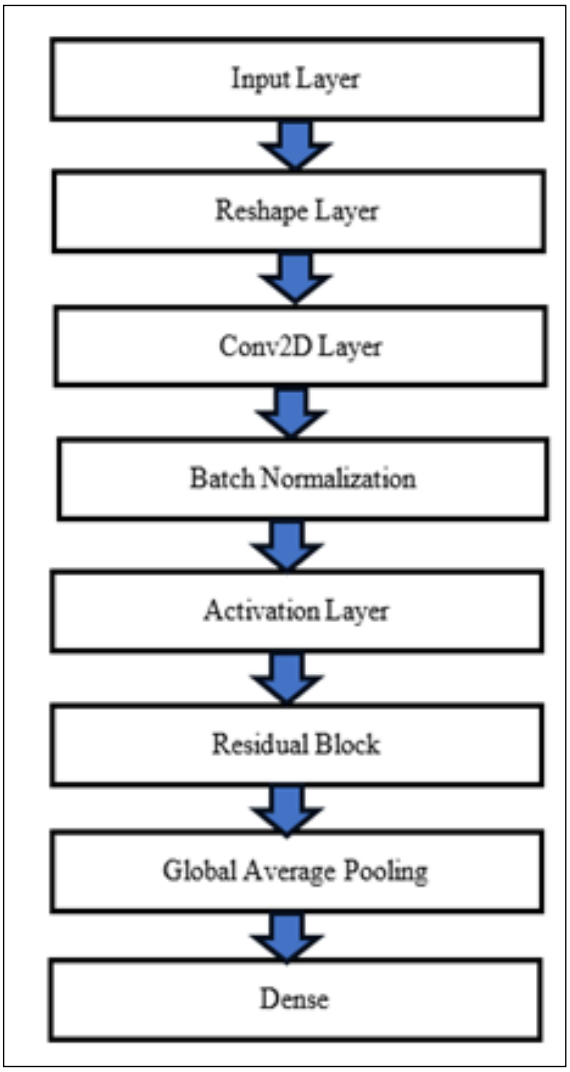

Figure 3.Proposed DL Architecture for Analysing Features

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This signifies that highly pertinent neurons will have greater values over other neurons. Depending on this, the important features can easily be identified in the output layer. Similarly, we have also utilised Extra tree in the proposed model which also evaluates the importance of features on each DL layer. Features that consistently lead to better predictions across multiple trees are considered more important. The importance scores of individual trees are added across the ensemble to obtain an aggregated feature importance score. These scores are then used to rank the input features in descending order of importance. This ranking helps identify which features have the most influence on model predictions. The outputs generated by the LRP and Extra tree are then combined to form the final feature vector which comprises only the 10 most important and informative features. This feature selection aids in improving the accuracy of the detection rate along with this, it also solves dimensionality and complexity issues. Table 3 shows the features selected from the processed feature set after implementing LRP and Extra tree on DL architecture. In addition to this, the process of feature selection by employing LRP and Extra Tree is explained in Algorithm 1.

The algorithm clearly describes the process of evaluating feature importance on each layer of the DL model. The LRP model is initialised to get the weight values and biases from the trained DL model. Then these weights and bias values are added and p_values or positive values are extracted. The relevance for each value is then calculated by using the following formula.

$$r_{values} = \frac{p_{values}}{\sum_1^n p_{values}} \quad (1)$$

By applying this formula, the relevance of the feature at each level of the DL model is evaluated. In the next step, the extra tree model is implemented on each DL layer for calculating the feature importance denoted by, f_{values}. Once this process is completed, the outputs produced by two FS models i.e., LRP and Extra Tree are combined for optimum feature selection. The formula used for combining the feature importance is shown below;

$$C_{values} = f_{values} + r_{values} \quad (2)$$

The final feature set obtained after following the above algorithm is shown in Table 3.

Numeric value	Attributes	Non-Null	Count	Data Type
0	patient_age_ quantile	5644	Non-null	int64
1	sars-cov-2_exam_ result	5644	Non-null	int64
2	Hematocrit	5644	Non-null	float64
3	serum_glucose	5644	Non-null	float64
4	respiratory_ syncytial_virus	5644	Non-null	int64
5	mycoplasma_ pneumoniae	5644	Non-null	float64
6	neutrophils	5644	Non-null	float64
7	urea	5644	Non-null	float64
8	proteina_c_reativa_ mg/dl	5644	Non-null	float64
9	potassium	5644	Non-null	float64

In addition to this, we have also generated the heat map for selected features. We are interested in using heatmaps to identify the characteristics that are essential for predicting True Positives (1) and True Negatives (0). Figure 4 represents the heat map of features.

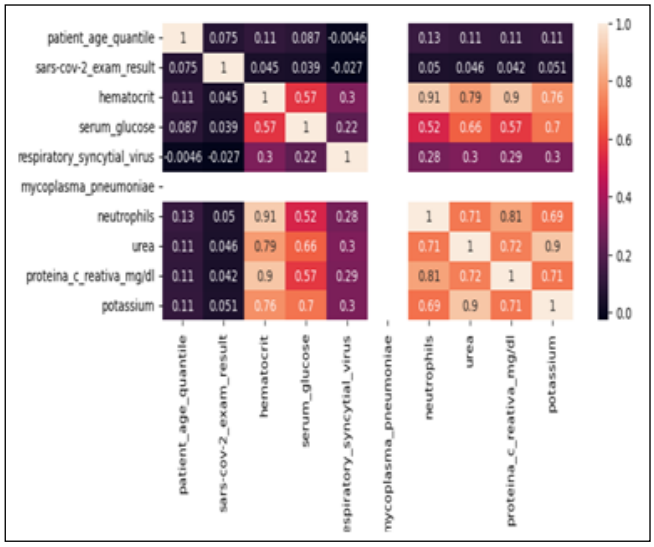

Figure 4.Heat Map Generated for Features

By analysing the heat maps, we aim to have a clear understanding of the multiple features in a dataset. These visualisations provide a way to quickly identify patterns, correlations, and trends within the data. This heat map clearly shows the 10 features extracted by our model are highly correlated and hence best feature subset is chosen.

Data Splitting

Once the process of feature selection is completed, a refined set of features is extracted, forming the final feature vector set. This carefully curated feature vector is of paramount importance as it constitutes the input for both the training and testing phases of the model development process. This feature vector is meticulously categorised into two distinct subsets: the training dataset and the testing dataset in the ratio of 80:20 respectively. The majority portion of data is preserved for training the model, while, a small portion of data i.e., 20% is utilised for

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testing. This distribution strategy ensures that the model is predominantly exposed to a substantial and diverse range of data during the training phase. This extended exposure empowers the model to capture intricate patterns, relationships, and nuances present within the dataset. On the other hand, the reserved testing dataset, although smaller in proportion, plays a critical role in validating the model's generalisation capabilities.

Multi-Agent-Based Classification Model

This section of the paper discusses the proposed multi-agent-based classification model. After splitting the data, we move to the next phase of the proposed model i.e., the classification process. In the proposed model, the concept of multi-agent is introduced to ensure a high detection rate in COVID-19 patients. The training dataset is divided into three subsets which are referred to as agents. These agents are then separately passed to the three classifiers used in our system which are SVM, LR and KNN. The novelty contribution of our work is that we are dividing the training dataset into three agents or subsets and each agent is passed to a specific classifier for making the predictions. This was not the case in current COVID-19 detection models, wherein the entire training dataset is passed to classifiers to make the final prediction. By introducing the concept of agents in the proposed work, the performance of ML classifiers can be increased significantly. To start with, the parameters of the three classifiers used in the proposed approach are initialised by defining their parameters.

SVM Classifier

One of the commonly utilised supervised ML techniques called SVM is applied to various classification and regression issues. It carries out classification by locating the hyper-plane which efficiently distinguishes each group. The hyper-plane of the SVM is discovered by increasing its margins. This classifier creates a model which categorises fresh samples into one or two groups for binary classification. An SVM enlarges the distance between the two categories by mapping training samples to points in space. Following that, depending on what side of the separation they fall, fresh samples are placed into the same space and projected to belong to a class. The configuration parameters of the SVM classifier are mentioned in Table 4.

Table 4.SVM Configuration Parameters

S. No.	Parameters	Values
1	C	1.0
2	Cache_Size	200
3	Decision_function_shape	oyr
4	Degree	3
5	Kernel	rbf
6	Tol	0.001

Logistic Regression (LR) Classifier

A popular analytical technique for forecasting binary results (y = 0 or 1) is logistic regression. While logistic regression is appropriate for categorising outcomes (binomial/ multinomial values of y), linear regression is useful for projecting outcomes with constant values. The common logistic function, having the shape of an S, is represented by the following formula (1). The LR is initialised by defining various parameters which are mentioned in Table 5.

$$f(x) = \frac{1}{1 + e^{-x}} \quad (3)$$

Table 5.LR Configuration Parameters

S.No.	Parameters	Values
1	C	1.0
2	Intercept_Scaling	1
3	Max_iter	100
4	Solver	Lbfgs
5	Tol	0.0001

KNN classifier

The non-parametric classifier is KNN. On the basis of the issue or dataset that has been provided, prediction and learning assessment is carried out. Despite making any assumptions about the information being used, the KNN classification model's prediction is only dependent on neighbor data values. The K in KNN stands for the quantity of closest neighbor reference values. The KNN method decides how to categorise the data set as "K," or the quantity of closest neighbors. In other words, the training set as a whole is searched for identical 'K' neighbor examples, and the most recent instance class is used to categorise the forecast of a new instance. The Euclidean distance equation is used to find another instance that is comparable. The total of the squared variations among the new instance (xi) and the current instance (yj) is what is known as the Euclidean distance. In our proposed model, the KNN classifier is initialised by defining its important parameters which are mentioned in Table 6.

$$Euclean_{i,j} = \sqrt{\sum_{k=1}^{n} (x_{ik} - y_{jk})^2} \quad (4)$$

Table 6.KNN Configuration Parameters

S. No.	Parameters	Values
1	Leaf size	30
2	Metric	Minkowski
3	n-neighbors	5
4	P	2
5	Weights	Uniform

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After the models are initialised, the three data subsets or agents are passed to each classifier. The main reason for doing so is that each model gets trained on new data which increases the accuracy of the proposed model. Moreover, this also solves overfitting issues among ML models because the dataset is divided into three agents which is a part of the dataset. The three classifiers are trained separately on this data and each classifier gives its output. In our approach, the outputs of the three classifiers are then combined by employing an ensemble learning method to make the final prediction.

Ensemble Learning Method

In a typical ensemble learning model, a number of base models are combined to create a more reliable and accurate approach. This technique involves combining various algorithms with the aim of solving any classification or regression problem which is not possible to solve by using individual models. By using this concept, we can really enhance the performance of the proposed approach, by employing an ensemble learning method which outperforms individual models' performance. In our approach, we have utilised a soft voting mechanism for making the final prediction for disease detection. The three base models i.e., SVM, LR and KNN are initially trained using agents or subsets of training data. Once the models are trained, we analyse their performance by passing testing data to them to evaluate the performance of our models. Each model generates its own output which is then combined by using a voting technique. Ensemble learning combines the predictions of multiple individual models to make a final prediction. This approach aims to improve the overall accuracy, robustness, and generalisation of predictions by leveraging the collective results generated by three classifiers. Figure 5 demonstrates the proposed ensemble learning model for classification.

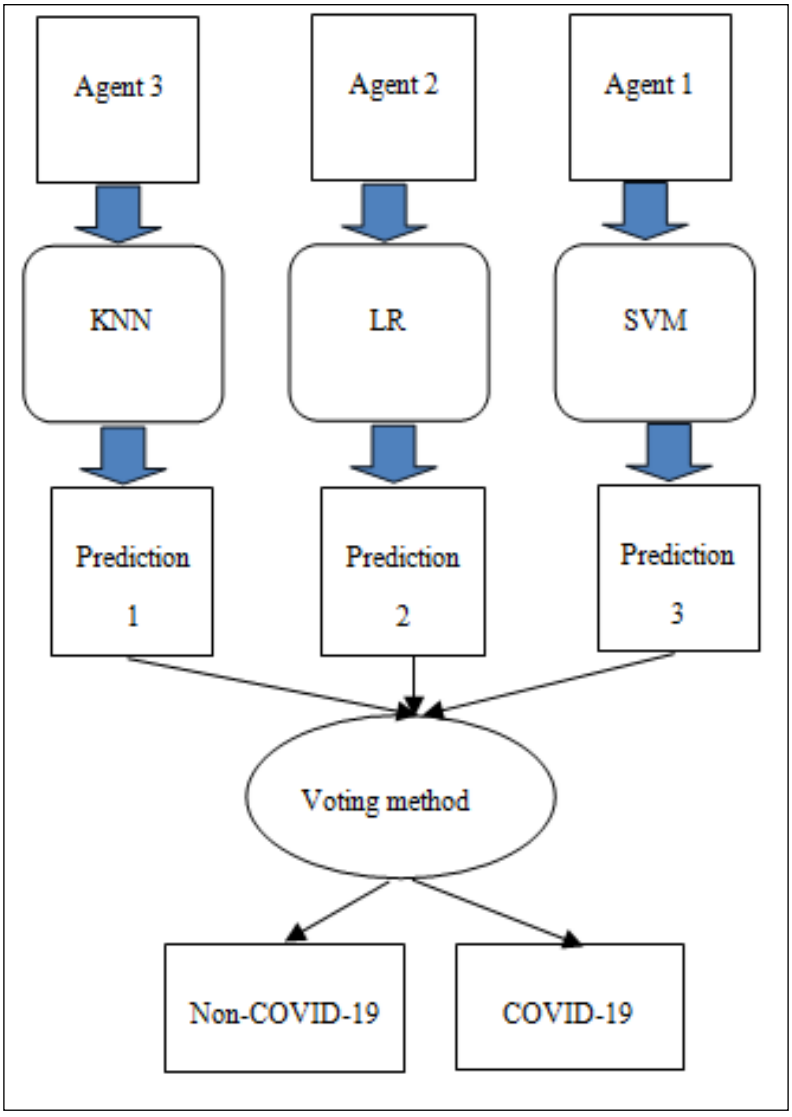

Figure 5.Proposed Classification Method

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Results and Discussion

In order to validate the effectiveness of our approach, we tested its performance along with a few traditional models using the Python Software tool. The simulating parameters were obtained in terms of confusion matrix, True positive rate, Accuracy, Precision, Recall and F1-Score. Additionally, we have also analysed the loss and accuracy results obtained for training and validation datasets. This section briefly discusses the results obtained from the proposed approach.

Performance Metrices

Before explaining the results of the proposed approach, let us understand the various performance dependency factors, based on which we prove its supremacy. Some of the performance metrices used in the proposed work are discussed below along with their mathematical formulas.

Confusion matrix: It is a table used to evaluate the performance of a classification model. It presents a summary of the model's predictions compared to the actual outcomes in a binary or multiclass classification problem.

True Positive Rate (TPR): It measures the proportion of actual positive instances that are correctly identified or predicted as positive by the classification model. Mathematically, it can be calculated as follows:

$$TPR = \frac{TP}{(TP + FN)} \quad (5)$$

Wherein, TP and FN represent the true positive and false negative values respectively.

Accuracy: It can be defined as the metric that measures the overall correctness of predictions made by the model. In other words, it's the ratio of correctly classified instances to the total number of instances in the dataset. Mathematically, it can be determined as;

$$Accuracy = \frac{(TP + TN)}{(TP + TN + FP + FN)} \quad (6)$$

Precision: It can be defined as the ratio of correctly predicted positive instances to the total instances predicted as positive by the model. Mathematically, it can be represented as;

$$Precision = \frac{TP}{(TP + FP)} \quad (7)$$

Recall: It can be defined as the ratio of true positive predictions to the total actual positive instances in the dataset. Mathematically, it can be represented as;

$$Recall = \frac{TP}{(TP + FN)} \quad (8)$$

F1-Score: It can be defined as the harmonic mean of precision and recall. Mathematically, F1-score can be defined as;

$$F1 - score = 2 \times \frac{Precision * Recall}{(Precision + Recall)} \quad (9)$$

Simulated Outcomes

The effectiveness of our approach is firstly validated by examining the loss curve attained by it during training and validating the model. Figure 6 shows the comparative line graph for the same. The x and y-axis of the given graph correspond to epoch and loss functions respectively. On analysing the given graph, it is observed that initially the training loss is high but with the increase in the number of epochs the loss curve steeps down ensuring effective training of the model. Similarly, the validation loss curve observed in the proposed model is very low initially, then the training loss curve reason because the model is effectively trained and handling large datasets.

In a similar manner, we have also examined the accuracy of the proposed approach during training and validation processes. The comparative graph obtained for the same is shown in Figure 7. The maximum number of epochs and accuracy rate of models are represented on the x-axis and y-axis, respectively. The graph clearly indicates that during training, the accuracy of the model is slightly low but during the validation process, the accuracy rate shoots to maximum values to showcase the effective training of the model.

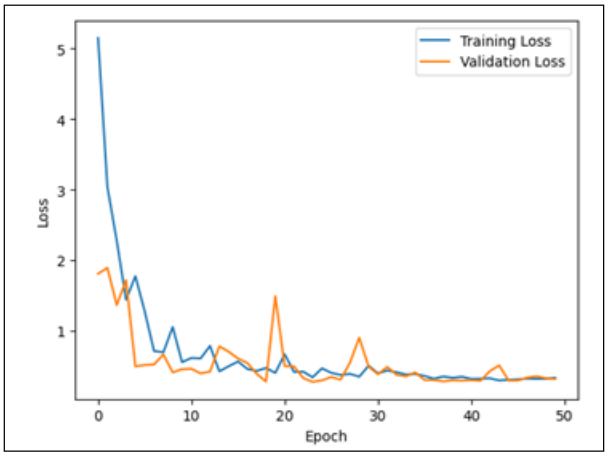

Figure 6.Loss Attained in Proposed Model During Training and Validation

Furthermore, we have evaluated the efficacy of the proposed model in terms of the confusion matrix that is shown in Figure 8. The x-axis and y-axis of the matrix depict predicted labels and true labels respectively. By analysing this matrix, we can assess the performance of our classification model based on its predictions with respect to the true class labels. It is a valuable tool to evaluate the model's accuracy, precision, recall, F1-score, and other performance metrics, providing insights into its strengths

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and weaknesses in making predictions for different classes.

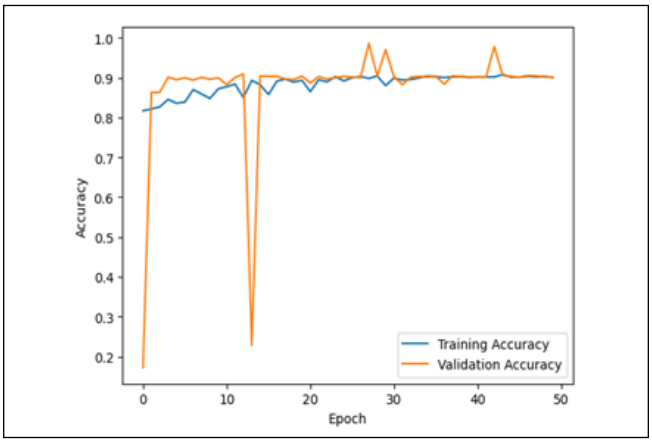

Figure 7.Accuracy Attained in Proposed Model During Training and Validation

Furthermore, to prove the effectiveness of the proposed approach, we examined its TPR value against FPR. The line graph obtained for the same is shown in Figure 9 with the x-axis and y-axis calibrating to FPR and TPR respectively. After carefully observing the graph, it is clear that the TPR value is initially low because the model is not yet trained effectively but, as training progresses and the model gains learning from more data samples, its ability to identify positive instances improves, resulting in a higher TPR i.e., 1.

Also, to further validate the efficacy of the proposed approach, its performance is compared with a few standard approaches like RF, Bernoulli and SVM in terms of overall accuracy detection rate. Figure 9 represents the comparative graph for the same, with x-axis showing different models and y-axis depicting their accuracy rates, respectively. The graph clearly indicates that among traditional models, the lowest accuracy of 92% is attained by Bernoulli, which is followed up by RF and SVM models with 94.16% and 95% respectively. Nevertheless, in the case of the proposed model, the accuracy rate came out to be highest at 97.5%, which is 5.5%, 3.34% and 2.5% higher than the other three models (RF, Bernoulli and SVM).

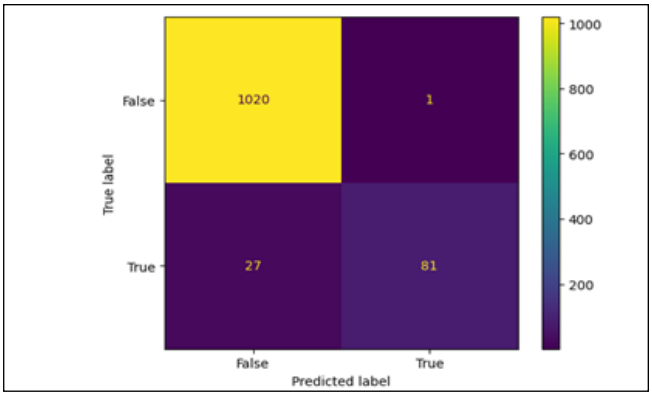

Figure 8.Confusion Matrix of Proposed Model

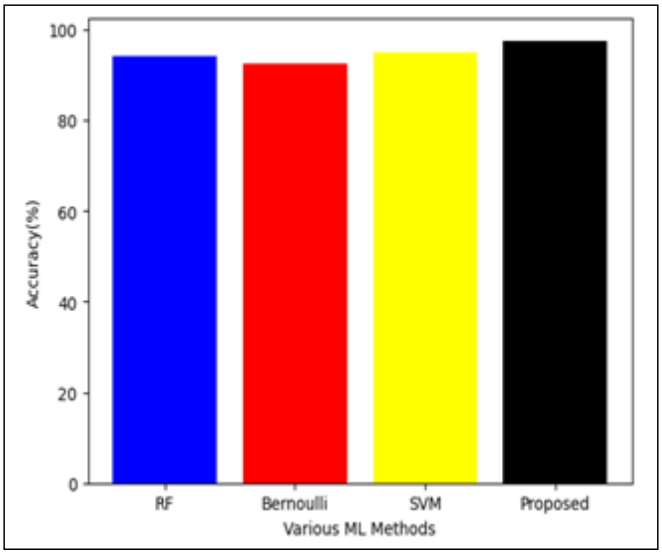

Figure 9.Comparative Graph for Accuracy

Moving on, we have also proved the supremacy of the proposed approach over other similar models in terms of their precision rate, whose comparative graph is shown in Figure 10. The x and y-axis of the given graph calibrates to various ML methods and their precision rate respectively. After carefully analysing the graph, we observed that the standard Bernoulli model is experiencing the lowest precision value of 89% as well, while, this rate was slightly better in SVM and RF models with 95%. However, in the proposed model, we were able to attain a precision rate of 98.7% which is significantly higher than the remaining three models. This high precision rate indicates that the model is correctly identifying positive cases as true positives and minimising false positives.

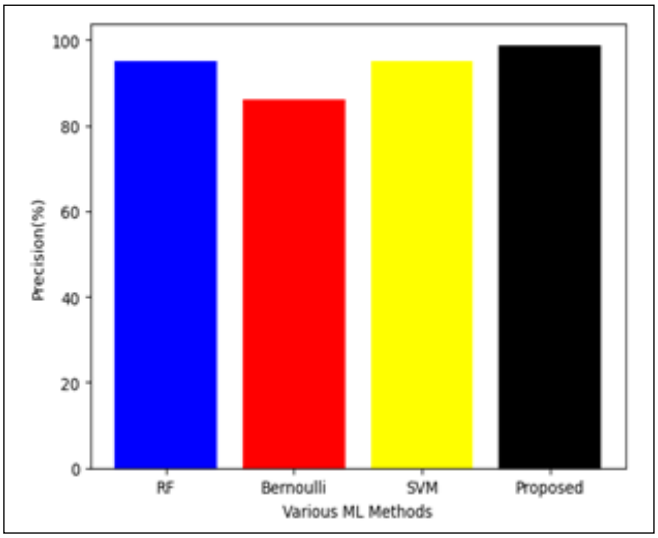

Figure 10.Comparative Graph for Precision

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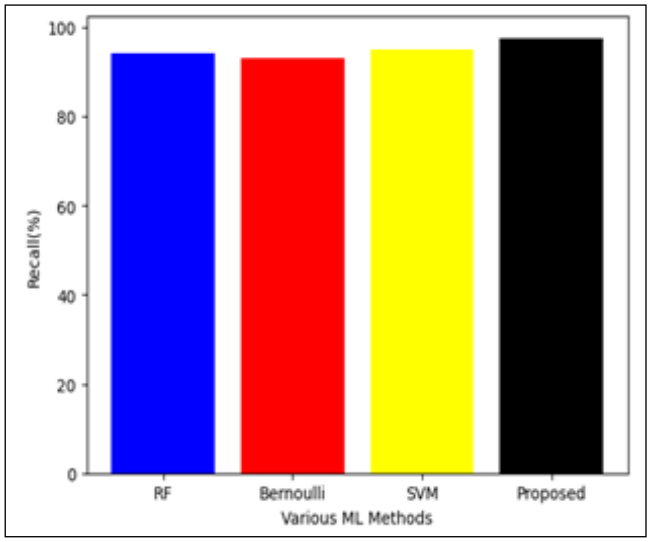

Figure 11.Comparative Graph for Recall

In addition to this, we have also tested the working of the proposed approach by comparing it with conventional approaches in terms of F1-Score. The graph obtained for the same is shown in Figure 7. Upon examining the graph, it is observed that traditional models like RF, Bernoulli and SVM were able to attain F1-Score of just 93%, 89% and 94% respectively. While as, this is not the case in the proposed model which attains an F1-Score of 97.5% to prove its supremacy. These results indicate that F1-Score is improved by around 4.5%, 8.5% and 3.5% in the proposed model as compared to RF, Bernoulli and SVM models, respectively and summarised graphically in Figures 11 and 12. The specific value of these parameters is recorded in tabular format and is given in Table 7.

Table 7.Comparative Values of Different Parameters

Model	Accuracy	Precision	Recall	F1-Score
RF	94.16	95	94	93
Bernoulli NB	92.5	86	93	89
SVM	95	95	95	94
Proposed model	97.5	98.7	97.5	97.51

The analysis of the graphs and tables reveals that the proposed model outperforms traditional models like RF, Bernoulli, and SVM across all given parameters. The proposed model shows significant improvements, with 5.5%, 3.34%, and 2.5% higher accuracy compared to RF, Bernoulli, and SVM models, respectively. Additionally, it demonstrates a notable enhancement of 3.5% in precision and recall over the RF model, while achieving improvements of 12.7% and 4.5% over the Bernoulli model. The proposed model also exhibits favourable results for precision and recall with 3.7% and 2.5% improvements over the SVM model. Moreover, the F1-Score in the proposed model is high by approximately 4.5%, 8.5%, and 3.5% in comparison to standard RF, Bernoulli, and SVM models, respectively. These findings conclusively demonstrate the superior effectiveness of our model in accurately detecting COVID-19 in patients.

Conclusion

This manuscript presents a highly accurate and robust multi-agent-based COVID-19 detection model. By harnessing the power of agent-based modelling, we have demonstrated the potential to significantly enhance the accuracy, adaptability, and contextual understanding of COVID-19 detection methods. Our study has highlighted the limitations of traditional methods in capturing the intricate heterogeneity and dynamic nature of the virus transmission, which the agent-based models excel in addressing. The performance of the proposed model was texted and validated in Python software where its performance is compared with traditional models in terms of various metrices. Results showcased that the proposed model was able to achieve a detection accuracy of 97.5% whereas, it was only 94%, 92% and 95% in conventional RF, Bernoulli NB and SVM models. This shows an accuracy improvement of 2.5% than the best-performing traditional model i.e., SVM. Similarly, the precision rate was observed in standard RF, Bernoulli NB and SVM models which came out to be 95%, 86% and 95%, while it was 98.7% in our proposed approach. Furthermore, the proposed model outperforms three standard models in terms of recall and F1-Score by achieving the highest values of 97.5% for each. In addition to this, our proposed model is showing effective results for training and validation loss and accuracy functions. These results showcase that the proposed model is able to detect COVID-19 more effectively than conventional models to prove its supremacy.

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Conflict of Interest: None

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